Package 'germinationmetrics'

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Title Seed Germination Indices and Curve Fitting

Version 0.1.0

Description Provides functions to compute various germination indices such as
germinability, median germination time, mean germination time, mean germination rate, speed of
germination, Timson's index, germination value, coefficient of uniformity of
germination, uncertainty of germination process, synchrony of germination
etc. from germination count data. Includes functions for fitting cumulative
seed germination curves using four-parameter hill function and computation
of associated parameters. See the vignette for more, including full list of
citations for the methods implemented.

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Encoding UTF-8

LazyData true

Depends R (>= 3.0.1)

VignetteBuilder knitr

RoxygenNote 6.0.1

Imports broom, ggplot2, ggrepel, minpack.lm, plyr, Rdpack, utils,
stats

Suggests knitr, rmarkdown, pander

RdMacros Rdpack

URL https://github.com/aravind-j/germinationmetrics,
https://aravind-j.github.io/germinationmetrics/

BugReports https://github.com/aravind-j/germinationmetrics/issues

NeedsCompilation no

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R topics documented:

CUGerm *Coefficient of uniformity of germination*

Description

Compute the coefficient of uniformity of germination (CUG).

Usage

```
CUGerm(germ.counts, intervals, partial = TRUE)
```

Arguments

germ.counts	Germination counts at each time interval. Can be partial or cumulative as specified in the argument `partial`.
intervals	The time intervals.
partial	logical. If `TRUE`, germ.counts is considered as partial and if `FALSE`, it is considered as cumulative. Default is `TRUE`.

Details

CUG is computed as follows (Heydecker, 1973, Bewley and Black, 1994).

$$CUG = \frac{\sum_{i=1}^{k} N_i}{\sum_{i=1}^{k} (\overline{T} - T_i)^2 N_i}$$

Where, $\overline{T}$ is the the mean germination time, T_i is the time from the start of the experiment to the ith observation (day for the example); N_i is the number of seeds germinated in the ith time (not the accumulated number, but the number correspondent to the ith observation), and k is the last time of germination.

Value

The value of the coefficient of uniformity of germination as time^{-2}.

References

Heydecker W (1972). *Seed Ecology. Proceedings of the Nineteenth Easter School in Agricultural Science, University of Nottingham, 1972*. Pennsylvania State University Press, University Park, USA.

Bewley JD and Black M (1994). *Seeds: Physiology of Development and Germination.*. Plenum Publishing Corporation, New York, USA. ISBN 0-306-44748-7, https://www.cabdirect.org/cabdirect/abstract/19950315483.

See Also

GermSynchrony, MeanGermTime

Examples

```
x <- c(0, 0, 0, 0, 4, 17, 10, 7, 1, 0, 1, 0, 0, 0)
y <- c(0, 0, 0, 0, 4, 21, 31, 38, 39, 39, 40, 40, 40, 40)
int <- 1:length(x)

# From partial germination counts
#----------------------------------------------------------------------------
CUGerm(germ.counts = x, intervals = int)

# From cumulative germination counts
#----------------------------------------------------------------------------
CUGerm(germ.counts = y, intervals = int, partial = FALSE)
```

| FirstGermTime | *Time for first, last and peak germination* |

Description

Compute the following metrics:

FirstGermTime Time of first germination or Germination time lag (t_0) (Edwards, 1932; Czabator, 1962; Goloff and Bazzaz, 1975; Labouriau, 1983; Ranal, 1999; Quintanilla et al., 2000).

LastGermTime Time of last germination (t_g) (Edwards, 1932; Labouriau, 1983; Ranal and de Santana, 2006).

PeakGermTime Time spread of germination (Al-Mudaris, 1998; Kader, 2005).

TimeSpreadGerm Peak time of germination or Modal time of germination (Ranal and de Santana, 2006).

Usage

```
FirstGermTime(germ.counts, intervals, partial = TRUE)

LastGermTime(germ.counts, intervals, partial = TRUE)

PeakGermTime(germ.counts, intervals, partial = TRUE)

TimeSpreadGerm(germ.counts, intervals, partial = TRUE)
```

Arguments

germ.counts	Germination counts at each time interval. Can be partial or cumulative as specified in the argument `partial`.
intervals	The time intervals.
partial	logical. If `TRUE`, germ.counts is considered as partial and if `FALSE`, it is considered as cumulative. Default is `TRUE`.

Details

Time of first germination indicates time of germination of the faster seeds in a seedlot.

Lower value of time of first germination indicates faster initiation of germination and lower value of time of last germination indicates faster termination of germination.

Time spread of germination ($t_g - t_0$) indicates difference between faster and slower germinating members of a sample.

Peak time of germination is the time in which highest frequency of germinated seeds are observed. Multiple peak times of germination are possible and if detected are indicated by a warning message.

Value

For `FirstGermTime`, the time of first germination value in the same unit of time as specified in the argument `intervals`.

For `LastGermTime`, the time of last germination value in the same unit of time as specified in the argument `intervals`.

For `TimeSpreadGerm`, the time spread of germination value in the same unit of time as specified in the argument `intervals`.

For `PeakGermTime`, the time(s) of peak germination value(s) as a numeric vector in the same unit of time as specified in the argument `intervals`.

References

Edwards TI (1932). "Temperature relations of seed germination." *The Quarterly Review of Biology*, **7**(4), pp. 428–443.

Czabator FJ (1962). "Germination value: An index combining speed and completeness of pine seed germination." *Forest Science*, **8**(4), pp. 386–396.

Goloff AA and Bazzaz FA (1975). "A germination model for natural seed populations." *Journal of Theoretical Biology*, **52**(2), pp. 259–283.

Labouriau L (1983). *A Germinacao Das Sementes*. Organizacao dos Estados Americanos. Programa Regional de Desenvolvimento Cientifico e Tecnologico. Serie de Biologia. Monografia 24.

Al-Mudaris M (1998). "Notes on various parameters recording the speed of seed germination." *Der Tropenlandwirt-Journal of Agriculture in the Tropics and Subtropics*, **99**(2), pp. 147–154.

Ranal MA (1999). "Effects of temperature on spore germination in some fern species from semideciduous mesophytic forest." *American Fern Journal*, **89**(2), pp. 149.

Quintanilla LG, Pajaron S, Pangua E and Amigo J (2000). "Effect of temperature on germination in northernmost populations of *Culcita macrocarpa* and *Woodwardia radicans*." *Plant Biology*, **2**(6), pp. 612–617.

Kader M (2005). "A comparison of seed germination calculation formulae and the associated interpretation of resulting data." *ournal and Proceedings of the Royal Society of New South Wales*, **138**, pp. 65–75.

Ranal MA and de Santana DG (2006). "How and why to measure the germination process?" *Brazilian Journal of Botany*, **29**(1), pp. 1–11.

Examples

```
x <- c(0, 0, 0, 0, 4, 17, 10, 7, 1, 0, 1, 0, 0, 0)
y <- c(0, 0, 0, 0, 4, 21, 31, 38, 39, 39, 40, 40, 40, 40)
z <- c(0, 0, 0, 0, 11, 11, 9, 7, 1, 0, 1, 0, 0, 0)
int <- 1:length(x)

# From partial germination counts
#----------------------------------------------------------------------------
FirstGermTime(germ.counts = x, intervals = int)
LastGermTime(germ.counts = x, intervals = int)
TimeSpreadGerm(germ.counts = x, intervals = int)
PeakGermTime(germ.counts = x, intervals = int)
```

```
# For multiple peak germination times
PeakGermTime(germ.counts = z, intervals = int)

# From cumulative germination counts
#--------------------------------------------------------------------------
FirstGermTime(germ.counts = y, intervals = int, partial = FALSE)
LastGermTime(germ.counts = y, intervals = int, partial = FALSE)
TimeSpreadGerm(germ.counts = y, intervals = int, partial = FALSE)
PeakGermTime(germ.counts = y, intervals = int, partial = FALSE)
# For multiple peak germination time
PeakGermTime(germ.counts = cumsum(z), intervals = int, partial = FALSE)
```

FourPHFfit   *Fit four-parameter hill function*

Description

Fit a four-parameter hill function (El-Kassaby, et al. 2008) to cumulative germination count data
and compute the associated parameters.

Usage

```
FourPHFfit(germ.counts, intervals, total.seeds, partial = TRUE,
  fix.y0 = TRUE, fix.a = TRUE, tmax, xp = c(10, 60), umin = 10,
  umax = 90, tries = 3, limits = TRUE, plotlabels = TRUE)
```

Arguments

germ.counts	Germination counts at each time interval. Can be partial or cumulative as specified in the argument `partial`.
intervals	The time intervals.
total.seeds	Total number of seeds.
partial	logical. If `TRUE`, germ.counts is considered as partial and if `FALSE`, it is considered as cumulative. Default is `TRUE`.
fix.y0	Force the intercept of the y axis through 0.
fix.a	Fix a as the actual maximum germination percentage at the end of the experiment.
tmax	The time up to which AUC is to be computed.
xp	Germination percentage value(s) for which the corresponding time is to be computed as a numeric vector. Default is `c(10, 60)`.
umin	The minimum germination percentage value for computing uniformity. Default is `10`. Seed `Details`.
umax	The maximum germination percentage value for computing uniformity. Default is `90`. Seed `Details`.

tries	The number of tries to be attempted to fit the curve. Default is 3.
limits	logical. If TRUE, set the limits of y axis (germination percentage) between 0 and 100 in the germination curve plot. If FALSE, limits are set according to the data. Default is TRUE.
plotlabels	logical. If TRUE, adds labels to the germination curve plot. Default is TRUE.

Details

The cumulative germination count data of a seed lot can be modelled to fit a four-parameter hill function defined as follows (El-Kassaby, et al. 2008):

$$y = y_0 + \frac{ax^b}{c^b + x^b}$$

Where, y is the cumulative germination percentage at time x, y_0 is the intercept on the y axis, a is the asymptote, or maximum cumulative germination percentage, which is equivalent to germination capacity, b is a mathematical parameter controlling the shape and steepness of the germination curve (the larger the b parameter, the steeper the rise toward the asymptote a, and the shorter the time between germination onset and maximum germination) and c is the "half-maximal activation level" and represents the time required for 50% of viable seeds to germinate (c is equivalent to the germination speed).

Once this function is fitted to the curve, FourPHFfit computes the time to 50% germination of total seeds (t50.total) or viable seeds (t50.Germinated). Similarly the time at any percentage of germination (in terms of both total and viable seeds) as specified in argument xp can be computed.

The time at germination onset (lag) can be computed as follows:

$$lag = b\sqrt{\frac{-y_0 c^b}{a + y_0}}$$

The value D_{lag-50} is defined as the duration between the time at germination onset (lag) and that at 50% germination (c).

The time interval between the percentages of viable seeds specified in the arguments umin and umin to germinate is computed as uniformity($U_{t_{max}-t_{min}}$).

$$U_{t_{max}-t_{min}} = t_{max} - t_{min}$$

The partial derivative of the four-parameter hill function gives the instantaneous rate of germination (s) as follows:

$$s = \frac{\partial y}{\partial x} = \frac{abc^b x^{b-1}}{(c^b + x^b)^2}$$

From this function for instantaneous rate of germination, the time at maximum germination rate ($TMGR$) can be estimated as follows:

$$TMGR = b\sqrt{\frac{c^b(b-1)}{b+1}}$$

TMGR represents the point in time when the instantaneous rate of germination starts to decline.

The area under the curve (AUC) is obtained by integration of the fitted curve between time 0 and time specified in the argument 'tmax'.

Integration of the fitted curve gives the value of mean germination time (MGT) and the skewness of the germination curve is computed as the ratio of MGT and the time for 50% of viable seeds to germinate (t_{50}).

$$Skewness = \frac{MGT}{t_{50}}$$

`FourPHFfit` plots the cumulative germination curve (FPHF curve) and the rate of germination curve (RoG curve) with different parameters annotated (if argument `plotlabels` is specified as `TRUE`).

If final germination percentage is less than 10%, a warning is given, as the results may not be informative.

Value

A list with the following components:

`Parameters`	A data.frame of parameter estimates, standard errors and p value.
`Fit`	A one-row data frame with estimates of model fitness such as log likelyhoods, Akaike Information Criterion, Bayesian Information Criterion, deviance and residual degrees of freedom.
`a`	The asymptote or the maximum cumulative germination percentage.
`b`	The mathematical parameter controlling the shape and steepness of the germination curve.
`c`	The half-maximal activation level
`y0`	The intercept on the y axis.
`lag`	Time at germination onset
`Dlag50`	duration between the time at germination onset (lag) and that at 50% germination.
`t50.total`	time required for 50% of total seeds to germinate.
`txp.total`	time required for x% (as specified in argument xp) of total seeds to germinate.
`t50.Germinated`	time required for 50% of viable/germinated seeds to germinate.
`txp.Germinated`	time required for x% (as specified in argument xp) of viable/germinated seeds to germinate.
`Uniformity`	Time interval between `umin`% and `umax`% of viable seeds to germinate.
`TMGR`	Time at maximum germination rate.
`AUC`	The estimate of area under the curve.
`MGT`	Mean germination time
`Skewness`	Skewness of mean germination time
`msg`	The message from `nls.lm`
`isConv`	Logical value indicating whether convergence was achieved.
`plot`	The plot of the cumulative germination curve as an object of class `ggplot`.

References

El-Kassaby YA, Moss I, Kolotelo D and Stoehr M (2008). "Seed germination: Mathematical representation and parameters extraction." *Forest Science*, **54**(2), pp. 220–227.

Examples

```
x <- c(0, 0, 0, 0, 4, 17, 10, 7, 1, 0, 1, 0, 0, 0)
y <- c(0, 0, 0, 0, 4, 21, 31, 38, 39, 39, 40, 40, 40, 40)
int <- 1:length(x)
total.seeds = 50

# From partial germination counts
#----------------------------------------------------------------------------
FourPHFfit(germ.counts = x, intervals = int, total.seeds = 50, tmax = 20)

# From cumulative germination counts
#----------------------------------------------------------------------------
FourPHFfit(germ.counts = y, intervals = int, total.seeds = 50, tmax = 20,
partial = FALSE)
```

GermPercent   *Germination percentage*

Description

Compute the germination percentage or germinability.

Usage

```
GermPercent(germinated.seeds, germ.counts, total.seeds, partial = TRUE)
```

Arguments

germinated.seeds
: Number of germinated seeds

germ.counts
: Germination counts at each time interval. Can be partial or cumulative as specified in the argument `partial`.

total.seeds
: Total number of seeds.

partial
: logical. If `TRUE`, `germ.counts` is considered as partial and if `FALSE`, it is considered as cumulative. Default is `TRUE`.

Details

Germination percentage is computed as follows:

$$GP = \frac{N_g}{N_t} \times 100$$

Where, N_g is the number of germinated seeds and N_t is the total number of seeds.

The value of N_g can be either specified using the argument `germinated.seeds` or is computed from the `germ.counts` argument.

Value

The germination percentage (%) value.

References

ISTA (2015). "Chapter 5: The germination test." *International Rules for Seed Testing. International Seed Testing Association, Zurich, Switzerland.*, **2015**, pp. i–5–56. https://doi.org/10.15258/istarules.2015.05.

Examples

```
x <- c(0, 0, 0, 0, 4, 17, 10, 7, 1, 0, 1, 0, 0, 0)
y <- c(0, 0, 0, 0, 4, 21, 31, 38, 39, 39, 40, 40, 40, 40)

# From partial germination counts
GermPercent(germ.counts = x, total.seeds = 50)

# From cumulative germination counts
GermPercent(germ.counts = y, total.seeds = 50, partial = FALSE)

# From number of germinated seeds
GermPercent(germinated.seeds = 40, total.seeds = 50)
```

GermSpeed *Speed of germination*

Description

Compute the following metrics:

GermSpeed Speed of germination or Germination rate index or Index of velocity of germination or Germination index (Kendrick and Frankland, 1969; AOSA, 1983)

GermSpeedAccumulated Speed of accumulated germination (Bradbeer, 1988; Wardle et al., 1991; Haugland and Brandsaeter, 1996; Santana and Ranal, 2004)

GermSpeedCorrected Corrected speed of germination or Corrected germination rate index

Usage

```
GermSpeed(germ.counts, intervals, partial = TRUE)

GermSpeedAccumulated(germ.counts, intervals, partial = TRUE)

GermSpeedCorrected(germ.counts, intervals, partial = TRUE, total.seeds)
```

Arguments

germ.counts   Germination counts at each time interval. Can be partial or cumulative as specified in the argument `partial`.

intervals   The time intervals.

partial   logical. If `TRUE`, germ.counts is considered as partial and if `FALSE`, it is considered as cumulative. Default is `TRUE`.

total.seeds   Total number of seeds.

Details

GermSpeed computes the speed of germination according to the following formula (Throneberry and Smith, 1955; Maguire, 1962; Kendrick and Frankland, 1969; AOSA, 1983; Khandakar and Bradbeer, 1983; Bradbeer, 1988; Wardle et al., 1991).

$$S = \frac{N_1}{T_1} + \frac{N_2}{T_2} + \frac{N_3}{T_3} + \cdots + \frac{N_n}{T_n}$$

Where, N_1, N_2, N_3, $\cdots$, N_n are the number of germinated seeds observed at time (days or hours) T_1, T_2, T_3, $\cdots$, T_n after sowing. (Not accumulated/cumulative number, but the number of seeds that germinated at the specific time).

Speed of germination expresses the rate of germination in terms of the total number of seeds that germinate in a time interval. Higher values indicate greater and faster germination. This is useful for comparisons only when samples or treatments possess similar germinabilities. This is overcome by using the corrected speed of germination.

GermSpeedCorrected computes the corrected speed of germination as follows (Evetts and Burnside, 1972).

$$S_{corrected} = \frac{S}{FGP}$$

Where, FGP is the final germination percentage or germinability.

GermSpeedAccumulated computes the speed of accumulated germination as follows (Bradbeer, 1988; Wardle et al., 1991; Haugland and Brandsaeter, 1996; Santana and Ranal, 2004).

$$S_{accumulated} = \frac{N_1}{T_1} + \frac{N_1 + N_2}{T_2} + \frac{N_1 + N_2 + N_3}{T_3} + \cdots + \frac{N_1 + N_2 + \cdots + N_n}{T_n}$$

Where, N_1, N_2, N_3, $\cdots$, N_n are the number of germinated seeds observed at time (days or hours) T_1, T_2, T_3, $\cdots$, T_n after sowing. (Not accumulated/cumulative number, but the number of seeds that germinated at the specific time).

Value

For `GermSpeed`, the value of germination speed as $\% \text{ time}^{-1}$.

For `GermSpeedAccumulated`, the value of accumulated germination speed as $\% \text{ time}^{-1}$.

For `GermSpeedCorrected`, the corrected speed of germination.

References

Throneberry GO and Smith FG (1955). "Relation of respiratory and enzymatic activity to corn seed viability." *Plant Physiology*, **30**(4), pp. 337–343.

Maguire JD (1962). "Speed of germination - Aid in selection and evaluation for seedling emergence and vigor." *Crop Science*, **2**(2), pp. 176–177.

Kendrick RE and Frankland B (1969). "Photocontrol of germination in *Amaranthus caudatus*." *Planta*, **85**(4), pp. 326–339.

Evetts LL and Burnside OC (1972). "Germination and seedling development of common milkweed and other species." *Weed Science*, **20**(4), pp. 371–378.

Khandakar A and Bradbeer J (1983). "Jute seed quality." *Bangladesh Agricultural Research Council, Dhaka*.

Bradbeer JW (1988). *Seed Dormancy and Germination*. Blackie, Glasgow and London. www. springer.com/in/book/9780216916364.

Wardle D, Ahmed M and Nicholson KS (1991). "Allelopathic influence of nodding thistle (*Carduus nutans* L.) seeds on germination and radicle growth of pasture plants." *New Zealand Journal of Agricultural Research*, **34**(2), pp. 185–191.

Haugland E and Brandsaeter LO (1996). "Experiments on bioassay sensitivity in the study of allelopathy." *Journal of Chemical Ecology*, **22**(10), pp. 1845–1859.

de Santana D and Ranal MA (2004). *Analise Da Germinacao: Um Enfoque Estatistico*. Universidade de Brasilia, Brasilia.

Examples

```
x <- c(0, 0, 0, 0, 4, 17, 10, 7, 1, 0, 1, 0, 0, 0)
y <- c(0, 0, 0, 0, 4, 21, 31, 38, 39, 39, 40, 40, 40, 40)
int <- 1:length(x)

# From partial germination counts
#----------------------------------------------------------------------
GermSpeed(germ.counts = x, intervals = int)
GermSpeedAccumulated(germ.counts = x, intervals = int)
GermSpeedCorrected(germ.counts = x, intervals = int, total.seeds = 50)

# From cumulative germination counts
#----------------------------------------------------------------------
GermSpeed(germ.counts = y, intervals = int, partial = FALSE)
GermSpeedAccumulated(germ.counts = y, intervals = int, partial = FALSE)
GermSpeedCorrected(germ.counts = y, intervals = int,
                   partial = FALSE, total.seeds = 50)
```

GermSynchrony   *Synchrony and uncertainty of germination*

Description

Compute the following metrics:

GermSynchrony Synchrony of germination (Z index).

GermUncertainty Synchronization index ($\overline{E}$) or Uncertainty of the germination process (U) or Informational entropy (H).

Usage

```
GermSynchrony(germ.counts, intervals, partial = TRUE)

GermUncertainty(germ.counts, intervals, partial = TRUE)
```

Arguments

germ.counts	Germination counts at each time interval. Can be partial or cumulative as specified in the argument partial.
intervals	The time intervals.
partial	logical. If TRUE, germ.counts is considered as partial and if FALSE, it is considered as cumulative. Default is TRUE.

Details

GermSynchrony computes the value of synchrony of germination (Z index) as follows (Primack, 1980; Ranal and Santana, 2006).

$$Z = \frac{\sum_{i=1}^{k} C_{N_i,2}}{C_{\Sigma N_i,2}}$$

Where, $C_{N_i,2}$ is the partial combination of the two germinated seeds from among N_i, the number of seeds germinated on the ith time (estimated as $C_{N_i,2} = \frac{Ni(Ni-1)}{2}$) and $C_{\Sigma N_i,2}$ is the partial combination of the two germinated seeds from among the total number of seeds germinated at the final count, assuming that all seeds that germinated did so simultaneously.

GermUncertainty computes the value of synchronization index ($\overline{E}$) or uncertainty of the germination process (U) or informational entropy (H) as follows (Shannon, 1948; Labouriau and Valadares, 1976; Labouriau 1983).

$$\overline{E} = -\sum_{i=1}^{k} f_i \log_2 f_i$$

Where, f_i is the relative frequency of germination (estimated as $f_i = \frac{N_i}{\sum_{i=1}^{k} N_i}$), N_i is the number of seeds germinated on the ith time and k is the last day of observation.

Value

For `GermUncertainty`, the value of uncertainty of germination process.

For `GermSynchrony`, the value of synchrony of germination.

References

Shannon CE (1948). "A mathematical theory of communication." *Bell System Technical Journal*, **27**(3), pp. 379–423.

Labouriau L and Viladares M (1976). "On the germination of seeds of *Calotropis procera* (Ait.) Ait. f." *Anais da Academia Brasileira de Ciencias*, **48**(263-284).

Labouriau L (1983). "Uma nova linha de pesquisa na fisiologia da germinacao das sementes." *Anais do XXXIV Congresso Nacional de Botanica. SBB, Porto Alegre*, pp. 11–50.

Primack RB (1985). "Longevity of individual flowers." *Annual Review of Ecology and Systematics*, **16**(1), pp. 15–37.

Ranal MA and de Santana DG (2006). "How and why to measure the germination process?" *Brazilian Journal of Botany*, **29**(1), pp. 1–11.

See Also

CUGerm

Examples

```
x <- c(0, 0, 0, 0, 4, 17, 10, 7, 1, 0, 1, 0, 0, 0)
y <- c(0, 0, 0, 0, 4, 21, 31, 38, 39, 39, 40, 40, 40, 40)
int <- 1:length(x)

# From partial germination counts
#----------------------------------------------------------------------------
GermSynchrony(germ.counts = x, intervals = int)
GermUncertainty(germ.counts = x, intervals = int)

# From cumulative germination counts
#----------------------------------------------------------------------------
GermSynchrony(germ.counts = y, intervals = int, partial = FALSE)
GermUncertainty(germ.counts = y, intervals = int, partial = FALSE)
```

GermValue　　　　　　　　　　　*Peak value and germination value*

Description

Compute the peak value (Czabator, 1962) and germination value (Czabator, 1962; Djavanshir and Pourbeik, 1976).

Usage

```
PeakValue(germ.counts, intervals, total.seeds, partial = TRUE)

GermValue(germ.counts, intervals, total.seeds, partial = TRUE,
  method = c("czabator", "dp"), k = 10)
```

Arguments

germ.counts	Germination counts at each time interval. Can be partial or cumulative as specified in the argument partial.
intervals	The time intervals.
total.seeds	Total number of seeds.
partial	logical. If TRUE, germ.counts is considered as partial and if FALSE, it is considered as cumulative. Default is TRUE.
method	The method for computing germination value. Either "czabator" or "dp".
k	Constant (See **Details**). Default is 10.

Details

Peak value (PV) is the maximum quotient obtained by dividing successive cumulative germination values by the relevant incubation time (Czabator, 1962). It represents the mean daily germination of the most vigorous component of the seed lot, and is a mathematical expression of the break, or shoulder, of a typical sigmoid germination curve (Djavanshir and Pourbeik, 1976).

For daily germination counts, germination value (GV) is computed as follows (Czabator, 1962).

$$GV = PV \times MDG$$

Where, PV is the peak value and MDG is the mean daily germination percentage.

GV can also be computed for other time intervals of successive germination counts, by replacing MDG with the mean germination percentage per unit time ($\overline{GP}$).

A new estimation of germination value was given by Djavanshir and Pourbeik (1976) as follows:

$$GV = \frac{\sum DGS}{N} \times GP \times k$$

Where, DGS is the daily germination speed computed by dividing cumulative germination percentage by the number of days since the beginning of the test, N is the frequency or number of DGS calculated during the test, GP is the germination percentage expressed over 100 and k is a constant. The value of k is decided on the basis of average daily speed of germination ($\frac{\sum DGS}{N}$). If it is less than 10, then k value of 10 can be used and if it is more than 10, then value of 7 or 8 can be used for k.

Value

A list with the following components:

```
Germination Value
```
>   The germination value

```
Calculations    The data frame of calculations.
```

```
testend         The end of test value (Only for method dp).
```

References

Czabator FJ (1962). "Germination value: An index combining speed and completeness of pine seed germination." *Forest Science*, **8**(4), pp. 386–396.

Khamassi K, Harbaoui K, Silva Td, A J and Jeddi FB (2013). "Optimal germination temperature assessed by indices and models in field bean (*Vicia faba* L. var. *minor*)." *Agriculturae Conspectus Scientificus*, **78**(2), pp. 131–136. <https://hrcak.srce.hr/104663>.

Examples

```
x <- c(0, 0, 34, 40, 21, 10, 4, 5, 3, 5, 8, 7, 7, 6, 6, 4, 0, 2, 0, 2)
y <- c(0, 0, 34, 74, 95, 105, 109, 114, 117, 122, 130, 137, 144, 150,
      156, 160, 160, 162, 162, 164)
int <- 1:length(x)
total.seeds = 200

# From partial germination counts
#----------------------------------------------------------------------------
PeakValue(germ.counts = x, intervals = int, total.seeds = 200)
GermValue(germ.counts = x, intervals = int, total.seeds = 200,
          method = "czabator")
GermValue(germ.counts = x, intervals = int, total.seeds = 200,
          method = "dp", k = 10)

# From cumulative germination counts
#----------------------------------------------------------------------------
PeakValue(germ.counts = y, interval = int, total.seeds = 200,
          partial = FALSE)
GermValue(germ.counts = y, intervals = int, total.seeds = 200,
          partial = FALSE, method = "czabator")
GermValue(germ.counts = y, intervals = int, total.seeds = 200,
          partial = FALSE, method = "dp", k = 10)
```

MeanGermPercent   *Mean germination percentage and number of seeds per time interval*

Description

Compute the following metrics:

MeanGermPercent Mean/average germination percentage per unit time ($\overline{GP}$).

MeanGermNumber Number of seeds germinated per unit time ($\overline{N}$).

Usage

```
MeanGermPercent(germinated.seeds, germ.counts, total.seeds, intervals,
  partial = TRUE)

MeanGermNumber(germ.counts, intervals, partial = TRUE)
```

Arguments

germinated.seeds
Number of germinated seeds

germ.counts   Germination counts at each time interval. Can be partial or cumulative as specified in the argument `partial`.

total.seeds   Total number of seeds.

intervals   The time intervals.

partial   logical. If TRUE, germ.counts is considered as partial and if FALSE, it is considered as cumulative. Default is TRUE.

Details

Mean germination percentage per unit time ($\overline{GP}$) is computed as follows (Czabator, 1962).

$$\overline{G} = \frac{GP}{T_n}$$

Where, GP is the final germination percentage and T_n is the total number of intervals(e.g. days) required for final germination.

Mean number of seeds germinated per unit time ($\overline{N}$) is computed as follows (Khamassi et al., 2013).

$$\overline{N} = \frac{N_g}{T_n}$$

Where, N_g is the number of germinated seeds and T_n is the total number of intervals (e.g. days) required for final germination.

Value

The value of mean germination percentage or mean number of seeds per time interval.

References

Czabator FJ (1962). "Germination value: An index combining speed and completeness of pine seed germination." *Forest Science*, **8**(4), pp. 386–396.

Djavanshir K and Pourbeik H (1976). "Germination value-A new formula." *Silvae genetica*, **25**(2), pp. 79–83.

See Also

GermPercent

Examples

```
x <- c(0, 0, 0, 0, 4, 17, 10, 7, 1, 0, 1, 0, 0, 0)
y <- c(0, 0, 0, 0, 4, 21, 31, 38, 39, 39, 40, 40, 40, 40)
int <- 1:length(x)

# From partial germination counts
#----------------------------------------------------------------------------
MeanGermPercent(germ.counts = x, total.seeds = 50, intervals = int)
MeanGermNumber(germ.counts = x, intervals = int)

# From cumulative germination counts
#----------------------------------------------------------------------------
MeanGermPercent(germ.counts = y, total.seeds = 50, intervals = int, partial = FALSE)
MeanGermNumber(germ.counts = y, intervals = int, partial = FALSE)

# From number of germinated seeds
#----------------------------------------------------------------------------
MeanGermPercent(germinated.seeds = 40, total.seeds = 50, intervals = int)
```

MeanGermRate   *Germination Rate*

Description

Compute the following metrics:

MeanGermRate Mean germination rate ($\overline{V}$).

VarGermRate Variance of germination rate (s_V^2).

SEGermRate Standard error of germination rate ($s_{\overline{V}}$).

CVG Coefficient of velocity/rate of germination or Kotowski's coefficient of velocity (CVG).

GermRateRecip Germination rate as reciprocal of median time (v_{50}).

Usage

```
MeanGermRate(germ.counts, intervals, partial = TRUE)

CVG(germ.counts, intervals, partial = TRUE)

VarGermRate(germ.counts, intervals, partial = TRUE)

SEGermRate(germ.counts, intervals, partial = TRUE)

GermRateRecip(germ.counts, intervals, partial = TRUE, method = c("coolbear",
    "farooq"))
```

Arguments

`germ.counts`	Germination counts at each time interval. Can be partial or cumulative as specified in the argument `partial`.
`intervals`	The time intervals.
`partial`	logical. If `TRUE`, `germ.counts` is considered as partial and if `FALSE`, it is considered as cumulative. Default is `TRUE`.
`method`	The method for computing median germination time. Either `"coolbear"` or `"farooq"`.

Details

`MeanGermRate` computes the mean germination rate ($\overline{V}$) according to the following formula (Labouriau and Viladares, 1976; Labouriau, 1983; Ranal and de Santana, 2006).

$$\overline{V} = \frac{\sum_{i=1}^{k} N_i}{\sum_{i=1}^{k} N_i T_i}$$

Where, T_i is the time from the start of the experiment to the ith observation, N_i is the number of seeds germinated in the ith time (not the accumulated number, but the number correspondent to the ith observation) and k is the last time of germination.

It is the inverse of mean germination time ($\overline{T}$).

$$\overline{V} = \frac{1}{\overline{T}}$$

`VarGermRate` computes the variance of germination rate (s_V^2) according to the following formula (Labouriau, 1983; Ranal and de Santana, 2006).

$$s_V^2 = \overline{V}^4 \times s_T^2$$

Where, s_T^2 is the variance of germination time.

`SEGermRate` computes the standard error of germination time ($s_{\overline{V}}$) according to the following formula (Labouriau, 1983; Ranal and de Santana, 2006).

$$s_{\overline{V}} = \sqrt{\frac{s_V^2}{\sum_{i=1}^{k} N_i}}$$

Where, N_i is the number of seeds germinated in the ith time (not the accumulated number, but the number correspondent to the ith observation) and k is the last time of germination.

CVG computes the coefficient of velocity/rate of germination or Kotowski's coefficient of velocity (CVG) according to the following formula (Kotowski, 1926; Nichols and Heydecker, 1968; Labouriau, 1983; Scott et al., 1984; Bewley and Black, 1985).

$$CVG = \frac{\sum_{i=1}^{k} N_i}{\sum_{i=1}^{k} N_i T_i} \times 100$$

$$CVG = \overline{V} \times 100$$

Where, T_i is the time from the start of the experiment to the ith observation, N_i is the number of seeds germinated in the ith time (not the accumulated number, but the number correspondent to the ith observation) and k is the last time of germination.

GermRateRecip computes the germination rate (v_{50}) as the reciprocal of the median germination time (t_{50}) (Went, 1957; Labouriau, 1983a; Ranal and de Santana, 2006) computed according to the methods of Coolbear et al., 1984 or Farooq et al., 2005 as follows:

$$v_{50} = \frac{1}{t_{50}}$$

Value

For MeanGermRate, the mean germination rate value as time^{-1}.

For VarGermTime, the variance of germination rate value as time^{-2}.

For SEGermTime, the standard error of germination rate as time^{-1}.

For CVG, the value of Coefficient of of velocity/rate of germination or Kotowski's coefficient of velocity.

For GermRateRecip, the value of germination rate as time^{-1}.

References

Kotowski F (1926). "Temperature relations to germination of vegetable seeds." *Proceedings of the American Society for Horticultural Science*, **23**, pp. 176–184.

Went FW (1957). *The experimental control of plant growth.*, volume 17. Chronica Botanica Co., Waltham, Mass., USA \& The Ronald Press Co., New York.

Nichols M and Heydecker W (1968). "Two approaches to the study of germination data." *Proceedings of the International Seed Testing Association*, **33**(3), pp. 531–540.

Labouriau L (1983). "Uma nova linha de pesquisa na fisiologia da germinacao das sementes." *Anais do XXXIV Congresso Nacional de Botanica. SBB, Porto Alegre*, pp. 11–50.

Coolbear P, Francis A and Grierson D (1984). "The effect of low temperature pre-sowing treatment on the germination performance and membrane integrity of artificially aged tomato seeds." *Journal of Experimental Botany*, **35**(11), pp. 1609–1617.

Scott SJ, Jones RA and Williams WA (1984). "Review of data analysis methods for seed germination." *Crop Science*, **24**(6), pp. 1192–1199.

Bewley JD and Black M (1994). *Seeds: Physiology of Development and Germination.*. Plenum Publishing Corporation, New York, USA. ISBN 0-306-44748-7, https://www.cabdirect.org/cabdirect/abstract/19950315483.

Farooq M, Basra SMA, Ahmad N and Hafeez K (2005). "Thermal hardening: A new seed vigor enhancement tool in rice." *Journal of Integrative Plant Biology*, **47**(2), pp. 187–193.

Ranal MA and de Santana DG (2006). "How and why to measure the germination process?" *Brazilian Journal of Botany*, **29**(1), pp. 1–11.

See Also

[MeanGermTime](), [t50]()

Examples

```
x <- c(0, 0, 0, 0, 4, 17, 10, 7, 1, 0, 1, 0, 0, 0)
y <- c(0, 0, 0, 0, 4, 21, 31, 38, 39, 39, 40, 40, 40, 40)
int <- 1:length(x)

# From partial germination counts
#---------------------------------------------------------------------------
MeanGermRate(germ.counts = x, intervals = int)
CVG(germ.counts = x, intervals = int)
VarGermRate(germ.counts = x, intervals = int)
SEGermRate(germ.counts = x, intervals = int)
GermRateRecip(germ.counts = x, intervals = int, method = "coolbear")
GermRateRecip(germ.counts = x, intervals = int, method = "farooq")


# From cumulative germination counts
#---------------------------------------------------------------------------
MeanGermRate(germ.counts = y, intervals = int, partial = FALSE)
CVG(germ.counts = y, intervals = int, partial = FALSE)
VarGermRate(germ.counts = y, intervals = int, partial = FALSE)
SEGermRate(germ.counts = y, intervals = int, partial = FALSE)
GermRateRecip(germ.counts = y, intervals = int,
              method = "coolbear", partial = FALSE)
GermRateRecip(germ.counts = y, intervals = int,
              method = "farooq", partial = FALSE)
```

MeanGermTime	*Germination Time*

Description

Compute the following metrics:

MeanGermTime Mean germination time ($\overline{T}$) or Mean length of incubation time.

VarGermTime Variance of germination time (s_T^2).

SEGermTime Standard error of germination time ($s_{\overline{T}}$).

CVSEGermTime Coefficient of variation of the germination time (CV_T).

Usage

```
MeanGermTime(germ.counts, intervals, partial = TRUE)

VarGermTime(germ.counts, intervals, partial = TRUE)

SEGermTime(germ.counts, intervals, partial = TRUE)

CVSEGermTime(germ.counts, intervals, partial = TRUE)
```

Arguments

germ.counts	Germination counts at each time interval. Can be partial or cumulative as specified in the argument `partial`.
intervals	The time intervals.
partial	logical. If `TRUE`, germ.counts is considered as partial and if `FALSE`, it is considered as cumulative. Default is `TRUE`.

Details

MeanGermTime computes the mean germination time according to the following formula (Edmond and Drapala, 1958; Czabator, 1962; Ellis and Roberts, 1980; Labouriau, 1983; Ranal and de Santana, 2006).

$$\overline{T} = \frac{\sum_{i=1}^{k} N_i T_i}{\sum_{i=1}^{k} N_i}$$

Where, T_i is the time from the start of the experiment to the ith observation, N_i is the number of seeds germinated in the ith time (not the accumulated number, but the number correspondent to the ith observation) and k is the last time of germination.

It is the inverse of mean germination rate ($\overline{V}$).

$$\overline{T} = \frac{1}{\overline{V}}$$

It indicates the average length of time required for maximum germination of a seed lot. Lower the $\overline{T}$, faster the sample has germinated and reflects seed vigor.

VarGermTime computes the variance of germination time according to the following formula.

$$s_T^2 = \frac{\sum_{i=1}^{k} N_i (T_i - \overline{T})^2}{\sum_{i=1}^{k} N_i - 1}$$

Where, T_i is the time from the start of the experiment to the ith observation, N_i is the number of seeds germinated in the ith time (not the accumulated number, but the number correspondent to the ith observation) and k is the last time of germination.

SEGermTime computes the standard error of germination time ($s_{\overline{T}}$) according to the following formula.

$$s_{\overline{T}} = \sqrt{\frac{s_T^2}{\sum_{i=1}^{k} N_i}}$$

Where, N_i is the number of seeds germinated in the ith time (not the accumulated number, but the number correspondent to the ith observation) and k is the last time of germination.

It signifies the accuracy of the calculation of the mean germination time.

CVGermTime computes the coefficient of variation of germination time (CV_T) according to the following formula (Ranal and de Santana, 2006).

$$CV_T = \sqrt{\frac{s_T^2}{\overline{T}}}$$

This indicates the uniformity of germination and permits comparisons irrespective of the magnitude of mean germination time ($\overline{T}$).

Value

For MeanGermTime, the mean germination time value in the same unit of time as specified in the argument intervals.

For VarGermTime, the variance of germination time value as time^2.

For SEGermTime, the standard error of germination time in the same unit of time specified in the argument intervals.

For CVSEGermTime, the value of coefficient of variation of the germination time.

References

Edmond J and Drapala W (1958). "The effects of temperature, sand and soil, and acetone on germination of okra seed." *Proceedings of the American Society for Horticultural Science*, **71**, pp. 428–434.

Czabator FJ (1962). "Germination value: An index combining speed and completeness of pine seed germination." *Forest Science*, **8**(4), pp. 386–396.

Ellis RH and Roberts EH (1980). "Improved equations for the prediction of seed longevity." *Annals of Botany*, **45**(1), pp. 13–30.

Labouriau L (1983). *A Germinacao Das Sementes*. Organizacao dos Estados Americanos. Programa Regional de Desenvolvimento Cientifico e Tecnologico. Serie de Biologia. Monografia 24.

Ranal MA and de Santana DG (2006). "How and why to measure the germination process?" *Brazilian Journal of Botany*, **29**(1), pp. 1–11.

See Also

[MeanGermRate](#)

Examples

```
x <- c(0, 0, 0, 0, 4, 17, 10, 7, 1, 0, 1, 0, 0, 0)
y <- c(0, 0, 0, 0, 4, 21, 31, 38, 39, 39, 40, 40, 40, 40)
int <- 1:length(x)

# From partial germination counts
#----------------------------------------------------------------------------
MeanGermTime(germ.counts = x, intervals = int)
VarGermTime(germ.counts = x, intervals = int)
SEGermTime(germ.counts = x, intervals = int)
CVSEGermTime(germ.counts = x, intervals = int)

# From cumulative germination counts
#----------------------------------------------------------------------------
MeanGermTime(germ.counts = y, intervals = int, partial = FALSE)
VarGermTime(germ.counts = y, intervals = int, partial = FALSE)
SEGermTime(germ.counts = y, intervals = int, partial = FALSE)
CVSEGermTime(germ.counts = y, intervals = int, partial = FALSE)
```

---

t50   *Median germination time*

Description

Compute the median germination time (t_{50}). Median germination time is the time to reach 50% of final/maximum germination.

Usage

```
t50(germ.counts, intervals, partial = TRUE, method = c("coolbear",
  "farooq"))
```

Arguments

germ.counts	Germination counts at each time interval. Can be partial or cumulative as specified in the argument `partial`.
intervals	The time intervals.
partial	logical. If TRUE, `germ.counts` is considered as partial and if FALSE, it is considered as cumulative. Default is TRUE.
method	The method for computing median germination time. Either "coolbear" or "farooq".

Details

With argument `method` specified as `"coolbear"`, median germination time is computed according to the formula by Coolbear et al., 1984 as follows:

$$t_{50} = T_i + \frac{(\frac{N+1}{2} - N_i)(T_j - T_i)}{N_j - N_i}$$

Where, t_{50} is the median germination time, N is the final number of germinated seeds and N_i and N_j are the total number of seeds germinated in adjacent counts at time T_i and T_j respectively, when $N_i < \frac{N+1}{2} < N_j$.

Similarly with argument `method` specified as `"farooq"`, median germination time is computed according to the formula by by Farooq et al., 2005 as follows:

$$t_{50} = T_i + \frac{(\frac{N}{2} - N_i)(T_j - T_i)}{N_j - N_i}$$

Where, t_{50} is the median germination time, N is the final number of germinated seeds and N_i and N_j are the total number of seeds germinated in adjacent counts at time T_i and T_j respectively, when $N_i < \frac{N}{2} < N_j$.

Value

The median germination time (t_{50}) value in the same unit of time as specified in the argument `intervals`.

References

Coolbear P, Francis A and Grierson D (1984). "The effect of low temperature pre-sowing treatment on the germination performance and membrane integrity of artificially aged tomato seeds." *Journal of Experimental Botany*, **35**(11), pp. 1609–1617.

Farooq M, Basra SMA, Ahmad N and Hafeez K (2005). "Thermal hardening: A new seed vigor enhancement tool in rice." *Journal of Integrative Plant Biology*, **47**(2), pp. 187–193.

See Also

MeanGermRate

Examples

```
x <- c(0, 0, 0, 0, 4, 17, 10, 7, 1, 0, 1, 0, 0, 0)
y <- c(0, 0, 0, 0, 4, 21, 31, 38, 39, 39, 40, 40, 40, 40)
int <- 1:length(x)

# From partial germination counts
#-------------------------------------------------------------------------
t50(germ.counts = x, intervals = int, method = "coolbear")
t50(germ.counts = x, intervals = int, method = "farooq")
```

```
# From cumulative germination counts
#--------------------------------------------------------------------------
t50(germ.counts = y, intervals = int, partial = FALSE, method = "coolbear")
t50(germ.counts = y, intervals = int, partial = FALSE, method = "farooq")
```

TimsonsIndex   *Timson's index*

Description

Compute George's index, Timson's index or Timson's germination velocity index and it's modifications by Labouriau (Ranal and de Santana, 2006) and Khan and Unger (1984).

Usage

```
TimsonsIndex(germ.counts, intervals, partial = TRUE, total.seeds, max,
  modification = c("none", "labouriau", "khanunger"))

GermRateGeorge(germ.counts, intervals, partial = TRUE, max)
```

Arguments

germ.counts	Germination counts at each time interval. Can be partial or cumulative as specified in the argument partial.
intervals	The time intervals.
partial	logical. If TRUE, germ.counts is considered as partial and if FALSE, it is considered as cumulative. Default is TRUE.
total.seeds	Total number of seeds.
max	The maximum interval value up to which Timson's index/George's germination rate is to be computed.
modification	The modification to be applied. Either "none", "labouriau" or "khanunger". Default is "none" (see **Details**).

Details

Timson's index (Timson, 1965) is computed as follows (Brown and Mayer, 1988; Baskin and Baskin, 1998).

$$\sum n = \sum_{i=1}^{t} G_i$$

Where, G_i is the cumulative germination percentage in time interval i and t is the total number of time intervals.

For example ten summation ($\Sigma 10$) is expressed as follows:

$$\sum 10 = G_1 + G_2 + \cdots + G_{10}$$

Where $G_1, G_2, \cdots G_{10}$ are the cumulative germination percentage at day 1, 2, 3, $\cdots$, 10 respectively.

Similarly $\Sigma 5$ or $\Sigma 20$ can be estimated. For $\Sigma 10$, the value can range from 0 (no germination) to 1,000 (100% germination after 24 hours).

It is the progressive total of cumulative germination percentage recorded at specific intervals for a set period of time. It combines onset, rate and total percentage of germination and estimates the area under the cumulative germination percentage curve.

Goodchild and Walker (1971), described the same in terms of partial germination percentage as follows:

$$\sum n = \sum_{i=1}^{t} g_i(t-j)$$

Where, g_i is the germination (not cumulative, but partial germination) in time interval i (i varying from 0 to t) and t is the total number of time intervals and $j = i - 1$.

Timson's index is similar to the germination rate proposed by George (1961) as follows (Tucker and Wright, 1965; Nichols and Heydecker, 1968).

$$GR = \sum_{i=1}^{t} N_i K_i$$

Where N_i is the number of seeds germinated by ith interval and K_i is the number of intervals(e.g. days) until the end of the test.

This index uses number of seeds germinated instead of germination percentage.

As Timson's index is useful for comparison only when samples have similar germinabilities or final germination percentage, the following modification was suggested by Labouriau (Ranal and de Santana, 2006).

$$T_{mod} = \frac{T}{\sum_{i=1}^{t} g_i}$$

Here Timson's index (t) is divided by the sum of partial germination percentages.

Similarly another modification was proposed by Khan and Unger (1984), where Timson's index (t) is divided by number of intervals (t).

$$T_{mod} = \frac{T}{t}$$

Value

For `TimsonsIndex` The value of Timson's index.

For `GermRateGeorge` The value of George's germination rate.

References

George D (1961). "Influence of germination temperature on the expression of post-harvest dormancy in wheat." *Crop Science Abstracts; Western Society of Crop Science Annual Meeting, 1961*, pp. 15.

Timson J (1965). "New Method of Recording Germination Data." *Nature*, **207**(4993), pp. 216.

Tucker H and Wright LN (1965). "Estimating rapidity of germination." *Crop Science*, **5**(5), pp. 398–399.

Nichols M and Heydecker W (1968). "Two approaches to the study of germination data." *Proceedings of the International Seed Testing Association*, **33**(3), pp. 531–540.

Goodchild NA and Walker MG (1971). "A method of measuring seed germination in physiological studies." *Annals of Botany*, **35**(141), pp. 615–621. http://www.jstor.org/stable/42908843.

Khan MA and Ungar IA (1984). "The effect of salinity and temperature on the germination of polymorphic seeds and growth of *Atriplex triangularis* Willd." *American Journal of Botany*, **71**(4), pp. 481–489.

Brown RF and Mayer DG (1988). "Representing cumulative germination. 1. A critical analysis of single-value germination indices." *Annals of Botany*, **61**(2), pp. 117–125.

Baskin CC and Baskin JM (1998). *Seeds: Ecology, Biogeography, and Evolution of Dormancy and Germination*. Academic Press, San Diego. ISBN 0-12-080260-0.

Ranal MA and de Santana DG (2006). "How and why to measure the germination process?" *Brazilian Journal of Botany*, **29**(1), pp. 1–11.

Examples

```
x <- c(0, 0, 0, 0, 4, 17, 10, 7, 1, 0, 1, 0, 0, 0)
y <- c(0, 0, 0, 0, 4, 21, 31, 38, 39, 39, 40, 40, 40, 40)
int <- 1:length(x)

# From partial germination counts
#----------------------------------------------------------------------------
# Wihout max specified
TimsonsIndex(germ.counts = x, intervals = int, total.seeds = 50)
TimsonsIndex(germ.counts = x, intervals = int, total.seeds = 50,
             modification = "none")
TimsonsIndex(germ.counts = x, intervals = int, total.seeds = 50,
             modification = "labouriau")
TimsonsIndex(germ.counts = x, intervals = int, total.seeds = 50,
             modification = "khanunger")
# With max specified
TimsonsIndex(germ.counts = x, intervals = int, total.seeds = 50, max = 10)
TimsonsIndex(germ.counts = x, intervals = int, total.seeds = 50,
             max = 10, modification = "none")
TimsonsIndex(germ.counts = x, intervals = int, total.seeds = 50,
             max = 10, modification = "labouriau")
TimsonsIndex(germ.counts = x, intervals = int, total.seeds = 50,
             max = 10, modification = "khanunger")

# Wihout max specified
GermRateGeorge(germ.counts = x, intervals = int)
```

```
# With max specified
GermRateGeorge(germ.counts = x, intervals = int, max = 10)
GermRateGeorge(germ.counts = x, intervals = int, max = 14)

# From cumulative germination counts
#---------------------------------------------------------------------------


# Wihout max specified
GermRateGeorge(germ.counts = x, intervals = int, partial = TRUE)
# With max specified
GermRateGeorge(germ.counts = x, intervals = int, partial = TRUE, max = 10)
GermRateGeorge(germ.counts = x, intervals = int, partial = TRUE, max = 14)
```

Index