

# Package ‘Surrogate’

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**Type** Package

**Title** Evaluation of Surrogate Endpoints in Clinical Trials

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**Description** In a clinical trial, it frequently occurs that the most credible outcome to evaluate the effec-  
tiveness of a new therapy (the true endpoint) is difficult to measure. In such a situa-  
tion, it can be an effective strategy to replace the true endpoint by a (bio)marker that is eas-  
ier to measure and that allows for a prediction of the treatment effect on the true endpoint (a sur-  
rogate endpoint). The package 'Surrogate' allows for an evaluation of the appropriate-  
ness of a candidate surrogate endpoint based on the meta-analytic, information-  
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## Depends

**Imports** MASS, rgl, lattice, latticeExtra, survival, nlme, lme4, msm,  
OrdinalLogisticBiplot, logistf, rms, mixtools, parallel, ks,  
rootSolve, extraDistr

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AA.MultS

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*Compute the multiple-surrogate adjusted association*


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### Description

The function `AA.MultS` computes the multiple-surrogate adjusted correlation. This is a generalisation of the adjusted association proposed by Buyse & Molenberghs (1998) (see `Single.Trial.RE.AA`) to the setting where there are multiple endpoints. See **Details** below.

**Usage**

```
AA.MultS(Sigma_gamma, N, Alpha=0.05)
```

**Arguments**

Sigma_gamma	The variance covariance matrix of the residuals of regression models in which the true endpoint ( $T$ ) is regressed on the treatment ( $Z$ ), the first surrogate ( $S1$ ) is regressed on $Z$ , ..., and the $k$ -th surrogate ( $Sk$ ) is regressed on $Z$ . See <b>Details</b> below.
N	The sample size (needed to compute a CI around the multiple adjusted association; $\gamma_M$ )
Alpha	The $\alpha$ -level that is used to determine the confidence interval around $\gamma_M$ . Default 0.05.

**Details**

The multiple-surrogate adjusted association ( $\gamma_M$ ) is obtained by regressing  $T$ ,  $S1$ ,  $S2$ , ...,  $Sk$  on the treatment ( $Z$ ):

$$\begin{aligned} T_j &= \mu_T + \beta Z_j + \varepsilon_{Tj}, \\ S1_j &= \mu_{S1} + \alpha_1 Z_j + \varepsilon_{S1j}, \\ &\dots, \\ Sk_j &= \mu_{Sk} + \alpha_k Z_j + \varepsilon_{Skj}, \end{aligned}$$

where the error terms have a joint zero-mean normal distribution with variance-covariance matrix:

$$\Sigma = \begin{pmatrix} \sigma_{TT} & \Sigma_{ST} \\ \Sigma'_{ST} & \Sigma_{SS} \end{pmatrix}.$$

The multiple adjusted association is then computed as

$$\gamma_M = \sqrt{\left( \frac{\Sigma'_{ST} \Sigma_{SS}^{-1} \Sigma_{ST}}{\sigma_{TT}} \right)}$$

**Value**

An object of class `AA.MultS` with components,

Gamma.Delta	An object of class <code>data.frame</code> that contains the multiple-surrogate adjusted association (i.e., $\gamma_M$ ), its standard error, and its confidence interval (based on the Fisher-Z transformation procedure).
Corr.Gamma.Delta	An object of class <code>data.frame</code> that contains the bias-corrected multiple-surrogate adjusted association (i.e., corrected $\gamma_M$ ), its standard error, and its confidence interval (based on the Fisher-Z transformation procedure).
Sigma_gamma	The variance covariance matrix of the residuals of regression models in which $T$ is regressed on $Z$ , $S1$ is regressed on $Z$ , ..., and $Sk$ is regressed on $Z$ .
N	The sample size (used to compute a CI around the multiple adjusted association; $\gamma_M$ )
Alpha	The $\alpha$ -level that is used to determine the confidence interval around $\gamma_M$ .

**Author(s)**

Wim Van der Elst, Ariel Alonso, & Geert Molenberghs

**References**

Buyse, M., & Molenberghs, G. (1998). The validation of surrogate endpoints in randomized experiments. *Biometrics*, *54*, 1014-1029.

Van der Elst, W., Alonso, A. A., & Molenberghs, G. (2017). A causal inference-based approach to evaluate surrogacy using multiple surrogates.

**See Also**

[Single.Trial.RE.AA](#)

**Examples**

```
data(ARMD.MultS)

# Regress T on Z, S1 on Z, ..., Sk on Z
# (to compute the covariance matrix of the residuals)
Res_T <- residuals(lm(Diff52~Treat, data=ARMD.MultS))
Res_S1 <- residuals(lm(Diff4~Treat, data=ARMD.MultS))
Res_S2 <- residuals(lm(Diff12~Treat, data=ARMD.MultS))
Res_S3 <- residuals(lm(Diff24~Treat, data=ARMD.MultS))
Residuals <- cbind(Res_T, Res_S1, Res_S2, Res_S3)

# Make covariance matrix of residuals, Sigma_gamma
Sigma_gamma <- cov(Residuals)

# Conduct analysis
Result <- AA.MultS(Sigma_gamma = Sigma_gamma, N = 188, Alpha = .05)

# Explore results
summary(Result)
```

**Description**

These are the data of a clinical trial involving patients suffering from age-related macular degeneration (ARMD), a condition that involves a progressive loss of vision. A total of 181 patients from 36 centers participated in the trial. Patients' visual acuity was assessed using standardized vision charts. There were two treatment conditions (placebo and interferon- $\alpha$ ). The potential surrogate endpoint is the change in the visual acuity at 24 weeks (6 months) after starting treatment. The true endpoint is the change in the visual acuity at 52 weeks.

**Usage**

```
data(ARMD)
```

**Format**

A data.frame with 181 observations on 5 variables.

Id The Patient ID.

Center The center in which the patient was treated.

Treat The treatment indicator, coded as  $-1$  = placebo and  $1$  = interferon- $\alpha$ .

Diff24 The change in the visual acuity at 24 weeks after starting treatment. This endpoint is a potential surrogate for Diff52.

Diff52 The change in the visual acuity at 52 weeks after starting treatment. This outcome serves as the true endpoint.

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ARMD.MultS

*Data of the Age-Related Macular Degeneration Study with multiple candidate surrogates*

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**Description**

These are the data of a clinical trial involving patients suffering from age-related macular degeneration (ARMD), a condition that involves a progressive loss of vision. A total of 181 patients participated in the trial. Patients' visual acuity was assessed using standardized vision charts. There were two treatment conditions (placebo and interferon- $\alpha$ ). The potential surrogate endpoints are the changes in the visual acuity at 4, 12, and 24 weeks after starting treatment. The true endpoint is the change in the visual acuity at 52 weeks.

**Usage**

```
data(ARMD.MultS)
```

**Format**

A data.frame with 181 observations on 6 variables.

Id The Patient ID.

Diff4 The change in the visual acuity at 4 weeks after starting treatment. This endpoint is a potential surrogate for Diff52.

Diff12 The change in the visual acuity at 12 weeks after starting treatment. This endpoint is a potential surrogate for Diff52.

Diff24 The change in the visual acuity at 24 weeks after starting treatment. This endpoint is a potential surrogate for Diff52.

Diff52 The change in the visual acuity at 52 weeks after starting treatment. This outcome serves as the true endpoint.

Treat The treatment indicator, coded as  $-1$  = placebo and  $1$  = interferon- $\alpha$ .

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BifixedContCont	<i>Fits a bivariate fixed-effects model to assess surrogacy in the meta-analytic multiple-trial setting (Continuous-continuous case)</i>
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## Description

The function `BifixedContCont` uses the bivariate fixed-effects approach to estimate trial- and individual-level surrogacy when the data of multiple clinical trials are available. The user can specify whether a (weighted or unweighted) full, semi-reduced, or reduced model should be fitted. See the **Details** section below. Further, the Individual Causal Association (ICA) is computed.

## Usage

```
BifixedContCont(Dataset, Surr, True, Treat, Trial.ID, Pat.ID, Model=c("Full"),
  Weighted=TRUE, Min.Trial.Size=2, Alpha=.05, T0T1=seq(-1, 1, by=.2),
  T0S1=seq(-1, 1, by=.2), T1S0=seq(-1, 1, by=.2), S0S1=seq(-1, 1, by=.2))
```

## Arguments

Dataset	A data.frame that should consist of one line per patient. Each line contains (at least) a surrogate value, a true endpoint value, a treatment indicator, a patient ID, and a trial ID.
Surr	The name of the variable in Dataset that contains the surrogate endpoint values.
True	The name of the variable in Dataset that contains the true endpoint values.
Treat	The name of the variable in Dataset that contains the treatment indicators. The treatment indicator should either be coded as 1 for the experimental group and -1 for the control group, or as 1 for the experimental group and 0 for the control group.
Trial.ID	The name of the variable in Dataset that contains the trial ID to which the patient belongs.
Pat.ID	The name of the variable in Dataset that contains the patient's ID.
Model	The type of model that should be fitted, i.e., <code>Model=c("Full")</code> , <code>Model=c("Reduced")</code> , or <code>Model=c("SemiReduced")</code> . See the <b>Details</b> section below. Default <code>Model=c("Full")</code> .
Weighted	Logical. If TRUE, then a weighted regression analysis is conducted at stage 2 of the two-stage approach. If FALSE, then an unweighted regression analysis is conducted at stage 2 of the two-stage approach. See the <b>Details</b> section below. Default TRUE.
Min.Trial.Size	The minimum number of patients that a trial should contain in order to be included in the analysis. If the number of patients in a trial is smaller than the value specified by <code>Min.Trial.Size</code> , the data of the trial are excluded from the analysis. Default 2.
Alpha	The $\alpha$ -level that is used to determine the confidence intervals around $R_{trial}^2$ , $R_{indiv}^2$ and $R_{indiv}$ . Default 0.05.

T0T1	A scalar or vector that contains the correlation(s) between the counterfactuals T0 and T1 that should be considered in the computation of $\rho_{\Delta}$ (ICA). For details, see function <code>ICA.ContCont</code> . Default <code>seq(-1, 1, by=.2)</code> .
T0S1	A scalar or vector that contains the correlation(s) between the counterfactuals T0 and S1 that should be considered in the computation of $\rho_{\Delta}$ . Default <code>seq(-1, 1, by=.2)</code> .
T1S0	A scalar or vector that contains the correlation(s) between the counterfactuals T1 and S0 that should be considered in the computation of $\rho_{\Delta}$ . Default <code>seq(-1, 1, by=.2)</code> .
S0S1	A scalar or vector that contains the correlation(s) between the counterfactuals S0 and S1 that should be considered in the computation of $\rho_{\Delta}$ . Default <code>seq(-1, 1, by=.2)</code> .

### Details

When the full bivariate mixed-effects model is fitted to assess surrogacy in the meta-analytic framework (for details, Buyse & Molenberghs, 2000), computational issues often occur. In that situation, the use of simplified model-fitting strategies may be warranted (for details, see Burzykowski et al., 2005; Tibaldi et al., 2003).

The function `BifixedContCont` implements one such strategy, i.e., it uses a two-stage bivariate fixed-effects modelling approach to assess surrogacy. In the first stage of the analysis, a bivariate linear regression model is fitted. When a full or semi-reduced model is requested (by using the argument `Model=c("Full")` or `Model=c("SemiReduced")` in the function call), the following bivariate model is fitted:

$$S_{ij} = \mu_{Si} + \alpha_i Z_{ij} + \varepsilon_{Sij},$$

$$T_{ij} = \mu_{Ti} + \beta_i Z_{ij} + \varepsilon_{Tij},$$

where  $S_{ij}$  and  $T_{ij}$  are the surrogate and true endpoint values of subject  $j$  in trial  $i$ ,  $Z_{ij}$  is the treatment indicator for subject  $j$  in trial  $i$ ,  $\mu_{Si}$  and  $\mu_{Ti}$  are the fixed trial-specific intercepts for S and T, and  $\alpha_i$  and  $\beta_i$  are the trial-specific treatment effects on S and T, respectively. When a reduced model is requested (by using the argument `Model=c("Reduced")` in the function call), the following bivariate model is fitted:

$$S_{ij} = \mu_S + \alpha_i Z_{ij} + \varepsilon_{Sij},$$

$$T_{ij} = \mu_T + \beta_i Z_{ij} + \varepsilon_{Tij},$$

where  $\mu_S$  and  $\mu_T$  are the common intercepts for S and T (i.e., it is assumed that the intercepts for the surrogate and the true endpoints are identical in all trials). The other parameters are the same as defined above.

In the above models, the error terms  $\varepsilon_{Sij}$  and  $\varepsilon_{Tij}$  are assumed to be mean-zero normally distributed with variance-covariance matrix  $\Sigma$ :

$$\Sigma = \begin{pmatrix} \sigma_{SS} & \\ \sigma_{ST} & \sigma_{TT} \end{pmatrix}.$$



Based on  $\Sigma$ , individual-level surrogacy is quantified as:

$$R_{indiv}^2 = \frac{\sigma_{ST}^2}{\sigma_{SS}\sigma_{TT}}.$$

Next, the second stage of the analysis is conducted. When a full model is requested by the user (by using the argument `Model=c("Full")` in the function call), the following model is fitted:

$$\widehat{\beta}_i = \lambda_0 + \lambda_1 \widehat{\mu_{Si}} + \lambda_2 \widehat{\alpha}_i + \varepsilon_i,$$

where the parameter estimates for  $\beta_i$ ,  $\mu_{Si}$ , and  $\alpha_i$  are based on the full model that was fitted in stage 1.

When a reduced or semi-reduced model is requested by the user (by using the arguments `Model=c("Reduced")` or `Model=c("SemiReduced")` in the function call), the following model is fitted:

$$\widehat{\beta}_i = \lambda_0 + \lambda_1 \widehat{\alpha}_i + \varepsilon_i.$$

where the parameter estimates for  $\beta_i$  and  $\alpha_i$  are based on the semi-reduced or reduced model that was fitted in stage 1.

When the argument `Weighted=FALSE` is used in the function call, the model that is fitted in stage 2 is an unweighted linear regression model. When a weighted model is requested (using the argument `Weighted=TRUE` in the function call), the information that is obtained in stage 1 is weighted according to the number of patients in a trial.

The classical coefficient of determination of the fitted stage 2 model provides an estimate of  $R_{trial}^2$ .

## Value

An object of class `BifixedContCont` with components,

<code>Data.Analyze</code>	Prior to conducting the surrogacy analysis, data of patients who have a missing value for the surrogate and/or the true endpoint are excluded. In addition, the data of trials (i) in which only one type of the treatment was administered, and (ii) in which either the surrogate or the true endpoint was a constant (i.e., all patients within a trial had the same surrogate and/or true endpoint value) are excluded. In addition, the user can specify the minimum number of patients that a trial should contain in order to include the trial in the analysis. If the number of patients in a trial is smaller than the value specified by <code>Min.Trial.Size</code> , the data of the trial are excluded. <code>Data.Analyze</code> is the dataset on which the surrogacy analysis was conducted.
<code>Obs.Per.Trial</code>	A <code>data.frame</code> that contains the total number of patients per trial and the number of patients who were administered the control treatment and the experimental treatment in each of the trials (in <code>Data.Analyze</code> ).
<code>Results.Stage.1</code>	The results of stage 1 of the two-stage model fitting approach: a <code>data.frame</code> that contains the trial-specific intercepts and treatment effects for the surrogate and the true endpoints (when a full or semi-reduced model is requested), or the trial-specific treatment effects for the surrogate and the true endpoints (when a reduced model is requested).

Residuals.Stage.1	A data.frame that contains the residuals for the surrogate and true endpoints that are obtained in stage 1 of the analysis ( $\varepsilon_{Sij}$ and $\varepsilon_{Tij}$ ).
Results.Stage.2	An object of class <code>lm</code> (linear model) that contains the parameter estimates of the regression model that is fitted in stage 2 of the analysis.
Trial.R2	A data.frame that contains the trial-level coefficient of determination ( $R_{trial}^2$ ), its standard error and confidence interval.
Indiv.R2	A data.frame that contains the individual-level coefficient of determination ( $R_{indiv}^2$ ), its standard error and confidence interval.
Trial.R	A data.frame that contains the trial-level correlation coefficient ( $R_{trial}$ ), its standard error and confidence interval.
Indiv.R	A data.frame that contains the individual-level correlation coefficient ( $R_{indiv}$ ), its standard error and confidence interval.
Cor.Endpoints	A data.frame that contains the correlations between the surrogate and the true endpoint in the control treatment group (i.e., $\rho_{T0S0}$ ) and in the experimental treatment group (i.e., $\rho_{T1S1}$ ), their standard errors and their confidence intervals.
D.Equiv	The variance-covariance matrix of the trial-specific intercept and treatment effects for the surrogate and true endpoints (when a full or semi-reduced model is fitted, i.e., when <code>Model=c("Full")</code> or <code>Model=c("SemiReduced")</code> is used in the function call), or the variance-covariance matrix of the trial-specific treatment effects for the surrogate and true endpoints (when a reduced model is fitted, i.e., when <code>Model=c("Reduced")</code> is used in the function call). The variance-covariance matrix <code>D.Equiv</code> is equivalent to the $D$ matrix that would be obtained when a (full or reduced) bivariate mixed-effect approach is used; see function <a href="#">BimixedContCont</a> .
Sigma	The 2 by 2 variance-covariance matrix of the residuals ( $\varepsilon_{Sij}$ and $\varepsilon_{Tij}$ ).
ICA	A fitted object of class <code>ICA.ContCont</code> .
T0T0	The variance of the true endpoint in the control treatment condition.
T1T1	The variance of the true endpoint in the experimental treatment condition.
S0S0	The variance of the surrogate endpoint in the control treatment condition.
S1S1	The variance of the surrogate endpoint in the experimental treatment condition.

### Author(s)

Wim Van der Elst, Ariel Alonso, & Geert Molenberghs

### References

- Burzykowski, T., Molenberghs, G., & Buyse, M. (2005). *The evaluation of surrogate endpoints*. New York: Springer-Verlag.
- Buyse, M., Molenberghs, G., Burzykowski, T., Renard, D., & Geys, H. (2000). The validation of surrogate endpoints in meta-analysis of randomized experiments. *Biostatistics*, 1, 49-67.
- Tibaldi, F., Abrahantes, J. C., Molenberghs, G., Renard, D., Burzykowski, T., Buyse, M., Parmar, M., et al., (2003). Simplified hierarchical linear models for the evaluation of surrogate endpoints. *Journal of Statistical Computation and Simulation*, 73, 643-658.

**See Also**

[UnifixedContCont](#), [UnimixedContCont](#), [BimixedContCont](#), [plot Meta-Analytic](#)

**Examples**

```
## Not run: # time consuming code part
# Example 1, based on the ARMD data
data(ARMD)

# Fit a full bivariate fixed-effects model with weighting according to the
# number of patients in stage 2 of the two stage approach to assess surrogacy:
Sur <- BifixedContCont(Dataset=ARMD, Surr=Diff24, True=Diff52, Treat=Treat, Trial.ID=Center,
Pat.ID=Id, Model="Full", Weighted=TRUE)

# Obtain a summary of the results
summary(Sur)

# Obtain a graphical representation of the trial- and individual-level surrogacy
plot(Sur)

# Example 2
# Conduct a surrogacy analysis based on a simulated dataset with 2000 patients,
# 100 trials, and Rindiv=Rtrial=.8
# Simulate the data:
Sim.Data.MTS(N.Total=2000, N.Trial=100, R.Trial.Target=.8, R.Indiv.Target=.8,
Seed=123, Model="Reduced")

# Fit a reduced bivariate fixed-effects model with no weighting according to the
# number of patients in stage 2 of the two stage approach to assess surrogacy:
\dontrun{ #time-consuming code parts
Sur2 <- BifixedContCont(Dataset=Data.Observed.MTS, Surr=Surr, True=True, Treat=Treat,
Trial.ID=Trial.ID, Pat.ID=Pat.ID, , Model="Reduced", Weighted=FALSE)

# Show summary and plots of results:
summary(Sur2)
plot(Sur2, Weighted=FALSE)}

## End(Not run)
```

---

BimixedCbCContCont	<i>Fits a bivariate mixed-effects model using the cluster-by-cluster (CbC) estimator to assess surrogacy in the meta-analytic multiple-trial setting (Continuous-continuous case)</i>
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---

**Description**

The function `BimixedCbCContCont` uses the cluster-by-cluster (CbC) estimator of the bivariate mixed-effects to estimate trial- and individual-level surrogacy when the data of multiple clinical trials are available. See the **Details** section below.

**Usage**

```
BimixedCbCContCont(Dataset, Surr, True, Treat, Trial.ID, Min.Treat.Size=2, Alpha=0.05)
```

**Arguments**

Dataset	A data.frame that should consist of one line per patient. Each line contains (at least) a surrogate value, a true endpoint value, a treatment indicator, and a trial ID.
Surr	The name of the variable in Dataset that contains the surrogate endpoint values.
True	The name of the variable in Dataset that contains the true endpoint values.
Treat	The name of the variable in Dataset that contains the treatment indicators. The treatment indicator should either be coded as 1 for the experimental group and -1 for the control group, or as 1 for the experimental group and 0 for the control group.
Trial.ID	The name of the variable in Dataset that contains the trial ID to which the patient belongs.
Min.Treat.Size	The minimum number of patients in each group (control or experimental) that a trial should contain to be included in the analysis. If the number of patients in a group of a trial is smaller than the value specified by Min.Treat.Size, the data of the trial are excluded from the analysis. Default 2.
Alpha	The $\alpha$ -level that is used to determine the confidence intervals around $R^2_{trial}$ and $R^2_{indiv}$ . Default 0.05.

**Details**

The function `BimixedContCont` fits a bivariate mixed-effects model using the CbC estimator (for details, see Florez et al., 2019) to assess surrogacy (for details, see Buyse et al., 2000). In particular, the following mixed-effects model is fitted:

$$\begin{aligned} S_{ij} &= \mu_S + m_{Si} + (\alpha + a_i)Z_{ij} + \varepsilon_{Sij}, \\ T_{ij} &= \mu_T + m_{Ti} + (\beta + b_i)Z_{ij} + \varepsilon_{Tij}, \end{aligned}$$

where  $i$  and  $j$  are the trial and subject indicators,  $S_{ij}$  and  $T_{ij}$  are the surrogate and true endpoint values of subject  $j$  in trial  $i$ ,  $Z_{ij}$  is the treatment indicator for subject  $j$  in trial  $i$ ,  $\mu_S$  and  $\mu_T$  are the fixed intercepts for S and T,  $m_{Si}$  and  $m_{Ti}$  are the corresponding random intercepts,  $\alpha$  and  $\beta$  are the fixed treatment effects for S and T, and  $a_i$  and  $b_i$  are the corresponding random treatment effects, respectively.

The vector of the random effects (i.e.,  $m_{Si}$ ,  $m_{Ti}$ ,  $a_i$  and  $b_i$ ) is assumed to be mean-zero normally distributed with variance-covariance matrix  $D$ :

$$D = \begin{pmatrix} d_{SS} & & & \\ d_{ST} & d_{TT} & & \\ d_{Sa} & d_{Ta} & d_{aa} & \\ d_{Sb} & d_{Tb} & d_{ab} & d_{bb} \end{pmatrix}.$$

The trial-level coefficient of determination (i.e.,  $R^2_{trial}$ ) is quantified as:

$$R_{trial}^2 = \frac{\begin{pmatrix} d_{Sb} \\ d_{ab} \end{pmatrix}' \begin{pmatrix} d_{SS} & d_{Sa} \\ d_{Sa} & d_{aa} \end{pmatrix}^{-1} \begin{pmatrix} d_{Sb} \\ d_{ab} \end{pmatrix}}{d_{bb}}.$$

The error terms  $\varepsilon_{Sij}$  and  $\varepsilon_{Tij}$  are assumed to be mean-zero normally distributed with variance-covariance matrix  $\Sigma$ :

$$\Sigma = \begin{pmatrix} \sigma_{SS} & \\ \sigma_{ST} & \sigma_{TT} \end{pmatrix}.$$

Based on  $\Sigma$ , individual-level surrogacy is quantified as:

$$R_{indiv}^2 = \frac{\sigma_{ST}^2}{\sigma_{SS}\sigma_{TT}}.$$

**Note** The CbC estimator for the full bivariate mixed-effects model is closed-form (for details, see Florez et al., 2019). Therefore, it is fast. Furthermore, it is recommended when computational issues occur with the full maximum likelihood estimator (implemented in function `BimixedContCont`).

The CbC estimator is performed in two stages: (1) a linear model is fitted in each trial. Evidently, it is require that the design matrix ( $X_i$ ) is full column rank within each trial, allowing estimation of the fixed effects. When  $X_i$  is not full rank, trial  $i$  is excluded from the analysis. (2) a global estimator of the fixed effects ( $\beta$ ) is obtained by weighted averaging the sets of estimates of each trial, and  $D$  is estimated using a method-of-moments estimator. Optimal weights (for details, see Molenberghs et al., 2018) are used as a weighting scheme.

The estimator of  $D$  might lead to a non-positive-definite solution. Therefore, the eigenvalue method (for details, see Rousseeuw and Molenberghs, 1993) is used for non-positive-definiteness adjustment.

## Value

An object of class `BimixedContCont` with components,

<code>Obs.Per.Trial</code>	A data.frame that contains the total number of patients per trial and the number of patients who were administered the control treatment and the experimental treatment in each of the trials (after excluding clusters). Clusters are excluded for two reasons: (i) the number of patients is smaller than the value especified by <code>Min.Trial.Size</code> , and (ii) the design matrix ( $X_i$ ) is not full rank.
<code>Trial.removed</code>	Number of trials excluded from the analysis
<code>Fixed.Effects</code>	A data.frame that contains the fixed intercept and treatment effects for the true and the surrogate endpoints (i.e., $\mu_S$ , $\mu_T$ , $\alpha$ , and $\beta$ ) and their corresponding standard error.
<code>Trial.R2</code>	A data.frame that contains the trial-level coefficient of determination ( $R_{trial}^2$ ), its standard error and confidence interval.
<code>Indiv.R2</code>	A data.frame that contains the individual-level coefficient of determination ( $R_{indiv}^2$ ), its standard error and confidence interval.

D	The variance-covariance matrix of the random effects (the $D$ matrix), i.e., a 4 by 4 variance-covariance matrix of the random intercept and treatment effects.
DH.pd	DH.pd=TRUE if an adjustment for non-positive definiteness was not needed to estimate $D$ . DH.pd=FALSE if this adjustment was required.
Sigma	The 2 by 2 variance-covariance matrix of the residuals ( $\varepsilon_{Sij}$ and $\varepsilon_{Tij}$ ).

### Author(s)

Alvaro J. Florez, Wim Van der Elst, Ariel Alonso, & Geert Molenberghs

### References

Buyse, M., Molenberghs, G., Burzykowski, T., Renard, D., & Geys, H. (2000). The validation of surrogate endpoints in meta-analysis of randomized experiments. *Biostatistics*, 1, 49-67.

Florez, A. J., Molenberghs G, Verbeke G, Alonso, A. (2019). A closed-form estimator for meta-analysis and surrogate markers evaluation. *Journal of Biopharmaceutical Statistics*, 29(2) 318-332.

Molenberghs, G., Hermans, L., Nassiri, V., Kenward, M., Van der Elst, W., Aerts, M. and Verbeke, G. (2018). Clusters with random size: maximum likelihood versus weighted estimation. *Statistica Sinica*, 28, 1107-1132.

Rousseeuw, P. J. and Molenberghs, G. (1993) Transformation of non positive semidefinite correlation matrices. *Communications in Statistics, Theory and Methods*, 22, 965-984.

### See Also

[BimixedContCont](#), [UnifixedContCont](#), [BifixedContCont](#), [UnimixedContCont](#)

### Examples

```
# Open the Schizo dataset (clinical trial in schizophrenic patients)
data(Schizo)

# Fit a full bivariate random-effects model by the cluster-by-cluster (CbC) estimator
# a minimum of 2 subjects per group are allowed in each trial
fit <- BimixedCbCContCont(Dataset=Schizo, Surr=BPRS, True=PANSS, Treat=Treat, Trial.ID=InvestId,
                          Alpha=0.05, Min.Treat.Size = 10)
# Note that an adjustment for non-positive definiteness was required and 113 trials were removed.

# Obtain a summary of the results
summary(fit)
```

---

BimixedContCont	<i>Fits a bivariate mixed-effects model to assess surrogacy in the meta-analytic multiple-trial setting (Continuous-continuous case)</i>
-----------------	--

---

### Description

The function `BimixedContCont` uses the bivariate mixed-effects approach to estimate trial- and individual-level surrogacy when the data of multiple clinical trials are available. The user can specify whether a full or reduced model should be fitted. See the **Details** section below. Further, the Individual Causal Association (ICA) is computed.

### Usage

```
BimixedContCont(Dataset, Surr, True, Treat, Trial.ID, Pat.ID, Model=c("Full"),
  Min.Trial.Size=2, Alpha=.05, T0T1=seq(-1, 1, by=.2), T0S1=seq(-1, 1, by=.2),
  T1S0=seq(-1, 1, by=.2), S0S1=seq(-1, 1, by=.2), ...)
```

### Arguments

Dataset	A data.frame that should consist of one line per patient. Each line contains (at least) a surrogate value, a true endpoint value, a treatment indicator, a patient ID, and a trial ID.
Surr	The name of the variable in Dataset that contains the surrogate endpoint values.
True	The name of the variable in Dataset that contains the true endpoint values.
Treat	The name of the variable in Dataset that contains the treatment indicators. The treatment indicator should either be coded as 1 for the experimental group and -1 for the control group, or as 1 for the experimental group and 0 for the control group.
Trial.ID	The name of the variable in Dataset that contains the trial ID to which the patient belongs.
Pat.ID	The name of the variable in Dataset that contains the patient's ID.
Model	The type of model that should be fitted, i.e., <code>Model=c("Full")</code> or <code>Model=c("Reduced")</code> . See the <b>Details</b> section below. Default <code>Model=c("Full")</code> .
Min.Trial.Size	The minimum number of patients that a trial should contain to be included in the analysis. If the number of patients in a trial is smaller than the value specified by <code>Min.Trial.Size</code> , the data of the trial are excluded from the analysis. Default 2.
Alpha	The $\alpha$ -level that is used to determine the confidence intervals around $R_{trial}^2$ , $R_{indiv}^2$ and $R_{indiv}$ . Default 0.05.
T0T1	A scalar or vector that contains the correlation(s) between the counterfactuals T0 and T1 that should be considered in the computation of $\rho_{\Delta}$ (ICA). For details, see function <code>ICA.ContCont</code> . Default <code>seq(-1, 1, by=.2)</code> .
T0S1	A scalar or vector that contains the correlation(s) between the counterfactuals T0 and S1 that should be considered in the computation of $\rho_{\Delta}$ . Default <code>seq(-1, 1, by=.2)</code> .

T1S0	A scalar or vector that contains the correlation(s) between the counterfactuals T1 and S0 that should be considered in the computation of $\rho_{\Delta}$ . Default <code>seq(-1, 1, by=.2)</code> .
S0S1	A scalar or vector that contains the correlation(s) between the counterfactuals S0 and S1 that should be considered in the computation of $\rho_{\Delta}$ . Default <code>seq(-1, 1, by=.2)</code> .
...	Other arguments to be passed to the function <code>lmer</code> (of the R package <code>lme4</code> ) that is used to fit the generalized linear mixed-effect models in the function <code>BimixedContCont</code> .

### Details

The function `BimixedContCont` fits a bivariate mixed-effects model to assess surrogacy (for details, see Buyse et al., 2000). In particular, the following mixed-effects model is fitted:

$$S_{ij} = \mu_S + m_{Si} + (\alpha + a_i)Z_{ij} + \varepsilon_{Sij},$$

$$T_{ij} = \mu_T + m_{Ti} + (\beta + b_i)Z_{ij} + \varepsilon_{Tij},$$

where  $i$  and  $j$  are the trial and subject indicators,  $S_{ij}$  and  $T_{ij}$  are the surrogate and true endpoint values of subject  $j$  in trial  $i$ ,  $Z_{ij}$  is the treatment indicator for subject  $j$  in trial  $i$ ,  $\mu_S$  and  $\mu_T$  are the fixed intercepts for S and T,  $m_{Si}$  and  $m_{Ti}$  are the corresponding random intercepts,  $\alpha$  and  $\beta$  are the fixed treatment effects for S and T, and  $a_i$  and  $b_i$  are the corresponding random treatment effects, respectively.

The vector of the random effects (i.e.,  $m_{Si}$ ,  $m_{Ti}$ ,  $a_i$  and  $b_i$ ) is assumed to be mean-zero normally distributed with variance-covariance matrix  $\mathbf{D}$ :

$$\mathbf{D} = \begin{pmatrix} d_{SS} & & & & \\ d_{ST} & d_{TT} & & & \\ d_{Sa} & d_{Ta} & d_{aa} & & \\ d_{Sb} & d_{Tb} & d_{ab} & d_{bb} & \end{pmatrix}.$$

The trial-level coefficient of determination (i.e.,  $R^2_{trial}$ ) is quantified as:

$$R^2_{trial} = \frac{\begin{pmatrix} d_{Sb} \\ d_{ab} \end{pmatrix}' \begin{pmatrix} d_{SS} & d_{Sa} \\ d_{Sa} & d_{aa} \end{pmatrix}^{-1} \begin{pmatrix} d_{Sb} \\ d_{ab} \end{pmatrix}}{d_{bb}}.$$

The error terms  $\varepsilon_{Sij}$  and  $\varepsilon_{Tij}$  are assumed to be mean-zero normally distributed with variance-covariance matrix  $\mathbf{\Sigma}$ :

$$\mathbf{\Sigma} = \begin{pmatrix} \sigma_{SS} & \\ \sigma_{ST} & \sigma_{TT} \end{pmatrix}.$$

Based on  $\mathbf{\Sigma}$ , individual-level surrogacy is quantified as:

$$R^2_{indiv} = \frac{\sigma_{ST}^2}{\sigma_{SS}\sigma_{TT}}.$$



**Note**

When the full bivariate mixed-effects approach is used to assess surrogacy in the meta-analytic framework (for details, see Buyse & Molenberghs, 2000), computational issues often occur. Such problems mainly occur when the number of trials is low, the number of patients in the different trials is low, and/or when the trial-level heterogeneity is small (Burzykowski et al., 2000).

In that situation, the use of a simplified model-fitting strategy may be warranted (for details, see Burzykowski et al., 2000; Tibaldi et al., 2003).

For example, a reduced bivariate-mixed effect model can be fitted instead of a full model (by using the `Model=c("Reduced")` argument in the function call). In the reduced model, the random-effects structure is simplified (i) by assuming that there is no heterogeneity in the random intercepts, or (ii) by assuming that the covariance between the random intercepts and random treatment effects is zero. Note that under this assumption, the computation of the trial-level coefficient of determination (i.e.,  $R^2_{trial}$ ) simplifies to:

$$R^2_{trial} = \frac{d_{ab}^2}{d_{aa}d_{bb}}.$$

Alternatively, the bivariate mixed-effects model may be abandoned and the user may fit a univariate fixed-effects model, a bivariate fixed-effects model, or a univariate mixed-effects model (for details, see Tibaldi et al., 2003). These models are implemented in the functions [UnifixedContCont](#), [BifixedContCont](#), and [UnimixedContCont](#)).

**Value**

An object of class `BimixedContCont` with components,

- |                                 |   |
|---------------------------------|---|
| <code>Data.Analyze</code>       | Prior to conducting the surrogacy analysis, data of patients who have a missing value for the surrogate and/or the true endpoint are excluded. In addition, the data of trials (i) in which only one type of the treatment was administered, and (ii) in which either the surrogate or the true endpoint was a constant (i.e., all patients within a trial had the same surrogate and/or true endpoint value) are excluded. In addition, the user can specify the minimum number of patients that a trial should contain in order to include the trial in the analysis. If the number of patients in a trial is smaller than the value specified by <code>Min.Trial.Size</code> , the data of the trial are excluded. <code>Data.Analyze</code> is the dataset on which the surrogacy analysis was conducted. |
| <code>Obs.Per.Trial</code>      | A <code>data.frame</code> that contains the total number of patients per trial and the number of patients who were administered the control treatment and the experimental treatment in each of the trials (in <code>Data.Analyze</code> ).   |
| <code>Trial.Spec.Results</code> | A <code>data.frame</code> that contains the trial-specific intercepts and treatment effects on the surrogate and the true endpoints when a full model is requested (i.e., $\mu_S + m_{Si}$ , $\mu_T + m_{Ti}$ , $\alpha + a_i$ , and $\beta + b_i$ ), or the trial-specific treatment effects on the surrogate and the true endpoints when a reduced model is requested (i.e., $\alpha + a_i$ , and $\beta + b_i$ ). Note that the results that are contained in <code>Trial.Spec.Results</code> are equivalent to the results in <code>Results.Stage.1</code> that are obtained when the functions <a href="#">UnifixedContCont</a> , <a href="#">UnimixedContCont</a> , or <a href="#">BifixedContCont</a> are used.  |

Residuals	A data.frame that contains the residuals for the surrogate and true endpoints ( $\varepsilon_{Sij}$ and $\varepsilon_{Tij}$ ).
Fixed.Effect.Pars	A data.frame that contains the fixed intercept and treatment effects for the surrogate and the true endpoints (i.e., $\mu_S$ , $\mu_T$ , $\alpha$ , and $\beta$ ).
Random.Effect.Pars	A data.frame that contains the random intercept and treatment effects for the surrogate and the true endpoints (i.e., $m_{Si}$ , $m_{Ti}$ , $a_i$ , and $b_i$ ) when a full model is fitted (i.e., when <code>Model=c("Full")</code> is used in the function call), or that contains the random treatment effects for the surrogate and the true endpoints (i.e., $a_i$ and $b_i$ ) when a reduced model is fitted (i.e., when <code>Model=c("Reduced")</code> is used in the function call).
Trial.R2	A data.frame that contains the trial-level coefficient of determination ( $R_{trial}^2$ ), its standard error and confidence interval.
Indiv.R2	A data.frame that contains the individual-level coefficient of determination ( $R_{indiv}^2$ ), its standard error and confidence interval.
Trial.R	A data.frame that contains the trial-level correlation coefficient ( $R_{trial}$ ), its standard error and confidence interval.
Indiv.R	A data.frame that contains the individual-level correlation coefficient ( $R_{indiv}$ ), its standard error and confidence interval.
Cor.Endpoints	A data.frame that contains the correlations between the surrogate and the true endpoint in the control treatment group (i.e., $\rho_{T0S0}$ ) and in the experimental treatment group (i.e., $\rho_{T1S1}$ ), their standard errors and their confidence intervals.
D	The variance-covariance matrix of the random effects (the <b>D</b> matrix), i.e., a 4 by 4 variance-covariance matrix of the random intercept and treatment effects when a full model is fitted (i.e., when <code>Model=c("Full")</code> is used in the function call), or a 2 by 2 variance-covariance matrix of the random treatment effects when a reduced model is fitted (i.e., when <code>Model=c("Reduced")</code> is used in the function call).
Sigma	The 2 by 2 variance-covariance matrix of the residuals ( $\varepsilon_{Sij}$ and $\varepsilon_{Tij}$ ).
ICA	A fitted object of class ICA.ContCont.
T0T0	The variance of the true endpoint in the control treatment condition.
T1T1	The variance of the true endpoint in the experimental treatment condition.
S0S0	The variance of the surrogate endpoint in the control treatment condition.
S1S1	The variance of the surrogate endpoint in the experimental treatment condition.

### Author(s)

Wim Van der Elst, Ariel Alonso, & Geert Molenberghs

### References

Burzykowski, T., Molenberghs, G., & Buyse, M. (2005). *The evaluation of surrogate endpoints*. New York: Springer-Verlag.

Buyse, M., Molenberghs, G., Burzykowski, T., Renard, D., & Geys, H. (2000). The validation of surrogate endpoints in meta-analysis of randomized experiments. *Biostatistics*, *1*, 49-67.

Tibaldi, F., Abrahantes, J. C., Molenberghs, G., Renard, D., Burzykowski, T., Buyse, M., Parmar, M., et al., (2003). Simplified hierarchical linear models for the evaluation of surrogate endpoints. *Journal of Statistical Computation and Simulation*, *73*, 643-658.

### See Also

[UnifixedContCont](#), [BifixedContCont](#), [UnimixedContCont](#), [plot Meta-Analytic](#)

### Examples

```
# Open the Schizo dataset (clinical trial in schizophrenic patients)
data(Schizo)

## Not run: #Time consuming (>5 sec) code part
# When a reduced bivariate mixed-effect model is used to assess surrogacy,
# the conditioning number for the D matrix is very high:
Sur <- BimixedContCont(Dataset=Schizo, Surr=BPRS, True=PANSS, Treat=Treat, Model="Reduced",
  Trial.ID=InvestId, Pat.ID=Id)

# Such problems often occur when the total number of patients, the total number
# of trials and/or the trial-level heterogeneity
# of the treatment effects is relatively small

# As an alternative approach to assess surrogacy, consider using the functions
# BifixedContCont, UnifixedContCont or UnimixedContCont in the meta-analytic framework,
# or use the information-theoretic approach

## End(Not run)
```

---

Bootstrap.MEP.BinBin *Bootstrap 95% CI around the maximum-entropy ICA and SPF (surrogate predictive function)*

---

### Description

Computes a 95% bootstrap-based CI around the maximum-entropy ICA and SPF (surrogate predictive function) in the binary-binary setting

### Usage

```
Bootstrap.MEP.BinBin(Data, Surr, True, Treat, M=100, Seed=123)
```

**Arguments**

Data	The dataset to be used.
Surr	The name of the surrogate variable.
True	The name of the true endpoint.
Treat	The name of the treatment indicator.
M	The number of bootstrap samples taken. Default M=1000.
Seed	The seed to be used. Default Seed=123.

**Value**

R2H	The vector the bootstrapped MEP ICA values.
r_1_1	The vector of the bootstrapped bootstrapped MEP $r(1, 1)$ values.
r_min1_1	The vector of the bootstrapped bootstrapped MEP $r(-1, 1)$ .
r_0_1	The vector of the bootstrapped bootstrapped MEP $r(0, 1)$ .
r_1_0	The vector of the bootstrapped bootstrapped MEP $r(1, 0)$ .
r_min1_0	The vector of the bootstrapped bootstrapped MEP $r(-1, 0)$ .
r_0_0	The vector of the bootstrapped bootstrapped MEP $r(0, 0)$ .
r_1_min1	The vector of the bootstrapped bootstrapped MEP $r(1, -1)$ .
r_min1_min1	The vector of the bootstrapped bootstrapped MEP $r(-1, -1)$ .
r_0_min1	The vector of the bootstrapped bootstrapped MEP $r(0, -1)$ .
vector_p	The matrix that contains all bootstrapped maximum entropy distributions of the vector of the potential outcomes.

**Author(s)**

Wim Van der Elst, Ariel Alonso, & Geert Molenberghs

**References**

Alonso, A., & Van der Elst, W. (2015). A maximum-entropy approach for the evaluation of surrogate endpoints based on causal inference.

**See Also**

[ICA.BinBin](#), [ICA.BinBin.Grid.Sample](#), [ICA.BinBin.Grid.Full](#), [plot MaxEntSPF BinBin](#)

**Examples**

```
## Not run: # time consuming code part
MEP_CI <- Bootstrap.MEP.BinBin(Data = Schizo_Bin, Surr = "BPRS_Bin", True = "PANSS_Bin",
                              Treat = "Treat", M = 500, Seed=123)
summary(MEP_CI)

## End(Not run)
```

---

CausalDiagramBinBin *Draws a causal diagram depicting the median informational coefficients of correlation (or odds ratios) between the counterfactuals for a specified range of values of the ICA in the binary-binary setting.*

---

### Description

This function provides a diagram that depicts the medians of the informational coefficients of correlation (or odds ratios) between the counterfactuals for a specified range of values of the individual causal association in the binary-binary setting ( $R_H^2$ ).

### Usage

```
CausalDiagramBinBin(x, Values="Corrs", Theta_T0S0, Theta_T1S1,
  Min=0, Max=1, Cex.Letters=3, Cex.Corr=2, Lines.Rel.Width=TRUE,
  Col.Pos.Neg=TRUE, Monotonicity, Histograms.Corr=FALSE,
  Densities.Corr=FALSE)
```

### Arguments

x	An object of class ICA.BinBin. See <a href="#">ICA.BinBin</a> .
Values	Specifies whether the median informational coefficients of correlation or median odds ratios between the counterfactuals should be depicted, i.e., Values="Corrs" or Values="ORs".
Theta_T0S0	The odds ratio between $T$ and $S$ in the control group. This quantity is estimable based on the observed data. Only has to be provided when Values="ORs".
Theta_T1S1	The odds ratio between $T$ and $S$ in the experimental treatment group. This quantity is estimable based on the observed data. Only has to be provided when Values="ORs".
Min	The minimum value of $R_H^2$ that should be considered. Default=-1.
Max	The maximum value of $R_H^2$ that should be considered. Default=1.
Cex.Letters	The size of the symbols for the counterfactuals ( $S_0, S_1, T_0, T_1$ ). Default=3.
Cex.Corr	The size of the text depicting the median odds ratios between the counterfactuals. Default=2.
Lines.Rel.Width	Logical. When Lines.Rel.Width=TRUE, the widths of the lines that represent the odds ratios between the counterfactuals are relative to the size of the odds ratios (i.e., a smaller/thicker line is used for smaller/higher odds ratios). When Lines.Rel.Width=FALSE, the width of all lines representing the odds ratios between the counterfactuals is identical. Default=TRUE. Only considered when Values="ORs".
Col.Pos.Neg	Logical. When Col.Pos.Neg=TRUE, the color of the lines that represent the odds ratios between the counterfactuals is red for odds ratios below 1 and black for the ones above 1. When Col.Pos.Neg=FALSE, all lines are in black. Default=TRUE. Only considered when Values="ORs".

- Monotonicity** Specifies the monotonicity scenario that should be considered (i.e., `Monotonicity=c("No")`, `Monotonicity=c("True.Endp")`, `Monotonicity=c("Surr.Endp")`, or `Monotonicity=c("Surr.True")`).
- Histograms.Correlations** Should histograms of the informational coefficients of association  $R_H^2$  be provided? Default `Histograms.Correlations=FALSE`.
- Densities.Correlations** Should densities of the informational coefficients of association  $R_H^2$  be provided? Default `Densities.Correlations=FALSE`.

## Value

The following components are stored in the fitted object if histograms of the informational correlations are requested in the function call (i.e., if `Histograms.Correlations=TRUE` and `Values="Corrs"` in the function call):

- `R2_H_T0T1` The informational coefficients of association  $R_H^2$  between  $T_0$  and  $T_1$ .
- `R2_H_S1T0` The informational coefficients of association  $R_H^2$  between  $S_1$  and  $T_0$ .
- `R2_H_S0T1` The informational coefficients of association  $R_H^2$  between  $S_0$  and  $T_1$ .
- `R2_H_S0S1` The informational coefficients of association  $R_H^2$  between  $S_0$  and  $S_1$ .
- `R2_H_S0T0` The informational coefficients of association  $R_H^2$  between  $S_0$  and  $T_0$ .
- `R2_H_S1T1` The informational coefficients of association  $R_H^2$  between  $S_1$  and  $T_1$ .

## Author(s)

Wim Van der Elst, Ariel Alonso, & Geert Molenberghs

## References

Alonso, A., Van der Elst, W., Molenberghs, G., Buyse, M., & Burzykowski, T. (submitted). On the relationship between the causal inference and meta-analytic paradigms for the validation of surrogate markers.

Van der Elst, W., Alonso, A., & Molenberghs, G. (submitted). An exploration of the relationship between causal inference and meta-analytic measures of surrogacy.

## See Also

[ICA.BinBin](#)

## Examples

```
# Compute R2_H given the marginals specified as the pi's
ICA <- ICA.BinBin.Grid.Sample(pi1_1_=0.2619048, pi1_0_=0.2857143,
pi_1_1=0.6372549, pi_1_0=0.07843137, pi0_1_=0.1349206, pi_0_1=0.127451,
Seed=1, Monotonicity=c("General"), M=1000)
```

```
# Obtain a causal diagram that provides the medians of the
# correlations between the counterfactuals for the range
# of R2_H values between 0.1 and 1
```

```

# Assume no monotonicity
CausalDiagramBinBin(x=ICA, Min=0.1, Max=1, Monotonicity="No")

# Assume monotonicity for S
CausalDiagramBinBin(x=ICA, Min=0.1, Max=1, Monotonicity="Surr.Endp")

# Now only consider the results that were obtained when
# monotonicity was assumed for the true endpoint
CausalDiagramBinBin(x=ICA, Values="ORs", Theta_T0S0=2.156, Theta_T1S1=10,
Min=0, Max=1, Monotonicity="True.Endp")

```

---

CausalDiagramContCont *Draws a causal diagram depicting the median correlations between the counterfactuals for a specified range of values of ICA or MICA in the continuous-continuous setting*

---

### Description

This function provides a diagram that depicts the medians of the correlations between the counterfactuals for a specified range of values of the individual causal association (ICA;  $\rho_{\Delta}$ ) or the meta-analytic individual causal association (MICA;  $\rho_M$ ).

### Usage

```

CausalDiagramContCont(x, Min=-1, Max=1, Cex.Letters=3, Cex.Corr=2,
Lines.Rel.Width=TRUE, Col.Pos.Neg=TRUE, Histograms.Counterfactuals=FALSE)

```

### Arguments

x	An object of class ICA.ContCont or MICA.ContCont. See <a href="#">ICA.ContCont</a> or <a href="#">MICA.ContCont</a> .
Min	The minimum values of (M)ICA that should be considered. Default=-1.
Max	The maximum values of (M)ICA that should be considered. Default=1.
Cex.Letters	The size of the symbols for the counterfactuals ( $S_0, S_1, T_0, T_1$ ). Default=3.
Cex.Corr	The size of the text depicting the median correlations between the counterfactuals. Default=2.
Lines.Rel.Width	Logical. When Lines.Rel.Width=TRUE, the widths of the lines that represent the correlations between the counterfactuals are relative to the size of the correlations (i.e., a smaller line is used for correlations closer to zero whereas a thicker line is used for (absolute) correlations closer to 1). When Lines.Rel.Width=FALSE, the width of all lines representing the correlations between the counterfactuals is identical. Default=TRUE.
Col.Pos.Neg	Logical. When Col.Pos.Neg=TRUE, the color of the lines that represent the correlations between the counterfactuals is red for negative correlations and black for positive ones. When Col.Pos.Neg=FALSE, all lines are in black. Default=TRUE.

Histograms.Counterfactuals

Should plots that shows the densities for the inidentifiable correlations be shown?  
Default =FALSE.

### Author(s)

Wim Van der Elst, Ariel Alonso, & Geert Molenberghs

### References

Alonso, A., Van der Elst, W., Molenberghs, G., Buyse, M., & Burzykowski, T. (submitted). On the relationship between the causal inference and meta-analytic paradigms for the validation of surrogate markers.

Van der Elst, W., Alonso, A., & Molenberghs, G. (submitted). An exploration of the relationship between causal inference and meta-analytic measures of surrogacy.

### See Also

[ICA.ContCont](#), [MICA.ContCont](#)

### Examples

```
## Not run: #Time consuming (>5 sec) code parts
# Generate the vector of ICA values when rho_T0S0=.91, rho_T1S1=.91, and when the
# grid of values {0, .1, ..., 1} is considered for the correlations
# between the counterfactuals:
SurICA <- ICA.ContCont(T0S0=.95, T1S1=.91, T0T1=seq(0, 1, by=.1), T0S1=seq(0, 1, by=.1),
T1S0=seq(0, 1, by=.1), S0S1=seq(0, 1, by=.1))

#obtain a plot of ICA

# Obtain a causal diagram that provides the medians of the
# correlations between the counterfactuals for the range
# of ICA values between .9 and 1 (i.e., which assumed
# correlations between the counterfactuals lead to a
# high ICA?)
CausalDiagramContCont(SurICA, Min=.9, Max=1)

# Same, for low values of ICA
CausalDiagramContCont(SurICA, Min=0, Max=.5)
## End(Not run)
```



## Description

The function `comb27.BinBin` assesses a surrogate predictive value of each of the 27 possible prediction functions in the single-trial causal-inference framework when both the surrogate and the true endpoints are binary outcomes. The distribution of frequencies at which each of the 27 possible prediction functions are selected provides additional insights regarding the association between  $S$  ( $\Delta_S$ ) and  $T$  ( $\Delta_T$ ). See **Details** below.

## Usage

```
comb27.BinBin(pi1_1_, pi1_0_, pi_1_1, pi_1_0,
pi0_1_, pi_0_1, Monotonicity=c("No"),M=1000, Seed=1)
```

## Arguments

<code>pi1_1_</code>	A scalar that contains values for $P(T = 1, S = 1 Z = 0)$ , i.e., the probability that $S = T = 1$ when under treatment $Z = 0$ .
<code>pi1_0_</code>	A scalar that contains values for $P(T = 1, S = 0 Z = 0)$ .
<code>pi_1_1</code>	A scalar that contains values for $P(T = 1, S = 1 Z = 1)$ .
<code>pi_1_0</code>	A scalar that contains values for $P(T = 1, S = 0 Z = 1)$ .
<code>pi0_1_</code>	A scalar that contains values for $P(T = 0, S = 1 Z = 0)$ .
<code>pi_0_1</code>	A scalar that contains values for $P(T = 0, S = 1 Z = 1)$ .
<code>Monotonicity</code>	Specifies which assumptions regarding monotonicity should be made, only one assumption can be made at the time: <code>Monotonicity=c("No")</code> , <code>Monotonicity=c("True.Endp")</code> , <code>Monotonicity=c("Surr.Endp")</code> , or <code>Monotonicity=c("Surr.True.Endp")</code> . Default <code>Monotonicity=c("No")</code> .
<code>M</code>	The number of random samples that have to be drawn for the freely varying parameters. Default <code>M=100000</code> .
<code>Seed</code>	The seed to be used to generate $\pi_r$ . Default <code>Seed=1</code> .

## Details

In the continuous normal setting, surrogacy can be assessed by studying the association between the individual causal effects on  $S$  and  $T$  (see [ICA.ContCont](#)). In that setting, the Pearson correlation is the obvious measure of association.

When  $S$  and  $T$  are binary endpoints, multiple alternatives exist. Alonso et al. (2016) proposed the individual causal association (ICA;  $R_H^2$ ), which captures the association between the individual causal effects of the treatment on  $S$  ( $\Delta_S$ ) and  $T$  ( $\Delta_T$ ) using information-theoretic principles.

The function `comb27.BinBin` computes  $R_H^2$  using a grid-based approach where all possible combinations of the specified grids for the parameters that are allowed to vary freely are considered. It computes the probability of a prediction error for each of the 27 possible prediction functions. The frequency at which each prediction function is selected provides additional insight about the minimal probability of a prediction error PPE which can be obtained with `PPE.BinBin`.

**Value**

An object of class `comb27.BinBin` with components,

<code>index</code>	count variable
<code>Monotonicity</code>	The vector of Monotonicity assumptions
<code>Pe</code>	The vector of the prediction error values.
<code>combo</code>	The vector containing the codes for the each of the 27 prediction functions.
<code>R2_H</code>	The vector of the $R_H^2$ values.
<code>H_Delta_T</code>	The vector of the entropies of $\Delta_T$ .
<code>H_Delta_S</code>	The vector of the entropies of $\Delta_S$ .
<code>I_Delta_T_Delta_S</code>	The vector of the mutual information of $\Delta_S$ and $\Delta_T$ .

**Author(s)**

Paul Meyvisch, Wim Van der Elst, Ariel Alonso, Geert Molenberghs

**References**

Alonso A, Van der Elst W, Molenberghs G, Buyse M and Burzykowski T. (2016). An information-theoretic approach for the evaluation of surrogate endpoints based on causal inference.

Alonso A, Van der Elst W and Meyvisch P (2016). Assessing a surrogate predictive value: A causal inference approach.

**See Also**

[PPE.BinBin](#)

**Examples**

```
# Conduct the analysis assuming no monotonicity

## Not run: # time consuming code part
comb27.BinBin(pi1_1_ = 0.3412, pi1_0_ = 0.2539, pi0_1_ = 0.119,
              pi_1_1 = 0.6863, pi_1_0 = 0.0882, pi_0_1 = 0.0784,
              Seed=1, Monotonicity=c("No"), M=500000)

## End(Not run)
```

---

ECT *Apply the Entropy Concentration Theorem*

---

### Description

The Entropy Concentration Theorem (ECT; Edwin, 1982) states that if  $N$  is large enough, then  $100(1 - F)\%$  of all  $\mathbf{p}^*$  and  $\Delta H$  is determined by the upper tail are  $1 - F$  of a  $\chi^2$  distribution, with  $DF = q - m - 1$  (which equals 8 in a surrogate evaluation context).

### Usage

```
ECT(Perc=.95, H_Max, N)
```

### Arguments

Perc	The desired interval. E.g., Perc=.05 will generate the lower and upper bounds for $H(\mathbf{p})$ that contain 95% of the cases (as determined by the ECT).
H_Max	The maximum entropy value. In the binary-binary setting, this can be computed using the function <a href="#">MaxEntICABinBin</a> .
N	The sample size.

### Value

An object of class ECT with components,

Lower_H	The lower bound of the requested interval.
Upper_H	The upper bound of the requested interval, which equals $H_{Max}$ .

### Author(s)

Wim Van der Elst, Paul Meyvisch, & Ariel Alonso

### References

Alonso, A., Van der Elst, W., & Molenberghs, G. (2016). Surrogate markers validation: the continuous-binary setting from a causal inference perspective.

### See Also

[MaxEntICABinBin](#), [ICA.BinBin](#)

### Examples

```
ECT_fit <- ECT(Perc = .05, H_Max = 1.981811, N=454)
summary(ECT_fit)
```

---

Fano.BinBin	<i>Evaluate the possibility of finding a good surrogate in the setting where both <math>S</math> and <math>T</math> are binary endpoints</i>
-------------	--

---

### Description

The function `Fano.BinBin` evaluates the existence of a good surrogate in the single-trial causal-inference framework when both the surrogate and the true endpoints are binary outcomes. See **Details** below.

### Usage

```
Fano.BinBin(pi1_, pi_1, rangepi10=c(0,min(pi1_,1-pi_1)),
fano_delta=c(0.1), M=1000, Seed=1)
```

### Arguments

<code>pi1_</code>	A scalar or a vector of plausible values that represents the proportion of responders under treatment.
<code>pi_1</code>	A scalar or a vector of plausible values that represents the proportion of responders under control.
<code>rangepi10</code>	Represents the range from which $\pi_{10}$ is sampled. By default, Monte Carlo simulation will be constrained to the interval $[0, \min(\pi_{1.}, \pi_{.0})]$ but this allows the user to specify a more narrow range. <code>rangepi10=c(0,0)</code> is equivalent to the assumption of monotonicity for the true endpoint.
<code>fano_delta</code>	A scalar or a vector that specifies the values for the upper bound of the prediction error $\delta$ . Default <code>fano_delta=c(0.2)</code> .
<code>M</code>	The number of random samples that have to be drawn for the freely varying parameter $\pi_{10}$ . Default <code>M=1000</code> . The number of random samples should be sufficiently large in relation to the length of the interval <code>rangepi10</code> . Typically <code>M=1000</code> yields a sufficiently fine grid. In case <code>rangepi10</code> is a single value: <code>M=1</code>
<code>Seed</code>	The seed to be used to sample the freely varying parameter $\pi_{10}$ . Default <code>Seed=1</code> .

### Details

Values for  $\pi_{10}$  have to be uniformly sampled from the interval  $[0, \min(\pi_{1.}, \pi_{.0})]$ . Any sampled value for  $\pi_{10}$  will fully determine the bivariate distribution of potential outcomes for the true endpoint. The treatment effect should be positive.

The vector  $\pi_{km}$  fully determines  $R_{HL}^2$ .

### Value

An object of class `Fano.BinBin` with components,

<code>R2_HL</code>	The sampled values for $R_{HL}^2$ .
<code>H_Delta_T</code>	The sampled values for $H\Delta T$ .

PPE_T	The sampled values for $PPE_T$ .
minpi10	The minimum value for $\pi_{10}$ .
maxpi10	The maximum value for $\pi_{10}$ .
samplepi10	The sampled value for $\pi_{10}$ .
delta	The specified vector of upper bounds for the prediction errors.
uncertainty	Indexes the sampling of $pi1_$ .
pi_00	The sampled values for $\pi_{00}$ .
pi_11	The sampled values for $\pi_{11}$ .
pi_01	The sampled values for $\pi_{01}$ .
pi_10	The sampled values for $\pi_{10}$ .

**Author(s)**

Paul Meyvisch, Wim Van der Elst, Ariel Alonso

**References**

Alonso, A., Van der Elst, W., & Molenberghs, G. (2014). Validation of surrogate endpoints: the binary-binary setting from a causal inference perspective.

**See Also**

[plot.Fano.BinBin](#)

**Examples**

```
# Conduct the analysis assuming no monotonicity
# for the true endpoint, using a range of
# upper bounds for prediction errors
Fano.BinBin(pi1_ = 0.5951 , pi_1 = 0.7745,
fano_delta=c(0.05, 0.1, 0.2), M=1000)

# Conduct the same analysis now sampling from
# a range of values to allow for uncertainty

Fano.BinBin(pi1_ = runif(n=20,min=0.504,max=0.681),
pi_1 = runif(n=20,min=0.679,max=0.849),
fano_delta=c(0.05, 0.1, 0.2), M=10, Seed=2)
```

---

FixedBinBinIT	<i>Fits (univariate) fixed-effect models to assess surrogacy in the binary-binary case based on the Information-Theoretic framework</i>
---------------	---

---

### Description

The function `FixedBinBinIT` uses the information-theoretic approach (Alonso & Molenberghs, 2007) to estimate trial- and individual-level surrogacy based on fixed-effect models when both S and T are binary variables. The user can specify whether a (weighted or unweighted) full, semi-reduced, or reduced model should be fitted. See the **Details** section below.

### Usage

```
FixedBinBinIT(Dataset, Surr, True, Treat, Trial.ID, Pat.ID,
              Model=c("Full"), Weighted=TRUE, Min.Trial.Size=2, Alpha=.05,
              Number.Bootstraps=50, Seed=sample(1:1000, size=1))
```

### Arguments

Dataset	A data frame that should consist of one line per patient. Each line contains (at least) a surrogate value, a true endpoint value, a treatment indicator, a patient ID, and a trial ID.
Surr	The name of the variable in <code>Dataset</code> that contains the surrogate endpoint values.
True	The name of the variable in <code>Dataset</code> that contains the true endpoint values.
Treat	The name of the variable in <code>Dataset</code> that contains the treatment indicators. The treatment indicator should either be coded as 1 for the experimental group and -1 for the control group, or as 1 for the experimental group and 0 for the control group.
Trial.ID	The name of the variable in <code>Dataset</code> that contains the trial ID to which the patient belongs.
Pat.ID	The name of the variable in <code>Dataset</code> that contains the patient's ID.
Model	The type of model that should be fitted, i.e., <code>Model=c("Full")</code> , <code>Model=c("Reduced")</code> , or <code>Model=c("SemiReduced")</code> . See the <b>Details</b> section below. Default <code>Model=c("Full")</code> .
Weighted	Logical. In practice it is often the case that different trials (or other clustering units) have different sample sizes. Univariate models are used to assess surrogacy in the information-theoretic approach, so it can be useful to adjust for heterogeneity in information content between the trial-specific contributions (particularly when trial-level surrogacy measures are of primary interest and when the heterogeneity in sample sizes is large). If <code>Weighted=TRUE</code> , weighted regression models are fitted. If <code>Weighted=FALSE</code> , unweighted regression analyses are conducted. See the <b>Details</b> section below. Default <code>TRUE</code> .
Min.Trial.Size	The minimum number of patients that a trial should contain to be included in the analysis. If the number of patients in a trial is smaller than the value specified by <code>Min.Trial.Size</code> , the data of the trial are excluded from the analysis. Default 2.

Alpha	The $\alpha$ -level that is used to determine the confidence intervals around $R_h^2$ and $R_{ht}^2$ . Default 0.05.
Number.Bootstraps	The standard errors and confidence intervals for $R_h^2$ , $R_{b.ind}^2$ and $R_{h.ind}^2$ are determined based on a bootstrap procedure. Number.Bootstraps specifies the number of bootstrap samples that are used. Default 50.
Seed	The seed to be used in the bootstrap procedure. Default <code>sample(1 : 1000, size = 1)</code> .

## Details

### *Individual-level surrogacy*

The following univariate generalised linear models are fitted:

$$g_T(E(T_{ij})) = \mu_{Ti} + \beta_i Z_{ij},$$

$$g_T(E(T_{ij}|S_{ij})) = \gamma_{0i} + \gamma_{1i} Z_{ij} + \gamma_{2i} S_{ij},$$

where  $i$  and  $j$  are the trial and subject indicators,  $g_T$  is an appropriate link function (i.e., a logit link when binary endpoints are considered),  $S_{ij}$  and  $T_{ij}$  are the surrogate and true endpoint values of subject  $j$  in trial  $i$ , and  $Z_{ij}$  is the treatment indicator for subject  $j$  in trial  $i$ .  $\mu_{Ti}$  and  $\beta_i$  are the trial-specific intercepts and treatment-effects on the true endpoint in trial  $i$ .  $\gamma_{0i}$  and  $\gamma_{1i}$  are the trial-specific intercepts and treatment-effects on the true endpoint in trial  $i$  after accounting for the effect of the surrogate endpoint.

The  $-2$  log likelihood values of the previous models in each of the  $i$  trials (i.e.,  $L_{1i}$  and  $L_{2i}$ , respectively) are subsequently used to compute individual-level surrogacy based on the so-called Variance Reduction Factor (VFR; for details, see Alonso & Molenberghs, 2007):

$$R_h^2 = 1 - \frac{1}{N} \sum_i \exp\left(-\frac{L_{2i} - L_{1i}}{n_i}\right),$$

where  $N$  is the number of trials and  $n_i$  is the number of patients within trial  $i$ .

When it can be assumed (i) that the treatment-corrected association between the surrogate and the true endpoint is constant across trials, or (ii) when all data come from a single clinical trial (i.e., when  $N = 1$ ), the previous expression simplifies to:

$$R_{h.ind}^2 = 1 - \exp\left(-\frac{L_2 - L_1}{N}\right).$$

The upper bound does not reach to 1 when  $T$  is binary, i.e., its maximum is 0.75. Kent (1983) claims that 0.75 is a reasonable upper bound and thus  $R_{h.ind}^2$  can usually be interpreted without paying special consideration to the discreteness of  $T$ . Alternatively, to address the upper bound problem, a scaled version of the mutual information can be used when both  $S$  and  $T$  are binary (Joe, 1989):

$$R_{b.ind}^2 = \frac{I(T, S)}{\min[H(T), H(S)]},$$

where the entropy of  $T$  and  $S$  in the previous expression can be estimated using the log likelihood functions of the GLMs shown above.

#### *Trial-level surrogacy*

When a full or semi-reduced model is requested (by using the argument `Model=c("Full")` or `Model=c("SemiReduced")` in the function call), trial-level surrogacy is assessed by fitting the following univariate models:

$$S_{ij} = \mu_{Si} + \alpha_i Z_{ij} + \varepsilon_{Sij}, (1)$$

$$T_{ij} = \mu_{Ti} + \beta_i Z_{ij} + \varepsilon_{Tij}, (1)$$

where  $i$  and  $j$  are the trial and subject indicators,  $S_{ij}$  and  $T_{ij}$  are the surrogate and true endpoint values of subject  $j$  in trial  $i$ ,  $Z_{ij}$  is the treatment indicator for subject  $j$  in trial  $i$ ,  $\mu_{Si}$  and  $\mu_{Ti}$  are the fixed trial-specific intercepts for S and T, and  $\alpha_i$  and  $\beta_i$  are the fixed trial-specific treatment effects on S and T, respectively. The error terms  $\varepsilon_{Sij}$  and  $\varepsilon_{Tij}$  are assumed to be independent.

When a reduced model is requested by the user (by using the argument `Model=c("Reduced")` in the function call), the following univariate models are fitted:

$$S_{ij} = \mu_S + \alpha_i Z_{ij} + \varepsilon_{Sij}, (2)$$

$$T_{ij} = \mu_T + \beta_i Z_{ij} + \varepsilon_{Tij}, (2)$$

where  $\mu_S$  and  $\mu_T$  are the common intercepts for S and T. The other parameters are the same as defined above, and  $\varepsilon_{Sij}$  and  $\varepsilon_{Tij}$  are again assumed to be independent.

When the user requested a full model approach (by using the argument `Model=c("Full")` in the function call, i.e., when models (1) were fitted), the following model is subsequently fitted:

$$\hat{\beta}_i = \lambda_0 + \lambda_1 \widehat{\mu_{Si}} + \lambda_2 \hat{\alpha}_i + \varepsilon_i, (3)$$

where the parameter estimates for  $\beta_i$ ,  $\mu_{Si}$ , and  $\alpha_i$  are based on models (1) (see above). When a weighted model is requested (using the argument `Weighted=TRUE` in the function call), model (3) is a weighted regression model (with weights based on the number of observations in trial  $i$ ). The  $-2$  log likelihood value of the (weighted or unweighted) model (3) ( $L_1$ ) is subsequently compared to the  $-2$  log likelihood value of an intercept-only model ( $\hat{\beta}_i = \lambda_3; L_0$ ), and  $R_{ht}^2$  is computed based on the Variance Reduction Factor (for details, see Alonso & Molenberghs, 2007):

$$R_{ht}^2 = 1 - \exp\left(-\frac{L_1 - L_0}{N}\right),$$

where  $N$  is the number of trials.

When a semi-reduced or reduced model is requested (by using the argument `Model=c("SemiReduced")` or `Model=c("Reduced")` in the function call), the following model is fitted:

$$\hat{\beta}_i = \lambda_0 + \lambda_1 \hat{\alpha}_i + \varepsilon_i,$$

where the parameter estimates for  $\beta_i$  and  $\alpha_i$  are based on models (1) when a semi-reduced model is fitted or on models (2) when a reduced model is fitted. The  $-2$  log likelihood value of this (weighted or unweighted) model ( $L_1$ ) is subsequently compared to the  $-2$  log likelihood value of an intercept-only model ( $\hat{\beta}_i = \lambda_3; L_0$ ), and  $R_{ht}^2$  is computed based on the reduction in the likelihood (as described above).



**Value**

An object of class FixedBinBinIT with components,

Data.Analyze	Prior to conducting the surrogacy analysis, data of patients who have a missing value for the surrogate and/or the true endpoint are excluded. In addition, the data of trials (i) in which only one type of the treatment was administered, and (ii) in which either the surrogate or the true endpoint was a constant (i.e., all patients within a trial had the same surrogate and/or true endpoint value) are excluded. In addition, the user can specify the minimum number of patients that a trial should contain in order to include the trial in the analysis. If the number of patients in a trial is smaller than the value specified by <code>Min.Trial.Size</code> , the data of the trial are excluded. <code>Data.Analyze</code> is the dataset on which the surrogacy analysis was conducted.
Obs.Per.Trial	A <code>data.frame</code> that contains the total number of patients per trial and the number of patients who were administered the control treatment and the experimental treatment in each of the trials (in <code>Data.Analyze</code> ).
Trial.Spec.Results	A <code>data.frame</code> that contains the trial-specific intercepts and treatment effects for the surrogate and the true endpoints (when a full or semi-reduced model is requested), or the trial-specific treatment effects for the surrogate and the true endpoints (when a reduced model is requested).
R2ht	A <code>data.frame</code> that contains the trial-level surrogacy estimate and its confidence interval.
R2h.ind	A <code>data.frame</code> that contains the individual-level surrogacy estimate $R_{h.ind}^2$ (single-trial based estimate) and its confidence interval.
R2h	A <code>data.frame</code> that contains the individual-level surrogacy estimate $R_h^2$ (cluster-based estimate) and its confidence interval (based on a bootstrap).
R2b.ind	A <code>data.frame</code> that contains the individual-level surrogacy estimate $R_{b.ind}^2$ (single-trial based estimate accounting for upper bound) and its confidence interval (based on a bootstrap).
R2h.Ind.By.Trial	A <code>data.frame</code> that contains individual-level surrogacy estimates $R_{hInd}^2$ (cluster-based estimates) and their confidence interval for each of the trials separately.

**Author(s)**

Wim Van der Elst, Ariel Alonso, & Geert Molenberghs

**References**

- Alonso, A, & Molenberghs, G. (2007). Surrogate marker evaluation from an information theory perspective. *Biometrics*, 63, 180-186.
- Joe, H. (1989). Relative entropy measures of multivariate dependence. *Journal of the American Statistical Association*, 84, 157-164.
- Kent, T. J. (1983). Information gain as a general measure of correlation. *Biometrika*, 70, 163-173.

**See Also**

[FixedBinContIT](#), [FixedContBinIT](#), [plot Information-Theoretic BinComb](#)

**Examples**

```
## Not run: # Time consuming (>5sec) code part
# Generate data with continuous Surr and True
Sim.Data.MTS(N.Total=5000, N.Trial=50, R.Trial.Target=.9, R.Indiv.Target=.9,
             Fixed.Effects=c(0, 0, 0, 0), D.aa=10, D.bb=10, Seed=1,
             Model=c("Full"))
# Dichotomize Surr and True
Surr_Bin <- Data.Observed.MTS$Surr
Surr_Bin[Data.Observed.MTS$Surr>.5] <- 1
Surr_Bin[Data.Observed.MTS$Surr<=.5] <- 0
True_Bin <- Data.Observed.MTS$True
True_Bin[Data.Observed.MTS$True>.15] <- 1
True_Bin[Data.Observed.MTS$True<=.15] <- 0
Data.Observed.MTS$Surr <- Surr_Bin
Data.Observed.MTS$True <- True_Bin

# Assess surrogacy using info-theoretic framework
Fit <- FixedBinBinIT(Dataset = Data.Observed.MTS, Surr = Surr,
                    True = True, Treat = Treat, Trial.ID = Trial.ID,
                    Pat.ID = Pat.ID, Number.Bootstraps=100)

# Examine results
summary(Fit)
plot(Fit, Trial.Level = FALSE, Indiv.Level.By.Trial=TRUE)
plot(Fit, Trial.Level = TRUE, Indiv.Level.By.Trial=FALSE)

## End(Not run)
```

---

FixedBinContIT

*Fits (univariate) fixed-effect models to assess surrogacy in the case where the true endpoint is binary and the surrogate endpoint is continuous (based on the Information-Theoretic framework)*

---

**Description**

The function `FixedBinContIT` uses the information-theoretic approach (Alonso & Molenberghs, 2007) to estimate trial- and individual-level surrogacy based on fixed-effect models when T is binary and S is continuous. The user can specify whether a (weighted or unweighted) full, semi-reduced, or reduced model should be fitted. See the **Details** section below.

**Usage**

```
FixedBinContIT(Dataset, Surr, True, Treat, Trial.ID, Pat.ID,
               Model=c("Full"), Weighted=TRUE, Min.Trial.Size=2, Alpha=.05,
               Number.Bootstraps=50, Seed=sample(1:1000, size=1))
```

**Arguments**

Dataset	A data.frame that should consist of one line per patient. Each line contains (at least) a surrogate value, a true endpoint value, a treatment indicator, a patient ID, and a trial ID.
Surr	The name of the variable in Dataset that contains the surrogate endpoint values.
True	The name of the variable in Dataset that contains the true endpoint values.
Treat	The name of the variable in Dataset that contains the treatment indicators. The treatment indicator should either be coded as 1 for the experimental group and -1 for the control group, or as 1 for the experimental group and 0 for the control group.
Trial.ID	The name of the variable in Dataset that contains the trial ID to which the patient belongs.
Pat.ID	The name of the variable in Dataset that contains the patient's ID.
Model	The type of model that should be fitted, i.e., Model=c("Full"), Model=c("Reduced"), or Model=c("SemiReduced"). See the <b>Details</b> section below. Default Model=c("Full").
Weighted	Logical. In practice it is often the case that different trials (or other clustering units) have different sample sizes. Univariate models are used to assess surrogacy in the information-theoretic approach, so it can be useful to adjust for heterogeneity in information content between the trial-specific contributions (particularly when trial-level surrogacy measures are of primary interest and when the heterogeneity in sample sizes is large). If Weighted=TRUE, weighted regression models are fitted. If Weighted=FALSE, unweighted regression analyses are conducted. See the <b>Details</b> section below. Default TRUE.
Min.Trial.Size	The minimum number of patients that a trial should contain to be included in the analysis. If the number of patients in a trial is smaller than the value specified by Min.Trial.Size, the data of the trial are excluded from the analysis. Default 2.
Alpha	The $\alpha$ -level that is used to determine the confidence intervals around $R_h^2$ and $R_{ht}^2$ . Default 0.05.
Number.Bootstraps	The standard errors and confidence intervals for $R_h^2$ and $R_{h.ind}^2$ are determined based on a bootstrap procedure. Number.Bootstraps specifies the number of bootstrap samples that are used. Default 50.
Seed	The seed to be used in the bootstrap procedure. Default <code>sample(1 : 1000, size = 1)</code> .

**Details***Individual-level surrogacy*

The following univariate generalised linear models are fitted:

$$g_T(E(T_{ij})) = \mu_{Ti} + \beta_i Z_{ij},$$

$$g_T(E(T_{ij}|S_{ij})) = \gamma_{0i} + \gamma_{1i} Z_{ij} + \gamma_{2i} S_{ij},$$

where  $i$  and  $j$  are the trial and subject indicators,  $g_T$  is an appropriate link function (i.e., a logit link for binary endpoints and an identity link for normally distributed continuous endpoints),  $S_{ij}$  and  $T_{ij}$  are the surrogate and true endpoint values of subject  $j$  in trial  $i$ , and  $Z_{ij}$  is the treatment indicator for subject  $j$  in trial  $i$ .  $\mu_{Ti}$  and  $\beta_i$  are the trial-specific intercepts and treatment-effects on the true endpoint in trial  $i$ .  $\gamma_{0i}$  and  $\gamma_{1i}$  are the trial-specific intercepts and treatment-effects on the true endpoint in trial  $i$  after accounting for the effect of the surrogate endpoint.

The  $-2$  log likelihood values of the previous models in each of the  $i$  trials (i.e.,  $L_{1i}$  and  $L_{2i}$ , respectively) are subsequently used to compute individual-level surrogacy based on the so-called Variance Reduction Factor (VFR; for details, see Alonso & Molenberghs, 2007):

$$R_h^2 = 1 - \frac{1}{N} \sum_i \exp\left(-\frac{L_{2i} - L_{1i}}{n_i}\right),$$

where  $N$  is the number of trials and  $n_i$  is the number of patients within trial  $i$ .

When it can be assumed (i) that the treatment-corrected association between the surrogate and the true endpoint is constant across trials, or (ii) when all data come from a single clinical trial (i.e., when  $N = 1$ ), the previous expression simplifies to:

$$R_{h.ind}^2 = 1 - \exp\left(-\frac{L_2 - L_1}{N}\right).$$

The upper bound does not reach to 1 when  $T$  is binary, i.e., its maximum is 0.75. Kent (1983) claims that 0.75 is a reasonable upper bound and thus  $R_{h.ind}^2$  can usually be interpreted without paying special consideration to the discreteness of  $T$ . Alternatively, to address the upper bound problem, a scaled version of the mutual information can be used when both  $S$  and  $T$  are binary (Joe, 1989):

$$R_{b.ind}^2 = \frac{I(T, S)}{\min[H(T), H(S)]},$$

where the entropy of  $T$  and  $S$  in the previous expression can be estimated using the log likelihood functions of the GLMs shown above.

#### *Trial-level surrogacy*

When a full or semi-reduced model is requested (by using the argument `Model=c("Full")` or `Model=c("SemiReduced")` in the function call), trial-level surrogacy is assessed by fitting the following univariate models:

$$S_{ij} = \mu_{Si} + \alpha_i Z_{ij} + \varepsilon_{Sij}, (1)$$

$$T_{ij} = \mu_{Ti} + \beta_i Z_{ij} + \varepsilon_{Tij}, (1)$$

where  $i$  and  $j$  are the trial and subject indicators,  $S_{ij}$  and  $T_{ij}$  are the surrogate and true endpoint values of subject  $j$  in trial  $i$ ,  $Z_{ij}$  is the treatment indicator for subject  $j$  in trial  $i$ ,  $\mu_{Si}$  and  $\mu_{Ti}$  are the fixed trial-specific intercepts for S and T, and  $\alpha_i$  and  $\beta_i$  are the fixed trial-specific treatment effects on S and T, respectively. The error terms  $\varepsilon_{Sij}$  and  $\varepsilon_{Tij}$  are assumed to be independent.

When a reduced model is requested by the user (by using the argument `Model=c("Reduced")` in the function call), the following univariate models are fitted:

$$S_{ij} = \mu_S + \alpha_i Z_{ij} + \varepsilon_{Sij}, (2)$$

$$T_{ij} = \mu_T + \beta_i Z_{ij} + \varepsilon_{Tij}, (2)$$

where  $\mu_S$  and  $\mu_T$  are the common intercepts for S and T. The other parameters are the same as defined above, and  $\varepsilon_{Sij}$  and  $\varepsilon_{Tij}$  are again assumed to be independent.

When the user requested a full model approach (by using the argument `Model=c("Full")`) in the function call, i.e., when models (1) were fitted), the following model is subsequently fitted:

$$\hat{\beta}_i = \lambda_0 + \lambda_1 \widehat{\mu_{Si}} + \lambda_2 \hat{\alpha}_i + \varepsilon_i, (3)$$

where the parameter estimates for  $\beta_i$ ,  $\mu_{Si}$ , and  $\alpha_i$  are based on models (1) (see above). When a weighted model is requested (using the argument `Weighted=TRUE` in the function call), model (3) is a weighted regression model (with weights based on the number of observations in trial  $i$ ). The  $-2$  log likelihood value of the (weighted or unweighted) model (3) ( $L_1$ ) is subsequently compared to the  $-2$  log likelihood value of an intercept-only model ( $\hat{\beta}_i = \lambda_3; L_0$ ), and  $R_{ht}^2$  is computed based on the Variance Reduction Factor (for details, see Alonso & Molenberghs, 2007):

$$R_{ht}^2 = 1 - \exp\left(-\frac{L_1 - L_0}{N}\right),$$

where  $N$  is the number of trials.

When a semi-reduced or reduced model is requested (by using the argument `Model=c("SemiReduced")` or `Model=c("Reduced")`) in the function call, the following model is fitted:

$$\hat{\beta}_i = \lambda_0 + \lambda_1 \hat{\alpha}_i + \varepsilon_i,$$

where the parameter estimates for  $\beta_i$  and  $\alpha_i$  are based on models (1) when a semi-reduced model is fitted or on models (2) when a reduced model is fitted. The  $-2$  log likelihood value of this (weighted or unweighted) model ( $L_1$ ) is subsequently compared to the  $-2$  log likelihood value of an intercept-only model ( $\hat{\beta}_i = \lambda_3; L_0$ ), and  $R_{ht}^2$  is computed based on the reduction in the likelihood (as described above).

## Value

An object of class `FixedBinContIT` with components,

`Data.Analyze` Prior to conducting the surrogacy analysis, data of patients who have a missing value for the surrogate and/or the true endpoint are excluded. In addition, the data of trials (i) in which only one type of the treatment was administered, and (ii) in which either the surrogate or the true endpoint was a constant (i.e., all patients within a trial had the same surrogate and/or true endpoint value) are excluded. In addition, the user can specify the minimum number of patients that a trial should contain in order to include the trial in the analysis. If the number of patients in a trial is smaller than the value specified by `Min.Trial.Size`, the data of the trial are excluded. `Data.Analyze` is the dataset on which the surrogacy analysis was conducted.

Obs.Per.Trial	A data.frame that contains the total number of patients per trial and the number of patients who were administered the control treatment and the experimental treatment in each of the trials (in Data.Analyze).
Trial.Spec.Results	A data.frame that contains the trial-specific intercepts and treatment effects for the surrogate and the true endpoints (when a full or semi-reduced model is requested), or the trial-specific treatment effects for the surrogate and the true endpoints (when a reduced model is requested).
R2ht	A data.frame that contains the trial-level surrogacy estimate and its confidence interval.
R2h.ind	A data.frame that contains the individual-level surrogacy estimate $R_{h.ind}^2$ (single-trial based estimate) and its confidence interval.
R2h	A data.frame that contains the individual-level surrogacy estimate $R_h^2$ (cluster-based estimate) and its confidence interval (bootstrap-based).
R2b.ind	A data.frame that contains the individual-level surrogacy estimate $R_{b.ind}^2$ (single-trial based estimate accounting for upper bound) and its confidence interval (based on a bootstrap).
R2h.Ind.By.Trial	A data.frame that contains individual-level surrogacy estimates $R_h^2$ (cluster-based estimate) and their confidence interval for each of the trials separately.

**Author(s)**

Wim Van der Elst, Ariel Alonso, & Geert Molenberghs

**References**

- Alonso, A, & Molenberghs, G. (2007). Surrogate marker evaluation from an information theory perspective. *Biometrics*, 63, 180-186.
- Joe, H. (1989). Relative entropy measures of multivariate dependence. *Journal of the American Statistical Association*, 84, 157-164.
- Kent, T. J. (1983). Information gain as a general measure of correlation. *Biometrika*, 70, 163-173.

**See Also**

[FixedBinBinIT](#), [FixedContBinIT](#), [plot Information-Theoretic BinComb](#)

**Examples**

```
## Not run: # Time consuming (>5sec) code part
# Generate data with continuous Surr and True
Sim.Data.MTS(N.Total=2000, N.Trial=100, R.Trial.Target=.8,
R.Indiv.Target=.8, Seed=123, Model="Full")

# Make T binary
Data.Observed.MTS$True_Bin <- Data.Observed.MTS$True
Data.Observed.MTS$True_Bin[Data.Observed.MTS$True>=0] <- 1
Data.Observed.MTS$True_Bin[Data.Observed.MTS$True<0] <- 0
```

```

# Analyze data
Fit <- FixedBinContIT(Dataset = Data.Observed.MTS, Surr = Surr,
  True = True_Bin, Treat = Treat, Trial.ID = Trial.ID, Pat.ID = Pat.ID,
  Model = "Full", Number.Bootstraps=50)

# Examine results
summary(Fit)
plot(Fit, Trial.Level = FALSE, Individ.Level.By.Trial=TRUE)
plot(Fit, Trial.Level = TRUE, Individ.Level.By.Trial=FALSE)

## End(Not run)

```

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FixedContBinIT	<i>Fits (univariate) fixed-effect models to assess surrogacy in the case where the true endpoint is continuous and the surrogate endpoint is binary (based on the Information-Theoretic framework)</i>
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### Description

The function FixedContBinIT uses the information-theoretic approach (Alonso & Molenberghs, 2007) to estimate trial- and individual-level surrogacy based on fixed-effect models when T is continuous normally distributed and S is binary. The user can specify whether a (weighted or unweighted) full, semi-reduced, or reduced model should be fitted. See the **Details** section below.

### Usage

```

FixedContBinIT(Dataset, Surr, True, Treat, Trial.ID, Pat.ID,
  Model=c("Full"), Weighted=TRUE, Min.Trial.Size=2, Alpha=.05,
  Number.Bootstraps=50, Seed=sample(1:1000, size=1))

```

### Arguments

Dataset	A data.frame that should consist of one line per patient. Each line contains (at least) a surrogate value, a true endpoint value, a treatment indicator, a patient ID, and a trial ID.
Surr	The name of the variable in Dataset that contains the surrogate endpoint values.
True	The name of the variable in Dataset that contains the true endpoint values.
Treat	The name of the variable in Dataset that contains the treatment indicators. The treatment indicator should either be coded as 1 for the experimental group and -1 for the control group, or as 1 for the experimental group and 0 for the control group.
Trial.ID	The name of the variable in Dataset that contains the trial ID to which the patient belongs.
Pat.ID	The name of the variable in Dataset that contains the patient's ID.
Model	The type of model that should be fitted, i.e., Model=c("Full"), Model=c("Reduced"), or Model=c("SemiReduced"). See the <b>Details</b> section below. Default Model=c("Full").

Weighted	Logical. In practice it is often the case that different trials (or other clustering units) have different sample sizes. Univariate models are used to assess surrogacy in the information-theoretic approach, so it can be useful to adjust for heterogeneity in information content between the trial-specific contributions (particularly when trial-level surrogacy measures are of primary interest and when the heterogeneity in sample sizes is large). If <code>Weighted=TRUE</code> , weighted regression models are fitted. If <code>Weighted=FALSE</code> , unweighted regression analyses are conducted. See the <b>Details</b> section below. Default <code>TRUE</code> .
Min.Trial.Size	The minimum number of patients that a trial should contain to be included in the analysis. If the number of patients in a trial is smaller than the value specified by <code>Min.Trial.Size</code> , the data of the trial are excluded from the analysis. Default 2.
Alpha	The $\alpha$ -level that is used to determine the confidence intervals around $R_h^2$ and $R_{ht}^2$ . Default 0.05.
Number.Bootstraps	The standard error and confidence interval for $R_{h.ind}^2$ is determined based on a bootstrap procedure. <code>Number.Bootstraps</code> specifies the number of bootstrap samples that are used. Default 50.
Seed	The seed to be used in the bootstrap procedure. Default <code>sample(1 : 1000, size = 1)</code> .

## Details

### Individual-level surrogacy

The following univariate generalised linear models are fitted:

$$g_T(E(T_{ij})) = \mu_{Ti} + \beta_i Z_{ij},$$

$$g_T(E(T_{ij}|S_{ij})) = \gamma_{0i} + \gamma_{1i} Z_{ij} + \gamma_{2i} S_{ij},$$

where  $i$  and  $j$  are the trial and subject indicators,  $g_T$  is an appropriate link function (i.e., a logit link for binary endpoints and an identity link for normally distributed continuous endpoints),  $S_{ij}$  and  $T_{ij}$  are the surrogate and true endpoint values of subject  $j$  in trial  $i$ , and  $Z_{ij}$  is the treatment indicator for subject  $j$  in trial  $i$ .  $\mu_{Ti}$  and  $\beta_i$  are the trial-specific intercepts and treatment-effects on the true endpoint in trial  $i$ .  $\gamma_{0i}$  and  $\gamma_{1i}$  are the trial-specific intercepts and treatment-effects on the true endpoint in trial  $i$  after accounting for the effect of the surrogate endpoint.

The  $-2$  log likelihood values of the previous models in each of the  $i$  trials (i.e.,  $L_{1i}$  and  $L_{2i}$ , respectively) are subsequently used to compute individual-level surrogacy based on the so-called Variance Reduction Factor (VFR; for details, see Alonso & Molenberghs, 2007):

$$R_h^2 = 1 - \frac{1}{N} \sum_i \exp\left(-\frac{L_{2i} - L_{1i}}{n_i}\right),$$

where  $N$  is the number of trials and  $n_i$  is the number of patients within trial  $i$ .

When it can be assumed (i) that the treatment-corrected association between the surrogate and the true endpoint is constant across trials, or (ii) when all data come from a single clinical trial (i.e., when  $N = 1$ ), the previous expression simplifies to:



$$R_{h.ind}^2 = 1 - \exp\left(-\frac{L_2 - L_1}{N}\right).$$

#### Trial-level surrogacy

When a full or semi-reduced model is requested (by using the argument `Model=c("Full")` or `Model=c("SemiReduced")` in the function call), trial-level surrogacy is assessed by fitting the following univariate models:

$$S_{ij} = \mu_{Si} + \alpha_i Z_{ij} + \varepsilon_{Sij}, (1)$$

$$T_{ij} = \mu_{Ti} + \beta_i Z_{ij} + \varepsilon_{Tij}, (1)$$

where  $i$  and  $j$  are the trial and subject indicators,  $S_{ij}$  and  $T_{ij}$  are the surrogate and true endpoint values of subject  $j$  in trial  $i$ ,  $Z_{ij}$  is the treatment indicator for subject  $j$  in trial  $i$ ,  $\mu_{Si}$  and  $\mu_{Ti}$  are the fixed trial-specific intercepts for S and T, and  $\alpha_i$  and  $\beta_i$  are the fixed trial-specific treatment effects on S and T, respectively. The error terms  $\varepsilon_{Sij}$  and  $\varepsilon_{Tij}$  are assumed to be independent.

When a reduced model is requested by the user (by using the argument `Model=c("Reduced")` in the function call), the following univariate models are fitted:

$$S_{ij} = \mu_S + \alpha_i Z_{ij} + \varepsilon_{Sij}, (2)$$

$$T_{ij} = \mu_T + \beta_i Z_{ij} + \varepsilon_{Tij}, (2)$$

where  $\mu_S$  and  $\mu_T$  are the common intercepts for S and T. The other parameters are the same as defined above, and  $\varepsilon_{Sij}$  and  $\varepsilon_{Tij}$  are again assumed to be independent.

When the user requested a full model approach (by using the argument `Model=c("Full")` in the function call, i.e., when models (1) were fitted), the following model is subsequently fitted:

$$\hat{\beta}_i = \lambda_0 + \lambda_1 \widehat{\mu_{Si}} + \lambda_2 \hat{\alpha}_i + \varepsilon_i, (3)$$

where the parameter estimates for  $\beta_i$ ,  $\mu_{Si}$ , and  $\alpha_i$  are based on models (1) (see above). When a weighted model is requested (using the argument `Weighted=TRUE` in the function call), model (3) is a weighted regression model (with weights based on the number of observations in trial  $i$ ). The  $-2$  log likelihood value of the (weighted or unweighted) model (3) ( $L_1$ ) is subsequently compared to the  $-2$  log likelihood value of an intercept-only model ( $\hat{\beta}_i = \lambda_3; L_0$ ), and  $R_{ht}^2$  is computed based on the Variance Reduction Factor (for details, see Alonso & Molenberghs, 2007):

$$R_{ht}^2 = 1 - \exp\left(-\frac{L_1 - L_0}{N}\right),$$

where  $N$  is the number of trials.

When a semi-reduced or reduced model is requested (by using the argument `Model=c("SemiReduced")` or `Model=c("Reduced")` in the function call), the following model is fitted:

$$\hat{\beta}_i = \lambda_0 + \lambda_1 \hat{\alpha}_i + \varepsilon_i,$$

where the parameter estimates for  $\beta_i$  and  $\alpha_i$  are based on models (1) when a semi-reduced model is fitted or on models (2) when a reduced model is fitted. The  $-2$  log likelihood value of this (weighted or unweighted) model ( $L_1$ ) is subsequently compared to the  $-2$  log likelihood value of an intercept-only model ( $\hat{\beta}_i = \lambda_3; L_0$ ), and  $R_{ht}^2$  is computed based on the reduction in the likelihood (as described above).

**Value**

An object of class FixedContBinIT with components,

Data.Analyze	Prior to conducting the surrogacy analysis, data of patients who have a missing value for the surrogate and/or the true endpoint are excluded. In addition, the data of trials (i) in which only one type of the treatment was administered, and (ii) in which either the surrogate or the true endpoint was a constant (i.e., all patients within a trial had the same surrogate and/or true endpoint value) are excluded. In addition, the user can specify the minimum number of patients that a trial should contain in order to include the trial in the analysis. If the number of patients in a trial is smaller than the value specified by <code>Min.Trial.Size</code> , the data of the trial are excluded. <code>Data.Analyze</code> is the dataset on which the surrogacy analysis was conducted.
Obs.Per.Trial	A <code>data.frame</code> that contains the total number of patients per trial and the number of patients who were administered the control treatment and the experimental treatment in each of the trials (in <code>Data.Analyze</code> ).
Trial.Spec.Results	A <code>data.frame</code> that contains the trial-specific intercepts and treatment effects for the surrogate and the true endpoints (when a full or semi-reduced model is requested), or the trial-specific treatment effects for the surrogate and the true endpoints (when a reduced model is requested).
R2ht	A <code>data.frame</code> that contains the trial-level surrogacy estimate and its confidence interval.
R2h	A <code>data.frame</code> that contains the individual-level surrogacy estimate $R_h^2$ (cluster-based estimate) and its confidence interval.
R2h.ind	A <code>data.frame</code> that contains the individual-level surrogacy estimate $R_{h.ind}^2$ (single-trial based estimate) and its confidence interval based on a bootstrap. The $R_{h.ind}^2$ shown is the mean of the bootstrapped values.
R2h.Ind.By.Trial	A <code>data.frame</code> that contains individual-level surrogacy estimates $R_h^2$ (cluster-based estimate) and their confidence interval for each of the trials separately.

**Author(s)**

Wim Van der Elst, Ariel Alonso, & Geert Molenberghs

**References**

Alonso, A, & Molenberghs, G. (2007). Surrogate marker evaluation from an information theory perspective. *Biometrics*, 63, 180-186.

**See Also**

[FixedBinBinIT](#), [FixedBinContIT](#), [plot Information-Theoretic BinComb](#)

## Examples

```
## Not run: # Time consuming (>5sec) code part
# Generate data with continuous Surr and True
Sim.Data.MTS(N.Total=2000, N.Trial=100, R.Trial.Target=.8,
R.Indiv.Target=.8, Seed=123, Model="Full")

# Make S binary
Data.Observed.MTS$Surr_Bin <- Data.Observed.MTS$Surr
Data.Observed.MTS$Surr_Bin[Data.Observed.MTS$Surr>=0] <- 1
Data.Observed.MTS$Surr_Bin[Data.Observed.MTS$Surr<0] <- 0

# Analyze data
Fit <- FixedContBinIT(Dataset = Data.Observed.MTS, Surr = Surr_Bin,
True = True, Treat = Treat, Trial.ID = Trial.ID, Pat.ID = Pat.ID,
Model = "Full", Number.Bootstraps=50)

# Examine results
summary(Fit)
plot(Fit, Trial.Level = FALSE, Indiv.Level.By.Trial=TRUE)
plot(Fit, Trial.Level = TRUE, Indiv.Level.By.Trial=FALSE)

## End(Not run)
```

---

FixedContContIT	<i>Fits (univariate) fixed-effect models to assess surrogacy in the continuous-continuous case based on the Information-Theoretic framework</i>
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## Description

The function `FixedContContIT` uses the information-theoretic approach (Alonso & Molenberghs, 2007) to estimate trial- and individual-level surrogacy based on fixed-effect models when both `S` and `T` are continuous variables. The user can specify whether a (weighted or unweighted) full, semi-reduced, or reduced model should be fitted. See the **Details** section below.

## Usage

```
FixedContContIT(Dataset, Surr, True, Treat, Trial.ID, Pat.ID,
Model=c("Full"), Weighted=TRUE, Min.Trial.Size=2,
Alpha=.05, Number.Bootstraps=500, Seed=sample(1:1000, size=1))
```

## Arguments

<code>Dataset</code>	A data.frame that should consist of one line per patient. Each line contains (at least) a surrogate value, a true endpoint value, a treatment indicator, a patient ID, and a trial ID.
<code>Surr</code>	The name of the variable in <code>Dataset</code> that contains the surrogate endpoint values.
<code>True</code>	The name of the variable in <code>Dataset</code> that contains the true endpoint values.

Treat	The name of the variable in Dataset that contains the treatment indicators. The treatment indicator should either be coded as 1 for the experimental group and $-1$ for the control group, or as 1 for the experimental group and 0 for the control group.
Trial.ID	The name of the variable in Dataset that contains the trial ID to which the patient belongs.
Pat.ID	The name of the variable in Dataset that contains the patient's ID.
Model	The type of model that should be fitted, i.e., Model=c("Full"), Model=c("Reduced"), or Model=c("SemiReduced"). See the <b>Details</b> section below. Default Model=c("Full").
Weighted	Logical. In practice it is often the case that different trials (or other clustering units) have different sample sizes. Univariate models are used to assess surrogacy in the information-theoretic approach, so it can be useful to adjust for heterogeneity in information content between the trial-specific contributions (particularly when trial-level surrogacy measures are of primary interest and when the heterogeneity in sample sizes is large). If Weighted=TRUE, weighted regression models are fitted. If Weighted=FALSE, unweighted regression analyses are conducted. See the <b>Details</b> section below. Default TRUE.
Min.Trial.Size	The minimum number of patients that a trial should contain to be included in the analysis. If the number of patients in a trial is smaller than the value specified by Min.Trial.Size, the data of the trial are excluded from the analysis. Default 2.
Alpha	The $\alpha$ -level that is used to determine the confidence intervals around $R_h^2$ and $R_{ht}^2$ . Default 0.05.
Number.Bootstraps	The standard error and confidence interval for $R_h^2$ is determined based on a bootstrap procedure. Number.Bootstraps specifies the number of bootstrap samples that are used. Default 500.
Seed	The seed to be used in the bootstrap procedure. Default <code>sample(1 : 1000, size = 1)</code> .

## Details

### Individual-level surrogacy

The following univariate generalised linear models are fitted:

$$g_T(E(T_{ij})) = \mu_{Ti} + \beta_i Z_{ij},$$

$$g_T(E(T_{ij}|S_{ij})) = \gamma_{0i} + \gamma_{1i} Z_{ij} + \gamma_{2i} S_{ij},$$

where  $i$  and  $j$  are the trial and subject indicators,  $g_T$  is an appropriate link function (i.e., an identity link when a continuous true endpoint is considered),  $S_{ij}$  and  $T_{ij}$  are the surrogate and true endpoint values of subject  $j$  in trial  $i$ , and  $Z_{ij}$  is the treatment indicator for subject  $j$  in trial  $i$ .  $\mu_{Ti}$  and  $\beta_i$  are the trial-specific intercepts and treatment-effects on the true endpoint in trial  $i$ .  $\gamma_{0i}$  and  $\gamma_{1i}$  are the trial-specific intercepts and treatment-effects on the true endpoint in trial  $i$  after accounting for the effect of the surrogate endpoint.

The  $-2$  log likelihood values of the previous models in each of the  $i$  trials (i.e.,  $L_{1i}$  and  $L_{2i}$ , respectively) are subsequently used to compute individual-level surrogacy based on the so-called Variance Reduction Factor (VFR; for details, see Alonso & Molenberghs, 2007):

$$R_{h.ind}^2 = 1 - \frac{1}{N} \sum_i \exp\left(-\frac{L_{2i} - L_{1i}}{n_i}\right),$$

where  $N$  is the number of trials and  $n_i$  is the number of patients within trial  $i$ .

When it can be assumed (i) that the treatment-corrected association between the surrogate and the true endpoint is constant across trials, or (ii) when all data come from a single clinical trial (i.e., when  $N = 1$ ), the previous expression simplifies to:

$$R_{h.ind.clust}^2 = 1 - \exp\left(-\frac{L_2 - L_1}{N}\right).$$

#### *Trial-level surrogacy*

When a full or semi-reduced model is requested (by using the argument `Model=c("Full")` or `Model=c("SemiReduced")` in the function call), trial-level surrogacy is assessed by fitting the following univariate models:

$$S_{ij} = \mu_{Si} + \alpha_i Z_{ij} + \varepsilon_{Sij}, (1)$$

$$T_{ij} = \mu_{Ti} + \beta_i Z_{ij} + \varepsilon_{Tij}, (1)$$

where  $i$  and  $j$  are the trial and subject indicators,  $S_{ij}$  and  $T_{ij}$  are the surrogate and true endpoint values of subject  $j$  in trial  $i$ ,  $Z_{ij}$  is the treatment indicator for subject  $j$  in trial  $i$ ,  $\mu_{Si}$  and  $\mu_{Ti}$  are the fixed trial-specific intercepts for S and T, and  $\alpha_i$  and  $\beta_i$  are the fixed trial-specific treatment effects on S and T, respectively. The error terms  $\varepsilon_{Sij}$  and  $\varepsilon_{Tij}$  are assumed to be independent.

When a reduced model is requested by the user (by using the argument `Model=c("Reduced")` in the function call), the following univariate models are fitted:

$$S_{ij} = \mu_S + \alpha_i Z_{ij} + \varepsilon_{Sij}, (2)$$

$$T_{ij} = \mu_T + \beta_i Z_{ij} + \varepsilon_{Tij}, (2)$$

where  $\mu_S$  and  $\mu_T$  are the common intercepts for S and T. The other parameters are the same as defined above, and  $\varepsilon_{Sij}$  and  $\varepsilon_{Tij}$  are again assumed to be independent.

When the user requested a full model approach (by using the argument `Model=c("Full")` in the function call, i.e., when models (1) were fitted), the following model is subsequently fitted:

$$\widehat{\beta}_i = \lambda_0 + \lambda_1 \widehat{\mu_{Si}} + \lambda_2 \widehat{\alpha}_i + \varepsilon_i, (3)$$

where the parameter estimates for  $\beta_i$ ,  $\mu_{Si}$ , and  $\alpha_i$  are based on models (1) (see above). When a weighted model is requested (using the argument `Weighted=TRUE` in the function call), model (3) is a weighted regression model (with weights based on the number of observations in trial  $i$ ). The  $-2$  log likelihood value of the (weighted or unweighted) model (3) ( $L_1$ ) is subsequently compared to the  $-2$  log likelihood value of an intercept-only model ( $\widehat{\beta}_i = \lambda_3; L_0$ ), and  $R_{ht}^2$  is computed based on the Variance Reduction Factor (for details, see Alonso & Molenberghs, 2007):

$$R_{ht}^2 = 1 - \exp\left(-\frac{L_1 - L_0}{N}\right),$$

where  $N$  is the number of trials.

When a semi-reduced or reduced model is requested (by using the argument `Model=c("SemiReduced")` or `Model=c("Reduced")` in the function call), the following model is fitted:

$$\hat{\beta}_i = \lambda_0 + \lambda_1 \hat{\alpha}_i + \varepsilon_i,$$

where the parameter estimates for  $\beta_i$  and  $\alpha_i$  are based on models (1) when a semi-reduced model is fitted or on models (2) when a reduced model is fitted. The  $-2 \log$  likelihood value of this (weighted or unweighted) model ( $L_1$ ) is subsequently compared to the  $-2 \log$  likelihood value of an intercept-only model ( $\hat{\beta}_i = \lambda_3; L_0$ ), and  $R_{ht}^2$  is computed based on the reduction in the likelihood (as described above).

## Value

An object of class `FixedContContIT` with components,

<code>Data.Analyze</code>	Prior to conducting the surrogacy analysis, data of patients who have a missing value for the surrogate and/or the true endpoint are excluded. In addition, the data of trials (i) in which only one type of the treatment was administered, and (ii) in which either the surrogate or the true endpoint was a constant (i.e., all patients within a trial had the same surrogate and/or true endpoint value) are excluded. In addition, the user can specify the minimum number of patients that a trial should contain in order to include the trial in the analysis. If the number of patients in a trial is smaller than the value specified by <code>Min.Trial.Size</code> , the data of the trial are excluded. <code>Data.Analyze</code> is the dataset on which the surrogacy analysis was conducted.
<code>Obs.Per.Trial</code>	A <code>data.frame</code> that contains the total number of patients per trial and the number of patients who were administered the control treatment and the experimental treatment in each of the trials (in <code>Data.Analyze</code> ).
<code>Trial.Spec.Results</code>	A <code>data.frame</code> that contains the trial-specific intercepts and treatment effects for the surrogate and the true endpoints (when a full or semi-reduced model is requested), or the trial-specific treatment effects for the surrogate and the true endpoints (when a reduced model is requested).
<code>R2ht</code>	A <code>data.frame</code> that contains the trial-level surrogacy estimate and its confidence interval.
<code>R2h.ind.clust</code>	A <code>data.frame</code> that contains the individual-level surrogacy estimate and its confidence interval.
<code>R2h.ind</code>	A <code>data.frame</code> that contains the individual-level surrogacy estimate and its confidence interval under the assumption that the treatment-corrected association between the surrogate and the true endpoints is constant across trials or when all data come from a single clinical trial.

Boot.CI	A data.frame that contains the bootstrapped R2h.Single values.
Cor.Endpoints	A data.frame that contains the correlations between the surrogate and the true endpoint in the control treatment group (i.e., $\rho_{T0S0}$ ) and in the experimental treatment group (i.e., $\rho_{T1S1}$ ), their standard errors and their confidence intervals.
Residuals	A data.frame that contains the residuals for the surrogate and true endpoints ( $\varepsilon_{Sij}$ and $\varepsilon_{Tij}$ ) that are obtained when models (1) or models (2) are fitted (see the <b>Details</b> section above).

### Author(s)

Wim Van der Elst, Ariel Alonso, & Geert Molenberghs

### References

Alonso, A, & Molenberghs, G. (2007). Surrogate marker evaluation from an information theory perspective. *Biometrics*, 63, 180-186.

### See Also

[MixedContContIT](#), [FixedContBinIT](#), [FixedBinContIT](#), [FixedBinBinIT](#), [plot Information-Theoretic](#)

### Examples

```
# Example 1
# Based on the ARMD data

data(ARMD)
# Assess surrogacy based on a full fixed-effect model
# in the information-theoretic framework:
Sur <- FixedContContIT(Dataset=ARMD, Surr=Diff24, True=Diff52, Treat=Treat, Trial.ID=Center,
Pat.ID=Id, Model="Full", Number.Bootstraps=50)
# Obtain a summary of the results:
summary(Sur)

## Not run: #time consuming code
# Example 2
# Conduct an analysis based on a simulated dataset with 2000 patients, 100 trials,
# and Rindiv=Rtrial=.8

# Simulate the data:
Sim.Data.MTS(N.Total=2000, N.Trial=100, R.Trial.Target=.8, R.Indiv.Target=.8,
Seed=123, Model="Full")
# Assess surrogacy based on a full fixed-effect model
# in the information-theoretic framework:
Sur2 <- FixedContContIT(Dataset=Data.Observed.MTS, Surr=Surr, True=True, Treat=Treat,
Trial.ID=Trial.ID, Pat.ID=Pat.ID, Model="Full", Number.Bootstraps=50)

# Show a summary of the results:
summary(Sur2)
## End(Not run)
```

---

FixedDiscrDiscrIT	<i>Investigates surrogacy for binary or ordinal outcomes using the Information Theoretic framework</i>
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---

### Description

The function `FixedDiscrDiscrIT` uses the information theoretic approach (Alonso and Molenberghs 2007) to estimate trial and individual level surrogacy based on fixed-effects models when the surrogate is binary and the true outcome is ordinal, the converse case or when both outcomes are ordinal (the user must specify which form the data is in). The user can specify whether a weighted or unweighted analysis is required at the trial level. The penalized likelihood approach of Firth (1993) is applied to resolve issues of separation in discrete outcomes for particular trials. Requires packages `OrdinalLogisticBiplot` and `logistf`.

### Usage

```
FixedDiscrDiscrIT(Dataset, Surr, True, Treat, Trial.ID,
  Weighted = TRUE, Setting = c("binord"))
```

### Arguments

Dataset	A data.frame that should consist of one line per patient. Each line contains (at least) a surrogate value, a true outcome value, a treatment indicator and a trial ID.
Surr	The name of the variable in Dataset that contains the surrogate outcome values.
True	The name of the variable in Dataset that contains the true outcome values.
Treat	The name of the in Dataset that contains the treatment group values, 0/1 or -1/+1 are recommended.
Trial.ID	The name of the variable in Dataset that contains the trial ID to which the patient belongs.
Weighted	Logical. In practice it is often the case that different trials (or other clustering units) have different sample sizes. Univariate models are used to assess surrogacy in the information-theoretic approach, so it can be useful to adjust for heterogeneity in information content between the trial-specific contributions (particularly when trial-level surrogacy measures are of primary interest and when the heterogeneity in sample sizes is large). If <code>Weighted=TRUE</code> , weighted regression models are fitted. If <code>Weighted=FALSE</code> , unweighted regression analyses are conducted. See the <b>Details</b> section below. Default <code>TRUE</code> .
Setting	Specifies whether an ordinal or binary surrogate or true outcome are present in Dataset. <code>Setting=c("binord")</code> for a binary surrogate and ordinal true outcome, <code>Setting=c("ordbin")</code> for an ordinal surrogate and binary true outcome and <code>Setting=c("ordord")</code> where both outcomes are ordinal.



## Details

### Individual level surrogacy

The following univariate logistic regression models are fitted when Setting=c("ordbin"):

$$\text{logit}(P(T_{ij} = 1)) = \mu_{T_i} + \beta_i Z_{ij}, (1)$$

$$\text{logit}(P(T_{ij} = 1 | S_{ij} = s)) = \gamma_{0i} + \gamma_{1i} Z_{ij} + \gamma_{2i} S_{ij}, (1)$$

where:  $i$  and  $j$  are the trial and subject indicators;  $S_{ij}$  and  $T_{ij}$  are the surrogate and true outcome values of subject  $j$  in trial  $i$ ; and  $Z_{ij}$  is the treatment indicator for subject  $j$  in trial  $i$ ;  $\mu_{T_i}$  and  $\beta_i$  are the trial-specific intercepts and treatment-effects on the true endpoint in trial  $i$ ; and  $\gamma_{0i}$  and  $\gamma_{1i}$  are the trial-specific intercepts and treatment-effects on the true endpoint in trial  $i$  after accounting for the effect of the surrogate endpoint. The  $-2$  log likelihood values of the previous models in each of the  $i$  trials (i.e.,  $L_{1i}$  and  $L_{2i}$ , respectively) are subsequently used to compute individual-level surrogacy based on the so-called Likelihood Reduction Factor (LRF; for details, see Alonso & Molenberghs, 2006):

$$R_h^2 = 1 - \frac{1}{N} \sum_i \exp\left(-\frac{L_{2i} - L_{1i}}{n_i}\right),$$

where  $N$  is the number of trials and  $n_i$  is the number of patients within trial  $i$ .

At the individual level in the discrete case  $R_h^2$  is bounded above by a number strictly less than one and is re-scaled (see Alonso & Molenberghs (2007)):

$$\widehat{R}_h^2 = \frac{R_h^2}{1 - e^{-2L_0}},$$

where  $L_0$  is the log-likelihood of the intercept only model of the true outcome ( $\text{logit}(P(T_{ij} = 1) = \gamma_3$ ).

In the case of Setting=c("binord") or Setting=c("ordord") proportional odds models in (1) are used to accommodate the ordinal true response outcome, in all other respects the calculation of  $R_h^2$  would proceed in the same manner.

### Trial-level surrogacy

When Setting=c("ordbin") trial-level surrogacy is assessed by fitting the following univariate logistic regression and proportional odds models for the ordinal surrogate and binary true response variables regressed on treatment for each trial  $i$ :

$$\text{logit}(P(S_{ij} \leq W)) = \mu_{S_{wi}} + \alpha_i Z_{ij}, (2)$$

$$\text{logit}(P(T_{ij} = 1)) = \mu_{T_i} + \beta_i Z_{ij}, (2)$$

where:  $i$  and  $j$  are the trial and subject indicators;  $S_{ij}$  and  $T_{ij}$  are the surrogate and true outcome values of subject  $j$  in trial  $i$ ;  $Z_{ij}$  is the treatment indicator for subject  $j$  in trial  $i$ ;  $\mu_{S_{wi}}$  are the trial-specific intercept values for each cut point  $w$ , where  $w = 1, \dots, W - 1$ , of the ordinal surrogate outcome;  $\mu_{T_i}$  are the fixed trial-specific intercepts for T; and  $\alpha_i$  and  $\beta_i$  are the fixed trial-specific treatment effects on S and T, respectively. The mean trial-specific intercepts for the surrogate are calculated,  $\bar{\mu}_{S_{wi}}$ . The following model is subsequently fitted:

$$\widehat{\beta}_i = \lambda_0 + \lambda_1 \widehat{\mu}_{S_{wi}} + \lambda_2 \widehat{\alpha}_i + \varepsilon_i, (3)$$

where the parameter estimates for  $\beta_i$ ,  $\bar{\mu}_{S_{wi}}$ , and  $\alpha_i$  are based on models (2) (see above). When a weighted model is requested (using the argument `Weighted=TRUE` in the function call), model (2) is a weighted regression model (with weights based on the number of observations in trial  $i$ ). The  $-2$  log likelihood value of the (weighted or unweighted) model (2) ( $L_1$ ) is subsequently compared to the  $-2$  log likelihood value of an intercept-only model ( $\hat{\beta}_i = \lambda_3; L_0$ ), and  $R_{ht}^2$  is computed based on the Likelihood Reduction Factor (for details, see Alonso & Molenberghs, 2006):

$$R_{ht}^2 = 1 - \exp\left(-\frac{L_1 - L_0}{N}\right),$$

where  $N$  is the number of trials.

When separation (the presence of zero cells) occurs in the cross tabs of treatment and the true or surrogate outcome for a particular trial in models (2) extreme bias can occur in  $R_{ht}^2$ . Under separation there are no unique maximum likelihood for parameters  $\beta_i$ ,  $\bar{\mu}_{S_{wi}}$  and  $\alpha_i$ , in (2), for the affected trial  $i$ . This typically leads to extreme bias in the estimation of these parameters and hence outlying influential points in model (3), bias in  $R_{ht}^2$  inevitably follows.

To resolve the issue of separation the penalized likelihood approach of Firth (1993) is applied. This approach adds an asymptotically negligible component to the score function to allow unbiased estimation of  $\beta_i$ ,  $\bar{\mu}_{S_{wi}}$ , and  $\alpha_i$  and in turn  $R_{ht}^2$ . The penalized likelihood R function `logitf` from the package of the same name is applied in the case of binary separation (Heinze and Schemper, 2002). The function `ordlogistf` from the package `OrdinalLogisticBioplot` is applied in the case of ordinal separation (Hern'andez, 2013). All instances of separation are reported.

In the case of `Setting=c("binord")` or `Setting=c("ordord")` the appropriate models (either logistic regression or a proportional odds models) are fitted in (2) to accommodate the form (either binary or ordinal) of the true or surrogate response variable. The rest of the analysis would proceed in a similar manner as that described above.

## Value

An object of class `FixedDiscrDiscrIT` with components,

`Trial.Spec.Results`

A `data.frame` that contains the trial-specific intercepts and treatment effects for the surrogate and the true endpoints. Also, the number of observations per trial; whether the trial was able to be included in the analysis for both  $R_h^2$  and  $R_{ht}^2$ ; whether separation occurred and hence the penalized likelihood approach used for the surrogate or true outcome.

`R2ht`

A `data.frame` that contains the trial-level surrogacy estimate and its confidence interval.

`R2h`

A `data.frame` that contains the individual-level surrogacy estimate and its confidence interval.

## Author(s)

Hannah M. Ensor & Christopher J. Weir

## References

- Alonso, A, & Molenberghs, G. (2007). Surrogate marker evaluation from an information theory perspective. *Biometrics*, *63*, 180-186.
- Alonso, A, & Molenberghs, G., Geys, H., Buyse, M. & Vangeneugden, T. (2006). A unifying approach for surrogate marker validation based on Prentice's criteria. *Statistics in medicine*, *25*, 205-221.
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- Heinze, G. & Schemper, M. 2002. A solution to the problem of separation in logistic regression. *Statistics in medicine*, *21*, 2409-2419.
- Hernandez, J. C. V.-V. O., J. L. 2013. OrdinalLogisticBiplot: Biplot representations of ordinal variables. R.

## See Also

[FixedContContIT](#), [plot Information-Theoretic](#), [logistf](#)

## Examples

```
## Not run: # Time consuming (>5sec) code part
# Example 1
# Conduct an analysis based on a simulated dataset with 2000 patients, 100 trials,
# and Rindiv=Rtrial=.8

# Simulate the data:
Sim.Data.MTS(N.Total=2000, N.Trial=100, R.Trial.Target=.8, R.Indiv.Target=.8,
Seed=123, Model="Full")

# create a binary true and ordinal surrogate outcome
Data.Observed.MTS$True<-findInterval(Data.Observed.MTS$True,
c(quantile(Data.Observed.MTS$True,0.5)))
Data.Observed.MTS$Surr<-findInterval(Data.Observed.MTS$Surr,
c(quantile(Data.Observed.MTS$Surr,0.333),quantile(Data.Observed.MTS$Surr,0.666)))

# Assess surrogacy based on a full fixed-effect model
# in the information-theoretic framework for a binary surrogate and ordinal true outcome:
SurEval <- FixedDiscrDiscrIT(Dataset=Data.Observed.MTS, Surr=Surr, True=True, Treat=Treat,
Trial.ID=Trial.ID, Setting="ordbin")

# Show a summary of the results:
summary(SurEval)
SurEval$Trial.Spec.Results
SurEval$R2h
SurEval$R2ht

## End(Not run)
```

---

ICA.BinBin	<i>Assess surrogacy in the causal-inference single-trial setting in the binary-binary case</i>
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---

### Description

The function `ICA.BinBin` quantifies surrogacy in the single-trial causal-inference framework (individual causal association and causal concordance) when both the surrogate and the true endpoints are binary outcomes. See **Details** below.

### Usage

```
ICA.BinBin(pi1_1_, pi1_0_, pi_1_1, pi_1_0, pi0_1_, pi_0_1,
Monotonicity=c("General"), Sum_Pi_f = seq(from=0.01, to=0.99, by=.01),
M=10000, Volume.Perc=0, Seed=sample(1:100000, size=1))
```

### Arguments

<code>pi1_1_</code>	A scalar or vector that contains values for $P(T = 1, S = 1 Z = 0)$ , i.e., the probability that $S = T = 1$ when under treatment $Z = 0$ . A vector is specified to account for uncertainty, i.e., rather than keeping $P(T = 1, S = 1 Z = 0)$ fixed at one estimated value, a distribution can be specified (see <b>examples</b> below) from which a value is drawn in each run.
<code>pi1_0_</code>	A scalar or vector that contains values for $P(T = 1, S = 0 Z = 0)$ .
<code>pi_1_1</code>	A scalar or vector that contains values for $P(T = 1, S = 1 Z = 1)$ .
<code>pi_1_0</code>	A scalar or vector that contains values for $P(T = 1, S = 0 Z = 1)$ .
<code>pi0_1_</code>	A scalar or vector that contains values for $P(T = 0, S = 1 Z = 0)$ .
<code>pi_0_1</code>	A scalar or vector that contains values for $P(T = 0, S = 1 Z = 1)$ .
<code>Monotonicity</code>	Specifies which assumptions regarding monotonicity should be made: <code>Monotonicity=c("General")</code> , <code>Monotonicity=c("No")</code> , <code>Monotonicity=c("True.Endp")</code> , <code>Monotonicity=c("Surr.Endp")</code> , or <code>Monotonicity=c("Surr.True.Endp")</code> . See <b>Details</b> below. Default <code>Monotonicity=c("General")</code> .
<code>Sum_Pi_f</code>	A scalar or vector that specifies the grid of values $G = g_1, g_2, \dots, g_k$ to be considered when the sensitivity analysis is conducted. See <b>Details</b> below. Default <code>Sum_Pi_f = seq(from=0.01, to=0.99, by=.01)</code> .
<code>M</code>	The number of runs that are conducted for a given value of <code>Sum_Pi_f</code> . This argument is not used when <code>Volume.Perc=0</code> . Default <code>M=10000</code> .
<code>Volume.Perc</code>	Note that the marginals that are observable in the data set a number of restrictions on the unidentified correlations. For example, under monotonicity for $S$ and $T$ , it holds that $\pi_{0111} \leq \min(\pi_{0.1}, \pi_{1.1})$ and $\pi_{1100} \leq \min(\pi_{1.0}, \pi_{1.0})$ . For example, when $\min(\pi_{0.1}, \pi_{1.1}) = 0.10$ and $\min(\pi_{1.0}, \pi_{1.0}) = 0.08$ , then all valid $\pi_{0111} \leq 0.10$ and all valid $\pi_{1100} \leq 0.08$ . The argument <code>Volume.Perc</code> specifies the fraction of the 'volume' of the parameter space that is explored. This volume is computed based on the grids $G=0, 0.01, \dots$ , maximum possible value for the counterfactual probability at hand. E.g., in the

previous example, the 'volume' of the parameter space would be  $11 * 9 = 99$ , and when e.g., the argument `Volume.Perc=1` is used a total of 99 runs will be conducted for each given value of `Sum_Pi_f`. Notice that when monotonicity is not assumed, relatively high values of `Volume.Perc` will lead to a large number of runs and consequently a long analysis time.

Seed            The seed to be used to generate  $\pi_r$ . Default `Seed=sample(1:100000, size=1)`.

## Details

In the continuous normal setting, surrogacy can be assessed by studying the association between the individual causal effects on  $S$  and  $T$  (see [ICA.ContCont](#)). In that setting, the Pearson correlation is the obvious measure of association.

When  $S$  and  $T$  are binary endpoints, multiple alternatives exist. Alonso et al. (2014) proposed the individual causal association (ICA;  $R_H^2$ ), which captures the association between the individual causal effects of the treatment on  $S$  ( $\Delta_S$ ) and  $T$  ( $\Delta_T$ ) using information-theoretic principles.

The function `ICA.BinBin` computes  $R_H^2$  based on plausible values of the potential outcomes. Denote by  $\mathbf{Y}' = (T_0, T_1, S_0, S_1)$  the vector of potential outcomes. The vector  $\mathbf{Y}$  can take 16 values and the set of parameters  $\pi_{ijpq} = P(T_0 = i, T_1 = j, S_0 = p, S_1 = q)$  (with  $i, j, p, q = 0/1$ ) fully characterizes its distribution.

However, the parameters in  $\pi_{ijpq}$  are not all functionally independent, e.g.,  $1 = \pi_{\dots}$ . When no assumptions regarding monotonicity are made, the data impose a total of 7 restrictions, and thus only 9 probabilities in  $\pi_{ijpq}$  are allowed to vary freely (for details, see Alonso et al., 2014). Based on the data and assuming SUTVA, the marginal probabilities  $\pi_{1\cdot\cdot}$ ,  $\pi_{1\cdot 0\cdot}$ ,  $\pi_{\cdot 1\cdot 1}$ ,  $\pi_{\cdot 1\cdot 0}$ ,  $\pi_{0\cdot 1\cdot}$ , and  $\pi_{0\cdot 0\cdot 1}$  can be computed (by hand or using the function `MarginalProbs`). Define the vector

$$\mathbf{b}' = (1, \pi_{1\cdot\cdot}, \pi_{1\cdot 0\cdot}, \pi_{\cdot 1\cdot 1}, \pi_{\cdot 1\cdot 0}, \pi_{0\cdot 1\cdot}, \pi_{0\cdot 0\cdot 1})$$

and  $\mathbf{A}$  is a contrast matrix such that the identified restrictions can be written as a system of linear equation

$$\mathbf{A}\pi = \mathbf{b}.$$

The matrix  $\mathbf{A}$  has rank 7 and can be partitioned as  $\mathbf{A} = (\mathbf{A}_r | \mathbf{A}_f)$ , and similarly the vector  $\pi$  can be partitioned as  $\pi' = (\pi_r' | \pi_f')$  (where  $f$  refers to the submatrix/vector given by the 9 last columns/components of  $\mathbf{A}/\pi$ ). Using these partitions the previous system of linear equations can be rewritten as

$$\mathbf{A}_r \pi_r + \mathbf{A}_f \pi_f = \mathbf{b}.$$

The following algorithm is used to generate plausible distributions for  $\mathbf{Y}$ . First, select a value of the specified grid of values (specified using `Sum_Pi_f` in the function call). For  $k = 1$  to  $M$  (specified using `M` in the function call), generate a vector  $\pi_f$  that contains 9 components that are uniformly sampled from hyperplane subject to the restriction that the sum of the generated components equals `Sum_Pi_f` (the function `RandVec`, which uses the `randfixedsum` algorithm written by Roger Stafford, is used to obtain these components). Next,  $\pi_r = \mathbf{A}_r^{-1}(\mathbf{b} - \mathbf{A}_f \pi_f)$  is computed and the  $\pi_r$  vectors where all components are in the  $[0; 1]$  range are retained. This procedure is repeated for each of the `Sum_Pi_f` values. Based on these results,  $R_H^2$  is estimated. The obtained values can be used to conduct a sensitivity analysis during the validation exercise.

The previous developments hold when no monotonicity is assumed. When monotonicity for  $S$ ,  $T$ , or for  $S$  and  $T$  is assumed, some of the probabilities of  $\pi$  are zero. For example, when monotonicity is

assumed for  $T$ , then  $P(T_0 \leq T_1) = 1$ , or equivalently,  $\pi_{1000} = \pi_{1010} = \pi_{1001} = \pi_{1011} = 0$ . When monotonicity is assumed, the procedure described above is modified accordingly (for details, see Alonso et al., 2014). When a general analysis is requested (using `Monotonicity=c("General")` in the function call), all settings are considered (no monotonicity, monotonicity for  $S$  alone, for  $T$  alone, and for both for  $S$  and  $T$ .)

To account for the uncertainty in the estimation of the marginal probabilities, a vector of values can be specified from which a random draw is made in each run (see **Examples** below).

### Value

An object of class `ICA.BinBin` with components,

<code>Pi.Vectors</code>	An object of class <code>data.frame</code> that contains the valid $\pi$ vectors.
<code>R2_H</code>	The vector of the $R_H^2$ values.
<code>Theta_T</code>	The vector of odds ratios for $T$ .
<code>Theta_S</code>	The vector of odds ratios for $S$ .
<code>H_Delta_T</code>	The vector of the entropies of $\Delta_T$ .
<code>Monotonicity</code>	The assumption regarding monotonicity that was made.
<code>Volume.No</code>	The 'volume' of the parameter space when monotonicity is not assumed. Is only provided when the argument <code>Volume.Perc</code> is used (i.e., when it is not equal to 0).
<code>Volume.T</code>	The 'volume' of the parameter space when monotonicity for $T$ is assumed. Is only provided when the argument <code>Volume.Perc</code> is used.
<code>Volume.S</code>	The 'volume' of the parameter space when monotonicity for $S$ is assumed. Is only provided when the argument <code>Volume.Perc</code> is used.
<code>Volume.ST</code>	The 'volume' of the parameter space when monotonicity for $S$ and $T$ is assumed. Is only provided when the argument <code>Volume.Perc</code> is used.

### Author(s)

Wim Van der Elst, Paul Meyvisch, Ariel Alonso & Geert Molenberghs

### References

Alonso, A., Van der Elst, W., & Molenberghs, G. (2015). Validation of surrogate endpoints: the binary-binary setting from a causal inference perspective.

### See Also

[ICA.ContCont](#), [MICA.ContCont](#)

### Examples

```
## Not run: # Time consuming code part
# Compute R2_H given the marginals specified as the pi's, making no
# assumptions regarding monotonicity (general case)
ICA <- ICA.BinBin(pi1_1=0.2619048, pi1_0=0.2857143, pi_1_1=0.6372549,
```

```

pi_1_0=0.07843137, pi_1_1=0.1349206, pi_0_1=0.127451, Seed=1,
Monotonicity=c("General"), Sum_Pi_f = seq(from=0.01, to=.99, by=.01), M=10000)

# obtain plot of the results
plot(ICA, R2_H=TRUE)

# Example 2 where the uncertainty in the estimation
# of the marginals is taken into account
ICA_BINBIN2 <- ICA.BinBin(pi1_1=runif(10000, 0.2573, 0.4252),
pi1_0=runif(10000, 0.1769, 0.3310),
pi_1_1=runif(10000, 0.5947, 0.7779),
pi_1_0=runif(10000, 0.0322, 0.1442),
pi0_1=runif(10000, 0.0617, 0.1764),
pi_0_1=runif(10000, 0.0254, 0.1315),
Monotonicity=c("General"),
Sum_Pi_f = seq(from=0.01, to=0.99, by=.01),
M=50000, Seed=1)

# Plot results
plot(ICA_BINBIN2)

## End(Not run)

```

---

ICA.BinBin.CounterAssum

*ICA (binary-binary setting) that is obtained when the counterfactual correlations are assumed to fall within some prespecified ranges.*

---

## Description

Shows the results of ICA (binary-binary setting) in the subgroup of results where the counterfactual correlations are assumed to fall within some prespecified ranges.

## Usage

```
ICA.BinBin.CounterAssum(x, r2_h_S0S1_min, r2_h_S0S1_max, r2_h_S0T1_min,
r2_h_S0T1_max, r2_h_T0T1_min, r2_h_T0T1_max, r2_h_T0S1_min, r2_h_T0S1_max,
Monotonicity="General", Type="Freq", MainPlot=" ", Cex.Legend=1,
Cex.Position="topright", ...)
```

## Arguments

x	An object of class ICA.BinBin. See <a href="#">ICA.BinBin</a> .
r2_h_S0S1_min	The minimum value to be considered for the counterfactual correlation $r_h^2(S_0, S_1)$ .
r2_h_S0S1_max	The maximum value to be considered for the counterfactual correlation $r_h^2(S_0, S_1)$ .
r2_h_S0T1_min	The minimum value to be considered for the counterfactual correlation $r_h^2(S_0, T_1)$ .
r2_h_S0T1_max	The maximum value to be considered for the counterfactual correlation $r_h^2(S_0, T_1)$ .

r2_h_T0T1_min	The minimum value to be considered for the counterfactual correlation $r_h^2(T_0, T_1)$ .
r2_h_T0T1_max	The maximum value to be considered for the counterfactual correlation $r_h^2(T_0, T_1)$ .
r2_h_T0S1_min	The minimum value to be considered for the counterfactual correlation $r_h^2(T_0, S_1)$ .
r2_h_T0S1_max	The maximum value to be considered for the counterfactual correlation $r_h^2(T_0, S_1)$ .
Monotonicity	Specifies whether the all results in the fitted object ICA.BinBin should be shown (i.e., Monotonicity=c("General")), or a subset of the results arising under specific assumptions (i.e., Monotonicity=c("No"), Monotonicity=c("True.Endp"), Monotonicity=c("Surr.Endp"), or Monotonicity=c("Surr.True.Endp")). Default Monotonicity=c("General").
Type	The type of plot that is produced. When Type="Freq" or Type="Density", the Y-axis shows frequencies or densities of $R_H^2$ . When Type="All.Densities" and the fitted object of class ICA.BinBin was obtained using a general analysis (i.e., conducting the analyses assuming no monotonicity, monotonicity for $S$ alone, monotonicity for $T$ alone, and for both $S$ and $T$ , so using Monotonicity=c("General") in the function call of ICA.BinBin), the density plots are shown for the four scenarios where different assumptions regarding monotonicity are made. Default "Freq".
MainPlot	The title of the plot. Default " ".
Cex.Legend	The size of the legend when Type="All.Densities" is used. Default Cex.Legend=1.
Cex.Position	The position of the legend, Cex.Position="topright" or Cex.Position="topleft". Default Cex.Position="topright".
...	Other arguments to be passed to the plot() function.

**Author(s)**

Wim Van der Elst, Ariel Alonso, & Geert Molenberghs

**References**

Alonso, A., Van der Elst, W., Molenberghs, G., Buyse, M., & Burzykowski, T. (submitted). On the relationship between the causal inference and meta-analytic paradigms for the validation of surrogate markers.

Van der Elst, W., Alonso, A., & Molenberghs, G. (submitted). An exploration of the relationship between causal inference and meta-analytic measures of surrogacy.

**See Also**

[ICA.BinBin](#)

**Examples**

```
## Not run: #Time consuming (>5 sec) code part
# Compute R2_H given the marginals specified as the pi's, making no
# assumptions regarding monotonicity (general case)
ICA <- ICA.BinBin.Grid.Sample(pi1_1=0.261, pi1_0=0.285,
pi_1_1=0.637, pi_1_0=0.078, pi0_1=0.134, pi_0_1=0.127,
Monotonicity=c("General"), M=5000, Seed=1)
```



```

# Obtain a density plot of R2_H, assuming that
# r2_h_S0S1>=.2, r2_h_S0T1>=0, r2_h_T0T1>=.2, and r2_h_T0S1>=0
ICA.BinBin.CounterAssum(ICA, r2_h_S0S1_min=.2, r2_h_S0S1_max=1,
r2_h_S0T1_min=0, r2_h_S0T1_max=1, r2_h_T0T1_min=0.2, r2_h_T0T1_max=1,
r2_h_T0S1_min=0, r2_h_T0S1_max=1, Monotonicity="General",
Type="Density")

# Now show the densities of R2_H under the different
# monotonicity assumptions
ICA.BinBin.CounterAssum(ICA, r2_h_S0S1_min=.2, r2_h_S0S1_max=1,
r2_h_S0T1_min=0, r2_h_S0T1_max=1, r2_h_T0T1_min=0.2, r2_h_T0T1_max=1,
r2_h_T0S1_min=0, r2_h_T0S1_max=1, Monotonicity="General",
Type="All.Densities", MainPlot=" ", Cex.Legend=1,
Cex.Position="topright", ylim=c(0, 20))

## End(Not run)

```

---

ICA.BinBin.Grid.Full *Assess surrogacy in the causal-inference single-trial setting in the binary-binary case when monotonicity for S and T is assumed using the full grid-based approach*

---

## Description

The function `ICA.BinBin.Grid.Full` quantifies surrogacy in the single-trial causal-inference framework (individual causal association and causal concordance) when both the surrogate and the true endpoints are binary outcomes. This method provides an alternative for `ICA.BinBin` and `ICA.BinBin.Grid.Sample`. It uses an alternative strategy to identify plausible values for  $\pi$ . See **Details** below.

## Usage

```

ICA.BinBin.Grid.Full(pi1_1_, pi1_0_, pi_1_1, pi_1_0, pi0_1_, pi_0_1,
Monotonicity=c("General"), pi_1001=seq(0, 1, by=.02),
pi_1110=seq(0, 1, by=.02), pi_1101=seq(0, 1, by=.02),
pi_1011=seq(0, 1, by=.02), pi_1111=seq(0, 1, by=.02),
pi_0110=seq(0, 1, by=.02), pi_0011=seq(0, 1, by=.02),
pi_0111=seq(0, 1, by=.02), pi_1100=seq(0, 1, by=.02),
Seed=sample(1:100000, size=1))

```

## Arguments

<code>pi1_1_</code>	A scalar that contains $P(T = 1, S = 1   Z = 0)$ , i.e., the probability that $S = T = 1$ when under treatment $Z = 0$ .
<code>pi1_0_</code>	A scalar that contains $P(T = 1, S = 0   Z = 0)$ .
<code>pi_1_1</code>	A scalar that contains $P(T = 1, S = 1   Z = 1)$ .
<code>pi_1_0</code>	A scalar that contains $P(T = 1, S = 0   Z = 1)$ .

pi0_1_	A scalar that contains $P(T = 0, S = 1   Z = 0)$ .
pi_0_1	A scalar that contains $P(T = 0, S = 1   Z = 1)$ .
Monotonicity	Specifies which assumptions regarding monotonicity should be made: <code>Monotonicity=c("General")</code> , <code>Monotonicity=c("No")</code> , <code>Monotonicity=c("True.Endp")</code> , <code>Monotonicity=c("Surr.Endp")</code> , or <code>Monotonicity=c("Surr.True.Endp")</code> . When a general analysis is requested (using <code>Monotonicity=c("General")</code> in the function call), all settings are considered (no monotonicity, monotonicity for $S$ alone, for $T$ alone, and for both for $S$ and $T$ . Default <code>Monotonicity=c("General")</code> ).
pi_1001	A vector that specifies the grid of values that should be considered for $\pi_{pi_1001}$ . Default <code>pi_1001=seq(0, 1, by=.02)</code> .
pi_1110	A vector that specifies the grid of values that should be considered for $\pi_{pi_1110}$ . Default <code>pi_1110=seq(0, 1, by=.02)</code> .
pi_1101	A vector that specifies the grid of values that should be considered for $\pi_{pi_1101}$ . Default <code>pi_1101=seq(0, 1, by=.02)</code> .
pi_1011	A vector that specifies the grid of values that should be considered for $\pi_{pi_1011}$ . Default <code>pi_1011=seq(0, 1, by=.02)</code> .
pi_1111	A vector that specifies the grid of values that should be considered for $\pi_{pi_1111}$ . Default <code>pi_1111=seq(0, 1, by=.02)</code> .
pi_0110	A vector that specifies the grid of values that should be considered for $\pi_{pi_0110}$ . Default <code>pi_0110=seq(0, 1, by=.02)</code> .
pi_0011	A vector that specifies the grid of values that should be considered for $\pi_{pi_0011}$ . Default <code>pi_0011=seq(0, 1, by=.02)</code> .
pi_0111	A vector that specifies the grid of values that should be considered for $\pi_{pi_0111}$ . Default <code>pi_0111=seq(0, 1, by=.02)</code> .
pi_1100	A vector that specifies the grid of values that should be considered for $\pi_{pi_1100}$ . Default <code>pi_1100=seq(0, 1, by=.02)</code> .
Seed	The seed to be used to generate $\pi_r$ . Default <code>Seed=sample(1:100000, size=1)</code> .

## Details

In the continuous normal setting, surrogacy can be assessed by studying the association between the individual causal effects on  $S$  and  $T$  (see [ICA.ContCont](#)). In that setting, the Pearson correlation is the obvious measure of association.

When  $S$  and  $T$  are binary endpoints, multiple alternatives exist. Alonso et al. (2014) proposed the individual causal association (ICA;  $R_H^2$ ), which captures the association between the individual causal effects of the treatment on  $S$  ( $\Delta_S$ ) and  $T$  ( $\Delta_T$ ) using information-theoretic principles.

The function `ICA.BinBin.Grid.Full` computes  $R_H^2$  using a grid-based approach where all possible combinations of the specified grids for the parameters that are allowed that are allowed to vary freely are considered. When it is not assumed that monotonicity holds for both  $S$  and  $T$ , the computationally less demanding algorithm `ICA.BinBin.Grid.Sample` may be preferred.

## Value

An object of class `ICA.BinBin` with components,

Pi.Vectors	An object of class <code>data.frame</code> that contains the valid $\pi$ vectors.
R2_H	The vector of the $R_H^2$ values.
Theta_T	The vector of odds ratios for $T$ .
Theta_S	The vector of odds ratios for $S$ .
H_Delta_T	The vector of the entropies of $\Delta_T$ .

**Author(s)**

Wim Van der Elst, Paul Meyvisch, Ariel Alonso & Geert Molenberghs

**References**

Alonso, A., Van der Elst, W., & Molenberghs, G. (2014). Validation of surrogate endpoints: the binary-binary setting from a causal inference perspective.

Buyse, M., Burzykowski, T., Alosa, A., & Molenberghs, G. (2014). Direct estimation of joint counterfactual probabilities, with application to surrogate marker validation.

**See Also**

[ICA.ContCont](#), [MICA.ContCont](#), [ICA.BinBin](#), [ICA.BinBin.Grid.Sample](#)

**Examples**

```
## Not run: # time consuming code part
# Compute R2_H given the marginals,
# assuming monotonicity for S and T and grids
# pi_0111=seq(0, 1, by=.001) and
# pi_1100=seq(0, 1, by=.001)
ICA <- ICA.BinBin.Grid.Full(pi1_1=0.2619048, pi1_0=0.2857143, pi_1_1=0.6372549,
pi_1_0=0.07843137, pi0_1=0.1349206, pi_0_1=0.127451,
pi_0111=seq(0, 1, by=.01), pi_1100=seq(0, 1, by=.01), Seed=1)

# obtain plot of R2_H
plot(ICA, R2_H=TRUE)

## End(Not run)
```

---

ICA.BinBin.Grid.Sample

*Assess surrogacy in the causal-inference single-trial setting in the binary-binary case when monotonicity for S and T is assumed using the grid-based sample approach*

---

## Description

The function `ICA.BinBin.Grid.Sample` quantifies surrogacy in the single-trial causal-inference framework (individual causal association and causal concordance) when both the surrogate and the true endpoints are binary outcomes. This method provides an alternative for `ICA.BinBin` and `ICA.BinBin.Grid.Full`. It uses an alternative strategy to identify plausible values for  $\pi$ . See **Details** below.

## Usage

```
ICA.BinBin.Grid.Sample(pi1_1_, pi1_0_, pi_1_1, pi_1_0, pi0_1_,
  pi_0_1, Monotonicity=c("General"), M=100000,
  Volume.Perc=0, Seed=sample(1:100000, size=1))
```

## Arguments

<code>pi1_1_</code>	A scalar that contains values for $P(T = 1, S = 1 Z = 0)$ , i.e., the probability that $S = T = 1$ when under treatment $Z = 0$ .
<code>pi1_0_</code>	A scalar that contains values for $P(T = 1, S = 0 Z = 0)$ .
<code>pi_1_1</code>	A scalar that contains values for $P(T = 1, S = 1 Z = 1)$ .
<code>pi_1_0</code>	A scalar that contains values for $P(T = 1, S = 0 Z = 1)$ .
<code>pi0_1_</code>	A scalar that contains values for $P(T = 0, S = 1 Z = 0)$ .
<code>pi_0_1</code>	A scalar that contains values for $P(T = 0, S = 1 Z = 1)$ .
<code>Monotonicity</code>	Specifies which assumptions regarding monotonicity should be made: <code>Monotonicity=c("General")</code> , <code>Monotonicity=c("No")</code> , <code>Monotonicity=c("True.Endp")</code> , <code>Monotonicity=c("Surr.Endp")</code> , or <code>Monotonicity=c("Surr.True.Endp")</code> . When a general analysis is requested (using <code>Monotonicity=c("General")</code> in the function call), all settings are considered (no monotonicity, monotonicity for $S$ alone, for $T$ alone, and for both for $S$ and $T$ . Default <code>Monotonicity=c("General")</code> ).
<code>M</code>	The number of random samples that have to be drawn for the freely varying parameters. Default <code>M=100000</code> . This argument is not used when <code>Volume.Perc=0</code> . Default <code>M=10000</code> .
<code>Volume.Perc</code>	Note that the marginals that are observable in the data set a number of restrictions on the unidentified correlations. For example, under monotonicity for $S$ and $T$ , it holds that $\pi_{0111} \leq \min(\pi_{0.1.}, \pi_{.1.1})$ and $\pi_{1100} \leq \min(\pi_{1.0.}, \pi_{.1.0})$ . For example, when $\min(\pi_{0.1.}, \pi_{.1.1}) = 0.10$ and $\min(\pi_{1.0.}, \pi_{.1.0}) = 0.08$ , then all valid $\pi_{0111} \leq 0.10$ and all valid $\pi_{1100} \leq 0.08$ . The argument <code>Volume.Perc</code> specifies the fraction of the 'volume' of the parameter space that is explored. This volume is computed based on the grids <code>G=0, 0.01, ...,</code> maximum possible value for the counterfactual probability at hand. E.g., in the previous example, the 'volume' of the parameter space would be $11 * 9 = 99$ , and when e.g., the argument <code>Volume.Perc=1</code> is used a total of 99 runs will be conducted. Notice that when monotonicity is not assumed, relatively high values of <code>Volume.Perc</code> will lead to a large number of runs and consequently a long analysis time.
<code>Seed</code>	The seed to be used to generate $\pi_r$ . Default <code>M=100000</code> .

## Details

In the continuous normal setting, surrogacy can be assessed by studying the association between the individual causal effects on  $S$  and  $T$  (see [ICA.ContCont](#)). In that setting, the Pearson correlation is the obvious measure of association.

When  $S$  and  $T$  are binary endpoints, multiple alternatives exist. Alonso et al. (2014) proposed the individual causal association (ICA;  $R_H^2$ ), which captures the association between the individual causal effects of the treatment on  $S$  ( $\Delta_S$ ) and  $T$  ( $\Delta_T$ ) using information-theoretic principles.

The function `ICA.BinBin.Grid.Full` computes  $R_H^2$  using a grid-based approach where all possible combinations of the specified grids for the parameters that are allowed that are allowed to vary freely are considered. When it is not assumed that monotonicity holds for both  $S$  and  $T$ , the number of possible combinations become very high. The function `ICA.BinBin.Grid.Sample` considers a random sample of all possible combinations.

## Value

An object of class `ICA.BinBin` with components,

<code>Pi.Vectors</code>	An object of class <code>data.frame</code> that contains the valid $\pi$ vectors.
<code>R2_H</code>	The vector of the $R_H^2$ values.
<code>Theta_T</code>	The vector of odds ratios for $T$ .
<code>Theta_S</code>	The vector of odds ratios for $S$ .
<code>H_Delta_T</code>	The vector of the entropies of $\Delta_T$ .
<code>Volume.No</code>	The 'volume' of the parameter space when monotonicity is not assumed.
<code>Volume.T</code>	The 'volume' of the parameter space when monotonicity for $T$ is assumed.
<code>Volume.S</code>	The 'volume' of the parameter space when monotonicity for $S$ is assumed.
<code>Volume.ST</code>	The 'volume' of the parameter space when monotonicity for $S$ and $T$ is assumed.

## Author(s)

Wim Van der Elst, Paul Meyvisch, Ariel Alonso & Geert Molenberghs

## References

Alonso, A., Van der Elst, W., & Molenberghs, G. (2014). Validation of surrogate endpoints: the binary-binary setting from a causal inference perspective.

Buyse, M., Burzykowski, T., Alosa, A., & Molenberghs, G. (2014). Direct estimation of joint counterfactual probabilities, with application to surrogate marker validation.

## See Also

[ICA.ContCont](#), [MICA.ContCont](#), [ICA.BinBin](#), [ICA.BinBin.Grid.Sample](#)

**Examples**

```
## Not run: #time-consuming code parts
# Compute R2_H given the marginals,
# assuming monotonicity for S and T and grids
# pi_0111=seq(0, 1, by=.001) and
# pi_1100=seq(0, 1, by=.001)
ICA <- ICA.BinBin.Grid.Sample(pi1_1_=0.261, pi1_0_=0.285,
pi_1_1=0.637, pi_1_0=0.078, pi0_1_=0.134, pi_0_1=0.127,
Monotonicity=c("Surr.True.Endp"), M=2500, Seed=1)

# obtain plot of R2_H
plot(ICA, R2_H=TRUE)

## End(Not run)
```

---

ICA.BinBin.Grid.Sample.Uncert

*Assess surrogacy in the causal-inference single-trial setting in the binary-binary case when monotonicity for S and T is assumed using the grid-based sample approach, accounting for sampling variability in the marginal  $\pi$ .*

---

**Description**

The function `ICA.BinBin.Grid.Sample.Uncert` quantifies surrogacy in the single-trial causal-inference framework (individual causal association and causal concordance) when both the surrogate and the true endpoints are binary outcomes. This method provides an alternative for `ICA.BinBin` and `ICA.BinBin.Grid.Full`. It uses an alternative strategy to identify plausible values for  $\pi$ . The function allows to account for sampling variability in the marginal  $\pi$ . See **Details** below.

**Usage**

```
ICA.BinBin.Grid.Sample.Uncert(pi1_1_, pi1_0_, pi_1_1, pi_1_0, pi0_1_,
pi_0_1, Monotonicity=c("General"), M=100000,
Volume.Perc=0, Seed=sample(1:100000, size=1))
```

**Arguments**

<code>pi1_1_</code>	A vector that contains values for $P(T = 1, S = 1 Z = 0)$ , i.e., the probability that $S = T = 1$ when under treatment $Z = 0$ . A vector is specified to account for uncertainty, i.e., rather than keeping $P(T = 1, S = 1 Z = 0)$ fixed at one estimated value, a distribution can be specified (see <b>examples</b> below) from which a value is drawn in each run.
<code>pi1_0_</code>	A vector that contains values for $P(T = 1, S = 0 Z = 0)$ .
<code>pi_1_1</code>	A vector that contains values for $P(T = 1, S = 1 Z = 1)$ .
<code>pi_1_0</code>	A vector that contains values for $P(T = 1, S = 0 Z = 1)$ .

pi0_1_	A vector that contains values for $P(T = 0, S = 1 Z = 0)$ .
pi_0_1	A vector that contains values for $P(T = 0, S = 1 Z = 1)$ .
Monotonicity	Specifies which assumptions regarding monotonicity should be made: Monotonicity=c("General"), Monotonicity=c("No"), Monotonicity=c("True.Endp"), Monotonicity=c("Surr.Endp"), or Monotonicity=c("Surr.True.Endp"). When a general analysis is requested (using Monotonicity=c("General") in the function call), all settings are considered (no monotonicity, monotonicity for $S$ alone, for $T$ alone, and for both for $S$ and $T$ . Default Monotonicity=c("General").
M	The number of random samples that have to be drawn for the freely varying parameters. Default M=100000. This argument is not used when Volume.Perc=0. Default M=10000.
Volume.Perc	Note that the marginals that are observable in the data set a number of restrictions on the unidentified correlations. For example, under monotonicity for $S$ and $T$ , it holds that $\pi_{0111} \leq \min(\pi_{0.1}, \pi_{1.1})$ and $\pi_{1100} \leq \min(\pi_{1.0}, \pi_{1.0})$ . For example, when $\min(\pi_{0.1}, \pi_{1.1}) = 0.10$ and $\min(\pi_{1.0}, \pi_{1.0}) = 0.08$ , then all valid $\pi_{0111} \leq 0.10$ and all valid $\pi_{1100} \leq 0.08$ . The argument Volume.Perc specifies the fraction of the 'volume' of the parameter space that is explored. This volume is computed based on the grids G=0, 0.01, ..., maximum possible value for the counterfactual probability at hand. E.g., in the previous example, the 'volume' of the parameter space would be $11 * 9 = 99$ , and when e.g., the argument Volume.Perc=1 is used a total of 99 runs will be conducted. Notice that when monotonicity is not assumed, relatively high values of Volume.Perc will lead to a large number of runs and consequently a long analysis time.
Seed	The seed to be used to generate $\pi_r$ . Default M=100000.

## Details

In the continuous normal setting, surrogacy can be assessed by studying the association between the individual causal effects on  $S$  and  $T$  (see ICA.ContCont). In that setting, the Pearson correlation is the obvious measure of association.

When  $S$  and  $T$  are binary endpoints, multiple alternatives exist. Alonso et al. (2014) proposed the individual causal association (ICA;  $R_H^2$ ), which captures the association between the individual causal effects of the treatment on  $S$  ( $\Delta_S$ ) and  $T$  ( $\Delta_T$ ) using information-theoretic principles.

The function ICA.BinBin.Grid.Full computes  $R_H^2$  using a grid-based approach where all possible combinations of the specified grids for the parameters that are allowed to vary freely are considered. When it is not assumed that monotonicity holds for both  $S$  and  $T$ , the number of possible combinations become very high. The function ICA.BinBin.Grid.Sample.Uncert considers a random sample of all possible combinations.

## Value

An object of class ICA.BinBin with components,

Pi.Vectors	An object of class data.frame that contains the valid $\pi$ vectors.
R2_H	The vector of the $R_H^2$ values.
Theta_T	The vector of odds ratios for $T$ .

Theta_S	The vector of odds ratios for $S$ .
H_Delta_T	The vector of the entropies of $\Delta_T$ .
Volume.No	The 'volume' of the parameter space when monotonicity is not assumed.
Volume.T	The 'volume' of the parameter space when monotonicity for $T$ is assumed.
Volume.S	The 'volume' of the parameter space when monotonicity for $S$ is assumed.
Volume.ST	The 'volume' of the parameter space when monotonicity for $S$ and $T$ is assumed.

**Author(s)**

Wim Van der Elst, Paul Meyvisch, Ariel Alonso & Geert Molenberghs

**References**

Alonso, A., Van der Elst, W., & Molenberghs, G. (2014). Validation of surrogate endpoints: the binary-binary setting from a causal inference perspective.

Buyse, M., Burzykowski, T., Alonso, A., & Molenberghs, G. (2014). Direct estimation of joint counterfactual probabilities, with application to surrogate marker validation.

**See Also**

[ICA.ContCont](#), [MICA.ContCont](#), [ICA.BinBin](#), [ICA.BinBin.Grid.Sample.Uncert](#)

**Examples**

```
# Compute R2_H given the marginals (sample from uniform),
# assuming no monotonicity
ICA_No2 <- ICA.BinBin.Grid.Sample.Uncert(pi1_1=runif(10000, 0.3562, 0.4868),
pi0_1=runif(10000, 0.0240, 0.0837), pi1_0=runif(10000, 0.0240, 0.0837),
pi_1_1=runif(10000, 0.4434, 0.5742), pi_1_0=runif(10000, 0.0081, 0.0533),
pi_0_1=runif(10000, 0.0202, 0.0763), Seed=1, Monotonicity=c("No"), M=1000)

summary(ICA_No2)

# obtain plot of R2_H
plot(ICA_No2)
```

---

ICA.BinCont

*Assess surrogacy in the causal-inference single-trial setting in the binary-continuous case*

---

**Description**

The function `ICA.BinCont` quantifies surrogacy in the single-trial causal-inference framework (individual causal association) when the surrogate endpoint is continuous (normally distributed) and the true endpoint is a binary outcome. For details, see Alonso *et al.* (2016).



**Usage**

```
ICA.BinCont(Dataset, Surr, True, Treat, Diff.Sigma=FALSE,
  G_pi_00=seq(0, 1, by=.01), G_rho_01_00=seq(-1, 1, by=.01),
  G_rho_01_01=seq(-1, 1, by=.01), G_rho_01_10=seq(-1, 1, by=.01),
  G_rho_01_11=seq(-1, 1, by=.01), M=1000, Seed=123,
  Plots=TRUE, Save.Plots="No", Test.Fit.Mixture=FALSE,
  Test.Fit.Mixture.Alpha=0.01, Test.Fit.Details=FALSE,
  Keep.All=FALSE)
```

**Arguments**

Dataset	A data frame that should consist of one line per patient. Each line contains (at least) a surrogate value, a true endpoint value, and a treatment indicator.
Surr	The name of the variable in Dataset that contains the surrogate endpoint values.
True	The name of the variable in Dataset that contains the true endpoint values.
Treat	The name of the variable in Dataset that contains the treatment indicators. The treatment indicator should be coded as 1 for the experimental group and $-1$ for the control group.
Diff.Sigma	Logical. If Diff.Sigma=TRUE, then the mixtures of normal distributions are allowed to have different variances. If Diff.Sigma=FALSE, then the mixtures of normal distributions are not allowed to have different variances (selecting the latter option speeds up the required calculations). Default Diff.Sigma=FALSE.
G_pi_00	A grid of values to be considered for $\pi_{11}$ , i.e., the unidentifiable probability $P(T_1 = 0, T_0 = 0)$ . Default seq(0, 1, by=.01).
G_rho_01_00	A grid of values to be considered for the association parameter $\rho_{01}^{00}$ . Default seq(-1, 1, by=.01).
G_rho_01_01	A grid of values to be considered for the association parameter $\rho_{01}^{01}$ . Default seq(-1, 1, by=.01).
G_rho_01_10	A grid of values to be considered for the association parameter $\rho_{01}^{10}$ . Default seq(-1, 1, by=.01).
G_rho_01_11	A grid of values to be considered for the association parameter $\rho_{01}^{11}$ . Default seq(-1, 1, by=.01).
M	The number of valid ICA values to be sampled. Default M=1000.
Seed	The seed to be used to generate $\pi_r$ . Default Seed=123.
Plots	Logical. Should histograms of $S_0$ (surrogate endpoint in control group) and $S_1$ (surrogate endpoint in experimental treatment group) be provided together with density of fitted mixtures? Default Plots=TRUE.
Save.Plots	Should the plots (see previous item) be saved? If Save.Plots="No", no plots are saved. If plots have to be saved, replace "No" by the desired location, e.g., Save.Plots="C:/". Default Save.Plots="No".
Test.Fit.Mixture	Should the fit of the densities of the mixture distributions with the observed densities of the surrogates in the control and experimental treatment groups be conducted? For details on the method used, see Wilcox (1995, 2014). The code used to conduct the analysis is provided by Wilcox, see <a href="http://dornsife.usc.edu/labs/rwilcox/software/">http://dornsife.usc.edu/labs/rwilcox/software/</a> . Default Test.Fit.Mixture=FALSE.

**Test.Fit.Mixture.Alpha**

The *alpha*-level that is used in comparing the observed densities of  $S[0]$  and  $S[1]$ , see previous points. Default Test.Fit.Mixture.Alpha=0.01.

**Test.Fit.Details**

Should the details of the Wilcox-testing procedure be saved? Default Test.Fit.Details=FALSE.

**Keep.All**

When Test.Fit.Mixture is used, the Wilcox-testing procedure is used to evaluate model fit and only models for which the fit is OK (i.e., all p-values above the specified  $\alpha$ -level) are retained. To keep all results (irrespective of whether or not model fit is OK), Keep.All=TRUE can be used. Default Keep.All=FALSE.

**Value**

An object of class ICA.BinCont with components,

R2_H	The vector of the $R_H^2$ values.
pi_00	The vector of $\pi_{00}^T$ values.
pi_01	The vector of $\pi_{01}^T$ values.
pi_10	The vector of $\pi_{10}^T$ values.
pi_11	The vector of $\pi_{11}^T$ values.
G_rho_01_00	The vector of the $R_{01}^{00}$ values.
G_rho_01_01	The vector of the $R_{01}^{01}$ values.
G_rho_01_10	The vector of the $R_{01}^{10}$ values.
G_rho_01_11	The vector of the $R_{01}^{11}$ values.
pi_Delta_T_min1	The vector of the $\pi_{-1}^{\Delta T}$ values.
pi_Delta_T_0	The vector of the $\pi_0^{\Delta T}$ values.
pi_Delta_T_1	The vector of the $\pi_1^{\Delta T}$ values.
pi_0_00	The vector of $\pi_{00}$ values of $f(S_0)$ .
pi_0_01	The vector of $\pi_{01}$ values of $f(S_0)$ .
pi_0_10	The vector of $\pi_{10}$ values of $f(S_0)$ .
pi_0_11	The vector of $\pi_{11}$ values of $f(S_0)$ .
mu_0_00	The vector of $\mu_0^{00}$ values of $f(S_0)$ .
mu_0_01	The vector of $\mu_0^{01}$ values of $f(S_0)$ .
mu_0_10	The vector of $\mu_0^{10}$ values of $f(S_0)$ .
mu_0_11	The vector of $\mu_0^{11}$ values of $f(S_0)$ .
sigma2_00_00	The vector of squared $\sigma_{00}^{00}$ values of $f(S_0)$ .
sigma2_00_01	The vector of squared $\sigma_{00}^{01}$ values of $f(S_0)$ .
sigma2_00_10	The vector of squared $\sigma_{00}^{10}$ values of $f(S_0)$ .
sigma2_00_11	The vector of squared $\sigma_{00}^{11}$ values of $f(S_0)$ .
pi_1_00	The vector of $\pi_{00}$ values of $f(S_1)$ .
pi_1_01	The vector of $\pi_{01}$ values of $f(S_1)$ .

pi_1_10	The vector of $\pi_{10}$ values of $f(S_1)$ .
pi_1_11	The vector of $\pi_{11}$ values of $f(S_1)$ .
mu_1_00	The vector of $\mu_1^{00}$ values of $f(S_1)$ .
mu_1_01	The vector of $\mu_1^{01}$ values of $f(S_1)$ .
mu_1_10	The vector of $\mu_1^{10}$ values of $f(S_1)$ .
mu_1_11	The vector of $\mu_1^{11}$ values of $f(S_1)$ .
sigma2_11_00	The vector of squared $\sigma_{11}^{00}$ values of $f(S_1)$ .
sigma2_11_01	The vector of squared $\sigma_{11}^{01}$ values of $f(S_1)$ .
sigma2_11_10	The vector of squared $\sigma_{11}^{10}$ values of $f(S_1)$ .
sigma2_11_11	The vector of squared $\sigma_{11}^{11}$ values of $f(S_1)$ .
Fit.Mixture_S_0_OK	Is the fit of the mixture distribution for $S[0]$ OK (i.e., all $p$ -values) of the test procedure above the specified $\alpha$ ?
Fit.Mixture_S_1_OK	Is the fit of the mixture distribution for $S[1]$ OK (i.e., all $p$ -values) of the test procedure above the specified $\alpha$ ?
Test.Fit.Details	Details of the Wilcox-testing procedure. This information is provided when the argument <code>Test.Fit.Details=FALSE</code> was used in the function call.

**Author(s)**

Wim Van der Elst & Ariel Alonso

**References**

- Alonso, A., Van der Elst, W., & Molenberghs, G. (2016). Surrogate markers validation: the continuous-binary setting from a causal inference perspective.
- Wilcox, R.R. (1995) Comparing Two Independent Groups Via Multiple Quantiles. *Journal of the Royal Statistical Society. Series D (The Statistician)*, 44, 91-99.
- Wilcox, R. R., Erceg-Hurn, D. M, Clark, F., & Carlson, M. (2014). Comparing two independent groups via the lower and upper quantiles. *Journal of Statistical Computation and Simulation*.

**See Also**

[ICA.ContCont](#), [MICA.ContCont](#), [ICA.BinBin](#)

**Examples**

```
## Not run: # Time consuming code part
data(Schizo)
Fit <- ICA.BinCont(Dataset = Schizo, Surr = BPRS, True = PANSS_Bin,
  Treat=Treat, M=50, Seed=1)

summary(Fit)
plot(Fit)

## End(Not run)
```

ICA.ContCont

*Assess surrogacy in the causal-inference single-trial setting (Individual Causal Association, ICA) in the Continuous-continuous case*

### Description

The function `ICA.ContCont` quantifies surrogacy in the single-trial causal-inference framework. See **Details** below.

### Usage

```
ICA.ContCont(T0S0, T1S1, T0T0=1, T1T1=1, S0S0=1, S1S1=1, T0T1=seq(-1, 1, by=.1),
T0S1=seq(-1, 1, by=.1), T1S0=seq(-1, 1, by=.1), S0S1=seq(-1, 1, by=.1))
```

### Arguments

<code>T0S0</code>	A scalar or vector that specifies the correlation(s) between the surrogate and the true endpoint in the control treatment condition that should be considered in the computation of $\rho_{\Delta}$ .
<code>T1S1</code>	A scalar or vector that specifies the correlation(s) between the surrogate and the true endpoint in the experimental treatment condition that should be considered in the computation of $\rho_{\Delta}$ .
<code>T0T0</code>	A scalar that specifies the variance of the true endpoint in the control treatment condition that should be considered in the computation of $\rho_{\Delta}$ . Default 1.
<code>T1T1</code>	A scalar that specifies the variance of the true endpoint in the experimental treatment condition that should be considered in the computation of $\rho_{\Delta}$ . Default 1.
<code>S0S0</code>	A scalar that specifies the variance of the surrogate endpoint in the control treatment condition that should be considered in the computation of $\rho_{\Delta}$ . Default 1.
<code>S1S1</code>	A scalar that specifies the variance of the surrogate endpoint in the experimental treatment condition that should be considered in the computation of $\rho_{\Delta}$ . Default 1.
<code>T0T1</code>	A scalar or vector that contains the correlation(s) between the counterfactuals T0 and T1 that should be considered in the computation of $\rho_{\Delta}$ . Default <code>seq(-1, 1, by=.1)</code> , i.e., the values $-1, -0.9, -0.8, \dots, 1$ .
<code>T0S1</code>	A scalar or vector that contains the correlation(s) between the counterfactuals T0 and S1 that should be considered in the computation of $\rho_{\Delta}$ . Default <code>seq(-1, 1, by=.1)</code> .
<code>T1S0</code>	A scalar or vector that contains the correlation(s) between the counterfactuals T1 and S0 that should be considered in the computation of $\rho_{\Delta}$ . Default <code>seq(-1, 1, by=.1)</code> .
<code>S0S1</code>	A scalar or vector that contains the correlation(s) between the counterfactuals S0 and S1 that should be considered in the computation of $\rho_{\Delta}$ . Default <code>seq(-1, 1, by=.1)</code> .

## Details

Based on the causal-inference framework, it is assumed that each subject  $j$  has four counterfactuals (or potential outcomes), i.e.,  $T_{0j}$ ,  $T_{1j}$ ,  $S_{0j}$ , and  $S_{1j}$ . Let  $T_{0j}$  and  $T_{1j}$  denote the counterfactuals for the true endpoint ( $T$ ) under the control ( $Z = 0$ ) and the experimental ( $Z = 1$ ) treatments of subject  $j$ , respectively. Similarly,  $S_{0j}$  and  $S_{1j}$  denote the corresponding counterfactuals for the surrogate endpoint ( $S$ ) under the control and experimental treatments, respectively. The individual causal effects of  $Z$  on  $T$  and  $S$  for a given subject  $j$  are then defined as  $\Delta_{T_j} = T_{1j} - T_{0j}$  and  $\Delta_{S_j} = S_{1j} - S_{0j}$ , respectively.

In the single-trial causal-inference framework, surrogacy can be quantified as the correlation between the individual causal effects of  $Z$  on  $S$  and  $T$  (for details, see Alonso et al., submitted):

$$\rho_{\Delta} = \rho(\Delta_{T_j}, \Delta_{S_j}) = \frac{\sqrt{\sigma_{S_0S_0}\sigma_{T_0T_0}}\rho_{S_0T_0} + \sqrt{\sigma_{S_1S_1}\sigma_{T_1T_1}}\rho_{S_1T_1} - \sqrt{\sigma_{S_0S_0}\sigma_{T_1T_1}}\rho_{S_0T_1} - \sqrt{\sigma_{S_1S_1}\sigma_{T_0T_0}}\rho_{S_1T_0}}{\sqrt{(\sigma_{T_0T_0} + \sigma_{T_1T_1} - 2\sqrt{\sigma_{T_0T_0}\sigma_{T_1T_1}}\rho_{T_0T_1})(\sigma_{S_0S_0} + \sigma_{S_1S_1} - 2\sqrt{\sigma_{S_0S_0}\sigma_{S_1S_1}}\rho_{S_0S_1})}},$$

where the correlations  $\rho_{S_0T_1}$ ,  $\rho_{S_1T_0}$ ,  $\rho_{T_0T_1}$ , and  $\rho_{S_0S_1}$  are not estimable. It is thus warranted to conduct a sensitivity analysis (by considering vectors of possible values for the correlations between the counterfactuals – rather than point estimates).

When the user specifies a vector of values that should be considered for one or more of the counterfactual correlations in the above expression, the function `ICA.ContCont` constructs all possible matrices that can be formed as based on these values, identifies the matrices that are positive definite (i.e., valid correlation matrices), and computes  $\rho_{\Delta}$  for each of these matrices. The obtained vector of  $\rho_{\Delta}$  values can subsequently be used to examine (i) the impact of different assumptions regarding the correlations between the counterfactuals on the results (see also [plot Causal-Inference ContCont](#)), and (ii) the extent to which proponents of the causal-inference and meta-analytic frameworks will reach the same conclusion with respect to the appropriateness of the candidate surrogate at hand.

The function `ICA.ContCont` also generates output that is useful to examine the plausibility of finding a good surrogate endpoint (see `GoodSurr` in the **Value** section below). For details, see Alonso et al. (submitted).

## Notes

A single  $\rho_{\Delta}$  value is obtained when all correlations in the function call are scalars.

## Value

An object of class `ICA.ContCont` with components,

`Total.Num.Matrices`

An object of class `numeric` that contains the total number of matrices that can be formed as based on the user-specified correlations in the function call.

`Pos.Def`

A `data.frame` that contains the positive definite matrices that can be formed based on the user-specified correlations. These matrices are used to compute the vector of the  $\rho_{\Delta}$  values.

`ICA`

A scalar or vector that contains the individual causal association (ICA;  $\rho_{\Delta}$ ) value(s).

`GoodSurr`

A `data.frame` that contains the ICA ( $\rho_{\Delta}$ ),  $\sigma_{\Delta_T}$ , and  $\delta$ .

**Author(s)**

Wim Van der Elst, Ariel Alonso, & Geert Molenberghs

**References**

Alonso, A., Van der Elst, W., Molenberghs, G., Buyse, M., & Burzykowski, T. (submitted). On the relationship between the causal-inference and meta-analytic paradigms for the validation of surrogate markers.

**See Also**

[MICA.ContCont](#), [ICA.Sample.ContCont](#), [Single.Trial.RE.AA](#), [plot Causal-Inference ContCont](#)

**Examples**

```
## Not run: #time-consuming code parts
# Generate the vector of ICA.ContCont values when rho_T0S0=rho_T1S1=.95,
# sigma_T0T0=90, sigma_T1T1=100,sigma_S0S0=10, sigma_S1S1=15, and
# the grid of values {0, .2, ..., 1} is considered for the correlations
# between the counterfactuals:
SurICA <- ICA.ContCont(T0S0=.95, T1S1=.95, T0T0=90, T1T1=100, S0S0=10, S1S1=15,
T0T1=seq(0, 1, by=.2), T0S1=seq(0, 1, by=.2), T1S0=seq(0, 1, by=.2),
S0S1=seq(0, 1, by=.2))

# Examine and plot the vector of generated ICA values:
summary(SurICA)
plot(SurICA)

# Obtain the positive definite matrices than can be formed as based on the
# specified (vectors) of the correlations (these matrices are used to
# compute the ICA values)
SurICA$Pos.Def

# Same, but specify vectors for rho_T0S0 and rho_T1S1: Sample from
# normal with mean .95 and SD=.05 (to account for uncertainty
# in estimation)
SurICA2 <- ICA.ContCont(T0S0=rnorm(n=10000000, mean=.95, sd=.05),
T1S1=rnorm(n=10000000, mean=.95, sd=.05),
T0T0=90, T1T1=100, S0S0=10, S1S1=15,
T0T1=seq(0, 1, by=.2), T0S1=seq(0, 1, by=.2), T1S0=seq(0, 1, by=.2),
S0S1=seq(0, 1, by=.2))

# Examine results
summary(SurICA2)
plot(SurICA2)

## End(Not run)
```

---

ICA.ContCont.MultS	<i>Assess surrogacy in the causal-inference single-trial setting (Individual Causal Association, ICA) using a continuous univariate T and multiple continuous S</i>
--------------------	---

---

## Description

The function `ICA.ContCont.MultS` quantifies surrogacy in the single-trial causal-inference framework where T is continuous and there are multiple continuous S.

## Usage

```
ICA.ContCont.MultS(M = 500, N, Sigma,
  G = seq(from=-1, to=1, by = .00001),
  Seed=c(123), Show.Progress=FALSE)
```

## Arguments

M	The number of multivariate ICA values ( $R_H^2$ ) that should be sampled. Default M=500.
N	The sample size of the dataset.
Sigma	A matrix that specifies the variance-covariance matrix between $T_0$ , $T_1$ , $S_{10}$ , $S_{11}$ , $S_{20}$ , $S_{21}$ , ..., $S_{k0}$ , and $S_{k1}$ (in this order, the $T_0$ and $T_1$ data should be in <code>Sigma[c(1, 2), c(1, 2)]</code> , the $S_{10}$ and $S_{11}$ data should be in <code>Sigma[c(3, 4), c(3, 4)]</code> , and so on). The unidentifiable covariances should be defined as NA (see example below).
G	A vector of the values that should be considered for the unidentified correlations. Default <code>G=seq(-1, 1, by=.00001)</code> , i.e., values with range $-1$ to $1$ .
Seed	The seed that is used. Default <code>Seed=123</code> .
Show.Progress	Should progress of runs be graphically shown? (i.e., 1% done..., 2% done..., etc). Mainly useful when a large number of S have to be considered (to follow progress and estimate total run time).

## Details

The multivariate ICA ( $R_H^2$ ) is not identifiable because the individual causal treatment effects on  $T$ ,  $S_1$ , ...,  $S_k$  cannot be observed. A simulation-based sensitivity analysis is therefore conducted in which the multivariate ICA ( $R_H^2$ ) is estimated across a set of plausible values for the unidentifiable correlations. To this end, consider the variance covariance matrix of the potential outcomes  $\Sigma$  (0





**Author(s)**

Wim Van der Elst, Ariel Alonso, & Geert Molenberghs

**References**

Van der Elst, W., Alonso, A. A., & Molenberghs, G. (2017). Univariate versus multivariate surrogate endpoints.

**See Also**

[MICA.ContCont](#), [ICA.ContCont](#), [Single.Trial.RE.AA](#), [plot Causal-Inference ContCont](#), [ICA.ContCont.MultS\\_alt](#)

**Examples**

```
## Not run: #time-consuming code parts
# Specify matrix Sigma (var-covar matrix T_0, T_1, S1_0, S1_1, ...)
# here for 1 true endpoint and 3 surrogates

s<-matrix(rep(NA, times=64),8)
s[1,1] <- 450; s[2,2] <- 413.5; s[3,3] <- 174.2; s[4,4] <- 157.5;
s[5,5] <- 244.0; s[6,6] <- 229.99; s[7,7] <- 294.2; s[8,8] <- 302.5
s[3,1] <- 160.8; s[5,1] <- 208.5; s[7,1] <- 268.4
s[4,2] <- 124.6; s[6,2] <- 212.3; s[8,2] <- 287.1
s[5,3] <- 160.3; s[7,3] <- 142.8
s[6,4] <- 134.3; s[8,4] <- 130.4
s[7,5] <- 209.3;
s[8,6] <- 214.7
s[upper.tri(s)] = t(s)[upper.tri(s)]

# Marix looks like (NA indicates unidentified covariances):
#           T_0   T_1  S1_0  S1_1  S2_0  S2_1  S2_0  S2_1
#           [,1] [,2] [,3] [,4] [,5] [,6] [,7] [,8]
# T_0 [1,] 450.0  NA 160.8   NA 208.5   NA 268.4   NA
# T_1 [2,]   NA 413.5   NA 124.6   NA 212.30   NA 287.1
# S1_0 [3,] 160.8   NA 174.2   NA 160.3   NA 142.8   NA
# S1_1 [4,]   NA 124.6   NA 157.5   NA 134.30   NA 130.4
# S2_0 [5,] 208.5   NA 160.3   NA 244.0   NA 209.3   NA
# S2_1 [6,]   NA 212.3   NA 134.3   NA 229.99   NA 214.7
# S3_0 [7,] 268.4   NA 142.8   NA 209.3   NA 294.2   NA
# S3_1 [8,]   NA 287.1   NA 130.4   NA 214.70   NA 302.5

# Conduct analysis
ICA <- ICA.ContCont.MultS(M=100, N=200, Show.Progress = TRUE,
  Sigma=s, G = seq(from=-1, to=1, by = .00001), Seed=c(123))

# Explore results
summary(ICA)
plot(ICA)

## End(Not run)
```

---

ICA.ContCont.MultS.PC *Assess surrogacy in the causal-inference single-trial setting (Individual Causal Association, ICA) using a continuous univariate T and multiple continuous S, by simulating correlation matrices using an algorithm based on partial correlations*

---

## Description

The function `ICA.ContCont.MultS` quantifies surrogacy in the single-trial causal-inference framework where T is continuous and there are multiple continuous S. This function provides an alternative for `ICA.ContCont.MultS`.

## Usage

```
ICA.ContCont.MultS.PC(M=1000,N,Sigma,Seed=123,Show.Progress=FALSE)
```

## Arguments

M	The number of multivariate ICA values ( $R_H^2$ ) that should be sampled. Default M=1000.
N	The sample size of the dataset.
Sigma	A matrix that specifies the variance-covariance matrix between $T_0$ , $T_1$ , $S_{10}$ , $S_{11}$ , $S_{20}$ , $S_{21}$ , ..., $S_{k0}$ , and $S_{k1}$ (in this order, the $T_0$ and $T_1$ data should be in <code>Sigma[c(1,2),c(1,2)]</code> , the $S_{10}$ and $S_{11}$ data should be in <code>Sigma[c(3,4),c(3,4)]</code> , and so on). The unidentifiable covariances should be defined as NA (see example below).
Seed	The seed that is used. Default Seed=123.
Show.Progress	Should progress of runs be graphically shown? (i.e., 1% done..., 2% done..., etc). Mainly useful when a large number of S have to be considered (to follow progress and estimate total run time).

## Details

The multivariate ICA ( $R_H^2$ ) is not identifiable because the individual causal treatment effects on  $T$ ,  $S_1$ , ...,  $S_k$  cannot be observed. A simulation-based sensitivity analysis is therefore conducted in which the multivariate ICA ( $R_H^2$ ) is estimated across a set of plausible values for the unidentifiable correlations. To this end, consider the variance covariance matrix of the potential outcomes  $\Sigma$  (0



**See Also**

[MICA.ContCont](#), [ICA.ContCont](#), [Single.Trial.RE.AA](#), [plot Causal-Inference ContCont](#), [ICA.ContCont.MultS](#), [ICA.ContCont.MultS\\_alt](#)

**Examples**

```
## Not run:
# Specify matrix Sigma (var-covar matrix T_0, T_1, S1_0, S1_1, ...)
# here for 1 true endpoint and 3 surrogates

s<-matrix(rep(NA, times=64),8)
s[1,1] <- 450; s[2,2] <- 413.5; s[3,3] <- 174.2; s[4,4] <- 157.5;
s[5,5] <- 244.0; s[6,6] <- 229.99; s[7,7] <- 294.2; s[8,8] <- 302.5
s[3,1] <- 160.8; s[5,1] <- 208.5; s[7,1] <- 268.4
s[4,2] <- 124.6; s[6,2] <- 212.3; s[8,2] <- 287.1
s[5,3] <- 160.3; s[7,3] <- 142.8
s[6,4] <- 134.3; s[8,4] <- 130.4
s[7,5] <- 209.3;
s[8,6] <- 214.7
s[upper.tri(s)] = t(s)[upper.tri(s)]

# Marix looks like (NA indicates unidentified covariances):
#           T_0   T_1  S1_0  S1_1  S2_0  S2_1  S2_0  S2_1
#           [,1] [,2] [,3] [,4] [,5] [,6] [,7] [,8]
# T_0 [1,] 450.0  NA 160.8   NA 208.5   NA 268.4   NA
# T_1 [2,]   NA 413.5   NA 124.6   NA 212.30   NA 287.1
# S1_0 [3,] 160.8   NA 174.2   NA 160.3   NA 142.8   NA
# S1_1 [4,]   NA 124.6   NA 157.5   NA 134.30   NA 130.4
# S2_0 [5,] 208.5   NA 160.3   NA 244.0   NA 209.3   NA
# S2_1 [6,]   NA 212.3   NA 134.3   NA 229.99   NA 214.7
# S3_0 [7,] 268.4   NA 142.8   NA 209.3   NA 294.2   NA
# S3_1 [8,]   NA 287.1   NA 130.4   NA 214.70   NA 302.5

# Conduct analysis
ICA <- ICA.ContCont.MultS.PC(M=1000, N=200, Show.Progress = TRUE,
Sigma=s, Seed=c(123))

# Explore results
summary(ICA)
plot(ICA)

## End(Not run)
```

---

ICA.ContCont.MultS\_alt

*Assess surrogacy in the causal-inference single-trial setting (Individual Causal Association, ICA) using a continuous univariate T and multiple continuous S, alternative approach*

---



The `ICA.ContCont.MultS_alt` function requires the user to specify a distribution  $G$  for the unidentified correlations. Next, the identifiable correlations are fixed at their estimated values and the unidentifiable correlations are independently and randomly sampled from  $G$ . In the function call, the unidentifiable correlations are marked by specifying NA in the Sigma matrix (see example section below). The algorithm generates a large number of 'completed' matrices, and only those that are positive definite are retained (the number of positive definite matrices that should be obtained is specified by the `M=` argument in the function call). Based on the identifiable variances, these positive definite correlation matrices are converted to covariance matrices  $\Sigma$  and the multiple-surrogate ICA are estimated.

An issue with this approach (i.e., substituting unidentified correlations by random and independent samples from  $G$ ) is that the probability of obtaining a positive definite matrix is very low when the dimensionality of the matrix increases. One approach to increase the efficiency of the algorithm is to build-up the correlation matrix in a gradual way. In particular, the property that a  $(k \times k)$  matrix is positive definite if and only if all principal minors are positive (i.e., Sylvester's criterion) can be used. In other words, a  $(k \times k)$  matrix is positive definite when the determinants of the upper-left  $(2 \times 2)$ ,  $(3 \times 3)$ , ...,  $(k \times k)$  submatrices all have a positive determinant. Thus, when a positive definite  $(k \times k)$  matrix has to be generated, one can start with the upper-left  $(2 \times 2)$  submatrix and randomly sample a value from the unidentified correlation (here:  $\rho_{T_0T_0}$ ) from  $G$ . When the determinant is positive (which will always be the case for a  $(2 \times 2)$  matrix), the same procedure is used for the upper-left  $(3 \times 3)$  submatrix, and so on. When a particular draw from  $G$  for a particular submatrix does not give a positive determinant, new values are sampled for the unidentified correlations until a positive determinant is obtained. In this way, it can be guaranteed that the final  $(k \times k)$  submatrix will be positive definite. The latter approach is used in the current function. This procedure is used to generate many positive definite matrices. These positive definite matrices are used to generate  $M$  datasets which contain  $\Delta T$ ,  $\Delta S_1$ ,  $\Delta S_2$ , ...,  $\Delta S_k$ . Finally, the multivariate ICA ( $R_H^2$ ) is estimated by regressing  $\Delta T$  on  $\Delta S_1$ ,  $\Delta S_2$ , ...,  $\Delta S_k$  and computing the multiple coefficient of determination.

### Value

An object of class `ICA.ContCont.MultS_alt` with components,

<code>R2_H</code>	The multiple-surrogate individual causal association value(s).
<code>Corr.R2_H</code>	The corrected multiple-surrogate individual causal association value(s).
<code>Res_Err_Delta_T</code>	The residual errors (prediction errors) for intercept-only models of $\Delta T$ (i.e., models that do not include $\Delta S_1$ , $\Delta S_2$ , etc as predictors).
<code>Res_Err_Delta_T_Given_S</code>	The residual errors (prediction errors) for models where $\Delta T$ is regressed on $\Delta S_1$ , $\Delta S_2$ , etc.
<code>Lower.Dig.Corr.All</code>	A <code>data.frame</code> that contains the matrix that contains the identifiable and unidentifiable correlations (lower diagonal elements) that were used to compute ( $R_H^2$ ) in the run.

### Author(s)

Wim Van der Elst, Ariel Alonso, & Geert Molenberghs

## References

Van der Elst, W., Alonso, A. A., & Molenberghs, G. (2017). Univariate versus multivariate surrogate endpoints.

## See Also

[MICA.ContCont](#), [ICA.ContCont](#), [Single.Trial.RE.AA](#), [plot Causal-Inference ContCont](#)

## Examples

```
## Not run: #time-consuming code parts
# Specify matrix Sigma (var-covar matrix T_0, T_1, S1_0, S1_1, ...)
# here for 1 true endpoint and 3 surrogates

s<-matrix(rep(NA, times=64),8)
s[1,1] <- 450; s[2,2] <- 413.5; s[3,3] <- 174.2; s[4,4] <- 157.5;
s[5,5] <- 244.0; s[6,6] <- 229.99; s[7,7] <- 294.2; s[8,8] <- 302.5
s[3,1] <- 160.8; s[5,1] <- 208.5; s[7,1] <- 268.4
s[4,2] <- 124.6; s[6,2] <- 212.3; s[8,2] <- 287.1
s[5,3] <- 160.3; s[7,3] <- 142.8
s[6,4] <- 134.3; s[8,4] <- 130.4
s[7,5] <- 209.3;
s[8,6] <- 214.7
s[upper.tri(s)] = t(s)[upper.tri(s)]

# Marix looks like (NA indicates unidentified covariances):
#      T_0  T_1  S1_0  S1_1  S2_0  S2_1  S2_0  S2_1
#      [,1] [,2] [,3] [,4] [,5] [,6] [,7] [,8]
# T_0 [1,] 450.0  NA 160.8  NA 208.5  NA 268.4  NA
# T_1 [2,]  NA 413.5  NA 124.6  NA 212.30  NA 287.1
# S1_0 [3,] 160.8  NA 174.2  NA 160.3  NA 142.8  NA
# S1_1 [4,]  NA 124.6  NA 157.5  NA 134.30  NA 130.4
# S2_0 [5,] 208.5  NA 160.3  NA 244.0  NA 209.3  NA
# S2_1 [6,]  NA 212.3  NA 134.3  NA 229.99  NA 214.7
# S3_0 [7,] 268.4  NA 142.8  NA 209.3  NA 294.2  NA
# S3_1 [8,]  NA 287.1  NA 130.4  NA 214.70  NA 302.5

# Conduct analysis
ICA <- ICA.ContCont.MultS_alt(M=100, N=200, Show.Progress = TRUE,
  Sigma=s, G = seq(from=-1, to=1, by = .00001), Seed=c(123),
  Model = "Delta_T ~ Delta_S1 + Delta_S2 + Delta_S3")

# Explore results
summary(ICA)
plot(ICA)

## End(Not run)
```

---

ICA.Sample.ContCont	<i>Assess surrogacy in the causal-inference single-trial setting (Individual Causal Association, ICA) in the Continuous-continuous case using the grid-based sample approach</i>
---------------------	--

---

### Description

The function `ICA.Sample.ContCont` quantifies surrogacy in the single-trial causal-inference framework. It provides a faster alternative for `ICA.ContCont`. See **Details** below.

### Usage

```
ICA.Sample.ContCont(T0S0, T1S1, T0T0=1, T1T1=1, S0S0=1, S1S1=1, T0T1=seq(-1, 1, by=.001),
  T0S1=seq(-1, 1, by=.001), T1S0=seq(-1, 1, by=.001), S0S1=seq(-1, 1, by=.001), M=50000)
```

### Arguments

T0S0	A scalar or vector that specifies the correlation(s) between the surrogate and the true endpoint in the control treatment condition that should be considered in the computation of $\rho_{\Delta}$ .
T1S1	A scalar or vector that specifies the correlation(s) between the surrogate and the true endpoint in the experimental treatment condition that should be considered in the computation of $\rho_{\Delta}$ .
T0T0	A scalar that specifies the variance of the true endpoint in the control treatment condition that should be considered in the computation of $\rho_{\Delta}$ . Default 1.
T1T1	A scalar that specifies the variance of the true endpoint in the experimental treatment condition that should be considered in the computation of $\rho_{\Delta}$ . Default 1.
S0S0	A scalar that specifies the variance of the surrogate endpoint in the control treatment condition that should be considered in the computation of $\rho_{\Delta}$ . Default 1.
S1S1	A scalar that specifies the variance of the surrogate endpoint in the experimental treatment condition that should be considered in the computation of $\rho_{\Delta}$ . Default 1.
T0T1	A scalar or vector that contains the correlation(s) between the counterfactuals T0 and T1 that should be considered in the computation of $\rho_{\Delta}$ . Default <code>seq(-1, 1, by=.001)</code> .
T0S1	A scalar or vector that contains the correlation(s) between the counterfactuals T0 and S1 that should be considered in the computation of $\rho_{\Delta}$ . Default <code>seq(-1, 1, by=.001)</code> .
T1S0	A scalar or vector that contains the correlation(s) between the counterfactuals T1 and S0 that should be considered in the computation of $\rho_{\Delta}$ . Default <code>seq(-1, 1, by=.001)</code> .
S0S1	A scalar or vector that contains the correlation(s) between the counterfactuals S0 and S1 that should be considered in the computation of $\rho_{\Delta}$ . Default <code>seq(-1, 1, by=.001)</code> .
M	The number of runs that should be conducted. Default 50000.



## Details

Based on the causal-inference framework, it is assumed that each subject  $j$  has four counterfactuals (or potential outcomes), i.e.,  $T_{0j}$ ,  $T_{1j}$ ,  $S_{0j}$ , and  $S_{1j}$ . Let  $T_{0j}$  and  $T_{1j}$  denote the counterfactuals for the true endpoint ( $T$ ) under the control ( $Z = 0$ ) and the experimental ( $Z = 1$ ) treatments of subject  $j$ , respectively. Similarly,  $S_{0j}$  and  $S_{1j}$  denote the corresponding counterfactuals for the surrogate endpoint ( $S$ ) under the control and experimental treatments, respectively. The individual causal effects of  $Z$  on  $T$  and  $S$  for a given subject  $j$  are then defined as  $\Delta_{T_j} = T_{1j} - T_{0j}$  and  $\Delta_{S_j} = S_{1j} - S_{0j}$ , respectively.

In the single-trial causal-inference framework, surrogacy can be quantified as the correlation between the individual causal effects of  $Z$  on  $S$  and  $T$  (for details, see Alonso et al., submitted):

$$\rho_{\Delta} = \rho(\Delta_{T_j}, \Delta_{S_j}) = \frac{\sqrt{\sigma_{S_0 S_0} \sigma_{T_0 T_0} \rho_{S_0 T_0}} + \sqrt{\sigma_{S_1 S_1} \sigma_{T_1 T_1} \rho_{S_1 T_1}} - \sqrt{\sigma_{S_0 S_0} \sigma_{T_1 T_1} \rho_{S_0 T_1}} - \sqrt{\sigma_{S_1 S_1} \sigma_{T_0 T_0} \rho_{S_1 T_0}}}{\sqrt{(\sigma_{T_0 T_0} + \sigma_{T_1 T_1} - 2\sqrt{\sigma_{T_0 T_0} \sigma_{T_1 T_1} \rho_{T_0 T_1}})(\sigma_{S_0 S_0} + \sigma_{S_1 S_1} - 2\sqrt{\sigma_{S_0 S_0} \sigma_{S_1 S_1} \rho_{S_0 S_1}})},$$

where the correlations  $\rho_{S_0 T_1}$ ,  $\rho_{S_1 T_0}$ ,  $\rho_{T_0 T_1}$ , and  $\rho_{S_0 S_1}$  are not estimable. It is thus warranted to conduct a sensitivity analysis.

The function `ICA.ContCont` constructs all possible matrices that can be formed based on the specified vectors for  $\rho_{S_0 T_1}$ ,  $\rho_{S_1 T_0}$ ,  $\rho_{T_0 T_1}$ , and  $\rho_{S_0 S_1}$ , and retains the positive definite ones for the computation of  $\rho_{\Delta}$ .

In contrast, the function `ICA.ContCont` samples random values for  $\rho_{S_0 T_1}$ ,  $\rho_{S_1 T_0}$ ,  $\rho_{T_0 T_1}$ , and  $\rho_{S_0 S_1}$  based on a uniform distribution with user-specified minimum and maximum values, and retains the positive definite ones for the computation of  $\rho_{\Delta}$ .

The obtained vector of  $\rho_{\Delta}$  values can subsequently be used to examine (i) the impact of different assumptions regarding the correlations between the counterfactuals on the results (see also [plot Causal-Inference ContCont](#)), and (ii) the extent to which proponents of the causal-inference and meta-analytic frameworks will reach the same conclusion with respect to the appropriateness of the candidate surrogate at hand.

The function `ICA.Sample.ContCont` also generates output that is useful to examine the plausibility of finding a good surrogate endpoint (see `GoodSurr` in the **Value** section below). For details, see Alonso et al. (submitted).

## Notes

A single  $\rho_{\Delta}$  value is obtained when all correlations in the function call are scalars.

## Value

An object of class `ICA.ContCont` with components,

`Total.Num.Matrices`

An object of class `numeric` that contains the total number of matrices that can be formed as based on the user-specified correlations in the function call.

`Pos.Def`

A `data.frame` that contains the positive definite matrices that can be formed based on the user-specified correlations. These matrices are used to compute the vector of the  $\rho_{\Delta}$  values.

`ICA`

A scalar or vector that contains the individual causal association (ICA;  $\rho_{\Delta}$ ) value(s).

`GoodSurr`

A `data.frame` that contains the ICA ( $\rho_{\Delta}$ ),  $\sigma_{\Delta_T}$ , and  $\delta$ .

**Author(s)**

Wim Van der Elst, Ariel Alonso, & Geert Molenberghs

**References**

Alonso, A., Van der Elst, W., Molenberghs, G., Buyse, M., & Burzykowski, T. (submitted). On the relationship between the causal-inference and meta-analytic paradigms for the validation of surrogate markers.

**See Also**

[MICA.ContCont](#), [ICA.ContCont](#), [Single.Trial.RE.AA](#), [plot Causal-Inference ContCont](#)

**Examples**

```
# Generate the vector of ICA values when rho_T0S0=rho_T1S1=.95,
# sigma_T0T0=90, sigma_T1T1=100, sigma_S0S0=10, sigma_S1S1=15, and
# min=-1 max=1 is considered for the correlations
# between the counterfactuals:
SurICA2 <- ICA.Sample.ContCont(T0S0=.95, T1S1=.95, T0T0=90, T1T1=100, S0S0=10,
S1S1=15, M=5000)

# Examine and plot the vector of generated ICA values:
summary(SurICA2)
plot(SurICA2)
```

---

ISTE.ContCont

*Individual-level surrogate threshold effect for continuous normally distributed surrogate and true endpoints.*

---

**Description**

Computes the individual-level surrogate threshold effect in the causal-inference single-trial setting where both the surrogate and the true endpoint are continuous normally distributed variables. For details, see paper in the references section.

**Usage**

```
ISTE.ContCont(Mean_T1, Mean_T0, Mean_S1, Mean_S0, N, Delta_S=c(-10, 0, 10),
zeta.PI=0.05, PI.Bound=0, PI.Lower=TRUE, Show.Prediction.Plots=TRUE, Save.Plots="No",
T0S0, T1S1, T0T0=1, T1T1=1, S0S0=1, S1S1=1, T0T1=seq(-1, 1, by=.001),
T0S1=seq(-1, 1, by=.001), T1S0=seq(-1, 1, by=.001),
S0S1=seq(-1, 1, by=.001), M.PosDef=500, Seed=123)
```

**Arguments**

Mean_T1	A scalar or vector that specifies the mean of the true endpoint in the experimental treatment condition (a vector is used to account for estimation uncertainty).
Mean_T0	A scalar or vector that specifies the mean of the true endpoint in the control condition (a vector is used to account for estimation uncertainty).
Mean_S1	A scalar or vector that specifies the mean of the surrogate endpoint in the experimental treatment condition (a vector is used to account for estimation uncertainty).
Mean_S0	A scalar or vector that specifies the mean of the surrogate endpoint in the control condition (a vector is used to account for estimation uncertainty).
N	The sample size of the clinical trial.
Delta_S	The vector or scalar of $\Delta S$ values for which the expected $\Delta T$ and its prediction error has to be computed.
zeta.PI	The alpha-level to be used in the computation of the prediction interval around $E(\Delta T)$ . Default <code>zeta.PI=0.05</code> , i.e., the 95% prediction interval.
PI.Bound	The ISTE is defined as the value of $\Delta S$ for which the lower (or upper) bound of the $(1 - \alpha)\%$ prediction interval around $E(\Delta T)$ is 0. If another threshold value than 0 is desired, this can be requested by using the <code>PI.Bound</code> argument. For example, the argument <code>PI.Bound=5</code> can be used in the function call to obtain the values of $\Delta S$ for which the lower (or upper) bound of the $(1 - \alpha)\%$ prediction intervals (in the different runs of the algorithm) around $\Delta T$ equal 5.
PI.Lower	Logical. Should a lower ( <code>PI.Lower=TRUE</code> ) or upper ( <code>PI.Lower=FALSE</code> ) prediction interval be used in the computation of ISTE? Default <code>PI.Lower=TRUE</code> .
Show.Prediction.Plots	Logical. Should plots that depict $E(\Delta T)$ against $\Delta S$ (prediction function), the prediction interval, and the ISTE for the different runs of the algorithm be shown? Default <code>Show.Prediction.Plots=TRUE</code> .
Save.Plots	Should the prediction plots (see previous item) be saved? If <code>Save.Plots="No"</code> is used (the default argument), the plots are not saved. If the plots have to be saved, replace "No" by the desired location, e.g., <code>Save.Plots="C:/Analysis directory/"</code> on a windows computer or <code>Save.Plots="/Users/wim/Desktop/Analysis directory/"</code> on macOS or Linux.
T0S0	A scalar or vector that specifies the correlation(s) between the surrogate and the true endpoint in the control treatment condition that should be considered in the computation of ISTE.
T1S1	A scalar or vector that specifies the correlation(s) between the surrogate and the true endpoint in the experimental treatment condition that should be considered in the computation of ISTE.
T0T0	A scalar that specifies the variance of the true endpoint in the control treatment condition that should be considered in the computation of ISTE. Default 1.
T1T1	A scalar that specifies the variance of the true endpoint in the experimental treatment condition that should be considered in the computation of ISTE. Default 1.

S0S0	A scalar that specifies the variance of the surrogate endpoint in the control treatment condition that should be considered in the computation of ISTE. Default 1.
S1S1	A scalar that specifies the variance of the surrogate endpoint in the experimental treatment condition that should be considered in the computation of ISTE. Default 1.
T0T1	A scalar or vector that contains the correlation(s) between the counterfactuals T0 and T1 that should be considered in the computation of ISTE. Default <code>seq(-1, 1, by=.001)</code> .
T0S1	A scalar or vector that contains the correlation(s) between the counterfactuals T0 and S1 that should be considered in the computation of ISTE. Default <code>seq(-1, 1, by=.001)</code> .
T1S0	A scalar or vector that contains the correlation(s) between the counterfactuals T1 and S0 that should be considered in the computation of ISTE. Default <code>seq(-1, 1, by=.001)</code> .
S0S1	A scalar or vector that contains the correlation(s) between the counterfactuals S0 and S1 that should be considered in the computation of ISTE. Default <code>seq(-1, 1, by=.001)</code> .
M.PosDef	The number of positive definite $\Sigma$ matrices that should be identified. This will also determine the amount of ISTE values that are identified. Default <code>M.PosDef=500</code> .
Seed	The seed to be used in the analysis (for reproducibility). Default <code>Seed=123</code> .

### Details

See paper in the references section.

### Value

An object of class `ICA.ContCont` with components,

ISTE_Low_PI	The vector of individual surrogate threshold effect (ISTE) values, i.e., the values of $\Delta S$ for which the lower bound of the $(1 - \alpha)\%$ prediction interval around $\Delta T$ is 0 (or another threshold value, which can be requested by using the <code>PI.Bound</code> argument in the function call).
ISTE_Up_PI	Same as <code>ISTE_Low_PI</code> , but using the upper bound of the $(1 - \alpha)\%$ prediction interval.
MSE	The vector of mean squared error values that are obtained in the prediction of $\Delta T$ based on $\Delta S$ .
gamma0	The vector of intercepts that are obtained in the prediction of $\Delta T$ based on $\Delta S$ .
gamma1	The vector of slope that are obtained in the prediction of $\Delta T$ based on $\Delta S$ .
Delta_S_For_Which_Delta_T_equal_0	The vector of $\Delta S$ values for which $E(\Delta T = 0)$ .
S_squared_pred	The vector of variances of the prediction errors for $\Delta T$ .

Predicted_Delta_T	The vector/matrix of predicted values of $\Delta T$ for the $\Delta S$ values that were requested in the function call (argument <code>Delta_S</code> ).
PI_Interval_Low	The vector/matrix of lower bound values of the $(1 - \alpha)\%$ prediction interval around $\Delta T$ for the $\Delta S$ values that were requested in the function call (argument <code>Delta_S</code> ).
PI_Interval_Up	The vector/matrix of upper bound values of the $(1 - \alpha)\%$ prediction interval around $\Delta T$ for the $\Delta S$ values that were requested in the function call (argument <code>Delta_S</code> ).
T0T0	The vector of variances of T0 (true endpoint in the control treatment) that are used in the computation (this is a constant if the variance is fixed in the function call).
T1T1	The vector of variances of T1 (true endpoint in the experimental treatment) that are used in the computations (this is a constant if the variance is fixed in the function call).
S0S0	The vector of variances of S0 (surrogate endpoint in the control treatment) that are used in the computations (this is a constant if the variance is fixed in the function call).
S1S1	The vector of variances of S1 (surrogate endpoint in the experimental treatment) that are used in the computations (this is a constant if the variance is fixed in the function call).
Mean_DeltaT	The vector of treatment effect values on the true endpoint that are used in the computations (this is a constant if the means of T0 and T1 are fixed in the function call).
Mean_DeltaS	The vector of treatment effect values on the surrogate endpoint that are used in the computations (this is a constant if the means of S0 and S1 are fixed in the function call).
Total.Num.Matrices	An object of class <code>numeric</code> that contains the total number of matrices that can be formed as based on the user-specified correlations in the function call.
Pos.Def	A <code>data.frame</code> that contains the positive definite matrices that can be formed based on the user-specified correlations. These matrices are used to compute the vector of the ISTE values.
ICA	Apart from ISTE, ICA is also computed (the individual causal association). For details, see <a href="#">ICA.ContCont</a> .
zeta.PI	The <code>zeta.PI</code> value specified in the function call.
PI.Bound	The <code>PI.Bound</code> value specified in the function call.
PI.Lower	The <code>PI.Lower</code> value specified in the function call.
Delta_S	The <code>Delta_S</code> value(s) specified in the function call.

**Author(s)**

Wim Van der Elst, Ariel Alonso, & Geert Molenberghs

## References

Van der Elst, W., Alonso, A. A., and Molenberghs, G. (submitted). The individual-level surrogate threshold effect in a causal-inference setting.

## See Also

[ICA.ContCont](#)

## Examples

```
# Define input for analysis using the Schizo dataset,
# with S=BPRS and T = PANSS.
# For each of the identifiable quantities,
# uncertainty is accounted for by specifying a uniform
# distribution with min, max values corresponding to
# the 95% confidence interval of the quantity.
T0S0 <- runif(min = 0.9524, max = 0.9659, n = 1000)
T1S1 <- runif(min = 0.9608, max = 0.9677, n = 1000)

S0S0 <- runif(min=160.811, max=204.5009, n=1000)
S1S1 <- runif(min=168.989, max = 194.219, n=1000)
T0T0 <- runif(min=484.462, max = 616.082, n=1000)
T1T1 <- runif(min=514.279, max = 591.062, n=1000)

Mean_T0 <- runif(min=-13.455, max=-9.489, n=1000)
Mean_T1 <- runif(min=-17.17, max=-14.86, n=1000)
Mean_S0 <- runif(min=-7.789, max=-5.503, n=1000)
Mean_S1 <- runif(min=-9.600, max=-8.276, n=1000)

# Do the ISTE analysis
## Not run:
ISTE <- ISTE.ContCont(Mean_T1=Mean_T1, Mean_T0=Mean_T0,
  Mean_S1=Mean_S1, Mean_S0=Mean_S0, N=2128, Delta_S=c(-50:50),
  zeta.PI=0.05, PI.Bound=0, Show.Prediction.Plots=TRUE,
  Save.Plots="No", T0S0=T0S0, T1S1=T1S1, T0T0=T0T0, T1T1=T1T1,
  S0S0=S0S0, S1S1=S1S1)

# Examine results:
summary(ISTE)

# Plots of results.
# Plot ISTE
plot(ISTE)
# Other plots, see plot.ISTE.ContCont for details
plot(ISTE, Outcome="MSE")
plot(ISTE, Outcome="gamma0")
plot(ISTE, Outcome="gamma1")
plot(ISTE, Outcome="Exp.DeltaT")
plot(ISTE, Outcome="Exp.DeltaT.Low.PI")
plot(ISTE, Outcome="Exp.DeltaT.Up.PI")

## End(Not run)
```

---

LongToWide	<i>Reshapes a dataset from the 'long' format (i.e., multiple lines per patient) into the 'wide' format (i.e., one line per patient)</i>
------------	---

---

**Description**

Reshapes a dataset that is in the 'long' format into the 'wide' format. The dataset should contain a single surrogate endpoint and a single true endpoint value per subject.

**Usage**

```
LongToWide(Dataset, OutcomeIndicator, IdIndicator, TreatIndicator, OutcomeValue)
```

**Arguments**

Dataset	A data.frame in the 'long' format that contains (at least) five columns, i.e., one that contains the subject ID, one that contains the trial ID, one that contains the endpoint indicator, one that contains the treatment indicator, and one that contains the endpoint values.
OutcomeIndicator	The name of the variable in Dataset that contains the indicator that distinguishes between the surrogate and true endpoints.
IdIndicator	The name of the variable in Dataset that contains the subject ID.
TreatIndicator	The name of the variable in Dataset that contains the treatment indicator. For the subsequent surrogacy analyses, the treatment indicator should either be coded as 1 for the experimental group and -1 for the control group, or as 1 for the experimental group and 0 for the control group. The -1/1 coding is recommended.
OutcomeValue	The name of the variable in Dataset that contains the endpoint values.

**Value**

A data.frame in the 'wide' format, i.e., a data.frame that contains one line per subject. Each line contains a surrogate value, a true endpoint value, a treatment indicator, a patient ID, and a trial ID.

**Author(s)**

Wim Van der Elst, Ariel Alonso, and Geert Molenberghs

**Examples**

```
# Generate a dataset in the 'long' format that contains
# S and T values for 100 patients
Outcome <- rep(x=c(0, 1), times=100)
ID <- rep(seq(1:100), each=2)
Treat <- rep(seq(c(0,1)), each=100)
Outcomes <- as.numeric(matrix(rnorm(1*200, mean=100, sd=10),
```

```

                                ncol=200))
Data <- data.frame(cbind(Outcome, ID, Treat, Outcomes))

# Reshapes the Data object
LongToWide(Dataset=Data, OutcomeIndicator=Outcome, IdIndicator=ID,
           TreatIndicator=Treat, OutcomeValue=Outcomes)

```

---

MarginalProbs                    *Computes marginal probabilities for a dataset where the surrogate and true endpoints are binary*

---

### Description

This function computes the marginal probabilities associated with the distribution of the potential outcomes for the true and surrogate endpoint.

### Usage

```
MarginalProbs(Dataset=Dataset, Surr=Surr, True=True, Treat=Treat)
```

### Arguments

Dataset	A <code>data.frame</code> that should consist of one line per patient. Each line contains (at least) a binary surrogate value, a binary true endpoint value, and a treatment indicator.
Surr	The name of the variable in <code>Dataset</code> that contains the binary surrogate endpoint values. Should be coded as 0 and 1.
True	The name of the variable in <code>Dataset</code> that contains the binary true endpoint values. Should be coded as 0 and 1.
Treat	The name of the variable in <code>Dataset</code> that contains the treatment indicators. The treatment indicator should be coded as 1 for the experimental group and $-1$ for the control group.

### Value

Theta_T0S0	The odds ratio for $S$ and $T$ in the control group.
Theta_T1S1	The odds ratio for $S$ and $T$ in the experimental group.
Freq.Cont	The frequencies for $S$ and $T$ in the control group.
Freq.Exp	The frequencies for $S$ and $T$ in the experimental group.
pi1_1_	The estimated $\pi_{1.1}$ .
pi0_1_	The estimated $\pi_{0.1}$ .
pi1_0_	The estimated $\pi_{1.0}$ .
pi0_0_	The estimated $\pi_{0.0}$ .
pi_1_1	The estimated $\pi_{.1.1}$ .
pi_1_0	The estimated $\pi_{.1.0}$ .
pi_0_1	The estimated $\pi_{.0.1}$ .
pi_0_0	The estimated $\pi_{.0.0}$ .



**Author(s)**

Wim Van der Elst, Ariel Alonso, & Geert Molenberghs

**See Also**

[ICA.BinBin](#)

**Examples**

```
# Open the ARMD dataset and recode Diff24 and Diff52 as 1
# when the original value is above 0, and 0 otherwise
data(ARMD)
ARMD$Diff24_Dich <- ifelse(ARMD$Diff24>0, 1, 0)
ARMD$Diff52_Dich <- ifelse(ARMD$Diff52>0, 1, 0)

# Obtain marginal probabilities and ORs
MarginalProbs(Dataset=ARMD, Surr=Diff24_Dich, True=Diff52_Dich,
Treat=Treat)
```

---

MaxEntContCont	<i>Use the maximum-entropy approach to compute ICA in the continuous-continuous single-trial setting</i>
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---

**Description**

In a surrogate evaluation setting where both  $S$  and  $T$  are continuous endpoints, a sensitivity-based approach where multiple 'plausible values' for ICA are retained can be used (see functions `ICA.ContCont`). The function `MaxEntContCont` identifies the estimate which has the maximum entropy.

**Usage**

```
MaxEntContCont(x, T0T0, T1T1, S0S0, S1S1)
```

**Arguments**

<code>x</code>	A fitted object of class <code>ICA.ContCont</code> .
<code>T0T0</code>	A scalar that specifies the variance of the true endpoint in the control treatment condition.
<code>T1T1</code>	A scalar that specifies the variance of the true endpoint in the experimental treatment condition.
<code>S0S0</code>	A scalar that specifies the variance of the surrogate endpoint in the control treatment condition.
<code>S1S1</code>	A scalar that specifies the variance of the surrogate endpoint in the experimental treatment condition.

**Value**

ICA.Max.Ent	The ICA value with maximum entropy.
Max.Ent	The maximum entropy.
Entropy	The vector of entropies corresponding to the vector of 'plausible values' for ICA.
Table.ICA.Entropy	A data.frame that contains the vector of ICA, their entropies, and the correlations between the counterfactuals.
ICA.Fit	The fitted ICA.ContCont object.

**Author(s)**

Wim Van der Elst, Ariel Alonso, Paul Meyvisch, & Geert Molenberghs

**References**

Add

**See Also**

[ICA.ContCont](#), [MaxEntICABinBin](#)

**Examples**

```
## Not run: #time-consuming code parts
# Compute ICA for ARMD dataset, using the grid
# G={-1, -.80, ..., 1} for the unidentifiable correlations

ICA <- ICA.ContCont(T0S0 = 0.769, T1S1 = 0.712, S0S0 = 188.926,
S1S1 = 132.638, T0T0 = 264.797, T1T1 = 231.771,
T0T1 = seq(-1, 1, by = 0.2), T0S1 = seq(-1, 1, by = 0.2),
T1S0 = seq(-1, 1, by = 0.2), S0S1 = seq(-1, 1, by = 0.2))

# Identify the maximum entropy ICA
MaxEnt_ARMD <- MaxEntContCont(x = ICA, S0S0 = 188.926,
S1S1 = 132.638, T0T0 = 264.797, T1T1 = 231.771)

# Explore results using summary() and plot() functions
summary(MaxEnt_ARMD)
plot(MaxEnt_ARMD)
plot(MaxEnt_ARMD, Entropy.By.ICA = TRUE)

## End(Not run)
```

---

MaxEntICABinBin	<i>Use the maximum-entropy approach to compute ICA in the binary-binary setting</i>
-----------------	---

---

### Description

In a surrogate evaluation setting where both  $S$  and  $T$  are binary endpoints, a sensitivity-based approach where multiple 'plausible values' for ICA are retained can be used (see functions `ICA.BinBin`, `ICA.BinBin.Grid.Full`, or `ICA.BinBin.Grid.Sample`). Alternatively, the maximum entropy distribution of the vector of potential outcomes can be considered, based upon which ICA is subsequently computed. The use of the distribution that maximizes the entropy can be justified based on the fact that any other distribution would necessarily (i) assume information that we do not have, or (ii) contradict information that we do have. The function `MaxEntICABinBin` implements the latter approach.

### Usage

```
MaxEntICABinBin(pi1_1_, pi1_0_, pi_1_1,
pi_1_0, pi0_1_, pi_0_1, Method="BFGS",
Fitted.ICA=NULL)
```

### Arguments

pi1_1_	A scalar that contains the estimated value for $P(T = 1, S = 1 Z = 0)$ , i.e., the probability that $S = T = 1$ when under treatment $Z = 0$ .
pi1_0_	A scalar that contains the estimated value for $P(T = 1, S = 0 Z = 0)$ .
pi_1_1	A scalar that contains the estimated value for $P(T = 1, S = 1 Z = 1)$ .
pi_1_0	A scalar that contains the estimated value for $P(T = 1, S = 0 Z = 1)$ .
pi0_1_	A scalar that contains the estimated value for $P(T = 0, S = 1 Z = 0)$ .
pi_0_1	A scalar that contains the estimated value for $P(T = 0, S = 1 Z = 1)$ .
Method	The maximum entropy frequency vector $p^*$ is calculated based on the optimal solution to an unconstrained dual convex programming problem (for details, see Alonso et al., 2015). Two different optimization methods can be specified, i.e., <code>Method="BFGS"</code> and <code>Method="CG"</code> , which implement the quasi-Newton BFGS (Broyden, Fletcher, Goldfarb, and Shanno) and the conjugent gradient (CG) methods (for details on these methods, see the help files of the <code>optim()</code> function and the references therein). Alternatively, the $\pi$ vector (obtained when the functions <code>ICA.BinBin</code> , <code>ICA.BinBin.Grid.Full</code> , or <code>ICA.BinBin.Grid.Sample</code> are executed) that is 'closest' to the vector $\pi$ can be retained. Here, the 'closest' vector is defined as the vector where the sum of the squared differences between the components in the vectors $\pi$ and $\pi$ is smallest. The latter 'Minimum Difference' method can be requested by specifying the argument <code>Method="MD"</code> in the function call. Default <code>Method="BFGS"</code> .
Fitted.ICA	A fitted object of class <code>ICA.BinBin</code> , <code>ICA.BinBin.Grid.Full</code> , or <code>ICA.BinBin.Grid.Sample</code> . Only required when <code>Method="MD"</code> is used.

**Value**

R2_H	The R2_H value.
Vector_p	The maximum entropy frequency vector $p^*$
H_max	The entropy of $p^*$

**Author(s)**

Wim Van der Elst, Ariel Alonso, & Geert Molenberghs

**References**

Alonso, A., & Van der Elst, W. (2015). A maximum-entropy approach for the evaluation of surrogate endpoints based on causal inference.

**See Also**

[ICA.BinBin](#), [ICA.BinBin.Grid.Sample](#), [ICA.BinBin.Grid.Full](#), [plot MaxEntICA BinBin](#)

**Examples**

```
# Sensitivity-based ICA results using ICA.BinBin.Grid.Sample
ICA <- ICA.BinBin.Grid.Sample(pi1_1=0.341, pi0_1=0.119, pi1_0=0.254,
  pi_1_1=0.686, pi_1_0=0.088, pi_0_1=0.078, Seed=1,
  Monotonicity=c("No"), M=5000)

# Maximum-entropy based ICA
MaxEnt <- MaxEntICABinBin(pi1_1=0.341, pi0_1=0.119, pi1_0=0.254,
  pi_1_1=0.686, pi_1_0=0.088, pi_0_1=0.078)

# Explore maximum-entropy results
summary(MaxEnt)

# Plot results
plot(x=MaxEnt, ICA.Fit=ICA)
```

---

MaxEntSPFBinBin	<i>Use the maximum-entropy approach to compute SPF (surrogate predictive function) in the binary-binary setting</i>
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---

**Description**

In a surrogate evaluation setting where both  $S$  and  $T$  are binary endpoints, a sensitivity-based approach where multiple 'plausible values' for vector  $\pi$  (i.e., vectors  $\pi$  that are compatible with the observable data at hand) can be used (for details, see [SPF.BinBin](#)). Alternatively, the maximum entropy distribution for vector  $\pi$  can be considered (Alonso et al., 2015). The use of the distribution that maximizes the entropy can be justified based on the fact that any other distribution would necessarily (i) assume information that we do not have, or (ii) contradict information that we do have. The function `MaxEntSPFBinBin` implements the latter approach.

Based on vector  $\pi$ , the surrogate predictive function (SPF) is computed, i.e.,  $r(i, j) = P(\Delta T = i | \Delta S = j)$ . For example,  $r(-1, 1)$  quantifies the probability that the treatment has a negative effect on the true endpoint ( $\Delta T = -1$ ) given that it has a positive effect on the surrogate ( $\Delta S = 1$ ).

### Usage

```
MaxEntSPFBinBin(pi1_1_, pi1_0_, pi_1_1,
pi_1_0, pi0_1_, pi_0_1, Method="BFGS",
Fitted.ICA=NULL)
```

### Arguments

pi1_1_	A scalar that contains the estimated value for $P(T = 1, S = 1   Z = 0)$ , i.e., the probability that $S = T = 1$ when under treatment $Z = 0$ .
pi1_0_	A scalar that contains the estimated value for $P(T = 1, S = 0   Z = 0)$ .
pi_1_1	A scalar that contains the estimated value for $P(T = 1, S = 1   Z = 1)$ .
pi_1_0	A scalar that contains the estimated value for $P(T = 1, S = 0   Z = 1)$ .
pi0_1_	A scalar that contains the estimated value for $P(T = 0, S = 1   Z = 0)$ .
pi_0_1	A scalar that contains the estimated value for $P(T = 0, S = 1   Z = 1)$ .
Method	The maximum entropy frequency vector $p^*$ is calculated based on the optimal solution to an unconstrained dual convex programming problem (for details, see Alonso et al., 2015). Two different optimization methods can be specified, i.e., Method="BFGS" and Method="CG", which implement the quasi-Newton BFGS (Broyden, Fletcher, Goldfarb, and Shanno) and the conjugent gradient (CG) methods (for details on these methods, see the help files of the <code>optim()</code> function and the references therein). Alternatively, the $\pi$ vector (obtained when the functions <code>ICA.BinBin</code> , <code>ICA.BinBin.Grid.Full</code> , or <code>ICA.BinBin.Grid.Sample</code> are executed) that is 'closest' to the vector $\pi$ can be retained. Here, the 'closest' vector is defined as the vector where the sum of the squared differences between the components in the vectors $\pi$ and $\pi$ is smallest. The latter 'Minimum Difference' method can be requested by specifying the argument Method="MD" in the function call. Default Method="BFGS".
Fitted.ICA	A fitted object of class <code>ICA.BinBin</code> , <code>ICA.BinBin.Grid.Full</code> , or <code>ICA.BinBin.Grid.Sample</code> . Only required when Method="MD" is used.

### Value

Vector_p	The maximum entropy frequency vector $p^*$
r_1_1	The vector of values for $r(1, 1)$ , i.e., $P(\Delta T = 1   \Delta S = 1)$ .
r_min1_1	The vector of values for $r(-1, 1)$ .
r_0_1	The vector of values for $r(0, 1)$ .
r_1_0	The vector of values for $r(1, 0)$ .
r_min1_0	The vector of values for $r(-1, 0)$ .
r_0_0	The vector of values for $r(0, 0)$ .
r_1_min1	The vector of values for $r(1, -1)$ .
r_min1_min1	The vector of values for $r(-1, -1)$ .
r_0_min1	The vector of values for $r(0, -1)$ .

**Author(s)**

Wim Van der Elst, Ariel Alonso, & Geert Molenberghs

**References**

Alonso, A., & Van der Elst, W. (2015). A maximum-entropy approach for the evaluation of surrogate endpoints based on causal inference.

**See Also**

[ICA.BinBin](#), [ICA.BinBin.Grid.Sample](#), [ICA.BinBin.Grid.Full](#), [plot MaxEntSPF BinBin](#)

**Examples**

```
# Sensitivity-based ICA results using ICA.BinBin.Grid.Sample
ICA <- ICA.BinBin.Grid.Sample(pi1_1=0.341, pi0_1=0.119, pi1_0=0.254,
pi_1_1=0.686, pi_1_0=0.088, pi_0_1=0.078, Seed=1,
Monotonicity=c("No"), M=5000)

# Sensitivity-based SPF
SPFSens <- SPF.BinBin(ICA)

# Maximum-entropy based SPF
SPFMaxEnt <- MaxEntSPFBinBin(pi1_1=0.341, pi0_1=0.119, pi1_0=0.254,
pi_1_1=0.686, pi_1_0=0.088, pi_0_1=0.078)

# Explore maximum-entropy results
summary(SPFMaxEnt)

# Plot results
plot(x=SPFMaxEnt, SPF.Fit=SPFSens)
```

---

MICA.ContCont

*Assess surrogacy in the causal-inference multiple-trial setting (Meta-analytic Individual Causal Association; MICA) in the continuous-continuous case*

---

**Description**

The function MICA.ContCont quantifies surrogacy in the multiple-trial causal-inference framework. See **Details** below.

**Usage**

```
MICA.ContCont(Trial.R, D.aa, D.bb, T0S0, T1S1, T0T0=1, T1T1=1, S0S0=1, S1S1=1,
T0T1=seq(-1, 1, by=.1), T0S1=seq(-1, 1, by=.1), T1S0=seq(-1, 1, by=.1),
S0S1=seq(-1, 1, by=.1))
```

**Arguments**

Trials.R	A scalar that specifies the trial-level correlation coefficient (i.e., $R_{trial}$ ) that should be used in the computation of $\rho_M$ .
D.aa	A scalar that specifies the between-trial variance of the treatment effects on the surrogate endpoint (i.e., $d_{aa}$ ) that should be used in the computation of $\rho_M$ .
D.bb	A scalar that specifies the between-trial variance of the treatment effects on the true endpoint (i.e., $d_{bb}$ ) that should be used in the computation of $\rho_M$ .
T0S0	A scalar or vector that specifies the correlation(s) between the surrogate and the true endpoint in the control treatment condition that should be considered in the computation of $\rho_M$ .
T1S1	A scalar or vector that specifies the correlation(s) between the surrogate and the true endpoint in the experimental treatment condition that should be considered in the computation of $\rho_M$ .
T0T0	A scalar that specifies the variance of the true endpoint in the control treatment condition that should be considered in the computation of $\rho_M$ . Default 1.
T1T1	A scalar that specifies the variance of the true endpoint in the experimental treatment condition that should be considered in the computation of $\rho_M$ . Default 1.
S0S0	A scalar that specifies the variance of the surrogate endpoint in the control treatment condition that should be considered in the computation of $\rho_M$ . Default 1.
S1S1	A scalar that specifies the variance of the surrogate endpoint in the experimental treatment condition that should be considered in the computation of $\rho_M$ . Default 1.
T0T1	A scalar or vector that contains the correlation(s) between the counterfactuals T0 and T1 that should be considered in the computation of $\rho_M$ . Default <code>seq(-1, 1, by=.1)</code> , i.e., the values $-1, -0.9, -0.8, \dots, 1$ .
T0S1	A scalar or vector that contains the correlation(s) between the counterfactuals T0 and S1 that should be considered in the computation of $\rho_M$ . Default <code>seq(-1, 1, by=.1)</code> .
T1S0	A scalar or vector that contains the correlation(s) between the counterfactuals T1 and S0 that should be considered in the computation of $\rho_M$ . Default <code>seq(-1, 1, by=.1)</code> .
S0S1	A scalar or vector that contains the correlation(s) between the counterfactuals S0 and S1 that should be considered in the computation of $\rho_M$ . Default <code>seq(-1, 1, by=.1)</code> .

**Details**

Based on the causal-inference framework, it is assumed that each subject  $j$  in trial  $i$  has four counterfactuals (or potential outcomes), i.e.,  $T_{0ij}$ ,  $T_{1ij}$ ,  $S_{0ij}$ , and  $S_{1ij}$ . Let  $T_{0ij}$  and  $T_{1ij}$  denote the counterfactuals for the true endpoint ( $T$ ) under the control ( $Z = 0$ ) and the experimental ( $Z = 1$ ) treatments of subject  $j$  in trial  $i$ , respectively. Similarly,  $S_{0ij}$  and  $S_{1ij}$  denote the corresponding counterfactuals for the surrogate endpoint ( $S$ ) under the control and experimental treatments of subject  $j$  in trial  $i$ , respectively. The individual causal effects of  $Z$  on  $T$  and  $S$  for a given subject  $j$  in trial  $i$  are then defined as  $\Delta_{T_{ij}} = T_{1ij} - T_{0ij}$  and  $\Delta_{S_{ij}} = S_{1ij} - S_{0ij}$ , respectively.

In the multiple-trial causal-inference framework, surrogacy can be quantified as the correlation between the individual causal effects of  $Z$  on  $S$  and  $T$  (for details, see Alonso et al., submitted):

$$\rho_M = \rho(\Delta_{Tij}, \Delta_{Sij}) = \frac{\sqrt{d_{bb}d_{aa}R_{trial}} + \sqrt{V(\varepsilon_{\Delta Tij})V(\varepsilon_{\Delta Sij})}\rho_{\Delta}}{\sqrt{V(\Delta_{Tij})V(\Delta_{Sij})}},$$

where

$$V(\varepsilon_{\Delta Tij}) = \sigma_{T_0T_0} + \sigma_{T_1T_1} - 2\sqrt{\sigma_{T_0T_0}\sigma_{T_1T_1}}\rho_{T_0T_1},$$

$$V(\varepsilon_{\Delta Sij}) = \sigma_{S_0S_0} + \sigma_{S_1S_1} - 2\sqrt{\sigma_{S_0S_0}\sigma_{S_1S_1}}\rho_{S_0S_1},$$

$$V(\Delta_{Tij}) = d_{bb} + \sigma_{T_0T_0} + \sigma_{T_1T_1} - 2\sqrt{\sigma_{T_0T_0}\sigma_{T_1T_1}}\rho_{T_0T_1},$$

$$V(\Delta_{Sij}) = d_{aa} + \sigma_{S_0S_0} + \sigma_{S_1S_1} - 2\sqrt{\sigma_{S_0S_0}\sigma_{S_1S_1}}\rho_{S_0S_1}.$$

The correlations between the counterfactuals (i.e.,  $\rho_{S_0T_1}$ ,  $\rho_{S_1T_0}$ ,  $\rho_{T_0T_1}$ , and  $\rho_{S_0S_1}$ ) are not identifiable from the data. It is thus warranted to conduct a sensitivity analysis (by considering vectors of possible values for the correlations between the counterfactuals – rather than point estimates).

When the user specifies a vector of values that should be considered for one or more of the correlations that are involved in the computation of  $\rho_M$ , the function `MICA.ContCont` constructs all possible matrices that can be formed as based on the specified values, identifies the matrices that are positive definite (i.e., valid correlation matrices), and computes  $\rho_M$  for each of these matrices. An examination of the vector of the obtained  $\rho_M$  values allows for a straightforward examination of the impact of different assumptions regarding the correlations between the counterfactuals on the results (see also `plot Causal-Inference ContCont`), and the extent to which proponents of the causal-inference and meta-analytic frameworks will reach the same conclusion with respect to the appropriateness of the candidate surrogate at hand.

### Notes

A single  $\rho_M$  value is obtained when all correlations in the function call are scalars.

### Value

An object of class `MICA.ContCont` with components,

`Total.Num.Matrices`

An object of class `numeric` which contains the total number of matrices that can be formed as based on the user-specified correlations.

`Pos.Def`

A `data.frame` that contains the positive definite matrices that can be formed based on the user-specified correlations. These matrices are used to compute the vector of the  $\rho_M$  values.

`ICA`

A scalar or vector of the  $\rho_{\Delta}$  values.

`MICA`

A scalar or vector of the  $\rho_M$  values.



**Warning**

The theory that relates the causal-inference and the meta-analytic frameworks in the multiple-trial setting (as developed in Alonso et al., submitted) assumes that a reduced or semi-reduced modelling approach is used in the meta-analytic framework. Thus  $R_{trial}$ ,  $d_{aa}$  and  $d_{bb}$  should be estimated based on a reduced model (i.e., using the `Model=c("Reduced")` argument in the functions `UnifixedContCont`, `UnimixedContCont`, `BifixedContCont`, or `BimixedContCont`) or based on a semi-reduced model (i.e., using the `Model=c("SemiReduced")` argument in the functions `UnifixedContCont`, `UnimixedContCont`, or `BifixedContCont`).

**Author(s)**

Wim Van der Elst, Ariel Alonso, & Geert Molenberghs

**References**

Alonso, A., Van der Elst, W., Molenberghs, G., Buyse, M., & Burzykowski, T. (submitted). On the relationship between the causal-inference and meta-analytic paradigms for the validation of surrogate markers.

**See Also**

[ICA.ContCont](#), [MICA.Sample.ContCont](#), [plot Causal-Inference ContCont](#), [UnifixedContCont](#), [UnimixedContCont](#), [BifixedContCont](#), [BimixedContCont](#)

**Examples**

```
## Not run: #time-consuming code parts
# Generate the vector of MICA values when R_trial=.8, rho_T0S0=rho_T1S1=.8,
# sigma_T0T0=90, sigma_T1T1=100, sigma_S0S0=10, sigma_S1S1=15, D.aa=5, D.bb=10,
# and when the grid of values {0, .2, ..., 1} is considered for the
# correlations between the counterfactuals:
SurMICA <- MICA.ContCont(Trial.R=.80, D.aa=5, D.bb=10, T0S0=.8, T1S1=.8,
T0T0=90, T1T1=100, S0S0=10, S1S1=15, T0T1=seq(0, 1, by=.2),
T0S1=seq(0, 1, by=.2), T1S0=seq(0, 1, by=.2), S0S1=seq(0, 1, by=.2))

# Examine and plot the vector of the generated MICA values:
summary(SurMICA)
plot(SurMICA)

# Same analysis, but now assume that D.aa=.5 and D.bb=.1:
SurMICA <- MICA.ContCont(Trial.R=.80, D.aa=.5, D.bb=.1, T0S0=.8, T1S1=.8,
T0T0=90, T1T1=100, S0S0=10, S1S1=15, T0T1=seq(0, 1, by=.2),
T0S1=seq(0, 1, by=.2), T1S0=seq(0, 1, by=.2), S0S1=seq(0, 1, by=.2))

# Examine and plot the vector of the generated MICA values:
summary(SurMICA)
plot(SurMICA)

# Same as first analysis, but specify vectors for rho_T0S0 and rho_T1S1:
```

```
# Sample from normal with mean .8 and SD=.1 (to account for uncertainty
# in estimation)
SurMICA <- MICA.ContCont(Trial.R=.80, D.aa=5, D.bb=10,
T0S0=rnorm(n=10000000, mean=.8, sd=.1),
T1S1=rnorm(n=10000000, mean=.8, sd=.1),
T0T0=90, T1T1=100, S0S0=10, S1S1=15, T0T1=seq(0, 1, by=.2),
T0S1=seq(0, 1, by=.2), T1S0=seq(0, 1, by=.2), S0S1=seq(0, 1, by=.2))

## End(Not run)
```

---

MICA.Sample.ContCont    *Assess surrogacy in the causal-inference multiple-trial setting (Meta-analytic Individual Causal Association; MICA) in the continuous-continuous case using the grid-based sample approach*

---

## Description

The function `MICA.Sample.ContCont` quantifies surrogacy in the multiple-trial causal-inference framework. It provides a faster alternative for `MICA.ContCont`. See **Details** below.

## Usage

```
MICA.Sample.ContCont(Trial.R, D.aa, D.bb, T0S0, T1S1, T0T0=1, T1T1=1, S0S0=1, S1S1=1,
T0T1=seq(-1, 1, by=.001), T0S1=seq(-1, 1, by=.001), T1S0=seq(-1, 1, by=.001),
S0S1=seq(-1, 1, by=.001), M=50000)
```

## Arguments

Trial.R	A scalar that specifies the trial-level correlation coefficient (i.e., $R_{trial}$ ) that should be used in the computation of $\rho_M$ .
D.aa	A scalar that specifies the between-trial variance of the treatment effects on the surrogate endpoint (i.e., $d_{aa}$ ) that should be used in the computation of $\rho_M$ .
D.bb	A scalar that specifies the between-trial variance of the treatment effects on the true endpoint (i.e., $d_{bb}$ ) that should be used in the computation of $\rho_M$ .
T0S0	A scalar or vector that specifies the correlation(s) between the surrogate and the true endpoint in the control treatment condition that should be considered in the computation of $\rho_M$ .
T1S1	A scalar or vector that specifies the correlation(s) between the surrogate and the true endpoint in the experimental treatment condition that should be considered in the computation of $\rho_M$ .
T0T0	A scalar that specifies the variance of the true endpoint in the control treatment condition that should be considered in the computation of $\rho_M$ . Default 1.
T1T1	A scalar that specifies the variance of the true endpoint in the experimental treatment condition that should be considered in the computation of $\rho_M$ . Default 1.

S0S0	A scalar that specifies the variance of the surrogate endpoint in the control treatment condition that should be considered in the computation of $\rho_M$ . Default 1.
S1S1	A scalar that specifies the variance of the surrogate endpoint in the experimental treatment condition that should be considered in the computation of $\rho_M$ . Default 1.
T0T1	A scalar or vector that contains the correlation(s) between the counterfactuals T0 and T1 that should be considered in the computation of $\rho_M$ . Default $\text{seq}(-1, 1, \text{by}=.001)$ .
T0S1	A scalar or vector that contains the correlation(s) between the counterfactuals T0 and S1 that should be considered in the computation of $\rho_M$ . Default $\text{seq}(-1, 1, \text{by}=.001)$ .
T1S0	A scalar or vector that contains the correlation(s) between the counterfactuals T1 and S0 that should be considered in the computation of $\rho_M$ . Default $\text{seq}(-1, 1, \text{by}=.001)$ .
S0S1	A scalar or vector that contains the correlation(s) between the counterfactuals S0 and S1 that should be considered in the computation of $\rho_M$ . Default $\text{seq}(-1, 1, \text{by}=.001)$ .
M	The number of runs that should be conducted. Default 50000.

### Details

Based on the causal-inference framework, it is assumed that each subject  $j$  in trial  $i$  has four counterfactuals (or potential outcomes), i.e.,  $T_{0ij}$ ,  $T_{1ij}$ ,  $S_{0ij}$ , and  $S_{1ij}$ . Let  $T_{0ij}$  and  $T_{1ij}$  denote the counterfactuals for the true endpoint ( $T$ ) under the control ( $Z = 0$ ) and the experimental ( $Z = 1$ ) treatments of subject  $j$  in trial  $i$ , respectively. Similarly,  $S_{0ij}$  and  $S_{1ij}$  denote the corresponding counterfactuals for the surrogate endpoint ( $S$ ) under the control and experimental treatments of subject  $j$  in trial  $i$ , respectively. The individual causal effects of  $Z$  on  $T$  and  $S$  for a given subject  $j$  in trial  $i$  are then defined as  $\Delta_{Tij} = T_{1ij} - T_{0ij}$  and  $\Delta_{Sij} = S_{1ij} - S_{0ij}$ , respectively.

In the multiple-trial causal-inference framework, surrogacy can be quantified as the correlation between the individual causal effects of  $Z$  on  $S$  and  $T$  (for details, see Alonso et al., submitted):

$$\rho_M = \rho(\Delta_{Tij}, \Delta_{Sij}) = \frac{\sqrt{d_{bb}d_{aa}}R_{\text{trial}} + \sqrt{V(\varepsilon_{\Delta T_{ij}})V(\varepsilon_{\Delta S_{ij}})}\rho_{\Delta}}{\sqrt{V(\Delta_{Tij})V(\Delta_{Sij})}},$$

where

$$\begin{aligned} V(\varepsilon_{\Delta T_{ij}}) &= \sigma_{T_0T_0} + \sigma_{T_1T_1} - 2\sqrt{\sigma_{T_0T_0}\sigma_{T_1T_1}}\rho_{T_0T_1}, \\ V(\varepsilon_{\Delta S_{ij}}) &= \sigma_{S_0S_0} + \sigma_{S_1S_1} - 2\sqrt{\sigma_{S_0S_0}\sigma_{S_1S_1}}\rho_{S_0S_1}, \\ V(\Delta_{Tij}) &= d_{bb} + \sigma_{T_0T_0} + \sigma_{T_1T_1} - 2\sqrt{\sigma_{T_0T_0}\sigma_{T_1T_1}}\rho_{T_0T_1}, \\ V(\Delta_{Sij}) &= d_{aa} + \sigma_{S_0S_0} + \sigma_{S_1S_1} - 2\sqrt{\sigma_{S_0S_0}\sigma_{S_1S_1}}\rho_{S_0S_1}. \end{aligned}$$

The correlations between the counterfactuals (i.e.,  $\rho_{S_0T_1}$ ,  $\rho_{S_1T_0}$ ,  $\rho_{T_0T_1}$ , and  $\rho_{S_0S_1}$ ) are not identifiable from the data. It is thus warranted to conduct a sensitivity analysis (by considering vectors of possible values for the correlations between the counterfactuals – rather than point estimates).

When the user specifies a vector of values that should be considered for one or more of the correlations that are involved in the computation of  $\rho_M$ , the function `MICA.ContCont` constructs all possible matrices that can be formed as based on the specified values, and retains the positive definite ones for the computation of  $\rho_M$ .

In contrast, the function `MICA.Sample.ContCont` samples random values for  $\rho_{S_0T_1}$ ,  $\rho_{S_1T_0}$ ,  $\rho_{T_0T_1}$ , and  $\rho_{S_0S_1}$  based on a uniform distribution with user-specified minimum and maximum values, and retains the positive definite ones for the computation of  $\rho_M$ .

An examination of the vector of the obtained  $\rho_M$  values allows for a straightforward examination of the impact of different assumptions regarding the correlations between the counterfactuals on the results (see also [plot Causal-Inference ContCont](#)), and the extent to which proponents of the causal-inference and meta-analytic frameworks will reach the same conclusion with respect to the appropriateness of the candidate surrogate at hand.

### Notes

A single  $\rho_M$  value is obtained when all correlations in the function call are scalars.

### Value

An object of class `MICA.ContCont` with components,

`Total.Num.Matrices`

An object of class `numeric` which contains the total number of matrices that can be formed as based on the user-specified correlations.

`Pos.Def`

A `data.frame` that contains the positive definite matrices that can be formed based on the user-specified correlations. These matrices are used to compute the vector of the  $\rho_M$  values.

`ICA`

A scalar or vector of the  $\rho_\Delta$  values.

`MICA`

A scalar or vector of the  $\rho_M$  values.

### Warning

The theory that relates the causal-inference and the meta-analytic frameworks in the multiple-trial setting (as developed in Alonso et al., submitted) assumes that a reduced or semi-reduced modelling approach is used in the meta-analytic framework. Thus  $R_{trial}$ ,  $d_{aa}$  and  $d_{bb}$  should be estimated based on a reduced model (i.e., using the `Model=c("Reduced")` argument in the functions [UnifixedContCont](#), [UnimixedContCont](#), [BifixedContCont](#), or [BimixedContCont](#)) or based on a semi-reduced model (i.e., using the `Model=c("SemiReduced")` argument in the functions [UnifixedContCont](#), [UnimixedContCont](#), or [BifixedContCont](#)).

### Author(s)

Wim Van der Elst, Ariel Alonso, & Geert Molenberghs

### References

Alonso, A., Van der Elst, W., Molenberghs, G., Buyse, M., & Burzykowski, T. (submitted). On the relationship between the causal-inference and meta-analytic paradigms for the validation of surrogate markers.

**See Also**

[ICA.ContCont](#), [MICA.ContCont](#), [plot Causal-Inference ContCont](#), [UnifixedContCont](#), [UnimixedContCont](#), [BifixedContCont](#), [BimixedContCont](#)

**Examples**

```
## Not run: #Time consuming (>5 sec) code part
# Generate the vector of MICA values when R_trial=.8, rho_T0S0=rho_T1S1=.8,
# sigma_T0T0=90, sigma_T1T1=100, sigma_S0S0=10, sigma_S1S1=15, D.aa=5, D.bb=10,
# and when the grid of values {-1, -0.999, ..., 1} is considered for the
# correlations between the counterfactuals:
SurMICA <- MICA.Sample.ContCont(Trial.R=.80, D.aa=5, D.bb=10, T0S0=.8, T1S1=.8,
T0T0=90, T1T1=100, S0S0=10, S1S1=15, T0T1=seq(-1, 1, by=.001),
T0S1=seq(-1, 1, by=.001), T1S0=seq(-1, 1, by=.001),
S0S1=seq(-1, 1, by=.001), M=10000)

# Examine and plot the vector of the generated MICA values:
summary(SurMICA)
plot(SurMICA, ICA=FALSE, MICA=TRUE)

# Same analysis, but now assume that D.aa=.5 and D.bb=.1:
SurMICA <- MICA.Sample.ContCont(Trial.R=.80, D.aa=.5, D.bb=.1, T0S0=.8, T1S1=.8,
T0T0=90, T1T1=100, S0S0=10, S1S1=15, T0T1=seq(-1, 1, by=.001),
T0S1=seq(-1, 1, by=.001), T1S0=seq(-1, 1, by=.001),
S0S1=seq(-1, 1, by=.001), M=10000)

# Examine and plot the vector of the generated MICA values:
summary(SurMICA)
plot(SurMICA)

## End(Not run)
```

---

MinSurrContCont	<i>Examine the plausibility of finding a good surrogate endpoint in the Continuous-continuous case</i>
-----------------	--

---

**Description**

The function `MinSurrContCont` examines the plausibility of finding a good surrogate endpoint in the continuous-continuous setting. For details, see Alonso et al. (submitted).

**Usage**

```
MinSurrContCont(T0T0, T1T1, Delta, T0T1=seq(from=0, to=1, by=.01))
```

**Arguments**

T0T0	A scalar that specifies the variance of the true endpoint in the control treatment condition.
T1T1	A scalar that specifies the variance of the true endpoint in the experimental treatment condition.
Delta	A scalar that specifies an upper bound for the prediction mean squared error when predicting the individual causal effect of the treatment on the true endpoint based on the individual causal effect of the treatment on the surrogate.
T0T1	A scalar or vector that contains the correlation(s) between the counterfactuals T0 and T1 that should be considered in the computation of $\rho_{min}^2$ . Default <code>seq(0, 1, by=.1)</code> , i.e., the values 0, 0.10, 0.20, ..., 1.

**Value**

An object of class `MinSurrContCont` with components,

T0T1	A scalar or vector that contains the correlation(s) between the counterfactuals T0 and T1 that were considered (i.e., $\rho_{T_0T_1}$ ).
Sigma.Delta.T	A scalar or vector that contains the standard deviations of the individual causal treatment effects on the true endpoint as a function of $\rho_{T_0T_1}$ .
Rho2.Min	A scalar or vector that contains the $\rho_{min}^2$ values as a function of $\rho_{T_0T_1}$ .

**Author(s)**

Wim Van der Elst, Ariel Alonso, & Geert Molenberghs

**References**

Alonso, A., Van der Elst, W., Molenberghs, G., Buyse, M., & Burzykowski, T. (submitted). On the relationship between the causal-inference and meta-analytic paradigms for the validation of surrogate markers.

**See Also**

[ICA.ContCont](#), [plot Causal-Inference ContCont](#), [plot MinSurrContCont](#)

**Examples**

```
# Assess the plausibility of finding a good surrogate when
# sigma_T0T0 = sigma_T1T1 = 8 and Delta = 1
## Not run:
MinSurr <- MinSurrContCont(T0T0 = 8, T1T1 = 8, Delta = 1)
summary(MinSurr)
plot(MinSurr)
## End(Not run)
```

---

MixedContContIT	<i>Fits (univariate) mixed-effect models to assess surrogacy in the continuous-continuous case based on the Information-Theoretic framework</i>
-----------------	---

---

### Description

The function `MixedContContIT` uses the information-theoretic approach (Alonso & Molenberghs, 2007) to estimate trial- and individual-level surrogacy based on mixed-effect models when both S and T are continuous endpoints. The user can specify whether a (weighted or unweighted) full, semi-reduced, or reduced model should be fitted. See the **Details** section below.

### Usage

```
MixedContContIT(Dataset, Surr, True, Treat, Trial.ID, Pat.ID,
Model=c("Full"), Weighted=TRUE, Min.Trial.Size=2, Alpha=.05, ...)
```

### Arguments

<code>Dataset</code>	A data frame that should consist of one line per patient. Each line contains (at least) a surrogate value, a true endpoint value, a treatment indicator, a patient ID, and a trial ID.
<code>Surr</code>	The name of the variable in <code>Dataset</code> that contains the surrogate endpoint values.
<code>True</code>	The name of the variable in <code>Dataset</code> that contains the true endpoint values.
<code>Treat</code>	The name of the variable in <code>Dataset</code> that contains the treatment indicators. The treatment indicator should either be coded as 1 for the experimental group and -1 for the control group, or as 1 for the experimental group and 0 for the control group.
<code>Trial.ID</code>	The name of the variable in <code>Dataset</code> that contains the trial ID to which the patient belongs.
<code>Pat.ID</code>	The name of the variable in <code>Dataset</code> that contains the patient's ID.
<code>Model</code>	The type of model that should be fitted, i.e., <code>Model=c("Full")</code> , <code>Model=c("Reduced")</code> , or <code>Model=c("SemiReduced")</code> . See the <b>Details</b> section below. Default <code>Model=c("Full")</code> .
<code>Weighted</code>	Logical. In practice it is often the case that different trials (or other clustering units) have different sample sizes. Univariate models are used to assess surrogacy in the information-theoretic approach, so it can be useful to adjust for heterogeneity in information content between the trial-specific contributions (particularly when trial-level surrogacy measures are of primary interest and when the heterogeneity in sample sizes is large). If <code>Weighted=TRUE</code> , weighted regression models are fitted. If <code>Weighted=FALSE</code> , unweighted regression analyses are conducted. See the <b>Details</b> section below. Default <code>TRUE</code> .
<code>Min.Trial.Size</code>	The minimum number of patients that a trial should contain to be included in the analysis. If the number of patients in a trial is smaller than the value specified by <code>Min.Trial.Size</code> , the data of the trial are excluded from the analysis. Default 2.

Alpha	The $\alpha$ -level that is used to determine the confidence intervals around $R_h^2$ and $R_{ht}^2$ . Default 0.05.
...	Other arguments to be passed to the function <code>lmer</code> (of the R package <code>lme4</code> ) that is used to fit the generalized linear mixed-effect models in the function <code>BimixedContCont</code> .

## Details

### Individual-level surrogacy

The following generalised linear mixed-effect models are fitted:

$$g_T(E(T_{ij})) = \mu_T + m_{Ti} + \beta Z_{ij} + b_i Z_{ij},$$

$$g_T(E(T_{ij}|S_{ij})) = \theta_0 + c_{Ti} + \theta_1 Z_{ij} + a_i Z_{ij} + \theta_{2i} S_{ij},$$

where  $i$  and  $j$  are the trial and subject indicators,  $g_T$  is an appropriate link function (i.e., an identity link when a continuous true endpoint is considered),  $S_{ij}$  and  $T_{ij}$  are the surrogate and true endpoint values of subject  $j$  in trial  $i$ , and  $Z_{ij}$  is the treatment indicator for subject  $j$  in trial  $i$ .  $\mu_T$  and  $\beta$  are a fixed intercept and a fixed treatment-effect on the true endpoint, while  $m_{Ti}$  and  $b_i$  are the corresponding random effects.  $\theta_0$  and  $\theta_1$  are the fixed intercept and the fixed treatment effect on the true endpoint after accounting for the effect of the surrogate endpoint, and  $c_{Ti}$  and  $a_i$  are the corresponding random effects.

The  $-2$  log likelihood values of the previous models (i.e.,  $L_1$  and  $L_2$ , respectively) are subsequently used to compute individual-level surrogacy (based on the so-called Variance Reduction Factor, VFR; for details, see Alonso & Molenberghs, 2007):

$$R_{hind}^2 = 1 - \exp\left(-\frac{L_2 - L_1}{N}\right),$$

where  $N$  is the number of trials.

### Trial-level surrogacy

When a full or semi-reduced model is requested (by using the argument `Model=c("Full")` or `Model=c("SemiReduced")` in the function call), trial-level surrogacy is assessed by fitting the following mixed models:

$$S_{ij} = \mu_S + m_{Si} + (\alpha + a_i) Z_{ij} + \varepsilon_{Sij}, (1)$$

$$T_{ij} = \mu_T + m_{Ti} + (\beta + b_i) Z_{ij} + \varepsilon_{Tij}, (1)$$

where  $i$  and  $j$  are the trial and subject indicators,  $S_{ij}$  and  $T_{ij}$  are the surrogate and true endpoint values of subject  $j$  in trial  $i$ ,  $Z_{ij}$  is the treatment indicator for subject  $j$  in trial  $i$ ,  $\mu_S$  and  $\mu_T$  are the fixed intercepts for S and T,  $m_{Si}$  and  $m_{Ti}$  are the corresponding random intercepts,  $\alpha$  and  $\beta$  are the fixed treatment effects on S and T, and  $a_i$  and  $b_i$  are the corresponding random effects. The error terms  $\varepsilon_{Sij}$  and  $\varepsilon_{Tij}$  are assumed to be independent.

When a reduced model is requested by the user (by using the argument `Model=c("Reduced")` in the function call), the following univariate models are fitted:

$$S_{ij} = \mu_S + (\alpha + a_i) Z_{ij} + \varepsilon_{Sij}, (2)$$



$$T_{ij} = \mu_T + (\beta + b_i)Z_{ij} + \varepsilon_{Tij}, (2)$$

where  $\mu_S$  and  $\mu_T$  are the common intercepts for S and T. The other parameters are the same as defined above, and  $\varepsilon_{Sij}$  and  $\varepsilon_{Tij}$  are again assumed to be independent.

When the user requested that a full model approach is used (by using the argument `Model=c("Full")` in the function call, i.e., when models (1) were fitted), the following model is subsequently fitted:

$$\hat{\beta}_i = \lambda_0 + \lambda_1 \widehat{\mu_{Si}} + \lambda_2 \hat{\alpha}_i + \varepsilon_i, (3)$$

where the parameter estimates for  $\beta_i$ ,  $\mu_{Si}$ , and  $\alpha_i$  are based on models (1) (see above). When a weighted model is requested (using the argument `Weighted=TRUE` in the function call), model (3) is a weighted regression model (with weights based on the number of observations in trial  $i$ ). The  $-2$  log likelihood value of the (weighted or unweighted) models (3) ( $L_1$ ) is subsequently compared to the  $-2$  log likelihood value of an intercept-only model ( $\hat{\beta}_i = \lambda_3; L_0$ ), and  $R_{ht}^2$  is computed based on the Variance Reduction Factor (VFR; for details, see Alonso & Molenberghs, 2007):

$$R_{ht}^2 = 1 - \exp\left(-\frac{L_1 - L_0}{N}\right),$$

where  $N$  is the number of trials.

When a semi-reduced or reduced model is requested (by using the argument `Model=c("SemiReduced")` or `Model=c("Reduced")` in the function call), the following model is fitted:

$$\hat{\beta}_i = \lambda_0 + \lambda_1 \hat{\alpha}_i + \varepsilon_i,$$

where the parameter estimates for  $\beta_i$  and  $\alpha_i$  are based on models (2). The  $-2$  log likelihood value of this (weighted or unweighted) model ( $L_1$ ) is subsequently compared to the  $-2$  log likelihood value of an intercept-only model ( $\hat{\beta}_i = \lambda_3; L_0$ ), and  $R_{ht}^2$  is computed based on the reduction in the likelihood (as described above).

## Value

An object of class `MixedContContIT` with components,

- |                            |   |
|----------------------------|---|
| <code>Data.Analyze</code>  | Prior to conducting the surrogacy analysis, data of patients who have a missing value for the surrogate and/or the true endpoint are excluded. In addition, the data of trials (i) in which only one type of the treatment was administered, and (ii) in which either the surrogate or the true endpoint was a constant (i.e., all patients within a trial had the same surrogate and/or true endpoint value) are excluded. In addition, the user can specify the minimum number of patients that a trial should contain in order to include the trial in the analysis. If the number of patients in a trial is smaller than the value specified by <code>Min.Trial.Size</code> , the data of the trial are excluded. <code>Data.Analyze</code> is the dataset on which the surrogacy analysis was conducted. |
| <code>Obs.Per.Trial</code> | A <code>data.frame</code> that contains the total number of patients per trial and the number of patients who were administered the control treatment and the experimental treatment in each of the trials (in <code>Data.Analyze</code> ).   |

## Trial.Spec.Results

	A data.frame that contains the trial-specific intercepts and treatment effects for the surrogate and the true endpoints (when a full or semi-reduced model is requested), or the trial-specific treatment effects for the surrogate and the true endpoints (when a reduced model is requested).
R2ht	A data.frame that contains the trial-level surrogacy estimate and its confidence interval.
R2h.ind	A data.frame that contains the individual-level surrogacy estimate and its confidence interval.
Cor.Endpoints	A data.frame that contains the correlations between the surrogate and the true endpoint in the control treatment group (i.e., $\rho_{T0S0}$ ) and in the experimental treatment group (i.e., $\rho_{T1S1}$ ), their standard errors and their confidence intervals.
Residuals	A data.frame that contains the residuals for the surrogate and true endpoints ( $\varepsilon_{Sij}$ and $\varepsilon_{Tij}$ ) that are obtained when models (1) or models (2) are fitted (see the <b>Details</b> section above).

**Author(s)**

Wim Van der Elst, Ariel Alonso, & Geert Molenberghs

**References**

Alonso, A, & Molenberghs, G. (2007). Surrogate marker evaluation from an information theory perspective. *Biometrics*, 63, 180-186.

**See Also**

[FixedContContIT, plot Information-Theoretic](#)

**Examples**

```
# Example 1
# Based on the ARMD data:
data(ARMD)
# Assess surrogacy based on a full mixed-effect model
# in the information-theoretic framework:
Sur <- MixedContContIT(Dataset=ARMD, Surr=Diff24, True=Diff52, Treat=Treat, Trial.ID=Center,
Pat.ID=Id, Model="Full")
# Obtain a summary of the results:
summary(Sur)

## Not run: # Time consuming (>5sec) code part
# Example 2
# Conduct an analysis based on a simulated dataset with 2000 patients, 200 trials,
# and Rindiv=Rtrial=.8
# Simulate the data:
Sim.Data.MTS(N.Total=2000, N.Trial=200, R.Trial.Target=.8, R.Indiv.Target=.8,
Seed=123, Model="Full")
# Assess surrogacy based on a full mixed-effect model
# in the information-theoretic framework:
```

```
Sur2 <- MixedContContIT(Dataset=Data.Observed.MTS, Surr=Surr, True=True, Treat=Treat,
  Trial.ID=Trials.ID, Pat.ID=Pat.ID, Model="Full")

# Show a summary of the results:
summary(Sur2)
## End(Not run)
```

---

Ovarian

*The Ovarian dataset*

---

### Description

This dataset combines the data that were collected in four double-blind randomized clinical trials in advanced ovarian cancer (Ovarian Cancer Meta-Analysis Project, 1991). In these trials, the objective was to examine the efficacy of cyclophosphamide plus cisplatin (CP) versus cyclophosphamide plus adriamycin plus cisplatin (CAP) to treat advanced ovarian cancer.

### Usage

```
data("Ovarian")
```

### Format

A data frame with 1192 observations on the following 7 variables.

Patient The ID number of a patient.

Center The center in which a patient was treated.

Treat The treatment indicator, coded as 0=CP (active control) and 1=CAP (experimental treatment).

Pfs Progression-free survival (the candidate surrogate).

PfsInd Censoring indicator for progression-free survival.

Surv Survival time (the true endpoint).

SurvInd Censoring indicator for survival time.

### References

Ovarian Cancer Meta-Analysis Project (1991). Cyclophosphamide plus cisplatin plus adriamycin versus cyclophosphamide, doxorubicin, and cisplatin chemotherapy of ovarian carcinoma: a meta-analysis. *Classic papers and current comments*, 3, 237-234.

### Examples

```
data(Ovarian)
str(Ovarian)
head(Ovarian)
```

---

plot Causal-Inference BinBin

*Plots the (Meta-Analytic) Individual Causal Association and related metrics when S and T are binary outcomes*

---

## Description

This function provides a plot that displays the frequencies, percentages, cumulative percentages or densities of the individual causal association (ICA;  $R_H^2$  or  $R_H$ ), and/or the odds ratios for  $S$  and  $T$  ( $\theta_S$  and  $\theta_T$ ).

## Usage

```
## S3 method for class 'ICA.BinBin'
plot(x, R2_H=TRUE, R_H=FALSE, Theta_T=FALSE,
     Theta_S=FALSE, Type="Density", Labels=FALSE, Xlab.R2_H,
     Main.R2_H, Xlab.R_H, Main.R_H, Xlab.Theta_S, Main.Theta_S, Xlab.Theta_T,
     Main.Theta_T, Cex.Legend=1, Cex.Position="topright",
     col, Par=par(oma=c(0, 0, 0, 0), mar=c(5.1, 4.1, 4.1, 2.1)), ylim, ...)
```

## Arguments

x	An object of class ICA.BinBin. See <a href="#">ICA.BinBin</a> .
R2_H	Logical. When R2_H=TRUE, a plot of the $R_H^2$ is provided. Default TRUE.
R_H	Logical. When R_H=TRUE, a plot of the $R_H$ is provided. Default FALSE.
Theta_T	Logical. When Theta_T=TRUE, a plot of the $\theta_T$ is provided. Default FALSE.
Theta_S	Logical. When Theta_S=TRUE, a plot of the $\theta_S$ is provided. Default FALSE.
Type	The type of plot that is produced. When Type="Freq" or Type="Percent", the Y-axis shows frequencies or percentages of $R_H^2$ , $R_H$ , $\theta_T$ , or $\theta_S$ . When Type="CumPerc", the Y-axis shows cumulative percentages. When Type="Density", the density is shown. When the fitted object of class ICA.BinBin was obtained using a general analysis (i.e., using the Monotonicity=c("General") argument in the function call), sperate plots are provided for the different monotonicity scenarios. Default "Density".
Labels	Logical. When Labels=TRUE, the percentage of $R_H^2$ , $R_H$ , $\theta_T$ , or $\theta_S$ values that are equal to or larger than the midpoint value of each of the bins are displayed (on top of each bin). Default FALSE.
Xlab.R2_H	The legend of the X-axis of the $R_H^2$ plot.
Main.R2_H	The title of the $R_H^2$ plot.
Xlab.R_H	The legend of the X-axis of the $R_H$ plot.
Main.R_H	The title of the $R_H$ plot.
Xlab.Theta_S	The legend of the X-axis of the $\theta_S$ plot.
Main.Theta_S	The title of the $\theta_S$ plot.

Xlab.Theta_T	The legend of the X-axis of the $\theta_T$ plot.
Main.Theta_T	The title of the $\theta_T$ plot.
Cex.Legend	The size of the legend when Type="All.Densities" is used. Default Cex.Legend=1.
Cex.Position	The position of the legend, Cex.Position="topright" or Cex.Position="topleft". Default Cex.Position="topright".
col	The color of the bins. Default col <-c(8).
Par	Graphical parameters for the plot. Default par(oma=c(0,0,0,0),mar=c(5.1,4.1,4.1,2.1)).
ylim	The (min, max) values for the Y-axis.
...	Extra graphical parameters to be passed to hist().

**Author(s)**

Wim Van der Elst, Ariel Alonso, & Geert Molenberghs

**References**

Alonso, A., Van der Elst, W., Molenberghs, G., Buyse, M., & Burzykowski, T. (submitted). A causal-inference approach for the validation of surrogate endpoints based on information theory and sensitivity analysis.

**See Also**

[ICA.BinBin](#)

**Examples**

```
# Compute R2_H given the marginals,
# assuming monotonicity for S and T and grids
# pi_0111=seq(0, 1, by=.001) and
# pi_1100=seq(0, 1, by=.001)
ICA <- ICA.BinBin.Grid.Sample(pi1_1_=0.261, pi1_0_=0.285,
pi_1_1=0.637, pi_1_0=0.078, pi0_1_=0.134, pi_0_1=0.127,
Monotonicity=c("General"), M=2500, Seed=1)

# Plot the results (density of R2_H):
plot(ICA, Type="Density", R2_H=TRUE, R_H=FALSE,
Theta_T=FALSE, Theta_S=FALSE)
```

---

plot Causal-Inference BinCont

*Plots the (Meta-Analytic) Individual Causal Association and related metrics when S is continuous and T is binary*

---

**Description**

This function provides a plot that displays the frequencies, percentages, cumulative percentages or densities of the individual causal association (ICA;  $R_H^2$ ) in the setting where S is continuous and T is binary.

**Usage**

```
## S3 method for class 'ICA.BinCont'
plot(x, Xlab, Main=" ", Type="Percent", Labels=FALSE, ...)
```

**Arguments**

x	An object of class ICA.BinCont. See <a href="#">ICA.BinCont</a> .
Xlab	The legend of the X-axis of the plot.
Main	The title of the plot.
Type	The type of plot that is produced. When Type="Freq" or Type="Percent", the Y-axis shows frequencies or percentages of $R_H^2$ . When Type="CumPerc", the Y-axis shows cumulative percentages. When Type="Density", the density is shown.
Labels	Logical. When Labels=TRUE, the percentage of $R_H^2$ values that are equal to or larger than the midpoint value of each of the bins are displayed (on top of each bin). Default FALSE.
...	Extra graphical parameters to be passed to hist().

**Author(s)**

Wim Van der Elst, Paul Meyvisch, & Ariel Alonso

**References**

Alonso, A., Van der Elst, W., & Meyvisch, P. (2016). Surrogate markers validation: the continuous-binary setting from a causal inference perspective.

**See Also**

[ICA.BinCont](#)

**Examples**

```
## Not run: # Time consuming code part
Fit <- ICA.BinCont(Dataset = Schizo, Surr = BPRS, True = PANSS_Bin,
Treat=Treat, M=50, Seed=1)

summary(Fit)
plot(Fit)

## End(Not run)
```

---

```
plot Causal-Inference ContCont
```

*Plots the (Meta-Analytic) Individual Causal Association when S and T are continuous outcomes*

---

## Description

This function provides a plot that displays the frequencies, percentages, or cumulative percentages of the individual causal association (ICA;  $\rho_{\Delta}$ ) and/or the meta-analytic individual causal association (MICA;  $\rho_M$ ) values. These figures are useful to examine the sensitivity of the obtained results with respect to the assumptions regarding the correlations between the counterfactuals (for details, see Alonso et al., submitted; Van der Elst et al., submitted). Optionally, it is also possible to obtain plots that are useful in the examination of the plausibility of finding a good surrogate endpoint when an object of class ICA.ContCont is considered.

## Usage

```
## S3 method for class 'ICA.ContCont'
plot(x, Xlab.ICA, Main.ICA, Type="Percent",
     Labels=FALSE, ICA=TRUE, Good.Surr=FALSE, Main.Good.Surr,
     Par=par(oma=c(0, 0, 0, 0), mar=c(5.1, 4.1, 4.1, 2.1)), col, ...)

## S3 method for class 'MICA.ContCont'
plot(x, ICA=TRUE, MICA=TRUE, Type="Percent",
     Labels=FALSE, Xlab.ICA, Main.ICA, Xlab.MICA, Main.MICA,
     Par=par(oma=c(0, 0, 0, 0), mar=c(5.1, 4.1, 4.1, 2.1)), col, ...)
```

## Arguments

x	An object of class ICA.ContCont or MICA.ContCont. See <a href="#">ICA.ContCont</a> or <a href="#">MICA.ContCont</a> .
ICA	Logical. When ICA=TRUE, a plot of the ICA is provided. Default TRUE.
MICA	Logical. This argument only has effect when the plot() function is applied to an object of class MICA.ContCont. When MICA=TRUE, a plot of the MICA is provided. Default TRUE.
Type	The type of plot that is produced. When Type=Freq or Type=Percent, the Y-axis shows frequencies or percentages of $\rho_{\Delta}$ , $\rho_M$ , and/or $\delta$ . When Type=CumPerc, the Y-axis shows cumulative percentages of $\rho_{\Delta}$ , $\rho_M$ , and/or $\delta$ . Default "Percent".
Labels	Logical. When Labels=TRUE, the percentage of $\rho_{\Delta}$ , $\rho_M$ , and/or $\delta$ values that are equal to or larger than the midpoint value of each of the bins are displayed (on top of each bin). Default FALSE.
Xlab.ICA	The legend of the X-axis of the ICA plot. Default " $\rho_{\Delta}$ ".
Main.ICA	The title of the ICA plot. Default "ICA".
Xlab.MICA	The legend of the X-axis of the MICA plot. Default " $\rho_M$ ".

Main.MICA	The title of the MICA plot. Default "MICA".
Good.Surr	Logical. When Good.Surr=TRUE, a plot of $\delta$ is provided. This plot is useful in the context of examining the plausibility of finding a good surrogate endpoint. Only applies when an object of class ICA.ContCont is considered. For details, see Alonso et al. (submitted). Default FALSE.
Main.Good.Surr	The title of the plot of $\delta$ . Only applies when an object of class ICA.ContCont is considered. For details, see Alonso et al. (submitted).
Par	Graphical parameters for the plot. Default <code>par(oma=c(0,0,0,0),mar=c(5.1,4.1,4.1,2.1))</code> .
col	The color of the bins. Default <code>col&lt;-c(8)</code> .
...	Extra graphical parameters to be passed to <code>hist()</code> .

**Author(s)**

Wim Van der Elst, Ariel Alonso, & Geert Molenberghs

**References**

Alonso, A., Van der Elst, W., Molenberghs, G., Buyse, M., & Burzykowski, T. (submitted). On the relationship between the causal inference and meta-analytic paradigms for the validation of surrogate markers.

Van der Elst, W., Alonso, A., & Molenberghs, G. (submitted). An exploration of the relationship between causal inference and meta-analytic measures of surrogacy.

**See Also**

[ICA.ContCont](#), [MICA.ContCont](#), [plot MinSurrContCont](#)

**Examples**

```
# Plot of ICA

# Generate the vector of ICA values when rho_T0S0=rho_T1S1=.95, and when the
# grid of values {0, .2, ..., 1} is considered for the correlations
# between the counterfactuals:
SurICA <- ICA.ContCont(T0S0=.95, T1S1=.95, T0T1=seq(0, 1, by=.2), T0S1=seq(0, 1, by=.2),
T1S0=seq(0, 1, by=.2), S0S1=seq(0, 1, by=.2))

# Plot the results:
plot(SurICA)

# Same plot but add the percentages of ICA values that are equal to or larger
# than the midpoint values of the bins
plot(SurICA, Labels=TRUE)

# Plot of both ICA and MICA

# Generate the vector of ICA and MICA values when R_trial=.8, rho_T0S0=rho_T1S1=.8,
# D.aa=5, D.bb=10, and when the grid of values {0, .2, ..., 1} is considered
# for the correlations between the counterfactuals:
```



```
SurMICA <- MICA.ContCont(Trial.R=.80, D.aa=5, D.bb=10, T0S0=.8, T1S1=.8,
T0T1=seq(0, 1, by=.2), T0S1=seq(0, 1, by=.2), T1S0=seq(0, 1, by=.2),
S0S1=seq(0, 1, by=.2))
```

```
# Plot the vector of generated ICA and MICA values
plot(SurMICA, ICA=TRUE, MICA=TRUE)
```

---

```
plot FixedDiscrDiscrIT
```

*Provides plots of trial-level surrogacy in the Information-Theoretic framework*

---

## Description

Produces plots that provide a graphical representation of trial level surrogacy  $R_{ht}^2$  based on the Information-Theoretic approach of Alonso & Molenberghs (2007).

## Usage

```
## S3 method for class 'FixedDiscrDiscrIT'
plot(x, Weighted=TRUE, Xlab.Trial, Ylab.Trial, Main.Trial,
     Par=par(oma=c(0, 0, 0, 0), mar=c(5.1, 4.1, 4.1, 2.1)), ...)
```

## Arguments

x	An object of class FixedDiscrDiscrIT.
Weighted	Logical. This argument only has effect when the user requests a trial-level surrogacy plot (i.e., when Trial.Level=TRUE in the function call). If Weighted=TRUE, the circles that depict the trial-specific treatment effects on the true endpoint against the surrogate endpoint are proportional to the number of patients in the trial. If Weighted=FALSE, all circles have the same size. Default TRUE.
Xlab.Trial	The legend of the X-axis of the plot that depicts trial-level surrogacy. Default "Treatment effect on the surrogate endpoint ( $\alpha_i$ )".
Ylab.Trial	The legend of the Y-axis of the plot that depicts trial-level surrogacy. Default "Treatment effect on the true endpoint ( $\beta_i$ )".
Main.Trial	The title of the plot that depicts trial-level surrogacy. Default "Trial-level surrogacy".
Par	Graphical parameters for the plot. Default par(oma=c(0, 0, 0, 0), mar=c(5.1, 4.1, 4.1, 2.1)).
...	Extra graphical parameters to be passed to plot().

## Author(s)

Hannah M. Ensor & Christopher J. Weir

**References**

Alonso, A, & Molenberghs, G. (2007). Surrogate marker evaluation from an information theory perspective. *Biometrics*, 63, 180-186.

**See Also**

[FixedDiscrDiscrIT](#)

**Examples**

```
## Not run: # Time consuming (>5sec) code part
# Simulate the data:
Sim.Data.MTS(N.Total=2000, N.Trial=100, R.Trial.Target=.8, R.Indiv.Target=.8,
             Seed=123, Model="Full")

# create a binary true and ordinal surrogate outcome
Data.Observed.MTS$True<-findInterval(Data.Observed.MTS$True,
                                     c(quantile(Data.Observed.MTS$True,0.5)))
Data.Observed.MTS$Surr<-findInterval(Data.Observed.MTS$Surr,
                                    c(quantile(Data.Observed.MTS$Surr,0.333),quantile(Data.Observed.MTS$Surr,0.666)))

# Assess surrogacy based on a full fixed-effect model
# in the information-theoretic framework for a binary surrogate and ordinal true outcome:
SurEval <- FixedDiscrDiscrIT(Dataset=Data.Observed.MTS, Surr=Surr, True=True, Treat=Treat,
                             Trial.ID=Trial.ID, Setting="ordbin")

## Request trial-level surrogacy plot. In the trial-level plot,
## make the size of the circles proportional to the number of patients in a trial:
plot(SurEval, Weighted=FALSE)

## End(Not run)
```

---

plot ICA.ContCont.MultS

*Plots the Individual Causal Association in the setting where there are multiple continuous S and a continuous T*

---

**Description**

This function provides a plot that displays the frequencies, percentages, or cumulative percentages of the multivariate individual causal association ( $R_H^2$ ). These figures are useful to examine the sensitivity of the obtained results with respect to the assumptions regarding the correlations between the counterfactuals.

**Usage**

```
## S3 method for class 'ICA.ContCont.MultS'
plot(x, R2_H=FALSE, Corr.R2_H=TRUE,
     Type="Percent", Labels=FALSE,
     Par=par(oma=c(0, 0, 0, 0), mar=c(5.1, 4.1, 4.1, 2.1)), col,
     Prediction.Error.Reduction=FALSE, ...)
```

**Arguments**

x	An object of class <code>ICA.ContCont.MultS</code> . See <code>ICA.ContCont.MultS</code> or <code>ICA.ContCont.MultS_alt</code> .
R2_H	Should a plot of the $R_H^2$ be provided? Default FALSE.
Corr.R2_H	Should a plot of the corrected $R_H^2$ be provided? Default TRUE.
Type	The type of plot that is produced. When <code>Type=Freq</code> or <code>Type=Percent</code> , the Y-axis shows frequencies or percentages of $R_H^2$ . When <code>Type=CumPerc</code> , the Y-axis shows cumulative percentages of $R_H^2$ . Default "Percent".
Labels	Logical. When <code>Labels=TRUE</code> , the percentage of $R_H^2$ values that are equal to or larger than the midpoint value of each of the bins are displayed (on top of each bin). Default FALSE.
Par	Graphical parameters for the plot. Default <code>par(oma=c(0, 0, 0, 0), mar=c(5.1, 4.1, 4.1, 2.1))</code> .
col	The color of the bins. Default <code>col &lt;- c(8)</code> .
Prediction.Error.Reduction	Should a plot be shown that shows the prediction error (reisdual error) in predicting $\Delta T$ using an intercept only model, and that shows the prediction error (reisdual error) in predicting $\Delta T$ using $\Delta S_1$ , $\Delta S_2$ , ...? Default <code>Prediction.Error.Reduction=FALSE</code> .
...	Extra graphical parameters to be passed to <code>hist()</code> .

**Author(s)**

Wim Van der Elst, Ariel Alonso, & Geert Molenberghs

**References**

Van der Elst, W., Alonso, A. A., & Molenberghs, G. (2017). Univariate versus multivariate surrogate endpoints.

**See Also**

[ICA.ContCont](#), [ICA.ContCont.MultS](#), [ICA.ContCont.MultS\\_alt](#), [MICA.ContCont](#), [plot MinSurContCont](#)

**Examples**

```
## Not run: #time-consuming code parts
# Specify matrix Sigma (var-covar matrix T_0, T_1, S1_0, S1_1, ...)
# here for 1 true endpoint and 3 surrogates
```

```

s<-matrix(rep(NA, times=64),8)
s[1,1] <- 450; s[2,2] <- 413.5; s[3,3] <- 174.2; s[4,4] <- 157.5;
s[5,5] <- 244.0; s[6,6] <- 229.99; s[7,7] <- 294.2; s[8,8] <- 302.5
s[3,1] <- 160.8; s[5,1] <- 208.5; s[7,1] <- 268.4
s[4,2] <- 124.6; s[6,2] <- 212.3; s[8,2] <- 287.1
s[5,3] <- 160.3; s[7,3] <- 142.8
s[6,4] <- 134.3; s[8,4] <- 130.4
s[7,5] <- 209.3;
s[8,6] <- 214.7
s[upper.tri(s)] = t(s)[upper.tri(s)]

# Marix looks like:
#           T_0   T_1  S1_0  S1_1  S2_0  S2_1  S2_0  S2_1
#           [,1] [,2] [,3] [,4] [,5] [,6] [,7] [,8]
# T_0 [1,] 450.0   NA 160.8   NA 208.5   NA 268.4   NA
# T_1 [2,]   NA 413.5   NA 124.6   NA 212.30   NA 287.1
# S1_0 [3,] 160.8   NA 174.2   NA 160.3   NA 142.8   NA
# S1_1 [4,]   NA 124.6   NA 157.5   NA 134.30   NA 130.4
# S2_0 [5,] 208.5   NA 160.3   NA 244.0   NA 209.3   NA
# S2_1 [6,]   NA 212.3   NA 134.3   NA 229.99   NA 214.7
# S3_0 [7,] 268.4   NA 142.8   NA 209.3   NA 294.2   NA
# S3_1 [8,]   NA 287.1   NA 130.4   NA 214.70   NA 302.5

# Conduct analysis
ICA <- ICA.ContCont.MultS(M=100, N=200, Show.Progress = TRUE,
  Sigma=s, G = seq(from=-1, to=1, by = .00001), Seed=c(123),
  Model = "Delta_T ~ Delta_S1 + Delta_S2 + Delta_S3")

# Explore results
summary(ICA)
plot(ICA)

## End(Not run)

```

---

plot Information-Theoretic

*Provides plots of trial- and individual-level surrogacy in the Information-Theoretic framework*

---

## Description

Produces plots that provide a graphical representation of trial- and/or individual-level surrogacy (R2\_ht and R2\_h) based on the Information-Theoretic approach of Alonso & Molenberghs (2007).

## Usage

```

## S3 method for class 'FixedContContIT'
plot(x, Trial.Level=TRUE, Weighted=TRUE, Individ.Level=TRUE,
  Xlab.Indiv, Ylab.Indiv, Xlab.Trial, Ylab.Trial, Main.Trial, Main.Indiv,
  Par=par(oma=c(0, 0, 0, 0), mar=c(5.1, 4.1, 4.1, 2.1)), ...)

```

```
## S3 method for class 'MixedContContIT'
plot(x, Trial.Level=TRUE, Weighted=TRUE, Individ.Level=TRUE,
     Xlab.Indiv, Ylab.Indiv, Xlab.Trial, Ylab.Trial, Main.Trial, Main.Indiv,
     Par=par(oma=c(0, 0, 0, 0), mar=c(5.1, 4.1, 4.1, 2.1)), ...)
```

### Arguments

x	An object of class MixedContContIT or FixedContContIT.
Trial.Level	Logical. If Trial.Level=TRUE, a plot of the trial-specific treatment effects on the true endpoint against the trial-specific treatment effect on the surrogate endpoints is provided (as a graphical representation of $R_{ht}$ ). Default TRUE.
Weighted	Logical. This argument only has effect when the user requests a trial-level surrogacy plot (i.e., when Trial.Level=TRUE in the function call). If Weighted=TRUE, the circles that depict the trial-specific treatment effects on the true endpoint against the surrogate endpoint are proportional to the number of patients in the trial. If Weighted=FALSE, all circles have the same size. Default TRUE.
Individ.Level	Logical. If Individ.Level=TRUE, a plot of the trial- and treatment-corrected residuals of the true and surrogate endpoints is provided. This plot provides a graphical representation of $R_h$ . Default TRUE.
Xlab.Indiv	The legend of the X-axis of the plot that depicts individual-level surrogacy. Default "Residuals for the surrogate endpoint ( $\varepsilon_{Sij}$ )".
Ylab.Indiv	The legend of the Y-axis of the plot that depicts individual-level surrogacy. Default "Residuals for the true endpoint ( $\varepsilon_{Tij}$ )".
Xlab.Trial	The legend of the X-axis of the plot that depicts trial-level surrogacy. Default "Treatment effect on the surrogate endpoint ( $\alpha_i$ )".
Ylab.Trial	The legend of the Y-axis of the plot that depicts trial-level surrogacy. Default "Treatment effect on the true endpoint ( $\beta_i$ )".
Main.Indiv	The title of the plot that depicts individual-level surrogacy. Default "Individual-level surrogacy".
Main.Trial	The title of the plot that depicts trial-level surrogacy. Default "Trial-level surrogacy".
Par	Graphical parameters for the plot. Default par(oma=c(0, 0, 0, 0), mar=c(5.1, 4.1, 4.1, 2.1)).
...	Extra graphical parameters to be passed to plot().

### Author(s)

Wim Van der Elst, Ariel Alonso, & Geert Molenberghs

### References

Alonso, A, & Molenberghs, G. (2007). Surrogate marker evaluation from an information theory perspective. *Biometrics*, 63, 180-186.

**See Also**

[MixedContContIT](#), [FixedContContIT](#)

**Examples**

```
## Load ARMD dataset
data(ARMD)

## Conduct a surrogacy analysis, using a weighted reduced univariate fixed effect model:
Sur <- MixedContContIT(Dataset=ARMD, Surr=Diff24, True=Diff52, Treat=Treat, Trial.ID=Center,
Pat.ID=Id, Model=c("Full"))

## Request both trial- and individual-level surrogacy plots. In the trial-level plot,
## make the size of the circles proportional to the number of patients in a trial:
plot(Sur, Trial.Level=TRUE, Weighted=TRUE, Individ.Level=TRUE)

## Make a trial-level surrogacy plot using filled blue circles that
## are transparent (to make sure that the results of overlapping trials remain
## visible), and modify the title and the axes labels of the plot:
plot(Sur, pch=16, col=rgb(.3, .2, 1, 0.3), Individ.Level=FALSE, Trial.Level=TRUE,
Weighted=TRUE, Main.Trial=c("Trial-level surrogacy (ARMD dataset)"),
Xlab.Trial=c("Difference in vision after 6 months (Surrogate)"),
Ylab.Trial=c("Difference in vision after 12 months (True endpoint)"))

## Add the estimated R2_ht value in the previous plot at position (X=-2.2, Y=0)
## (the previous plot should not have been closed):
R2ht <- format(round(as.numeric(Sur$R2ht[1]), 3))
text(x=-2.2, y=0, cex=1.4, labels=(bquote(paste("R"[ht]^{2}, "="~.(R2ht)))))

## Make an Individual-level surrogacy plot with red squares to depict individuals
## (rather than black circles):
plot(Sur, pch=15, col="red", Individ.Level=TRUE, Trial.Level=FALSE)
```

---

plot Information-Theoretic BinComb

*Provides plots of trial- and individual-level surrogacy in the Information-Theoretic framework when both S and T are binary, or when S is binary and T is continuous (or vice versa)*

---

**Description**

Produces plots that provide a graphical representation of trial- and/or individual-level surrogacy (R2\_ht and R2\_hInd per cluster) based on the Information-Theoretic approach of Alonso & Molenberghs (2007).

**Usage**

```
## S3 method for class 'FixedBinBinIT'
plot(x, Trial.Level=TRUE, Weighted=TRUE, Individ.Level.By.Trial=TRUE,
```

```
Xlab.Indiv, Ylab.Indiv, Xlab.Trial, Ylab.Trial, Main.Trial, Main.Indiv,
Par=par(oma=c(0, 0, 0, 0), mar=c(5.1, 4.1, 4.1, 2.1)), ...)
```

```
## S3 method for class 'FixedBinContIT'
plot(x, Trial.Level=TRUE, Weighted=TRUE, Indiv.Level.By.Trial=TRUE,
Xlab.Indiv, Ylab.Indiv, Xlab.Trial, Ylab.Trial, Main.Trial, Main.Indiv,
Par=par(oma=c(0, 0, 0, 0), mar=c(5.1, 4.1, 4.1, 2.1)), ...)
```

```
## S3 method for class 'FixedContBinIT'
plot(x, Trial.Level=TRUE, Weighted=TRUE, Indiv.Level.By.Trial=TRUE,
Xlab.Indiv, Ylab.Indiv, Xlab.Trial, Ylab.Trial, Main.Trial, Main.Indiv,
Par=par(oma=c(0, 0, 0, 0), mar=c(5.1, 4.1, 4.1, 2.1)), ...)
```

## Arguments

<code>x</code>	An object of class <code>FixedBinBinIT</code> , <code>FixedBinContIT</code> , or <code>FixedContBinIT</code> .
<code>Trial.Level</code>	Logical. If <code>Trial.Level=TRUE</code> , a plot of the trial-specific treatment effects on the true endpoint against the trial-specific treatment effect on the surrogate endpoints is provided (as a graphical representation of $R_{ht}$ ). Default <code>TRUE</code> .
<code>Weighted</code>	Logical. This argument only has effect when the user requests a trial-level surrogacy plot (i.e., when <code>Trial.Level=TRUE</code> in the function call). If <code>Weighted=TRUE</code> , the circles that depict the trial-specific treatment effects on the true endpoint against the surrogate endpoint are proportional to the number of patients in the trial. If <code>Weighted=FALSE</code> , all circles have the same size. Default <code>TRUE</code> .
<code>Indiv.Level.By.Trial</code>	Logical. If <code>Indiv.Level.By.Trial=TRUE</code> , a plot that shows the estimated $R_{h.ind}^2$ for each trial (and confidence intervals) is provided. Default <code>TRUE</code> .
<code>Xlab.Indiv</code>	The legend of the X-axis of the plot that depicts the estimated $R_{h.ind}^2$ per trial. Default <code>"R[h.ind]<sup>2</sup>"</code> .
<code>Ylab.Indiv</code>	The legend of the Y-axis of the plot that shows the estimated $R_{h.ind}^2$ per trial. Default <code>"Trial"</code> .
<code>Xlab.Trial</code>	The legend of the X-axis of the plot that depicts trial-level surrogacy. Default <code>"Treatment effect on the surrogate endpoint (<math>\alpha_i</math>)"</code> .
<code>Ylab.Trial</code>	The legend of the Y-axis of the plot that depicts trial-level surrogacy. Default <code>"Treatment effect on the true endpoint (<math>\beta_i</math>)"</code> .
<code>Main.Indiv</code>	The title of the plot that depicts individual-level surrogacy. Default <code>"Individual-level surrogacy"</code> .
<code>Main.Trial</code>	The title of the plot that depicts trial-level surrogacy. Default <code>"Trial-level surrogacy"</code> .
<code>Par</code>	Graphical parameters for the plot. Default <code>par(oma=c(0, 0, 0, 0), mar=c(5.1, 4.1, 4.1, 2.1))</code> .
<code>...</code>	Extra graphical parameters to be passed to <code>plot()</code> .

## Author(s)

Wim Van der Elst, Ariel Alonso, & Geert Molenberghs

**References**

Alonso, A, & Molenberghs, G. (2007). Surrogate marker evaluation from an information theory perspective. *Biometrics*, 63, 180-186.

**See Also**

[FixedBinBinIT](#), [FixedBinContIT](#), [FixedContBinIT](#)

**Examples**

```
## Not run: # Time consuming (>5sec) code part
# Generate data with continuous Surr and True
Sim.Data.MTS(N.Total=5000, N.Trial=50, R.Trial.Target=.9, R.Indiv.Target=.9,
             Fixed.Effects=c(0, 0, 0, 0), D.aa=10, D.bb=10, Seed=1,
             Model=c("Full"))
# Dichtomize Surr and True
Surr_Bin <- Data.Observed.MTS$Surr
Surr_Bin[Data.Observed.MTS$Surr>.5] <- 1
Surr_Bin[Data.Observed.MTS$Surr<=.5] <- 0
True_Bin <- Data.Observed.MTS$True
True_Bin[Data.Observed.MTS$True>.15] <- 1
True_Bin[Data.Observed.MTS$True<=.15] <- 0
Data.Observed.MTS$Surr <- Surr_Bin
Data.Observed.MTS$True <- True_Bin

# Assess surrogacy using info-theoretic framework
Fit <- FixedBinBinIT(Dataset = Data.Observed.MTS, Surr = Surr,
                    True = True, Treat = Treat, Trial.ID = Trial.ID,
                    Pat.ID = Pat.ID, Number.Bootstraps=100)

# Examine results
summary(Fit)
plot(Fit, Trial.Level = FALSE, Indiv.Level.By.Trial=TRUE)
plot(Fit, Trial.Level = TRUE, Indiv.Level.By.Trial=FALSE)

## End(Not run)
```

---

plot ISTE.ContCont	<i>Plots the individual-level surrogate threshold effect (STE) values and related metrics</i>
--------------------	---

---

**Description**

This function plots the individual-level surrogate threshold effect (STE) values and related metrics, e.g., the expected  $\Delta T$  values for a vector of  $\Delta S$  values.

**Usage**

```
## S3 method for class 'ISTE.ContCont'
plot(x, Outcome="ISTE", breaks=50, ...)
```



**Arguments**

x	An object of class ISTE.ContCont. See <a href="#">ISTE.ContCont</a> .
Outcome	The outcome for which a histogram has to be produced. When Outcome="ISTE", a histogram of the ISTE is produced. When Outcome="MSE", a histogram of the MSE values (of regression models in which $\Delta T$ is regressed on $\Delta S$ ) is given. When Outcome="gamma0", a histogram of $\gamma[0]$ values (of regression models in which $\Delta T$ is regressed on $\Delta S$ ) is given. When Outcome="gamma1", a histogram of $\gamma[1]$ values (of regression models in which $\Delta T$ is regressed on $\Delta S$ ) is given. When Outcome="Exp.DeltaT", a histogram of the expected $\Delta T$ values for a vector of $\Delta S$ values (specified in the call of the ISTE.ContCont function) values is given. When Outcome="Exp.DeltaT.Low.PI", a histogram of the lower prediction intervals of the expected $\Delta T$ values for a vector of $\Delta S$ values (specified in the call of the ISTE.ContCont function) values is given. When Outcome="Exp.DeltaT.Up.PI", a histogram of the upper prediction intervals of the expected $\Delta T$ values for a vector of $\Delta S$ values (specified in the call of the ISTE.ContCont function) values is given. Default Outcome="ISTE". When Outcome="Delta_S_For_Which_Delta_T_equal_0", a histogram of $\omega$ is shown with $E(\Delta T   \Delta S > \omega) > 0$ .
breaks	The number of breaks used in the histogram(s). Default breaks=50.
...	Extra graphical parameters to be passed to hist().

**Author(s)**

Wim Van der Elst, Ariel Alonso, & Geert Molenberghs

**References**

Van der Elst, W., Alonso, A. A., and Molenberghs, G. (submitted). The individual-level surrogate threshold effect in a causal-inference setting.

**See Also**

[ISTE.ContCont](#)

**Examples**

```
# Define input for analysis using the Schizo dataset,
# with S=BPRS and T = PANSS.
# For each of the identifiable quantities,
# uncertainty is accounted for by specifying a uniform
# distribution with min, max values corresponding to
# the 95% confidence interval of the quantity.
T0S0 <- runif(min = 0.9524, max = 0.9659, n = 1000)
T1S1 <- runif(min = 0.9608, max = 0.9677, n = 1000)

S0S0 <- runif(min=160.811, max=204.5009, n=1000)
S1S1 <- runif(min=168.989, max = 194.219, n=1000)
T0T0 <- runif(min=484.462, max = 616.082, n=1000)
T1T1 <- runif(min=514.279, max = 591.062, n=1000)
```

```

Mean_T0 <- runif(min=-13.455, max=-9.489, n=1000)
Mean_T1 <- runif(min=-17.17, max=-14.86, n=1000)
Mean_S0 <- runif(min=-7.789, max=-5.503, n=1000)
Mean_S1 <- runif(min=-9.600, max=-8.276, n=1000)

# Do the ISTE analysis
## Not run:
ISTE <- ISTE.ContCont(Mean_T1=Mean_T1, Mean_T0=Mean_T0,
  Mean_S1=Mean_S1, Mean_S0=Mean_S0, N=2128, Delta_S=c(-50:50),
  alpha.PI=0.05, PI.Bound=0, Show.Prediction.Plots=TRUE,
  Save.Plots="No", T0S0=T0S0, T1S1=T1S1, T0T0=T0T0, T1T1=T1T1,
  S0S0=S0S0, S1S1=S1S1)

# Examine results:
summary(ISTE)

# Plots of results.
# Plot main ISTE results
plot(ISTE)
# Other plots
plot(ISTE, Outcome="MSE")
plot(ISTE, Outcome="gamma0")
plot(ISTE, Outcome="gamma1")
plot(ISTE, Outcome="Exp.DeltaT")
plot(ISTE, Outcome="Exp.DeltaT.Low.PI")
plot(ISTE, Outcome="Exp.DeltaT.Up.PI")

## End(Not run)

```

---

plot MaxEnt ContCont *Plots the sensitivity-based and maximum entropy based Individual Causal Association when S and T are continuous outcomes in the single-trial setting*

---

## Description

This function provides a plot that displays the frequencies or densities of the individual causal association (ICA;  $\rho[\Delta]$ ) as identified based on the sensitivity- (using the functions [ICA.ContCont](#)) and maximum entropy-based (using the function [MaxEntContCont](#)) approaches.

## Usage

```

## S3 method for class 'MaxEntContCont'
plot(x, Type="Freq", Xlab, col,
  Main, Entropy.By.ICA=FALSE, ...)

```

**Arguments**

x	An object of class MaxEntContCont. See <a href="#">MaxEntContCont</a> .
Type	The type of plot that is produced. When Type="Freq", the Y-axis shows frequencies of ICA. When Type="Density", the density is shown. Default Type="Freq".
Xlab	The legend of the X-axis of the plot.
col	The color of the bins (frequency plot) or line (density plot). Default col <-c(8).
Main	The title of the plot.
Entropy.By.ICA	Plot with ICA on Y-axis and entropy on X-axis.
...	Other arguments to be passed to plot()

**Author(s)**

Wim Van der Elst, Ariel Alonso, Paul Meyvisch, & Geert Molenberghs

**References**

Add

**See Also**

[ICA.ContCont](#), [MaxEntContCont](#)

**Examples**

```
## Not run: #time-consuming code parts
# Compute ICA for ARMD dataset, using the grid
# G={-1, -.80, ..., 1} for the unidentifiable correlations

ICA <- ICA.ContCont(T0S0 = 0.769, T1S1 = 0.712, S0S0 = 188.926,
S1S1 = 132.638, T0T0 = 264.797, T1T1 = 231.771,
T0T1 = seq(-1, 1, by = 0.2), T0S1 = seq(-1, 1, by = 0.2),
T1S0 = seq(-1, 1, by = 0.2), S0S1 = seq(-1, 1, by = 0.2))

# Identify the maximum entropy ICA
MaxEnt_ARMD <- MaxEntContCont(x = ICA, S0S0 = 188.926,
S1S1 = 132.638, T0T0 = 264.797, T1T1 = 231.771)

# Explore results using summary() and plot() functions
summary(MaxEnt_ARMD)
plot(MaxEnt_ARMD)
plot(MaxEnt_ARMD, Entropy.By.ICA = TRUE)

## End(Not run)
```

---

plot MaxEntICA BinBin *Plots the sensitivity-based and maximum entropy based Individual Causal Association when S and T are binary outcomes*

---

### Description

This function provides a plot that displays the frequencies or densities of the individual causal association (ICA;  $R_H^2$ ) as identified based on the sensitivity- (using the functions [ICA.BinBin](#), [ICA.BinBin.Grid.Sample](#), or [ICA.BinBin.Grid.Full](#)) and maximum entropy-based (using the function [MaxEntICABinBin](#)) approaches.

### Usage

```
## S3 method for class 'MaxEntICA.BinBin'
plot(x, ICA.Fit,
     Type="Density", Xlab, col, Main, ...)
```

### Arguments

x	An object of class MaxEntICABinBin. See <a href="#">MaxEntICABinBin</a> .
ICA.Fit	An object of class ICA.BinBin. See <a href="#">ICA.BinBin</a> .
Type	The type of plot that is produced. When Type="Freq", the Y-axis shows frequencies of $R_H^2$ . When Type="Density", the density is shown.
Xlab	The legend of the X-axis of the plot.
col	The color of the bins (frequency plot) or line (density plot). Default col <-c(8).
Main	The title of the plot.
...	Other arguments to be passed to plot()

### Author(s)

Wim Van der Elst, Ariel Alonso, & Geert Molenberghs

### References

Alonso, A., & Van der Elst, W. (2015). A maximum-entropy approach for the evaluation of surrogate endpoints based on causal inference.

### See Also

[ICA.BinBin](#), [MaxEntICABinBin](#)

**Examples**

```
# Sensitivity-based ICA results using ICA.BinBin.Grid.Sample
ICA <- ICA.BinBin.Grid.Sample(pi1_1=0.341, pi0_1=0.119, pi1_0=0.254,
  pi_1_1=0.686, pi_1_0=0.088, pi_0_1=0.078, Seed=1,
  Monotonicity=c("No"), M=5000)

# Maximum-entropy based ICA
MaxEnt <- MaxEntICABinBin(pi1_1=0.341, pi0_1=0.119, pi1_0=0.254,
  pi_1_1=0.686, pi_1_0=0.088, pi_0_1=0.078)

# Plot results
plot(x=MaxEnt, ICA.Fit=ICA)
```

---

plot MaxEntSPF BinBin *Plots the sensitivity-based and maximum entropy based surrogate predictive function (SPF) when S and T are binary outcomes.*

---

**Description**

Plots the sensitivity-based (Alonso et al., 2015a) and maximum entropy based (Alonso et al., 2015b) surrogate predictive function (SPF), i.e.,  $r(i, j) = P(\Delta T = i | \Delta S = j)$ , in the setting where both  $S$  and  $T$  are binary endpoints. For example,  $r(-1, 1)$  quantifies the probability that the treatment has a negative effect on the true endpoint ( $\Delta T = -1$ ) given that it has a positive effect on the surrogate ( $\Delta S = 1$ ).

**Usage**

```
## S3 method for class 'MaxEntSPF.BinBin'
plot(x, SPF.Fit, Type="All.Histograms", Col="grey", ...)
```

**Arguments**

x	A fitted object of class MaxEntSPF.BinBin. See <a href="#">MaxEntSPFBinBin</a> .
SPF.Fit	A fitted object of class SPF.BinBin. See <a href="#">SPF.BinBin</a> .
Type	The type of plot that is requested. Possible choices are: Type="All.Histograms", the histograms of all 9 $r(i, j) = P(\Delta T = i   \Delta S = j)$ vectors arranged in a 3 by 3 grid; Type="All.Densities", plots of densities of all $r(i, j) = P(\Delta T = i   \Delta S = j)$ vectors. Default Type="All.Densities".
Col	The color of the bins or lines when histograms or density plots are requested. Default "grey".
...	Other arguments to be passed to the plot() function.

**Author(s)**

Wim Van der Elst, Ariel Alonso, & Geert Molenberghs

**References**

Alonso, A., Van der Elst, W., & Molenberghs, G. (2015a). Assessing a surrogate effect predictive value in a causal inference framework.

Alonso, A., & Van der Elst, W. (2015b). A maximum-entropy approach for the evaluation of surrogate endpoints based on causal inference.

**See Also**

[SPF.BinBin](#)

**Examples**

```
# Sensitivity-based ICA results using ICA.BinBin.Grid.Sample
ICA <- ICA.BinBin.Grid.Sample(pi1_1=0.341, pi0_1=0.119, pi1_0=0.254,
pi_1_1=0.686, pi_1_0=0.088, pi_0_1=0.078, Seed=1,
Monotonicity=c("No"), M=5000)

# Sensitivity-based SPF
SPFSens <- SPF.BinBin(ICA)

# Maximum-entropy based SPF
SPFMaxEnt <- MaxEntSPFBinBin(pi1_1=0.341, pi0_1=0.119, pi1_0=0.254,
pi_1_1=0.686, pi_1_0=0.088, pi_0_1=0.078)

# Plot results
plot(x=SPFMaxEnt, SPF.Fit=SPFSens)
```

---

plot Meta-Analytic      *Provides plots of trial- and individual-level surrogacy in the meta-analytic framework*

---

**Description**

Produces plots that provide a graphical representation of trial- and/or individual-level surrogacy based on the meta-analytic approach of Buyse & Molenberghs (2000) in the single- and multiple-trial settings.

**Usage**

```
## S3 method for class 'BifixedContCont'
plot(x, Trial.Level=TRUE, Weighted=TRUE,
Indiv.Level=TRUE, ICA=TRUE, Entropy.By.ICA=FALSE, Xlab.Indiv, Ylab.Indiv,
Xlab.Trial, Ylab.Trial, Main.Trial, Main.Indiv, Par=par(oma=c(0, 0, 0, 0),
mar=c(5.1, 4.1, 4.1, 2.1)), ...)

## S3 method for class 'BimixedContCont'
plot(x, Trial.Level=TRUE, Weighted=TRUE,
Indiv.Level=TRUE, ICA=TRUE, Entropy.By.ICA=FALSE, Xlab.Indiv, Ylab.Indiv,
```

```
Xlab.Trial, Ylab.Trial, Main.Trial, Main.Indiv, Par=par(oma=c(0, 0, 0, 0),
mar=c(5.1, 4.1, 4.1, 2.1)), ...)
```

```
## S3 method for class 'UnifixedContCont'
plot(x, Trial.Level=TRUE, Weighted=TRUE,
Indiv.Level=TRUE, ICA=TRUE, Entropy.By.ICA=FALSE,
Xlab.Indiv, Ylab.Indiv, Xlab.Trial, Ylab.Trial,
Main.Trial, Main.Indiv, Par=par(oma=c(0, 0, 0, 0),
mar=c(5.1, 4.1, 4.1, 2.1)), ...)
```

```
## S3 method for class 'UnimixedContCont'
plot(x, Trial.Level=TRUE, Weighted=TRUE,
Indiv.Level=TRUE, ICA=TRUE, Entropy.By.ICA=FALSE,
Xlab.Indiv, Ylab.Indiv, Xlab.Trial, Ylab.Trial,
Main.Trial, Main.Indiv, Par=par(oma=c(0, 0, 0, 0),
mar=c(5.1, 4.1, 4.1, 2.1)), ...)
```

## Arguments

x	An object of class <code>UnifixedContCont</code> , <code>BifixedContCont</code> , <code>UnimixedContCont</code> , <code>BimixedContCont</code> , or <code>Single.Trial.RE.AA</code> .
<code>Trial.Level</code>	Logical. If <code>Trial.Level=TRUE</code> and an object of class <code>UnifixedContCont</code> , <code>BifixedContCont</code> , <code>UnimixedContCont</code> , or <code>BimixedContCont</code> is considered, a plot of the trial-specific treatment effects on the true endpoint against the trial-specific treatment effect on the surrogate endpoints is provided (as a graphical representation of $R_{trial}$ ). If <code>Trial.Level=TRUE</code> and an object of class <code>Single.Trial.RE.AA</code> is considered, a plot of the treatment effect on the true endpoint against the treatment effect on the surrogate endpoint is provided, and a regression line that goes through the origin with slope RE is added to the plot (to depict the constant RE assumption, see <a href="#">Single.Trial.RE.AA</a> for details). If <code>Trial.Level=FALSE</code> , this plot is not provided. Default TRUE.
<code>Weighted</code>	Logical. This argument only has effect when the user requests a trial-level surrogacy plot (i.e., when <code>Trial.Level=TRUE</code> in the function call) and when an object of class <code>UnifixedContCont</code> , <code>BifixedContCont</code> , <code>UnimixedContCont</code> , or <code>BimixedContCont</code> is considered (not when an object of class <code>Single.Trial.RE.AA</code> is considered). If <code>Weighted=TRUE</code> , the circles that depict the trial-specific treatment effects on the true endpoint against the surrogate endpoint are proportional to the number of patients in the trial. If <code>Weighted=FALSE</code> , all circles have the same size. Default TRUE.
<code>Indiv.Level</code>	Logical. If <code>Indiv.Level=TRUE</code> , a plot of the trial- and treatment-corrected residuals of the true and surrogate endpoints is provided (when an object of class <code>UnifixedContCont</code> , <code>BifixedContCont</code> , <code>UnimixedContCont</code> , or <code>BimixedContCont</code> is considered), or a plot of the treatment-corrected residuals (when an object of class <code>Single.Trial.RE.AA</code> is considered). This plot provides a graphical representation of $R_{indiv}$ . If <code>Indiv.Level=FALSE</code> , this plot is not provided. Default TRUE.

ICA	Logical. Should a plot of the individual level causal association be shown? Default ICA=TRUE.
Entropy.By.ICA	Logical. Should a plot that shows ICA against the entropy be shown? Default Entropy.By.ICA=FALSE.
Xlab.Indiv	The legend of the X-axis of the plot that depicts individual-level surrogacy. Default "Residuals for the surrogate endpoint ( $\varepsilon_{Sij}$ )" (without the $i$ subscript when an object of class <code>Single.Trial.RE.AA</code> is considered).
Ylab.Indiv	The legend of the Y-axis of the plot that depicts individual-level surrogacy. Default "Residuals for the true endpoint ( $\varepsilon_{Tij}$ )" (without the $i$ subscript when an object of class <code>Single.Trial.RE.AA</code> is considered).
Xlab.Trial	The legend of the X-axis of the plot that depicts trial-level surrogacy. Default "Treatment effect on the surrogate endpoint ( $\alpha_i$ )" (without the $i$ subscript when an object of class <code>Single.Trial.RE.AA</code> is considered).
Ylab.Trial	The legend of the Y-axis of the plot that depicts trial-level surrogacy. Default "Treatment effect on the true endpoint ( $\beta_i$ )" (without the $i$ subscript when an object of class <code>Single.Trial.RE.AA</code> is considered).
Main.Indiv	The title of the plot that depicts individual-level surrogacy. Default "Individual-level surrogacy" when an object of class <code>UnifixedContCont</code> , <code>BifixedContCont</code> , <code>UnimixedContCont</code> , or <code>BimixedContCont</code> is considered, and "Adjusted Association ( $\rho_{0z}$ )" when an object of class <code>Single.Trial.RE.AA</code> is considered.
Main.Trial	The title of the plot that depicts trial-level surrogacy. Default "Trial-level surrogacy" (when an object of class <code>UnifixedContCont</code> , <code>BifixedContCont</code> , <code>UnimixedContCont</code> , or <code>BimixedContCont</code> is considered) or "Relative Effect (RE)" (when an object of class <code>Single.Trial.RE.AA</code> is considered).
Par	Graphical parameters for the plot. Default <code>par(oma=c(0,0,0,0),mar=c(5.1,4.1,4.1,2.1))</code> .
...	Extra graphical parameters to be passed to <code>plot()</code> .

**Author(s)**

Wim Van der Elst, Ariel Alonso, & Geert Molenberghs

**References**

Buyse, M., Molenberghs, G., Burzykowski, T., Renard, D., & Geys, H. (2000). The validation of surrogate endpoints in meta-analysis of randomized experiments. *Biostatistics*, 1, 49-67.

**See Also**

[UnifixedContCont](#), [BifixedContCont](#), [UnifixedContCont](#), [BimixedContCont](#), [Single.Trial.RE.AA](#)

**Examples**

```
## Not run: # time consuming code part
##### Multiple-trial setting

## Load ARMD dataset
data(ARMD)
```



```

## Conduct a surrogacy analysis, using a weighted reduced univariate fixed effect model:
Sur <- UnifixedContCont(Dataset=ARMD, Surr=Diff24, True=Diff52, Treat=Treat, Trial.ID=Center,
Pat.ID=Id, Number.Bootstraps=100, Model=c("Reduced"), Weighted=TRUE)

## Request both trial- and individual-level surrogacy plots. In the trial-level plot,
## make the size of the circles proportional to the number of patients in a trial:
plot(Sur, Trial.Level=TRUE, Weighted=TRUE, Individ.Level=TRUE)

## Make a trial-level surrogacy plot using filled blue circles that
## are transparent (to make sure that the results of overlapping trials remain
## visible), and modify the title and the axes labels of the plot:
plot(Sur, pch=16, col=rgb(.3, .2, 1, 0.3), Individ.Level=FALSE, Trial.Level=TRUE,
Weighted=TRUE, Main.Trial=c("Trial-level surrogacy (ARMD dataset)"),
Xlab.Trial=c("Difference in vision after 6 months (Surrogate)"),
Ylab.Trial=c("Difference in vision after 12 months (True endpoint)"))

## Add the estimated R2_trial value in the previous plot at position (X=-7, Y=11)
## (the previous plot should not have been closed):
R2trial <- format(round(as.numeric(Sur$Trial.R2[1]), 3))
text(x=-7, y=11, cex=1.4, labels=(bquote(paste("R"[trial]^2}, "~.(R2trial))))))

## Make an Individual-level surrogacy plot with red squares to depict individuals
## (rather than black circles):
plot(Sur, pch=15, col="red", Individ.Level=TRUE, Trial.Level=FALSE)

## Same plot as before, but now with smaller squares, a y-axis with range [-40; 40],
## and the estimated R2_indiv value in the title of the plot:
R2ind <- format(round(as.numeric(Sur$Indiv.R2[1]), 3))
plot(Sur, pch=15, col="red", Individ.Level=TRUE, Trial.Level=FALSE, cex=.5,
ylim=c(-40, 40), Main.Indiv=bquote(paste("R"[indiv]^2}, "~.(R2ind))))

##### Single-trial setting

## Conduct a surrogacy analysis in the single-trial meta-analytic setting:
SurSTS <- Single.Trial.RE.AA(Dataset=ARMD, Surr=Diff24, True=Diff52, Treat=Treat, Pat.ID=Id)

# Request a plot of individual-level surrogacy and a plot that depicts the Relative effect
# and the constant RE assumption:
plot(SurSTS, Trial.Level=TRUE, Individ.Level=TRUE)

## End(Not run)

```

---

plot MinSurrContCont    *Graphically illustrates the theoretical plausibility of finding a good surrogate endpoint in the continuous-continuous case*

---

**Description**

This function provides a plot that displays the frequencies, percentages, or cumulative percentages of  $\rho_{min}^2$  for a fixed value of  $\delta$  (given the observed variances of the true endpoint in the control and experimental treatment conditions and a specified grid of values for the unidentified parameter  $\rho_{T_0T_1}$ ; see [MinSurrContCont](#)). For details, see the online appendix of Alonso et al., submitted.

**Usage**

```
## S3 method for class 'MinSurrContCont'
plot(x, main, col, Type="Percent", Labels=FALSE,
     Par=par(oma=c(0, 0, 0, 0), mar=c(5.1, 4.1, 4.1, 2.1)), ...)
```

**Arguments**

x	An object of class <code>MinSurrContCont</code> . See <a href="#">MinSurrContCont</a> .
main	The title of the plot.
col	The color of the bins.
Type	The type of plot that is produced. When <code>Type=Freq</code> or <code>Type=Percent</code> , the Y-axis shows frequencies or percentages of $\rho_{min}^2$ . When <code>Type=CumPerc</code> , the Y-axis shows cumulative percentages of $\rho_{min}^2$ . Default "Percent".
Labels	Logical. When <code>Labels=TRUE</code> , the percentage of $\rho_{min}^2$ values that are equal to or larger than the midpoint value of each of the bins are displayed (on top of each bin). Only applies when <code>Type=Freq</code> or <code>Type=Percent</code> . Default FALSE.
Par	Graphical parameters for the plot. Default <code>par(oma=c(0, 0, 0, 0), mar=c(5.1, 4.1, 4.1, 2.1))</code> .
...	Extra graphical parameters to be passed to <code>hist()</code> .

**Author(s)**

Wim Van der Elst, Ariel Alonso, & Geert Molenberghs

**References**

Alonso, A., Van der Elst, W., Molenberghs, G., Buyse, M., & Burzykowski, T. (submitted). On the relationship between the causal inference and meta-analytic paradigms for the validation of surrogate markers.

**See Also**

[MinSurrContCont](#)

**Examples**

```
# compute rho^2_min in the setting where the variances of T in the control
# and experimental treatments equal 100 and 120, delta is fixed at 50,
# and the grid G={0, .01, ..., 1} is considered for the counterfactual
# correlation rho_T0T1:
MinSurr <- MinSurrContCont(T0T0 = 100, T1T1 = 120, Delta = 50,
T0T1 = seq(0, 1, by = 0.01))
```

```
# Plot the results (use percentages on Y-axis)
plot(MinSurr, Type="Percent")

# Same plot, but add the percentages of ICA values that are equal to or
# larger than the midpoint values of the bins
plot(MinSurr, Labels=TRUE)
```

---

```
plot PredTrialTContCont
```

*Plots the expected treatment effect on the true endpoint in a new trial  
(when both S and T are normally distributed continuous endpoints)*

---

## Description

The key motivation to evaluate a surrogate endpoint is to be able to predict the treatment effect on the true endpoint  $T$  based on the treatment effect on  $S$  in a new trial  $i = 0$ . The function `Pred.TrialT.ContCont` allows for making such predictions. The present plot function shows the results graphically.

## Usage

```
## S3 method for class 'PredTrialTContCont'
plot(x, Size.New.Trial=5, CI.Segment=1, ...)
```

## Arguments

<code>x</code>	A fitted object of class <code>Pred.TrialT.ContCont</code> , for details see <a href="#">Pred.TrialT.ContCont</a> .
<code>Size.New.Trial</code>	The expected treatment effect on $T$ is drawn as a black circle with size specified by <code>Size.New.Trial</code> . Default <code>Size.New.Trial=5</code> .
<code>CI.Segment</code>	The confidence interval around the expected treatment effect on $T$ is depicted by a dashed horizontal line. By default, the width of the horizontal line of the horizontal section of the confidence interval indicator is 2 times the values specified by <code>CI.Segment</code> . Default <code>CI.Segment = 1</code> .
<code>...</code>	Extra graphical parameters to be passed to <code>plot()</code> .

## Author(s)

Wim Van der Elst, Ariel Alonso, & Geert Molenberghs

## See Also

[Pred.TrialT.ContCont](#)

**Examples**

```
## Not run: # time consuming code part
# Generate dataset
Sim.Data.MTS(N.Total=2000, N.Trial=15, R.Trial.Target=.95,
R.Indiv.Target=.8, D.aa=10, D.bb=50,
Fixed.Effects=c(1, 2, 30, 90), Seed=1)

# Evaluate surrogacy using a reduced bivariate mixed-effects model
BimixedFit <- BimixedContCont(Dataset = Data.Observed.MTS,
Surr = Surr, True = True, Treat = Treat, Trial.ID = Trial.ID,
Pat.ID = Pat.ID, Model="Reduced")

# Suppose that in a new trial, it was estimated alpha_0 = 30
# predict beta_0 in this trial
Pred_Beta <- Pred.TrialT.ContCont(Object = BimixedFit,
alpha_0 = 30)

# Examine the results
summary(Pred_Beta)

# Plot the results
plot(Pred_Beta)

## End(Not run)
```

---

plot SPF BinBin	<i>Plots the surrogate predictive function (SPF) in the binary-binary setting.</i>
-----------------	--

---

**Description**

Plots the surrogate predictive function (SPF), i.e.,  $r(i, j) = P(\Delta T = i | \Delta S = j)$ , in the setting where both  $S$  and  $T$  are binary endpoints. For example,  $r(-1, 1)$  quantifies the probability that the treatment has a negative effect on the true endpoint ( $\Delta T = -1$ ) given that it has a positive effect on the surrogate ( $\Delta S = 1$ ).

**Usage**

```
## S3 method for class 'SPF.BinBin'
plot(x, Type="All.Histograms", Specific.Pi="r_0_0", Col="grey",
Box.Plot.Outliers=FALSE, Legend.Pos="topleft", Legend.Cex=1, ...)
```

**Arguments**

x	A fitted object of class <code>SPF.BinBin</code> . See <a href="#">ICA.BinBin</a> .
Type	The type of plot that is requested. Possible choices are: <code>Type="All.Histograms"</code> , the histograms of all 9 $r(i, j) = P(\Delta T = i   \Delta S = j)$ vectors arranged in a 3 by 3 grid; <code>Type="All.Densities"</code> , plots of densities of all $r(i, j) = P(\Delta T =$

$i|\Delta S = j$ ) vectors; Type="Histogram", the histogram of a particular  $r(i, j) = P(\Delta T = i|\Delta S = j)$  vector (the Specific.Pi= argument has to be used to specify the desired  $r(i, j)$ ); Type="Density", the density of a particular  $r(i, j) = P(\Delta T = i|\Delta S = j)$  vector (the Specific.Pi= argument has to be used to specify the desired  $r(i, j)$ ); Type="Box.Plot", a box plot of all  $r(i, j) = P(\Delta T = i|\Delta S = j)$  vectors; Type="Lines.Mean", a line plot the depicts the means of all  $r(i, j) = P(\Delta T = i|\Delta S = j)$  vectors; Type="Lines.Median", a line plot the depicts the medians of all  $r(i, j) = P(\Delta T = i|\Delta S = j)$  vectors; Type="Lines.Mode", a line plot the depicts the modes of all  $r(i, j) = P(\Delta T = i|\Delta S = j)$  vectors; Type="3D.Mean", a 3D bar plot the depicts the means of all  $r(i, j) = P(\Delta T = i|\Delta S = j)$  vectors; Type="3D.Median", a 3D bar plot the depicts the medians of all  $r(i, j) = P(\Delta T = i|\Delta S = j)$  vectors; Type="3D.Mode", a 3D bar plot the depicts the modes of all  $r(i, j) = P(\Delta T = i|\Delta S = j)$  vectors; Type="3D.Spinning.Mean", a spinning 3D plot that depicts the means of all  $r(i, j) = P(\Delta T = i|\Delta S = j)$  vectors that can be rotated; Type="3D.Spinning.Median", a spinning 3D plot that depicts the medians of all  $r(i, j) = P(\Delta T = i|\Delta S = j)$  vectors that can be rotated; Type="3D.Spinning.Mode", a spinning 3D plot that depicts the modes of all  $r(i, j) = P(\Delta T = i|\Delta S = j)$  vectors that can be rotated.

Specific.Pi	When Type="Histogram" or Type="Density" , the histogram/density of a particular $r(i, j) = P(\Delta T = i \Delta S = j)$ vector is shown. The Specific.Pi= argument is used to specify the desired $r(i, j)$ . Default <code>r_0_0</code> .
Col	The color of the bins or lines when histograms or density plots are requested. Default "grey".
Box.Plot.Outliers	Logical. Should outliers be depicted in the box plots?. Default FALSE.
Legend.Pos	Position of the legend when a type="Box.Plot", type="Lines.Mean", type="Lines.Median", or type="Lines.Mode" is requested. Default "topleft".
Legend.Cex	Size of the legend when a type="Box.Plot", type="Lines.Mean", type="Lines.Median", or type="Lines.Mode" is requested. Default 1.
...	Arguments to be passed to the plot, histogram, ... functions.

### Author(s)

Wim Van der Elst, Ariel Alonso, & Geert Molenberghs

### References

Alonso, A., Van der Elst, W., & Molenberghs, G. (2015). Assessing a surrogate effect predictive value in a causal inference framework.

### See Also

[SPF.BinBin](#)

**Examples**

```
## Not run:
# Generate plausible values for Pi
ICA <- ICA.BinBin.Grid.Sample(pi1_1_=0.341, pi0_1_=0.119,
pi1_0_=0.254, pi_1_1=0.686, pi_1_0=0.088, pi_0_1=0.078, Seed=1,
Monotonicity=c("General"), M=2500)

# Compute the surrogate predictive function (SPF)
SPF <- SPF.BinBin(ICA)

# Explore the results
summary(SPF)

# Examples of plots
plot(SPF, Type="All.Histograms")
plot(SPF, Type="All.Densities")
plot(SPF, Type="Histogram", Specific.Pi="r_0_0")
plot(SPF, Type="Box.Plot", Legend.Pos="topleft", Legend.Cex=.7)
plot(SPF, Type="Lines.Mean")
plot(SPF, Type="Lines.Median")
plot(SPF, Type="3D.Mean")
plot(SPF, Type="3D.Median")
plot(SPF, Type="3D.Spining.Mean")
plot(SPF, Type="3D.Spining.Median")

## End(Not run)
```

---

plot SPF BinCont	<i>Plots the surrogate predictive function (SPF) in the binary-continuous setting.</i>
------------------	--

---

**Description**

Plots the surrogate predictive function (SPF) based on sensitivity-analysis, i.e.,  $P(\Delta T | \Delta S \in I[ab])$ , in the setting where  $S$  is continuous and  $T$  is a binary endpoint.

**Usage**

```
## S3 method for class 'SPF.BinCont'
plot(x, Type="Frequency", Col="grey", Main, Xlab=TRUE, ...)
```

**Arguments**

x	A fitted object of class <code>SPF.BinCont</code> . See <a href="#">ICA.BinCont</a> .
Type	The type of plot that is requested. The argument <code>Type="Frequency"</code> requests histograms for $P(\Delta T   \Delta S \in I[ab])$ . The argument <code>Type="Percentage"</code> requests relative frequencies for $P(\Delta T   \Delta S \in I[ab])$ . The argument <code>Type="Most.Likely.DeltaT"</code> requests a histogram of the most likely $\Delta T$ values. For example, when in one

run of the sensitivity analysis,  $P(\Delta T = -1|\Delta S \in I[ab]) = .6$ ,  $P(\Delta T = 0|\Delta S \in I[ab]) = .3$ , and  $P(\Delta T = -1|\Delta S \in I[ab]) = .1$ , the most likely outcome in this run would be  $P(\Delta T = -1)$ . The argument `Type="Most.Likely.DeltaT"` generates a plot with percentages for the most likely  $P(\Delta T)$  value across all obtained values in the sensitivity analysis.

Col	The color of the bins or lines when histograms or density plots are requested. Default "grey".
Main	The title of the plot.
Xlab	Logical. Should labels on the X-axis be shown? Default Xlab=TRUE.
...	Arguments to be passed to the plot, histogram, ... functions.

### Author(s)

Wim Van der Elst & Ariel Alonso

### References

Alonso, A., Van der Elst, W., Molenberghs, G., & Verbeke, G. (2017). Assessing the predictive value of a continuous surrogate for a binary true endpoint based on causal inference.

### See Also

[SPF.BinCont](#)

### Examples

```
## Not run: # time consuming code part
data(Schizo_BinCont)
# Use ICA.BinCont to examine surrogacy
Result_BinCont <- ICA.BinCont(M = 1000, Dataset = Schizo_BinCont,
Surr = PANSS, True = CGI_Bin, Treat=Treat, Diff.Sigma=TRUE)

# Obtain SPF
Fit <- SPF.BinCont(x=Result_BinCont, a = -30, b = -3)

# examine results
summary(Fit1)
plot(Fit1)

plot(Fit1, Type="Most.Likely.DeltaT")

## End(Not run)
```

---

plot TrialLevelIT      *Provides a plots of trial-level surrogacy in the information-theoretic framework based on the output of the TrialLevelIT() function*

---

### Description

Produces a plot that provides a graphical representation of trial-level surrogacy based on the output of the TrialLevelIT() function (information-theoretic framework).

### Usage

```
## S3 method for class 'TrialLevelIT'
plot(x, Xlab.Trial,
     Ylab.Trial, Main.Trial, Par=par(oma=c(0, 0, 0, 0),
     mar=c(5.1, 4.1, 4.1, 2.1)), ...)
```

### Arguments

x	An object of class TrialLevelIT.
Xlab.Trial	The legend of the X-axis of the plot that depicts trial-level surrogacy. Default "Treatment effect on the surrogate endpoint ( $\alpha_i$ )".
Ylab.Trial	The legend of the Y-axis of the plot that depicts trial-level surrogacy. Default "Treatment effect on the true endpoint ( $\beta_i$ )".
Main.Trial	The title of the plot that depicts trial-level surrogacy. Default "Trial-level surrogacy".
Par	Graphical parameters for the plot. Default par(oma=c(0, 0, 0, 0), mar=c(5.1, 4.1, 4.1, 2.1)).
...	Extra graphical parameters to be passed to plot().

### Author(s)

Wim Van der Elst, Ariel Alonso, & Geert Molenberghs

### References

Buyse, M., Molenberghs, G., Burzykowski, T., Renard, D., & Geys, H. (2000). The validation of surrogate endpoints in meta-analysis of randomized experiments. *Biostatistics*, 1, 49-67.

### See Also

[UnifixedContCont](#), [BifixedContCont](#), [UnifixedContCont](#), [BimixedContCont](#), [TrialLevelIT](#)



**Examples**

```
# Generate vector treatment effects on S
set.seed(seed = 1)
Alpha.Vector <- seq(from = 5, to = 10, by=.1) + runif(min = -.5, max = .5, n = 51)

# Generate vector treatment effects on T
set.seed(seed=2)
Beta.Vector <- (Alpha.Vector * 3) + runif(min = -5, max = 5, n = 51)

# Apply the function to estimate R^2_{h.t}
Fit <- TrialLevelIT(Alpha.Vector=Alpha.Vector,
Beta.Vector=Beta.Vector, N.Trial=50, Model="Reduced")

# Plot the results
plot(Fit)
```

---

plot TrialLevelMA	<i>Provides a plots of trial-level surrogacy in the meta-analytic framework based on the output of the TrialLevelMA() function</i>
-------------------	--

---

**Description**

Produces a plot that provides a graphical representation of trial-level surrogacy based on the output of the TrialLevel() function (meta-analytic framework).

**Usage**

```
## S3 method for class 'TrialLevelMA'
plot(x, Weighted=TRUE, Xlab.Trial,
Ylab.Trial, Main.Trial, Par=par(oma=c(0, 0, 0, 0),
mar=c(5.1, 4.1, 4.1, 2.1)), ...)
```

**Arguments**

x	An object of class TrialLevelMA.
Weighted	Logical. If Weighted=TRUE, the circles that depict the trial-specific treatment effects on the true endpoint against the surrogate endpoint are proportional to the number of patients in the trial. If Weighted=FALSE, all circles have the same size. Default TRUE.
Xlab.Trial	The legend of the X-axis of the plot that depicts trial-level surrogacy. Default "Treatment effect on the surrogate endpoint ( $\alpha_i$ )".
Ylab.Trial	The legend of the Y-axis of the plot that depicts trial-level surrogacy. Default "Treatment effect on the true endpoint ( $\beta_i$ )".
Main.Trial	The title of the plot that depicts trial-level surrogacy. Default "Trial-level surrogacy".
Par	Graphical parameters for the plot. Default par(oma=c(0, 0, 0, 0), mar=c(5.1, 4.1, 4.1, 2.1)).
...	Extra graphical parameters to be passed to plot().

**Author(s)**

Wim Van der Elst, Ariel Alonso, & Geert Molenberghs

**References**

Buyse, M., Molenberghs, G., Burzykowski, T., Renard, D., & Geys, H. (2000). The validation of surrogate endpoints in meta-analysis of randomized experiments. *Biostatistics*, 1, 49-67.

**See Also**

[UnifixedContCont](#), [BifixedContCont](#), [UnifixedContCont](#), [BimixedContCont](#), [TrialLevelMA](#)

**Examples**

```
# Generate vector treatment effects on S
set.seed(seed = 1)
Alpha.Vector <- seq(from = 5, to = 10, by=.1) + runif(min = -.5, max = .5, n = 51)
# Generate vector treatment effects on T
set.seed(seed=2)
Beta.Vector <- (Alpha.Vector * 3) + runif(min = -5, max = 5, n = 51)
# Vector of sample sizes of the trials (here, all n_i=10)
N.Vector <- rep(10, times=51)

# Apply the function to estimate R^2_{trial}
Fit <- TrialLevelMA(Alpha.Vector=Alpha.Vector,
Beta.Vector=Beta.Vector, N.Vector=N.Vector)

# Plot the results and obtain summary
plot(Fit)
summary(Fit)
```

---

plot TwoStageSurvSurv *Plots trial-level surrogacy in the meta-analytic framework when two survival endpoints are considered.*

---

**Description**

Produces a plot that graphically depicts trial-level surrogacy when the surrogate and true endpoints are survival endpoints.

**Usage**

```
## S3 method for class 'TwoStageSurvSurv'
plot(x, Weighted=TRUE, xlab, ylab, main,
Par=par(oma=c(0, 0, 0, 0), mar=c(5.1, 4.1, 4.1, 2.1)), ...)
```

**Arguments**

x	An object of class TwoStageContCont.
Weighted	Logical. If Weighted=TRUE, the circles that depict the trial-specific treatment effects on the true endpoint against the surrogate endpoint are proportional to the number of patients in the trial. If Weighted=FALSE, all circles have the same size. Default TRUE.
xlab	The legend of the X-axis, default "Treatment effect on the surrogate endpoint ( $\alpha_i$ )".
ylab	The legend of the Y-axis, default "Treatment effect on the true endpoint ( $\beta_i$ )".
main	The title of the plot, default "Trial-level surrogacy".
Par	Graphical parameters for the plot. Default par(oma=c(0, 0, 0, 0), mar=c(5.1, 4.1, 4.1, 2.1)).
...	Extra graphical parameters to be passed to plot().

**Author(s)**

Wim Van der Elst, Ariel Alonso, & Geert Molenberghs

**See Also**

[TwoStageSurvSurv](#)

**Examples**

```
# Open Ovarian dataset
data(Ovarian)
# Conduct analysis
Results <- TwoStageSurvSurv(Dataset = Ovarian, Surr = Pfs, SurrCens = PfsInd,
True = Surv, TrueCens = SurvInd, Treat = Treat, Trial.ID = Center)
# Examine results of analysis
summary(Results)
plot(Results)
```

---

plot.comb27.BinBin     *Plots the distribution of prediction error functions in decreasing order of appearance.*

---

**Description**

The function plot.comb27.BinBin plots each of the selected prediction functions in decreasing order in the single-trial causal-inference framework when both the surrogate and the true endpoints are binary outcomes. The distribution of frequencies at which each of the 27 possible prediction functions are selected provides additional insights regarding the association between  $S$  ( $\Delta_S$ ) and  $T$  ( $\Delta_T$ ). See **Details** below.

**Usage**

```
## S3 method for class 'comb27.BinBin'
plot(x, lab, ...)
```

**Arguments**

`x` An object of class `comb27.BinBin`. See [comb27.BinBin](#).

`lab` a supplementary label to the graph.

`...` Other arguments to be passed

**Details**

Each of the 27 prediction functions is coded as  $x/y/z$  with  $x$ ,  $y$  and  $z$  taking values in  $-1, 0, 1$ . As an example, the combination  $0/0/0$  represents the prediction function that projects every value of  $\Delta_S$  to 0. Similarly, the combination  $-1/0/1$  is the identity function projecting every value of  $\Delta_S$  to the same value for  $\Delta_T$ .

**Value**

An object of class `comb27.BinBin` with components,

<code>index</code>	count variable
<code>Monotonicity</code>	The vector of Monotonicity assumptions
<code>Pe</code>	The vector of the prediction error values.
<code>combo</code>	The vector containing the codes for the each of the 27 prediction functions.
<code>R2_H</code>	The vector of the $R_H^2$ values.
<code>H_Delta_T</code>	The vector of the entropies of $\Delta_T$ .
<code>H_Delta_S</code>	The vector of the entropies of $\Delta_S$ .
<code>I_Delta_T_Delta_S</code>	The vector of the mutual information of $\Delta_S$ and $\Delta_T$ .

**Author(s)**

Paul Meyvisch, Wim Van der Elst, Ariel Alonso

**References**

Alonso A, Van der Elst W, Molenberghs G, Buyse M and Burzykowski T. (2016). An information-theoretic approach for the evaluation of surrogate endpoints based on causal inference.

Alonso A, Van der Elst W and Meyvisch P (2016). Assessing a surrogate predictive value: A causal inference approach.

**See Also**

[comb27.BinBin](#)

**Examples**

```
## Not run: # time consuming code part
CIGTS_27 <- comb27.BinBin(pi1_1_ = 0.3412, pi1_0_ = 0.2539, pi0_1_ = 0.119,
                        pi_1_1 = 0.6863, pi_1_0 = 0.0882, pi_0_1 = 0.0784,
                        Seed=1, Monotonicity=c("No"), M=500000)
plot.comb27.BinBin(CIGTS_27, lab="CIGTS")

## End(Not run)
```

---

plot.Fano.BinBin	<i>Plots the distribution of <math>R^2_{HL}</math> either as a density or as function of <math>\pi_{10}</math> in the setting where both <math>S</math> and <math>T</math> are binary endpoints</i>
------------------	---

---

**Description**

The function `plot.Fano.BinBin` plots the distribution of  $R^2_{HL}$  which is fully identifiable for given values of  $\pi_{10}$ . See **Details** below.

**Usage**

```
## S3 method for class 'Fano.BinBin'
plot(x, Type="Density", Xlab.R2_HL, main.R2_HL,
     ylab="density", Par=par(mfrow=c(1,1), oma=c(0,0,0,0), mar=c(5.1,4.1,4.1,2.1)),
     Cex.Legend=1, Cex.Position="top", lwd=3, linety=c(5,6,7), color=c(8,9,3), ...)
```

**Arguments**

<code>x</code>	An object of class <code>Fano.BinBin</code> . See <a href="#">Fano.BinBin</a> .
<code>Type</code>	The type of plot that is produced. When <code>Type="Freq"</code> , a histogram of $R^2_{HL}$ is produced. When <code>Type="Density"</code> , the density of $R^2_{HL}$ is produced. When <code>Type="Scatter"</code> , a scatter plot of $R^2_{HL}$ is produced as a function of $\pi_{10}$ . Default <code>Type="Scatter"</code> .
<code>Xlab.R2_HL</code>	The label of the X-axis when density plots or histograms are produced.
<code>main.R2_HL</code>	Title of the density plot or histogram.
<code>ylab</code>	The label of the Y-axis when density plots or histograms are produced. Default <code>ylab="density"</code> .
<code>Par</code>	Graphical parameters for the plot. Default <code>par(mfrow=c(1,1), oma=c(0,0,0,0), mar=c(5.1,4.1,4.1,</code>
<code>Cex.Legend</code>	The size of the legend. Default <code>Cex.Legend=1</code> .
<code>Cex.Position</code>	The position of the legend. Default <code>Cex.Position="top"</code> .
<code>lwd</code>	The line width for the density plot. Default <code>lwd=3</code> .
<code>linety</code>	The line types corresponding to each level of <code>fano_delta</code> . Default <code>linety=c(5,6,7)</code> .
<code>color</code>	The color corresponding to each level of <code>fano_delta</code> . Default <code>color=c(8,9,3)</code> .
<code>...</code>	Other arguments to be passed.

**Details**

Values for  $\pi_{10}$  have to be uniformly sampled from the interval  $[0, \min(\pi_{1\cdot}, \pi_{\cdot 0})]$ . Any sampled value for  $\pi_{10}$  will fully determine the bivariate distribution of potential outcomes for the true endpoint.

The vector  $\pi_{km}$  fully determines  $R_{HL}^2$ .

**Value**

An object of class `Fano.BinBin` with components,

<code>R2_HL</code>	The sampled values for $R_{HL}^2$ .
<code>H_Delta_T</code>	The sampled values for $H\Delta T$ .
<code>minpi10</code>	The minimum value for $\pi_{10}$ .
<code>maxpi10</code>	The maximum value for $\pi_{10}$ .
<code>samplepi10</code>	The sampled value for $\pi_{10}$ .
<code>delta</code>	The specified vector of upper bounds for the prediction errors.
<code>uncertainty</code>	Indexes the sampling of $pi1_{\cdot}$ .
<code>pi_00</code>	The sampled values for $\pi_{00}$ .
<code>pi_11</code>	The sampled values for $\pi_{11}$ .
<code>pi_01</code>	The sampled values for $\pi_{01}$ .
<code>pi_10</code>	The sampled values for $\pi_{10}$ .

**Author(s)**

Paul Meyvisch, Wim Van der Elst, Ariel Alonso

**References**

Alonso, A., Van der Elst, W., & Molenberghs, G. (2014). Validation of surrogate endpoints: the binary-binary setting from a causal inference perspective.

**See Also**

[Fano.BinBin](#)

**Examples**

```
# Conduct the analysis assuming no monotonicity
# for the true endpoint, using a range of
# upper bounds for prediction errors
FANO<-Fano.BinBin(pi1_ = 0.5951 , pi_1 = 0.7745,
fano_delta=c(0.05, 0.1, 0.2), M=1000)

plot(FANO, Type="Scatter", color=c(3,4,5), Cex.Position="bottom")
```

---

plot.PPE.BinBin	<i>Plots the distribution of either PPE, RPE or <math>R^2_H</math> either as a density or as a histogram in the setting where both S and T are binary endpoints</i>
-----------------	---

---

### Description

The function `plot.PPE.BinBin` plots the distribution of *PPE*, *RPE* or  $R^2_H$  in the setting where both surrogate and true endpoints are binary in the single-trial causal-inference framework. See **Details** below.

### Usage

```
## S3 method for class 'PPE.BinBin'
plot(x, Type="Density", Param="PPE", Xlab=PE, main=PE,
     ylab="density", Cex.Legend=1, Cex.Position="bottomright", lwd=3, linety=1, color=1,
     Breaks=0.05, xlimits=c(0,1), ...)
```

### Arguments

<code>x</code>	An object of class <code>PPE.BinBin</code> . See <a href="#">PPE.BinBin</a> .
<code>Type</code>	The type of plot that is produced. When <code>Type="Freq"</code> , a histogram is produced. When <code>Type="Density"</code> , a density is produced. Default <code>Type="Density"</code> .
<code>Param</code>	Parameter to be plotted: is either "PPE", "RPE" or "ICA"
<code>Xlab=PE</code>	The label of the X-axis when density plots or histograms are produced.
<code>main=PE</code>	Title of the density plot or histogram.
<code>ylab</code>	The label of the Y-axis for the density plots. Default <code>ylab="density"</code> .
<code>Cex.Legend</code>	The size of the legend. Default <code>Cex.Legend=1</code> .
<code>Cex.Position</code>	The position of the legend. Default <code>Cex.Position="bottomright"</code> .
<code>lwd</code>	The line width for the density plot. Default <code>lwd=3</code> .
<code>linety</code>	The line types for the density. Default <code>linety=1</code> .
<code>color</code>	The color of the density or histogram. Default <code>color=1</code> .
<code>Breaks</code>	The breaks for the histogram. Default <code>Breaks=0.05</code> .
<code>xlimits</code>	The limits for the X-axis. Default <code>xlimits=c(0,1)</code> .
<code>...</code>	Other arguments to be passed.

### Details

In the continuous normal setting, surrogacy can be assessed by studying the association between the individual causal effects on *S* and *T* (see [ICA.ContCont](#)). In that setting, the Pearson correlation is the obvious measure of association.

When  $S$  and  $T$  are binary endpoints, multiple alternatives exist. Alonso et al. (2016) proposed the individual causal association (ICA;  $R_H^2$ ), which captures the association between the individual causal effects of the treatment on  $S$  ( $\Delta_S$ ) and  $T$  ( $\Delta_T$ ) using information-theoretic principles.

The function `PPE.BinBin` computes  $R_H^2$  using a grid-based approach where all possible combinations of the specified grids for the parameters that are allowed to vary freely are considered. It additionally computes the minimal probability of a prediction error (PPE) and the reduction on the PPE using information that  $S$  conveys on  $T$ . Both measures provide complementary information over the  $R_H^2$  and facilitate more straightforward clinical interpretation.

### Value

An object of class `PPE.BinBin` with components,

<code>index</code>	count variable
<code>PPE</code>	The vector of the PPE values.
<code>RPE</code>	The vector of the RPE values.
<code>PPE_T</code>	The vector of the $PPE_T$ values indicating the probability on a prediction error without using information on $S$ .
<code>R2_H</code>	The vector of the $R_H^2$ values.
<code>H_Delta_T</code>	The vector of the entropies of $\Delta_T$ .
<code>H_Delta_S</code>	The vector of the entropies of $\Delta_S$ .
<code>I_Delta_T_Delta_S</code>	The vector of the mutual information of $\Delta_S$ and $\Delta_T$ .
<code>Pi.Vectors</code>	An object of class <code>data.frame</code> that contains the valid $\pi$ vectors.

### Author(s)

Paul Meyvisch, Wim Van der Elst, Ariel Alonso, Geert Molenberghs

### References

Alonso A, Van der Elst W, Molenberghs G, Buyse M and Burzykowski T. (2016). An information-theoretic approach for the evaluation of surrogate endpoints based on causal inference.

Meyvisch P., Alonso A., Van der Elst W, Molenberghs G. (2018). Assessing the predictive value of a binary surrogate for a binary true endpoint, based on the minimum probability of a prediction error.

### See Also

[PPE.BinBin](#)

### Examples

```
## Not run: # Time consuming part
PANSS <- PPE.BinBin(pi1_1=0.4215, pi0_1=0.0538, pi1_0=0.0538,
                   pi_1_1=0.5088, pi_1_0=0.0307, pi_0_1=0.0482,
                   Seed=1, M=2500)
```



```
plot(PANSS,Type="Freq",Param="RPE",color="grey",Breaks=0.05,xlimits=c(0,1),main="PANSS")

## End(Not run)
```

---

plot.SurvSurv	<i>Provides plots of trial- and individual-level surrogacy in the Information-Theoretic framework when both S and T are time-to-event endpoints</i>
---------------	---

---

## Description

Produces plots that provide a graphical representation of trial- and/or individual-level surrogacy ( $R2\_ht$  and  $R2\_hInd$  per cluster) based on the Information-Theoretic approach of Alonso & Molenaar (2007).

## Usage

```
## S3 method for class 'SurvSurv'
plot(x, Trial.Level=TRUE, Weighted=TRUE,
     Individ.Level.By.Trial=TRUE, Xlab.Indiv, Ylab.Indiv, Xlab.Trial,
     Ylab.Trial, Main.Trial, Main.Indiv,
     Par=par(oma=c(0, 0, 0, 0), mar=c(5.1, 4.1, 4.1, 2.1)), ...)
```

## Arguments

x	An object of class FixedBinBinIT.
Trial.Level	Logical. If Trial.Level=TRUE, a plot of the trial-specific treatment effects on the true endpoint against the trial-specific treatment effect on the surrogate endpoints is provided (as a graphical representation of $R_{ht}$ ). Default TRUE.
Weighted	Logical. This argument only has effect when the user requests a trial-level surrogacy plot (i.e., when Trial.Level=TRUE in the function call). If Weighted=TRUE, the circles that depict the trial-specific treatment effects on the true endpoint against the surrogate endpoint are proportional to the number of patients in the trial. If Weighted=FALSE, all circles have the same size. Default TRUE.
Individ.Level.By.Trial	Logical. If Individ.Level.By.Trial=TRUE, a plot that shows the estimated $R_{h.ind}^2$ for each trial (and confidence intervals) is provided. Default TRUE.
Xlab.Indiv	The legend of the X-axis of the plot that depicts the estimated $R_{h.ind}^2$ per trial. Default " $R[h.ind]^2$ ".
Ylab.Indiv	The legend of the Y-axis of the plot that shows the estimated $R_{h.ind}^2$ per trial. Default "Trial".
Xlab.Trial	The legend of the X-axis of the plot that depicts trial-level surrogacy. Default "Treatment effect on the surrogate endpoint ( $\alpha_i$ )".
Ylab.Trial	The legend of the Y-axis of the plot that depicts trial-level surrogacy. Default "Treatment effect on the true endpoint ( $\beta_i$ )".

Main.Indiv	The title of the plot that depicts individual-level surrogacy. Default "Individual-level surrogacy".
Main.Trial	The title of the plot that depicts trial-level surrogacy. Default "Trial-level surrogacy".
Par	Graphical parameters for the plot. Default <code>par(oma=c(0,0,0,0),mar=c(5.1,4.1,4.1,2.1))</code> .
...	Extra graphical parameters to be passed to <code>plot()</code> .

**Author(s)**

Wim Van der Elst, Ariel Alonso, & Geert Molenberghs

**References**

Alonso, A, & Molenberghs, G. (2007). Surrogate marker evaluation from an information theory perspective. *Biometrics*, 63, 180-186.

**See Also**

[SurvSurv](#)

**Examples**

```
# Open Ovarian dataset
data(Ovarian)

# Conduct analysis
Fit <- SurvSurv(Dataset = Ovarian, Surr = Pfs, SurrCens = PfsInd,
True = Surv, TrueCens = SurvInd, Treat = Treat,
Trial.ID = Center, Alpha=.05)

# Examine results
summary(Fit)
plot(Fit, Trial.Level = FALSE, Individ.Level.By.Trial=TRUE)
plot(Fit, Trial.Level = TRUE, Individ.Level.By.Trial=FALSE)
```

---

Pos.Def.Matrices

*Generate 4 by 4 correlation matrices and flag the positive definite ones*

---

**Description**

Based on vectors (or scalars) for the six off-diagonal correlations of a 4 by 4 matrix, the function `Pos.Def.Matrices` constructs all possible matrices that can be formed by combining the specified values, computes the minimum eigenvalues for each of these matrices, and flags the positive definite ones (i.e., valid correlation matrices).

**Usage**

```
Pos.Def.Matrices(T0T1=seq(0, 1, by=.2), T0S0=seq(0, 1, by=.2), T0S1=seq(0, 1,
by=.2), T1S0=seq(0, 1, by=.2), T1S1=seq(0, 1, by=.2), S0S1=seq(0, 1, by=.2))
```

**Arguments**

T0T1	A vector or scalar that specifies the correlation(s) between T0 and T1 that should be considered to construct all possible 4 by 4 matrices. Default <code>seq(0, 1, by=.2)</code> , i.e., the values 0, 0.20, ..., 1.
T0S0	A vector or scalar that specifies the correlation(s) between T0 and S0 that should be considered to construct all possible 4 by 4 matrices. Default <code>seq(0, 1, by=.2)</code> .
T0S1	A vector or scalar that specifies the correlation(s) between T0 and S1 that should be considered to construct all possible 4 by 4 matrices. Default <code>seq(0, 1, by=.2)</code> .
T1S0	A vector or scalar that specifies the correlation(s) between T1 and S0 that should be considered to construct all possible 4 by 4 matrices. Default <code>seq(0, 1, by=.2)</code> .
T1S1	A vector or scalar that specifies the correlation(s) between T1 and S1 that should be considered to construct all possible 4 by 4 matrices. Default <code>seq(0, 1, by=.2)</code> .
S0S1	A vector or scalar that specifies the correlation(s) between S0 and S1 that should be considered to construct all possible 4 by 4 matrices. Default <code>seq(0, 1, by=.2)</code> .

**Details**

The generated object `Generated.Matrices` (of class `data.frame`) is placed in the workspace (for easy access).

**Author(s)**

Wim Van der Elst, Ariel Alonso, & Geert Molenberghs

**See Also**

[Sim.Data.Counterfactuals](#)

**Examples**

```
## Generate all 4x4 matrices that can be formed using rho(T0,S0)=rho(T1,S1)=.5
## and the grid of values 0, .2, ..., 1 for the other off-diagonal correlations:
Pos.Def.Matrices(T0T1=seq(0, 1, by=.2), T0S0=.5, T0S1=seq(0, 1, by=.2),
T1S0=seq(0, 1, by=.2), T1S1=.5, S0S1=seq(0, 1, by=.2))

## Examine the first 10 rows of the the object Generated.Matrices:
Generated.Matrices[1:10,]

## Check how many of the generated matrices are positive definite
## (counts and percentages):
table(Generated.Matrices$Pos.Def.Status)
table(Generated.Matrices$Pos.Def.Status)/nrow(Generated.Matrices)

## Make an object PosDef which contains the positive definite matrices:
PosDef <- Generated.Matrices[Generated.Matrices$Pos.Def.Status==1,]

## Shows the 10 first matrices that are positive definite:
PosDef[1:10,]
```

---

PPE.BinBin	<i>Evaluate a surrogate predictive value based on the minimum probability of a prediction error in the setting where both <math>S</math> and <math>T</math> are binary endpoints</i>
------------	--

---

### Description

The function `PPE.BinBin` assesses a surrogate predictive value using the probability of a prediction error in the single-trial causal-inference framework when both the surrogate and the true endpoints are binary outcomes. It additionally assesses the individual causal association (ICA). See **Details** below.

### Usage

```
PPE.BinBin(pi1_1_, pi1_0_, pi_1_1, pi_1_0,
pi0_1_, pi_0_1, M=10000, Seed=1)
```

### Arguments

<code>pi1_1_</code>	A scalar that contains values for $P(T = 1, S = 1 Z = 0)$ , i.e., the probability that $S = T = 1$ when under treatment $Z = 0$ .
<code>pi1_0_</code>	A scalar that contains values for $P(T = 1, S = 0 Z = 0)$ .
<code>pi_1_1</code>	A scalar that contains values for $P(T = 1, S = 1 Z = 1)$ .
<code>pi_1_0</code>	A scalar that contains values for $P(T = 1, S = 0 Z = 1)$ .
<code>pi0_1_</code>	A scalar that contains values for $P(T = 0, S = 1 Z = 0)$ .
<code>pi_0_1</code>	A scalar that contains values for $P(T = 0, S = 1 Z = 1)$ .
<code>M</code>	The number of valid vectors that have to be obtained. Default <code>M=10000</code> .
<code>Seed</code>	The seed to be used to generate $\pi_r$ . Default <code>Seed=1</code> .

### Details

In the continuous normal setting, surrogacy can be assessed by studying the association between the individual causal effects on  $S$  and  $T$  (see [ICA.ContCont](#)). In that setting, the Pearson correlation is the obvious measure of association.

When  $S$  and  $T$  are binary endpoints, multiple alternatives exist. Alonso et al. (2016) proposed the individual causal association (ICA;  $R_H^2$ ), which captures the association between the individual causal effects of the treatment on  $S$  ( $\Delta_S$ ) and  $T$  ( $\Delta_T$ ) using information-theoretic principles.

The function `PPE.BinBin` computes  $R_H^2$  using a grid-based approach where all possible combinations of the specified grids for the parameters that are allowed to vary freely are considered. It additionally computes the minimal probability of a prediction error (PPE) and the reduction on the PPE using information that  $S$  conveys on  $T$ . Both measures provide complementary information over the  $R_H^2$  and facilitate more straightforward clinical interpretation. No assumption about monotonicity can be made.

**Value**

An object of class `PPE.BinBin` with components,

<code>index</code>	count variable
<code>PPE</code>	The vector of the PPE values.
<code>RPE</code>	The vector of the RPE values.
<code>PPE_T</code>	The vector of the $PPE_T$ values indicating the probability on a prediction error without using information on $S$ .
<code>R2_H</code>	The vector of the $R_H^2$ values.
<code>H_Delta_T</code>	The vector of the entropies of $\Delta_T$ .
<code>H_Delta_S</code>	The vector of the entropies of $\Delta_S$ .
<code>I_Delta_T_Delta_S</code>	The vector of the mutual information of $\Delta_S$ and $\Delta_T$ .

**Author(s)**

Paul Meyvisch, Wim Van der Elst, Ariel Alonso, Geert Molenberghs

**References**

Alonso A, Van der Elst W, Molenberghs G, Buyse M and Burzykowski T. (2016). An information-theoretic approach for the evaluation of surrogate endpoints based on causal inference.

Meyvisch P., Alonso A., Van der Elst W, Molenberghs G. (2018). Assessing the predictive value of a binary surrogate for a binary true endpoint, based on the minimum probability of a prediction error.

**See Also**

[ICA.BinBin.Grid.Sample](#)

**Examples**

```
# Conduct the analysis

## Not run: # time consuming code part
PPE.BinBin(pi1_1=0.4215, pi0_1=0.0538, pi1_0=0.0538,
           pi_1_1=0.5088, pi_1_0=0.0307, pi_0_1=0.0482,
           Seed=1, M=10000)

## End(Not run)
```

---

Pred.TrialT.ContCont *Compute the expected treatment effect on the true endpoint in a new trial (when both  $S$  and  $T$  are normally distributed continuous endpoints)*

---

## Description

The key motivation to evaluate a surrogate endpoint is to be able to predict the treatment effect on the true endpoint  $T$  based on the treatment effect on  $S$  in a new trial  $i = 0$ . The function `Pred.TrialT.ContCont` allows for making such predictions based on fitted models of class `BimixedContCont`, `BifixedContCont`, `UnimixedContCont` and `UnifixedContCont`.

## Usage

```
Pred.TrialT.ContCont(Object, mu_S0, alpha_0, alpha.CI=0.05)
```

## Arguments

Object	A fitted object of class <code>BimixedContCont</code> , <code>BifixedContCont</code> , <code>UnimixedContCont</code> and <code>UnifixedContCont</code> . Some of the components in these fitted objects are needed to estimate $E(\beta + b_0)$ and its variance.
mu_S0	The intercept of a regression model in the new trial $i = 0$ where the surrogate endpoint is regressed on the true endpoint, i.e., $S_{0j} = \mu_{S0} + \alpha_0 Z_{0j} + \varepsilon_{S0j}$ , where $S$ is the surrogate endpoint, $j$ is the patient indicator, and $Z$ is the treatment. This argument only needs to be specified when a full model was used to examine surroacy.
alpha_0	The regression weight of the treatment in the regression model specified under argument <code>mu_S0</code> .
alpha.CI	The $\alpha$ -level to be used to determine the confidence interval around $E(\beta + b_0)$ . Default <code>alpha.CI=0.05</code> .

## Details

The key motivation to evaluate a surrogate endpoint is to be able to predict the treatment effect on the true endpoint  $T$  based on the treatment effect on  $S$  in a new trial  $i = 0$ .

When a so-called full (fixed or mixed) bi- or univariate model was fitted in the surrogate evaluation phase (for details, see `BimixedContCont`, `BifixedContCont`, `UnimixedContCont` and `UnifixedContCont`), this prediction is made as:

$$E(\beta + b_0 | m_{S0}, a_0) = \beta + \begin{pmatrix} d_{Sb} \\ d_{ab} \end{pmatrix}^T \begin{pmatrix} d_{SS} & D_{Sa} \\ d_{Sa} & d_{aa} \end{pmatrix}^{-1} \begin{pmatrix} \mu_{S0} - \mu_S \\ \alpha_0 - \alpha \end{pmatrix}$$

$$Var(\beta + b_0 | m_{S0}, a_0) = d_{bb} + \begin{pmatrix} d_{Sb} \\ d_{ab} \end{pmatrix}^T \begin{pmatrix} d_{SS} & D_{Sa} \\ d_{Sa} & d_{aa} \end{pmatrix}^{-1} \begin{pmatrix} d_{Sb} \\ d_{ab} \end{pmatrix},$$

where all components are defined as in [BimixedContCont](#). When the univariate mixed-effects models are used or the (univariate or bivariate) fixed effects models, the fitted components contained in `D.Equiv` are used instead of those in `D`.

When a reduced-model approach was used in the surrogate evaluation phase, the prediction is made as:

$$E(\beta + b_0|a_0) = \beta + \frac{d_{ab}}{d_{aa}} + (\alpha_0 - \alpha),$$

$$Var(\beta + b_0|a_0) = d_{bb} - \frac{d_{ab}^2}{d_{aa}},$$

where all components are defined as in [BimixedContCont](#). When the univariate mixed-effects models are used or the (univariate or bivariate) fixed effects models, the fitted components contained in `D.Equiv` are used instead of those in `D`.

A  $(1 - \gamma)100\%$  prediction interval for  $E(\beta + b_0|m_{S0}, a_0)$  can be obtained as  $E(\beta + b_0|m_{S0}, a_0) \pm z_{1-\gamma/2}\sqrt{Var(\beta + b_0|m_{S0}, a_0)}$  (and similarly for  $E(\beta + b_0|a_0)$ ).

### Value

<code>Beta_0</code>	The predicted $\beta_0$ .
<code>Variance</code>	The variance of the prediction.
<code>Lower</code>	The lower bound of the confidence interval around the expected $\beta_0$ , see <a href="#">Details</a> above.
<code>Upper</code>	The upper bound of the confidence interval around the expected $\beta_0$ .
<code>alpha.CI</code>	The $\alpha$ -level used to establish the confidence interval.
<code>Surr.Model</code>	The model that was used to compute $\beta_0$ .
<code>alpha_0</code>	The slope of the regression model specified in the <a href="#">Arguments</a> section.

### Author(s)

Wim Van der Elst, Ariel Alonso, & Geert Molenberghs

### References

Burzykowski, T., Molenberghs, G., & Buyse, M. (2005). *The evaluation of surrogate endpoints*. New York: Springer-Verlag.

### See Also

[UnifixedContCont](#), [BifixedContCont](#), [UnimixedContCont](#)

## Examples

```
## Not run: #time-consuming code parts
# Generate dataset
Sim.Data.MTS(N.Total=2000, N.Trial=15, R.Trial.Target=.8,
R.Indiv.Target=.8, D.aa=10, D.bb=50, Fixed.Effects=c(1, 2, 30, 90),
Seed=1)

# Evaluate surrogacy using a reduced bivariate mixed-effects model
BimixedFit <- BimixedContCont(Dataset = Data.Observed.MTS, Surr = Surr,
True = True, Treat = Treat, Trial.ID = Trial.ID, Pat.ID = Pat.ID,
Model="Reduced")

# Suppose that in a new trial, it was estimated alpha_0 = 30
# predict beta_0 in this trial
Pred_Beta <- Pred.TrialT.ContCont(Object = BimixedFit,
alpha_0 = 30)

# Examine the results
summary(Pred_Beta)

# Plot the results
plot(Pred_Beta)

## End(Not run)
```

---

Prentice

*Evaluates surrogacy based on the Prentice criteria for continuous end-points (single-trial setting)*

---

## Description

The function `Prentice` evaluates the validity of a potential surrogate based on the Prentice criteria (Prentice, 1989) in the setting where the candidate surrogate and the true endpoint are normally distributed endpoints.

**Warning** The Prentice approach is included in the *Surrogate* package for illustrative purposes (as it was the first formal approach to assess surrogacy), but this method has some severe problems that renders its use problematic (see **Details** below). It is recommended to replace the Prentice approach by a more statistically-sound approach to evaluate a surrogate (e.g., the meta-analytic methods; see the functions [UnifixedContCont](#), [BifixedContCont](#), [UnimixedContCont](#), [BimixedContCont](#)).

## Usage

```
Prentice(Dataset, Surr, True, Treat, Pat.ID, Alpha=.05)
```

## Arguments

`Dataset` A data.frame that should consist of one line per patient. Each line contains (at least) a surrogate value, a true endpoint value, a treatment indicator, a patient ID, and a trial ID.



Surr	The name of the variable in Dataset that contains the surrogate values.
True	The name of the variable in Dataset that contains the true endpoint values.
Treat	The name of the variable in Dataset that contains the treatment indicators. The treatment indicator should either be coded as 1 for the experimental group and -1 for the control group, or as 1 for the experimental group and 0 for the control group.
Pat.ID	The name of the variable in Dataset that contains the patient's ID.
Alpha	The $\alpha$ -level that is used to examine whether the Prentice criteria are fulfilled. Default 0.05.

### Details

The Prentice criteria are examined by fitting the following regression models (when the surrogate and true endpoints are continuous variables):

$$S_j = \mu_S + \alpha Z_j + \varepsilon_{Sj}, (1)$$

$$T_j = \mu_T + \beta Z_j + \varepsilon_{Tj}, (2)$$

$$T_j = \mu + \gamma Z_j + \varepsilon_j, (3)$$

$$T_j = \tilde{\mu}_T + \beta_S Z_j + \gamma_Z S_j + \tilde{\varepsilon}_{Tj}, (4)$$

where the error terms of (1) and (2) have a joint zero-mean normal distribution with variance-covariance matrix

$$\Sigma = \begin{pmatrix} \sigma_{SS} & \\ \sigma_{ST} & \sigma_{TT} \end{pmatrix}$$

,

and where  $j$  is the subject indicator,  $S_j$  and  $T_j$  are the surrogate and true endpoint values of subject  $j$ , and  $Z_j$  is the treatment indicator for subject  $j$ .

To be in line with the Prentice criteria,  $Z$  should have a significant effect on  $S$  in model 1 (Prentice criterion 1),  $Z$  should have a significant effect on  $T$  in model 2 (Prentice criterion 2),  $S$  should have a significant effect on  $T$  in model 3 (Prentice criterion criterion 3), and the effect of  $Z$  on  $T$  should be fully captured by  $S$  in model 4 (Prentice criterion 4).

The Prentice approach to assess surrogacy has some fundamental limitations. For example, the fourth Prentice criterion requires that the statistical test for the  $\beta_S$  in model 4 is non-significant. This criterion is useful to reject a poor surrogate, but it is not suitable to validate a good surrogate (i.e., a non-significant result may always be attributable to a lack of statistical power). Even when lack of power would not be an issue, the result of the statistical test to evaluate the fourth Prentice criterion cannot prove that the effect of the treatment on the true endpoint is fully captured by the surrogate.

The use of the Prentice approach to evaluate a surrogate is not recommended. Instead, consider using the single-trial meta-analytic method (if no multiple clinical trials are available or if there is no other clustering unit in the data; see function [Single.Trial.RE.AA](#)) or the multiple-trial meta-analytic methods (see [UnifixedContCont](#), [BifixedContCont](#), [UnimixedContCont](#), and [BimixedContCont](#)).

**Value**

Prentice.Model.1  
An object of class `lm` that contains the fitted model 1 (using the Prentice approach).

Prentice.Model.2  
An object of class `lm` that contains the fitted model 2 (using the Prentice approach).

Prentice.Model.3  
An object of class `lm` that contains the fitted model 3 (using the Prentice approach).

Prentice.Model.4  
An object of class `lm` that contains the fitted model 4 (using the Prentice approach).

Prentice.Passed  
Logical. If all four Prentice criteria are fulfilled, `Prentice.Passed=TRUE`. If at least one criterion is not fulfilled, `Prentice.Passed=FALSE`.

**Author(s)**

Wim Van der Elst, Ariel Alonso, & Geert Molenberghs

**References**

Burzykowski, T., Molenberghs, G., & Buyse, M. (2005). *The evaluation of surrogate endpoints*. New York: Springer-Verlag.

Prentice, R. L. (1989). Surrogate endpoints in clinical trials: definitions and operational criteria. *Statistics in Medicine*, 8, 431-440.

**Examples**

```
## Load the ARMD dataset
data(ARMD)

## Evaluate the Prentice criteria in the ARMD dataset
Prent <- Prentice(Dataset=ARMD, Surr=Diff24, True=Diff52, Treat=Treat, Pat.ID=Id)

# Summary of results
summary(Prent)
```

---

PROC.BinBin

*Evaluate the individual causal association (ICA) and reduction in probability of a prediction error (RPE) in the setting where both  $S$  and  $T$  are binary endpoints*

---

## Description

The function PROC.BinBin assesses the ICA and RPE in the single-trial causal-inference framework when both the surrogate and the true endpoints are binary outcomes. It additionally allows to account for sampling variability by means of bootstrap. See **Details** below.

## Usage

```
PROC.BinBin(Dataset=Dataset, Surr=Surr, True=True, Treat=Treat,
BS=FALSE, seqs=250, MC_samples=1000, Seed=1)
```

## Arguments

Dataset	A data.frame that should consist of one line per patient. Each line contains (at least) a binary surrogate value, a binary true endpoint value, and a treatment indicator.
Surr	The name of the variable in Dataset that contains the binary surrogate endpoint values. Should be coded as 0 and 1.
True	The name of the variable in Dataset that contains the binary true endpoint values. Should be coded as 0 and 1.
Treat	The name of the variable in Dataset that contains the treatment indicators. The treatment indicator should be coded as 1 for the experimental group and -1 for the control group.
BS	Logical. If TRUE, then Dataset will be bootstrapped to account for sampling variability. If FALSE, then no bootstrap is performed. See the <b>Details</b> section below. Default FALSE.
seqs	The number of copies of the dataset that are produced or alternatively the number of bootstrap datasets that are produced. Default seqs=250.
MC_samples	The number of Monte Carlo samples that need to be obtained per copy of the data set. Default MC_samples=1000.
Seed	The seed to be used. Default Seed=1.

## Details

In the continuous normal setting, surrogacy can be assessed by studying the association between the individual causal effects on  $S$  and  $T$  (see [ICA.ContCont](#)). In that setting, the Pearson correlation is the obvious measure of association.

When  $S$  and  $T$  are binary endpoints, multiple alternatives exist. Alonso et al. (2016) proposed the individual causal association (ICA;  $R_H^2$ ), which captures the association between the individual causal effects of the treatment on  $S$  ( $\Delta_S$ ) and  $T$  ( $\Delta_T$ ) using information-theoretic principles.

The function PPE.BinBin computes  $R_H^2$  using a grid-based approach where all possible combinations of the specified grids for the parameters that are allowed to vary freely are considered. It additionally computes the minimal probability of a prediction error (PPE) and the reduction on the PPE using information that  $S$  conveys on  $T$  (RPE). Both measures provide complementary information over the  $R_H^2$  and facilitate more straightforward clinical interpretation. No assumption about monotonicity can be made. The function PROC.BinBin makes direct use of the function PPE.BinBin. However, it is computationally much faster thanks to equally dividing the number of

Monte Carlo samples over copies of the input data. In addition, it allows to account for sampling variability using a bootstrap procedure. Finally, the function PROC.BinBin computes the marginal probabilities directly from the input data set.

### Value

An object of class PPE.BinBin with components,

PPE	The vector of the PPE values.
RPE	The vector of the RPE values.
PPE_T	The vector of the $PPE_T$ values indicating the probability on a prediction error without using information on $S$ .
R2_H	The vector of the $R_H^2$ values.

### Author(s)

Paul Meyvisch, Wim Van der Elst, Ariel Alonso, Geert Molenberghs

### References

Alonso A, Van der Elst W, Molenberghs G, Buyse M and Burzykowski T. (2016). An information-theoretic approach for the evaluation of surrogate endpoints based on causal inference.

Meyvisch P., Alonso A., Van der Elst W, Molenberghs G.. Assessing the predictive value of a binary surrogate for a binary true endpoint, based on the minimum probability of a prediction error.

### See Also

[PPE.BinBin](#)

### Examples

```
# Conduct the analysis

## Not run: # time consuming code part
library(Surrogate)
# load the CIGTS data
data(CIGTS)
CIGTS_25000<-PROC.BinBin(Dataset=CIGTS, Surr=IOP_12, True=IOP_96,
Treat=Treat, BS=FALSE,seqs=250, MC_samples=100, Seed=1)

## End(Not run)
```

---

**RandVec***Generate random vectors with a fixed sum*

---

**Description**

This function generates an  $n$  by  $m$  array  $x$ , each of whose  $m$  columns contains  $n$  random values lying in the interval  $[a,b]$ , subject to the condition that their sum be equal to  $s$ . The distribution of values is uniform in the sense that it has the conditional probability distribution of a uniform distribution over the whole  $n$ -cube, given that the sum of the  $x$ 's is  $s$ . The function uses the `randfixedsum` algorithm, written by Roger Stafford and implemented in MatLab. For details, see <http://www.mathworks.com/matlabcentral/fileexchange/9700-random-vectors-with-fixed-sum/content/randfixedsum.m>

**Usage**

```
RandVec(a=0, b=1, s=1, n=9, m=1, Seed=sample(1:1000, size = 1))
```

**Arguments**

<code>a</code>	The function <code>RandVec</code> generates an $n$ by $m$ matrix $x$ . Each of the $m$ columns contain $n$ random values lying in the interval $[a,b]$ . The argument <code>a</code> specifies the lower limit of the interval. Default $0$ .
<code>b</code>	The argument <code>b</code> specifies the upper limit of the interval. Default $1$ .
<code>s</code>	The argument <code>s</code> specifies the value to which each of the $m$ generated columns should sum to. Default $1$ .
<code>n</code>	The number of requested elements per column. Default $9$ .
<code>m</code>	The number of requested columns. Default $1$ .
<code>Seed</code>	The seed that is used. Default <code>sample(1:1000, size = 1)</code> .

**Value**

An object of class `RandVec` with components,

`RandVecOutput` The randomly generated vectors.

**Author(s)**

Wim Van der Elst, Ariel Alonso, & Geert Molenberghs

**References**

The function is an R adaptation of a matlab program written by Roger Stafford. For details on the original Matlab algorithm, see: <http://www.mathworks.com/matlabcentral/fileexchange/9700-random-vectors-with-fixed-sum/content/randfixedsum.m>

**Examples**

```
# generate two vectors with 10 values ranging between 0 and 1
# where each vector sums to 1
# (uniform distribution over the whole n-cube)
Vectors <- RandVec(a=0, b=1, s=1, n=10, m=2)
sum(Vectors$RandVecOutput[,1])
sum(Vectors$RandVecOutput[,2])
```

---

Restrictions.BinBin    *Examine restrictions in  $\pi_f$  under different monotonicity assumptions for binary  $S$  and  $T$*

---

**Description**

The function Restrictions.BinBin gives an overview of the restrictions in  $\pi_f$  under different assumptions regarding monotonicity when both  $S$  and  $T$  are binary.

**Usage**

```
Restrictions.BinBin(pi1_1_, pi1_0_, pi_1_1, pi_1_0, pi0_1_, pi_0_1)
```

**Arguments**

pi1_1_	A scalar that contains $P(T = 1, S = 1 Z = 0)$ , i.e., the probability that $S = T = 1$ when under treatment $Z = 0$ .
pi1_0_	A scalar that contains $P(T = 1, S = 0 Z = 0)$ .
pi_1_1	A scalar that contains $P(T = 1, S = 1 Z = 1)$ .
pi_1_0	A scalar that contains $P(T = 1, S = 0 Z = 1)$ .
pi0_1_	A scalar that contains $P(T = 0, S = 1 Z = 0)$ .
pi_0_1	A scalar that contains $P(T = 0, S = 1 Z = 1)$ .

**Value**

An overview of the restrictions for the freely varying parameters imposed by the data is provided

**Author(s)**

Wim Van der Elst, Ariel Alonso, & Geert Molenberghs

**References**

Alonso, A., Van der Elst, W., & Molenberghs, G. (2014). Validation of surrogate endpoints: the binary-binary setting from a causal inference perspective.

**See Also**

[MarginalProbs](#)

**Examples**

```
Restrictions.BinBin(pi1_1=0.262, pi0_1=0.135, pi1_0=0.286,
pi_1_1=0.637, pi_1_0=0.078, pi_0_1=0.127)
```

---

 Schizo

---

*Data of five clinical trials in schizophrenia*


---

**Description**

These are the data of five clinical trials in schizophrenia. A total of 2128 patients were treated by 198 investigators (psychiatrists). Patients' schizophrenic symptoms were measured using the PANSS, BPRS, and CGI. There were two treatment conditions (risperidone and control).

**Usage**

```
data(Schizo)
```

**Format**

A data.frame with 2128 observations on 9 variables.

Id The patient ID.

InvestID The ID of the investigator (psychiatrist) who treated the patient.

Treat The treatment indicator, coded as  $-1$  = control and  $1$  = Risperidone.

CGI The change in the CGI score (= score at the start of the treatment - score at the end of the treatment).

PANSS The change in the PANSS score (= score at the start of the treatment - score at the end of the treatment).

BPRS The change in the PANSS score (= score at the start of the treatment - score at the end of the treatment).

PANSS\_Bin The dichotomized PANSS change score, coded as  $1$  = a reduction of 20% or more in the PANSS score (score at the end of the treatment relative to score at the beginning of the treatment),  $0$  = otherwise.

BPRS\_Bin The dichotomized BPRS change score, coded as  $1$  = a reduction of 20% or more in the BPRS score (score at the end of the treatment relative to score at the beginning of the treatment),  $0$  = otherwise.

CGI\_Bin The dichotomized change in the CGI score, coded as  $1$  = a change of more than 3 points on the original scale (score at the end of the treatment relative to score at the beginning of the treatment),  $0$  = otherwise.

Schizo\_Bin

*Data of a clinical trial in Schizophrenia (with binary outcomes).***Description**

These are the data of a clinical trial in Schizophrenia (a subset of the dataset Schizo\_Bin, study 1 where the patients were administered 10 mg. of haloperidol or 8 mg. of risperidone). A total of 454 patients were treated by 117 investigators (psychiatrists). Patients' schizophrenia symptoms at baseline and at the end of the study (after 8 weeks) were measured using the PANSS and BPRS. The variables BPRS\_Bin and PANSS\_Bin are binary outcomes that indicate whether clinically meaningful change had occurred (1 = a reduction of 20% or higher in the PANSS/BPRS scores at the last measurement compared to baseline; 0 = no such reduction; Leucht et al., 2005; Kay et al., 1988).

**Usage**

```
data(Schizo_Bin)
```

**Format**

A data.frame with 454 observations on 5 variables.

Id The patient ID.

InvestI The ID of the investigator (psychiatrist) who treated the patient.

Treat The treatment indicator, coded as -1 = control treatment (10 mg. haloperidol) and 1 = experimental treatment (8 mg. risperidone).

PANSS\_Bin The dichotomized change in the PANSS score (1 = a reduction of 20% or more in the PANSS score, 0=otherwise)

BPRS\_Bin The dichotomized change in the BPRS score (1 = a reduction of 20% or more in the BPRS score, 0=otherwise)

CGI\_Bin The dichotomized change in the CGI score, coded as 1 = a change of more than 3 points on the original scale (score at the end of the treatment relative to score at the beginning of the treatment), 0 = otherwise.

**References**

Kay, S.R., Opler, L.A., & Lindenmayer, J.P. (1988). Reliability and validity of the Positive and Negative Syndrome Scale for schizophrenics. *Psychiatric Research*, 23, 99-110.

Leucht, S., et al. (2005). Clinical implications of Brief Psychiatric Rating Scale scores. *The British Journal of Psychiatry*, 187, 366-371.



---

Schizo_BinCont	<i>Data of a clinical trial in schizophrenia, with binary and continuous endpoints</i>
----------------	--

---

### Description

These are the data of a clinical trial in schizophrenia. Patients' schizophrenic symptoms were measured using the PANSS, BPRS, and CGI. There were two treatment conditions (risperidone and control).

### Usage

```
data(Schizo)
```

### Format

A data.frame with 446 observations on 9 variables.

Id The patient ID.

InvestID The ID of the investigator (psychiatrist) who treated the patient.

Treat The treatment indicator, coded as  $-1$  = control and  $1$  = Risperidone.

CGI The change in the CGI score (= score at the start of the treatment - score at the end of the treatment).

PANSS The change in the PANSS score (= score at the start of the treatment - score at the end of the treatment).

BPRS The change in the PANSS score (= score at the start of the treatment - score at the end of the treatment).

PANSS\_Bin The dichotomized PANSS change score, coded as  $1$  = a reduction of 20% or more in the PANSS score (score at the end of the treatment relative to score at the beginning of the treatment),  $0$  = otherwise.

BPRS\_Bin The dichotomized BPRS change score, coded as  $1$  = a reduction of 20% or more in the BPRS score (score at the end of the treatment relative to score at the beginning of the treatment),  $0$  = otherwise.

CGI\_Bin The dichotomized change in the CGI score, coded as  $1$  = a change of more than 3 points on the original scale (score at the end of the treatment relative to score at the beginning of the treatment),  $0$  = otherwise.

Schizo\_PANSS

*Longitudinal PANSS data of five clinical trials in schizophrenia***Description**

These are the longitudinal PANSS data of five clinical trial in schizophrenia. A total of 2151 patients were treated by 198 investigators (psychiatrists). There were two treatment conditions (risperidone and control). Patients' schizophrenic symptoms were measured using the PANSS at different time moments following start of the treatment. The variables Week1-Week8 express the change scores over time using the raw (semi-continuous) PANSS scores. The variables Week1\_bin - Week8\_bin are binary indicators of a 20% or higher reduction in PANSS score versus baseline. The latter corresponds to a commonly accepted criterion for defining a clinically meaningful response (Kay et al., 1988).

**Usage**

```
data(Schizo_PANSS)
```

**Format**

A data.frame with 2151 observations on 6 variables.

Id The patient ID.

InvestID The ID of the investigator (psychiatrist) who treated the patient.

Treat The treatment indicator, coded as -1 = placebo and 1 = Risperidone.

Week1 The change in the PANSS score 1 week after starting the treatment (= score at the start of the treatment - score at 1 week after starting the treatment).

Week2 The change in the PANSS score 2 weeks after starting the treatment.

Week4 The change in the PANSS score 4 weeks after starting the treatment.

Week6 The change in the PANSS score 6 weeks after starting the treatment.

Week8 The change in the PANSS score 8 weeks after starting the treatment.

Week1\_bin The dichotomized change in the PANSS score 1 week after starting the treatment (1=a 20% or higher reduction in PANSS score versus baseline, 0=otherwise).

Week2\_bin The dichotomized change in the PANSS score 2 weeks after starting the treatment.

Week4\_bin The dichotomized change in the PANSS score 4 weeks after starting the treatment.

Week6\_bin The dichotomized change in the PANSS score 6 weeks after starting the treatment.

Week8\_bin The dichotomized change in the PANSS score 8 weeks after starting the treatment.

**References**

Kay, S.R., Opler, L.A., & Lindenmayer, J.P. (1988). Reliability and validity of the Positive and Negative Syndrome Scale for schizophrenics. *Psychiatric Research*, 23, 99-110.

---

 Sim.Data.Counterfactuals

*Simulate a dataset that contains counterfactuals*


---

## Description

The function `Sim.Data.Counterfactuals` simulates a dataset that contains four (continuous) counterfactuals (i.e., potential outcomes) and a (binary) treatment indicator. The counterfactuals  $T_0$  and  $T_1$  denote the true endpoints of a patient under the control and the experimental treatments, respectively, and the counterfactuals  $S_0$  and  $S_1$  denote the surrogate endpoints of the patient under the control and the experimental treatments, respectively. The user can specify the number of patients, the desired mean values for the counterfactuals (i.e.,  $\mu_c$ ), and the desired correlations between the counterfactuals (i.e., the off-diagonal values in the standardized  $\Sigma_c$  matrix). For details, see the papers of Alonso et al. (submitted) and Van der Elst et al. (submitted).

## Usage

```
Sim.Data.Counterfactuals(N.Total=2000,
  mu_c=c(0, 0, 0, 0), T0S0=0, T1S1=0, T0T1=0, T0S1=0,
  T1S0=0, S0S1=0, Seed=sample(1:1000, size=1))
```

## Arguments

<code>N.Total</code>	The total number of patients in the simulated dataset. Default 2000.
<code>mu_c</code>	A vector that specifies the desired means for the counterfactuals $S_0$ , $S_1$ , $T_0$ , and $T_1$ , respectively. Default <code>c(0, 0, 0, 0)</code> .
<code>T0S0</code>	A scalar that specifies the desired correlation between the counterfactuals $T_0$ and $S_0$ that should be used in the generation of the data. Default 0.
<code>T1S1</code>	A scalar that specifies the desired correlation between the counterfactuals $T_1$ and $S_1$ that should be used in the generation of the data. Default 0.
<code>T0T1</code>	A scalar that specifies the desired correlation between the counterfactuals $T_0$ and $T_1$ that should be used in the generation of the data. Default 0.
<code>T0S1</code>	A scalar that specifies the desired correlation between the counterfactuals $T_0$ and $S_1$ that should be used in the generation of the data. Default 0.
<code>T1S0</code>	A scalar that specifies the desired correlation between the counterfactuals $T_1$ and $S_0$ that should be used in the generation of the data. Default 0.
<code>S0S1</code>	A scalar that specifies the desired correlation between the counterfactuals $T_0$ and $T_1$ that should be used in the generation of the data. Default 0.
<code>Seed</code>	A seed that is used to generate the dataset. Default <code>sample(x=1:1000, size=1)</code> , i.e., a random number between 1 and 1000.

**Details**

The generated object `Data.Counterfactuals` (of class `data.frame`) is placed in the workspace.

The specified values for `T0S0`, `T1S1`, `T0T1`, `T0S1`, `T1S0`, and `S0S1` in the function call should form a matrix that is positive definite (i.e., they should form a valid correlation matrix). When the user specifies values that form a matrix that is not positive definite, an error message is given and the object `Data.Counterfactuals` is not generated. The function `Pos.Def.Matrices` can be used to examine beforehand whether a 4 by 4 matrix is positive definite.

**Author(s)**

Wim Van der Elst, Ariel Alonso, & Geert Molenberghs

**References**

Alonso, A., Van der Elst, W., Molenberghs, G., Buyse, M., & Burzykowski, T. (submitted). On the relationship between the causal inference and meta-analytic paradigms for the validation of surrogate markers.

Van der Elst, W., Alonso, A., & Molenberghs, G. (submitted). An exploration of the relationship between causal inference and meta-analytic measures of surrogacy.

**See Also**

[Sim.Data.MTS](#), [Sim.Data.STS](#)

**Examples**

```
## Generate a dataset with 2000 patients, cor(S0,T0)=cor(S1,T1)=.5,
## cor(T0,T1)=cor(T0,S1)=cor(T1,S0)=cor(S0,S1)=0, with means
## 5, 9, 12, and 15 for S0, S1, T0, and T1, respectively:
Sim.Data.Counterfactuals(N=2000, T0S0=.5, T1S1=.5, T0T1=0, T0S1=0, T1S0=0, S0S1=0,
mu_c=c(5, 9, 12, 15), Seed=1)
```

---

`Sim.Data.CounterfactualsBinBin`

*Simulate a dataset that contains counterfactuals for binary endpoints*

---

**Description**

The function `Sim.Data.CounterfactualsBinBin` simulates a dataset that contains four (binary) counterfactuals (i.e., potential outcomes) and a (binary) treatment indicator. The counterfactuals  $T_0$  and  $T_1$  denote the true endpoints of a patient under the control and the experimental treatments, respectively, and the counterfactuals  $S_0$  and  $S_1$  denote the surrogate endpoints of the patient under the control and the experimental treatments, respectively. The user can specify the number of patients and the desired probabilities of the vector of potential outcomes (i.e.,  $\mathbf{Y}'_c=(T_0, T_1, S_0, S_1)$ ).

**Usage**

```
Sim.Data.CounterfactualsBinBin(Pi_s=rep(1/16, 16),
N.Total=2000, Seed=sample(1:1000, size=1))
```

**Arguments**

Pi_s	The vector of probabilities of the potential outcomes, i.e., $p^{i_{0000}}, p^{i_{0100}}, p^{i_{0010}}, p^{i_{0001}}, p^{i_{0101}}, p^{i_{1000}}, p^{i_{1010}}, p^{i_{1001}}, p^{i_{1110}}, p^{i_{1101}}, p^{i_{1011}}, p^{i_{1111}}, p^{i_{0110}}, p^{i_{0011}}, p^{i_{0111}}, p^{i_{1100}}$ . Default <code>rep(1/16, 16)</code> .
N.Total	The desired number of patients in the simulated dataset. Default 2000.
Seed	A seed that is used to generate the dataset. Default <code>sample(x=1:1000, size=1)</code> , i.e., a random number between 1 and 1000.

**Details**

The generated object `Data.STSBinBin.Counter` (which contains the counterfactuals) and `Data.STSBinBin.Obs` (the "observable data") (of class `data.frame`) is placed in the workspace.

**Value**

An object of class `Sim.Data.CounterfactualsBinBin` with components,

<code>Data.STSBinBin.Obs</code>	The generated dataset that contains the "observed" surrogate endpoint, true endpoint, and assigned treatment.
<code>Data.STSBinBin.Counter</code>	The generated dataset that contains the counterfactuals.
<code>Vector_Pi</code>	The vector of probabilities of the potential outcomes, i.e., $p^{i_{0000}}, p^{i_{0100}}, p^{i_{0010}}, p^{i_{0001}}, p^{i_{0101}}, p^{i_{1000}}, p^{i_{1010}}, p^{i_{1001}}, p^{i_{1110}}, p^{i_{1101}}, p^{i_{1011}}, p^{i_{1111}}, p^{i_{0110}}, p^{i_{0011}}, p^{i_{0111}}, p^{i_{1100}}$ .
<code>Pi_Marginals</code>	The vector of marginal probabilities $\pi_{1.1.}, \pi_{0.1.}, \pi_{1.0.}, \pi_{0.0.}, \pi_{.1.1}, \pi_{.1.0}, \pi_{.0.1}, \pi_{.0.0}$ .
<code>True.R2_H</code>	The true $R_H^2$ value.
<code>True.Theta_T</code>	The true odds ratio for $T$ .
<code>True.Theta_S</code>	The true odds ratio for $S$ .

**Author(s)**

Wim Van der Elst, Ariel Alonso, & Geert Molenberghs

**Examples**

```
## Generate a dataset with 2000 patients, and values 1/16
## for all probabilities between the counterfactuals:
Sim.Data.CounterfactualsBinBin(N.Total=2000)
```

---

Sim.Data.MTS	<i>Simulates a dataset that can be used to assess surrogacy in the multiple-trial setting</i>
--------------	---

---

### Description

The function `Sim.Data.MTS` simulates a dataset that contains the variables `Treat`, `Trial.ID`, `Surr.True`, and `Pat.ID`. The user can specify the number of patients and the number of trials that should be included in the simulated dataset, the desired  $R_{trial}$  and  $R_{indiv}$  values, the desired variability of the trial-specific treatment effects for the surrogate and the true endpoints (i.e.,  $d_{aa}$  and  $d_{bb}$ , respectively), and the desired fixed-effect parameters of the intercepts and treatment effects for the surrogate and the true endpoints.

### Usage

```
Sim.Data.MTS(N.Total=2000, N.Trial=50, R.Trial.Target=.8, R.Indiv.Target=.8,
Fixed.Effects=c(0, 0, 0, 0), D.aa=10, D.bb=10, Seed=sample(1:1000, size=1),
Model=c("Full"))
```

### Arguments

<code>N.Total</code>	The total number of patients in the simulated dataset. Default 2000.
<code>N.Trial</code>	The number of trials. Default 50.
<code>R.Trial.Target</code>	The desired $R_{trial}$ value in the simulated dataset. Default 0.80
<code>R.Indiv.Target</code>	The desired $R_{indiv}$ value in the simulated dataset. Default 0.80.
<code>Fixed.Effects</code>	A vector that specifies the desired fixed-effect intercept for the surrogate, fixed-effect intercept for the true endpoint, fixed treatment effect for the surrogate, and fixed treatment effect for the true endpoint, respectively. Default <code>c(0, 0, 0, 0)</code> .
<code>D.aa</code>	The desired variability of the trial-specific treatment effects on the surrogate endpoint. Default 10.
<code>D.bb</code>	The desired variability of the trial-specific treatment effects on the true endpoint. Default 10.
<code>Model</code>	The type of model that will be fitted on the data when surrogacy is assessed, i.e., a full, semireduced, or reduced model (for details, see <a href="#">UnifixedContCont</a> , <a href="#">UnimixedContCont</a> , <a href="#">BifixedContCont</a> , <a href="#">BimixedContCont</a> ).
<code>Seed</code>	The seed that is used to generate the dataset. Default <code>sample(x=1:1000, size=1)</code> , i.e., a random number between 1 and 1000.

### Details

The generated object `Data.Observed.MTS` (of class `data.frame`) is placed in the workspace (for easy access).

The number of patients per trial in the simulated dataset is identical in each trial, and equals the requested total number of patients divided by the requested number of trials ( $=N.Total/N.Trial$ ).

If this is not a whole number, a warning is given and the number of patients per trial is automatically rounded up to the nearest whole number. See **Examples** below.

Treatment allocation is balanced when the number of patients per trial is an odd number. If this is not the case, treatment allocation is balanced up to one patient (the remaining patient is randomly allocated to the experimental or the control treatment groups in each of the trials).

### Author(s)

Wim Van der Elst, Ariel Alonso, & Geert Molenberghs

### See Also

[UnifixedContCont](#), [BifixedContCont](#), [UnimixedContCont](#), [BimixedContCont](#), [Sim.Data.STS](#)

### Examples

```
# Simulate a dataset with 2000 patients, 50 trials, R.indiv=R.trial=.8, D.aa=10,
# D.bb=50, and fixed effect values 1, 2, 30, and 90:
Sim.Data.MTS(N.Total=2000, N.Trial=50, R.Trial.Target=.8, R.Indiv.Target=.8, D.aa=10,
D.bb=50, Fixed.Effects=c(1, 2, 30, 90), Seed=1)
```

```
# Sample output, the first 10 rows of Data.Observed.MTS:
Data.Observed.MTS[1:10,]
```

```
# Note: When the following code is used to generate a dataset:
Sim.Data.MTS(N.Total=2000, N.Trial=99, R.Trial.Target=.5, R.Indiv.Target=.8,
D.aa=10, D.bb=50, Fixed.Effects=c(1, 2, 30, 90), Seed=1)
```

```
# R gives the following warning:
```

```
# > NOTE: The number of patients per trial requested in the function call
# > equals 20.20202 (=N.Total/N.Trial), which is not a whole number.
# > To obtain a dataset where the number of patients per trial is balanced for
# > all trials, the number of patients per trial was rounded to 21 to generate
# > the dataset. Data.Observed.MTS thus contains a total of 2079 patients rather
# > than the requested 2000 in the function call.
```

---

Sim.Data.STS

*Simulates a dataset that can be used to assess surrogacy in the single-trial setting*

---

### Description

The function `Sim.Data.STS` simulates a dataset that contains the variables `Treat`, `Surr`, `True`, and `Pat.ID`. The user can specify the total number of patients, the desired  $R_{indiv}$  value (also referred to as the adjusted association ( $\gamma$ ) in the single-trial meta-analytic setting), and the desired means of the surrogate and the true endpoints in the experimental and control treatment groups.

**Usage**

```
Sim.Data.STS(N.Total=2000, R.Indiv.Target=.8, Means=c(0, 0, 0, 0), Seed=
sample(1:1000, size=1))
```

**Arguments**

N.Total	The total number of patients in the simulated dataset. Default 2000.
R.Indiv.Target	The desired $R_{indiv}$ (or $\gamma$ ) value in the simulated dataset. Default 0.80.
Means	A vector that specifies the desired mean for the surrogate in the control treatment group, mean for the surrogate in the experimental treatment group, mean for the true endpoint in the control treatment group, and mean for the true endpoint in the experimental treatment group, respectively. Default $c(0, 0, 0, 0)$ .
Seed	The seed that is used to generate the dataset. Default <code>sample(x=1:1000, size=1)</code> , i.e., a random number between 1 and 1000.

**Details**

The generated object `Data.Observed.STS` (of class `data.frame`) is placed in the workspace (for easy access).

**Author(s)**

Wim Van der Elst, Ariel Alonso, & Geert Molenberghs

**See Also**

[Sim.Data.MTS](#), [Single.Trial.RE.AA](#)

**Examples**

```
# Simulate a dataset:
Sim.Data.STS(N.Total=2000, R.Indiv.Target=.8, Means=c(1, 5, 20, 37), Seed=1)
```

---

<code>Sim.Data.STSBinBin</code>	<i>Simulates a dataset that can be used to assess surrogacy in the single trial setting when <math>S</math> and <math>T</math> are binary endpoints</i>
---------------------------------	---

---

**Description**

The function `Sim.Data.STSBinBin` simulates a dataset that contains four (binary) counterfactuals (i.e., potential outcomes) and a (binary) treatment indicator. The counterfactuals  $T_0$  and  $T_1$  denote the true endpoints of a patient under the control and the experimental treatments, respectively, and the counterfactuals  $S_0$  and  $S_1$  denote the surrogate endpoints of the patient under the control and the experimental treatments, respectively. In addition, the function provides the "observable" data based on the dataset of the counterfactuals, i.e., the  $S$  and  $T$  endpoints given the treatment that was allocated to a patient. The user can specify the assumption regarding monotonicity that should be made to generate the data (no monotonicity, monotonicity for  $S$  alone, monotonicity for  $T$  alone, or monotonicity for both  $S$  and  $T$ ).



**Usage**

```
Sim.Data.STSBinBin(Monotonicity=c("No"), N.Total=2000, Seed)
```

**Arguments**

Monotonicity	The assumption regarding monotonicity that should be made when the data are generated, i.e., <code>Monotonicity="No"</code> (no monotonicity assumed), <code>Monotonicity="True.Endp"</code> (monotonicity assumed for the true endpoint alone), <code>Monotonicity="Surr.Endp"</code> (monotonicity assumed for the surrogate endpoint alone), and <code>Monotonicity="Surr.True.Endp"</code> (monotonicity assumed for both endpoints). Default <code>Monotonicity="No"</code> .
N.Total	The desired number of patients in the simulated dataset. Default 2000.
Seed	A seed that is used to generate the dataset. Default <code>sample(x=1:1000, size=1)</code> , i.e., a random number between 1 and 1000.

**Details**

The generated objects `Data.STSBinBin_Counterfactuals` (which contains the counterfactuals) and `Data.STSBinBin_Obs` (which contains the observable data) of class `data.frame` are placed in the workspace. Other relevant output can be accessed based on the fitted object (see *Value* below)

**Value**

An object of class `Sim.Data.STSBinBin` with components,

<code>Data.STSBinBin.Obs</code>	The generated dataset that contains the "observed" surrogate endpoint, true endpoint, and assigned treatment.
<code>Data.STSBinBin.Counter</code>	The generated dataset that contains the counterfactuals.
<code>Vector_Pi</code>	The vector of probabilities of the potential outcomes, i.e., $p^{i_{0000}}, p^{i_{0100}}, p^{i_{0010}}, p^{i_{0001}}, p^{i_{0101}}, p^{i_{1000}}, p^{i_{1010}}, p^{i_{1001}}, p^{i_{1110}}, p^{i_{1101}}, p^{i_{1011}}, p^{i_{1111}}, p^{i_{0110}}, p^{i_{0011}}, p^{i_{0111}}, p^{i_{1100}}$ .
<code>Pi_Marginals</code>	The vector of marginal probabilities $\pi_{1.1.}, \pi_{0.1.}, \pi_{1.0.}, \pi_{0.0.}, \pi_{.1.1}, \pi_{.1.0}, \pi_{.0.1}, \pi_{.0.0}$ .
<code>True.R2_H</code>	The true $R_H^2$ value.
<code>True.Theta_T</code>	The true odds ratio for $T$ .
<code>True.Theta_S</code>	The true odds ratio for $S$ .

**Author(s)**

Wim Van der Elst, Ariel Alonso, & Geert Molenberghs

**Examples**

```
## Generate a dataset with 2000 patients,
## assuming no monotonicity:
Sim.Data.STSBinBin(Monotonicity=c("No"), N.Total=200)
```

---

Single.Trial.RE.AA	<i>Conducts a surrogacy analysis based on the single-trial meta-analytic framework</i>
--------------------	--

---

### Description

The function `Single.Trial.RE.AA` conducts a surrogacy analysis based on the single-trial meta-analytic framework of Buyse & Molenberghs (1998). See **Details** below.

### Usage

```
Single.Trial.RE.AA(Dataset, Surr, True, Treat, Pat.ID, Alpha=.05,
  Number.Bootstraps=500, Seed=sample(1:1000, size=1))
```

### Arguments

Dataset	A data.frame that should consist of one line per patient. Each line contains (at least) a surrogate value, a true endpoint value, a treatment indicator, and a patient ID.
Surr	The name of the variable in Dataset that contains the surrogate values.
True	The name of the variable in Dataset that contains the true endpoint values.
Treat	The name of the variable in Dataset that contains the treatment indicators. The treatment indicator should either be coded as 1 for the experimental group and -1 for the control group, or as 1 for the experimental group and 0 for the control group. The -1/1 coding is recommended.
Pat.ID	The name of the variable in Dataset that contains the patient's ID.
Alpha	The $\alpha$ -level that is used to determine the confidence intervals around Alpha (which is a parameter estimate of a model where the surrogate is regressed on the treatment indicator, see <b>Details</b> below), Beta, RE, and $\gamma$ . Default 0.05.
Number.Bootstraps	The number of bootstrap samples that are used to obtain the bootstrapp-based confidence intervals for RE and the adjusted association ( $\gamma$ ). Default 500.
Seed	The seed that is used to generate the bootstrap samples. Default <code>sample(x=1:1000, size=1)</code> , i.e., a random number between 1 and 1000.

### Details

The Relative Effect (RE) and the adjusted association ( $\gamma$ ) are based on the following bivariate regression model (when the surrogate and the true endpoints are continuous variables):

$$S_j = \mu_S + \alpha Z_j + \varepsilon_{Sj},$$

$$T_j = \mu_T + \beta Z_j + \varepsilon_{Tj},$$

where the error terms have a joint zero-mean normal distribution with variance-covariance matrix:

$$\Sigma = \begin{pmatrix} \sigma_{SS} & \\ \sigma_{ST} & \sigma_{TT} \end{pmatrix},$$

and where  $j$  is the subject indicator,  $S_j$  and  $T_j$  are the surrogate and true endpoint values of patient  $j$ , and  $Z_j$  is the treatment indicator for patient  $j$ .

The parameter estimates of the fitted regression model and the variance-covariance matrix of the residuals are used to compute RE and the adjusted association ( $\gamma$ ), respectively:

$$RE = \frac{\beta}{\alpha},$$

$$\gamma = \frac{\sigma_{ST}}{\sqrt{\sigma_{SS}\sigma_{TT}}}.$$

### Note

The single-trial meta-analytic framework is hampered by a number of issues (Burzykowski et al., 2005). For example, a key motivation to validate a surrogate endpoint is to be able to predict the effect of  $Z$  on  $T$  as based on the effect of  $Z$  on  $S$  in a new clinical trial where  $T$  is not (yet) observed. The RE allows for such a prediction, but this requires the assumption that the relation between  $\alpha$  and  $\beta$  can be described by a linear regression model that goes through the origin. In other words, it has to be assumed that the RE remains constant across clinical trials. The constant RE assumption is unverifiable in a single-trial setting, but a way out of this problem is to combine the information of multiple clinical trials and generalize the RE concept to a multiple-trial setting (as is done in the multiple-trial meta-analytic approach, see [UnifixedContCont](#), [BifixedContCont](#), [UnimixedContCont](#), and [BimixedContCont](#)).

### Value

An object of class `Single.Trial.RE.AA` with components,

<code>Data.Analyze</code>	Prior to conducting the surrogacy analysis, data of patients who have a missing value for the surrogate and/or the true endpoint are excluded. <code>Data.Analyze</code> is the dataset on which the surrogacy analysis was conducted.
<code>Alpha</code>	An object of class <code>data.frame</code> that contains the parameter estimate for $\alpha$ , its standard error, and its confidence interval. Note that <code>Alpha</code> is not to be confused with the <code>Alpha</code> argument in the function call, which specifies the $\alpha$ -level of the confidence intervals of the parameters.
<code>Beta</code>	An object of class <code>data.frame</code> that contains the parameter estimate for $\beta$ , its standard error, and its confidence interval.
<code>RE.Delta</code>	An object of class <code>data.frame</code> that contains the estimated RE, its standard error, and its confidence interval (based on the Delta method).
<code>RE.Fieller</code>	An object of class <code>data.frame</code> that contains the estimated RE, its standard error, and its confidence interval (based on Fieller's theorem).
<code>RE.Boot</code>	An object of class <code>data.frame</code> that contains the estimated RE, its standard error, and its confidence interval (based on bootstrapping). Note that the occurrence of outliers in the sample of bootstrapped RE values may lead to standard errors

and/or confidence intervals that are not trustworthy. Such problems mainly occur when the parameter estimate for  $\alpha$  is close to 0 (taking its standard error into account). To detect possible outliers, studentized deleted residuals are computed (by fitting an intercept-only model with the bootstrapped RE values as the outcome variable). Bootstrapped RE values with an absolute studentized residual larger than  $t(1 - \alpha/2n; n - 2)$  are marked as outliers (where  $n$  = the number of bootstrapped RE values; Kutner et al., 2005). A warning is given when outliers are found, and the position of the outlier(s) in the bootstrap sample is identified. Inspection of the vector of bootstrapped RE values (see RE.Boot.Samples below) is recommended in this situation, and/or the use of the confidence intervals that are based on the Delta method or Fieller's theorem (rather than the bootstrap-based confidence interval).

AA	An object of class <code>data.frame</code> that contains the adjusted association (i.e., $\gamma$ ), its standard error, and its confidence interval (based on the Fisher-Z transformation procedure).
AA.Boot	An object of class <code>data.frame</code> that contains the adjusted association (i.e., $\gamma$ ), its standard error, and its confidence interval (based on a bootstrap procedure).
RE.Boot.Samples	A vector that contains the RE values that were generated during the bootstrap procedure.
AA.Boot.Samples	A vector that contains the adjusted association (i.e., $\gamma$ ) values that were generated during the bootstrap procedure.
Cor.Endpoints	A <code>data.frame</code> that contains the correlations between the surrogate and the true endpoint in the control treatment group (i.e., $\rho_{T_0T_1}$ ) and in the experimental treatment group (i.e., $\rho_{T_1S_1}$ ), their standard errors and their confidence intervals.
Residuals	A <code>data.frame</code> that contains the residuals for the surrogate and true endpoints that are obtained when the surrogate and the true endpoint are regressed on the treatment indicator.

### Author(s)

Wim Van der Elst, Ariel Alonso, & Geert Molenberghs

### References

- Burzykowski, T., Molenberghs, G., & Buyse, M. (2005). *The evaluation of surrogate endpoints*. New York: Springer-Verlag.
- Buyse, M., & Molenberghs, G. (1998). The validation of surrogate endpoints in randomized experiments. *Biometrics*, *54*, 1014-1029.
- Buyse, M., Molenberghs, G., Burzykowski, T., Renard, D., & Geys, H. (2000). The validation of surrogate endpoints in meta-analysis of randomized experiments. *Biostatistics*, *1*, 49-67.
- Kutner, M. H., Nachtsheim, C. J., Neter, J., & Li, W. (2005). *Applied linear statistical models (5th ed.)*. New York: McGraw Hill.

### See Also

[UnifixedContCont](#), [BifixedContCont](#), [UnimixedContCont](#), [BimixedContCont](#), [ICA.ContCont](#)

**Examples**

```
## Not run: # time consuming code part
# Example 1, based on the ARMD data:
data(ARMD)

# Assess surrogacy based on the single-trial meta-analytic approach:
Sur <- Single.Trial.RE.AA(Dataset=ARMD, Surr=Diff24, True=Diff52, Treat=Treat, Pat.ID=Id)

# Obtain a summary and plot of the results
summary(Sur)
plot(Sur)

# Example 2
# Conduct an analysis based on a simulated dataset with 2000 patients
# and Rindiv=.8
# Simulate the data:
Sim.Data.STS(N.Total=2000, R.Indiv.Target=.8, Seed=123)

# Assess surrogacy:
Sur2 <- Single.Trial.RE.AA(Dataset=Data.Observed.STS, Surr=Surr, True=True, Treat=Treat,
Pat.ID=Pat.ID)

# Show a summary and plots of results
summary(Sur2)
plot(Sur2)

## End(Not run)
```

SPF.BinBin

*Evaluate the surrogate predictive function (SPF) in the binary-binary setting (sensitivity-analysis based approach)*

**Description**

Computes the surrogate predictive function (SPF) based on sensitivity-analysis, i.e.,  $r(i, j) = P(\Delta T = i | \Delta S = j)$ , in the setting where both  $S$  and  $T$  are binary endpoints. For example,  $r(-1, 1)$  quantifies the probability that the treatment has a negative effect on the true endpoint ( $\Delta T = -1$ ) given that it has a positive effect on the surrogate ( $\Delta S = 1$ ). All quantities of interest are derived from the vectors of 'plausible values' for  $\pi$  (i.e., vectors  $\pi$  that are compatible with the observable data at hand). See **Details** below.

**Usage**

```
SPF.BinBin(x)
```

**Arguments**

`x` A fitted object of class ICA.BinBin, ICA.BinBin.Grid.Full, or ICA.BinBin.Grid.Sample.

### Details

All  $r(i, j) = P(\Delta T = i | \Delta S = j)$  are derived from  $\pi$  (vector of potential outcomes). Denote by  $\mathbf{Y}' = (T_0, T_1, S_0, S_1)$  the vector of potential outcomes. The vector  $\mathbf{Y}$  can take 16 values and the set of parameters  $\pi_{ijpq} = P(T_0 = i, T_1 = j, S_0 = p, S_1 = q)$  (with  $i, j, p, q = 0/1$ ) fully characterizes its distribution.

Based on the data and assuming SUTVA, the marginal probabilities  $\pi_{1\cdot 1\cdot}, \pi_{1\cdot 0\cdot}, \pi_{\cdot 1\cdot 1\cdot}, \pi_{\cdot 1\cdot 0\cdot}, \pi_{0\cdot 1\cdot},$  and  $\pi_{0\cdot 0\cdot}$  can be computed (by hand or using the function [MarginalProbs](#)). Define the vector

$$\mathbf{b}' = (1, \pi_{1\cdot 1\cdot}, \pi_{1\cdot 0\cdot}, \pi_{\cdot 1\cdot 1\cdot}, \pi_{\cdot 1\cdot 0\cdot}, \pi_{0\cdot 1\cdot}, \pi_{0\cdot 0\cdot})$$

and  $\mathbf{A}$  is a contrast matrix such that the identified restrictions can be written as a system of linear equation

$$\mathbf{A}\pi = \mathbf{b}.$$

The matrix  $\mathbf{A}$  has rank 7 and can be partitioned as  $\mathbf{A} = (\mathbf{A}_r | \mathbf{A}_f)$ , and similarly the vector  $\pi$  can be partitioned as  $\pi' = (\pi'_r | \pi'_f)$  (where  $f$  refers to the submatrix/vector given by the 9 last columns/components of  $\mathbf{A}/\pi$ ). Using these partitions the previous system of linear equations can be rewritten as

$$\mathbf{A}_r \pi_r + \mathbf{A}_f \pi_f = \mathbf{b}.$$

The functions [ICA.BinBin](#), [ICA.BinBin.Grid.Sample](#), and [ICA.BinBin.Grid.Full](#) contain algorithms that generate plausible distributions for  $\mathbf{Y}$  (for details, see the documentation of these functions). Based on the output of these functions, [SPF.BinBin](#) computes the surrogate predictive function.

### Value

<code>r_1_1</code>	The vector of values for $r(1, 1)$ , i.e., $P(\Delta T = 1   \Delta S = 1)$ .
<code>r_min1_1</code>	The vector of values for $r(-1, 1)$ .
<code>r_0_1</code>	The vector of values for $r(0, 1)$ .
<code>r_1_0</code>	The vector of values for $r(1, 0)$ .
<code>r_min1_0</code>	The vector of values for $r(-1, 0)$ .
<code>r_0_0</code>	The vector of values for $r(0, 0)$ .
<code>r_1_min1</code>	The vector of values for $r(1, -1)$ .
<code>r_min1_min1</code>	The vector of values for $r(-1, -1)$ .
<code>r_0_min1</code>	The vector of values for $r(0, -1)$ .
<code>Monotonicity</code>	The assumption regarding monotonicity under which the result was obtained.

### Author(s)

Wim Van der Elst, Paul Meyvisch, Ariel Alonso, & Geert Molenberghs

### References

Alonso, A., Van der Elst, W., & Molenberghs, G. (2015). Assessing a surrogate effect predictive value in a causal inference framework.

**See Also**

[ICA.BinBin](#), [ICA.BinBin.Grid.Sample](#), [ICA.BinBin.Grid.Full](#), [plot.SPF.BinBin](#)

**Examples**

```
# Use ICA.BinBin.Grid.Sample to obtain plausible values for pi
ICA_BINBIN_Grid_Sample <- ICA.BinBin.Grid.Sample(pi1_1=0.341, pi0_1=0.119,
pi1_0=0.254, pi_1_1=0.686, pi_1_0=0.088, pi_0_1=0.078, Seed=1,
Monotonicity=c("General"), M=2500)

# Obtain SPF
SPF <- SPF.BinBin(ICA_BINBIN_Grid_Sample)

# examine results
summary(SPF)
plot(SPF)
```

---

SPF.BinCont	<i>Evaluate the surrogate predictive function (SPF) in the binary-continuous setting (sensitivity-analysis based approach)</i>
-------------	--

---

**Description**

Computes the surrogate predictive function (SPF) based on sensitivity-analysis, i.e.,  $P(\Delta T | \Delta S \in I[ab])$ , in the setting where  $S$  is continuous and  $T$  is a binary endpoint.

**Usage**

```
SPF.BinCont(x, a, b)
```

**Arguments**

x	A fitted object of class <code>ICA.BinCont</code> .
a	The lower interval $a$ in $P(\Delta T   \Delta S \in I[ab])$ .
b	The upper interval $b$ in $P(\Delta T   \Delta S \in I[ab])$ .

**Value**

a	The lower interval $a$ in $P(\Delta T   \Delta S \in I[ab])$ .
b	The upper interval $b$ in $P(\Delta T   \Delta S \in I[ab])$ .
P_Delta_T_min1	The vector of values for $P(\Delta T = -1   \Delta S \in I[ab])$ .
P_Delta_T_0	The vector of values for $P(\Delta T = 0   \Delta S \in I[ab])$ .
P_Delta_T_1	The vector of values for $P(\Delta T = 1   \Delta S \in I[ab])$ .

**Author(s)**

Wim Van der Elst & Ariel Alonso

## References

Alonso, A., Van der Elst, W., Molenberghs, G., & Verbeke, G. (2017). Assessing the predictive value of a continuous surrogate for a binary true endpoint based on causal inference.

## See Also

[ICA.BinBin](#), [plot.SPF.BinCont](#)

## Examples

```
## Not run: # time consuming code part
# Use ICA.BinCont to examine surrogacy
data(Schizo_BinCont)
Result_BinCont <- ICA.BinCont(M = 1000, Dataset = Schizo_BinCont,
Surr = PANSS, True = CGI_Bin, Treat=Treat, Diff.Sigma=TRUE)

# Obtain SPF
Fit <- SPF.BinCont(x=Result_BinCont, a = -30, b = -3)

# examine results
summary(Fit1)
plot(Fit1)

## End(Not run)
```

---

SurvSurv

*Assess surrogacy for two survival endpoints based on information theory and a two-stage approach*

---

## Description

The function `SurvSurv` implements the information-theoretic approach to estimate individual-level surrogacy (i.e.,  $R_{h.ind}^2$ ) and the two-stage approach to estimate trial-level surrogacy ( $R_{trial}^2$ ,  $R_{ht}^2$ ) when both endpoints are time-to-event variables (Alonso & Molenberghs, 2008). See the **Details** section below.

## Usage

```
SurvSurv(Dataset, Surr, SurrCens, True, TrueCens, Treat,
Trial.ID, Weighted=TRUE, Alpha=.05)
```

## Arguments

Dataset	A data.frame that should consist of one line per patient. Each line contains (at least) a surrogate value and censoring indicator, a true endpoint value and censoring indicator, a treatment indicator, and a trial ID.
Surr	The name of the variable in Dataset that contains the surrogate endpoint values.



SurrCens	The name of the variable in Dataset that contains the censoring indicator for the surrogate endpoint values (1 = event, 0 = censored).
True	The name of the variable in Dataset that contains the true endpoint values.
TrueCens	The name of the variable in Dataset that contains the censoring indicator for the true endpoint values (1 = event, 0 = censored).
Treat	The name of the variable in Dataset that contains the treatment indicators.
Trial.ID	The name of the variable in Dataset that contains the trial ID to which the patient belongs.
Weighted	Logical. If TRUE, then a weighted regression analysis is conducted at stage 2 of the two-stage approach. If FALSE, then an unweighted regression analysis is conducted at stage 2 of the two-stage approach. See the <b>Details</b> section below. Default TRUE.
Alpha	The $\alpha$ -level that is used to determine the confidence intervals around $R_{trial}^2$ and $R_{trial}$ . Default 0.05.

## Details

### *Individual-level surrogacy*

Alonso & Molenbergs (2008) proposed to redefine the surrogate endpoint  $S$  as a time-dependent covariate  $S(t)$ , taking value 0 until the surrogate endpoint occurs and 1 thereafter. Furthermore, these author considered the models

$$\lambda[t | x_{ij}, \beta] = K_{ij}(t)\lambda_{0i}(t)\exp(\beta x_{ij}),$$

$$\lambda[t | x_{ij}, s_{ij}, \beta, \phi] = K_{ij}(t)\lambda_{0i}(t)\exp(\beta x_{ij} + \phi S_{ij}),$$

where  $K_{ij}(t)$  is the risk function for patient  $j$  in trial  $i$ ,  $x_{ij}$  is a  $p$ -dimensional vector of (possibly) time-dependent covariates,  $\beta$  is a  $p$ -dimensional vector of unknown coefficients,  $\lambda_{0i}(t)$  is a trial-specific baseline hazard function,  $S_{ij}$  is a time-dependent covariate version of the surrogate endpoint, and  $\phi$  its associated effect.

The mutual information between  $S$  and  $T$  is estimated as  $I(T, S) = 1G^2$ , where  $n$  is the number of patients and  $G^2$  is the log likelihood test comparing the previous two models. Individual-level surrogacy can then be estimated as

$$R_{h.ind}^2 = 1 - \exp\left(-\frac{1}{n}G^2\right).$$

O'Quigley and Flandre (2006) pointed out that the previous estimator depends upon the censoring mechanism, even when the censoring mechanism is non-informative. For low levels of censoring this may not be an issue of much concern but for high levels it could lead to biased results. To properly cope with the censoring mechanism in time-to-event outcomes, these authors proposed to estimate the mutual information as  $I(T, S) = \frac{1}{k}G^2$ , where  $k$  is the total number of events experienced. Individual-level surrogacy is then estimated as

$$R_{h.ind}^2 = 1 - \exp\left(-\frac{1}{k}G^2\right).$$

*Trial-level surrogacy*

A two-stage approach is used to estimate trial-level surrogacy, following a procedure proposed by Buyse et al. (2011). In stage 1, the following trial-specific Cox proportional hazard models are fitted:

$$S_{ij}(t) = S_{i0}(t)\exp(\alpha_i Z_{ij}),$$

$$T_{ij}(t) = T_{i0}(t)\exp(\beta_i Z_{ij}),$$

where  $S_{i0}(t)$  and  $T_{i0}(t)$  are the trial-specific baseline hazard functions,  $Z_{ij}$  is the treatment indicator for subject  $j$  in trial  $i$ , and  $\alpha_i, \beta_i$  are the trial-specific treatment effects on S and T, respectively.

Next, the second stage of the analysis is conducted:

$$\hat{\beta}_i = \lambda_0 + \lambda_1 \hat{\alpha}_i + \varepsilon_i,$$

where the parameter estimates for  $\beta_i$  and  $\alpha_i$  are based on the full model that was fitted in stage 1.

When the argument `Weighted=FALSE` is used in the function call, the model that is fitted in stage 2 is an unweighted linear regression model. When a weighted model is requested (using the argument `Weighted=TRUE` in the function call), the information that is obtained in stage 1 is weighted according to the number of patients in a trial.

The classical coefficient of determination of the fitted stage 2 model provides an estimate of  $R_{trial}^2$ .

**Value**

An object of class `SurvSurv` with components,

**Results.Stage.1**

The results of stage 1 of the two-stage model fitting approach: a `data.frame` that contains the trial-specific log hazard ratio estimates of the treatment effects for the surrogate and the true endpoints.

**Results.Stage.2**

An object of class `lm` (linear model) that contains the parameter estimates of the regression model that is fitted in stage 2 of the analysis.

**R2.ht**

A `data.frame` that contains the trial-level coefficient of determination ( $R_{ht}^2$ ), its standard error and confidence interval.

**R2.hind**

A `data.frame` that contains the individual-level coefficient of determination ( $R_{hind}^2$ ), its standard error and confidence interval.

**R2h.ind.QF**

A `data.frame` that contains the individual-level coefficient of determination using the correction proposed by O'Quigley and Flandre (2006), its standard error and confidence interval.

**R2.hInd.By.Trial.QF**

A `data.frame` that contains individual-level surrogacy estimates using the correction proposed by O'Quigley and Flandre (2006), (cluster-based estimates) and their confidence interval for each of the trials separately.

**Author(s)**

Wim Van der Elst, Ariel Alonso, & Geert Molenberghs

## References

Alonso, A. A., & Molenberghs, G. (2008). Evaluating time-to-cancer recurrence as a surrogate marker for survival from an information theory perspective. *Statistical Methods in Medical Research*, 17, 497-504.

Buyse, M., Michiels, S., Squifflet, P., Lucchesi, K. J., Hellstrand, K., Brune, M. L., Castaigne, S., Rowe, J. M. (2011). Leukemia-free survival as a surrogate end point for overall survival in the evaluation of maintenance therapy for patients with acute myeloid leukemia in complete remission. *Haematologica*, 96, 1106-1112.

O'Quigly, J., & Flandre, P. (2006). Quantification of the Prentice criteria for surrogate endpoints. *Biometrics*, 62, 297-300.

## See Also

[plot.SurvSurv](#)

## Examples

```
# Open Ovarian dataset
data(Ovarian)

# Conduct analysis
Fit <- SurvSurv(Dataset = Ovarian, Surr = Pfs, SurrCens = PfsInd,
  True = Surv, TrueCens = SurvInd, Treat = Treat,
  Trial.ID = Center)

# Examine results
plot(Fit)
summary(Fit)
```

---

Test.Mono	<i>Test whether the data are compatible with monotonicity for S and/or T (binary endpoints)</i>
-----------	---

---

## Description

For some situations, the observable marginal probabilities contain sufficient information to exclude a particular monotonicity scenario. For example, under monotonicity for  $S$  and  $T$ , one of the restrictions that the data impose is  $\pi_{0111} < \min(\pi_{0.1}, \pi_{.1.1})$ . If the latter condition does not hold in the dataset at hand, monotonicity for  $S$  and  $T$  can be excluded.

## Usage

```
Test.Mono(pi1_1_, pi0_1_, pi1_0_, pi_1_1, pi_1_0, pi_0_1)
```

**Arguments**

pi1_1_	A scalar that contains $P(T = 1, S = 1 Z = 0)$ .
pi0_1_	A scalar that contains $P(T = 0, S = 1 Z = 0)$ .
pi1_0_	A scalar that contains $P(T = 1, S = 0 Z = 0)$ .
pi_1_1	A scalar that contains $P(T = 1, S = 1 Z = 1)$ .
pi_1_0	A scalar that contains $P(T = 1, S = 0 Z = 1)$ .
pi_0_1	A scalar that contains $P(T = 0, S = 1 Z = 1)$ .

**Author(s)**

Wim Van der Elst, Ariel Alonso, Marc Buyse, & Geert Molenberghs

**References**

Alonso, A., Van der Elst, W., & Molenberghs, G. (2015). Validation of surrogate endpoints: the binary-binary setting from a causal inference perspective.

**Examples**

```
Test.Mono(pi1_1=0.2619048, pi1_0=0.2857143, pi_1_1=0.6372549,
pi_1_0=0.07843137, pi0_1=0.1349206, pi_0_1=0.127451)
```

---

TrialLevelIT	<i>Estimates trial-level surrogacy in the information-theoretic framework</i>
--------------	---

---

**Description**

The function TrialLevelIT estimates trial-level surrogacy based on the vectors of treatment effects on  $S$  (i.e.,  $\alpha_i$ ), intercepts on  $S$  (i.e.,  $\mu_i$ ) and  $T$  (i.e.,  $\beta_i$ ) in the different trials. See the **Details** section below.

**Usage**

```
TrialLevelIT(Alpha.Vector, Mu_S.Vector=NULL,
Beta.Vector, N.Trial, Model="Reduced", Alpha=.05)
```

**Arguments**

Alpha.Vector	The vector of treatment effects on $S$ in the different trials, i.e., $\alpha_i$ .
Mu_S.Vector	The vector of intercepts for $S$ in the different trials, i.e., $\mu_{Si}$ . Only required when a full model is requested.
Beta.Vector	The vector of treatment effects on $T$ in the different trials, i.e., $\beta_i$ .
N.Trial	The total number of available trials.
Model	The type of model that should be fitted, i.e., Model=c("Full") or Model=c("Reduced"). See the <b>Details</b> section below. Default Model=c("Reduced").
Alpha	The $\alpha$ -level that is used to determine the confidence intervals around $R_{trial}^2$ and $R_{trial}$ . Default 0.05.

## Details

When a full model is requested (by using the argument `Model=c("Full")` in the function call), trial-level surrogacy is assessed by fitting the following univariate model:

$$\beta_i = \lambda_0 + \lambda_1 \mu_{Si} + \lambda_2 \alpha_i + \varepsilon_i, (1)$$

where  $\beta_i$  = the trial-specific treatment effects on  $T$ ,  $\mu_{Si}$  = the trial-specific intercepts for  $S$ , and  $\alpha_i$  = the trial-specific treatment effects on  $S$ . The  $-2 \log$  likelihood value of model (1) ( $L_1$ ) is subsequently compared to the  $-2 \log$  likelihood value of an intercept-only model ( $\beta_i = \lambda_3; L_0$ ), and  $R_{ht}^2$  is computed based on the Variance Reduction Factor (for details, see Alonso & Molenberghs, 2007):

$$R_{ht}^2 = 1 - \exp\left(-\frac{L_1 - L_0}{N}\right),$$

where  $N$  is the number of trials.

When a reduced model is requested (by using the argument `Model=c("Reduced")` in the function call), the following model is fitted:

$$\beta_i = \lambda_0 + \lambda_1 \alpha_i + \varepsilon_i.$$

The  $-2 \log$  likelihood value of this model ( $L_1$  for the reduced model) is subsequently compared to the  $-2 \log$  likelihood value of an intercept-only model ( $\beta_i = \lambda_3; L_0$ ), and  $R_{ht}^2$  is computed based on the reduction in the likelihood (as described above).

## Value

An object of class `TrialLevelIT` with components,

<code>Alpha.Vector</code>	The vector of treatment effects on $S$ in the different trials.
<code>Beta.Vector</code>	The vector of treatment effects on $T$ in the different trials.
<code>N.Trial</code>	The total number of trials.
<code>R2.ht</code>	A data.frame that contains the trial-level coefficient of determination ( $R_{ht}^2$ ), its standard error and confidence interval.

## Author(s)

Wim Van der Elst, Ariel Alonso, & Geert Molenberghs

## References

- Burzykowski, T., Molenberghs, G., & Buyse, M. (2005). *The evaluation of surrogate endpoints*. New York: Springer-Verlag.
- Buyse, M., Molenberghs, G., Burzykowski, T., Renard, D., & Geys, H. (2000). The validation of surrogate endpoints in meta-analysis of randomized experiments. *Biostatistics*, 1, 49-67.

**See Also**

[UnimixedContCont](#), [UnifixedContCont](#), [BifixedContCont](#), [BimixedContCont](#), [plot.TrialLevelIT](#)

**Examples**

```
# Generate vector treatment effects on S
set.seed(seed = 1)
Alpha.Vector <- seq(from = 5, to = 10, by=.1) + runif(min = -.5, max = .5, n = 51)

# Generate vector treatment effects on T
set.seed(seed=2)
Beta.Vector <- (Alpha.Vector * 3) + runif(min = -5, max = 5, n = 51)

# Apply the function to estimate R^2_{h.t}
Fit <- TrialLevelIT(Alpha.Vector=Alpha.Vector,
Beta.Vector=Beta.Vector, N.Trial=50, Model="Reduced")

summary(Fit)
plot(Fit)
```

---

TrialLevelMA

*Estimates trial-level surrogacy in the meta-analytic framework*

---

**Description**

The function `TrialLevelMA` estimates trial-level surrogacy based on the vectors of treatment effects on  $S$  (i.e.,  $\alpha_i$ ) and  $T$  (i.e.,  $\beta_i$ ) in the different trials. In particular,  $\beta_i$  is regressed on  $\alpha_i$  and the classical coefficient of determination of the fitted model provides an estimate of  $R_{trial}^2$ . In addition, the standard error and CI are provided.

**Usage**

```
TrialLevelMA(Alpha.Vector, Beta.Vector,
N.Vector, Weighted=TRUE, Alpha=.05)
```

**Arguments**

Alpha.Vector	The vector of treatment effects on $S$ in the different trials, i.e., $\alpha_i$ .
Beta.Vector	The vector of treatment effects on $T$ in the different trials, i.e., $\beta_i$ .
N.Vector	The vector of trial sizes $N_i$ .
Weighted	Logical. If TRUE, then a weighted regression analysis is conducted. If FALSE, then an unweighted regression analysis is conducted. Default TRUE.
Alpha	The $\alpha$ -level that is used to determine the confidence intervals around $R_{trial}^2$ and $R_{trial}$ . Default 0.05.

**Value**

An object of class TrialLevelMA with components,

Alpha.Vector	The vector of treatment effects on $S$ in the different trials.
Beta.Vector	The vector of treatment effects on $T$ in the different trials.
N.Vector	The vector of trial sizes $N_i$ .
Trial.R2	A data.frame that contains the trial-level coefficient of determination ( $R_{trial}^2$ ), its standard error and confidence interval.
Trial.R	A data.frame that contains the trial-level correlation coefficient ( $R_{trial}$ ), its standard error and confidence interval.
Model.2.Fit	The fitted stage 2 model.

**Author(s)**

Wim Van der Elst, Ariel Alonso, & Geert Molenberghs

**References**

Burzykowski, T., Molenberghs, G., & Buyse, M. (2005). *The evaluation of surrogate endpoints*. New York: Springer-Verlag.

Buyse, M., Molenberghs, G., Burzykowski, T., Renard, D., & Geys, H. (2000). The validation of surrogate endpoints in meta-analysis of randomized experiments. *Biostatistics*, 1, 49-67.

**See Also**

[UnimixedContCont](#), [UnifixedContCont](#), [BifixedContCont](#), [BimixedContCont](#), [plot Meta-Analytic](#)

**Examples**

```
# Generate vector treatment effects on S
set.seed(seed = 1)
Alpha.Vector <- seq(from = 5, to = 10, by=.1) + runif(min = -.5, max = .5, n = 51)
# Generate vector treatment effects on T
set.seed(seed=2)
Beta.Vector <- (Alpha.Vector * 3) + runif(min = -5, max = 5, n = 51)
# Vector of sample sizes of the trials (here, all n_i=10)
N.Vector <- rep(10, times=51)

# Apply the function to estimate R^2_{trial}
Fit <- TrialLevelMA(Alpha.Vector=Alpha.Vector,
Beta.Vector=Beta.Vector, N.Vector=N.Vector)

# Plot the results and obtain summary
plot(Fit)
summary(Fit)
```

---

TwoStageSurvSurv	<i>Assess trial-level surrogacy for two survival endpoints using a two-stage approach</i>
------------------	---

---

### Description

The function `TwoStageSurvSurv` uses a two-stage approach to estimate  $R_{trial}^2$ . In stage 1, trial-specific Cox proportional hazard models are fitted and in stage 2 the trial-specific estimated treatment effects on  $T$  are regressed on the trial-specific estimated treatment effects on  $S$  (measured on the log hazard ratio scale). The user can specify whether a weighted or unweighted model should be fitted at stage 2. See the **Details** section below.

### Usage

```
TwoStageSurvSurv(Dataset, Surr, SurrCens, True, TrueCens, Treat,
  Trial.ID, Weighted=TRUE, Alpha=.05)
```

### Arguments

Dataset	A data.frame that should consist of one line per patient. Each line contains (at least) a surrogate value and censoring indicator, a true endpoint value and censoring indicator, a treatment indicator, and a trial ID.
Surr	The name of the variable in Dataset that contains the surrogate endpoint values.
SurrCens	The name of the variable in Dataset that contains the censoring indicator for the surrogate endpoint values (1 = event, 0 = censored).
True	The name of the variable in Dataset that contains the true endpoint values.
TrueCens	The name of the variable in Dataset that contains the censoring indicator for the true endpoint values (1 = event, 0 = censored).
Treat	The name of the variable in Dataset that contains the treatment indicators.
Trial.ID	The name of the variable in Dataset that contains the trial ID to which the patient belongs.
Weighted	Logical. If TRUE, then a weighted regression analysis is conducted at stage 2 of the two-stage approach. If FALSE, then an unweighted regression analysis is conducted at stage 2 of the two-stage approach. See the <b>Details</b> section below. Default TRUE.
Alpha	The $\alpha$ -level that is used to determine the confidence intervals around $R_{trial}^2$ and $R_{trial}$ . Default 0.05.

### Details

A two-stage approach is used to estimate trial-level surrogacy, following a procedure proposed by Buyse et al. (2011). In stage 1, the following trial-specific Cox proportional hazard models are fitted:

$$S_{ij}(t) = S_{i0}(t) \exp(\alpha_i Z_{ij}),$$



$$T_{ij}(t) = T_{i0}(t) \exp(\beta_i Z_{ij}),$$

where  $S_{i0}(t)$  and  $T_{i0}(t)$  are the trial-specific baseline hazard functions,  $Z_{ij}$  is the treatment indicator for subject  $j$  in trial  $i$ ,  $\mu_{Si}$ , and  $\alpha_i$  and  $\beta_i$  are the trial-specific treatment effects on S and T, respectively.

Next, the second stage of the analysis is conducted:

$$\hat{\beta}_i = \lambda_0 + \lambda_1 \hat{\alpha}_i + \varepsilon_i,$$

where the parameter estimates for  $\beta_i$ ,  $\mu_{Si}$ , and  $\alpha_i$  are based on the full model that was fitted in stage 1.

When the argument `Weighted=FALSE` is used in the function call, the model that is fitted in stage 2 is an unweighted linear regression model. When a weighted model is requested (using the argument `Weighted=TRUE` in the function call), the information that is obtained in stage 1 is weighted according to the number of patients in a trial.

The classical coefficient of determination of the fitted stage 2 model provides an estimate of  $R_{trial}^2$ .

### Value

An object of class `TwoStageSurvSurv` with components,

<code>Data.Analyze</code>	Prior to conducting the surrogacy analysis, data of trials that do not have at least three patients per treatment arm are excluded due to estimation constraints (Burzykowski et al., 2001). <code>Data.Analyze</code> is the dataset on which the surrogacy analysis was conducted.
<code>Results.Stage.1</code>	The results of stage 1 of the two-stage model fitting approach: a <code>data.frame</code> that contains the trial-specific log hazard ratio estimates of the treatment effects for the surrogate and the true endpoints.
<code>Results.Stage.2</code>	An object of class <code>lm</code> (linear model) that contains the parameter estimates of the regression model that is fitted in stage 2 of the analysis.
<code>Trial.R2</code>	A <code>data.frame</code> that contains the trial-level coefficient of determination ( $R_{trial}^2$ ), its standard error and confidence interval.
<code>Trial.R</code>	A <code>data.frame</code> that contains the trial-level correlation coefficient ( $R_{trial}$ ), its standard error and confidence interval.

### Author(s)

Wim Van der Elst, Ariel Alonso, & Geert Molenberghs

### References

Burzykowski, T., Molenberghs, G., Buyse, M., Geys, H., & Renard, D. (2001). Validation of surrogate endpoints in multiple randomized clinical trials with failure-time endpoints. *Applied Statistics*, 50, 405-422.

Buyse, M., Michiels, S., Squifflet, P., Lucchesi, K. J., Hellstrand, K., Brune, M. L., Castaigne, S., Rowe, J. M. (2011). Leukemia-free survival as a surrogate end point for overall survival in the evaluation of maintenance therapy for patients with acute myeloid leukemia in complete remission. *Haematologica*, 96, 1106-1112.

### See Also

[plot.TwoStageSurvSurv](#)

### Examples

```
# Open Ovarian dataset
data(Ovarian)

# Conduct analysis
Results <- TwoStageSurvSurv(Dataset = Ovarian, Surr = Pfs, SurrCens = PfsInd,
True = Surv, TrueCens = SurvInd, Treat = Treat, Trial.ID = Center)

# Examine results of analysis
summary(Results)
plot(Results)
```

---

UnifixedContCont	<i>Fits univariate fixed-effect models to assess surrogacy in the meta-analytic multiple-trial setting (continuous-continuous case)</i>
------------------	---

---

### Description

The function `UnifixedContCont` uses the univariate fixed-effects approach to estimate trial- and individual-level surrogacy when the data of multiple clinical trials are available. The user can specify whether a (weighted or unweighted) full, semi-reduced, or reduced model should be fitted. See the **Details** section below. Further, the Individual Causal Association (ICA) is computed.

### Usage

```
UnifixedContCont(Dataset, Surr, True, Treat, Trial.ID, Pat.ID, Model=c("Full"),
Weighted=TRUE, Min.Trial.Size=2, Alpha=.05, Number.Bootstraps=500,
Seed=sample(1:1000, size=1), T0T1=seq(-1, 1, by=.2), T0S1=seq(-1, 1, by=.2),
T1S0=seq(-1, 1, by=.2), S0S1=seq(-1, 1, by=.2))
```

### Arguments

Dataset	A data.frame that should consist of one line per patient. Each line contains (at least) a surrogate value, a true endpoint value, a treatment indicator, a patient ID, and a trial ID.
Surr	The name of the variable in Dataset that contains the surrogate endpoint values.
True	The name of the variable in Dataset that contains the true endpoint values.

Treat	The name of the variable in Dataset that contains the treatment indicators. The treatment indicator should either be coded as 1 for the experimental group and -1 for the control group, or as 1 for the experimental group and 0 for the control group.
Trial.ID	The name of the variable in Dataset that contains the trial ID to which the patient belongs.
Pat.ID	The name of the variable in Dataset that contains the patient's ID.
Model	The type of model that should be fitted, i.e., Model=c("Full"), Model=c("Reduced"), or Model=c("SemiReduced"). See the <b>Details</b> section below. Default Model=c("Full").
Weighted	Logical. If TRUE, then a weighted regression analysis is conducted at stage 2 of the two-stage approach. If FALSE, then an unweighted regression analysis is conducted at stage 2 of the two-stage approach. See the <b>Details</b> section below. Default TRUE.
Min.Trial.Size	The minimum number of patients that a trial should contain to be included in the analysis. If the number of patients in a trial is smaller than the value specified by Min.Trial.Size, the data of the trial are excluded from the analysis. Default 2.
Alpha	The $\alpha$ -level that is used to determine the confidence intervals around $R_{trial}^2$ , $R_{indiv}^2$ , and $R_{indiv}$ . Default 0.05.
Number.Bootstraps	The standard errors and confidence intervals for $R_{indiv}^2$ and $R_{indiv}$ are determined as based on a bootstrap procedure. Number.Bootstraps specifies the number of bootstrap samples that are used. Default 500.
Seed	The seed to be used in the bootstrap procedure. Default <code>sample(1 : 1000, size = 1)</code> .
T0T1	A scalar or vector that contains the correlation(s) between the counterfactuals T0 and T1 that should be considered in the computation of $\rho_{\Delta}$ (ICA). For details, see function <code>ICA.ContCont</code> . Default <code>seq(-1, 1, by=.2)</code> .
T0S1	A scalar or vector that contains the correlation(s) between the counterfactuals T0 and S1 that should be considered in the computation of $\rho_{\Delta}$ . Default <code>seq(-1, 1, by=.2)</code> .
T1S0	A scalar or vector that contains the correlation(s) between the counterfactuals T1 and S0 that should be considered in the computation of $\rho_{\Delta}$ . Default <code>seq(-1, 1, by=.2)</code> .
S0S1	A scalar or vector that contains the correlation(s) between the counterfactuals S0 and S1 that should be considered in the computation of $\rho_{\Delta}$ . Default <code>seq(-1, 1, by=.2)</code> .

## Details

When the full bivariate mixed-effects model is fitted to assess surrogacy in the meta-analytic framework (for details, Buyse & Molenberghs, 2000), computational issues often occur. In that situation, the use of simplified model-fitting strategies may be warranted (for details, see see Burzykowski et al., 2005; Tibaldi et al., 2003).

The function `UnifixedContCont` implements one such strategy, i.e., it uses a two-stage univariate fixed-effects modelling approach to assess surrogacy. In the first stage of the analysis, two univariate

linear regression models are fitted to the data of each of the  $i$  trials. When a full or semi-reduced model is requested (by using the argument `Model=c("Full")` or `Model=c("SemiReduced")` in the function call), the following univariate models are fitted:

$$S_{ij} = \mu_{Si} + \alpha_i Z_{ij} + \varepsilon_{Sij},$$

$$T_{ij} = \mu_{Ti} + \beta_i Z_{ij} + \varepsilon_{Tij},$$

where  $i$  and  $j$  are the trial and subject indicators,  $S_{ij}$  and  $T_{ij}$  are the surrogate and true endpoint values of subject  $j$  in trial  $i$ ,  $Z_{ij}$  is the treatment indicator for subject  $j$  in trial  $i$ ,  $\mu_{Si}$  and  $\mu_{Ti}$  are the fixed trial-specific intercepts for S and T, and  $\alpha_i$  and  $\beta_i$  are the fixed trial-specific treatment effects on S and T, respectively. The error terms  $\varepsilon_{Sij}$  and  $\varepsilon_{Tij}$  are assumed to be independent.

When a reduced model is requested by the user (by using the argument `Model=c("Reduced")` in the function call), the following univariate models are fitted:

$$S_{ij} = \mu_S + \alpha_i Z_{ij} + \varepsilon_{Sij},$$

$$T_{ij} = \mu_T + \beta_i Z_{ij} + \varepsilon_{Tij},$$

where  $\mu_S$  and  $\mu_T$  are the common intercepts for S and T (i.e., it is assumed that the intercepts for the surrogate and the true endpoints are identical in each of the trials). The other parameters are the same as defined above, and  $\varepsilon_{Sij}$  and  $\varepsilon_{Tij}$  are again assumed to be independent.

An estimate of  $R_{indiv}^2$  is provided by  $r(\varepsilon_{Sij}, \varepsilon_{Tij})^2$ .

Next, the second stage of the analysis is conducted. When a full model is requested (by using the argument `Model=c("Full")` in the function call), the following model is fitted:

$$\widehat{\beta}_i = \lambda_0 + \lambda_1 \widehat{\mu_{Si}} + \lambda_2 \widehat{\alpha}_i + \varepsilon_i,$$

where the parameter estimates for  $\beta_i$ ,  $\mu_{Si}$ , and  $\alpha_i$  are based on the full models that were fitted in stage 1.

When a semi-reduced or reduced model is requested (by using the argument `Model=c("SemiReduced")` or `Model=c("Reduced")` in the function call), the following model is fitted:

$$\widehat{\beta}_i = \lambda_0 + \lambda_1 \widehat{\alpha}_i + \varepsilon_i.$$

where the parameter estimates for  $\beta_i$  and  $\alpha_i$  are based on the semi-reduced or reduced models that were fitted in stage 1.

When the argument `Weighted=FALSE` is used in the function call, the model that is fitted in stage 2 is an unweighted linear regression model. When a weighted model is requested (using the argument `Weighted=TRUE` in the function call), the information that is obtained in stage 1 is weighted according to the number of patients in a trial.

The classical coefficient of determination of the fitted stage 2 model provides an estimate of  $R_{trial}^2$ .

**Value**

An object of class `UnifixedContCont` with components,

<code>Data.Analyze</code>	Prior to conducting the surrogacy analysis, data of patients who have a missing value for the surrogate and/or the true endpoint are excluded. In addition, the data of trials (i) in which only one type of the treatment was administered, and (ii) in which either the surrogate or the true endpoint was a constant (i.e., all patients within a trial had the same surrogate and/or true endpoint value) are excluded. In addition, the user can specify the minimum number of patients that a trial should contain in order to include the trial in the analysis. If the number of patients in a trial is smaller than the value specified by <code>Min.Trial.Size</code> , the data of the trial are excluded. <code>Data.Analyze</code> is the dataset on which the surrogacy analysis was conducted.
<code>Obs.Per.Trial</code>	A <code>data.frame</code> that contains the total number of patients per trial and the number of patients who were administered the control treatment and the experimental treatment in each of the trials (in <code>Data.Analyze</code> ).
<code>Results.Stage.1</code>	The results of stage 1 of the two-stage model fitting approach: a <code>data.frame</code> that contains the trial-specific intercepts and treatment effects for the surrogate and the true endpoints (when a full or semi-reduced model is requested), or the trial-specific treatment effects for the surrogate and the true endpoints (when a reduced model is requested).
<code>Residuals.Stage.1</code>	A <code>data.frame</code> that contains the residuals for the surrogate and true endpoints that are obtained in stage 1 of the analysis ( $\varepsilon_{Sij}$ and $\varepsilon_{Tij}$ ).
<code>Results.Stage.2</code>	An object of class <code>lm</code> (linear model) that contains the parameter estimates of the regression model that is fitted in stage 2 of the analysis.
<code>Trial.R2</code>	A <code>data.frame</code> that contains the trial-level coefficient of determination ( $R_{trial}^2$ ), its standard error and confidence interval.
<code>Indiv.R2</code>	A <code>data.frame</code> that contains the individual-level coefficient of determination ( $R_{indiv}^2$ ), its standard error and confidence interval.
<code>Trial.R</code>	A <code>data.frame</code> that contains the trial-level correlation coefficient ( $R_{trial}$ ), its standard error and confidence interval.
<code>Indiv.R</code>	A <code>data.frame</code> that contains the individual-level correlation coefficient ( $R_{indiv}$ ), its standard error and confidence interval.
<code>Cor.Endpoints</code>	A <code>data.frame</code> that contains the correlations between the surrogate and the true endpoint in the control treatment group (i.e., $\rho_{T0S0}$ ) and in the experimental treatment group (i.e., $\rho_{T1S1}$ ), their standard errors and their confidence intervals.
<code>D.Equiv</code>	The variance-covariance matrix of the trial-specific intercept and treatment effects for the surrogate and true endpoints (when a full or semi-reduced model is fitted, i.e., when <code>Model=c("Full")</code> or <code>Model=c("SemiReduced")</code> is used in the function call), or the variance-covariance matrix of the trial-specific treatment effects for the surrogate and true endpoints (when a reduced model is fitted, i.e., when <code>Model=c("Reduced")</code> is used in the function call). The variance-covariance matrix <code>D.Equiv</code> is equivalent to the $D$ matrix that would be obtained

	when a (full or reduced) bivariate mixed-effect approach is used; see function <a href="#">BimixedContCont</a> ).
ICA	A fitted object of class ICA. ContCont.
T0T0	The variance of the true endpoint in the control treatment condition.
T1T1	The variance of the true endpoint in the experimental treatment condition.
S0S0	The variance of the surrogate endpoint in the control treatment condition.
S1S1	The variance of the surrogate endpoint in the experimental treatment condition.

**Author(s)**

Wim Van der Elst, Ariel Alonso, & Geert Molenberghs

**References**

Burzykowski, T., Molenberghs, G., & Buyse, M. (2005). *The evaluation of surrogate endpoints*. New York: Springer-Verlag.

Buyse, M., Molenberghs, G., Burzykowski, T., Renard, D., & Geys, H. (2000). The validation of surrogate endpoints in meta-analysis of randomized experiments. *Biostatistics*, *1*, 49-67.

Tibaldi, F., Abrahantes, J. C., Molenberghs, G., Renard, D., Burzykowski, T., Buyse, M., Parmar, M., et al., (2003). Simplified hierarchical linear models for the evaluation of surrogate endpoints. *Journal of Statistical Computation and Simulation*, *73*, 643-658.

**See Also**

[UnimixedContCont](#), [BifixedContCont](#), [BimixedContCont](#), [plot Meta-Analytic](#)

**Examples**

```
## Not run: #Time consuming (>5 sec) code parts
# Example 1, based on the ARMD data
data(ARMD)

# Fit a full univariate fixed-effects model with weighting according to the
# number of patients in stage 2 of the two stage approach to assess surrogacy:
Sur <- UnifixedContCont(Dataset=ARMD, Surr=Diff24, True=Diff52, Treat=Treat, Trial.ID=Center,
Pat.ID=Id, Model="Full", Weighted=TRUE)

# Obtain a summary and plot of the results
summary(Sur)
plot(Sur)

# Example 2
# Conduct an analysis based on a simulated dataset with 2000 patients, 100 trials,
# and Rindiv=Rtrial=.8
# Simulate the data:
Sim.Data.MTS(N.Total=2000, N.Trial=100, R.Trial.Target=.8, R.Indiv.Target=.8,
Seed=123, Model="Reduced")

# Fit a reduced univariate fixed-effects model without weighting to assess
```

```
# surrogacy:
Sur2 <- UnifixedContCont(Dataset=Data.Observed.MTS, Surr=Surr, True=True, Treat=Treat,
  Trial.ID=Trial.ID, Pat.ID=Pat.ID, Model="Reduced", Weighted=FALSE)

# Show a summary and plots of results:
summary(Sur2)
plot(Sur2, Weighted=FALSE)
## End(Not run)
```

---

UnimixedContCont	<i>Fits univariate mixed-effect models to assess surrogacy in the meta-analytic multiple-trial setting (continuous-continuous case)</i>
------------------	---

---

## Description

The function `UnimixedContCont` uses the univariate mixed-effects approach to estimate trial- and individual-level surrogacy when the data of multiple clinical trials are available. The user can specify whether a (weighted or unweighted) full, semi-reduced, or reduced model should be fitted. See the **Details** section below. Further, the Individual Causal Association (ICA) is computed.

## Usage

```
UnimixedContCont(Dataset, Surr, True, Treat, Trial.ID, Pat.ID, Model=c("Full"),
  Weighted=TRUE, Min.Trial.Size=2, Alpha=.05, Number.Bootstraps=500,
  Seed=sample(1:1000, size=1), T0T1=seq(-1, 1, by=.2), T0S1=seq(-1, 1, by=.2),
  T1S0=seq(-1, 1, by=.2), S0S1=seq(-1, 1, by=.2), ...)
```

## Arguments

Dataset	A data.frame that should consist of one line per patient. Each line contains (at least) a surrogate value, a true endpoint value, a treatment indicator, a patient ID, and a trial ID.
Surr	The name of the variable in Dataset that contains the surrogate endpoint values.
True	The name of the variable in Dataset that contains the true endpoint values.
Treat	The name of the variable in Dataset that contains the treatment indicators. The treatment indicator should either be coded as 1 for the experimental group and -1 for the control group, or as 1 for the experimental group and 0 for the control group.
Trial.ID	The name of the variable in Dataset that contains the trial ID to which the patient belongs.
Pat.ID	The name of the variable in Dataset that contains the patient's ID.
Model	The type of model that should be fitted, i.e., <code>Model=c("Full")</code> , <code>Model=c("Reduced")</code> , or <code>Model=c("SemiReduced")</code> . See the <b>Details</b> section below. Default <code>Model=c("Full")</code> .
Weighted	Logical. If TRUE, then a weighted regression analysis is conducted at stage 2 of the two-stage approach. If FALSE, then an unweighted regression analysis is conducted at stage 2 of the two-stage approach. See the <b>Details</b> section below. Default TRUE.

Min.Trial.Size	The minimum number of patients that a trial should contain to be included in the analysis. If the number of patients in a trial is smaller than the value specified by Min.Trial.Size, the data of the trial are excluded from the analysis. Default 2.
Alpha	The $\alpha$ -level that is used to determine the confidence intervals around $R_{trial}^2$ , $R_{indiv}^2$ , and $R_{indiv}$ . Default 0.05.
Number.Bootstraps	The confidence intervals for $R_{indiv}^2$ and $R_{indiv}$ are determined as based on a bootstrap procedure. Number.Bootstraps specifies the number of bootstrap samples that are to be used. Default 500.
Seed	The seed to be used in the bootstrap procedure. Default <code>sample(1 : 1000, size = 1)</code> .
T0T1	A scalar or vector that contains the correlation(s) between the counterfactuals T0 and T1 that should be considered in the computation of $\rho_{\Delta}$ (ICA). For details, see function <code>ICA.ContCont</code> . Default <code>seq(-1, 1, by=.2)</code> .
T0S1	A scalar or vector that contains the correlation(s) between the counterfactuals T0 and S1 that should be considered in the computation of $\rho_{\Delta}$ . Default <code>seq(-1, 1, by=.2)</code> .
T1S0	A scalar or vector that contains the correlation(s) between the counterfactuals T1 and S0 that should be considered in the computation of $\rho_{\Delta}$ . Default <code>seq(-1, 1, by=.2)</code> .
S0S1	A scalar or vector that contains the correlation(s) between the counterfactuals S0 and S1 that should be considered in the computation of $\rho_{\Delta}$ . Default <code>seq(-1, 1, by=.2)</code> .
...	Other arguments to be passed to the function <code>lmer</code> (of the R package <code>lme4</code> ) that is used to fit the generalized linear mixed-effect models in the function <code>BimixedContCont</code> .

## Details

When the full bivariate mixed-effects model is fitted to assess surrogacy in the meta-analytic framework (for details, Buyse & Molenberghs, 2000), computational issues often occur. In that situation, the use of simplified model-fitting strategies may be warranted (for details, see Burzykowski et al., 2005; Tibaldi et al., 2003).

The function `UnimixedContCont` implements one such strategy, i.e., it uses a two-stage univariate mixed-effects modelling approach to assess surrogacy. In the first stage of the analysis, two univariate mixed-effects models are fitted to the data. When a full or semi-reduced model is requested (by using the argument `Model=c("Full")` or `Model=c("SemiReduced")` in the function call), the following univariate models are fitted:

$$S_{ij} = \mu_S + m_{Si} + (\alpha + a_i)Z_{ij} + \varepsilon_{Sij},$$

$$T_{ij} = \mu_T + m_{Ti} + (\beta + b_i)Z_{ij} + \varepsilon_{Tij},$$

where  $i$  and  $j$  are the trial and subject indicators,  $S_{ij}$  and  $T_{ij}$  are the surrogate and true endpoint values of subject  $j$  in trial  $i$ ,  $Z_{ij}$  is the treatment indicator for subject  $j$  in trial  $i$ ,  $\mu_S$  and  $\mu_T$  are the fixed intercepts for S and T,  $m_{Si}$  and  $m_{Ti}$  are the corresponding random intercepts,  $\alpha$  and  $\beta$  are the fixed treatment effects for S and T, and  $a_i$  and  $b_i$  are the corresponding random treatment effects, respectively. The error terms  $\varepsilon_{Sij}$  and  $\varepsilon_{Tij}$  are assumed to be independent.



When a reduced model is requested (by using the argument `Model=c("Reduced")` in the function call), the following two univariate models are fitted:

$$S_{ij} = \mu_S + (\alpha + a_i)Z_{ij} + \varepsilon_{Sij},$$

$$T_{ij} = \mu_T + (\beta + b_i)Z_{ij} + \varepsilon_{Tij},$$

where  $\mu_S$  and  $\mu_T$  are the common intercepts for S and T (i.e., it is assumed that the intercepts for the surrogate and the true endpoints are identical in each of the trials). The other parameters are the same as defined above, and  $\varepsilon_{Sij}$  and  $\varepsilon_{Tij}$  are again assumed to be independent.

An estimate of  $R_{indiv}^2$  is computed as  $r(\varepsilon_{Sij}, \varepsilon_{Tij})^2$ .

Next, the second stage of the analysis is conducted. When a full model is requested by the user (by using the argument `Model=c("Full")` in the function call), the following model is fitted:

$$\hat{\beta}_i = \lambda_0 + \lambda_1 \widehat{\mu_{Si}} + \lambda_2 \widehat{\alpha}_i + \varepsilon_i,$$

where the parameter estimates for  $\beta_i$ ,  $\mu_{Si}$ , and  $\alpha_i$  are based on the models that were fitted in stage 1, i.e.,  $\beta_i = \beta + b_i$ ,  $\mu_{Si} = \mu_S + m_{Si}$ , and  $\alpha_i = \alpha + a_i$ .

When a reduced or semi-reduced model is requested by the user (by using the arguments `Model=c("SemiReduced")` or `Model=c("Reduced")` in the function call), the following model is fitted:

$$\hat{\beta}_i = \lambda_0 + \lambda_1 \widehat{\alpha}_i + \varepsilon_i,$$

where the parameters are the same as defined above.

When the argument `Weighted=FALSE` is used in the function call, the model that is fitted in stage 2 is an unweighted linear regression model. When a weighted model is requested (using the argument `Weighted=TRUE` in the function call), the information that is obtained in stage 1 is weighted according to the number of patients in a trial.

The classical coefficient of determination of the fitted stage 2 model provides an estimate of  $R_{trial}^2$ .

## Value

An object of class `UnimixedContCont` with components,

<code>Data.Analyze</code>	Prior to conducting the surrogacy analysis, data of patients who have a missing value for the surrogate and/or the true endpoint are excluded. In addition, the data of trials (i) in which only one type of the treatment was administered, and (ii) in which either the surrogate or the true endpoint was a constant (i.e., all patients within a trial had the same surrogate and/or true endpoint value) are excluded. In addition, the user can specify the minimum number of patients that a trial should contain in order to include the trial in the analysis. If the number of patients in a trial is smaller than the value specified by <code>Min.Trial.Size</code> , the data of the trial are excluded. <code>Data.Analyze</code> is the dataset on which the surrogacy analysis was conducted.
<code>Obs.Per.Trial</code>	A <code>data.frame</code> that contains the total number of patients per trial and the number of patients who were administered the control treatment and the experimental treatment in each of the trials (in <code>Data.Analyze</code> ).

Results.Stage.1	The results of stage 1 of the two-stage model fitting approach: a <code>data.frame</code> that contains the trial-specific intercepts and treatment effects for the surrogate and the true endpoints (when a full or semi-reduced model is requested), or the trial-specific treatment effects for the surrogate and the true endpoints (when a reduced model is requested).
Residuals.Stage.1	A <code>data.frame</code> that contains the residuals for the surrogate and true endpoints that are obtained in stage 1 of the analysis ( $\varepsilon_{Sij}$ and $\varepsilon_{Tij}$ ).
Fixed.Effect.Pars	A <code>data.frame</code> that contains the fixed intercept and treatment effects for S and T (i.e., $\mu_S$ , $\mu_T$ , $\alpha$ , and $\beta$ ) when a full, semi-reduced, or reduced model is fitted in stage 1.
Random.Effect.Pars	A <code>data.frame</code> that contains the random intercept and treatment effects for S and T (i.e., $m_{Si}$ , $m_{Ti}$ , $a_i$ and $b_i$ ) when a full or semi-reduced model is fitted in stage 1, or that contains the random treatment effects for S and T (i.e., $a_i$ , and $b_i$ ) when a reduced model is fitted in stage 1.
Results.Stage.2	An object of class <code>lm</code> (linear model) that contains the parameter estimates of the regression model that is fitted in stage 2 of the analysis.
Trial.R2	A <code>data.frame</code> that contains the trial-level coefficient of determination ( $R_{trial}^2$ ), its standard error and confidence interval.
Indiv.R2	A <code>data.frame</code> that contains the individual-level coefficient of determination ( $R_{indiv}^2$ ), its standard error and confidence interval.
Trial.R	A <code>data.frame</code> that contains the trial-level correlation coefficient ( $R_{trial}$ ), its standard error and confidence interval.
Indiv.R	A <code>data.frame</code> that contains the individual-level correlation coefficient ( $R_{indiv}$ ), its standard error and confidence interval.
Cor.Endpoints	A <code>data.frame</code> that contains the correlations between the surrogate and the true endpoint in the control treatment group (i.e., $\rho_{T0S0}$ ) and in the experimental treatment group (i.e., $\rho_{T1S1}$ ), their standard errors and their confidence intervals.
D.Equiv	The variance-covariance matrix of the trial-specific intercept and treatment effects for the surrogate and true endpoints (when a full or semi-reduced model is fitted, i.e., when <code>Model=c("Full")</code> or <code>Model=c("SemiReduced")</code> is used in the function call), or the variance-covariance matrix of the trial-specific treatment effects for the surrogate and true endpoints (when a reduced model is fitted, i.e., when <code>Model=c("Reduced")</code> is used in the function call). The variance-covariance matrix <code>D.Equiv</code> is equivalent to the $D$ matrix that would be obtained when a (full or reduced) bivariate mixed-effects approach is used; see function <a href="#">BimixedContCont</a> .
ICA	A fitted object of class <code>ICA.ContCont</code> .
T0T0	The variance of the true endpoint in the control treatment condition.
T1T1	The variance of the true endpoint in the experimental treatment condition.
S0S0	The variance of the surrogate endpoint in the control treatment condition.
S1S1	The variance of the surrogate endpoint in the experimental treatment condition.

**Author(s)**

Wim Van der Elst, Ariel Alonso, & Geert Molenberghs

**References**

Burzykowski, T., Molenberghs, G., & Buyse, M. (2005). *The evaluation of surrogate endpoints*. New York: Springer-Verlag.

Buyse, M., Molenberghs, G., Burzykowski, T., Renard, D., & Geys, H. (2000). The validation of surrogate endpoints in meta-analysis of randomized experiments. *Biostatistics*, 1, 49-67.

Tibaldi, F., Abrahantes, J. C., Molenberghs, G., Renard, D., Burzykowski, T., Buyse, M., Parmar, M., et al., (2003). Simplified hierarchical linear models for the evaluation of surrogate endpoints. *Journal of Statistical Computation and Simulation*, 73, 643-658.

**See Also**

[UnifixedContCont](#), [BifixedContCont](#), [BimixedContCont](#), [plot Meta-Analytic](#)

**Examples**

```
## Not run: #Time consuming code part
# Conduct an analysis based on a simulated dataset with 2000 patients, 100 trials,
# and Rindiv=Rtrial=.8
# Simulate the data:
Sim.Data.MTS(N.Total=2000, N.Trial=100, R.Trial.Target=.8, R.Indiv.Target=.8,
Seed=123, Model="Reduced")

# Fit a reduced univariate mixed-effects model without weighting to assess surrogacy:
Sur <- UnimixedContCont(Dataset=Data.Observed.MTS, Surr=Surr, True=True, Treat=Treat,
Trial.ID=Trial.ID, Pat.ID=Pat.ID, Model="Reduced", Weighted=FALSE)

# Show a summary and plots of the results:
summary(Sur)
plot(Sur, Weighted=FALSE)
## End(Not run)
```

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