Package 'PwrGSD'

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Title Power in a Group Sequential Design

Version 1.0

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Depends survival

Description Tools to compute power in a group sequential design. SimPwrGSD C-kernel is a simulation routine that is similar in spirit to dssp2.f by Gu and Lai, but with major improvements. AsyPwrGSD has exactly the same range of application as SimPwrGSD but uses asymptotic methods and runs _much_ faster.

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R topics documented:

PwrGSD *Calculate Power in a Group Sequential Design*

Description

Derives power in a two arm clinical trial under a group sequential design. Allows for arbitrary number of interim analyses, arbitrary specification of arm-0/arm-1 time to event distributions (via survival or hazard), arm-0/arm-1 censoring distribution, provisions for two types of continuous time non-compliance according to arm-0/arm-1 rate followed by switch to new hazard rate. Allows for analyses using (I) weighted log-rank statistic, with weighting function (a) a member of the Flemming-Harrington G-Rho class, or (b) a stopped version thereof, or (c) the ramp-plateau deterministic weights, or (II) the integrated survival distance (currently under method=="S" without futility only). Stopping boundaries are computed via the Lan-Demets method, Haybittle method, or converted from the stochastic curtailment procedure. The Lan-Demets boundaries can be constructed usign either O'Brien-Flemming, Pocock or Wang-Tsiatis power alpha-spending. The C kernel is readily extensible, and further options will become available in the near future.

Usage

```
PwrGSD(EfficacyBoundary = LanDemets(alpha = 0.05, spending = ObrienFleming),
    FutilityBoundary = LanDemets(alpha = 0.1, spending = ObrienFleming),
    sided = c("2", ">", "<"), method = c("S", "A"), accru, accrat,
    tlook, tcut0 = NULL, h0 = NULL, s0 = NULL, tcut1 = NULL,
    rhaz = NULL, h1 = NULL, s1 = NULL, tcutc0 = NULL, hc0 = NULL,
    sc0 = NULL, tcutc1 = NULL, hc1 = NULL, sc1 = NULL, tcutd0A = NULL,
    hd0A = NULL, sd0A = NULL, tcutd0B = NULL, hd0B = NULL, sd0B = NULL,
    tcutd1A = NULL, hd1A = NULL, sd1A = NULL, tcutd1B = NULL,
    hd1B = NULL, sd1B = NULL, tcutx0A = NULL, hx0A = NULL, sx0A = NULL,
    tcutx0B = NULL, hx0B = NULL, sx0B = NULL, tcutx1A = NULL,
    hx1A = NULL, sx1A = NULL, tcutx1B = NULL, hx1B = NULL, sx1B = NULL,
    noncompliance = c("none", "crossover", "mixed", "user"),
    gradual = FALSE, WtFun = c("FH", "SFH", "Ramp"), ppar = cbind(c(0, 0)),
    Spend.Info = c("Variance", "Events", "Hybrid(k)", "Calendar"), RR.Futility = NULL,
    qProp.one.or.Q = c("one", "Q"), Nsim = NULL, detail = FALSE, StatType = c("WLR",
        "ISD"))
```

Arguments

`EfficacyBoundary`

This specifies the method used to construct the efficacy boundary. The available choices are

(i) `Lan-Demets(alpha=<total type I error>, spending=<spending function>)`. The Lan-Demets method is based upon a error probability spending approach. The spending function can be set to `ObrienFleming`, `Pocock`, or `Power(rho)`, where `rho` is the the power argument for the power spending function: rho=3 is roughly equivalent to the O'Brien-Fleming spending function and smaller powers result in a less conservative spending function.

(ii) `Haybittle(alpha=<total type I error>, b.Haybittle=<user specified boundary point>)`. The Haybittle approach is the simplest, which sets

the boundary points equal to `b.Haybittle`, a user specified value (try 3) for all analyses except the last, which is calculated so as to result in the total type I error, set with the argument `alpha`.

(iii) `SC(alpha=<total type I error>, crit=<threshold for conditional type I error for efficacy stopping>)`. The stochastic curtailment method is based upon the conditional probability of type I error given the current value of the statistic. Under this method, a sequence of boundary points on the standard normal scale (as are boundary points under all other methods) is calculated so that the total probability of type I error, `alpha`, is maintained. This is done by considering the joint probabilities of continuing to the current analysis and then exceeding the threshold at the current analysis. A good value for the threshold value for the conditional type I error, `crit` is 0.90 or greater.

(iv) User supplied boundary points in the form `c(b1, b2, b3, ..., b_m)`, where `m` is the number of looks.

`FutilityBoundary`

This specifies the method used to construct the futility boundary. The available choices are

(i) `Lan-Demets(alpha=<total type II error>, spending=<spending function>)`. The Lan-Demets method is based upon a error probability spending approach. The spending function can be set to `ObrienFleming`, `Pocock`, or `Power(rho)`, where `rho` is the the power argument for the power spending function: rho=3 is roughly equivalent to the O'Brien-Fleming spending function and smaller powers result in a less conservative spending function.

(ii) `Haybittle(alpha=<total type I error>, b.Haybittle=<user specified boundary point>)`. The Haybittle approach is the simplest, which sets the boundary points equal to `b.Haybittle`, a user specified value (try 3) for all analyses except the last, which is calculated so as to result in the total type II error, set with the argument `alpha`.

(iii) `SC(alpha=<total type II error>, crit=<threshold for conditional type II error for futility stopping>, drift.end=<projected drift at end of trial>)`. The stochastic curtailment method is based upon the conditional probability of type II error given the current value of the statistic. Under this method, a sequence of boundary points on the standard normal scale (as are boundary points under all other methods) is calculated so that the total probability of type II error, `alpha`, is maintained. This is done by considering the joint probabilities of continuing to the current analysis and then exceeding the threshold at the current analysis. A good value for the threshold value for the conditional type I error, `crit` is 0.90 or greater.

(iv) User supplied boundary points in the form `c(b1, b2, b3, ..., b_m)`, where `m` is the number of looks.

`sided` If two-sided tests of H0, set to "2" (quoted). If one-sided test of H0, set to ">" for upper tail, "<" for lower tail. If `method`=="S" then this must be of the same length as `StatType` because the interpretation of `sided` is different depending upon whether `StatType`=="WLR" (negative is benefit) or `StatType`=="ISD" (positive is benefit)

`method` Determines how to calculate the power. Set to "A" (Asymptotic method, the default) or "S" (Simulation method)

accru	The upper endpoint of the accrual period beginning with time 0.
accrat	The rate of accrual per unit of time.
tlook	The times of planned interim analyses.
tcut0	Left hand endpoints for intervals upon which the arm-0 specific mortality is constant. The last given component is the left hand endpoint of the interval having right hand endpoint infinity.
h0	A vector of the same length as tcut0 which specifies the piecewise constant arm-0 mortality rate.
s0	Alternatively, the arm-0 mortality distribution can be supplied via this argument, in terms of of the corresponding survival function values at the times given in the vector tcut0. If s0 is supplied, then h0is derived internally, assuming the piecewise exponential distrubiton. If you specify s0, the first element must be 1, and correspondingly, the first component of tcut0 will be the lower support point of the distribution. You must supply either h0 or s0 but not both.
tcut1	Left hand endpoints for intervals upon which the arm-1 specific mortality is constant. The last given component is the left hand endpoint of the interval having right hand endpoint infinity.
rhaz	A vector of piecewise constant arm-1 versus arm-0 mortality rate ratios. If tcut1 and tcut0 are not identical, then tcut1, h0, and rhaz are internally rederived at the union of the sequences tcut0 and tcut1. In all cases the arm-1 mortality rate is then derived at the time cutpoints tcut1 as rhaz $\times$ h0.
h1	Alternatively, the arm-1 mortality distribution can be supplied via this argument by specifying the piecewise constant arm-1 mortality rate. See the comments above.
s1	Alternatively, the arm-1 mortality distribution can be supplied via this argument, in terms of of the corresponding survival function values at the times given in the vector tcut1. Comments regarding s0 above apply here as well. You must supply exactly one of the following: h1, rhaz, or s1.
tcutc0	Left hand endpoints for intervals upon which the arm-0 specific censoring distribution hazard function is constant. The last given component is the left hand endpoint of the interval having right hand endpoint infinity.
hc0	A vector of the same length as tcutc0 which specifies the arm-0 censoring distribution in terms of a piecewise constant hazard function.
sc0	Alternatively, the arm-0 censoring distribution can be supplied via this argument, in terms of of the corresponding survival function values at the times given in the vector tcutc0. See comments above. You must supply either hc0 or sc0 but not both.
tcutc1	Left hand endpoints for intervals upon which the arm-1 specific censoring distribution hazard function is constant. The last given component is the left hand endpoint of the interval having right hand endpoint infinity.
hc1	A vector of the same length as tcutc1 which specifies the arm-1 censoring distribution in terms of a piecewise constant hazard function.
sc1	Alternatively, the arm-1 censoring distribution can be supplied via this argument, in terms of of the corresponding survival function values at the times given in the vector tcutc1. See comments above. You must supply either hc1 or sc1 but not both.

`noncompliance` (i) Seting `noncompliance` to "none" for no non-compliance will automatically set the non-compliance arguments, below, to appropriate values for no compliance. This requires no additional user specification of non-compliance parameters. (ii) Setting `noncompliance` to "crossover" will automatically set crossover values in the arm 0/1 specific *post-cause-B-delay-mortality* for cross-over, i.e. simple interchange of the arm 0 and arm 1 mortalities. The user is required to specify all parameters corresponding to the arm 0/1 specific *cause-B-delay* distributions. The *cause-A-delay* and *post-cause-A-delay-mortality* are automatically set so as not to influence the calculations. Setting `noncompliance` to "mixed" will set the arm 0/1 specific *post-cause-B-delay-mortality* distributions for crossover as defined above. The user specifies the arm 0/1 specific *cause-B-delay* distribution as above, and in addition, all parameters related to the arm 0/1 specific *cause-A-delay* distributions and corresponding arm 0/1 specific *post-cause-A-delay-mortality* distributions. (iii) Setting `noncompliance` to "user" requires the user to specify all non-compliance distribution parameters.

`tcutd0A` Left hand endpoints for intervals upon which the arm-0 specific *cause-A delay* distribution hazard function is constant. The last given component is the left hand endpoint of the interval having right hand endpoint infinity. Required only when `noncompliance` is set to "mixed" or "user".

`hd0A` A vector of the same length as `tcutd0A` containing peicewise constant hazard rates for the arm-0 *cause-A delay* distribution. Required only when `noncompliance` is set to "mixed" or "user".

`sd0A` When required, the arm-0 *cause-A-delay* distribution is alternately specified via a survival function. A vector of the same length as `tcutd0A`.

`tcutd0B` Left hand endpoints for intervals upon which the arm-0 specific *cause-B delay* distribution hazard function is constant. The last given component is the left hand endpoint of the interval having right hand endpoint infinity. Always required when `noncompliance` is set to any value other than "none".

`hd0B` A vector of the same length as `tcutd0B` containing peicewise constant hazard rates for the arm-0 *cause-B delay* distribution. Always required when `noncompliance` is set to any value other than "none".

`sd0B` When required, the arm-0 *cause-B-delay* distribution is alternately specified via a survival function. A vector of the same length as `tcutd0B`.

`tcutd1A` Left hand endpoints for intervals upon which the arm-1 specific *cause-A delay* distribution hazard function is constant. The last given component is the left hand endpoint of the interval having right hand endpoint infinity. Required only when `noncompliance` is set to "mixed" or "user".

`hd1A` A vector of the same length as `tcutd1A` containing peicewise constant hazard rates for the arm-1 *cause-A delay* distribution. Required only when `noncompliance` is set to "mixed" or "user".

`sd1A` When required, the arm-1 *cause-A-delay* distribution is alternately specified via a survival function. A vector of the same length as `tcutd1A`.

`tcutd1B` Left hand endpoints for intervals upon which the arm-1 specific *cause-B delay* distribution hazard function is constant. The last given component is the left hand endpoint of the interval having right hand endpoint infinity. Always required when `noncompliance` is set to any value other than "none".

`hd1B` A vector of the same length as `tcutd1B` containing peicewise constant hazard rates for the arm-1 *cause-B delay* distribution. Always required when `noncompliance` is set to any value other than "none".

`sd1B` When required, the arm-1 *cause-A-delay* distribution is alternately specified via a survival function. A vector of the same length as `tcutd1A`.

`tcutx0A` Left hand endpoints for intervals upon which the arm-0 specific *post-cause-A-delay-mortality* rate is constant. The last given component is the left hand endpoint of the interval having right hand endpoint infinity. Required only when `noncompliance` is set to "mixed" or "user".

`hx0A` A vector of the same length as `tcutx0A` containing the arm-0 *post-cause-A-delay mortality* rates. Required only when `noncompliance` is set to "mixed" or "user".

`sx0A` When required, the arm-0 *post-cause-A-delay mortality* distribution is alternately specified via a survival function. A vector of the same length as `tcutx0A`.

`tcutx0B` Left hand endpoints for intervals upon which the arm-0 specific *post-cause-B-delay-mortality* rate is constant. The last given component is the left hand endpoint of the interval having right hand endpoint infinity. Always required when `noncompliance` is set to any value other than "none".

`hx0B` A vector of the same length as `tcutx0B` containing the arm-0 *post-cause-B-delay mortality* rates. Always required when `noncompliance` is set to any value other than "none".

`sx0B` When required, the arm-0 *post-cause-B-delay mortality* distribution is alternately specified via a survival function. A vector of the same length as `tcutx0B`.

`tcutx1A` Left hand endpoints for intervals upon which the arm-1 specific *post-cause-A-delay-mortality* rate is constant. The last given component is the left hand endpoint of the interval having right hand endpoint infinity. Required only when `noncompliance` is set to "mixed" or "user".

`hx1A` A vector of the same length as `tcutx1A` containing the arm-1 *post-cause-A-delay mortality* rates. Required only when `noncompliance` is set to "mixed" or "user".

`sx1A` When required, the arm-1 *post-cause-A-delay mortality* distribution is alternately specified via a survival function. A vector of the same length as `tcutx1A`.

`tcutx1B` Left hand endpoints for intervals upon which the arm-1 specific *post-cause-B-delay-mortality* rate is constant. The last given component is the left hand endpoint of the interval having right hand endpoint infinity. Always required when `noncompliance` is set to any value other than "none".

`hx1B` A vector of the same length as `tcutx1B` containing the arm-1 *post-cause-B-delay mortality* rates. Always required when `noncompliance` is set to any value other than "none".

`sx1B` When required, the arm-1 *post-cause-B-delay mortality* distribution is alternately specified via a survival function. A vector of the same length as `tcutx1B`.

`gradual` Should the conversion to post-noncompliance mortality be gradual. Under the default behavior, `gradual=FALSE`, there is an immediate conversion to the post-noncompliance mortality rate function. If `gradual` is set to

TRUE then this conversion is done "gradually". In truth, at the individual level what is done is that the new mortality rate function is a convex combination of the pre-noncompliance mortality and the post-noncompliance mortality, with the weighting in proportion to the time spent in compliance with the study arm protocal.

WtFun — Specifies the name of a weighting function (of time) for assigning relative weights to events according to the times at which they occur. The default, "FH", a two parameter weight function, specifies the 'Fleming-Harrington' g-rho family of weighting functions defined as the pooled arm survival function (Kaplan-Meier estimate) raised to the g times its complement raised to the rho. Note that g=rho=0 corresponds to the unweighted log-rank statistic. A second choice is the "SFH" function, (for 'Stopped Fleming-Harrington'), meaning that the "FH" weights are capped at their value at a user specified time, which has a total of 3 parameters. A third choice is Ramp(tcut). Under this choice, weights are assigned in a linearly manner from time 0 until a user specified cut-off time, tcut, after which events are weighted equally. It is possible to conduct computations on nstat candidate statistics within a single run. In this case, WtFun should be a character vector of length nstat having components set from among the available choices.

ppar — A vector containing all the weight function parameters, in the order determined by that of "WtFun". For example, if WtFun is set to c("FH","SFH","Ramp") then ppar should be a vector of length six, with the "FH" parameters in the first two elements, "SFH" parameters in the next 3 elements, and "Ramp" parameter in the last element.

RR.Futility — The relative risk corresponding to the alternative alternative hypothesis that is required in the construction of the futility boundary. Required if Boundary.Futility is set to a non-null value.

Spend.Info — When the test statistic is something other than the unweighted log-rank statistic, the variance information, i.e. the ratio of variance at interim analysis to variance at the end of trial, is something other than the ratio of events at interim analysis to the events at trial end. The problem is that in practice one doesn't necessarily have a good idea what the end of trial variance should be. In this case the user may wish to spend the type I and type II error probabilities according to a different time scale. Possible choices are "Variance", (default), which just uses the variance ratio scale, "Events", which uses the events ratio scale, "Hybrid(k)", which makes a linear transition from the "Variance" scale to the "Events" scale beginning with analysis number k. The last choice, "Calendar", uses the calendar time scale

qProp.one.or.Q — If a futility boundary is specified, what assumption should be made about the drift function (the mean value of the weighted log-rank statistic at analysis j normalized by the square root of the variance function at analysis k). In practice we don't presume to know the shape of the drift function. Set to "one" or "Q". The choice "one" results in a more conservative boundary.

Nsim — If you specify method=="S", then you must specify the number of simulations. 1000 should be sufficient.

detail — If you specify method=="S", and want to see the full level of detail regarding arguments returned from the C level code, specify detail==TRUE

`StatType` If you specify `method`=="S", then the available choices are "WLR" (weighted log-rank) and "ISD" (integrated survival difference).

Value

Returns a value of class `PwrGSD` which has components listed below. Note that the print method will display a summary table of estimated powers and type I errors as a `nstat` by 2 matrix. The summary method returns the same object invisibly, but after computing the summary table mentioned above, and it is included in the returned value as a commponent `TBL`. See examples below.

`dPower` A `length(tlook)` by `nstat` matrix containing in each column, an increment in power that resulted at that analysis time for the given statistic.

`dErrorI` A `length(tlook)` by `nstat` matrix containing in each column, an increment in type I error that resulted at that analysis time for the given statistic. Always sums to the total alpha specified in `alphatot`

`detail` A list with components equal to the arguments of the C-call, which correspond in a natural way to the arguments specified in the R call, along with the computed results in `palpha0vec`, `palpha1vec`, `inffrac`, and `mu`. The first two are identical to `dErrorI` and `dPower`, explained above. The last two are `length(tlook)` by `nstat` matrices. For each statistic specified in `par`, the corresponding columns of `pinffrac` and `mu` contain the information fraction and drift at each of the analysis times.

`call` the call

Author(s)

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References

Gu, M.-G. and Lai, T.-L. "Determination of power and sample size in the design of clinical trials with failure-time endpoints and interim analyses." Controlled Clinical Trials 20 (5): 423-438. 1999

Izmirlian, G. "The PwrGSD package." NCI Div. of Cancer Prevention Technical Report. 2004

Jennison, C. and Turnbull, B.W. (1999) Group Sequential Methods: Applications to Clinical Trials Chapman & Hall/Crc, Boca Raton FL

Proschan, M.A., Lan, K.K.G., Wittes, J.T. (2006), corr 2nd printing (2008) Statistical Monitoring of Clinical Trials A Unified Approach Springer Verlag, New York

See Also

`cpd.PwrGSD`

Examples

```
library(PwrGSD)

test.example <-
  PwrGSD(EfficacyBoundary = LanDemets(alpha = 0.05, spending = ObrienFleming),
         FutilityBoundary = LanDemets(alpha = 0.1, spending = ObrienFleming),
         RR.Futility = 0.82, sided="<",method="A",accru =7.73, accrat =9818.65,
```

```
tlook =c(7.14, 8.14, 9.14, 10.14, 10.64, 11.15, 12.14, 13.14,
         14.14, 15.14, 16.14, 17.14, 18.14, 19.14, 20.14),
tcut0 =0:19, h0 =c(rep(3.73e-04, 2), rep(7.45e-04, 3),
                   rep(1.49e-03, 15)),
tcut1 =0:19, rhaz =c(1, 0.9125, 0.8688, 0.7814, 0.6941,
                     0.6943, 0.6072, 0.5202, 0.4332, 0.6520,
                     0.6524, 0.6527, 0.6530, 0.6534, 0.6537,
                     0.6541, 0.6544, 0.6547, 0.6551, 0.6554),
tcutc0 =0:19, hc0 =c(rep(1.05e-02, 2), rep(2.09e-02, 3),
                     rep(4.19e-02, 15)),
tcutc1 =0:19, hc1 =c(rep(1.05e-02, 2), rep(2.09e-02, 3),
                     rep(4.19e-02, 15)),
tcutd0B =c(0, 13), hd0B =c(0.04777, 0),
tcutd1B =0:6, hd1B =c(0.1109, 0.1381, 0.1485, 0.1637, 0.2446,
                      0.2497, 0),
noncompliance =crossover, gradual =TRUE,
WtFun =c("FH", "SFH", "Ramp"),
ppar =c(0, 1, 0, 1, 10, 10))
```

`cpd.PwrGSD` *Create a skeleton compound PwrGSD object*

Description

Given a user defined indexing dataframe as its only argument, creates a skeleton compound PwrGSD object having a component `Elements`, a list of `PwrGSD` objects, of length equal to the number of rows in the indexing dataframe

Usage

```
cpd.PwrGSD(descr)
```

Arguments

`descr`	A dataframe of a number of rows equal to the length of the resulting list, `Elements`, of `PwrGSD` objects. The user defines the mapping between rows of `descr` and components of `Elements` and uses it to set up a loop over scenarios. There are several S3 classes and methods for example `plot.cpd.PwrGSD`, which exploit this mapping between characteristics of a run and the rows of `desr` for subsetting and constructing conditioned plots. See the example below.

Value

An object of class `cpd.PwrGSD` containing elements:

`date`	the POSIX date that the object was created–its quite useful
`Elements`	a list of length equal to the number of rows of `descr` which will later contain objects of class `PwrGSD`
`descr`	a copy of the indexing dataframe argument for use in navigating the compound object in subsequent calls to other functions such as the related `plot` method, and the subset extractor, `Elements`

Note

A `cpd.PwrGSD` object essentially a list of `PwrGSD` objects that a user may set up in order to investigate the space of possible trial scenarios, test statistics, and boundary construction options. One could store a list of results without appealing at all to these internal indexing capabilities. The advantage of setting up a `cpd.PwrGSD` object is the nice summarization functionality provided, for example the plot method for the `cpd.PwrGSD` class.

The key ingredient to (i) the construction of the empty object, (ii) and summarizing the results in tabular or plotted form via its manipulation in subsequent function calls, is the indexing dataset, `descr` (for description). The correspondence between rows of `descr` and elements in the list of `PwrGSD` objects is purposely left very loose. In the example outlined below, the user creates a "base case" call to `PwrGSD` and then decides which quantities in this "base case" call to vary in order to navigate the space of possible trial scenarios, monitoring statistics and boundary construction methods. Next, for each one of these settings being varied, a variable with levels that determine each possible setting is created. The dataset `descr` is created with one line corresponding to each combination of the selection variables so created. In order to ensure that there is 1-1 correspondence between the order of the rows in `descr` and the order in the list `Elements` of `PwrGSD` objects, the user carries out the computation in a loop over rows of `descr` in which the values of the selection variables in each given row of `descr` are used to create the corresponding component of `Elements` via an update the "base case" call.

Author(s)

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See Also

`Elements`, `plot.cpd.PwrGSD` and `Power`

Examples

```
## don't worry--these examples are guaranteed to work,
## its just inconvenient for the package checker
## Not run:
  library(PwrGSD)

## In order to set up a compound object of class `cpd.PwrGSD'
## we first construct a base case: a two arm trial randomized in just
## under eight years with a maximum of 20 years of follow-up.
## We compute power at a specific alternative, `rhaz', under
## an interim analysis plan with roughly one annual analysis, some
## crossover between intervention and control arms, with Efficacy
## and futility boundaries constructed via the Lan-Demets procedure
## with O'Brien-Fleming spending on the hybrid scale. Investigate
## the behavior of three weighted log-rank statistics.

test.example <-
  PwrGSD(EfficacyBoundary = LanDemets(alpha = 0.05, spending = ObrienFleming),
         FutilityBoundary = LanDemets(alpha = 0.1, spending = ObrienFleming),
         RR.Futility = 0.82, sided="<",method="A",accru =7.73, accrat =9818.65,
         tlook =c(7.14, 8.14, 9.14, 10.14, 10.64, 11.15, 12.14, 13.14,
                  14.14, 15.14, 16.14, 17.14, 18.14, 19.14, 20.14),
         tcut0 =0:19, h0 =c(rep(3.73e-04, 2), rep(7.45e-04, 3),
                            rep(1.49e-03, 15)),
```

```
          tcut1 =0:19, rhaz =c(1, 0.9125, 0.8688, 0.7814, 0.6941,
                               0.6943, 0.6072, 0.5202, 0.4332, 0.6520,
                               0.6524, 0.6527, 0.6530, 0.6534, 0.6537,
                               0.6541, 0.6544, 0.6547, 0.6551, 0.6554),
          tcutc0 =0:19, hc0 =c(rep(1.05e-02, 2), rep(2.09e-02, 3),
                               rep(4.19e-02, 15)),
          tcutc1 =0:19, hc1 =c(rep(1.05e-02, 2), rep(2.09e-02, 3),
                               rep(4.19e-02, 15)),
          tcutd0B =c(0, 13), hd0B =c(0.04777, 0),
          tcutd1B =0:6, hd1B =c(0.1109, 0.1381, 0.1485, 0.1637, 0.2446,
                                0.2497, 0),
          noncompliance =crossover, gradual =TRUE,
          WtFun =c("FH", "SFH", "Ramp"),
          ppar =c(0, 1, 0, 1, 10, 10))

## we will construct a variety of alternate hypotheses relative to the
## base case specified above

  rhaz <-
    c(1, 0.9125, 0.8688, 0.7814, 0.6941, 0.6943, 0.6072, 0.5202, 0.4332,
    0.652, 0.6524, 0.6527, 0.653, 0.6534, 0.6537, 0.6541, 0.6544,
    0.6547, 0.6551, 0.6554)

  max.effect <- 0.80 + 0.05*(0:8)
  n.me <- length(max.effect)

## we will also vary extent of censoring relative to the base case
## specified above

  hc <- c(rep(0.0105, 2), rep(0.0209, 3), rep(0.0419, 15))

  cens.amt <- 0.75 + 0.25*(0:2)
  n.ca <- length(cens.amt)

## we may also wish to compare the Lan-Demets/O'Brien-Fleming efficacy
## boundary with a Pocock efficacy boundary

  Eff.bound.choice <- 1:2
  ebc.nms <- c("LanDemets(alpha=0.05, spending=ObrienFleming)",
               "SC(alpha=0.05, crit=0.90)")
  n.ec <- length(Eff.bound.choice)

## The following line creates the indexing dataframe, `descr', with one
## line for each possible combination of the selection variables we've
## created.

  descr <- as.data.frame(
              cbind(Eff.bound.choice=rep(Eff.bound.choice, each=n.ca*n.me),
                    cens.amt=rep(rep(cens.amt, each=n.me), n.ec),
                    max.effect=rep(max.effect, n.ec*n.ca)))

  descr$Eff.bound.choice <- ebc.nms[descr$Eff.bound.choice]

## Now descr contains one row for each combination of the levels of
## the user defined selection variables, `Eff.bound.choice',
## `max.effect' and `cens.amt'. Keep in mind that the names and number
## of these variables is arbitrary. Next we create a skeleton
```

```
## `cpd.PwrGSD' object with a call to the function `cpd.PwrGSD' with
## argument `descr'

  test.example.set <- cpd.PwrGSD(descr)

## Now, the newly created object, of class `cpd.PwrGSD', contains
## an element `descr', a component `date', the date created
## and a component `Elements', an empty list of length equal
## to the number of rows in `descr'.  Next we do the computation in
## a loop over the rows of `descr'.

  n.descr <- nrow(descr)

  for(k in 1:n.descr){

    ## First, we copy the original call to the current call,
    ## `Elements[[k]]$call'

    test.example.set$Elements[[k]]$call <- test.example$call

    ## Use the efficacy boundary choice in the kth row of `descr'
    ## to set the efficacy boundary choice in the current call

    test.example.set$Elements[[k]]$call$EfficacyBoundary <-
    parse(text=as.character(descr[k,"Eff.bound.choice"]))[[1]]

    ## Derive the `rhaz' defined by the selection variable "max.effect"
    ## in the kth row of `descr' and use this to set the `rhaz'
    ## components of the current call

    test.example.set$Elements[[k]]$call$rhaz <-
                           exp(descr[k,"max.effect"] * log(rhaz))

    ## Derive the censoring components from the selection variable
    ## "cens.amt" in the kth row of `descr' and place that result
    ## into the current call

    test.example.set$Elements[[k]]$call$hc0 <-
    test.example.set$Elements[[k]]$call$hc1 <-
                              exp(descr[k, "cens.amt"] * log(hc))

    ## Now the current call corresponds exactly to the selection
    ## variable values in row `k' of `descr'. The computation is
    ## done by calling `update'

    test.example.set$Elements[[k]] <-
                         update(test.example.set$Elements[[k]])
    cat(k/n.descr, "\r")
  }

  ## We can create a new `cpd.PwrGSD' object by subsetting on
  ## the selection variables in `descr':

  Elements(test.example.set,
           subset=(substring(Eff.bound.choice, 1,9)=="LanDemets" &
                           max.effect >= 1))
```

```
## or we can plot the results -- see the help under `plot.cpd.PwrGSD'

plot(test.example.set, formula = ~ max.effect | stat * cens.amt,
     subset=(substring(Eff.bound.choice, 1,9)=="LanDemets"))

plot(test.example.set, formula = ~ max.effect | stat * cens.amt,
     subset=(substring(Eff.bound.choice, 1,2)=="SC"))

## Notice the appearance of the selection variable `stat' which was
## not defined in the dataset `descr'.

## Recall that each single "PwrGSD" object can contain results
## for a list of test statistics, as in the example shown here where
## we have results on three statistics per component of `Elements'.
## For this reason the variable `stat' can be also be referenced in
## the `subset' or `formula' arguments of calls to this `plot' method,
## and in the `subset' argument of the function `Power' shown below.

## The function `Power' is used to convert the `cpd.PwrGSD' object
## into  a dataframe, stacked by rows of `descr' and by `stat'
## (there are three statistics being profiled per each component of
## `Elements'), for generating tables or performing other
## computations.

Power(test.example.set,
      subset=(substring(Eff.bound.choice, 1,2)=="SC" & stat %in% c(1,3)))

## End(Not run)
```

`Power` *Extract the Power results*

Description

Extract the Power results from a compound object into a Stacked Dataframe

Usage

```
Power(object, subset)
```

Arguments

`object`	an object of class `cpd.PwrGSD`
`subset`	you may extract a subset via a logical expression in the variables of the index dataframe, `descr`

Value

an object of class `cpd.PwrGSD`. See help on that topic for details.

Author(s)

Grant Izmirlian <izmirlian@nih.gov>

See Also

`cpd.PwrGSD` and `PwrGSD`

Examples

```
## See the `cpd.PwrGSD' example
```

`Elements` *Create a subset of a "cpd.PwrGSD" object*

Description

Create a subset of a `cpd.PwrGSD` object

Usage

```
Elements(object, subset, na.action = na.pass)
```

Arguments

`object`	an object of class `cpd.PwrGSD`
`subset`	you may extract a subset via a logical expression in the variables of the index dataframe, `descr`
`na.action`	a method for handling `NA` values in the variables in the subset expression.

Value

an object of class `cpd.PwrGSD`. See help on that topic for details.

Author(s)

Grant Izmirlian <izmirlian@nih.gov>

See Also

`cpd.PwrGSD` and `PwrGSD`

Examples

```
## See the `cpd.PwrGSD' example
```

`plot.cpd.PwrGSD` *Plot Method for cpd.PwrGSD objects*

Description

Creates a trellis plot of type II error probability and power at each interim analysis, stacked, versus an effect size variable, conditioned upon levels of up to two factors.

Usage

```
## S3 method for class 'cpd.PwrGSD':
plot(x, formula, subset, na.action,...)
```

Arguments

`x`	an object of class `cpd.PwrGSD`
`formula`	a one sided formula of the form `~ effect | f1` or `~ effect | f1 * f2` where `effect`, `f1`, and `f2` are variables in the indexing dataframe `descr`, or the special variable `stat` which may be used when there are multiple test statistics per component of `Elements`. See the example in the documentation for `cpd.PwrGSD`
`subset`	the plot can be applied to a subset of rows of `descr` via a logical expression on its variables in combination with the special variable, `stat` when applicable.
`na.action`	a `na.action` method for handling `NA` values
`...`	other parameters to pass to the R function `coplot` usually not neccesary

Value

Returns the object, `x`, invisibly

Note

This processes the `cpd.PwrGSD` object into a dataframe, stacked on interim looks and then passes the results to the R function `coplot`

Author(s)

Abovementioned `cpd.PwrGSD` processing done by Grant Izmirlian <izmirlian@nih.gov>

References

Chambers, J. M. (1992) *Data for models.* Chapter 3 of *Statistical Models in S* eds J. M. Chambers and T. J. Hastie, Wadsworth & Brooks/Cole.

Cleveland, W. S. (1993) *Visualizing Data.* New Jersey: Summit Press.

See Also

`cpd.PwrGSD` `Power` and `Elements`

Examples

```
## See the example in the 'cpd.PwrGSD' documentation
```

`GrpSeqBnds` *Computes efficacy and futility boundaries*

Description

This computes efficacy and futility boundaries for interim analysis and sequential designs. Two sided symmetric efficacy boundaries can be computed by specifying half of the intended total type I error probability in the argument, `Alpha.Efficacy`. Otherwise, especially in the case of efficacy and futility bounds only one sided boundaries are currently computed. The computation allows for two different time scales–one must be the variance ratio, and the second can be a user chosen increasing scale beginning with 0 that takes the value 1 at the conclusion of the trial.

Usage

```
GrpSeqBnds(EfficacyBoundary = LanDemets(alpha = 0.05, spending = ObrienFleming),
           FutilityBoundary = LanDemets(alpha = 0.1, spending = ObrienFleming),
           frac, frac.ii = NULL, drift = rep(0, length(frac)))
```

Arguments

`EfficacyBoundary`

This specifies the method used to construct the efficacy boundary. The available choices are

(i) `Lan-Demets(alpha=<total type I error>, spending=<spending function>)`. The Lan-Demets method is based upon a error probability spending approach. The spending function can be set to `ObrienFleming`, `Pocock`, or `Power(rho)`, where `rho` is the the power argument for the power spending function: rho=3 is roughly equivalent to the O'Brien-Fleming spending function and smaller powers result in a less conservative spending function.

(ii) `Haybittle(alpha=<total type I error>, b.Haybittle=<user specified boundary point>)`. The Haybittle approach is the simplest, which sets the boundary points equal to `b.Haybittle`, a user specified value (try 3) for all analyses except the last, which is calculated so as to result in the total type I error, set with the argument `alpha`.

(iii) `SC(alpha=<total type I error>, crit=<threshold for conditional type I error for efficacy stopping>)`. The stochastic curtailment method is based upon the conditional probability of type I error given the current value of the statistic. Under this method, a sequence of boundary points on the standard normal scale (as are boundary points under all other methods) is calculated so that the total probability of type I error, `alpha`, is maintained. This is done by considering the joint probabilities of continuing to the current analysis and then exceeding the threshold at the current analysis. A good value for the threshold value for the conditional type I error, `crit` is 0.90 or greater.

(iv) User supplied boundary points in the form `c(b1, b2, b3, ..., b_m)`, where `m` is the number of looks.

`FutilityBoundary`

This specifies the method used to construct the futility boundary. The available choices are

(i) `Lan-Demets(alpha=<total type II error>, spending=<spending function>)`. The Lan-Demets method is based upon a error probability spending approach. The spending function can be set to `ObrienFleming`, `Pocock`, or `Power(rho)`, where `rho` is the the power argument for the power spending function: rho=3 is roughly equivalent to the O'Brien-Fleming spending function and smaller powers result in a less conservative spending function.

(ii) `Haybittle(alpha=<total type I error>, b.Haybittle=<user specified boundary point>)`. The Haybittle approach is the simplest, which sets the boundary points equal to `b.Haybittle`, a user specified value (try 3) for all analyses except the last, which is calculated so as to result in the total type II error, set with the argument `alpha`.

(iii) `SC(alpha=<total type II error>, crit=<threshold for conditional type II error for futility stopping>, drift.end=<projected drift at end of trial>)`. The stochastic curtailment method is based upon the conditional probability of type II error given the current value of the statistic. Under this method, a sequence of boundary points on the standard normal scale (as are boundary points under all other methods) is calculated so that the total probability of type II error, `alpha`, is maintained. This is done by considering the joint probabilities of continuing to the current analysis and then exceeding the threshold at the current analysis. A good value for the threshold value for the conditional type I error, `crit` is 0.90 or greater.

(iv) User supplied boundary points in the form `c(b1, b2, b3,..., b_m)`, where `m` is the number of looks.

`frac` The variance ratio. If the end of trial variance is unknown then normalize all previous variances by the current variance. In this case you must specify a second scale that is monotone increasing from 0 to 1 at the end of the trial. Required.

`frac.ii` The second information scale that is used for type I and type II error probability spending. Optional (see above)

`drift` The drift function of the underlying brownian motion, which is the expected value under the design alternative of the un-normalized weighted log-rank statistic, then normalized to have variance one when the variance ratio equals 1. See the examples below.

Value

An object of class `boundaries` with components: "table" "frac" "frac.ii" "drift" "call"

`call` The call that produced the returned results.

`frac` The vector of variance ratios.

`frac.ii` The vector of information ratios for type I and type II error probability spending, which differs from the above if the user sets the argument `frac.ii` to a second scale as mentioned above.

`drift` The drift vector that is required as an argument when futility boundaries are calculated.

`table` A matrix with components

frac The information ratio for type I and type II error probability spending.

b.f The calculated futility boundary (if requested).

alpha.f	The type II error probability spent at that analysis (if doing futility bounds).
cum-alpha.f	Cumulative sum of `alpha.f` (if doing futility bounds).
b.e	The calculated efficacy boundary.
alpha.e	The type I error probability spent at that analysis.
cum-alpha.e	Cumulative sum of `alpha.e`.

Author(s)

Grant Izmirlian <izmirlian@nih.gov>

References

Gu, M.-G. and Lai, T.-L. "Determination of power and sample size in the design of clinical trials with failure-time endpoints and interim analyses." Controlled Clinical Trials 20 (5): 423-438. 1999

Izmirlian, G. "The PwrGSD package." NCI Div. of Cancer Prevention Technical Report. 2004

Jennison, C. and Turnbull, B.W. (1999) Group Sequential Methods: Applications to Clinical Trials Chapman & Hall/Crc, Boca Raton FL

Proschan, M.A., Lan, K.K.G., Wittes, J.T. (2006), corr 2nd printing (2008) Statistical Monitoring of Clinical Trials A Unified Approach Springer Verlag, New York

See Also

`PwrGSD`

Examples

```
## NOTE: In an unweighted analysis, the variance ratios and event ratios
## are the same, whereas in a weighted analysis, they are quite different.
##
## For example, in a trial with 7 or so years of accrual and maximum follow-up of 20 years
## using the stopped Fleming-Harrington weights, `WtFun' = "SFH", with paramaters
## `ppar' = c(0, 1, 10) we might get the following vector of variance ratios:

frac    <- c(0.006995655, 0.01444565, 0.02682463, 0.04641363, 0.0585665,
             0.07614902, 0.1135391, 0.168252, 0.2336901, 0.3186155, 0.4164776,
             0.5352199, 0.670739, 0.8246061, 1)

## and the following vector of event ratios:

frac.ii <- c(0.1494354, 0.1972965, 0.2625075, 0.3274323, 0.3519184, 0.40231,
             0.4673037, 0.5579035, 0.6080742, 0.6982293, 0.7671917, 0.8195019,
             0.9045182, 0.9515884, 1)

## and the following drift under a given alternative hypothesis

drift <-   c(0.06214444, 0.1061856, 0.1731267, 0.2641265, 0.3105231, 0.3836636,
             0.5117394, 0.6918584, 0.8657705, 1.091984, 1.311094, 1.538582,
             1.818346, 2.081775, 2.345386)

## JUST ONE SIDED EFFICACY BOUNDARY
```

```
## In this call, we calculate a one sided efficacy boundary at each of 15 analyses
## which will occur at the given (known) variance ratios, and we use the variance
## ratio for type I error probability spending, with a total type I error probabilty
## of 0.05, using the Lan-Demets method with Obrien-Fleming spending (the default).

gsb.all.just.eff <- GrpSeqBnds(frac=frac,
                               EfficacyBoundary=LanDemets(alpha=0.05, spending=ObrienFleming))

## ONE SIDED EFFICACY AND FUTILTY BOUNDARIES
## In this call, we calculate a one sided efficacy boundary at each of 15 analyses
## which will occur at the given (known) variance ratios, and we use the variance
## ratio for type I and type II error probability spending, with a total type I error
## probabilty of 0.05 and a total type II error probability of 0.10, using the Lan-Demets
## method with Obrien-Fleming spending (the default) for both efficacy and futilty.

gsb.all.eff.fut <- GrpSeqBnds(frac=frac,
                              EfficacyBoundary=LanDemets(alpha=0.05, spending=ObrienFleming),
                              FutilityBoundary=LanDemets(alpha=0.10, spending=ObrienFleming),
                              drift=drift)

## Now suppose that we are performing the 7th interim analysis. We don't know what the variance
## will be at the end of the trial, so we normalize variances of the current and previous
## statistics by the variance of the current statistic.  This is equivalent to the following
## length 7 vector of variance ratios:

frac7 <- frac[1:7]/frac[7]

## To proceed under the "unknown variance at end of trial" case, we must use a second
## scale for spending type I and II error probabilty. Unlike the above scale
## which is renormalized at each analysis to have value 1 at the current analysis, the
## alpha spending scale must be monotone increasing and attain the value 1 only at the
## end of the trial. A natural choice is the event ratio, which is known in advance if
## the trial is run until a required number of events is obtained, a so called
## maximum information trial:

frac7.ii <- frac.ii[1:7]

## the first seven values of the drift function

drift7 <- drift[1:7]/frac[7]^0.5

gsb.1st7.eff.fut <- GrpSeqBnds(frac=frac7, frac.ii=frac7.ii,
                               EfficacyBoundary=LanDemets(alpha=0.05, spending=ObrienFleming),
                               FutilityBoundary=LanDemets(alpha=0.10, spending=ObrienFleming),
                               drift=drift7)

## Of course there are other options not covered in these examples but this should get you
## started
```

`CondPower` *Conditional type I and type II error probabilities given current value of the test statistic*

Description

Computes conditional type I and type II error probabilities given current value of the test statistic for monitoring based upon stochastic curtailment. This is now obsolete and included in the functionality of "GrpSeqBnds" and is here for instructional purposes only.

Usage

```
CondPower(Z, frac, drift, drift.end, err.I, sided = 1)
```

Arguments

`Z`	Current value of test statistic standardized to unit variance.
`frac`	Current value of the information fraction (variance fraction).
`drift`	Current value of the drift, i.e. the expected value of the test statistic normalized to have variance equal to the information fraction. Required if you want to compute conditional type II error, otherwise enter 0.
`drift.end`	Projected value of the drift at the end of the trial.
`err.I`	Overall (total) type I error probability
`sided`	Enter 1 or 2 for sided-ness of the test.

Value

A named numeric vector containing the two components "Pr.cond.typeIerr" and "Pr.cond.typeIIerr"

Author(s)

Grant Izmirlian <izmirlian@nih.gov>

References

A General Theory on Stochastic Curtailment for Censored Survival Data D. Y. Lin, Q. Yao, Zhiliang Ying Journal of the American Statistical Association, Vol. 94, No. 446 (Jun., 1999), pp. 510-521

See Also

`GrpSeqBnds`

Examples

```
## None as yet
```

`SimGSB` *Verifies the results of "GrpSeqBnds" via simulation*

Description

Verifies the results of `GrpSeqBnds` via simulation

Usage

```
SimGSB(object, nsim = 1e+05, ...)
```

Arguments

`object`	an object of class either `boundaries` or `PwrGSD`
`nsim`	number of simulations to do
`...`	if `object` is of class `PwrGSD` and there are more than one statistic under investigation, then you may specify an argument `stat`. The default value is 1, meaning the first one.

Value

A tabulation of the results

Author(s)

Grant Izmirlian <izmirlian@nih.gov

See Also

`GrpSeqBnds`

Examples

```
## none as yet
```

`as.boundaries` *Convert a "PwrGSD" object to a "boundaries" object*

Description

Convert a `PwrGSD` object to a `boundaries` object

Usage

```
as.boundaries(object, ...)
```

Arguments

`object`	an object of class `PwrGSD`
`...`	if `object` is of class `PwrGSD` and there are more than one statistic under investigation, then you may specify an argument `stat`. The default value is 1, meaning the first one.

Value

an object of class `boundaries`. See the documentation for `GrpSeqBnds`

Author(s)

Grant Izmirlian <izmirlian@nih.gov

See Also

`GrpSeqBnds`

Examples

```
## none as yet
```

`wtdlogrank` *Weighted log-rank test*

Description

Computes a two sample weighted log-rank statistic with events weighted according to one of the available weighting function choices

Usage

```
wtdlogrank(formula = formula(data), data = parent.frame(), WtFun = c("FH", "SFH", "Ramp"),
param = c(0, 0), sided = c(2, 1), subset, na.action, w = FALSE)
```

Arguments

`formula`	a formula of the form `Surv(Time, Event) ~ arm` where `arm` is a dichotomous variable with values 0 and 1.
`data`	a dataframe
`WtFun`	a selection from the available list: "FH" (Fleming-Harrington), "SFH" (stopped Fleming-Harrington) or "Ramp". See `param` in the following line.
`param`	Weight function parameters. Length and interpretation depends upon the selected value of `WtFun`: If `WtFun==\dQuote{FH}` then `param` is a length 2 vector specifying the power of the pooled (across arms) kaplan meier estimate and its complement. If `WtFun==\dQuote{SFH}` then `param` is a length 3 vector with first two components as in the "FH" case, and third component the time (in the same units as the time to event) at which the "FH" weight function is capped off at its current value. If `WtFun==\dQuote{SFH}` then `param` is of length 1 specifying the time (same units as time to event) at which events begin to get equal weight. The "Ramp" weight function is a linearly increasing deterministic weight function which is capped off at 1 at the user specified time.
`sided`	One or Two sided test? Set to 1 or 2
`subset`	Analysis can be applied to a subset of the dataframe based upon a logical expression in its variables
`na.action`	Method for handling `NA` values in the covariate, `arm`
`w`	currently no effect

Value

An object of class `survtest` containing components

`pn`	sample size
`wttyp`	internal representation of the `WtFun` argument
`par`	internal representation of the `param` argument
`time`	unique times of events accross all arms
`nrisk`	number at risk accross all arms at each event time
`nrisk1`	Number at risk in the experimental arm at each event time
`nevent`	Number of events accross all arms at each event time
`nevent1`	Number of events in the experimental arm at each event time
`wt`	Values of the weight function at each event time
`pntimes`	Number of event times
`stat`	The un-normalized weighted log-rank statistic, i.e. the summed weighted observed minus expected differences at each event time
`var`	Variance estimate for the above
`UQt`	Cumulative sum of increments in the sum resulting in `stat` above
`varQt`	Cumulative sum of increments in the sum resulting in `var` above
`var1t`	Cumulative sum of increments in the sum resulting in the variance of an unweighted version of the statistic
`pu0`	person units of follow-up time in the control arm
`pu1`	person units of follow-up time in the intervention arm
`n0`	events in the control arm
`n1`	events in the intervention arm
`n`	sample size, same as `pn`
`call`	the call that created the object

Author(s)

Grant Izmirlian <izmirlian@nih.gov>

References

Harrington, D. P. and Fleming, T. R. (1982). A class of rank test procedures for censored survival data. *Biometrika* **69**, 553-566.

See Also

`IntSurvDiff`

Examples

```
library(PwrGSD)
data(lung)
fit.wlr <- wtdlogrank(Surv(time, I(status==2))~I(sex==2), data=lung, WtFun="SFH", param=c(0,1,300))
```

IntSurvDiff *Weighted Integrated Survival function test*

Description

Computes a two sample weighted integrated survival function log-rank statistic with events weighted according to one of the available weighting function choices

Usage

```
IntSurvDiff(formula = formula(data), data = parent.frame(), WtFun = c("FH", "SFH", "Ramp")
            param = c(0, 0), sided = c(2, 1), subset, na.action, w = FALSE)
```

Arguments

formula	a formula of the form `Surv(Time, Event) ~ arm` where `arm` is a dichotomous variable with values 0 and 1.
data	a dataframe
WtFun	a selection from the available list: "FH" (Fleming-Harrington), "SFH" (stopped Fleming-Harrington) or "Ramp". See `param` in the following line.
param	Weight function parameters. Length and interpretation depends upon the selected value of `WtFun`: If `WtFun==\dQuote{FH}` then `param` is a length 2 vector specifying the power of the pooled (across arms) kaplan meier estimate and its complement. If `WtFun==\dQuote{SFH}` then `param` is a length 3 vector with first two components as in the "FH" case, and third component the time (in the same units as the time to event) at which the "FH" weight function is capped off at its current value. If `WtFun==\dQuote{SFH}` then `param` is of length 1 specifying the time (same units as time to event) at which events begin to get equal weight. The "Ramp" weight function is a linearly increasing deterministic weight function which is capped off at 1 at the user specified time.
sided	One or Two sided test? Set to 1 or 2
subset	Analysis can be applied to a subset of the dataframe based upon a logical expression in its variables
na.action	Method for handling `NA` values in the covariate, `arm`
w	currently no effect

Value

An object of class `survtest` containing components

pn	sample size
wttyp	internal representation of the `WtFun` argument
par	internal representation of the `param` argument
time	unique times of events accross all arms
nrisk	number at risk accross all arms at each event time
nrisk1	Number at risk in the experimental arm at each event time

`nevent`	Number of events accross all arms at each event time
`nevent1`	Number of events in the experimental arm at each event time
`wt`	Values of the weight function at each event time
`pntimes`	Number of event times
`stat`	The un-normalized weighted log-rank statistic, i.e. the summed weighted observed minus expected differences at each event time
`var`	Variance estimate for the above
`pu0`	person units of follow-up time in the control arm
`pu1`	person units of follow-up time in the intervention arm
`n0`	events in the control arm
`n1`	events in the intervention arm
`n`	sample size, same as `pn`
`call`	the call that created the object

Author(s)

Grant Izmirlian <izmirlian@nih.gov

References

Weiand S, Gail MH, James BR, James KL. (1989). A family of nonparametric statistics for comparing diagnostic makers with paired or unpaired data. *Biometrika* **76**, 585-592.

See Also

`wtdlogrank`

Examples

```
library(PwrGSD)
data(lung)
fit.isd <- IntSurvDiff(Surv(time, I(status==2))~I(sex==2), data=lung, WtFun="SFH", param=c(0,1,300))
```

`mysurvfit` *My Survfit*

Description

Computes numbers at risk, numbers of events at each unique event time within levels of a blocking factor

Usage

```
mysurvfit(formula = formula(data), data = parent.frame(), subset, na.action = na.fail)
```

Arguments

formula	Should be a formula of the form `Surv(ti, ev) ~ block` where `block` is the blocking factor. It need not be a factor per se but should have relatively few discrete levels. Sorry, no staggered entry allowed at present
data	a dataframe
subset	you can subset the analysis via logical expression in variables in the dataframe
na.action	pass a method for handling `NA` values in `block` such as `na.omit`, or `na.fail`

Value

A dataframe of `2*NLEV + 1` columns where `NLEV` is the number of levels of the factor `block`.

time	The sorted vector of unique event times from all blocks
nrisk1	The number at risk in block level 1 at each event time
nevent1	The number of events in block level 1 at each event time
...	
nriskNLEV	The number at risk in block level NLEV at each event time
neventNLEV	The number of events in block level NLEV at each event time

Author(s)

Grant Izmirlian <izmirlian@nih.gov>

Examples

```
library(PwrGSD)
data(lung)

fit.msf <- mysurvfit(Surv(time, I(status==2)) ~ sex, data=lung)

fit.msf
## Not run:
plot(fit.msf)

## End(Not run)
```

---

agghaz *Aggregated Hazard*

Description

Computes the MLE for the model that assumes piecewise constant hazards on intervals defined by a grid of points. One applications for example is to calculate monthly hazard rates given numbers of events, numbers at risk and event times reported to the day. Can also handle time to event data stratified on a blocking factor.

Usage

```
agghaz(t.agg, time, nrisk, nevent)
```

Arguments

`t.agg`	Vector defining intervals upon which the user wants constant hazard rates.
`time`	Event times, possibly stratified on a blocking factor into multiple columns, in units that occur in enough numbers per interval specified above. If there is just a single column then it must be in column form (see example below).
`nrisk`	Numbers at risk at specified event times
`nevent`	Numbers of events at specified event times

Value

`time.a`	User supplied left-hand endpoints of intervals of hazard constancy
`nrisk.a`	Numbers at risk on specified intervals
`nevent.a`	Numbers of events on specified intervals

Author(s)

Grant Izmirlian <izmirlian@nih.gov>

Examples

```
library(PwrGSD)
data(lung)
fit.msf <- mysurvfit(Surv(time, I(status==2)) ~ sex, data=lung)

## A single stratum:
with(fit.msf$Table, agghaz(30, time, cbind(nrisk1), cbind(nevent1)))

## Multiple strata--pooled and group 1:
with(fit.msf$Table, agghaz(30, time, cbind(nrisk1+nrisk2,nrisk1), cbind(nevent1+nevent2,nevent1)))
```

`mystack` *Stack a dataset*

Description

Given a dataframe containing one or more variables named with a common prefix, this function creates a stacked dataset with one set of observed values of the variables (in order of occurence) per line.

Usage

```
mystack(object, fu.vars, create.idvar = FALSE)
```

Arguments

`object`	a dataframe containing one or more variables named with a common prefix
`fu.vars`	a list of the unique prefixes
`create.idvar`	Do you want to add an ID variable with a common value given to all records resulting from a given input record? Default is `FALSE`

Value

A stacked dataframe

Author(s)

Grant Izmirlian <izmirlian@nih.gov>

Examples

```
## none as yet
```

`CDFOR2LRR` *Convert CDF Odds Ratio to Logged Relative Risks*

Description

A concise (1-5 lines) description of what the function does.

Usage

```
CDFOR2LRR(tcut, tmax, h0, CDFOR)
```

Arguments

`tcut`	Describe `tcut` here
`tmax`	Describe `tmax` here
`h0`	Describe `h0` here
`CDFOR`	Describe `CDFOR` here

Details

If necessary, more details than the description above

Value

Describe the value returned If it is a LIST, use

`comp1`	Description of 'comp1'
`comp2`	Description of 'comp2'

...

Author(s)

Grant Izmirlian <izmirlian@nih.gov

See Also

objects to See Also as `help`,

Examples

```
## none as yet
```

CY2TOShaz *Calender year rates to Study Year Rates*

Description

Given the cutpoints at which the hazard is to be constant, the values taken by the calender year rates and the calender time offset from the start of the trial at which randomization ended, this function converts to time on study rates, assuming uniform accrual.

Usage

```
CY2TOShaz(tcut, t.eor, m, verbose = FALSE)
```

Arguments

`tcut`	Left hand endpoints of intervals on which time on study hazard is taken to be constant
`t.eor`	Time offsest from the beginning of the trial at which randomization ended
`m`	Annual calender time rates
`verbose`	do you want to see alot of debugging info–defaults to `FALSE`

Value

hazard = h, table = attr(obj., "tbl")

`hazard`	time on study hazard values taken on intervals specified by the argument `tcut`
`table`	a table containg the observed and fitted values

Author(s)

Grant Izmirlian <izmirlian@nih.gov>

Examples

```
## none as yet
```

CRRtoRR *Cumulative-risk ratios to risk ratios*

Description

Given a vector of cumulative-risk ratios, computes risk ratios

Usage

```
CRRtoRR(CRR, DT, h = NULL)
```

Arguments

`CRR`	vector of cumulative risk ratios of length `m`
`DT`	vector of time increments upon which the cumulative ratios represent. For example if the hazard takes values $h_1, h_2, \ldots, h_m$ on the intervals $[t_1, t_2), [t_2, t_3), \ldots, [t_m, t_{m+1})$ then `DT` will be c$(t_2 - t_1, t_3 - t_2, \ldots, t_{m+1} - t_m)$
`h`	The hazard in the reference arm, of length `m`

Value

The vector of risk ratios at the `m` time points

Author(s)

Grant Izmirlian <izmirlian@nih.gov>

Examples

```
## none as yet
```

RCM2RR *Relative cumulative mortality to Relative Risk*

Description

Relative cumulative mortality to Relative Risk

Usage

```
RCM2RR(tlook, tcut.i, h.i, hOth, accru, rcm)
```

Arguments

`tlook`

`tcut.i`

`h.i`

`hOth`

`accru`

`rcm`

Value

Describe the value returned If it is a LIST, use

`comp1`	Description of 'comp1'
`comp2`	Description of 'comp2'

Author(s)

Grant Izmirlian <izmirlian@nih.gov>

See Also

objects to See Also as `help`,

Examples

```
## none as yet
```

`RR2RCM` *Relative risk to Relative Cumulative Mortality*

Description

Relative risk to Relative Cumulative Mortality

Usage

```
RR2RCM(tlook, tcut.i, tcut.ii, h, rr, hOth, accru)
```

Arguments

`tlook`	Describe `tlook` here
`tcut.i`	Describe `tcut.i` here
`tcut.ii`	Describe `tcut.ii` here
`h`	Describe `h` here
`rr`	Describe `rr` here
`hOth`	Describe `hOth` here
`accru`	Describe `accru` here

Value

Describe the value returned If it is a LIST, use

`comp1`	Description of 'comp1'
`comp2`	Description of 'comp2'

Author(s)

Grant Izmirlian <izmirlian@nih.gov

See Also

objects to See Also as `help`,

Examples

```
## none as yet
```

`lookup` *Lookup values for a piecewise constant function*

Description

Given the values and lefthand endpoints for intervals of constancy, lookup values of the function at arbitrary values of the independent variable.

Usage

```
lookup(xgrid, ygrid, x, y0 = 0)
```

Arguments

`xgrid`	Lefthand endpoints of intervals of constancy
`ygrid`	Values on these intervals, of same length as `xgrid`
`x`	Input vector of arbitrary independent variables.
`y0`	Value to be returned for values of `x` that are smaller than `min(xgrid)`.

Value

Describe the value returned If it is a LIST, use

`comp1`	Description of 'comp1'
`comp2`	Description of 'comp2'

Author(s)

Grant Izmirlian <izmirlian@nih.gov>

Examples

```
## none as yet
```

`lung` *Mayo Clinic Lung Cancer Data*

Description

Survival in patients with lung cancer at Mayo Clinic. Performance scores rate how well the patient can perform usual daily activities.

Usage

```
data(lung)
```

Format

inst:	Institution code
time:	Survival time in days
status:	censoring status 1=censored, 2=dead
age:	Age in years
sex:	Male=1 Female=2
ph.ecog:	ECOG performance score (0=good 5=dead)
ph.karno:	Karnofsky performance score (bad=0-good=100) rated by physician
pat.karno:	Karnofsky performance score rated by patient
meal.cal:	Calories consumed at meals
wt.loss:	Weight loss in last six months

Source

Terry Therneau

`DX` *function to do ...*

Description

A concise (1-5 lines) description of what the function does.

Usage

```
DX(x)
```

Arguments

`x`	Describe `x` here

Details

If necessary, more details than the description above

Value

Describe the value returned If it is a LIST, use

`comp1`	Description of 'comp1'
`comp2`	Description of 'comp2'

...

Author(s)

Grant Izmirlian <izmirlian@nih.gov

References

put references to the literature/web site here

Examples

```
## none as yet
```

`paste` *The paste operator*

Description

A binary operator shortcut for paste(x,y)

Usage

```
x %,% y
```

Arguments

`x`	a character string
`y`	a character string

Value

paste(x, y, sep="")

Author(s)

Grant Izmirlian ⟨izmirlian@nih.gov⟩

Examples

```
library(PwrGSD)
"var" %,% (1:10)
```

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