Package 'currentSurvival'

May 12, 2022

Version 1.1

Date 2022-05-03

Title Estimation of CCI and CLFS Functions

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Depends R (>= 4.2.0), survival, cmprsk

Description The currentSurvival package contains functions for the estimation of the current cumulative incidence (CCI) and the current leukaemia-free survival (CLFS). The CCI is the probability that a patient is alive and in any disease remission (e.g. complete cytogenetic remission in chronic myeloid leukaemia) after initiating his or her therapy (e.g. tyrosine kinase therapy for chronic myeloid leukaemia). The CLFS is the probability that a patient is alive and in any disease remission after achieving the first disease remission.

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NeedsCompilation no

Repository CRAN

Date/Publication 2022-05-12 07:20:02 UTC

R topics documented:

`cci` *Estimates Current Cumulative Incidence (CCI) and Common Cumulative Incidence (comCI) Functions*

Description

This function estimates the current cumulative incidence (CCI), i.e. the probability that a patient is alive and in any disease remission (e.g. complete cytogenetic remission in chronic myeloid leukaemia) after initiating his or her therapy (e.g. tyrosine kinase therapy for chronic myeloid leukaemia). Optionally, this function estimates the common cumulative incidence (comCI), i.e. the probability that a patient is alive and in the first disease remission after therapy initiation. The CCI and comCI curves can also be stratified by risk factors. Moreover, statistical test can be applied to compare the risk groups.

Usage

```
cci(data, maxx = NULL, com.est = TRUE, conf.int = FALSE,
    conf.int.level = NULL, no.iter = NULL, points = NULL,
    fig = TRUE, strat = FALSE, pvals = FALSE, pval.test = NULL)
```

Arguments

`data` a matrix with ascending times from therapy initiation to occurrence of individual events (in days, i.e. positive integer values), total follow-up times from therapy initiation to data cut-off date (in days), and censoring indicators; moreover, a vector for stratification factor may be included;
if no stratification factor is included, the size of the data matrix is n times (2*r+2), where n is the number of patients and r is the maximum number of disease remissions achieved by patients;
if the data contain a stratification factor, the size of the data matrix is n times (2*r+3), where n is the number of patients and r is the maximum number of disease remissions achieved by patients;
the data matrix consists of the following columns:
data[,1] is the time from therapy initiation to achievement of the first disease remission
data[,2] is the time from therapy initiation to loss of the first disease remission
data[,3] is the time from therapy initiation to achievement of the second disease remission

	... data[,2*r-1] is the time from therapy initiation to achievement of the *r*th disease remission data[,2*r] is the time from therapy initiation to loss of the *r*th disease remission data[,2*r+1] is the follow-up time (time from the therapy initiation to death or to the date of last contact with a patient) data[,2*r+2] is the censoring indicator (1..patient died, 0..patient is censored) (data[,2*r+3] is the stratification factor (maximum number of stratification levels is 8 because of figure clarity))
`maxx`	maximum follow-up time calculated from therapy initiation in years (defining time period for which the point estimates will be computed and curves will be plotted). Setting `maxx` smaller than the maximum follow-up time enables creating plots without fluctuating curve ends that may be caused by small number of patients. The default value is the maximum follow-up time (i.e. max(data[,2*r+1])/365).
`com.est`	a logical value indicating whether common cumulative incidence function should be estimated. The default value is TRUE.
`conf.int`	a logical value indicating whether confidence interval for the function(s) should be estimated. The default value is FALSE.
`conf.int.level`	two-sided confidence interval level (must be in range 0.9 and 0.99). The default value is 0.95.
`no.iter`	a number of bootstrap iterations for confidence interval computation (must be in range between 10 and 10,000). The default value is 100.
`points`	time points in which the point estimates will be computed (in months). The default values are 0, 12, 24, ..., floor(`maxx`/(365/12)).
`fig`	a logical value indicating whether a figure should be plotted. The default value is TRUE.
`strat`	a logical value indicating whether a stratification factor is included. The default value is FALSE.
`pvals`	a logical value indicating whether p-values for the comparison of stratified curves at pre-defined time points should be computed. The default value is FALSE.
`pval.test`	a type of a test that will be used for the computation of p-values. Possible values are "naive", "log", "loglog". The default value is "loglog".

Value

a list containing the following elements:

`no.risk`	numbers of patients at risk at the defined time points
`pest`	a matrix of point estimates (accompanied with confidence intervals) at the defined time points
`pest.day`	a matrix of point estimates (accompanied with confidence intervals) at each day of the follow-up time
`pval`	p-values for the comparison of point estimates at the defined time points
`summary`	summary of input data

Author(s)

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References

Pavlik T., Janousova E., Pospisil Z., et al. (2011). Estimation of current cumulative incidence of leukaemia-free patients and current leukaemia-free survival in chronic myeloid leukaemia in the era of modern pharmacotherapy. *BMC Med Res Methodol* **11**:140.

See Also

clfs

Examples

```
## 4 examples of CCI estimation without stratification (and
## comCI estimation) with and without confidence intervals:
data(cml)  # load example data set
cml <- cml[,c(1:7)] # select event and follow-up times and death
          # (stratification factor is not included)
res <- cci(cml) # CCI + comCI without confidence intervals
res <- cci(cml, com.est=FALSE) # CCI without confidence intervals
## Not run:
res <- cci(cml, conf.int=TRUE, no.iter=10) # CCI + comCI with
          # confidence intervals
res <- cci(cml, com.est=FALSE, conf.int=TRUE, no.iter=10) # CCI
          # with confidence intervals
## End(Not run)

## 4 examples of CCI estimation with stratification (and comCI
## estimation) with and without confidence intervals:
data(cml)  # load example data set
cml <- cml[,c(1:7,10)] # select event and follow-up times, death,
          # and the EUTOS score as a stratification parameter
res <- cci(cml, strat=TRUE) # stratified CCI + comCI without
          # confidence intervals
res <- cci(cml, com.est=FALSE, strat=TRUE) # stratified CCI
          # without confidence intervals
## Not run:
res <- cci(cml, conf.int=TRUE, no.iter=10, strat=TRUE, pvals=TRUE)
          # stratified CCI + comCI with confidence intervals
res <- cci(cml, com.est=FALSE, conf.int=TRUE, no.iter=10,
          strat=TRUE, pvals=TRUE) # stratified CCI with
          # confidence intervals
## End(Not run)

## Not run:
## As the function does not allow setting plot option (e.g. line
```

```
## colour, width and type), you can create a plot using the
## following commands:
data(cml)  # load example data set
cml <- cml[,c(1:7)] # select event and follow-up times and death
          # (stratification factor is not included)
res <- cci(cml, conf.int=TRUE, no.iter=10) # CCI + comCI with
          # confidence intervals
maxx <- max(res$pest.day[,1]) # maximum follow-up time in days
x=0:maxx
yrs <- floor(maxx/365) # maximum follow-up time in years
plot(0,0,pch='.',cex=0.01,xlab="Years after therapy initiation",
     ylab="Probability",axes=FALSE,xlim=c(0,maxx),ylim=c(0,1))
     # plot initialization
axis(2,at=seq(0,1,0.2)) # setting of points where tick-marks are
     # to be drawn on the y-axis
axis(1,at=seq(0,((yrs+1)*365),365),labels=seq(0,(yrs+1),1))
     # setting of points where tick-marks are to be drawn on the
     # x-axis
lines(x,res$pest.day[,2],type="S",lty=1,lwd=1) # lower confidence
     # interval for the CCI function estimate
lines(x,res$pest.day[,3],type="S",lty=1,lwd=2) # CCI estimate
lines(x,res$pest.day[,4],type="S",lty=1,lwd=1) # upper confidence
     # interval for the CCI function estimate
lines(x,res$pest.day[,5],type="S",lty=2,lwd=1) # lower confidence
     # interval for the comCI function estimate
lines(x,res$pest.day[,6],type="S",lty=2,lwd=2) # comCI estimate
lines(x,res$pest.day[,7],type="S",lty=2,lwd=1) # upper confidence
     # interval for the comCI function estimate
legend("bottomright",legend=c("CCI","95% conf. int.","comCI",
       "95% conf. int."),lwd=c(2,1,2,1),lty=c(1,1,2,2),bty="n",
       cex=0.9)
## End(Not run)
```

`cci.nostrat` *Estimates Current Cumulative Incidence (CCI) and Common Cumulative Incidence (comCI) Functions Without Stratification*

Description

This is an internal function and is not usually called by user.
This function estimates the unstratified current cumulative incidence (CCI), i.e. the probability that a patient is alive and in any disease remission after initiating his or her therapy. Optionally, this function estimates the unstratified common cumulative incidence (comCI) function.

Usage

```
cci.nostrat(data, maxx = NULL, com.est = TRUE, conf.int = FALSE,
            conf.int.level = NULL, no.iter = NULL,
            points = NULL, fig = TRUE)
```

Arguments

`data`	a matrix with ascending times from therapy initiation to occurrence of individual events (in days, i.e. positive integer values), total follow-up times from therapy initiation to data cut-off date (in days), and censoring indicators; the size of the data matrix is n times (2*r+2), where n is the number of patients and r is the maximum number of disease remissions achieved by patients; the data matrix consists of the following columns: data[,1] is the time from therapy initiation to achievement of the first disease remission data[,2] is the time from therapy initiation to loss of the first disease remission data[,3] is the time from therapy initiation to achievement of the second disease remission ... data[,2*r-1] is the time from therapy initiation to achievement of the rth disease remission data[,2*r] is the time from therapy initiation to loss of the rth disease remission data[,2*r+1] is the follow-up time (time from the therapy initiation to death or to the date of last contact with a patient) data[,2*r+2] is the censoring indicator (1..patient died, 0..patient is censored)
`maxx`	maximum follow-up time calculated from therapy initiation in days (defining time period for which the point estimates will be computed and curves will be plotted). Setting `maxx` smaller than the maximum follow-up time enables creating plots without fluctuating curve ends that may be caused by small number of patients. The default value is the maximum follow-up time (i.e. max(data[,2*r+1])).
`com.est`	a logical value indicating whether common cumulative incidence function should be estimated. The default value is TRUE.
`conf.int`	a logical value indicating whether confidence interval for the function(s) should be estimated. The default value is FALSE.
`conf.int.level`	two-sided confidence interval level (must be in range 0.9 and 0.99). The default value is 0.95.
`no.iter`	a number of bootstrap iterations for confidence interval computation (must be in range between 10 and 10,000). The default value is 100.
`points`	time points in which the point estimates will be computed (in months). The default values are 0, 12, 24, ..., floor(`maxx`/(365/12)).
`fig`	a logical value indicating whether a figure should be plotted. The default value is TRUE.

Value

a list containing the following elements:

`no.risk`	numbers of patients at risk at the defined time points
`pest`	a matrix of point estimates (accompanied with confidence intervals) at the defined time points
`pest.day`	a matrix of point estimates (accompanied with confidence intervals) at each day of the follow-up time
`summary`	summary of input data

Author(s)

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References

Pavlik T., Janousova E., Pospisil Z., et al. (2011). Estimation of current cumulative incidence of leukaemia-free patients and current leukaemia-free survival in chronic myeloid leukaemia in the era of modern pharmacotherapy. *BMC Med Res Methodol* **11**:140.

See Also

cci

Examples

```
# This is an internal function and is not usually called by user.
```

---

cci.pest *Estimates Current Cumulative Incidence (CCI) Function*

Description

This is an internal function and is not usually called by user.
This function estimates the current cumulative incidence (CCI), i.e. the probability that a patient is alive and in any disease remission after initiating his or her therapy.

Usage

```
cci.pest(E, LastContact, Exitus, maxx)
```

Arguments

E	a matrix with ascending times from therapy initiation to occurrence of individual events (in days); the size of the data matrix is *n* times (2**r*), where *n* is the number of patients and *r* is the maximum number of disease remissions achieved by patients; the data matrix consists of the following columns: E[,1] is the time from therapy initiation to achievement of the first disease remission E[,2] is the time from therapy initiation to loss of the first disease remission E[,3] is the time from therapy initiation to achievement of the second disease remission ... E[,2**r*-1] is the time from therapy initiation to achievement of the *r*th disease remission E[,2**r*] is the time from therapy initiation to loss of the *r*th disease remission

LastContact	a vector containing the follow-up time (time from therapy initiation to death or to the date of last contact with a patient)
Exitus	a vector containing the censoring indicators (1..patient died, 0..patient is censored)
maxx	maximum follow-up time in days

Value

x	days from 0 to maximum follow-up time maxx
y	CCI function estimates at each day

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References

Pavlik T., Janousova E., Pospisil Z., et al. (2011). Estimation of current cumulative incidence of leukaemia-free patients and current leukaemia-free survival in chronic myeloid leukaemia in the era of modern pharmacotherapy. *BMC Med Res Methodol* **11**:140.

See Also

cci

Examples

```
# This is an internal function and is not usually called by user.
```

---

cci.strat *Estimates Stratified Current Cumulative Incidence (CCI) and Common Cumulative Incidence (comCI) Functions*

Description

This is an internal function and is not usually called by user.
This function estimates the stratified current cumulative incidence (CCI), i.e. the probability that a patient is alive and in any disease remission after initiating his or her therapy. Optionally, this function estimates the stratified common cumulative incidence (comCI) function. Moreover, statistical test can be applied to compare the risk groups.

Usage

```
cci.strat(data, stratf = NULL, maxx = NULL, com.est = TRUE,
          conf.int = FALSE, conf.int.level = NULL,
          no.iter = NULL, points = NULL, fig = TRUE,
          pvals = FALSE, pval.test = NULL)
```

Arguments

`data`	a matrix with ascending times from therapy initiation to occurrence of individual events (in days, i.e. positive integer values), total follow-up times from therapy initiation to data cut-off date (in days), and censoring indicators; the size of the data matrix is n times (2*r+2), where n is the number of patients and r is the maximum number of disease remissions achieved by patients; the data matrix consists of the following columns: data[,1] is the time from therapy initiation to achievement of the first disease remission data[,2] is the time from therapy initiation to loss of the first disease remission data[,3] is the time from therapy initiation to achievement of the second disease remission ... data[,2*r-1] is the time from therapy initiation to achievement of the rth disease remission data[,2*r] is the time from therapy initiation to loss of the rth disease remission data[,2*r+1] is the follow-up time (time from the therapy initiation to death or to the date of last contact with a patient) data[,2*r+2] is the censoring indicator (1..patient died, 0..patient is censored)
`stratf`	stratification factor (maximum number of stratification levels is 8 because of figure clarity)
`maxx`	maximum follow-up time calculated from therapy initiation in days (defining time period for which the point estimates will be computed and curves will be plotted). Setting `maxx` smaller than the maximum follow-up time enables creating plots without fluctuating curve ends that may be caused by small number of patients. The default value is the maximum follow-up time (i.e. max(data[,2*r+1])).
`com.est`	a logical value indicating whether common cumulative incidence function should be estimated. The default value is TRUE.
`conf.int`	a logical value indicating whether confidence interval for the function(s) should be estimated. The default value is FALSE.
`conf.int.level`	two-sided confidence interval level (must be in range 0.9 and 0.99). The default value is 0.95.
`no.iter`	a number of bootstrap iterations for confidence interval computation (must be in range between 10 and 10,000). The default value is 100.
`points`	time points in which the point estimates will be computed (in months). The default values are 0, 12, 24, ..., floor(`maxx`/(365/12)).
`fig`	a logical value indicating whether a figure should be plotted. The default value is TRUE.

pvals	a logical value indicating whether p-values for the comparison of stratified curves at pre-defined time points should be computed. The default value is FALSE.
pval.test	a type of a test that will be used for the computation of p-values. Possible values are "naive", "log", "loglog". The default value is "loglog".

Value

a list containing the following elements:

no.risk	numbers of patients at risk at the defined time points
pest	a matrix of point estimates (accompanied with confidence intervals) at the defined time points
pest.day	a matrix of point estimates (accompanied with confidence intervals) at each day of the follow-up time
pval	p-values for the comparison of point estimates at the defined time points
summary	summary of input data

Author(s)

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References

Pavlik T., Janousova E., Pospisil Z., et al. (2011). Estimation of current cumulative incidence of leukaemia-free patients and current leukaemia-free survival in chronic myeloid leukaemia in the era of modern pharmacotherapy. *BMC Med Res Methodol* **11**:140.

See Also

cci

Examples

```
# This is an internal function and is not usually called by user.
```

---

chisq.log *Compares Three or More Survival Estimates Using Log Test*

Description

This is an internal function and is not usually called by user.
This function computes chi-square test for the comparison of three or more survival curves at fixed points in time using log transformation of the survival estimates.

Usage

```
chisq.log(st, ot.sq)
```

Arguments

st	point estimates at fixed points in time
ot.sq	estimated variance

Value

chi-square test statistic

Author(s)

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References

Klein J.P., Logan B., Harhoff M., et al. (2007). Analyzing survival curves at a fixed point in time. *Statistics in Medicine* **26**:4505–4519.

See Also

cci, clfs, chisq.loglog, chisq.naive

Examples

```
# This is an internal function and is not usually called by user.
```

---

chisq.loglog *Compares Three or More Survival Estimates Using Complementary Log-log Test*

Description

This is an internal function and is not usually called by user.
This function computes chi-square test for the comparison of three or more survival curves at fixed points in time using complementary log-log transformation of the survival estimates.

Usage

```
chisq.loglog(st, ot.sq)
```

Arguments

st	point estimates at fixed points in time
ot.sq	estimated variance

Value

chi-square test statistic

Author(s)

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References

Klein J.P., Logan B., Harhoff M., et al. (2007). Analyzing survival curves at a fixed point in time. *Statistics in Medicine* **26**:4505–4519.

See Also

cci, clfs, chisq.log, chisq.naive

Examples

```
# This is an internal function and is not usually called by user.
```

---

chisq.naive *Compares Three or More Survival Estimates Using Naive Chi-square Test*

Description

This is an internal function and is not usually called by user.
This function computes naive chi-square test for the comparison of three or more survival curves at fixed points in time.

Usage

```
chisq.naive(st, ot.sq)
```

Arguments

st	point estimates at fixed points in time
ot.sq	estimated variance

Value

chi-square test statistic

Author(s)

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References

Klein J.P., Logan B., Harhoff M., et al. (2007). Analyzing survival curves at a fixed point in time. *Statistics in Medicine* **26**:4505–4519.

See Also

cci, clfs, chisq.log, chisq.loglog

Examples

```
# This is an internal function and is not usually called by user.
```

---

clfs *Estimates Current Leukaemia-Free Survival (CLFS) and Common Leukaemia-Free Survival (LFS) Functions*

Description

This function estimates the current leukaemia-free survival (CLFS), i.e. the probability that a patient is alive and in any disease remission (e.g. complete cytogenetic remission in chronic myeloid leukaemia) after achieving the first disease remission. Optionally, this function estimates the common leukaemia-free survival (LFS), i.e. the probability that a patient is alive and in the first disease remission after achieving the first disease remission. The CLFS and LFS curves can also be stratified by risk factors. Moreover, statistical test can be applied to compare the risk groups. Only patients who achieved at least one disease remission during their treatment course are used for the estimation of the CLFS and LFS functions.

Usage

```
clfs(data, maxx = NULL, com.est = TRUE, conf.int = FALSE,
     conf.int.level = NULL, no.iter = NULL, points = NULL,
     fig = TRUE, strat = FALSE, pvals = FALSE, pval.test = NULL)
```

Arguments

`data`	a matrix with ascending times from therapy initiation to occurrence of individual events (in days, i.e. positive integer values), total follow-up times from therapy initiation to data cut-off date (in days), and censoring indicators; moreover, a vector for stratification factor may be included; if no stratification factor is included, the size of the data matrix is *n* times (2**r*+2), where *n* is the number of patients and *r* is the maximum number of disease remissions achieved by patients; if the data contain a stratification factor, the size of the data matrix is *n* times (2**r*+3), where *n* is the number of patients and *r* is the maximum number of disease remissions achieved by patients; the data matrix consists of the following columns: data[,1] is the time from therapy initiation to achievement of the first disease remission data[,2] is the time from therapy initiation to loss of the first disease remission data[,3] is the time from therapy initiation to achievement of the second disease remission ... data[,2**r*-1] is the time from therapy initiation to achievement of the *r*th disease remission data[,2**r*] is the time from therapy initiation to loss of the *r*th disease remission data[,2**r*+1] is the follow-up time (time from the therapy initiation to death or to the date of last contact with a patient) data[,2**r*+2] is the censoring indicator (1..patient died, 0..patient is censored) (data[,2**r*+3] is the stratification factor (maximum number of stratification levels is 8 because of figure clarity))
`maxx`	maximum follow-up time calculated from the achievement of the first disease remission in years (defining time period for which the point estimates will be computed and curves will be plotted). Setting `maxx` smaller than the maximum follow-up time enables creating plots without fluctuating curve ends that may be caused by small number of patients. The default value is the maximum follow-up time except the time from therapy initiation to achievement of the first disease remission (i.e. max(data[,2**r*+1]-data[,1])/365).
`com.est`	a logical value indicating whether common leukaemia-free survival function should be estimated. The default value is TRUE.
`conf.int`	a logical value indicating whether confidence interval for the function(s) should be estimated. The default value is FALSE.
`conf.int.level`	two-sided confidence interval level (must be in range 0.9 and 0.99). The default value is 0.95.
`no.iter`	a number of bootstrap iterations for confidence interval computation (must be in range between 10 and 10,000). The default value is 100.
`points`	time points in which the point estimates will be computed (in months). The default values are 0, 12, 24, ..., floor(`maxx`/(365/12)).
`fig`	a logical value indicating whether a figure should be plotted. The default value is TRUE.

strat	a logical value indicating whether a stratification factor is included. The default value is FALSE.
pvals	a logical value indicating whether p-values for the comparison of stratified curves at pre-defined time points should be computed. The default value is FALSE.
pval.test	a type of a test that will be used for the computation of p-values. Possible values are "naive", "log", "loglog". The default value is "loglog".

Value

a list containing the following elements:

no.risk	numbers of patients at risk at the defined time points
pest	a matrix of point estimates (accompanied with confidence intervals) at the defined time points
pest.day	a matrix of point estimates (accompanied with confidence intervals) at each day of the follow-up time
pval	p-values for the comparison of point estimates at the defined time points
summary	summary of input data

Author(s)

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References

Pavlik T., Janousova E., Pospisil Z., et al. (2011). Estimation of current cumulative incidence of leukaemia-free patients and current leukaemia-free survival in chronic myeloid leukaemia in the era of modern pharmacotherapy. *BMC Med Res Methodol* **11**:140.

See Also

cci

Examples

```
## 4 examples of CLFS estimation without stratification (and
## LFS estimation) with and without confidence intervals:
data(cml)  # load example data set
cml <- cml[,c(1:7)] # select event and follow-up times and death
          # (stratification factor is not included)
res <- clfs(cml) # CLFS + LFS without confidence intervals
res <- clfs(cml, com.est=FALSE) # CLFS without confidence
          # intervals
## Not run:
res <- clfs(cml, conf.int=TRUE, no.iter=10) # CLFS + LFS with
          # confidence intervals
```

```
res <- clfs(cml, com.est=FALSE, conf.int=TRUE, no.iter=10) # CLFS
          # with confidence intervals
## End(Not run)

## 4 examples of CLFS estimation with stratification (and LFS
## estimation) with and without confidence intervals:
data(cml)  # load example data set
cml <- cml[,c(1:7,10)] # select event and follow-up times, death,
          # and the EUTOS score as a stratification parameter
res <- clfs(cml, strat=TRUE) # stratified CLFS + LFS without
          # confidence intervals
res <- clfs(cml, com.est=FALSE, strat=TRUE) # stratified CLFS
          # without confidence intervals
## Not run:
res <- clfs(cml, conf.int=TRUE, no.iter=10, strat=TRUE, pvals=TRUE)
          # stratified CLFS + LFS with confidence intervals
res <- clfs(cml, com.est=FALSE, conf.int=TRUE, no.iter=10,
          strat=TRUE, pvals=TRUE) # stratified CLFS with
          # confidence intervals
## End(Not run)

## Not run:
## As the function does not allow setting plot option (e.g. line
## colour, width and type), you can create a plot using the
## following commands:
data(cml)  # load example data set
cml <- cml[,c(1:7)] # select event and follow-up times and death
          # (stratification factor is not included)
res <- clfs(cml, conf.int=TRUE, no.iter=10) # CLFS + LFS with
          # confidence intervals
maxx <- max(res$pest.day[,1]) # maximum follow-up time in days
x=0:maxx
yrs <- floor(maxx/365) # maximum follow-up time in years
plot(0,1,pch='.',cex=0.01,xlim=c(0,maxx),ylim=c(0,1),axes=FALSE,
     xlab="Years after achievement of the first remission",
     ylab="Probability") # plot initialization
axis(2,at=seq(0,1,0.2)) # setting of points where tick-marks are
     # to be drawn on the y-axis
axis(1,at=seq(0,((yrs+1)*365),365),labels=seq(0,(yrs+1),1))
     # setting of points where tick-marks are to be drawn on the
     # x-axis
lines(x,res$pest.day[,2],type="S",lty=1,lwd=1) # lower confidence
     # interval for the CLFS function estimate
lines(x,res$pest.day[,3],type="S",lty=1,lwd=2) # CLFS estimate
lines(x,res$pest.day[,4],type="S",lty=1,lwd=1) # upper confidence
     # interval for the CLFS function estimate
lines(x,res$pest.day[,5],type="S",lty=2,lwd=1) # lower confidence
     # interval for the LFS function estimate
lines(x,res$pest.day[,6],type="S",lty=2,lwd=2) # LFS estimate
lines(x,res$pest.day[,7],type="S",lty=2,lwd=1) # upper confidence
     # interval for the LFS function estimate
legend("bottomright",legend=c("CLFS","95% conf. int.","LFS",
       "95% conf. int."),lwd=c(2,1,2,1),lty=c(1,1,2,2),bty="n",
```

```
       cex=0.9)
## End(Not run)
```

---

clfs.nostrat *Estimates Current Leukaemia-Free Survival (CLFS) and Common Leukaemia-Free Survival (LFS) Functions Without Stratification*

Description

This is an internal function and is not usually called by user.
This function estimates the unstratified current leukaemia-free survival (CLFS), i.e. the probability that a patient is alive and in any disease remission after achieving the first disease remission. Optionally, this function estimates the unstratified common leukaemia-free survival (LFS) function. Only patients who achieved at least one disease remission during their treatment course are used for the estimation of the CLFS and LFS functions.

Usage

```
clfs.nostrat(data, maxx = NULL, com.est = TRUE, conf.int = FALSE,
             conf.int.level = NULL, no.iter = NULL,
             points = NULL, fig = TRUE)
```

Arguments

data	a matrix with ascending times from therapy initiation to occurrence of individual events (in days, i.e. positive integer values), total follow-up times from therapy initiation to data cut-off date (in days), and censoring indicators; the size of the data matrix is n times (2*r+2), where n is the number of patients and r is the maximum number of disease remissions achieved by patients; the data matrix consists of the following columns: data[,1] is the time from therapy initiation to achievement of the first disease remission data[,2] is the time from therapy initiation to loss of the first disease remission data[,3] is the time from therapy initiation to achievement of the second disease remission ... data[,2*r-1] is the time from therapy initiation to achievement of the rth disease remission data[,2*r] is the time from therapy initiation to loss of the rth disease remission data[,2*r+1] is the follow-up time (time from the therapy initiation to death or to the date of last contact with a patient) data[,2*r+2] is the censoring indicator (1..patient died, 0..patient is censored)
maxx	maximum follow-up time calculated from the achievement of the first disease remission in days (defining time period for which the point estimates will be computed and curves will be plotted). Setting maxx smaller than the maximum follow-up time enables creating plots without fluctuating curve ends that may be

	caused by small number of patients. The default value is the maximum follow-up time except the time from therapy initiation to achievement of the first disease remission (i.e. max(data[,2*r+1]-data[,1])).
`com.est`	a logical value indicating whether common cumulative incidence function should be estimated. The default value is TRUE.
`conf.int`	a logical value indicating whether confidence interval for the function(s) should be estimated. The default value is FALSE.
`conf.int.level`	two-sided confidence interval level (must be in range 0.9 and 0.99). The default value is 0.95.
`no.iter`	a number of bootstrap iterations for confidence interval computation (must be in range between 10 and 10,000). The default value is 100.
`points`	time points in which the point estimates will be computed (in months). The default values are 0, 12, 24, ..., floor(`maxx`/(365/12)).
`fig`	a logical value indicating whether a figure should be plotted. The default value is TRUE.

Value

a list containing the following elements:

`no.risk`	numbers of patients at risk at the defined time points
`pest`	a matrix of point estimates (accompanied with confidence intervals) at the defined time points
`pest.day`	a matrix of point estimates (accompanied with confidence intervals) at each day of the follow-up time
`summary`	summary of input data

Author(s)

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References

Pavlik T., Janousova E., Pospisil Z., et al. (2011). Estimation of current cumulative incidence of leukaemia-free patients and current leukaemia-free survival in chronic myeloid leukaemia in the era of modern pharmacotherapy. *BMC Med Res Methodol* **11**:140.

See Also

`clfs`

Examples

```
# This is an internal function and is not usually called by user.
```

clfs.pest *Estimates Current Leukaemia-Free Survival (CLFS) Function*

Description

This is an internal function and is not usually called by user.
This function estimates the current leukaemia-free survival (CLFS) function, i.e. the probability that a patient is alive and in any disease remission after achieving the first disease remission. Only patients who achieved at least one disease remission during their treatment course are used for the estimation of the CLFS function.

Usage

```
clfs.pest(E, LastContact, Exitus, maxx)
```

Arguments

E	a matrix with ascending times from achievement of the first disease remission to occurrence of individual events (in days); the size of the data matrix is *n* times (2**r*-1), where *n* is the number of patients and *r* is the maximum number of disease remissions achieved by patients; the data matrix consists of the following columns: E[,1] is the time from achievement of the first disease remission to loss of the first disease remission E[,2] is the time from achievement of the first disease remission to achievement of the second disease remission E[,3] is the time from achievement of the first disease remission to loss of the second disease remission ... E[,2**r*-2] is the time from achievement of the first disease remission to achievement of the *r*th disease remission E[,2**r*-1] is the time from achievement of the first disease remission to loss of the *r*th disease remission
LastContact	a vector containing the follow-up time (time from achievement of the first disease remission to death or to the date of last contact with a patient)
Exitus	a vector containing the censoring indicators (1..patient died, 0..patient is censored)
maxx	maximum follow-up time in days

Value

a list containing the following elements:

x	days from 0 to maximum follow-up time maxx
y	CLFS function estimates at each day

Author(s)

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References

Pavlik T., Janousova E., Pospisil Z., et al. (2011). Estimation of current cumulative incidence of leukaemia-free patients and current leukaemia-free survival in chronic myeloid leukaemia in the era of modern pharmacotherapy. *BMC Med Res Methodol* **11**:140.

See Also

clfs

Examples

```
# This is an internal function and is not usually called by user.
```

---

clfs.strat *Estimates Stratified Current Leukaemia-Free Survival (CLFS) and Common Leukaemia-Free Survival (LFS) Functions*

Description

This is an internal function and is not usually called by user.
This function estimates the stratified current leukaemia-free survival (CLFS), i.e. the probability that a patient is alive and in any disease remission after achieving the first disease remission. Optionally, this function estimates the stratified common leukaemia-free survival (LFS) function. Moreover, statistical test can be applied to compare the risk groups. Only patients who achieved at least one disease remission during their treatment course are used for the estimation of the CLFS and LFS functions.

Usage

```
clfs.strat(data, stratf = NULL, maxx = NULL, com.est = TRUE,
           conf.int = FALSE, conf.int.level = NULL,
           no.iter = NULL, points = NULL, fig = TRUE,
           pvals = FALSE, pval.test = NULL)
```

Arguments

data	a matrix with ascending times from therapy initiation to occurrence of individual events (in days, i.e. positive integer values), total follow-up times from therapy initiation to data cut-off date (in days), and censoring indicators; the size of the data matrix is n times (2*r+2), where n is the number of patients and r is the

maximum number of disease remissions achieved by patients; the data matrix consists of the following columns:
data[,1] is the time from therapy initiation to achievement of the first disease remission
data[,2] is the time from therapy initiation to loss of the first disease remission
data[,3] is the time from therapy initiation to achievement of the second disease remission
...
data[,2*r-1] is the time from therapy initiation to achievement of the rth disease remission
data[,2*r] is the time from therapy initiation to loss of the rth disease remission
data[,2*r+1] is the follow-up time (time from the therapy initiation to death or to the date of last contact with a patient)
data[,2*r+2] is the censoring indicator (1..patient died, 0..patient is censored)

`stratf` stratification factor (maximum number of stratification levels is 8 because of figure clarity)

`maxx` maximum follow-up time calculated from the achievement of the first disease remission in days (defining time period for which the point estimates will be computed and curves will be plotted). Setting `maxx` smaller than the maximum follow-up time enables creating plots without fluctuating curve ends that may be caused by small number of patients. The default value is the maximum follow-up time except the time from therapy initiation to achievement of the first disease remission (i.e. max(data[,2*r+1]-data[,1])).

`com.est` a logical value indicating whether common cumulative incidence function should be estimated. The default value is TRUE.

`conf.int` a logical value indicating whether confidence interval for the function(s) should be estimated. The default value is FALSE.

`conf.int.level` two-sided confidence interval level (must be in range 0.9 and 0.99). The default value is 0.95.

`no.iter` a number of bootstrap iterations for confidence interval computation (must be in range between 10 and 10,000). The default value is 100.

`points` time points in which the point estimates will be computed (in months). The default values are 0, 12, 24, ..., floor(`maxx`/(365/12)).

`fig` a logical value indicating whether a figure should be plotted. The default value is TRUE.

`pvals` a logical value indicating whether p-values for the comparison of stratified curves at pre-defined time points should be computed. The default value is FALSE.

`pval.test` a type of a test that will be used for the computation of p-values. Possible values are "naive", "log", "loglog". The default value is "loglog".

Value

a list containing the following elements:

`no.risk` numbers of patients at risk at the defined time points

pest	a matrix of point estimates (accompanied with confidence intervals) at the defined time points
pest.day	a matrix of point estimates (accompanied with confidence intervals) at each day of the follow-up time
pval	p-values for the comparison of point estimates at the defined time points
summary	summary of input data

Author(s)

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References

Pavlik T., Janousova E., Pospisil Z., et al. (2011). Estimation of current cumulative incidence of leukaemia-free patients and current leukaemia-free survival in chronic myeloid leukaemia in the era of modern pharmacotherapy. *BMC Med Res Methodol* **11**:140.

See Also

clfs

Examples

```
# This is an internal function and is not usually called by user.
```

---

cml *Data of Patients With Chronic Myeloid Leukaemia*

Description

data of patients with chronic myeloid leukaemia

Usage

```
data(cml)
```

Format

A data frame with 104 observations on the following 10 variables.

`CCgR01` time from therapy initiation to achievement of the first disease remission

`loss_CCgR01` time from therapy initiation to loss of the first disease remission

`CCgR02` time from therapy initiation to achievement of the second disease remission

`loss_CCgR02` time from therapy initiation to loss of the second disease remission

`CCgR03` time from therapy initiation to achievement of the third disease remission

`follow.up` follow-up time (time from therapy initiation to death or to the date of last contact with a patient)

`death` censoring indicator (1..patient died, 0..patient is censored)

`sokal` Sokal score (1..low-risk, 2..intermediate-risk, 3..high-risk)

`euro` Euro score (1..low-risk, 2..intermediate-risk, 3..high-risk)

`eutos` EUTOS score (0..low-risk, 1..high-risk)

Source

population-based, observational study, INFINITY (https://www.leukemia-cell.org/index-en.php?pg=infinity--project-information)

References

Pavlik T., Janousova E., Pospisil Z., et al. (2011). Estimation of current cumulative incidence of leukaemia-free patients and current leukaemia-free survival in chronic myeloid leukaemia in the era of modern pharmacotherapy. *BMC Med Res Methodol* **11**:140.

Examples

```
data(cml)
str(cml)
```

---

comci.pest *Estimates Common Cumulative Incidence (comCI) Function*

Description

This is an internal function and is not usually called by user.
This function estimates the common cumulative incidence (comCI), i.e. the probability that a patient is alive and in the first disease remission after initiating his or her therapy.

Usage

```
comci.pest(t, LastContact, Exitus, maxx)
```

Arguments

`t`	a vector containing the time from therapy initiation to achievement of the first disease remission (in days)
`LastContact`	a vector containing the follow-up time (time from therapy initiation to death or to the date of last contact with a patient)
`Exitus`	a vector containing the censoring indicators (1..patient died, 0..patient is censored)
`maxx`	maximum follow-up time in days

Value

a list containing the following elements:

x	days from 0 to maximum follow-up time maxx
y	comCI function estimates at each day

Author(s)

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References

Pavlik T., Janousova E., Pospisil Z., et al. (2011). Estimation of current cumulative incidence of leukaemia-free patients and current leukaemia-free survival in chronic myeloid leukaemia in the era of modern pharmacotherapy. *BMC Med Res Methodol* **11**:140.

See Also

cci

Examples

```
# This is an internal function and is not usually called by user.
```

---

lfs.pest *Estimates Common Leukaemia-Free Survival (LFS) Function*

Description

This is an internal function and is not usually called by user.
This function estimates the common leukaemia-free survival (LFS) function, i.e. the probability that a patient is alive and in the first disease remission after achieving the first disease remission. Only patients who achieved at least one disease remission during their treatment course are used for the estimation of the LFS function.

Usage

```
lfs.pest(t, LastContact, Exitus, maxx)
```

Arguments

t	a vector containing the time from achievement of the first disease remission to loss of the first disease remission (in days)
LastContact	a vector containing the follow-up time (time from achievement of the first disease remission to death or to the date of last contact with a patient)
Exitus	a vector containing the censoring indicators (1..patient died, 0..patient is censored)
maxx	maximum follow-up time in days

Value

a list containing the following elements:

x	days from 0 to maximum follow-up time maxx
y	LFS function estimates at each day

Author(s)

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References

Pavlik T., Janousova E., Pospisil Z., et al. (2011). Estimation of current cumulative incidence of leukaemia-free patients and current leukaemia-free survival in chronic myeloid leukaemia in the era of modern pharmacotherapy. *BMC Med Res Methodol* **11**:140.

See Also

clfs

Examples

```
# This is an internal function and is not usually called by user.
```

---

pvals.2cat *Computes p-Values for The Comparison of Two Survival Curves at Fixed Points in Time*

Description

This is an internal function and is not usually called by user.
This function computes p-values for the comparison of two survival curves at fixed time points.

Usage

```
pvals.2cat(pest, pval.test)
```

Arguments

pest	a matrix of point estimates accompanied with confidence intervals at fixed time points
pval.test	a type of a test used for the computation of p-values. Possible values are "naive", "log", "loglog". The default value is "loglog".

Value

a vector containing p-values for the comparison of the point estimates at fixed time points

Author(s)

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References

Klein J.P., Logan B., Harhoff M., et al. (2007). Analyzing survival curves at a fixed point in time. *Statistics in Medicine* **26**:4505–4519.

See Also

cci, clfs, pvals.cat

Examples

```
# This is an internal function and is not usually called by user.
```

---

pvals.cat *Computes p-Values for The Comparison of Three or More Survival Curves at Fixed Points in Time*

Description

This is an internal function and is not usually called by user.
This function computes p-values for the comparison of three or more survival curves at fixed time points.

Usage

```
pvals.cat(pest, pval.test)
```

Arguments

pest	a matrix of point estimates accompanied with confidence intervals at fixed time points
pval.test	a type of a test used for the computation of p-values. Possible values are "naive", "log", "loglog". The default value is "loglog".

Value

a vector containing p-values for the comparison of the point estimates at fixed time points

Author(s)

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References

Klein J.P., Logan B., Harhoff M., et al. (2007). Analyzing survival curves at a fixed point in time. *Statistics in Medicine* **26**:4505–4519.

See Also

cci, clfs, pvals.2cat

Examples

```
# This is an internal function and is not usually called by user.
```

---

stretch *Assigns Survival Estimates to Each Day of the Follow-up*

Description

This is an internal function and is not usually called by user.
This function assigns survival estimates to each day of the follow-up.

Usage

```
stretch(S, maxx)
```

Arguments

S	a list containing: x - the time points in which the survival curve has a step y - survival estimates at the time points in which the survival curve has a step
maxx	maximum follow-up time in days

Value

a list containing the following elements:

x	days from 0 to maximum follow-up time maxx
y	survival estimates at each day

Author(s)

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Masaryk University, Brno, Czech Republic
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References

Pavlik T., Janousova E., Pospisil Z., et al. (2011). Estimation of current cumulative incidence of leukaemia-free patients and current leukaemia-free survival in chronic myeloid leukaemia in the era of modern pharmacotherapy. *BMC Med Res Methodol* **11**:140.

See Also

clfs

Examples

```
# This is an internal function and is not usually called by user.
```

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