

# Package ‘stepp’

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**Type** Package

**Title** Subpopulation Treatment Effect Pattern Plot (STEPP)

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**Depends** methods, car, survival, splines

**Collate** 'stutil.R' 'stwin.R' 'stsubpop.R' 'stmodelKM.R' 'stmodelCI.R'  
'stmodelGLM.R' 'stmodel.R' 'stepes.R' 'stepp.R'

**Description** A method to explore the treatment-covariate interactions in survival or generalized linear model (GLM) for continuous, binomial and count data arising from two or more treatment arms of a clinical trial. A permutation distribution approach to inference is implemented, based on permuting the covariate values within each treatment group.  
Bonetti M, Gelber RD (2004) <DOI:10.1093/biostatistics/5.3.465>.  
Marco Bonetti, David Zahrieh, Bernard F. Cole, and Richard D. Gelber (2009) <doi:10.1002/sim.3524>.  
Ann A. Lazar, Bernard F. Cole, Marco Bonetti, and Richard D. Gelber (2010) <doi:10.1200/JCO.2009.27.9182>.  
Lazar AA, Bonetti M, Cole BF, Yip WK, Gelber RD (2016) <doi:10.1177/1740774515609106>.  
Wai-Ki Yip, Marco Bonetti, Bernard F Cole, William Barcella, Xin Victoria Wang, Ann Lazar, and Richard D Gelber (2016) <doi:10.1177/1740774516643297>.  
Wang XV, Cole B, Bonetti M, Gelber RD (2016) < doi:10.1002/sim.6958>.  
Wai-Ki Yip (2017, ISBN:978-3-319-48846-2).

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analyze.CumInc.stepp    *Analyze competing risks data using Cumulative Incidence method*

---

**Description**

This method will be deprecated in the future. Please use the constructor function `stepp.CI` to create a STEPP Cumulative Incidence model for future development.

A method to explore the treatment-effect interactions in competing risks data arising from two treatment arms of a clinical trial. A permutation distribution approach to inference is implemented that permutes covariate values within a treatment group. The statistical significance of observed heterogeneity of treatment effects is calculated using permutation tests:

- 1) for the maximum difference between each subpopulation effect and the overall population treatment effect or supremum based test statistic;

2) for the difference between each subpopulation effect and the overall population treatment effect, which resembles the chi-square statistic.

### Usage

```
analyze.CumInc.stepp(coltrt, coltime, coltype, colvar, trts, patspop, minpatpop,
  timest, noperm=2500, ncex = 0.7, legendy = 30, pline = -2.5,
  color = c("red", "black"),
  xlabel = "Subpopulations by Median Covariate",
  ylabel = "?-year Disease-Free Survival",
  tlegend = c("1st Treatment", "2nd Treatment"),
  nlas = 3, pointwise = FALSE)
```

### Arguments

coltrt	the treatment variable
coltime	the time to event variable
coltype	variable with distinct codes for different causes of failure where coltype=0 for censored observations; coltype=1 for event of interest; coltype=2 for other causes of failure
colvar	the covariate of interest
trts	a vector containing the codes for the 2 treatment arms, 1st and 2nd treatment arms, respectively
patspop	larger parameter(r2) for subpopulation construction that determines how many patients are in each subpopulation
minpatpop	smaller parameter(r1) for subpopulation construction that determines the largest number of patients in common among consecutive subpopulations
timest	timepoint to estimate survival
noperm	the desired number of permutations; must be 0 or above
ncex	optional - specify the size of the text for the sample size annotation, that is, the character expansion factor
legendy	optional - the vertical location of the legend according to the units on the y-axis
pline	optional - specify the vertical location of the p-value, that is, on which margin line, starting at 0 counting outwards
color	optional - a vector containing the line colors for the 1st and 2nd treatment, respectively
ylabel	optional - specify the label for the y-axis
xlabel	optional - specify the label for the x-axis
tlegend	optional - a vector containing the treatment labels, 1st and 2nd treatment, respectively
nlas	optional - specify the las parameter (0,1,2,3) to determine the orientation of the sample size annotation
pointwise	optional -specify pointwise confidence intervals (pointwise=TRUE), or confidence bands (pointwise=FALSE, default) to be displayed

## Details

A statistical method to explore treatment by covariate interactions in competing risks data arising from two treatment arms of a clinical trial. The method is based on constructing overlapping subpopulations of patients with respect to a covariate of interest, and in observing the pattern of the treatment effects estimated across subpopulations. A plot of these treatment effects is called STEPP, or Subpopulation Treatment Effect Pattern Plot. STEPP uses the permutation distribution based approach for inference.

One can explore the window parameters without invoking the permutation analysis by setting `noperm` to 0. In that case, `pvalue` and the covariance matrix will not be available.

We acknowledge Robert J. Gray for permitting us to use the `cmprsk` package.

## Value

`analyze.CumInc.stepp` generates a Subpopulation Treatment Effect Pattern Plot (STEPP) displaying the p-value from the test for interaction. Descriptive summaries of the dataset and the estimated variance-covariance matrix are returned through the `steppes` object. See documentation on `steppes` object for details on how you can use it.

## Warning

This function together with other old functions will be depreciated in the future. A new set of S4 classes are implemented to replace old interfaces. Please use them for future development.

A few tips to keep in mind:

The variables `coltrt`, `coltime`, `coltype`, and `colvar` must be numeric. No formatting allowed.

If you receive the error "Error in solve.default(sigma): system is computationally singular; reciprocal condition number = 0" then we recommend changing the seed by re-running `analyze.KM.stepp`. If this error persists after several runs, then the program cannot provide reliable results. Please try modifying your choices of the two parameters `minpatspop(r1)` and `patspop(r2)` that define the subpopulation.

The number of permutations specified in `noperm`, the sample size, and the number of subpopulations generated will affect how long `analyze.CumInc.stepp` takes to execute. The results are stable if 2500 or more permutations are specified. Furthermore, varying the number of subpopulations will affect inference.

The time point selected to estimate survival in `timest` must be in the same units (e.g., months) as the `coltime` variable.

The order of the treatments in the vector `trts` must be in the same order in the vector `tlegend`.

## Note

STEPP is an exploratory tool, with graphical features that make it easy for clinicians to interpret the results of the analysis. Positive results should prompt the need for confirmation from other datasets investigating similar treatment comparisons. It should also be clear that STEPP is not meant to estimate specific cutpoints in the range of values of the covariate of interest, but rather to provide some indication on ranges of values where treatment effect might have a particular behavior.

STEPP considers the case in which the subpopulations are constructed according to a sliding window pattern. The larger parameter (patspop) determines how many patients are in each subpopulation, and the smaller parameter (minpatspop) determines the largest number of patients in common among consecutive subpopulations. A minimum of 80-100 patients should be in each subpopulation, but that is not strictly necessary. The difference (patspop-minpatspop) is the approximate number of patients replaced between any two subsequent subpopulations, and can be used to determine the number of subpopulations once patspop is fixed. The choice of the values of the parameters patspop and minpatspop to be used does change the appearance of the plot and the corresponding p-value. It is probably reasonable to experiment with a few combinations to ensure that the significance (or lack of significance) is stable with respect to that choice.

For best results, consider implementing 2500 permutations of the covariate (vector of subpopulations) to obtain a rich distribution in which to draw inference.

### Author(s)

Ann Lazar, Wai-ki Yip, David Zahrieh, Bernard Cole, Marco Bonetti, Richard Gelber

### References

Bonetti M, Gelber RD. Patterns of treatment effects in subsets of patients in clinical trials. *Biostatistics* 2004; 5(3):465-481.

Bonetti M, Zahrieh D, Cole BF, Gelber RD. A small sample study of the STEPP approach to assessing treatment-covariate interactions in survival data. *Statistics in Medicine* 2009; 28(8):1255-68.

Lazar AA, Cole BF, Bonetti M, Gelber RD. Evaluation of treatment-effect heterogeneity using biomarkers measured on a continuous scale: subpopulation treatment effect pattern plot. *Journal of Clinical Oncology*, 2010; 28(29): 4539-4544.

### See Also

[stwin](#), [stsubpop](#), [stmodelCI](#), [steppes](#), [stmodel](#), [stepp.win](#), [stepp.subpop](#), [stepp.CI](#), [stepp.GLM](#), [stepp.test](#), [estimate](#), [generate](#),

Old functions to be deprecated: [stepp](#), [stepp\\_summary](#), [stepp\\_print](#), [stepp\\_plot](#), and [analyze.KM.stepp](#).

### Examples

```
#GENERATE TREATMENT VARIABLE:
n <- 1000 # set the sample size
mu <- 0 # set the mean and sd of the covariate
sigma <- 1

beta0 <- log(-log(0.5)) # set the intercept for the log hazard
beta1 <- -0.2 # set the slope on the covariate
beta2 <- 0.5 # set the slope on the treatment indicator
beta3 <- 0.7 # set the slope on the interaction

prob2 <- 0.2 # set the proportion type 2 events
cprob <- 0.3 # set the proportion censored

set.seed(7775432) # set the random number seed
```

```

covariate <- rnorm(n,mean=mu,sd=sigma) # generate the covariate values
Txassign <- rbinom(n,1,0.5) # generate the treatment indicator
x3 <- covariate*Txassign # compute interaction term
# compute the hazard for type 1 event
lambda1 <- exp(beta0+beta1*covariate+beta2*Txassign+beta3*x3)
lambda2 <- prob2*lambda1/(1-prob2) # compute the hazard for the type 2 event
# compute the hazard for censoring time
lambda0 <- cprob*(lambda1+lambda2)/(1-cprob)
t1 <- rexp(n,rate=lambda1) # generate the survival time for type 1 event
t2 <- rexp(n,rate=lambda2) # generate the survival time for type 2 event
t0 <- rexp(n,rate=lambda0) # generate the censoring time
time <- pmin(t0,t1,t2) # compute the observed survival time
type <- rep(0,n)
type[(t1 < t0)&(t1 < t2)] <- 1
type[(t2 < t0)&(t2 < t1)] <- 2

# Call analyze.CumInc.stepp to analyze the data
# Warning: In this example, the permutations have been set to 0 to allow the stepp function
# to finish in a short amount of time. IT IS RECOMMEND TO USE AT LEAST 2500 PERMUTATIONS TO
# PROVIDE STABLE RESULTS.
analyze.CumInc.stepp (coltrt=Txassign, trts=c(0,1), coltime=time, coltype=type, colvar=covariate,
  patpop=300, minpatpop=200, timest=1.0, noperm=0,
  ncex=0.70,legendy=30,pline=-2.5,color=c("red", "black"),
  xlabel="Subpopulations by Median Age",ylabel="4-year Cancer Relapse",
  tlegend=c("Treatment A", "Treatment B"), nlas=3,pointwise=FALSE)

```

---

analyze.KM.stepp

*Analyze survival data using Kaplan-Meier method*


---

## Description

This method will be deprecated in the future. Please use the constructor function `stepp.KM` to create a STEPP Kaplan-Meier model for future development.

A method to explore the treatment-covariate interactions in survival data arising from two treatment arms of a clinical trial. The treatment effects are measured using survival functions at a specified time point estimated from the Kaplan-Meier method and the hazard ratio based on observed-minus-expected estimation. A permutation distribution approach to inference is implemented, based on permuting the covariate values within each treatment group. The statistical significance of observed heterogeneity of treatment effects is calculated using permutation tests:

- 1) for the maximum difference between each subpopulation effect and the overall population treatment effect or supremum based test statistic;
- 2) for the difference between each subpopulation effect and the overall population treatment effect, which resembles the chi-square statistic.

## Usage

```

analyze.KM.stepp(coltrt, coltime, colcens, colvar, trts, patpop, minpatpop,
  timest, noperm=2500, ncex = 0.7, legendy = 30, pline = -2.5,

```

```

color = c("red", "black"),
xlabel = "Subpopulations by Median Covariate",
ylabel = "?-year Disease-Free Survival",
tlegend = c("1st Treatment", "2nd Treatment"),
nlas = 3, pointwise = FALSE)

```

### Arguments

coltrt	the treatment variable
coltime	the time to event variable
colcens	the censoring variable
colvar	the covariate of interest
trts	a vector containing the codes for the 2 treatment arms, 1st and 2nd treatment arms, respectively
patpop	larger parameter(r2) for subpopulation construction that determines how many patients are in each subpopulation
minpatpop	smaller parameter(r1) for subpopulation construction that determines the largest number of patients in common among consecutive subpopulations
timest	timepoint to estimate survival
nperm	the desired number of permutations; must be 0 or above
ncex	optional - specify the size of the text for the sample size annotation, that is, the character expansion factor
legendy	optional - the vertical location of the legend according to the units on the y-axis
pline	optional - specify the vertical location of the p-value, that is, on which margin line, starting at 0 counting outwards
color	optional - a vector containing the line colors for the 1st and 2nd treatment, respectively
ylabel	optional - specify the label for the y-axis
xlabel	optional - specify the label for the x-axis
tlegend	optional - a vector containing the treatment labels, 1st and 2nd treatment, respectively
nlas	optional - specify the las parameter (0,1,2,3) to determine the orientation of the sample size annotation
pointwise	optional -specify pointwise confidence intervals (pointwise=TRUE), or confidence bands (pointwise=FALSE, default) to be displayed

### Details

A statistical method to explore treatment-covariate interactions in survival data arising from two treatment arms of a clinical trial. The method is based on constructing overlapping subpopulations of patients with respect to one covariate of interest, and in observing the pattern of the treatment effects estimated across subpopulations. A plot of these treatment effects is called STEPP, or Subpopulation Treatment Effect Pattern Plot. STEPP uses the permutation distribution based approach for inference.

One can explore the window parameters without invoking the permutation analysis by setting nperm to 0. In that case, pvalue and the covariance matrix will not be available.

**Value**

analyze.KM.stepp generates a Subpopulation Treatment Effect Pattern Plot (STEPP) displaying the p-value from the test for interaction. Descriptive summaries of the dataset and the estimated variance-covariance matrix are returned through the `steppes` object. See documentation on `steppes` object for details on how you can use it.

**Warning**

This function together with other old functions will be depreciated in the future. A new set of S4 classes are implemented to replace old interfaces. Please use them for future development.

A few tips to keep in mind:

The variables `coltrt`, `coltime`, `colcens`, and `colvar` must be numeric. No formatting allowed.

If you receive the error "Error in solve.default(sigma): system is computationally singular; reciprocal condition number = 0" then we recommend changing the seed by re-running `analyze.KM.stepp`. If this error persists after several runs, then the program cannot provide reliable results. Please try modifying your choices of the two parameters `minpatspop(r1)` and `patspop(r2)` that define the subpopulation.

The number of permutations specified in `noperm`, the sample size, and the number of subpopulations generated will affect how long `analyze.KM.stepp` takes to execute. The results are stable if 2500 or more permutations are specified. Furthermore, varying the number of subpopulations will affect inference.

The time point selected to estimate survival in `timest` must be in the same units (e.g., months) as the `coltime` variable.

The order of the treatments in the vector `trts` must be in the same order in the vector `tlegend`.

**Note**

STEPP is an exploratory tool, with graphical features that make it easy for clinicians to interpret the results of the analysis. The method provides an opportunity to detect interactions other than those that may be apparent for example by using Cox models. Positive results should prompt the need for confirmation from other datasets investigating similar treatment comparisons. It should also be clear that STEPP is not meant to estimate specific cutpoints in the range of values of the covariate of interest, but rather to provide some indication on ranges of values where treatment effect might have a particular behavior.

STEPP considers the case in which the subpopulations are constructed according to a sliding window pattern. The larger parameter (`patspop`) determines how many patients are in each subpopulation, and the smaller parameter (`minpatspop`) determines the largest number of patients in common among consecutive subpopulations. A minimum of 80-100 patients should probably be in each subpopulation, but that is not strictly necessary. The difference (`patspop-minpatspop`) is the approximate number of patients replaced between any two subsequent subpopulations, and can be used to determine the number of subpopulations once `patspop` is fixed. The choice of the values of the parameters `patspop` and `minpatspop` to be used does change the appearance of the plot and the corresponding p-value. It is probably reasonable to experiment with a few combinations to ensure that the significance (or lack of significance) is stable with respect to that choice.

For best results, consider implementing 2500 permutations of the covariate (vector of subpopulations) to obtain a rich distribution in which to draw inference.



**Author(s)**

Wai-ki Yip, David Zahrieh, Marco Bonetti, Bernard Cole, Ann Lazar, Richard Gelber

**References**

Bonetti M, Gelber RD. Patterns of treatment effects in subsets of patients in clinical trials. *Biostatistics* 2004; 5(3):465-481.

Bonetti M, Zahrieh D, Cole BF, Gelber RD. A small sample study of the STEPP approach to assessing treatment-covariate interactions in survival data. *Statistics in Medicine* 2009; 28(8):1255-68.

**See Also**

[stwin](#), [stsubpop](#), [stmodelKM](#), [steppes](#), [stmodel](#), [stepp.win](#), [stepp.subpop](#), [stepp.KM](#), [stepp.test](#), [estimate](#), [generate](#)

Old functions to be deprecated: [stepp](#), [stepp\\_summary](#), [stepp\\_print](#), [stepp\\_plot](#), and [analyze.CumInc.stepp](#).

**Examples**

```
#GENERATE TREATMENT VARIABLE:
N <- 1000
Txassign <- sample(c(1,2), N, replace=TRUE, prob=c(1/2, 1/2))
n1 <- length(Txassign[Txassign==1])
n2 <- N - n1
#GENERATE A COVARIATE:
covariate <- rnorm(N, 55, 7)
#GENERATE SURVIVAL AND CENSORING VARIABLES ASSUMING A TREATMENT COVARIATE INTERACTION:
Entry <- sort( runif(N, 0, 5) )
SurvT1 <- .5
beta0 <- -65 / 75
beta1 <- 2 / 75
Surv <- rep(0, N)
lambda1 <- -log(SurvT1) / 4
Surv[Txassign==1] <- rexp(n1, lambda1)
Surv[Txassign==2] <- rexp(n2, (lambda1*(beta0+beta1*covariate[Txassign==2])))
EventTimes <- rep(0, N)
EventTimes <- Entry + Surv
censor <- rep(0, N)
time <- rep(0,N)
for ( i in 1:N )
{
  censor[i] <- ifelse( EventTimes[i] <= 7, 1, 0 )
  time[i] <- ifelse( EventTimes[i] < 7, Surv[i], 7 - Entry[i] )
}

#CALL analyze.KM.stepp to analyze the data
# Warning: In this example, the permutations have been set to 0 to allow
# the stepp function to finish in a short amount of time. IT IS RECOMMEND
# TO USE AT LEAST 2500 PERMUTATIONS TO PROVIDE STABLE RESULTS.
output <- analyze.KM.stepp ( coltrt=Txassign, coltime=time,
  colcens=censor, colvar=covariate, trts=c(1,2), patpop=300,
  minpatpop=200, timest=4, noperm=0, ncex=0.70, legendy=30,
```

```
pline=-2.5, color=c("red", "black"),
xlabel="Subpopulations by Median Age", ylabel="4-year Disease-Free Survival",
tlegend=c("Treatment A", "Treatment B"), nlas=3, pointwise=FALSE)
```

---

aspirin

*The aspirin data set.*


---

### Description

The "aspirin" data set was obtained with permission from the Polyp Prevention Study Group. The data are from a randomized clinical trial comparing two dosages of daily aspirin (81 mg or 325 mg/day) versus placebo for the prevention of colorectal adenomas among people having a prior history of these lesions. The study randomized a total of 1,121 participants to the three treatment groups. After an approximately three-year treatment period, 1,084 participants underwent follow-up colonoscopy. The primary endpoint of the trial was the occurrence of one or more large-bowel adenomas. Secondary endpoints included the occurrence of any advanced lesion (i.e., adenomas having high-risk characteristics or invasive cancer).

### Usage

```
data(aspirin)
```

### Format

The data set has the following columns: DOSE - Randomized aspirin dose (0=placebo); AGE - Age of the participant in years at baseline; G - Gender of the participant (M or F) AD - Occurrence of any adenoma at follow-up (0=no, 1=yes, .=missing); AL - Occurrence of any advanced lesion at follow-up(0=no, 1=yes, .=missing)

### Source

The Polyp Prevention Study Group is acknowledged for granting permission to use the data from the Aspirin/Folate Polyp Prevention study.

### References

Baron J, Cole BF, Sandler RS, et al (2003), "A Randomized Trial of Aspirin to prevent Colorectal Adenomas." *n engl j med* 2003;234:891-9.

### Examples

```
data(aspirin)

# remove cases with missing data
aspirinc <- aspirin[complete.cases(aspirin),]

# make a subset of patients with placebo and 81 mg
attach(aspirinc)
subset1 <- DOSE == 0 | DOSE == 81
```

```

aspirin1 <- aspirinc[subset1,]
detach(aspirinc)

# set up treatment assignment
trtA <- rep(0, dim(aspirin1)[1])
trtA[aspirin1[,"DOSE"] == 81] <- 1

# STEPP analysis A: placebo vs 81 mg aspirin
attach(aspirin1)
inc_win <- stepp.win(type="sliding", r1=30, r2=100)
inc_sp <- stepp.subpop(swin=inc_win, cov=AGE)

ADorLE <- as.numeric(AD==1 | AL==1)
modelA <- stepp.GLM(coltrt=trtA, trts=c(0,1), colY=ADorLE, glm="binomial", debug=0)
# Warning: In this example, the permutations have been set to 50 to allow the function
# to finish in a short amount of time. IT IS RECOMMEND TO USE AT LEAST 2500 PERMUTATIONS TO
# PROVIDE STABLE RESULTS.
steppGLMA <- stepp.test(inc_sp, modelA, nperm=50)
summary(steppGLMA)
print(steppGLMA)
plot(steppGLMA, ncex=0.70, legendy=30,
     pline=-4.5, color=c("red","black"),
     xlabel="Subpopulations by Median Age", ylabel="Risk",
     tlegend=c("Placebo", "81 mg aspirin"), nlas=3, pointwise=FALSE, noyscale=TRUE, rug=FALSE)

detach(aspirin1)

```

---

bigCI

*The BIG 1-98 trial dataset for cumulative incidence STEPP.*


---

## Description

This data set contains 2,685 patients in the Breast International Group (BIG) 1-98 randomized clinical trial. The BIG 1-98 is a Phase III clinical trial of 8,010 post menopausal women with hormone-receptor-positive early invasive breast cancer who were randomly assigned adjuvant therapy of letrozole or tamoxifen. Patterns of treatment effects for varying levels of the biomarker Ki-67 labeling index, a measure of cell proliferation, were analyzed using STEPP. The STEPP analysis showed that letrozole was more effective than tamoxifen for patients with tumors expressing the highest levels of the Ki-67 labeling index. The two treatment arms are letrozole and tamoxifen.

## Usage

```
data(bigCI)
```

## Format

There are four columns of numeric values: trt (treatment group), time (time to event), event (competing event types), and ki67 (continuous measurement of biomarker Ki-67).

## Source

The Breast International Group (BIG) 1-98 Steering Committee and the International Breast Cancer Study Group (IBCSG) are acknowledged for permission to use the data from the BIG 1-98 trial.

## References

Lazar A, Cole B, Bonetti M, Gelber R (2010), "Evaluation of treatment-effect heterogeneity using biomarkers measured on a continuous scale: subpopulation treatment effect pattern plot." *J Clin Oncol*, 28(29), 4539-44.

Viale G et al (2008), "Prognostic and predictive value of centrally reviewed Ki-67 labeling index in postmenopausal women with endocrine-responsive breast cancer: results from Breast International Group Trial 1-98 comparing adjuvant tamoxifen and letrozole." *J Clin Oncol*, 28(34), 5569-75.

## Examples

```
data(bigCI)

rxgroup <- bigCI$trt
time <- bigCI$time
evt <- bigCI$event
cov <- bigCI$ki67

# analyze using Cumulative Incidence method with
# sliding window size of 150 patients and a maximum of 50 patients in common
#
swin <- new("stwin", type="sliding", r1=50, r2=150) # create a sliding window
subp <- new("stsubpop") # create subpopulation object
subp <- generate(subp, win=swin, covariate=cov) # generate the subpopulations
summary(subp) # summary of the subpopulations

# create a stepp model using Cumulative Incidences to analyze the data
#
smodel <- new("stmodelCI", coltrt=rxgroup, trts=c(1,2), coltime=time, coltype=evt, timePoint=4)

statCI <- new("steppes") # create a test object based on subpopulation and window
statCI <- estimate(statCI, subp, smodel) # estimate the subpopulation results
# Warning: In this example, the permutations have been set to 0 to allow the function
# to finish in a short amount of time. IT IS RECOMMEND TO USE AT LEAST 2500 PERMUTATIONS TO
# PROVIDE STABLE RESULTS.
statCI <- test(statCI, nperm=0) # permutation test with 0 iterations

print(statCI) # print the estimates and test statistics
plot(statCI, ncex=0.65, legendy=30, pline=-15.5, color=c("blue","gold"),
      pointwise=FALSE,
      xlabel="Median Ki-67 LI in Subpopulation (% immunoreactivity)",
      ylabel="4-year Cumulative Incidence",
      tlegend=c("Tamoxifen", "Letrozole"), nlas=3)
```

---

`bigKM`*The BIG 1-98 trial dataset for Kaplan-Meier STEPP.*

---

**Description**

This data set contains 2,685 patients in the Breast International Group (BIG) 1-98 randomized clinical trial. The BIG 1-98 is a Phase III clinical trial of 8,010 post menopausal women with hormone-receptor-positive early invasive breast cancer who were randomly assigned adjuvant therapy of letrozole or tamoxifen. Patterns of treatment effects for varying levels of the biomarker Ki-67 labeling index, a measure of cell proliferation, were analyzed using STEPP. The STEPP analysis showed that letrozole was more effective than tamoxifen for patients with tumors expressing the highest levels of the Ki-67 labeling index. The two treatment arms are letrozole and tamoxifen.

**Usage**

```
data(bigKM)
```

**Format**

There are four columns of numeric values: `trt` (treatment group), `time` (time to event), `event` (competing event types), and `ki67` (continuous measurement of biomarker Ki-67).

**Source**

The Breast International Group (BIG) 1-98 Steering Committee and the International Breast Cancer Study Group (IBCSG) are acknowledged for permission to use the data from the BIG 1-98 trial.

**References**

Lazar A, Cole B, Bonetti M, Gelber R (2010), "Evaluation of treatment-effect heterogeneity using biomarkers measured on a continuous scale: subpopulation treatment effect pattern plot." *J Clin Oncol*, 28(29), 4539-44.

Viale G et al (2008), "Prognostic and predictive value of centrally reviewed Ki-67 labeling index in postmenopausal women with endocrine-responsive breast cancer: results from Breast International Group Trial 1-98 comparing adjuvant tamoxifen and letrozole." *J Clin Oncol*, 28(34), 5569-75.

**Examples**

```
data(bigKM)
```

```
rxgroup <- bigKM$trt
time <- bigKM$time
evt <- bigKM$event
cov <- bigKM$ki67
```

```
# analyze using Cumulative Incidence method with
# sliding window size of 150 patients and a maximum of 50 patients in common
#
```

```

swin <- new("stwin", type="sliding", r1=50, r2=150) # create a sliding window
subp <- new("stsubpop") # create subpopulation object
subp <- generate(subp, win=swin, covariate=cov) # generate the subpopulations
summary(subp) # summary of the subpopulations

# create a stepp model using Kaplan Meier Method to analyze the data
#
smodel <- new("stmodelKM", coltrt=rxgroup, trts=c(1,2), survTime=time, censor=evt, timePoint=4)

statKM <- new("steppes") # create a test object based on subpopulation and window
statKM <- estimate(statKM, subp, smodel) # estimate the subpopulation results
# Warning: In this example, the permutations have been set to 0 to allow the function
# to finish in a short amount of time. IT IS RECOMMEND TO USE AT LEAST 2500 PERMUTATIONS TO
# PROVIDE STABLE RESULTS.
statKM <- test(statKM, nperm=0) # permutation test with 0 iterations

print(statKM) # print the estimates and test statistics
plot(statKM, ncex=0.65, legendy=30, pline=-15.5, color=c("blue","gold"),
      pointwise=FALSE,
      xlabel="Median Ki-67 LI in Subpopulation (% immunoreactivity)",
      ylabel="4-year Disease Free Survival",
      tlegend=c("Taxmoxifen", "Letrozole"), nlas=3)

```

---

estimate

*The standard generic function for all estimate methods*

---

### Description

The default generic function for estimate methods for all stepp models classes and the steppes class.

For detail, please refer to the documentation in the estimate method in the S4 class: steppes.

### Author(s)

Wai-ki Yip

### See Also

[stwin](#), [stsubpop](#), [stmodelKM](#), [stmodelCI](#), [stmodelGLM](#), [steppes](#), [stmodel](#), [stepp.win](#), [stepp.subpop](#), [stepp.KM](#), [stepp.CI](#), [stepp.GLM](#), [stepp.test](#), [generate](#)

---

gen.tailwin	<i>Utility function to generate tail-oriented window</i>
-------------	--

---

### Description

Utility function to generate tail-oriented windows inputs given the approximate number of subpopulations desired.

### Usage

```
gen.tailwin(covariate, nsub, dir="LE")
```

### Arguments

covariate	covariate values
nsub	number of tail-oriented subpopulations to be generated
dir	"LE" (default) or "GE" - subpopulations with covariate values less than or equal/greater than or equal to the generated values

### Details

Use this together with the constructor, `stepp.win`, to generate tail-oriented windows.

### Value

It returns a list with fields: `$v` - vector of covariate values to be used in the constructor `stepp.win`.  
`$np` - vector of subpopulation size associate with each tail-oriented window defined by `$v`.

### Author(s)

Wai-ki Yip

### See Also

[stwin](#), [stepp.win](#)

---

generate	<i>The standard generic function for the generate method in stsubpop class</i>
----------	--

---

### Description

The default generic function for the generate method for stsubpop class.

For detail, please refer to the documentation in the generate method in the S4 class: stsubpop.

### Author(s)

Wai-ki Yip

### See Also

[stwin](#), [stsubpop](#), [stmodelKM](#), [stmodelCI](#), [stmodelGLM](#), [steppes](#), [stmodel](#), [stepp.win](#), [stepp.subpop](#), [stepp.KM](#), [stepp.CI](#), [stepp.GLM](#), [stepp.test](#), [estimate](#)

---

stepp	<i>Analyze survival or competing risks data</i>
-------	---

---

### Description

This method will be deprecated in the future. Please use S4 classes (stmodelCI, stmodelKM) and corresponding constructors (stepp.CI and stepp.KM) for future development.

A method to explore the treatment-effect interactions in either survival or competing risks data arising from two treatment arms of a clinical trial. A permutation distribution approach to inference is implemented, based on permuting covariate values within each treatment group. The statistical significance of observed heterogeneity of treatment effects is calculated using permutation tests:

- 1) for the maximum difference between each subpopulation effect and the overall population treatment effect or supremum based test statistic;
- 2) for the difference between each subpopulation effect and the overall population treatment effect, which resembles the chi-square statistic.

### Usage

```
stepp(trttype, coltrt, coltime, colcens=0, coltype=0, colvar, trts,
      patpop, minpatpop, timest, noperm)
```



**Arguments**

<code>trttype</code>	type of analysis methods to use: "KM" for Kaplan-Maier and "CI" for Cumulative Incidence
<code>coltrt</code>	the treatment variable
<code>coltime</code>	the time to event variable
<code>colcens</code>	the censoring variable. If specified, the KM method will be used
<code>coltype</code>	variable with distinct codes for different causes of failure where <code>coltype=0</code> for censored observations; <code>coltype=1</code> for event of interest; <code>coltype=2</code> for other causes of failure. If specified, the cumulative incidence method will be used.
<code>colvar</code>	the covariate of interest
<code>trts</code>	a vector containing the codes for the 2 treatment arms, 1st and 2nd treatment arms, respectively
<code>patpop</code>	larger parameter( <code>r2</code> ) for subpopulation construction that determines how many patients are in each subpopulation
<code>minpatpop</code>	smaller parameter( <code>r1</code> ) for subpopulation construction that determines the largest number of patients in common among consecutive subpopulations
<code>timest</code>	timepoint to estimate survival
<code>noperm</code>	the desired number of permutations; must be 0 or above

**Details**

A statistical method to explore treatment by covariate interactions in survival or competing risks data arising from two treatment arms of a clinical trial. The method is based on constructing overlapping subpopulations of patients with respect to a covariate of interest, and in observing the pattern of the treatment effects estimated across subpopulations. A plot of these treatment effects is called STEPP, or Subpopulation Treatment Effect Pattern Plot. STEPP uses the permutation distribution based approach for inference.

One can explore the window parameters without invoking the permutation analysis by setting `noperm` to 0. In that case, `pvalue` and the covariance matrix will not be available.

We acknowledge Robert J. Gray for permitting us to use the `cmprsk` package.

**Value**

`stepp` does all the computation and analysis but does not generate any Subpopulation Treatment Effect Pattern Plot (STEPP). A `stepes` object is returned and the user can use `stepp_summary`, `stepp_print`, or `stepp_plot` to display the information and to generate the plots for further analysis.

**Warning**

This function together with other old functions will be depreciated in the future. A new set of S4 classes are implemented to replace old interfaces. Please use them for future development.

A few tips to keep in mind:

The variables `coltrt`, `coltime`, `coltype`, and `colvar` must be numeric. No formatting allowed.

If you receive the error "Error in solve.default(sigma): system is computationally singular; reciprocal condition number = 0" then we recommend changing the seed by re-running stepp. If this error persists after several runs, then the program cannot provide reliable results. Please try modifying your choices of the two parameters minpatspop(r1) and patspop(r2) that define the subpopulation.

The number of permutations specified in noperm, the sample size, and the number of subpopulations generated will affect how long stepp takes to execute. The results are stable if 2500 or more permutations are specified. Furthermore, varying the number of subpopulations will affect inference.

The time point selected to estimate survival in timest must be in the same units (e.g., months) as the coltime variable.

The order of the treatments in the vector trts must be in the same order in the vector tlegend.

### Note

STEPP is an exploratory tool, with graphical features that make it easy for clinicians to interpret the results of the analysis. Positive results should prompt the need for confirmation from other datasets investigating similar treatment comparisons. It should also be clear that STEPP is not meant to estimate specific cutpoints in the range of values of the covariate of interest, but rather to provide some indication on ranges of values where treatment effect might have a particular behavior.

STEPP considers the case in which the subpopulations are constructed according to a sliding window pattern. The larger parameter (patspop) determines how many patients are in each subpopulation, and the smaller parameter (minpatspop) determines the largest number of patients in common among consecutive subpopulations. A minimum of 80-100 patients should be in each subpopulation, but that is not strictly necessary. The difference (patspop-minpatspop) is the approximate number of patients replaced between any two subsequent subpopulations, and can be used to determine the number of subpopulations once patspop is fixed. The choice of the values of the parameters patspop and minpatspop to be used does change the appearance of the plot and the corresponding p-value. It is probably reasonable to experiment with a few combinations to ensure that the significance (or lack of significance) is stable with respect to that choice.

For best results, consider implementing 2500 permutations of the covariate (vector of subpopulations) to obtain a rich distribution in which to draw inference.

### Author(s)

Ann Lazar, Wai-ki Yip, David Zahrieh, Bernard Cole, Marco Bonetti, Richard Gelber

### References

- Bonetti M, Gelber RD. Patterns of treatment effects in subsets of patients in clinical trials. *Bio-statistics* 2004; 5(3):465-481.
- Bonetti M, Zahrieh D, Cole BF, Gelber RD. A small sample study of the STEPP approach to assessing treatment-covariate interactions in survival data. *Statistics in Medicine* 2009; 28(8):1255-68.
- Lazar AA, Cole BF, Bonetti M, Gelber RD. Evaluation of treatment-effect heterogeneity using biomarkers measured on a continuous scale: subpopulation treatment effect pattern plot. *Journal of Clinical Oncology*, 2010; 28(29): 4539-4544.

**See Also**

[stwin](#), [stsubpop](#), [stmodelKM](#), [stmodelCI](#), [steppes](#), [stmodel](#), [stepp.win](#), [stepp.subpop](#), [stepp.KM](#), [stepp.CI](#), [stepp.test](#), [estimate](#), [generate](#),

Old functions to be deprecated: [stepp\\_summary](#), [stepp\\_print](#), [stepp\\_plot](#), [analyze.KM.stepp](#) and [analyze.CumInc.stepp](#).

**Examples**

```
#GENERATE TREATMENT VARIABLE:
n <- 1000 # set the sample size
mu <- 0 # set the mean and sd of the covariate
sigma <- 1

beta0 <- log(-log(0.5)) # set the intercept for the log hazard
beta1 <- -0.2 # set the slope on the covariate
beta2 <- 0.5 # set the slope on the treatment indicator
beta3 <- 0.7 # set the slope on the interaction

prob2 <- 0.2 # set the proportion type 2 events
cprob <- 0.3 # set the proportion censored

set.seed(7775432) # set the random number seed
covariate <- rnorm(n,mean=mu,sd=sigma) # generate the covariate values
Txassign <- rbinom(n,1,0.5) # generate the treatment indicator
x3 <- covariate*Txassign # compute interaction term
# compute the hazard for type 1 event
lambda1 <- exp(beta0+beta1*covariate+beta2*Txassign+beta3*x3)
lambda2 <- prob2*lambda1/(1-prob2) # compute the hazard for the type 2 event
# compute the hazard for censoring time
lambda0 <- cprob*(lambda1+lambda2)/(1-cprob)
t1 <- rexp(n,rate=lambda1) # generate the survival time for type 1 event
t2 <- rexp(n,rate=lambda2) # generate the survival time for type 2 event
t0 <- rexp(n,rate=lambda0) # generate the censoring time
time <- pmin(t0,t1,t2) # compute the observed survival time
type <- rep(0,n)
type[(t1 < t0)&(t1 < t2)] <- 1
type[(t2 < t0)&(t2 < t1)] <- 2

# Call stepp to analyze the data
# Warning: In this example, the permutations have been set to 0 to allow the stepp function
# to finish in a short amount of time. IT IS RECOMMEND TO USE AT LEAST 2500 PERMUTATIONS TO
# PROVIDE STABLE RESULTS.
steppCI <- stepp("CI", coltrt=Txassign, trts=c(0,1), coltime=time, coltype=type,
  colvar=covariate, patpop=300, minpatpop=200, timest=1.0, noperm=0)

stepp_summary(steppCI)
stepp_print(steppCI)
stepp_plot(steppCI,
  ncex=0.70,legendy=30,pline=-2.5,color=c("red", "black"),
  xlabel="Subpopulations by Median Age",ylabel="4-year Cancer Relapse",
  tlegend=c("Treatment A", "Treatment B"), nlas=3,pointwise=FALSE)
```

---

`stepp.CI`*The constructor to create the stmodelCI object*

---

## Description

This is the constructor function for the `stmodelCI` object. This object sets up the data with a `stepp` model using competing risks method for analysis. (CI stands for Cumulative Incidence.)

The model explores the treatment-effect interactions in competing risks data arising from two or more treatment arms of a clinical trial. A permutation distribution approach to inference is implemented that permutes covariate values within a treatment group. The statistical significance of observed heterogeneity of treatment effects is calculated using permutation tests:

- 1) for the maximum difference between each subpopulation effect and the overall population treatment effect or supremum based test statistic;
- 2) for the difference between each subpopulation effect and the overall population treatment effect, which resembles the chi-square statistic.

## Usage

```
stepp.CI(coltrt, coltime, coltype, trts, timePoint)
```

## Arguments

<code>coltrt</code>	the treatment variable
<code>coltime</code>	the time to event variable
<code>coltype</code>	variable with distinct codes for different causes of failure where <code>coltype=0</code> for censored observations; <code>coltype=1</code> for event of interest; <code>coltype=2</code> for other causes of failure
<code>trts</code>	a vector containing the codes for the 2 treatment groups, 1st and 2nd treatment groups, respectively
<code>timePoint</code>	timepoint to estimate survival

## Value

It returns the `stmodelCI` object.

## Author(s)

Wai-Ki Yip

## References

Bonetti M, Gelber RD. Patterns of treatment effects in subsets of patients in clinical trials. *Bio-statistics* 2004; 5(3):465-481.

Bonetti M, Zahrieh D, Cole BF, Gelber RD. A small sample study of the STEPP approach to assessing treatment-covariate interactions in survival data. *Statistics in Medicine* 2009; 28(8):1255-68.

Lazar AA, Cole BF, Bonetti M, Gelber RD. Evaluation of treatment-effect heterogeneity using biomarkers measured on a continuous scale: subpopulation treatment effect pattern plot. *Journal of Clinical Oncology*, 2010; 28(29): 4539-4544.

## See Also

[stwin](#), [stsubpop](#), [stmodelKM](#), [stmodelCI](#), [stmodelGLM](#), [stepes](#), [stmodel](#), [stepp.win](#), [stepp.subpop](#), [stepp.KM](#), [stepp.GLM](#), [stepp.test](#), [estimate](#), [generate](#)

## Examples

```
##
n <- 1000 # set the sample size
mu <- 0 # set the mean and sd of the covariate
sigma <- 1

beta0 <- log(-log(0.5)) # set the intercept for the log hazard
beta1 <- -0.2 # set the slope on the covariate
beta2 <- 0.5 # set the slope on the treatment indicator
beta3 <- 0.7 # set the slope on the interaction

prob2 <- 0.2 # set the proportion type 2 events
cprob <- 0.3 # set the proportion censored

set.seed(7775432) # set the random number seed
covariate <- rnorm(n,mean=mu,sd=sigma) # generate the covariate values
Txassign <- rbinom(n,1,0.5) # generate the treatment indicator
x3 <- covariate*Txassign # compute interaction term
# compute the hazard for type 1 event
lambda1 <- exp(beta0+beta1*covariate+beta2*Txassign+beta3*x3)
lambda2 <- prob2*lambda1/(1-prob2) # compute the hazard for the type 2 event
# compute the hazard for censoring time
lambda0 <- cprob*(lambda1+lambda2)/(1-cprob)
t1 <- rexp(n,rate=lambda1) # generate the survival time for type 1 event
t2 <- rexp(n,rate=lambda2) # generate the survival time for type 2 event
t0 <- rexp(n,rate=lambda0) # generate the censoring time
time <- pmin(t0,t1,t2) # compute the observed survival time
type <- rep(0,n)
type[(t1 < t0)&(t1 < t2)] <- 1
type[(t2 < t0)&(t2 < t1)] <- 2

# create the stepp model object to analyze the data using Cumulative Incidence approach
x <- stepp.CI(coltrt=Txassign, trts=c(0,1), coltime=time, coltype=type, timePoint=1.0)
```

---

stepp.edge	<i>The method performs an edge analysis on the STEPP GLM model estimate objects.</i>
------------	--

---

### Description

Perform an edge analysis on the STEPP GLM model estimate objects.

### Usage

```
stepp.edge(est, criteria, j=2, boot=0, seed=17, showstatus=TRUE, debug=0)
```

### Arguments

est	a STEPP estimate object.
criteria	criteria to be used to identify the cut point; abs or rel scale and by how much.
j	number of treatment, default to 2
boot	perform a bootstrap analysis, default is none (0).
seed	seed used for bootstrap, default is 17.
showstatus	show the status of bootstrap, default is TRUE.
debug	internal debug flag, default is 0

### Details

The criteria argument is a list with three elements:

trtid - the treatment id;

scale - "A" for absolute scale or "R" for relative scale;

threshold - amount in either absolute or relative scale that would consider a jump.

e.g. `crit <- list(trtid=1, scale="A", threshold=-0.03)`

Only support for STEPP GLM models for now. Bootstrap is computational time intensive but it will provide you with a quantification of the variability of the edge identified.

### Value

It returns the result of the identified edge with the STEPP subpopulations.

### Author(s)

Wai-ki Yip

### See Also

[stwin](#)

stepp.GLM

*The constructor to create the stmodelGLM object***Description**

This is the constructor function for stmodelGLM object. Three kinds of GLMs are supported at this time: gaussian with identity link, binomial with logit link and Poisson with log link.

**Usage**

```
stepp.GLM(coltrt, trts, colY, MM, glm, debug)
```

**Arguments**

coltrt	the treatment variable
trts	a vector containing the codes for the 2 treatment arms, 1st and 2nd treatment groups, respectively
colY	a vector containing the outcome
MM	a model matrix for additional covariates; default is NULL no logical values or factors allowed these values need to be converted to numeric with some encoding scheme
glm	the glm to be used for analysis: "gaussian", "binomial", "poisson"
debug	for internal debugging use only

**Value**

It returns a stmodelGLM object.

**Author(s)**

Wai-Ki Yip

**References**

Yip WK, Bonetti M, Cole BF, Barcella W, Wang XV, Lazar A and Gelber R (2016), "STEPP-Subpopulation Analysis for Continuous, Binary and Count Outcomes", Clinical Trials 2016 August ; 13(4): 382-290, doi:10.1177/1740774516643297.

**See Also**

[stwin](#), [stsubpop](#), [stmodelKM](#), [stmodelCI](#), [stmodelGLM](#), [steppes](#), [stmodel](#), [stepp.win](#), [stepp.subpop](#), [stepp.KM](#), [stepp.CI](#), [stepp.test](#), [estimate](#), [generate](#)

**Examples**

```
#
# see the example for the aspirin data for an example for a binomial glm model
```

---

`stepp.KM`*The constructor to create the stmodelKM object*

---

**Description**

This is the constructor function for the `stmodelKM` object. This object sets up the data with a `stepp` model using the Kaplan-Meier method for analysis.

The model explores the treatment-covariate interactions in survival data arising from two treatment arms of a clinical trial. The treatment effects are measured using survival functions at a specified time point estimated from the Kaplan-Meier method and the hazard ratio based on observed-minus-expected estimation. A permutation distribution approach to inference is implemented, based on permuting the covariate values within each treatment group. The statistical significance of observed heterogeneity of treatment effects is calculated using permutation tests:

- 1) for the maximum difference between each subpopulation effect and the overall population treatment effect or supremum based test statistic;
- 2) for the difference between each subpopulation effect and the overall population treatment effect, which resembles the chi-square statistic.

**Usage**

```
stepp.KM(coltrt, survTime, censor, trts, timePoint)
```

**Arguments**

<code>coltrt</code>	the treatment variable
<code>survTime</code>	the time to event variable
<code>censor</code>	the censor variable
<code>trts</code>	a vector containing the codes for the 2 treatment arms, 1st and 2nd treatment groups, respectively
<code>timePoint</code>	timepoint to estimate survival

**Value**

It returns the `stmodelKM` object.

**Author(s)**

Wai-Ki Yip

**References**

- Bonetti M, Gelber RD. Patterns of treatment effects in subsets of patients in clinical trials. *Bio-statistics* 2004; 5(3):465-481.
- Bonetti M, Zahrieh D, Cole BF, Gelber RD. A small sample study of the STEPP approach to assessing treatment-covariate interactions in survival data. *Statistics in Medicine* 2009; 28(8):1255-68.



**See Also**

[stwin](#), [stsubpop](#), [stmodelKM](#), [stmodelCI](#), [stmodelGLM](#), [steppes](#), [stmodel](#), [stepp.win](#), [stepp.subpop](#), [stepp.CI](#), [stepp.GLM](#), [stepp.test](#), [estimate](#), [generate](#)

**Examples**

```
#GENERATE TREATMENT VARIABLE:
N <- 1000
Txassign <- sample(c(1,2), N, replace=TRUE, prob=c(1/2, 1/2))
n1 <- length(Txassign[Txassign==1])
n2 <- N - n1
#GENERATE A COVARIATE:
covariate <- rnorm(N, 55, 7)
#GENERATE SURVIVAL AND CENSORING VARIABLES ASSUMING A TREATMENT COVARIATE INTERACTION:
Entry <- sort( runif(N, 0, 5) )
SurvT1 <- .5
beta0 <- -65 / 75
beta1 <- 2 / 75
Surv <- rep(0, N)
lambda1 <- -log(SurvT1) / 4
Surv[Txassign==1] <- rexp(n1, lambda1)
Surv[Txassign==2] <- rexp(n2, (lambda1*(beta0+beta1*covariate[Txassign==2])))
EventTimes <- rep(0, N)
EventTimes <- Entry + Surv
censor <- rep(0, N)
time <- rep(0,N)
for ( i in 1:N )
  {
    censor[i] <- ifelse( EventTimes[i] <= 7, 1, 0 )
    time[i] <- ifelse( EventTimes[i] < 7, Surv[i], 7 - Entry[i] )
  }

modKM <- stepp.KM( coltrt=Txassign, survTime=time, censor=censor, trts=c(1,2), timePoint=4)
```

---

stepp.rnote

*The method to print the release note for STEPP.*


---

**Description**

This method will print the current stepp version and the corresponding release note.

**Usage**

```
stepp.rnote()
```

**Author(s)**

Wai-ki Yip, Marco Bonetti, Bernard Cole, Ann Lazar, Victoria Xin Wang, Richard Gelber

**Examples**

```
stepp.rnote()
```

---

stepp.subpop	<i>The constructor to create the stsubpop object and generate the subpopulations based on the specified stepp window and covariate of interest</i>
--------------	--

---

**Description**

This is the constructor function to create a stepp subpopulation object. In addition, it will also generate the stepp subpopulations based on the stepp window and covariate specified.

**Usage**

```
stepp.subpop(swin, cov)
```

**Arguments**

swin	the stepp window set up for the analysis
cov	the covariate of interest

**Value**

It returns the stsubpop object with subpopulations generated.

**Author(s)**

Wai-Ki Yip

**See Also**

[stwin](#), [stsubpop](#), [stmodelKM](#), [stmodelCI](#), [stmodelGLM](#), [steppes](#), [stmodel](#), [stepp.win](#), [stepp.KM](#), [stepp.CI](#), [stepp.GLM](#), [stepp.test](#), [estimate](#), [generate](#)

**Examples**

```
# create a stepp window
win1 <- stepp.win(type="sliding", r1=5,r2=10)

# generate the covariate of interest
Y <- rnorm(100)

# create and generate the stepp subpopulation
sp <- stepp.subpop(swin=win1, cov=Y)
```

---

stepp.test	<i>The constructor to generate a complete steppes object with effect estimates and test statistics</i>
------------	--

---

### Description

This is a constructor function for the steppes object. In addition, it estimates all the effects of each subpopulations, performs permutation tests and generates all covariance matrices and statistics.

### Usage

```
stepp.test(subpop, model, nperm, showstatus = TRUE)
```

### Arguments

subpop	the filled stepp subpopulation object
model	the model of the data to be used for stepp analysis
nperm	number of permutation used in the permutation test
showstatus	display the progress bar for the permutation test; default is TRUE

### Details

Permutation tests for all the statistics are done (see ref below). For best results, considering using 2500 permutations to obtain a rich distribution from which to draw inference.

### Value

It returns a steppes object with all effects estimates, covariance matrices and statistics.

### Author(s)

Wai-ki Yip

### References

Bonetti M, Zahrieh D, Cole BF, Gelber RD. A small sample study of the STEPP approach to assessing treatment-covariate interactions in survival data. *Statistics in Medicine* 2009; 28(8):1255-68.

### See Also

[stwin](#), [stsubpop](#), [stmodelKM](#), [stmodelCI](#), [stmodelGLM](#), [steppes](#), [stmodel](#), [stepp.win](#), [stepp.subpop](#), [stepp.KM](#), [stepp.CI](#), [stepp.GLM](#), [estimate](#), [generate](#)

**Examples**

```

data(bigCI)

rxgroup <- bigCI$trt
time    <- bigCI$time
evt     <- bigCI$event
cov     <- bigCI$ki67

#
# using constructor functions
swin    <- stepp.win(type="sliding", r1=50, r2=150)
subp    <- stepp.subpop(swin=swin, cov=cov)
summary(subp)

smodel <- stepp.CI(coltrt=rxgroup, trts=c(1,2), coltime=time, coltype=evt, timePoint=4)
# Warning: In this example, the permutations have been set to 0 to allow the function
# to finish in a short amount of time. IT IS RECOMMEND TO USE AT LEAST 2500 PERMUTATIONS TO
# PROVIDE STABLE RESULTS.
statCI <- stepp.test(subpop=subp, model=smodel, nperm=0)

```

---

stepp.win

*The constructor to create the stepp window object*


---

**Description**

This is the constructor function to create a stepp window object.

**Usage**

```
stepp.win(type, r1, r2, basedon="all")
```

**Arguments**

type	type of stepp window; "sliding" or "tail-oriented"
r1	sliding window: minimum number of patients allowed in overlapping windows; tail-oriented window: a vector of maximum covariate values for each subpopulation
r2	sliding window: size of subpopulation in each window; tail-oriented window: a vector of minimum covariate values for each subpopulation
basedon	what the window is based on - "all" (default)

**Details**

This is the functional interface to construct a stepp window object besides using `new("stwin", ...)`. A STEPP window specifies a pattern of subpopulation you would like to explore. There are two kinds of patterns: "sliding window" and "tail-oriented window". Both patterns are specified through a set of (r1, r2) values: 1. for sliding windows, r1 is the minimum number of patients allowed in overlapping windows and r2 is the approximate size of subpopulation in each window; 2. for tail-oriented window, r1 is a vector of maximum covariate value for each subpopulation from the minimum value of the entire subpopulation, and r2 is a vector of minimum covariate values for each subpopulation from the maximum value of the window. The utility function, `gen.tailwin`, can be used to generate these two vectors based on the number of desired subpopulations.

Both pattern are based on all patients.

**Author(s)**

Wai-ki Yip

**See Also**

[stwin](#), [stsubpop](#), [stmodelKM](#), [stmodelCI](#), [stmodelGLM](#), [steppes](#), [stmodel](#), [stepp.subpop](#), [stepp.KM](#), [stepp.CI](#), [stepp.GLM](#), [stepp.test](#), [estimate](#), [generate](#)

**Examples**

```
# create a stepp window object of type "sliding",
# subpopulation size is 200 and allows only 50 patients
# between overlapping windows
mywin <- stepp.win(type="sliding", r1=50, r2=200)

# print a summary of the stepp window object
summary(mywin)
```

---

steppes-class

*Class "steppes"*

---

**Description**

This is the stepp object for stepp results. It keeps track of all the estimates, covariance matrices and the test statistics

**Value**

The new method returns the steppes object.

**Objects from the Class**

Objects can be created by calls of the form `new("steppes", ...)` or by the constructor function `stepp.test`.

**Slots**

- subpop:** Object of class "stsubpop"  
the filled stepp subpopulation object
- model:** Object of class "stmodel"  
the model of the data to be used for stepp analysis
- effect:** Object of class "ANY"  
effect estimates of each subpopulation in absolute and relative scales  
list return from the estimate methods of various stepp models  
see documentation in various stepp models for details on what is in the list
- result:** Object of class "ANY"  
permutation and gee test results and various covariance matrices  
list return from the test methods of various stepp models  
see documentation in various stepp models for details on what is in the list
- nperm:** Object of class "numeric"  
number of permutation for the permutation test; default is 2500

**Methods**

- estimate** signature(.Object = "steppes", sp, model):  
estimate the effect in absolute and relative scale of the overall and each subpopulation for the specified subpopulation using the specified model.
- plot** signature(.Object = "steppes"):  
generate the three stepp plots
- print** signature(.Object = "steppes", estimate=TRUE, cov=TRUE, test=TRUE):  
print the estimates, covariance matrices and statistics from the stepp analysis
- summary** signature(.Object = "steppes"):  
produce a summary of the steppes object
- test** signature(.Object = "steppes", nperm=100, showstatus=TRUE):  
perform the permutation tests and obtain various statistics. Number of permutation is default to 100 and status bar to show.

**Note**

The plot function for steppes class generates 3 plots at once. If you are using R studio for development, you can only get the last plot as R studio only allows one graphical device. There is a simple workaround. By writing the plots to pdf files in your working directory, you can display them outside of R studio.

**Author(s)**

Wai-Ki Yip

**See Also**

[stwin](#), [stsubpop](#), [stmodelKM](#), [stmodelCI](#), [stmodelGLM](#), [stmodel](#), [stepp.win](#), [stepp.subpop](#), [stepp.KM](#), [stepp.CI](#), [stepp.GLM](#), [stepp.test](#), [estimate](#), [generate](#)

**Examples**

```
showClass("steppes")
```

---

stepp\_plot

*A function to generate the stepp plots*


---

**Description**

This function will be deprecated in the future. Please use S4 classes and its generic function e.g. summary, print and plot for future development.

A method to generate the 3 stepp plots for users to examine the treatment-covariate interactions in various models data arising from two treatment arms of a clinical trial. Three plots are generated:

1. effect estimates of both treatments against the median of each subpopulation
2. effect differences (in absolute scale) between the two treatments against the median of each subpopulation.
3. effect ratios (in relative scale) between the two treatments against the median of each subpopulation.

**Usage**

```
stepp_plot(x, legendy = 30, pline = -2.5, color = c("red", "black"),
  ylabel= "Specify Timepoint & Endpoint", xlabel="Subpopulations by Median Covariate",
  ncex = 0.7, tlegend=c("Specify 1st Treatment", "Specify 2nd Treatment"),
  nlas = 0, alpha = 0.05, pointwise = FALSE, diff = TRUE, ci = TRUE, pv = TRUE,
  showss = TRUE, ylimit=c(0,100,-100,100,0,3), dev="", together=FALSE,
  noyscale=FALSE, at=NA, subplot=FALSE)
```

**Arguments**

x	the steppes object returned from stepp, analyze.KM.stepp or analyze.CumInc.stepp
legendy	optional - the vertical location of the legend according to the units on the y-axis; default is 30
pline	optional - specify the vertical location of the p-value, that is, on which MARGIN line, starting at 0 counting outwards; default is -2.5
color	optional - a vector containing the line colors for the 1st and 2nd treatment, respectively; default is "red" and "black"
ylabel	optional - specify the label for the y-axis; default is "Specify Timepoint & Endpoint"
xlabel	optional - specify the label for the x-axis; default is "Subpopulations by Median Covariate"
ncex	optional - specify the size of the text for the sample size annotation, that is, the character expansion factor; default is 0.7
tlegend	optional - a vector containing the treatment labels, 1st and 2nd treatment, respectively; default is c("Specify 1st Treatment", "Specify 2nd Treatment")

nlas	optional - specify the las paramter (0,1,2,3) to determine the orientation of the sample size annotation; default is 0
alpha	optional - specify the significance level; default is 0.05
pointwise	optional - specify pointwise confidence intervals (pointwise=TRUE), or confidence bands; default is FALSE
diff	optional - specify if you want just the first plot; default is TRUE (all three plots)
ci	optional - specify if you want to display the conf. interval or band; default is TRUE
pv	optional - pvalue will be displayed in the plots; FALSE: pvalue will not be displayed in the plots; default is TRUE
showss	optional - specify the label for the x-axis optional - show the sample size; FALSE: sample size will not be shown in the plots; default is TRUE
ylimit	optional - pvalue will be displayed in the plots; FALSE: pvalue will not be displayed in the plots; default is TRUE
dev	optional - output device control. Output the plots to the specified output format. postscript for .ps; eps (encapsulated postscript) for .eps; pdf for .pdf; png for .png; bmp for .bmp; tiff for .tif and jpeg for .jpeg. The filenames are always SteppPlot1, SteppPlot2 and SteppPlot3 in the R working directory; default is ""
together	optional - output the plots to a single file instead of 3 separate files; default is FALSE
noyscale	optional - do not scale to the y-axis; default is FALSE
at	optional - specify the horizontal position of the p-value; use together with pline; default is at the minimal value of x
subplot	optional - generate a subpopulation distribution subplot on top of the first STEPP plot; default is FALSE (no subplot)

### Details

This is the function to generate three stepp plots for user to explore treatment-covariate interactions in various models data arising from two treatment arms of a clinical trial. The output is usually directed to the R console output and will appear in separate windows. You can also direct the plots to various files in different formats: postscript for .ps; eps (encapsulated postscript) for .eps; pdf for .pdf; png for .png; bmp for .bmp; tiff for .tif and jpeg for .jpeg through the use of the dev parameter. The filenames are always SteppPlot1, SteppPlot2 and SteppPlot3 in the R working directory. You can also direct the plots to one file only by setting the together parameter to TRUE.

Through these plots, the user can examine the differences in effects (either in absolute or relative scale) with respect to each subpopulation.

This is mainly a graphics function. The STEPP analysis is done. Most of the parameters are for graphics control so that one can customize the plots for presentation purposes.

### Warning

This function together with other old functions will be depreciated in the future. A new set of S4 classes are implemented to replace old interfaces. Please use them for future development.



**Author(s)**

Wai-ki Yip, David Zahrieh, Marco Bonetti, Bernard Cole, Ann Lazar, Richard Gelber

**See Also**

The S4 classes: stwin, stsubpop, stmodelKM, stmodelCI, stmodelCOX, stmodelGLM, and steppes. Old functions to be deprecated: stepp, stepp\_summary, stepp\_print, analyze.KM.stepp and analyze.CumInc.stepp.

**Examples**

```
# see example in the documentation for the function stepp.
```

---

stepp_print	<i>The function to print the estimate, covariance matrices and test statistics.</i>
-------------	---

---

**Description**

This function will be deprecated in the future. Please use S4 classes and generic functions summary, print and plot for future development.

A method to print three essential information resulting from the STEPP analysis.

**Usage**

```
stepp_print(x, estimate=TRUE, cov=TRUE, test=TRUE)
```

**Arguments**

x	a steppes object returned from stepp, analyze.KM.stepp or analyze.CumInc.stepp function
estimate	whether to print the effect estimates; default to yes
cov	whether to print the covariance matrices; default to yes
test	whether to print the test statistics; default to yes

**Details**

The STEPP analysis produces three important pieces of information. User can decide to print them all or individually. The three pieces of information are:

1. effect estimates of each subpopulation for the two treatments, the differences in absolute scale of the effects and the ratio in relative scale of the effects.
2. covariance matrices of the differences, logratios, differences in homogeneous association and logratios in homogeneous association.
3. various permutation p values based on test statistics: supremum pvalues, homogeneous association pvalues, chisquare pvalue. Not all statistics are available for all models.

**Warning**

This function together with other old functions will be depreciated in the future. A new set of S4 classes are implemented to replace old interfaces. Please use them for future development.

**Author(s)**

Wai-ki Yip, David Zahrieh, Marco Bonetti, Bernard Cole, Ann Lazar, Richard Gelber

**See Also**

The S4 classes: stwin, stsubpop, stmodelKM, stmodelCI, stmodelCOX, stmodelGLM, and steppes.  
Old functions to be deprecated: stepp, stepp\_summary, stepp\_plot, analyze.CumInc.stepp and analyze.KM.stepp.

**Examples**

```
# see example in the documentation for the function stepp.
```

---

stepp_summary	<i>The function to produce a summary of the size and various attributes of each subpopulation</i>
---------------	---

---

**Description**

This function will be deprecated in the future. Please use S4 classes and corresponding generic functions e.g. summary, print and plot for future development.

A method to print the summary of the size and various attributes for each subpopulation used in the STEPP analysis.

**Usage**

```
stepp_summary(x)
```

**Arguments**

x	a steppes object returned from stepp, analyze.KM.stepp or analyze.CumInc.stepp function
---	---

**Warning**

This function together with other old functions will be depreciated in the future. A new set of S4 classes are implemented to replace old interfaces. Please use them for future development.

**Author(s)**

Wai-ki Yip, David Zahrieh, Marco Bonetti, Bernard Cole, Ann Lazar, Richard Gelber

**See Also**

The S4 classes: stwin, stsubpop, stmodelKM, stmodelCI, stmodelCOX, stmodelGLM, and steppes.

Old functions to be deprecated: stepp, stepp\_print, stepp\_plot, analyze.KM.stepp, and analyze.CumInc.stepp

**Examples**

```
# set example in the documentation for the function stepp.
```

---

stmodel-class	Class "stmodel"
---------------	-----------------

---

**Description**

This is the S4 virtual class of all stepp models.

**Objects from the Class**

A virtual Class: No objects may be created from it.

**Methods**

No methods defined with class "stmodel" in the signature.

**Author(s)**

Wai-Ki Yip

**See Also**

[stwin](#), [stsubpop](#), [stmodelKM](#), [stmodelCI](#), [stmodelGLM](#), [steppes](#), [stepp.win](#), [stepp.subpop](#), [stepp.KM](#), [stepp.CI](#), [stepp.GLM](#), [stepp.test](#), [estimate](#), [generate](#)

**Examples**

```
showClass("stmodel")
```

---

stmodelCI-class	Class "stmodelCI"
-----------------	-------------------

---

### Description

This is the stepp model of survival data with competing risks.

### Value

The new method returns the stmodelCI object.

The estimate method returns a list with the following fields:

model	the stepp model - "CIe"
sObs1	a vector of effect estimates of all subpopulations based on the 1st treatment
sSE1	a vector of standard errors of effect estimates of all subpopulations based on the 1st treatment
oObs1	effect estimate of the entire population based on the 1st treatment
oSE1	the standard error of the effect estimate of the entire population based on the 1st treatment
sObs2	a vector of effect estimates of all subpopulations based on the 1st treatment
sSE2	a vector of standard errors of effect estimates of all subpopulations based on the 1st treatment
oObs2	effect estimate of the entire population based on the 1st treatment
oSE2	the standard error of the effect estimate of the entire population based on the 1st treatment
skmw	Wald's statistics for the effect estimate differences between the two treatments
logHR	a vector of log hazard ratio estimate of the subpopulations comparing 1st and 2nd treatments
logHRSE	a vector of standard error of the log hazard ratio estimate of the subpopulations comparing 1st and 2nd treatments
ologHR	the log hazard ratio estimate of the entire population comparing 1st and 2nd treatments
ologHRSE	the standard error of the log hazard ratio estimate of the entire population comparing 1st and 2nd treatments
logHRw	Wald's statistics for the log hazard ratio between the two treatments

The test method returns a list with the following fields:

model	the stepp model - "CIi"
sigma	the covariance matrix for subpopulations based on effect differences
hasigma	the homogeneous association covariance matrix for subpopulations based on effect differences

HRsigma	the covariance matrix for the subpopulations based on hazard ratio
haHRsigma	the homogeneous association covariance matrix for subpopulations based on hazard ratio
pvalue	the supremum pvalue based on effect difference
chi2pvalue	the chisquare pvalue based on effect difference
hapvalue	the homogeneous association pvalue based on effect difference
HRpvalue	the supremum pvalue based on hazard ratio
haHRpvalue	the homogeneous association pvalue based on hazard ratio

### Objects from the Class

Objects can be created by calls of the form `new("stmodelCI", ...)` or by the constructor function `stepp.CI`.

### Slots

<code>coltrt</code>	Object of class "numeric" the treatment variable
<code>coltime</code>	Object of class "numeric" the time to event variable
<code>coltype</code>	Object of class "numeric" variable with distinct codes for different causes of failure where <code>coltype=0</code> for censored observations; <code>coltype=1</code> for event of interest; <code>coltype=2</code> for other causes of failure
<code>trts</code>	Object of class "numeric" a vector containing the codes for the 2 treatment groups, 1st and 2nd treatment groups, respectively
<code>timePoint</code>	Object of class "numeric" timepoint to estimate survival

### Extends

Class "`stmodel`", directly.

### Methods

**estimate** signature(.Object = "stmodelCI"):  
estimate the effect in absolute and relative scale of the overall and each subpopulation

**print** signature(.Object = "stmodelCI"):  
print the estimate, covariance matrices and statistics

**test** signature(.Object = "stmodelCI"):  
perform the permutation tests or GEE and obtain various statistics

### Author(s)

Wai-Ki Yip

**See Also**

[stwin](#), [stsubpop](#), [stmodelKM](#), [stmodelCI](#), [stmodelGLM](#), [steppes](#), [stmodel](#), [stepp.win](#), [stepp.subpop](#), [stepp.KM](#), [stepp.GLM](#), [stepp.test](#), [estimate](#), [generate](#)

**Examples**

```
showClass("stmodelCI")

##
n <- 1000 # set the sample size
mu <- 0 # set the mean and sd of the covariate
sigma <- 1

beta0 <- log(-log(0.5)) # set the intercept for the log hazard
beta1 <- -0.2 # set the slope on the covariate
beta2 <- 0.5 # set the slope on the treatment indicator
beta3 <- 0.7 # set the slope on the interaction

prob2 <- 0.2 # set the proportion type 2 events
cprob <- 0.3 # set the proportion censored

set.seed(7775432) # set the random number seed
covariate <- rnorm(n,mean=mu,sd=sigma) # generate the covariate values
Txassign <- rbinom(n,1,0.5) # generate the treatment indicator
x3 <- covariate*Txassign # compute interaction term
# compute the hazard for type 1 event
lambda1 <- exp(beta0+beta1*covariate+beta2*Txassign+beta3*x3)
lambda2 <- prob2*lambda1/(1-prob2) # compute the hazard for the type 2 event
# compute the hazard for censoring time
lambda0 <- cprob*(lambda1+lambda2)/(1-cprob)
t1 <- rexp(n,rate=lambda1) # generate the survival time for type 1 event
t2 <- rexp(n,rate=lambda2) # generate the survival time for type 2 event
t0 <- rexp(n,rate=lambda0) # generate the censoring time
time <- pmin(t0,t1,t2) # compute the observed survival time
type <- rep(0,n)
type[(t1 < t0)&(t1 < t2)] <- 1
type[(t2 < t0)&(t2 < t1)] <- 2

# create the stepp model object to analyze the data using Cumulative Incidence approach
x <- new ("stmodelCI", coltrt=Txassign, trts=c(0,1), coltime=time, coltype=type, timePoint=1.0)
```

---

stmodelGLM-class

*Class "stmodelGLM"*


---

**Description**

This is the stepp model for data arising from the following Generalized Linear Models: 1. gaussian with identity link, 2. binomial with logit link, and 3. Poisson with log link.

One can specify additional covariates in the model using `model.matrix` in R.

**Value**

The new method returns the stmodelGLM object.

The estimate method returns a list with the following fields:

model	the stepp model - "GLMGe" - Gaussian model, "GLMBe" - binomial model, and "GLMPe" - Poisson model
sObs1	a vector of effect estimates of all subpopulations based on the first treatment
sSE1	a vector of standard errors of effect estimates of all subpopulations based on the first treatment
oObs1	effect estimate of the entire population based on the first treatment
oSE1	the standard error of the effect estimate of the entire population based on the first treatment
sObs2	a vector of effect estimates of all subpopulations based on the first treatment
sSE2	a vector of standard errors of effect estimates of all subpopulations based on the first treatment
oObs2	effect estimate of the entire population based on the first treatment
oSE2	the standard error of the effect estimate of the entire population based on the first treatment
sglmw	Wald's statistics for the effect estimate differences between the two treatments
RD	a vector of effect estimates difference of all subpopulations between the two treatments
RDSE	a vector of the standard error effect estimates difference of all subpopulations between the two treatments
ORD	overall difference of effect estimates of the entire population between the two treatments
ORDSE	the standard error of the overall difference of the effect estimates of the entire population between the two treatments
logR	a vector of log ratio of effect estimates of all subpopulations between the two treatments
logRSE	a vector of standard error of log ratio of effect estimates of all subpopulations between the two treatments
ologR	log ratio of effect estimates of the entire population between the two treatments
ologRSE	the standard error of the log ratio of effect estimates of the entire population between the two treatments
sglmlogrw	Wald's statistics for the log ratio of effect estimates between the two treatments

The test method returns a list with the following fields:

model	the stepp model - "GLMt"
sigma	the covariance matrix for subpopulations based on effect differences
hasigma	the homogeneous association covariance matrix for subpopulations based on effect differences

HRsigma	the covariance matrix for the subpopulations based on hazard ratio
haHRsigma	the homogeneous association covariance matrix for subpopulations based on hazard ratio
pvalue	the supremum pvalue based on effect difference
chi2pvalue	the chisquare pvalue based on effect difference
hapvalue	the homogeneous association pvalue based on effect difference
HRpvalue	the supremum pvalue based on hazard ratio
haHRpvalue	the homogeneous association pvalue based on hazard ratio

### Objects from the Class

Objects can be created by calls of the form `new("stmodelGLM", ...)` or by the construction function `stmodel.GLM`.

### Slots

<code>coltrt</code>	Object of class "numeric" the treatment variable
<code>colY</code>	Object of class "numeric" a vector containing the outcome
<code>trts</code>	Object of class "numeric" a vector containing the codes for the 2 treatment groups, first and second treatment groups, respectively
<code>MM</code>	Object of class "ANY" a model matrix for extra adjustment covariates; default is NULL currently, <code>stepp</code> can only support covariates with numeric values, no logical values or factors allowed these values need to be converted to numeric with some encoding schemes
<code>glm</code>	Object of class "character" the glm to be used for analysis: "gaussian", "binomial", "poisson"
<code>link</code>	Object of class "character" the link function; reserved for future use
<code>debug</code>	Object of class "numeric"

### Extends

Class "`stmodel`", directly.

### Methods

<b>estimate</b>	signature(.Object = "stmodelGLM"): estimate the effect in absolute and relative scale of the overall and each subpopulation
<b>print</b>	signature(.Object = "stmodelGLM"): print the estimate, covariance matrices and statistics
<b>test</b>	signature(.Object = "stmodelGLM"): perform the permutation tests or GEE and obtain various statistics



**Author(s)**

Wai-Ki Yip

**See Also**

[stwin](#), [stsubpop](#), [stmodelKM](#), [stmodelCI](#), [steppes](#), [stmodel](#), [stepp.win](#), [stepp.subpop](#), [stepp.KM](#), [stepp.CI](#), [stepp.GLM](#), [stepp.test](#), [estimate](#), [generate](#)

**Examples**

```
showClass("stmodelGLM")
```

---

stmodelKM-class	Class "stmodelKM"
-----------------	-------------------

---

**Description**

This is the S4 class for the stepp model of survival data using Kaplan-Meier method.

**Value**

The new method returns the stmodelKM object.

The estimate method returns a list with the following fields:

model	the stepp model - "KMe"
sObs1	a vector of effect estimates of all subpopulations based on the first treatment
sSE1	a vector of standard errors of effect estimates of all subpopulations based on the first treatment
oObs1	effect estimate of the entire population based on the first treatment
oSE1	the standard error of the effect estimate of the entire population based on the first treatment
sObs2	a vector of effect estimates of all subpopulations based on the group treatment
sSE2	a vector of standard errors of effect estimates of all subpopulations based on the first treatment
oObs2	effect estimate of the entire population based on the first treatment
oSE2	the standard error of the effect estimate of the entire population based on the first treatment
skmw	Wald's statistics for the effect estimate differences between the two treatments
logHR	a vector of log hazard ratio estimate of the subpopulations comparing first and second treatments
logHRSE	a vector of standard error of the log hazard ratio estimate of the subpopulations comparing first and second treatment
ologHR	the log hazard ratio estimate of the entire population comparing first and second treatment

ologHRSE	the standard error of the log hazard ratio estimate of the entire population comparing first and second treatment
logHRw	Wald's statistics for the log hazard ratio between the two treatment

The test method returns a list with the following fields:

model	the stepp model - "KMt"
sigma	the covariance matrix for subpopulations based on effect differences
hasigma	the homogeneous association covariance matrix for subpopulations based on effect differences
HRsigma	the covariance matrix for the subpopulations based on hazard ratios
haHRsigma	the homogeneous association covariance matrix for subpopulations based on hazard ratios
pvalue	the supremum pvalue based on effect difference
chi2pvalue	the chisquare pvalue based on effect difference
hapvalue	the homogeneous association pvalue based on effect difference

### Objects from the Class

Objects can be created by calls of the form `new("stmodelKM", ...)` or by the constructor function `stmodel.KM`.

### Slots

<code>coltrt</code> :	Object of class "numeric" the treatment variable
<code>survTime</code> :	Object of class "numeric" the time to event variable
<code>censor</code> :	Object of class "numeric" the censor variable
<code>trts</code> :	Object of class "numeric" a vector containing the codes for the 2 treatment groups, first and second treatment groups, respectively
<code>timePoint</code> :	Object of class "numeric" timepoint to estimate survival

### Extends

Class `"stmodel"`, directly.

### Methods

**estimate** `signature(.Object = "stmodelKM")`:  
estimate the effect in absolute and relative scale of the overall population and each subpopulation.

```

print signature(.Object = "stmodelKM"):
  print the estimate, covariance matrices and statistics.

test signature(.Object = "stmodelKM"):
  perform the permutation tests or GEE and obtain various statistics.

```

**Author(s)**

Wai-Ki YIp

**See Also**

[stwin](#), [stsubpop](#), [stmodelCI](#), [stmodelGLM](#), [steples](#), [stmodel](#), [stepp.win](#), [stepp.subpop](#), [stepp.KM](#), [stepp.CI](#), [stepp.GLM](#), [stepp.test](#), [estimate](#), [generate](#)

**Examples**

```

showClass("stmodelKM")

#GENERATE TREATMENT VARIABLE:
N <- 1000
Txassign <- sample(c(1,2), N, replace=TRUE, prob=c(1/2, 1/2))
n1 <- length(Txassign[Txassign==1])
n2 <- N - n1
#GENERATE A COVARIATE:
covariate <- rnorm(N, 55, 7)
#GENERATE SURVIVAL AND CENSORING VARIABLES ASSUMING A TREATMENT COVARIATE INTERACTION:
Entry <- sort( runif(N, 0, 5) )
SurvT1 <- .5
beta0 <- -65 / 75
beta1 <- 2 / 75
Surv <- rep(0, N)
lambda1 <- -log(SurvT1) / 4
Surv[Txassign==1] <- rexp(n1, lambda1)
Surv[Txassign==2] <- rexp(n2, (lambda1*(beta0+beta1*covariate[Txassign==2])))
EventTimes <- rep(0, N)
EventTimes <- Entry + Surv
censor <- rep(0, N)
time <- rep(0,N)
for ( i in 1:N )
{
  censor[i] <- ifelse( EventTimes[i] <= 7, 1, 0 )
  time[i] <- ifelse( EventTimes[i] < 7, Surv[i], 7 - Entry[i] )
}

modKM <- new("stmodelKM", coltrt=Txassign, survTime=time, censor=censor, trts=c(1,2), timePoint=4)

```

---

stsubpop-class	Class "stsubpop"
----------------	------------------

---

### Description

This is the S4 class for stepp subpopulation object. The subpopulations are generated based on the stepp windows and the covariate of interest.

### Objects from the Class

Objects can be created by calls of the form `new("stsubpop")` or the constructor method `stepp.subpop`.

### Slots

**win:** Object of class "stwin"  
the stepp window set up for the analysis

**colvar:** Object of class "numeric"  
the covariate of interest

**nsubpop:** Object of class "numeric"  
the number of subpopulations generated

**subpop:** Object of class "ANY"  
a matrix of subpopulations generated based on the stepp window and the specified covariate of interest

**npatsub:** Object of class "numeric" a vector of size of each subpopulation

**medianz:** Object of class "numeric"  
a vector of median value of the covariate of interest for each subpopulation

**minz:** Object of class "numeric"  
a vector of rounded minimum value of the covariate of interest for each subpopulation

**minc:** Object of class "numeric"  
a vector of the minimum value of the covariate of interest for each subpopulation

**maxz:** Object of class "numeric"  
a vector of rounded maximum value of the covariate of interest for each subpopulation

**maxc:** Object of class "numeric"  
a vector of the maximum value of the covariate of interest for each subpopulation

**init:** Object of class "logical"  
a logical value indicating if the subpopulations are generated or not

### Methods

**generate** signature(.Object = "stsubpop", win, covariate):  
a method to generate the subpopulations based on the stepp window object and the specified covariate of interest

**summary** signature(.Object = "stsubpop"):  
a method to display the summary of the subpopulations generated

**Author(s)**

Wai-Ki Yip

**See Also**

[stwin](#), [stmodelKM](#), [stmodelCI](#), [stmodelGLM](#), [steppes](#), [stmodel](#), [stepp.win](#), [stepp.subpop](#), [stepp.KM](#), [stepp.CI](#), [stepp.GLM](#), [stepp.test](#), [estimate](#), [generate](#)

**Examples**

```
showClass("stsubpop")

# create a stepp window
win1 <- stepp.win(type="sliding", r1=5,r2=10)

# generate the covariate of interest
Y <- rnorm(100)

# create and generate the stepp subpopulation
sp <- new("stsubpop")
sp <- generate(sp, win=win1, cov=Y)
summary(sp)
```

---

stwin-class

*Class "stwin"*


---

**Description**

This is the S4 class for the stepp window object. The stepp window class describes the way to set up the subpopulation for a stepp analysis. It specifies a pattern of subpopulation you would like to explore. There are two kinds of patterns: "sliding window" and "tail-oriented window".

Both patterns are specified through a set of (r1, r2) values: 1. for sliding windows, r1 is the minimum number of patients allowed in overlapping windows and r2 is the approximate size of subpopulation in each window; 2. for tail-oriented window, r1 is a vector of maximum covariate value for each subpopulation from the minimum value of the entire subpopulation, and r2 is a vector of minimum covariate values for each subpopulation from the maximum value of the window. The utility function, `gen.tailwin`, can be used to generate these two vectors based on the number of desired subpopulations.

Both patterns are based on all patients.

**Objects from the Class**

Objects can be created by calls of the form `new("stwin", type="sliding", r1=5, r2=20 )` or the constructor function `stepp.win`.

**Slots**

type: Object of class "character"  
 stepp window type; "sliding" or "tail-oriented"

r1: Object of class "numeric"  
 sliding window: minimum number of patients allowed in overlapping windows;  
 tail-oriented window: a vector of maximum covariate value for each subpopulation

r2: Object of class "numeric"  
 sliding window: size of subpopulation in each window;  
 tail-oriented window: a vector of minimum covariate value for each subpopulation

basedon: Object of class "character"  
 what the window is based on: all patients - "all" (default)

**Methods**

**summary** signature(object = "stwin"):  
 print a summary of the stepp windows object

**Author(s)**

Wai-Ki Yip

**See Also**

[stsubpop](#), [stmodelKM](#), [stmodelCI](#), [stmodelGLM](#), [steppes](#), [stmodel](#), [stepp.win](#), [stepp.subpop](#),  
[stepp.KM](#), [stepp.CI](#), [stepp.GLM](#), [stepp.test](#), [estimate](#), [generate](#)

**Examples**

```
showClass("stwin")

# create a stepp window of type "sliding" with (r2) size of subpopulation
# in each window to be 200 and (r1) allows only 50 patients in the
# overlapping windows
mywin <- new("stwin", type="sliding", r1=50, r2=200)

# print a summary of the stepp window object created
summary(mywin)
```

---

test

---

*the standard generic function for all test methods*


---

**Description**

The default generic function for test methods for all stepp models classes and the steppes class.

For detail, please refer to the documentation in the test method in the S4 class: `stmodelCI`, `stmodelKM` and `stmodelGLM`.

**Author(s)**

Wai-ki Yip

**See Also**

[stwin](#), [stsubpop](#), [stmodelKM](#), [stmodelCI](#), [stmodelGLM](#), [stepes](#), [stmodel](#), [stepp.win](#), [stepp.subpop](#), [stepp.KM](#), [stepp.CI](#), [stepp.GLM](#), [generate](#), [estimate](#)

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