Package 'BCEA'

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Type Package

Title Bayesian Cost Effectiveness Analysis

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Suggests R2jags, R2OpenBUGS, ggplot2, grid, INLA, splancs, mgcv, ldr, shiny, shinythemes, knitr, rmarkdown, plotly

Imports MASS, dplyr, rlang

Additional_repositories https://inla.r-inla-download.org/R/stable/

Description Produces an economic evaluation of a Bayesian model in the form of MCMC simulations. Given suitable variables of cost and effectiveness / utility for two or more interventions, This package computes the most cost-effective alternative and produces graphical summaries and probabilistic sensitivity analysis.

License GPL (>= 2)

URL http://www.statistica.it/gianluca/BCEA, http://www.statistica.it/gianluca

Depends R (>= 2.10)

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R topics documented:

BCEA-package   *BCEA: A package for Bayesian Cost-Effectiveness Analysis*

Description

A package to post-process the results of a Bayesian health economic model and produce standardised output for the analysis of the results

Details

Package:	BCEA
Type:	Package
Version:	2.3-1
Date:	2019-08-05
License:	GPL2
LazyLoad:	yes

Given the results of a Bayesian model (possibly based on MCMC) in the form of simulations from the posterior distributions of suitable variables of costs and clinical benefits for two or more interventions, produces a health economic evaluation. Compares one of the interventions (the "reference") to the others ("comparators"). Produces many summary and plots to analyse the results

Author(s)

Gianluca Baio, Andrea Berardi, Anna Heath

Maintainer: Gianluca Baio <gianluca@stats.ucl.ac.uk>

References

Baio, G., Dawid, A. P. (2011). Probabilistic Sensitivity Analysis in Health Economics. Statistical Methods in Medical Research doi:10.1177/0962280211419832.

Baio G. (2012). Bayesian Methods in Health Economics. CRC/Chapman Hall, London

Baio G., Berardi A., Heath A. (forthcoming). Bayesian Cost Effectiveness Analysis with the R package BCEA. Springer

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bcea	*Bayesian Cost-Effectiveness Analysis*

Description

Cost-effectiveness analysis based on the results of a simulation model for a variable of clinical benefits (e) and of costs (c). Produces results to be post-processed to give the health economic analysis. The output is stored in an object of the class "bcea"

Usage

```
bcea(e, c, ref = 1, interventions = NULL, Kmax = 50000,
     wtp = NULL, plot = FALSE)

## Default S3 method:
bcea(e, c, ref = 1, interventions = NULL, Kmax = 50000,
     wtp = NULL, plot = FALSE)
```

Arguments

e	An object containing nsim simulations for the variable of clinical effectiveness for each intervention being considered. In general it is a matrix with nsim rows and nint columns.
c	An object containing nsim simulations for the variable of cost for each intervention being considered. In general it is a matrix with nsim rows and nint columns.

ref	Defines which intervention (columns of e or c) is considered to be the reference strategy. The default value ref=1 means that the intervention associated with the first column of e or c is the reference and the one(s) associated with the other column(s) is(are) the comparators.
interventions	Defines the labels to be associated with each intervention. By default and if NULL, assigns labels in the form "Intervention1", ... , "Intervention T".
Kmax	Maximum value of the willingness to pay to be considered. Default value is k=50000. The willingness to pay is then approximated on a discrete grid in the interval [0,Kmax]. The grid is equal to wtp if the parameter is given, or composed of 501 elements if wtp=NULL (the default).
wtp	A(n optional) vector wtp including the values of the willingness to pay grid. If not specified then BCEA will construct a grid of 501 values from 0 to Kmax. This option is useful when performing intensive computations (eg for the EVPPI).
plot	A logical value indicating whether the function should produce the summary plot or not.

Value

An object of the class "bcea" containing the following elements

n.sim	Number of simulations produced by the Bayesian model
n.comparators	Number of interventions being analysed
n.comparisons	Number of possible pairwise comparisons
delta.e	For each possible comparison, the differential in the effectiveness measure
delta.c	For each possible comparison, the differential in the cost measure
ICER	The value of the Incremental Cost-Effectiveness Ratio
Kmax	The maximum value assumed for the willingness to pay threshold
k	The vector of values for the grid approximation of the willingness to pay
ceac	The value for the Cost-Effectiveness Acceptability Curve, as a function of the willingness to pay
ib	The distribution of the Incremental Benefit, for a given willingness to pay
eib	The value for the Expected Incremental Benefit, as a function of the willingness to pay
kstar	The grid approximation of the break even point(s)
best	A vector containing the numeric label of the intervention that is the most cost-effective for each value of the willingness to pay in the selected grid approximation
U	An array including the value of the expected utility for each simulation from the Bayesian model, for each value of the grid approximation of the willingness to pay and for each intervention being considered
vi	An array including the value of information for each simulation from the Bayesian model and for each value of the grid approximation of the willingness to pay

Ustar	An array including the maximum "known-distribution" utility for each simulation from the Bayesian model and for each value of the grid approximation of the willingness to pay
ol	An array including the opportunity loss for each simulation from the Bayesian model and for each value of the grid approximation of the willingness to pay
evi	The vector of values for the Expected Value of Information, as a function of the willingness to pay
interventions	A vector of labels for all the interventions considered
ref	The numeric index associated with the intervention used as reference in the analysis
comp	The numeric index(es) associated with the intervention(s) used as comparator(s) in the analysis
step	The step used to form the grid approximation to the willingness to pay
e	The e matrix used to generate the object (see Arguments)
c	The c matrix used to generate the object (see Arguments)

Author(s)

Gianluca Baio, Andrea Berardi

References

Baio, G., Dawid, A. P. (2011). Probabilistic Sensitivity Analysis in Health Economics. Statistical Methods in Medical Research doi:10.1177/0962280211419832.

Baio G. (2012). Bayesian Methods in Health Economics. CRC/Chapman Hall, London

Examples

```
# See Baio G., Dawid A.P. (2011) for a detailed description of the
# Bayesian model and economic problem
#
# Load the processed results of the MCMC simulation model
data(Vaccine)
#
# Runs the health economic evaluation using BCEA
m <- bcea(e=e,c=c,          # defines the variables of
                            #  effectiveness and cost
      ref=2,                # selects the 2nd row of (e,c)
                            #  as containing the reference intervention
      interventions=treats, # defines the labels to be associated
                            #  with each intervention
      Kmax=50000,           # maximum value possible for the willingness
                            #  to pay threshold; implies that k is chosen
                            #  in a grid from the interval (0,Kmax)
      plot=TRUE         # plots the results
)
#
# Creates a summary table
```

```
summary(m,        # uses the results of the economic evalaution
                  #  (a "bcea" object)
        wtp=25000 # selects the particular value for k
)


#
# Plots the cost-effectiveness plane using base graphics
ceplane.plot(m,       # plots the Cost-Effectiveness plane
        comparison=1,  # if more than 2 interventions, selects the
                        #  pairwise comparison
        wtp=25000,      # selects the relevant willingness to pay
                        #  (default: 25,000)
        graph="base"   # selects base graphics (default)
)
#
# Plots the cost-effectiveness plane using ggplot2
if(requireNamespace("ggplot2")){
ceplane.plot(m,       # plots the Cost-Effectiveness plane
        comparison=1,  # if more than 2 interventions, selects the
                        #  pairwise comparison
        wtp=25000,      # selects the relevant willingness to pay
                        #  (default: 25,000)
        graph="ggplot2"# selects ggplot2 as the graphical engine
)
#
# Some more options
ceplane.plot(m,
        graph="ggplot2",
        pos="top",
        size=5,
        ICER.size=1.5,
        label.pos=FALSE,
        opt.theme=ggplot2::theme(text=ggplot2::element_text(size=8))
)
}
#
# Plots the contour and scatterplot of the bivariate
# distribution of (Delta_e,Delta_c)
contour(m,            # uses the results of the economic evalaution
                        #  (a "bcea" object)
        comparison=1, # if more than 2 interventions, selects the
                        #  pairwise comparison
        nlevels=4,     # selects the number of levels to be
                        #  plotted (default=4)
        levels=NULL,  # specifies the actual levels to be plotted
                        #  (default=NULL, so that R will decide)
        scale=0.5,     # scales the bandwiths for both x- and
                        #  y-axis (default=0.5)
        graph="base"  # uses base graphics to produce the plot
)
#
# Plots the contour and scatterplot of the bivariate
```

```
#    distribution of (Delta_e,Delta_c)
contour2(m,          # uses the results of the economic evalaution
                     #  (a "bcea" object)
         wtp=25000,  # selects the willingness-to-pay threshold
         xl=NULL,    # assumes default values
         yl=NULL     # assumes default values
)
#
# Using ggplot2
if(requireNamespace("ggplot2")){
contour2(m,              # uses the results of the economic evalaution
                         #  (a "bcea" object)
         graph="ggplot2",# selects the graphical engine
         wtp=25000,      # selects the willingness-to-pay threshold
         xl=NULL,        # assumes default values
         yl=NULL,        # assumes default values
         label.pos=FALSE # alternative position for the wtp label
)
}
#
# Plots the Expected Incremental Benefit for the "bcea" object m
eib.plot(m)
#
# Plots the distribution of the Incremental Benefit
ib.plot(m,          # uses the results of the economic evalaution
                    #  (a "bcea" object)
     comparison=1,  # if more than 2 interventions, selects the
                    #  pairwise comparison
     wtp=25000,     # selects the relevant willingness
                    #  to pay (default: 25,000)
     graph="base"   # uses base graphics
)
#
# Produces a plot of the CEAC against a grid of values for the
# willingness to pay threshold
ceac.plot(m)
#
# Plots the Expected Value of Information for the "bcea" object m
evi.plot(m)
#
```

BCEAweb   *BCEAweb*

Description

Launches the web-app

Usage

```
BCEAweb(e = NULL, c = NULL, parameters = NULL, ...)
```

Arguments

e	A matrix containing the simulations for the effectiveness variable (with number of simulation rows and number of interventions columns). Defaults at NULL, which means the user has to load their own values using the web-interface
c	A matrix containing the simulations for the cost variable (with number of simulation rows and number of interventions columns). Defaults at NULL, which means the user has to load their own values using the web-interface
parameters	A matrix with the simulations for all the relevant model parameters. Defaults at NULL, which means the user has to load their own values using the web-interface
...	Additional parameters.

Author(s)

Gianluca Baio

References

Baio, G., Dawid, A. P. (2011). Probabilistic Sensitivity Analysis in Health Economics. Statistical Methods in Medical Research doi:10.1177/0962280211419832.

Baio G. (2012). Bayesian Methods in Health Economics. CRC/Chapman Hall, London

See Also

bcea

Examples

```
data(Vaccine)
BCEAweb(e,c,vaccine)
```

---

ceac.plot	*Cost-Effectiveness Acceptability Curve (CEAC) plot*

Description

Produces a plot of the Cost-Effectiveness Acceptability Curve (CEAC) against the willingness to pay threshold

Usage

```
ceac.plot(he, comparison = NULL, pos = c(1, 0), graph = c("base",
  "ggplot2", "plotly"), ...)
```

Arguments

he	A bcea object containing the results of the Bayesian modelling and the economic evaluation.
comparison	Selects the comparator, in case of more than two interventions being analysed. Default as NULL plots all the comparisons together. Any subset of the possible comparisons can be selected (e.g., comparison=c(1,3) or comparison=2).
pos	Parameter to set the position of the legend (only relevant for multiple interventions, ie more than 2 interventions being compared). Can be given in form of a string (bottom|top)(right|left) for base graphics and bottom, top, left or right for ggplot2. It can be a two-elements vector, which specifies the relative position on the x and y axis respectively, or alternatively it can be in form of a logical variable, with FALSE indicating to use the default position and TRUE to place it on the bottom of the plot. Default value is c(1,0), that is the bottomright corner inside the plot area.
graph	A string used to select the graphical engine to use for plotting. Should (partial-)match the three options "base", "ggplot2" or "plotly". Default value is "base".
...	If graph="ggplot2" and a named theme object is supplied, it will be added to the ggplot object. Additional arguments:

- line_colors: specifies the line colour(s) - all graph types.
- line_types: specifies the line type(s) as lty numeric values - all graph types.
- area_include: logical, include area under the CEAC curves - plotly only.
- area_color: specifies the AUC colour - plotly only.

Value

ceac	If graph="ggplot2" a ggplot object, or if graph="plotly" a plotly object containing the requested plot. Nothing is returned when graph="base", the default.

The function produces a plot of the cost-effectiveness acceptability curve against the discrete grid of possible values for the willingness to pay parameter. Values of the CEAC closer to 1 indicate that uncertainty in the cost-effectiveness of the reference intervention is very low. Similarly, values of the CEAC closer to 0 indicate that uncertainty in the cost-effectiveness of the comparator is very low.

Author(s)

Gianluca Baio, Andrea Berardi

References

Baio, G., Dawid, A. P. (2011). Probabilistic Sensitivity Analysis in Health Economics. Statistical Methods in Medical Research doi:10.1177/0962280211419832.

Baio G. (2012). Bayesian Methods in Health Economics. CRC/Chapman Hall, London

See Also

[bcea](#)

---

ceaf.plot   *Cost-Effectiveness Acceptability Frontier (CEAF) plot*

Description

Produces a plot the Cost-Effectiveness Acceptability Frontier (CEAF) against the willingness to pay threshold

Usage

```
ceaf.plot(mce, graph=c("base","ggplot2"))
```

Arguments

mce   The output of the call to the function [multi.ce](#)

graph   A string used to select the graphical engine to use for plotting. Should (partial-)match the two options "base" or "ggplot2". Default value is "base".

Value

ceaf   A ggplot object containing the plot. Returned only if graph="ggplot2".

Author(s)

Gianluca Baio, Andrea Berardi

References

Baio, G., Dawid, A. P. (2011). Probabilistic Sensitivity Analysis in Health Economics. Statistical Methods in Medical Research doi:10.1177/0962280211419832.

Baio G. (2012). Bayesian Methods in Health Economics. CRC/Chapman Hall, London

See Also

[bcea](#), [multi.ce](#)

Examples

```
# See Baio G., Dawid A.P. (2011) for a detailed description of the
# Bayesian model and economic problem
#
# Load the processed results of the MCMC simulation model
data(Vaccine)
#
# Runs the health economic evaluation using BCEA
m <- bcea(e=e,c=c,          # defines the variables of
                            #  effectiveness and cost
      ref=2,                # selects the 2nd row of (e,c)
                            #  as containing the reference intervention
      interventions=treats, # defines the labels to be associated
                            #  with each intervention
      Kmax=50000,           # maximum value possible for the willingness
                            #  to pay threshold; implies that k is chosen
                            #  in a grid from the interval (0,Kmax)
      plot=FALSE            # inhibits graphical output
)
#

mce <- multi.ce(m)          # uses the results of the economic analysis

#

ceaf.plot(mce)              # plots the CEAF

#

ceaf.plot(mce, graph="g")   # uses ggplot2


# Use the smoking cessation dataset
data(Smoking)
m <- bcea(e,c,ref=4,intervention=treats,Kmax=500,plot=FALSE)
mce <- multi.ce(m)
ceaf.plot(mce)
```

---

ceef.plot   *Cost-Effectiveness Efficiency Frontier (CEAF) plot*

Description

Produces a plot of the Cost-Effectiveness Efficiency Frontier (CEEF)

Usage

```
ceef.plot(he, comparators = NULL, pos = c(1, 1),
start.from.origins = TRUE, threshold = NULL, flip = FALSE,
dominance = TRUE, relative = FALSE, print.summary = TRUE,
graph = c("base", "ggplot2"), ...)
```

Arguments

he	A bcea object containing the results of the Bayesian modelling and the economic evaluation. The list needs to include the e and c matrices used to generate the object; see Details.
comparators	Vector specifying the comparators to be included in the frontier analysis. Must be of length > 1. Default as NULL includes all the available comparators.
pos	Parameter to set the position of the legend. Can be given in form of a string (bottom|top)(right|left) for base graphics and bottom, top, left or right for ggplot2. It can be a two-elements vector, which specifies the relative position on the x and y axis respectively, or alternatively it can be in form of a logical variable, with FALSE indicating to use the default position and TRUE to place it on the bottom of the plot. Default value is c(1,1), that is the topright corner inside the plot area.
start.from.origins	
	Logical. Should the frontier start from the origins of the axes? The argument is reset to FALSE if the average effectiveness and/or costs of at least one comparator are negative.
threshold	Specifies if the efficiency should be defined based on a willingness-to-pay threshold value. If set to NULL (the default), no conditions are included on the slope increase. If a positive value is passed as argument, to be efficient an intervention also requires to have an ICER for the comparison versus the last efficient strategy not greater than the specified threshold value. A negative value will be ignored with a warning.
flip	Logical. Should the axes of the plane be inverted?
dominance	Logical. Should the dominance regions be included in the plot?
relative	Logical. Should the plot display the absolute measures (the default as FALSE) or the differential outcomes versus the reference comparator?
print.summary	Logical. Should the efficiency frontier summary be printed along with the graph? See Details for additional information.
graph	A string used to select the graphical engine to use for plotting. Should (partial-)match the two options "base" or "ggplot2". Default value is "base".
...	If graph="ggplot2" and a named theme object is supplied, it will be added to the ggplot object. Ignored if graph="base". Setting the optional argument include.ICER to TRUE will print the ICERs in the summary tables, if produced.

Details

The bcea objects did not include the generating e and c matrices in BCEA versions <2.1-0. This function is not compatible with objects created with previous versions. The matrices can be ap-

pended to bcea objects obtained using previous versions, making sure that the class of the object remains unaltered.

The argument print.summary allows for printing a brief summary of the efficiency frontier, with default to TRUE. Two tables are plotted, one for the interventions included in the frontier and one for the dominated interventions. The average costs and clinical benefits are included for each intervention. The frontier table includes the slope for the increase in the frontier and the non-frontier table displays the dominance type of each dominated intervention. Please note that the slopes are defined as the increment in the costs for a unit increment in the benefits even if flip = TRUE for consistency with the ICER definition. The angle of increase is in radians and depends on the definition of the axes, i.e. on the value given to the flip argument.

If the argument relative is set to TRUE, the graph will not display the absolute measures of costs and benefits. Instead the axes will represent differential costs and benefits compared to the reference intervention (indexed by ref in the bcea function).

Value

ceplane   A ggplot object containing the plot. Returned only if graph="ggplot2".

The function produces a plot of the cost-effectiveness efficiency frontier. The dots show the simulated values for the intervention-specific distributions of the effectiveness and costs. The circles indicate the average of each bivariate distribution, with the numbers referring to each included intervention. The numbers inside the circles are black if the intervention is included in the frontier and grey otherwise. If the option dominance is set to TRUE, the dominance regions are plotted, indicating the areas of dominance. Interventions in the areas between the dominance region and the frontier are in a situation of extended dominance.

Author(s)

Andrea Berardi, Gianluca Baio

References

Baio G. (2012). Bayesian Methods in Health Economics. CRC/Chapman Hall, London.

IQWIG (2009). General methods for the Assessment of the Relation of Benefits to Cost, Version 1.0. IQWIG, November 2009.

See Also

bcea

Examples

```
### create the bcea object m for the smoking cessation example
data(Smoking)
m <- bcea(e,c,ref=4,Kmax=500,interventions=treats)
### produce the plot
ceef.plot(m,graph="base")

### tweak the options
ceef.plot(m,flip=TRUE,dominance=FALSE,start.from.origins=FALSE,
```

```
            print.summary=FALSE,graph="base")
### or use ggplot2 instead
if(require(ggplot2)){
ceef.plot(m,dominance=TRUE,start.from.origins=FALSE,pos=TRUE,
            print.summary=FALSE,graph="ggplot2")
}
```

---

ceplane.plot   *Cost-effectiveness plane plot*

Description

Produces a scatter plot of the cost-effectiveness plane, together with the sustainability area, as a function of the selected willingness to pay threshold

Usage

```
ceplane.plot(he, comparison = NULL, wtp = 25000, pos = c(1, 1),
  size = NULL, graph = c("base", "ggplot2"), xlim = NULL,
  ylim = NULL, ...)
```

Arguments

he	A bcea object containing the results of the Bayesian modelling and the economic evaluation.
comparison	Selects the comparator, in case of more than two interventions being analysed. Default as NULL plots all the comparisons together. Any subset of the possible comparisons can be selected (e.g., comparison=c(1,3) or comparison=2).
wtp	The value of the willingness to pay parameter. Not used iff graph="base" for multiple comparisons.
pos	Parameter to set the position of the legend; for a single comparison plot, the ICER legend position. Can be given in form of a string (bottom|top)(right|left) for base graphics and bottom|top|left|right for ggplot2. It can be a two-elements vector, which specifies the relative position on the x and y axis respectively, or alternatively it can be in form of a logical variable, with FALSE indicating to use the default position and TRUE to place it on the bottom of the plot. Default value is c(1,1), that is the topright corner inside the plot area.
size	Value (in millimetres) of the size of the willingness to pay label. Used only if graph="ggplot2", otherwise is ignored with a message.
graph	A string used to select the graphical engine to use for plotting. Should (partial-)match the two options "base" or "ggplot2". Default value is "base".
xlim	The range of the plot along the x-axis. If NULL (default) it is determined by the range of the simulated values for delta.e
ylim	The range of the plot along the y-axis. If NULL (default) it is determined by the range of the simulated values for delta.c

...	If graph="ggplot2" and a named theme object is supplied, it will be added to the ggplot object. Additional graphical arguments:

- label.pos=FALSE will place the willingness to pay label in a different position at the bottom of the graph - base and ggplot2 only (no label in plotly);
- point_colors: a vector of colours specifying the colour(s) associated to the cloud of points. Should be of length 1 or equal to the number of comparisons.
- point_sizes: a vector of colours specifying the size(s) of the points. Should be of length 1 or equal to the number of comparisons.
- ICER_colors: a vector of colours specifying the colour(s) of the ICER points. Should be of length 1 or equal to the number of comparisons.
- ICER_sizes: a vector of colours specifying the size(s) of the ICER points. Should be of length 1 or equal to the number of comparisons.
- area_include: logical, include or exclude the cost-effectiveness acceptability area (default is TRUE).
- area_color: a color specifying the colour of the cost-effectiveness acceptability area

Details

In the plotly version, point_colors, ICER_colors and area_color can also be specified as rgba colours using either the [toRGB](){plotly::toRGB} function or a rgba colour string, e.g. 'rgba(1,1,1,1)'.

Value

ceplane	If graph="ggplot2" a ggplot object, or if graph="plotly" a plotly object containing the requested plot. Nothing is returned when graph="base", the default.

The function produces a plot of the cost-effectiveness plane. Grey dots show the simulated values for the joint distribution of the effectiveness and cost differentials. The larger red dot shows the ICER and the grey area identifies the sustainability area, i.e. the part of the plan for which the simulated values are below the willingness to pay threshold. The proportion of points in the sustainability area effectively represents the CEAC for a given value of the willingness to pay. If the comparators are more than 2 and no pairwise comparison is specified, all scatterplots are graphed using different colors.

Author(s)

Gianluca Baio, Andrea Berardi

References

Baio, G., Dawid, A. P. (2011). Probabilistic Sensitivity Analysis in Health Economics. Statistical Methods in Medical Research doi:10.1177/0962280211419832.

Baio G. (2012). Bayesian Methods in Health Economics. CRC/Chapman Hall, London

See Also

[bcea]()

Examples

```
### create the bcea object m for the smoking cessation example
data(Smoking)
m <- bcea(e,c,ref=4,Kmax=500,interventions=treats)
### produce the plot
ceplane.plot(m,wtp=200,graph="base")
### select only one comparator
ceplane.plot(m,wtp=200,graph="base",comparator=3)
### or use ggplot2 instead
if(requireNamespace("ggplot2")){
ceplane.plot(m,wtp=200,pos="right",ICER_sizes=2,graph="ggplot2")
}
```

CEriskav   *Cost-effectiveness analysis including a parameter of risk aversion*

Description

Extends the standard cost-effectiveness analysis to modify the utility function so that risk aversion of the decision maker is explicitly accounted for

Usage

```
CEriskav(he, r = NULL, comparison = 1)

## Default S3 method:
CEriskav(he, r = NULL, comparison = 1)
```

Arguments

he   A bcea object containing the results of the Bayesian modelling and the eco-
                nomic evaluation.

r   A vector of values for the risk aversion parameter. If NULL, default values are
                assigned by R. The first (smallest) value (r -> 0) produces the standard analysis
                with no risk aversion.

comparison   In case of more than 2 interventions being analysed, selects which plot should
                be made. By default the first possible choice is selected as the comparator.

Value

An object of the class CEriskav containing the following elements:

Ur   An array containing the simulated values for all the "known-distribution" utili-
                ties for all interventions, all the values of the willingness to pay parameter and
                for all the possible values of r

Urstar	An array containing the simulated values for the maximum "known-distribution" expected utility for all the values of the willingness to pay parameter and for all the possible values of r
IBr	An array containing the simulated values for the distribution of the Incremental Benefit for all the values of the willingness to pay and for all the possible values of r
eibr	An array containing the Expected Incremental Benefit for each value of the willingness to pay parameter and for all the possible values of r
vir	An array containing all the simulations for the Value of Information for each value of the willingness to pay parameter and for all the possible values of r
evir	An array containing the Expected Value of Information for each value of the willingness to pay parameter and for all the possible values of r
R	The number of possible values for the parameter of risk aversion r
r	The vector containing all the possible values for the parameter of risk aversion r

Author(s)

Gianluca Baio

References

Baio, G., Dawid, A. P. (2011). Probabilistic Sensitivity Analysis in Health Economics. Statistical Methods in Medical Research doi:10.1177/0962280211419832.

Baio G. (2012). Bayesian Methods in Health Economics. CRC/Chapman Hall, London

See Also

bcea

Examples

```
# See Baio G., Dawid A.P. (2011) for a detailed description of the
# Bayesian model and economic problem
#
# Load the processed results of the MCMC simulation model
data(Vaccine)
#
# Runs the health economic evaluation using BCEA
m <- bcea(e=e,c=c,          # defines the variables of
                            #  effectiveness and cost
     ref=2,                 # selects the 2nd row of (e,c)
                            #  as containing the reference intervention
     interventions=treats,  # defines the labels to be associated
                            #  with each intervention
     Kmax=50000             # maximum value possible for the willingness
                            #  to pay threshold; implies that k is chosen
                            #  in a grid from the interval (0,Kmax)
)
```

```
#
# Define the vector of values for the risk aversion parameter, r, eg:
r <- c(0.0000000001,0.005,0.020,0.035)
#
# Run the cost-effectiveness analysis accounting for risk aversion

cr <- CEriskav(m,       # uses the results of the economic evalaution
                        #  (a "bcea" object)
            r=r,        # defines the vector of values for the risk
                        #  aversion parameter
         comparison=1  # if more than 2 interventions, selects the
                        #  pairwise comparison
)
```

---

contour.bcea   *Contour method for objects in the class* bcea

---

Description

Produces a scatterplot of the cost-effectiveness plane, with a contour-plot of the bivariate density of
the differentials of cost (y-axis) and effectiveness (x-axis)

Usage

```
## S3 method for class 'bcea'
contour(x, comparison = 1, scale = 0.5, nlevels = 4, levels = NULL,
  pos = c(1,0), xlim=NULL, ylim=NULL, graph=c("base","ggplot2"), ...)
```

Arguments

x	A bcea object containing the results of the Bayesian modelling and the economic evaluation
comparison	In case of more than 2 interventions being analysed, selects which plot should be made. By default the first comparison among the possible ones will be plotted. If graph="ggplot2" any subset of the possible comparisons can be selected, and comparison=NULL will yield a plot of all the possible comparisons together.
scale	Scales the plot as a function of the observed standard deviation.
levels	Numeric vector of levels at which to draw contour lines. Will be ignored using graph="ggplot2".
nlevels	Number of levels to be plotted in the contour.
pos	Parameter to set the position of the legend. Can be given in form of a string (bottom|top)(right|left) for base graphics and bottom, top, left or right for ggplot2. It can be a two-elements vector, which specifies the relative position on the x and y axis respectively, or alternatively it can be in form of a logical variable, with FALSE indicating to use the default position and TRUE to place the legend on the bottom of the plot. Default value is c(1,0), that is the bottomright corner inside the plot area.

graph	A string used to select the graphical engine to use for plotting. Should (partial-)match the two options "base" or "ggplot2". Default value is "base".
xlim	The range of the plot along the x-axis. If NULL (default) it is determined by the range of the simulated values for delta.e
ylim	The range of the plot along the y-axis. If NULL (default) it is determined by the range of the simulated values for delta.c
...	Additional arguments to 'plot.window', 'title', 'Axis' and 'box', typically graphical parameters such as 'cex.axis'. Will be ignored if graph="ggplot2".

Value

ceplane	A ggplot object containing the plot. Returned only if graph="ggplot2".

Plots the cost-effectiveness plane with a scatterplot of all the simulated values from the (posterior) bivariate distribution of (Delta_e,Delta_c), the differentials of effectiveness and costs; superimposes a contour of the distribution and prints the estimated value of the probability of each quadrant (combination of positive/negative values for both Delta_e and Delta_c)

Author(s)

Gianluca Baio, Andrea Berardi

References

Baio, G., Dawid, A. P. (2011). Probabilistic Sensitivity Analysis in Health Economics. Statistical Methods in Medical Research doi:10.1177/0962280211419832.

Baio G. (2012). Bayesian Methods in Health Economics. CRC/Chapman Hall, London

See Also

bcea, ceplane.plot, contour2

---

contour2   *Specialised contour plot for objects in the class "bcea"*

Description

Produces a scatterplot of the cost-effectiveness plane, with a contour-plot of the bivariate density of the differentials of cost (y-axis) and effectiveness (x-axis). Also adds the sustainability area (i.e. below the selected value of the willingness-to-pay threshold).

Usage

```
contour2(he, wtp=25000, xlim=NULL, ylim=NULL, comparison=NULL,
          graph=c("base","ggplot2"),...)
```

Arguments

he	A "bcea" object containing the results of the Bayesian modelling and the economic evaluation
wtp	The selected value of the willingness-to-pay. Default is 25000.
xlim	Limits on the x-axis (default=NULL, so that R will select appropriate limits).
ylim	Limits on the y-axis (default=NULL, so that R will select appropriate limits).
comparison	The comparison being plotted. Default to NULL chooses the first comparison if graph="base". If graph="ggplot2" the default value will choose all the possible comparisons. Any subset of the possible comparisons can be selected (e.g., comparison=c(1,3)).
graph	A string used to select the graphical engine to use for plotting. Should (partial-)match the two options "base" or "ggplot2". Default value is "base".
...	Arguments to be passed to ceplane.plot. See the relative manual page for more details.

Value

contour	A ggplot item containing the requested plot. Returned only if graph="ggplot2".

Plots the cost-effectiveness plane with a scatterplot of all the simulated values from the (posterior) bivariate distribution of (Delta_e,Delta_c), the differentials of effectiveness and costs; superimposes a contour of the distribution and prints the value of the ICER, together with the sustainability area.

Author(s)

Gianluca Baio, Andrea Berardi

References

Baio, G., Dawid, A. P. (2011). Probabilistic Sensitivity Analysis in Health Economics. Statistical Methods in Medical Research doi:10.1177/0962280211419832.

Baio G. (2012). Bayesian Methods in Health Economics. CRC/Chapman Hall, London

See Also

bcea, ceplane.plot, contour.bcea

Examples

```
### create the bcea object m for the smoking cessation example
data(Smoking)
m=bcea(e,c,ref=4,interventions=treats,Kmax=500)
### produce the plot
contour2(m,wtp=200,graph="base")

### or use ggplot2 to plot multiple comparisons
contour2(m,wtp=200,ICER.size=2,graph="ggplot2")
```

CreateInputs   *CreateInputs*

Description

Creates an object containing the matrix with the parameters simulated using the MCMC procedure (using JAGS, BUGS or Stan) and a vector of parameters (strings) that can be used to perform the expected value of partial information analysis. In the process, CreateInputs also checks for linear dependency among columns of the PSA samples or columns having constant values and removes them to only leave the fundamental parameters (to run VoI analysis). This also deals with simulations stored in a .csv or .txt file (eg as obtained using bootstrapping from a non-Bayesian model)

Usage

```
CreateInputs(x, print.lincom = TRUE)
```

Arguments

x	A rjags, bugs or stanfit object, containing the results of a call to either jags, (under R2jags), bugs (under R2WinBUGS or R2OpenBUGS), or stan (under rstan).
print.lincom	A TRUE/FALSE indicator. If set to TRUE (default) then prints the output of the procedure trying to assess whether there are some parameters that are a linear combination of others (in which case they are removed).

Value

mat	A data.frame contaning all the simulations for all the monitored parameters
parameters	A character vectors listing the names of all the monitored parameters

Author(s)

Gianluca Baio and Mark Strong

See Also

bcea, evppi

`diag.evppi`	*diag.evppi*

Description

Performs diagnostic plots for the results of the EVPPI

Usage

```
diag.evppi(x,y,diag=c("residuals","qqplot"),int=1)
```

Arguments

x	A evppi object obtained by running the function evppi on a bcea model.
y	A bcea object containing the results of the Bayesian modelling and the economic evaluation.
diag	The type of diagnostics to be performed. It can be the 'residual plot' or the 'qqplot plot'.
int	Specifies the interventions for which diagnostic tests should be performed (if there are many options being compared)

Value

The function produces either a residual plot comparing the fitted values from the INLA-SPDE Gaussian Process regression to the residuals. This is a scatter plot of residuals on the y axis and fitted values (estimated responses) on the x axis. The plot is used to detect non-linearity, unequal error variances, and outliers. A well-behaved residual plot supporting the appropriateness of the simple linear regression model has the following characteristics: 1) The residuals bounce randomly around the 0 line. This suggests that the assumption that the relationship is linear is reasonable. 2) The residuals roughly form a horizontal band around the 0 line. This suggests that the variances of the error terms are equal. 3) None of the residual stands out from the basic random pattern of residuals. This suggests that there are no outliers.

The second possible diagnostic is the qqplot for the fitted value. This is a graphical method for comparing the fitted values distributions with the assumed underlying normal distribution by plotting their quantiles against each other. First, the set of intervals for the quantiles is chosen. A point (x,y) on the plot corresponds to one of the quantiles of the second distribution (y-coordinate) plotted against the same quantile of the first distribution (x-coordinate). If the two distributions being compared are identical, the Q-Q plot follows the 45 degrees line.

Author(s)

Gianluca Baio, Anna Heath

References

Baio, G., Dawid, A. P. (2011). Probabilistic Sensitivity Analysis in Health Economics. Statistical Methods in Medical Research doi:10.1177/0962280211419832.

Baio G. (2012). Bayesian Methods in Health Economics. CRC/Chapman Hall, London

See Also

bcea, evppi

---

eib.plot	*Expected Incremental Benefit (EIB) plot*

Description

Produces a plot of the Expected Incremental Benefit (EIB) as a function of the willingness to pay

Usage

```
eib.plot(he, comparison = NULL, pos = c(1, 0), size = NULL,
  plot.cri = NULL, graph = c("base", "ggplot2", "plotly"), ...)
```

Arguments

he	A bcea object containing the results of the Bayesian modelling and the economic evaluation.
comparison	Selects the comparator, in case of more than two interventions being analysed. Default as NULL plots all the comparisons together. Any subset of the possible comparisons can be selected (e.g., comparison=c(1,3) or comparison=2).
pos	Parameter to set the position of the legend; for a single comparison plot, the ICER legend position. Can be given in form of a string (bottom|top)(right|left) for base graphics and bottom|top|left|right for ggplot2. It can be a two-elements vector, which specifies the relative position on the x and y axis respectively, or alternatively it can be in form of a logical variable, with FALSE indicating to use the default position and TRUE to place it on the bottom of the plot. Default value is c(1,0), that is the bottomright corner inside the plot area.
size	Value (in millimetres) of the size of the willingness to pay label. Used only if graph="ggplot2", otherwise it will be ignored with a message. If set to NA, the break-even point line(s) and label(s) are suppressed, with both base graphics and ggplot2.
plot.cri	Logical value. Should the credible intervals be plotted along with the expected incremental benefit? Default as NULL draws the 95% credible intervals if only one comparison is selected, and does not include them for multiple comparisons. Setting plot.cri=TRUE or plot.cri=FALSE forces the function to add the intervals or not. The level of the intervals can be also set, see ... for more details.

graph   A string used to select the graphical engine to use for plotting. Should (partial-
)match the three options `"base"`, `"ggplot2"` or `"plotly"`. Default value is
                        `"base"`.

...   If `graph="ggplot2"` and a named theme object is supplied, it will be added to
                        the ggplot object. Additional arguments:

- `alpha` can be used to set the CrI level when `plot.cri=TRUE`, with a default
  value of `alpha=0.05`.
- `cri.quantile` controls the the method of calculation of the credible inter-
  vals. The default value `cri.quantile=TRUE` defines the CrI as the interval
  between the `alpha/2`-th and `1-alpha/2`-th quantiles of the IB distribution.
  Setting `cri.quantile=FALSE` will use a normal approximation on the IB
  distribution to calculate the intervals.
- `line_colors`: specifies the line colour(s) - all graph types.
- `line_types`: specifies the line type(s) as lty numeric values - all graph
  types.
- `area_include`: include area under the EIB curve - plotly only.
- `area_color`: specifies the AUC curve - plotly only.

Value

eib   If `graph="ggplot2"` a ggplot object, or if `graph="plotly"` a plotly object con-
                        taining the requested plot. Nothing is returned when `graph="base"`, the default.

The function produces a plot of the Expected Incremental Benefit as a function of the discrete grid
approximation of the willingness to pay parameter. The break even point (i.e. the point in which
the EIB=0, ie when the optimal decision changes from one intervention to another) is also showed
by default. The value k* is the discrete grid approximation of the ICER.

Author(s)

Gianluca Baio, Andrea Berardi

References

Baio, G., Dawid, A. P. (2011). Probabilistic Sensitivity Analysis in Health Economics. Statistical
Methods in Medical Research doi:10.1177/0962280211419832.

Baio G. (2012). Bayesian Methods in Health Economics. CRC/Chapman Hall, London

See Also

bcea, ib.plot, ceplane.plot

---

evi.plot   *Expected Value of Information (EVI) plot*

Description

Plots the Expected Value of Information (EVI) against the willingness to pay

Usage

```
evi.plot(he, graph = c("base", "ggplot2", "plotly"), ...)
```

Arguments

he	A bcea object containing the results of the Bayesian modelling and the economic evaluation.
graph	A string used to select the graphical engine to use for plotting. Should (partial-)match the three options "base", "ggplot2" or "plotly". Default value is "base".
...	Additional graphical arguments:

- line_colors to specify the EVPI line colour - all graph types.
- line_types to specify the line type (lty) - all graph types.
- area_include to specify whether to include the area under the EVPI curve - plotly only.
- area_color to specify the area under the colour curve - plotly only.

Value

eib	If graph="ggplot2" a ggplot object, or if graph="plotly" a plotly object containing the requested plot. Nothing is returned when graph="base", the default.

The function produces a plot of the Expected Value of Information as a function of the discrete grid approximation of the willingness to pay parameter. The break even point(s) (i.e. the point in which the EIB=0, ie when the optimal decision changes from one intervention to another) is(are) also showed.

Author(s)

Gianluca Baio, Andrea Berardi

References

Baio, G., Dawid, A. P. (2011). Probabilistic Sensitivity Analysis in Health Economics. Statistical Methods in Medical Research doi:10.1177/0962280211419832.

Baio G. (2012). Bayesian Methods in Health Economics. CRC/Chapman Hall, London

See Also

bcea, ceac.plot, ceplane.plot

---

evppi	*Expected Value of Perfect Partial Information (EVPPI) for selected parameters*

Description

Calculates the Expected Value of Perfect Partial Information (EVPPI) for subsets of parameters. Uses GAM non-parameteric regression for single parameter EVPPI and the SPDE-INLA method for larger parameter subsets.

Usage

```
evppi(parameter, input, he, N = NULL, plot = F, residuals = T, ...)
```

Arguments

parameter	A vector of parameters for which the EVPPI should be calculated. This can be given as a string (or vector of strings) of names or a numeric vector, corresponding to the column numbers of important parameters.
input	A matrix containing the simulations for all the parameters monitored by the call to JAGS or BUGS. The matrix should have column names matching the names of the parameters and the values in the vector parameter should match at least one of those values.
he	A bcea object (the result of the call to the function [bcea](#)).
N	The number of PSA simulations used to calculate the EVPPI. The default uses all the available samples.
plot	A logical value indicating whether the triangular mesh for SPDE-INLA should be plotted. Default set to F.
residuals	A logical value indicating whether the fitted values for the SPDE-INLA method should be outputted. Default set to T.
...	Additional arguments. The default methods to compute the EVPPI are: - For single-parameter: GAM regression. - For multi-parameter: INLA/SPDE. However, it is possible (mainly for backward compatibility) to use different methods. For single-parameter, the user can specify the method of Sadatsafavi et al or the method of Strong & Oakley. In order to do so, it is necessary to include the extra parameter method which takes as value a string ″sad″ in the former case and a string ″so″ in the latter. In case "sal" is selected, then it is possible to also specify the number of "separators" (e.g. n.seps=3). If none is specified, the default value n.seps=1 is used. If ″so″ is used as method for the calculation of the EVPPI, then the user *needs* to also specify the number of "blocks" (e.g. n.blocks=20).
	For multi-parameter, the user can select 3 possible methods. If method="GAM" (BCEA will accept also ″gam″, ″G″ or ″g″), then the computations are based on GAM regression. The user can also specify the formula for the regression. The default option is to use a tensor product (e.g. if there are two main parameters, p1

and p2, this amounts to setting formula="te(p1,p2)", which indicates that the two parameters interact). Alternatively, it is possible to specify a model in which the parameters are independent using the notation formula="s(p1)+s(p2)". This may lead to worse accuracy in the estimates.

The second possible method is the GP regression derived by Strong et al. This is used if method="GP" (BCEA will also accept the specification method="gp"). In this case, the user can also specify the number of PSA runs that should be used to estimate the hyperparameters of the model (e.g. n.sim=100). This value is set by default to 500. Finally, it is also possible to specify some INLA-related options. These are all rather technical and are described in detail in Baio, Berardi and Heath. The optional parameter vector int.ord can take integer values (c(1,1) is default) and will force the predictor to include interactions: if int.ord=c(k,h), then all k-way interactions will be used for the effects and all h-way interactions will be used for the costs. Also, the user can specify the feature of the mesh for the "spatial" part of the model. The optional parameter cutoff (default 0.3) controls the density of the points inside the mesh. Acceptable values are typically in the interval (0.1,0.5), with lower values implying more points (and thus better approximation and greatercomputational time). The construction of the boundaries for the mesh can becontrolled by the optional inputs convex.inner (default = -0.4) and convex.outer (default = -0.7). These should be negative values and can be decreased (say to -0.7 and -1, respectively) to increase the distance between the points and the outer boundary, which also increases precision and computational time. The optional argumentrobust can be set to TRUE, in which case INLA will use a t prior distribution for the coefficients of the linear predictor. Finally, the user can control the accuracy of the INLA grid-search for the estimation of the hyperparameters. This is done by setting a value h.value (default=0.00005). Lower values imply a more refined search (and hence better accuracy), at the expense of computational speed. The method argument can also be given as a list allowing different regression methods for the effects and costs, and the different incremental decisions. The first list element should contain a vector of methods for the incremental effects and the second for the costs, for example method=list(c("GAM"),c("INLA")). The int.ord argument can also be given as a list to give different interaction levels for each regression curve.

By default, when no method is specified by the user, evppi will use GAM if the number of parameters is <5 and INLA otherwise.

Details

The single parameter EVPPI has been calculated using the non-parametric GAM regression developed by Strong et al. (2014). The multi-parameter EVPPI is calculated using the SPDE-INLA regression method for Gaussian Process regression developed by Heath et al. (2015)

Value

evppi	The computed values of evppi for all values of the parameter of willingness to pay
index	A numerical vector with the index associated with the parameters for which the EVPPI was calculated

k	The vector of values for the willingness to pay
evi	The vector of values for the overall EVPPI
fitted.costs	The fitted values for the costs
fitted.effects	The fitted values for the effects
parameters	A single string containing the names of the parameters for which the EVPPI was calculated, used for plotting the EVPPI
time	Computational time (in seconds)
fit.c	The object produced by the model fit for the costs
fit.e	The object produced by the model fit for the effects
formula	The formula used to fit the model
method	A string indicating the method used to estimate the EVPPI

Author(s)

Anna Heath, Gianluca Baio

References

Strong M., Oakley J. and Brennan A. (2014). Estimating multi-parameter partial Expected Value of Perfect Information from a probabilistic sensitivity analysis sample: a non-parametric regression approach. Medical Decision Making.

Sadatsafavi M., Bansback N., Zafari Z., Najafzadeh M., Marra C. (2013). Need for speed: an efficient algorithm for calculation of single-parameter expected value of partial perfect information. Value in Health

Baio G. (2012). Bayesian Methods in Health Economics. CRC/Chapman Hall, London

Heath A., Manolopoulou I., Baio G. (2016). Estimating the Expected Value of Partial Perfect Information in Health Economic Evaluations using Integrated Nested Laplace Approximation. Statistics in Medicine. http://onlinelibrary.wiley.com/doi/10.1002/sim.6983/full

See Also

plot.evppi, bcea

Examples

```
# See Baio G., Dawid A.P. (2011) for a detailed description of the
# Bayesian model and economic problem
#
# Load the processed results of the MCMC simulation model
# data(Vaccine)
#
# Runs the health economic evaluation using BCEA
# m <- bcea(e,c,ref=2,interventions=treats)
#
# Computes the EVPPI for a bunch of parameters
# inp <- CreateInputs(vaccine)
```

```
# Computes the EVPPI using INLA/SPDE
# x0 <- evppi(parameter=c(38:40),input=inp$mat,he=m)
# Now uses GAM regression
# x1 <- evppi(parameter=c(38:40),input=inp$mat,he=m,method="GAM")
# Now uses the GP regression
# x2 <- evppi(parameter=c(38:40),input=inp$mat,he=m,method="GP")
# Now plots the results
# plot(x0)
# points(x0$k,x0$evppi,lwd=2,lty=2,t="l")
# points(x1$k,x1$evppi,t="l",col="red")
# points(x2$k,x2$evppi,t="l",col="blue")
```

---

ib.plot   *Incremental Benefit (IB) distribution plot*

Description

Plots the distribution of the Incremental Benefit (IB) for a given value of the willingness to pay threshold

Usage

```
ib.plot(he, comparison = NULL, wtp = 25000, bw = nbw, n = 512,
  xlim = NULL, graph=c("base","ggplot2"))
```

Arguments

he	A bcea object containing the results of the Bayesian modelling and the economic evaluation.
comparison	In the case of multiple interventions, specifies the one to be used in comparison with the reference. Default value of NULL forces R to consider the first non-reference intervention as the comparator.
wtp	The value of the willingness to pay threshold. Default value at 25000.
bw	Identifies the smoothing bandwith used to construct the kernel estimation of the IB density.
n	The number of equally spaced points at which the density is to be estimated.
xlim	The limits of the plot on the x-axis.
graph	A string used to select the graphical engine to use for plotting. Should (partial-)match the two options "base" or "ggplot2". Default value is "base".

Value

ib	A ggplot object containing the requested plot. Returned only if graph="ggplot2".

The function produces a plot of the distribution of the Incremental Benefit for a given value of the willingness to pay parameter. The dashed area indicates the positive part of the distribution (ie when the reference is more cost-effective than the comparator).

Author(s)

Gianluca Baio, Andrea Berardi

References

Baio, G., Dawid, A. P. (2011). Probabilistic Sensitivity Analysis in Health Economics. Statistical Methods in Medical Research doi:10.1177/0962280211419832.

Baio G. (2012). Bayesian Methods in Health Economics. CRC/Chapman Hall, London

See Also

bcea, ib.plot, ceplane.plot

---

info.rank   *Info-rank plot*

Description

Produces a plot similar to a Tornado-plot, but based on the analysis of the EVPPI. For each parameter and value of the willingness-to-pay threshold, a barchart is plotted to describe the ratio of EVPPI (specific to that parameter) to EVPI. This represents the relative 'importance' of each parameter in terms of the expected value of information.

Usage

```
info.rank(parameter, input, he, wtp = he$k[min(which(he$k >= he$ICER))],
  howManyPars = NULL, graph = c("base", "plotly"), ...)
```

Arguments

parameter	A vector of parameters for which the individual EVPPI should be calculated. This can be given as a string (or vector of strings) of names or a numeric vector, corresponding to the column numbers of important parameters.
input	A matrix containing the simulations for all the parameters monitored by the call to JAGS or BUGS. The matrix should have column names matching the names of the parameters and the values in the vector parameter should match at least one of those values.
he	A bcea object (the result of the call to the function bcea).
wtp	A value of the wtp for which the analysis should be performed. If not specified then the break-even point for the current model will be used.
howManyPars	Optional maximum number of parameters to be included in the bar plot. Includes all parameters by default.
graph	A string used to select the graphical enging to use for plotting. Should (partial-)match one of the two options "base" or "plotly". Default value is "base"

... Additional options. These include graphical parameters that the user can specify:

- `xlim` = limits of the x-axis; `ca` = font size for the axis label (default = 0.7 of full size).
- `cn` = font size for the parameter names vector (default = 0.7 of full size) - base graphics only.
- `mai` = margins of the graph (default = c(1.36,1.5,1,1)) - base graphics only.
- `rel` = logical argument that specifies whether the ratio of EVPPI to EVPI (`rel=TRUE`, default) or the absolute value of the EVPPI should be used for the analysis.

Value

res With base graphics: A data.frame containing the ranking of the parameters with the value of the selected summary, for the chosen wtp; with plotly: a plotly object, incorporating in the $rank element the data.frame as above.

The function produces a 'Info-rank' plot. This is an extension of standard 'Tornado plots' and presents a ranking of the model parameters in terms of their impact on the expected value of information. For each parameter, the specific individual EVPPI is computed and used to measure the impact of uncertainty in that parameter over the decision-making process, in terms of how large the expected value of gaining more information is.

Author(s)

Anna Heath, Gianluca Baio, Andrea Berardi

References

Baio, G., Dawid, A. P. (2011). Probabilistic Sensitivity Analysis in Health Economics. Statistical Methods in Medical Research doi:10.1177/0962280211419832.

Baio G. (2012). Bayesian Methods in Health Economics. CRC/Chapman Hall, London

See Also

bcea, evppi

---

make.report *make.report*

Description

Constructs the automated report from the output of the BCEA

Usage

```
make.report(he, evppi = NULL, ext = "pdf", echo = FALSE, ...)
```

Arguments

he	An object obtained as output to a call to bcea
evppi	An object obtained as output to a call to evppi (default is NULL, so not essential to producing the report).
ext	A string of text to indicate the extension of the resulting output file. Possible options are "pdf", "docx". This requires the use of pandoc, knitr and rmarkdown.
echo	A string (default to FALSE) to instruct whether the report should also include the BCEA commands used to produce the analyses. If the optional argument echo is set to TRUE (default = FALSE), then the commands are also printed.
...	Additional parameters. For example, the user can specify the value of the willingness to pay wtp, which is used in some of the resulting analyses (default at the break even point). Another additional parameter that the user can specify is the name of the file to which the report should be written. This can be done by simply passing the optional argument filename="NAME". The user can also specify an object including the PSA simulations for all the relevant model parameters. If this is passed to the function (in the object psa_sims), then make.report will automatically construct an "Info-rank plot", which is a probabilistic form of tornado plot, based on the Expcted Value of Partial Information. The user can also specify the optional argument show.tab (default=FALSE); if set to TRUE, then a table with the values of the Info-rank is also shown.

Author(s)

Gianluca Baio

References

Baio, G., Dawid, A. P. (2011). Probabilistic Sensitivity Analysis in Health Economics. Statistical Methods in Medical Research doi:10.1177/0962280211419832.

Baio G. (2012). Bayesian Methods in Health Economics. CRC/Chapman Hall, London

See Also

bcea

Examples

```
data(Vaccine)
m=bcea(e,c,ref=2)
makeReport(m)
```

mce.plot	*Plots the probability that each intervention is the most cost-effective*

Description

Plots the probability that each of the n_int interventions being analysed is the most cost-effective.

Usage

```
mce.plot(mce,pos=c(1,0.5),graph=c("base","ggplot2"),...)
```

Arguments

mce	The output of the call to the function [multi.ce](#).
pos	Parameter to set the position of the legend. Can be given in form of a string (bottom|top)(right|left) for base graphics and bottom|top|left|right for ggplot2. It can be a two-elements vector, which specifies the relative position on the x and y axis respectively, or alternatively it can be in form of a logical variable, with TRUE indicating to use the first standard and FALSE to use the second one. Default value is c(1,0.5), that is on the right inside the plot area.
graph	A string used to select the graphical engine to use for plotting. Should (partial-)match the two options "base" or "ggplot2". Default value is "base".
...	Optional arguments. For example, it is possible to specify the colours to be used in the plot. This is done in a vector color=c(...). The length of the vector colors needs to be the same as the number of comparators included in the analysis, otherwise BCEA will fall back to the default values (all black, or shades of grey)

Value

mceplot	A ggplot object containing the plot. Returned only if graph="ggplot2".

Author(s)

Gianluca Baio, Andrea Berardi

References

Baio, G., Dawid, A. P. (2011). Probabilistic Sensitivity Analysis in Health Economics. Statistical Methods in Medical Research doi:10.1177/0962280211419832.

Baio G. (2012). Bayesian Methods in Health Economics. CRC/Chapman Hall, London

See Also

[bcea](#)

Examples

```
# See Baio G., Dawid A.P. (2011) for a detailed description of the
# Bayesian model and economic problem
#
# Load the processed results of the MCMC simulation model
data(Vaccine)
#
# Runs the health economic evaluation using BCEA
m <- bcea(e=e,c=c,          # defines the variables of
                            #  effectiveness and cost
      ref=2,                # selects the 2nd row of (e,c)
                            #  as containing the reference intervention
      interventions=treats, # defines the labels to be associated
                            #  with each intervention
      Kmax=50000,           # maximum value possible for the willingness
                            #  to pay threshold; implies that k is chosen
                            #  in a grid from the interval (0,Kmax)
      plot=FALSE            # inhibits graphical output
)
#
mce <- multi.ce(m)          # uses the results of the economic analysis
#
mce.plot(mce,               # plots the probability of being most cost-effective
      graph="base")         #  using base graphics
#
if(require(ggplot2)){
mce.plot(mce,               # the same plot
      graph="ggplot2")      #  using ggplot2 instead
}
```

---

mixedAn | *Cost-effectiveness analysis when multiple (possibly non cost-effective) interventions are present on the market*

Description

Runs the cost-effectiveness analysis, but accounts for the fact that more than one intervention is present on the market

Usage

```
mixedAn(he, mkt.shares = NULL, plot = FALSE)

## Default S3 method:
mixedAn(he, mkt.shares = NULL, plot = FALSE)
```

Arguments

he	A bcea object containing the results of the Bayesian modelling and the economic evaluation.
mkt.shares	A vector of market shares associated with the interventions. Its size is the same as the number of possible comparators. By default, assumes uniform distribution for each intervention.
plot	Logical value indicating whether the function should produce graphical output, via [plot.mixedAn](), or not. Default is set to FALSE.

Value

Creates an object in the class mixedAn which contains the results of the health economic evaluation in the mixed analysis case

Ubar	An array with the simulations of the "known-distribution" mixed utilities, for each value of the discrete grid approximation of the willingness to pay parameter
OL.star	An array with the simulations of the distribution of the Opportunity Loss for the mixed strategy, for each value of the discrete grid approximation of the willingness to pay parameter
evi.star	The Expected Value of Information for the mixed strategy, for each value of the discrete grid approximation of the willingness to pay parameter
k	The discrete grid approximation of the willingness to pay parameter used for the mixed strategy analysis
Kmax	The maximum value of the discrete grid approximation for the willingness to pay parameter
step	The step used to form the grid approximation to the willingness to pay
ref	The numeric index associated with the intervention used as reference in the analysis
comp	The numeric index(es) associated with the intervention(s) used as comparator(s) in the analysis
mkt.shares	The vector of market shares associated with each available intervention
n.comparisons	The total number of pairwise comparisons available
interventions	A vector of labels for all the interventions considered
evi	The vector of values for the "optimal" Expected Value of Information, as a function of the willingness to pay

The function can also produce a graph showing the difference between the "optimal" version of the EVPI (when only the most cost-effective intervention is included in the market) and the mixed strategy one (when more than one intervention is considered in the market)

Author(s)

Gianluca Baio

References

Baio, G. and Russo, P. (2009).A decision-theoretic framework for the application of cost-effectiveness analysis in regulatory processes. Pharmacoeconomics 27(8), 645-655 doi:10.2165/11310250

Baio, G., Dawid, A. P. (2011). Probabilistic Sensitivity Analysis in Health Economics. Statistical Methods in Medical Research doi:10.1177/0962280211419832.

Baio G. (2012). Bayesian Methods in Health Economics. CRC/Chapman Hall, London

See Also

bcea

Examples

```
# See Baio G., Dawid A.P. (2011) for a detailed description of the
# Bayesian model and economic problem
#
# Load the processed results of the MCMC simulation model
data(Vaccine)
#
# Runs the health economic evaluation using BCEA
m <- bcea(e=e,c=c,          # defines the variables of
                            #  effectiveness and cost
      ref=2,                # selects the 2nd row of (e,c)
                            #  as containing the reference intervention
      interventions=treats, # defines the labels to be associated
                            #  with each intervention
      Kmax=50000,           # maximum value possible for the willingness
                            #  to pay threshold; implies that k is chosen
                            #  in a grid from the interval (0,Kmax)
      plot=FALSE            # inhibits graphical output
)
#
ma <- mixedAn(m,        # uses the results of the mixed strategy
                        #  analysis (a "mixedAn" object)
      mkt.shares=NULL,  # the vector of market shares can be defined
                        #  externally. If NULL, then each of the T
                        #  interventions will have 1/T market share
      plot=TRUE         # produces the plots
)
```

---

multi.ce   *Cost-effectiveness analysis with multiple comparison*

Description

Computes and plots the probability that each of the n_int interventions being analysed is the most cost-effective and the cost-effectiveness acceptability frontier

Usage

```
multi.ce(he)
```

Arguments

he   A bcea object containing the results of the Bayesian modelling and the eco-
            nomic evaluation.

Value

m.ce   A matrix including the probability that each intervention is the most cost-effective
             for all values of the willingness to pay parameter

ceaf   A vector containing the cost-effectiveness acceptability frontier

Author(s)

Gianluca Baio

See Also

bcea, mce.plot, ceaf.plot

Examples

```
# See Baio G., Dawid A.P. (2011) for a detailed description of the
# Bayesian model and economic problem
#
# Load the processed results of the MCMC simulation model
data(Vaccine)
#
# Runs the health economic evaluation using BCEA
m <- bcea(e=e,c=c,          # defines the variables of
                            #  effectiveness and cost
      ref=2,                # selects the 2nd row of (e,c)
                            #  as containing the reference intervention
      interventions=treats, # defines the labels to be associated
                            #  with each intervention
      Kmax=50000,           # maximum value possible for the willingness
                            #  to pay threshold; implies that k is chosen
                            #  in a grid from the interval (0,Kmax)
      plot=FALSE            # inhibits graphical output
)
#
mce <- multi.ce(m          # uses the results of the economic analysis
)
```

| plot.bcea | *Summary plot of the health economic analysis* |

Description

Plots in a single graph the Cost-Effectiveness plane, the Expected Incremental Benefit, the CEAC and the EVPI

Usage

```
## S3 method for class 'bcea'
plot(x, comparison=NULL, wtp=25000, pos=FALSE,
graph=c("base","ggplot2"), ...)
```

Arguments

x	A bcea object containing the results of the Bayesian modelling and the economic evaluation.
comparison	Selects the comparator, in case of more than two interventions being analysed. The value is passed to [ceplane.plot](), [eib.plot]() and [ceac.plot]().
wtp	The value of the willingness to pay parameter. It is passed to [ceplane.plot]().
pos	Parameter to set the position of the legend. Can be given in form of a string, a single logical value, or a two-element vector with the respective relative positions on the x and y axis. Default as FALSE sets the legend position to the default one for each plot (see the details section), while TRUE puts it on the bottom of each plot. Changes will affect all the individual plots.
graph	A string used to select the graphical engine to use for plotting. Should (partial-)match the two options ″base″ or ″ggplot2″. Default value is ″base″.
...	Arguments to be passed to the methods [ceplane.plot]() and [eib.plot](). Please see the manual pages for the individual functions. Arguments like size, ICER.size and plot.cri can be supplied to the functions in this way. In addition if graph=″ggplot2″ and the arguments are named theme objects they will be added to each plot.

Details

The default position of the legend for the cost-effectiveness plane (produced by [ceplane.plot]()) is set to c(1,1.025) overriding its default for pos=FALSE, since multiple ggplot2 plots are rendered in a slightly different way than single plots.

For more information see the documentation of each individual plot function.

Value

The function produces a plot with four graphical summaries of the health economic evaluation.

Author(s)

Gianluca Baio, Andrea Berardi

References

Baio, G., Dawid, A. P. (2011). Probabilistic Sensitivity Analysis in Health Economics. Statistical Methods in Medical Research doi:10.1177/0962280211419832.

Baio G. (2012). Bayesian Methods in Health Economics. CRC/Chapman Hall, London

See Also

bcea, ceplane.plot, eib.plot, ceac.plot, evi.plot

Examples

```
# See Baio G., Dawid A.P. (2011) for a detailed description of the
# Bayesian model and economic problem
#
# Load the processed results of the MCMC simulation model
data(Vaccine)
#
# Runs the health economic evaluation using BCEA
m <- bcea(e=e,c=c,          # defines the variables of
                            #  effectiveness and cost
      ref=2,                # selects the 2nd row of (e,c)
                            #  as containing the reference intervention
      interventions=treats, # defines the labels to be associated
                            #  with each intervention
      Kmax=50000,           # maximum value possible for the willingness
                            #  to pay threshold; implies that k is chosen
                            #  in a grid from the interval (0,Kmax)
      plot=FALSE            # does not produce graphical outputs
)
#
# Plots the summary plots for the "bcea" object m using base graphics
plot(m,graph="base")

# Plots the same summary plots using ggplot2
if(require(ggplot2)){
plot(m,graph="ggplot2")

##### Example of a customized plot.bcea with ggplot2
plot(m,
  graph="ggplot2",                                   # use ggplot2
  theme=theme(plot.title=element_text(size=rel(1.25))), # theme elements must have a name
  ICER.size=1.5,                                     # hidden option in ceplane.plot
  size=rel(2.5)                                      # modifies the size of k= labels
)                                                    #  in ceplane.plot and eib.plot
}
```

---

plot.CEriskav	*Summary plot of the health economic analysis when risk aversion is included*

Description

Plots the EIB and the EVPI when risk aversion is included in the utility function

Usage

```
## S3 method for class 'CEriskav'
plot(x, pos=c(0,1), graph=c("base","ggplot2"), ...)
```

Arguments

x	An object of the class CEriskav, containing the results of the economic analysis performed accounting for a risk aversion parameter (obtained as output of the function CEriskav).
pos	Parameter to set the position of the legend. Can be given in form of a string (bottom|top)(right|left) for base graphics and bottom|top|left|right for ggplot2. It can be a two-elements vector, which specifies the relative position on the x and y axis respectively, or alternatively it can be in form of a logical variable, with FALSE indicating to use the default position and TRUE to place it on the bottom of the plot. Default value is c(0,1), that is in the topleft corner inside the plot area.
graph	A string used to select the graphical engine to use for plotting. Should (partial-)match the two options "base" or "ggplot2". Default value is "base".
...	Arguments to be passed to methods, such as graphical parameters (see par).

Value

list(eib,evi)	A two-elements named list of the ggplot objects containing the requested plots. Returned only if graph="ggplot2".

The function produces two plots for the risk aversion analysis. The first one is the EIB as a function of the discrete grid approximation of the willingness parameter for each of the possible values of the risk aversion parameter, r. The second one is a similar plot for the EVPI.

Author(s)

Gianluca Baio, Andrea Berardi

References

Baio, G., Dawid, A. P. (2011). Probabilistic Sensitivity Analysis in Health Economics. Statistical Methods in Medical Research doi:10.1177/0962280211419832.

Baio G. (2012). Bayesian Methods in Health Economics. CRC/Chapman Hall, London

See Also

bcea, CEriskav

Examples

```
# See Baio G., Dawid A.P. (2011) for a detailed description of the
# Bayesian model and economic problem
#
# Load the processed results of the MCMC simulation model
data(Vaccine)
#
# Runs the health economic evaluation using BCEA
m <- bcea(e=e,c=c,          # defines the variables of
                            #  effectiveness and cost
      ref=2,                # selects the 2nd row of (e,c)
                            #  as containing the reference intervention
      interventions=treats, # defines the labels to be associated
                            #  with each intervention
      Kmax=50000,           # maximum value possible for the willingness
                            #  to pay threshold; implies that k is chosen
                            #  in a grid from the interval (0,Kmax)
      plot=FALSE            # inhibits graphical output
)
#
# Define the vector of values for the risk aversion parameter, r, eg:
r <- c(0.000000000001,0.005,0.020,0.035)
#
# Run the cost-effectiveness analysis accounting for risk aversion

cr <- CEriskav(m,     # uses the results of the economic evalaution
                      #  (a "bcea" object)
        r=r,          # defines the vector of values for the risk
                      #  aversion parameter
        comparison=1  # if more than 2 interventions, selects the
                      #  pairwise comparison
)

#
# Now produce the plots

plot(cr # uses the results of the risk aversion
        #  analysis (a "CEriskav" object)
)

### Alternative options, using ggplot2

plot(cr,
  graph="ggplot2",
  plot="ask"          # plot option can be specified as
                      #  "dev.new" (default), "x11" or "ask"
  )
```

---

plot.evppi   *plot.evppi*

Description

Plots a graph of the Expected Value of Partial Information with respect to a set of parameters

Usage

```
## S3 method for class 'evppi'
plot(x, pos = c(0, 0.8), graph = c("base", "ggplot2"),
col = NULL,...)
```

Arguments

x	An object in the class evppi, obtained by the call to the function evppi.
pos	Parameter to set the position of the legend. Can be given in form of a string (bottom|top)(right|left) for base graphics and bottom|top|left|right for ggplot2. It can be a two-elements vector, which specifies the relative position on the x and y axis respectively, or alternatively it can be in form of a logical variable, with FALSE indicating to use the default position and TRUE to place it on the bottom of the plot. Default value is c(0,1), that is in the topleft corner inside the plot area.
graph	A string used to select the graphical engine to use for plotting. Should (partial-)match the two options "base" or "ggplot2". Default value is "base".
col	Sets the color for the lines depicted in the graph.
...	Arguments to be passed to methods, such as graphical parameters (see par).

Author(s)

Gianluca Baio, Andrea Berardi

References

Baio G. (2012). Bayesian Methods in Health Economics. CRC/Chapman Hall, London

See Also

bcea, evppi

---

plot.mixedAn	*Summary plot of the health economic analysis when the mixed analysis is considered*

Description

Compares the optimal scenario to the mixed case in terms of the EVPI

Usage

```
## S3 method for class 'mixedAn'
plot(x, y.limits = NULL, pos=c(0,1), graph=c("base","ggplot2"), ...)
```

Arguments

x	An object of class mixedAn, given as output of the call to the function mixedAn.
y.limits	Range of the y-axis for the graph. The default value is NULL, in which case the maximum range between the optimal and the mixed analysis scenarios is considered.
pos	Parameter to set the position of the legend. Can be given in form of a string (bottom|top)(right|left) for base graphics and bottom|top|left|right for ggplot2. It can be a two-elements vector, which specifies the relative position on the x and y axis respectively, or alternatively it can be in form of a logical variable, with FALSE indicating to use the default position and TRUE to place it on the bottom of the plot. Default value is c(0,1), that is in the topleft corner inside the plot area.
graph	A string used to select the graphical engine to use for plotting. Should (partial-)match the two options "base" or "ggplot2". Default value is "base".
...	Arguments to be passed to methods, such as graphical parameters (see par).

Value

evi	A ggplot object containing the plot. Returned only if graph="ggplot2".

The function produces a graph showing the difference between the "optimal" version of the EVPI (when only the most cost-effective intervention is included in the market) and the mixed strategy one (when more than one intervention is considered in the market).

Author(s)

Gianluca Baio, Andrea Berardi

References

Baio, G. and Russo, P. (2009).A decision-theoretic framework for the application of cost-effectiveness analysis in regulatory processes. Pharmacoeconomics 27(8), 645-655 doi:10.2165/11310250

Baio, G., Dawid, A. P. (2011). Probabilistic Sensitivity Analysis in Health Economics. Statistical Methods in Medical Research doi:10.1177/0962280211419832.

Baio G. (2012). Bayesian Methods in Health Economics. CRC/Chapman Hall, London

See Also

bcea, mixedAn

Examples

```
# See Baio G., Dawid A.P. (2011) for a detailed description of the
# Bayesian model and economic problem
#
# Load the processed results of the MCMC simulation model
data(Vaccine)
#
# Runs the health economic evaluation using BCEA
m <- bcea(e=e,c=c,          # defines the variables of
                            #  effectiveness and cost
      ref=2,                # selects the 2nd row of (e,c)
                            #  as containing the reference intervention
      interventions=treats, # defines the labels to be associated
                            #  with each intervention
      Kmax=50000,           # maximum value possible for the willingness
                            #  to pay threshold; implies that k is chosen
                            #  in a grid from the interval (0,Kmax)
      plot=FALSE            # inhibits graphical output
)
#
ma <- mixedAn(m,       # uses the results of the mixed strategy
                       #  analysis (a "mixedAn" object)
      mkt.shares=NULL  # the vector of market shares can be defined
                       #  externally. If NULL, then each of the T
                       #  interventions will have 1/T market share
)
#
# Can also plot the summary graph
plot(ma,graph="base")
#
# Or with ggplot2
if(require(ggplot2)){
plot(ma,graph="ggplot2")
}
```

---

sim.table   *Table of simulations for the health economic model*

Description

Using the input in the form of MCMC simulations and after having run the health economic model, produces a summary table of the simulations from the cost-effectiveness analysis

Usage

```
sim.table(he, wtp = 25000)
```

Arguments

he	A bcea object containing the results of the Bayesian modelling and the economic evaluation.
wtp	The value of the willingness to pay threshold to be used in the summary table.

Value

Produces the following elements:

Table	A table with the simulations from the economic model
names.cols	A vector of labels to be associated with each column of the table
wtp	The selected value of the willingness to pay
ind.table	The index associated with the selected value of the willingness to pay threshold in the grid used to run the analysis

Author(s)

Gianluca Baio

References

Baio, G., Dawid, A. P. (2011). Probabilistic Sensitivity Analysis in Health Economics. Statistical Methods in Medical Research doi:10.1177/0962280211419832.

Baio G. (2012). Bayesian Methods in Health Economics. CRC/Chapman Hall, London

See Also

bcea

Examples

```
# See Baio G., Dawid A.P. (2011) for a detailed description of the
# Bayesian model and economic problem
#
# Load the processed results of the MCMC simulation model
data(Vaccine)
#
# Runs the health economic evaluation using BCEA
m <- bcea(e=e,c=c,            # defines the variables of
                              #  effectiveness and cost
       ref=2,                 # selects the 2nd row of (e,c)
                              #  as containing the reference intervention
       interventions=treats,  # defines the labels to be associated
                              #  with each intervention
       Kmax=50000             # maximum value possible for the willingness
                              #  to pay threshold; implies that k is chosen
                              #  in a grid from the interval (0,Kmax)
)
#
# Now can save the simulation exercise in an object using sim.table()
st <- sim.table(m, # uses the results of the economic evalaution
                   #  (a "bcea" object)
         wtp=25000  # selects the particular value for k
)
#
# The table can be explored. For example, checking the
#  element 'Table' of the object 'st'
```

Smoking   *Data set for the Bayesian model for the cost-effectiveness of smoking*
                                  cessation interventions

Description

This data set contains the results of the Bayesian analysis used to model the clinical output and the costs associated with the health economic evaluation of four different smoking cessation interventions.

Usage

```
data(Smoking)
```

Format

A data list including the variables needed for the smoking cessation cost-effectiveness analysis. The variables are as follows:

c a matrix of 500 simulations from the posterior distribution of the overall costs associated with the four strategies

data a dataset containing the characteristics of the smokers in the UK population

e a matrix of 500 simulations from the posterior distribution of the clinical benefits associated with the four strategies

life.years a matrix of 500 simulations from the posterior distribution of the life years gained with each strategy

pi a matrix of 500 simulations from the posterior distribution of the event of smoking cessation with each strategy

smoking a data frame containing the inputs needed for the network meta-analysis model. The data.frame object contains: nobs: the record ID number, s: the study ID number, i: the intervention ID number, r_i: the number of patients who quit smoking, n_i: the total number of patients for the row-specific arm and b_i: the reference intervention for each study

smoking_output a rjags object obtained by running the network meta-analysis model based on the data contained in the smoking object

smoking_mat a matrix obtained by running the network meta-analysis model based on the data contained in the smoking object

treats a vector of labels associated with the four strategies

Source

Effectiveness data adapted from Hasselblad V. (1998). Meta-analysis of Multitreatment Studies. Medical Decision Making 1998;18:37-43.

Cost and population characteristics data adapted from various sources:

- Taylor, D.H. Jr, et al. (2002). Benefits of smoking cessation on longevity. American Journal of Public Health 2002;92(6)

- ASH: Action on Smoking and Health (2013). ASH fact sheet on smoking statistics, http://ash.org.uk/files/documents/ASH_106.pdf

- Flack, S., et al. (2007). Cost-effectiveness of interventions for smoking cessation. York Health Economics Consortium, January 2007

- McGhan, W.F.D., and Smith, M. (1996). Pharmacoeconomic analysis of smoking-cessation interventions. American Journal of Health-System Pharmacy 1996;53:45-52

References

Baio G. (2012). Bayesian Methods in Health Economics. CRC/Chapman Hall, London

Examples

```
data(Smoking)
```

```
m=bcea(e,c,ref=4,interventions=treats,Kmax=500)
```

---

struct.psa   *Structural PSA*

Description

Computes the weights to be associated with a set of competing models in order to perform structural
PSA

Usage

```
struct.psa(models, effect, cost, ref = 1, interventions = NULL,
          Kmax = 50000, plot = F)
```

Arguments

models	A list containing the output from either R2jags or R2OpenBUGS/R2WinBUGS for all the models that need to be combined in the model average
effect	A list containing the measure of effectiveness computed from the various models (one matrix with n.sim x n.ints simulations for each model)
cost	A list containing the measure of costs computed from the various models (one matrix with n.sim x n.ints simulations for each model)
ref	Defines which intervention is considered to be the reference strategy. The default value ref=1 means that the intervention appearing first is the reference and the other(s) is(are) the comparator(s)
interventions	Defines the labels to be associated with each intervention. By default and if NULL, assigns labels in the form "Intervention1", ... , "Intervention T"
Kmax	Maximum value of the willingness to pay to be considered. Default value is k=50000. The willingness to pay is then approximated on a discrete grid in the interval [0,Kmax]. The grid is equal to wtp if the parameter is given, or composed of 501 elements if wtp=NULL (the default)
plot	A logical value indicating whether the function should produce the summary plot or not

Author(s)

Gianluca Baio

References

Baio G. (2012). Bayesian Methods in Health Economics. CRC/Chapman Hall, London

See Also

bcea

---

summary.bcea   *Summary method for objects in the class* bcea

---

Description

Produces a table printout with some summary results of the health economic evaluation

Usage

```
## S3 method for class 'bcea'
summary(object, wtp = 25000, ...)
```

Arguments

object	A bcea object containing the results of the Bayesian modelling and the economic evaluation.
wtp	The value of the willingness to pay threshold to be used in the summary table.
...	Additional arguments affecting the summary produced.

Value

Prints a summary table with some information on the health economic output and synthetic information on the economic measures (EIB, CEAC, EVPI).

Author(s)

Gianluca Baio

References

Baio, G., Dawid, A. P. (2011). Probabilistic Sensitivity Analysis in Health Economics. Statistical Methods in Medical Research doi:10.1177/0962280211419832.

Baio G. (2012). Bayesian Methods in Health Economics. CRC/Chapman Hall, London

See Also

bcea

---

summary.mixedAn   *Summary methods for objects in the class* mixedAn *(mixed analysis)*

Description

Prints a summary table for the results of the mixed analysis for the economic evaluation of a given model

Usage

```
## S3 method for class 'mixedAn'
summary(object, wtp = 25000,...)
```

Arguments

object	An object of the class mixedAn, which is the results of the function [mixedAn](#), generating the economic evaluation of a set of interventions, considering given market shares for each option.
wtp	The value of the willingness to pay choosen to present the analysis.
...	Additional arguments affecting the summary produced.

Value

Produces a table with summary information on the loss in expected value of information generated by the inclusion of non cost-effective interventions in the market.

Author(s)

Gianluca Baio

References

Baio, G. and Russo, P. (2009).A decision-theoretic framework for the application of cost-effectiveness analysis in regulatory processes. Pharmacoeconomics 27(8), 645-655 doi:10.2165/11310250

Baio, G., Dawid, A. P. (2011). Probabilistic Sensitivity Analysis in Health Economics. Statistical Methods in Medical Research doi:10.1177/0962280211419832.

Baio G. (2012). Bayesian Methods in Health Economics. CRC/Chapman Hall, London

See Also

[bcea](#), [mixedAn](#)

Examples

```
# See Baio G., Dawid A.P. (2011) for a detailed description of the
# Bayesian model and economic problem
#
# Load the processed results of the MCMC simulation model
data(Vaccine)
#
# Runs the health economic evaluation using BCEA
m <- bcea(e=e,c=c,          # defines the variables of
                            #  effectiveness and cost
     ref=2,                 # selects the 2nd row of (e,c)
                            #  as containing the reference intervention
     interventions=treats,  # defines the labels to be associated
                            #  with each intervention
     Kmax=50000             # maximum value possible for the willingness
                            #  to pay threshold; implies that k is chosen
                            #  in a grid from the interval (0,Kmax)
)
#
ma <- mixedAn(m,            # uses the results of the mixed strategy
                            #  analysis (a "mixedAn" object)
     mkt.shares=NULL        # the vector of market shares can be defined
                            #  externally. If NULL, then each of the T
                            #  interventions will have 1/T market share
)
#
# Prints a summary of the results
summary(ma,         # uses the results of the mixed strategy analysis
                    #  (a "mixedAn" object)
     wtp=25000      # selects the relevant willingness to pay
                    #  (default: 25,000)
)
```

Vaccine   *Data set for the Bayesian model for the cost-effectiveness of influenza vaccination*

Description

This data set contains the results of the Bayesian analysis used to model the clinical output and the costs associated with an influenza vaccination.

Usage

```
data(Vaccine)
```

Format

A data list including the variables needed for the influenza vaccination. The variables are as follows:

c a matrix of simulations from the posterior distribution of the overall costs associated with the two treatments

cost.GP a matrix of simulations from the posterior distribution of the costs for GP visits associated with the two treatments

cost.hosp a matrix of simulations from the posterior distribution of the costs for hospitalisations associated with the two treatments

cost.otc a matrix of simulations from the posterior distribution of the costs for over-the-counter medications associated with the two treatments

cost.time.off a matrix of simulations from the posterior distribution of the costs for time off work associated with the two treatments

cost.time.vac a matrix of simulations from the posterior distribution of the costs for time needed to get the vaccination associated with the two treatments

cost.travel a matrix of simulations from the posterior distribution of the costs for travel to get vaccination associated with the two treatments

cost.trt1 a matrix of simulations from the posterior distribution of the overall costs for first line of treatment associated with the two interventions

cost.trt2 a matrix of simulations from the posterior distribution of the overall costs for second line of treatment associated with the two interventions

cost.vac a matrix of simulations from the posterior distribution of the costs for vaccination

c.pts a matrix of simulations from the posterior distribution of the clinical benefits associated with the two treatments

e a matrix of simulations from the posterior distribution of the clinical benefits associated with the two treatments

e.pts a matrix of simulations from the posterior distribution of the clinical benefits associated with the two treatments

N the number of subjects in the reference population

N.outcomes the number of clinical outcomes analysed

N.resources the number of health-care resources under study

QALYs.adv a vector from the posterior distribution of the QALYs associated with advert events

QALYs.death a vector from the posterior distribution of the QALYs associated with death

QALYs.hosp a vector from the posterior distribution of the QALYs associated with hospitalisation

QALYs.inf a vector from the posterior distribution of the QALYs associated with influenza infection

QALYs.pne a vector from the posterior distribution of the QALYs associated with penumonia

treats a vector of labels associated with the two treatments

vaccine a rjags object containing the simulations for the parameters used in the original model

vaccine_mat a matrix containing the simulations for the parameters used in the original model

Source

Adapted from Turner D, Wailoo A, Cooper N, Sutton A, Abrams K, Nicholson K. The cost-effectiveness of influenza vaccination of healthy adults 50-64 years of age. Vaccine. 2006;24:1035-1043.

References

Baio, G., Dawid, A. P. (2011). Probabilistic Sensitivity Analysis in Health Economics. Statistical Methods in Medical Research doi:10.1177/0962280211419832.

Examples

```
data(Vaccine)


m=bcea(e,c,ref=1,interventions=treats)
```

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