Package 'germinationmetrics'

October 29, 2018

Title Seed Germination Indices and Curve Fitting

Version 0.1.1.9000

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 (>= 3.5.0)

VignetteBuilder knitr

RoxygenNote 6.1.0

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

Suggests knitr,
    rmarkdown,
    pander,
    XML,
    httr,
    RCurl

RdMacros Rdpack

URL https://github.com/aravind-j/germinationmetrics,
    https://aravind-j.github.io/germinationmetrics/
    https://CRAN.R-project.org/package=germinationmetrics
    https://doi.org/10.5281/zenodo.1219630

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

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 1972; 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

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

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.

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 speci-
               fied in the argument `partial`.

intervals   The time intervals.

partial   logical. If `TRUE`, `germ.counts` is considered as partial and if `FALSE`, it is consid-
               ered 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

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

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

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

Goloff AA, Bazzaz FA (1975). "A germination model for natural seed populations." *Journal of*

Theoretical Biology, **52**(2), 259–283.

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

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

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

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

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

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.

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}).

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

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.

References

El-Kassaby YA, Moss I, Kolotelo D, Stoehr M (2008). "Seed germination: Mathematical representation and parameters extraction." *Forest Science*, **54**(2), 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 (ISTA 2015):

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

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**, i–5–56.

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; de Santana and Ranal 2004)

GermSpeedCorrected Corrected speed of germination or Corrected germination rate index (Evetts and Burnside 1972)

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; de 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 % time^{-1}.

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

For `GermSpeedCorrected`, the corrected speed of germination.

References

AOSA (1983). *Seed Vigor Testing Handbook*. Association of Official Seed Analysts, Ithaca, NY, USA.

Bradbeer JW (1988). *Seed Dormancy and Germination*. Blackie, Glasgow and London.

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

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

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

Khandakar AL, Bradbeer JW (1983). "Jute seed quality." *Bangladesh Agricultural Research Council, Dhaka*.

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

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

Wardle DA, Ahmed M, 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), 185–191.

de Santana DG, 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) (Primack 1985; Ranal and de Santana 2006).

GermUncertainty Synchronization index ($\overline{E}$) or Uncertainty of the germination process (U) or Informational entropy (H) (Shannon 1948; Labouriau and Valadares 1976; Labouriau 1983).

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 1985; Ranal and de 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

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

Labouriau LG, Valadares MEB (1976). "On the germination of seeds of *Calotropis procera* (Ait.) Ait. f." *Anais da Academia Brasileira de Ciencias*, **48**(263-284).

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

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

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

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.

Germination value (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), 386–396.

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

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 ($\overline{GP}$) (Czabator 1962).

MeanGermNumber Number of seeds germinated per unit time ($\overline{N}$) (Khamassi et al. 2013).

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), 386–396.

Khamassi K, Harbaoui K, Jaime ATdS, Jeddi FB, Jeddi FB (2013). "Optimal germination temperature assessed by indices and models in field bean (*Vicia faba* L. var. *minor*)." *Agriculturae Conspectus Scientificus*, **78**(2), 131–136.

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 ($\overline{V}$) (Labouriau and Valadares 1976; Labouriau 1983; Ranal and de Santana 2006).

VarGermRate Variance of germination rate (s_V^2) (Labouriau 1983; Ranal and de Santana 2006).

SEGermRate Standard error of germination rate ($s_{\overline{V}}$) (Labouriau 1983; Ranal and de Santana 2006).

CVG Coefficient of velocity/rate of germination or Kotowski's coefficient of velocity (CVG) (Kotowski 1926; Nichols and Heydecker 1968; Labouriau 1983; Scott et al. 1984; Bewley and Black 1994).

GermRateRecip Germination rate as reciprocal of median time (v_{50}) (Went 1957; Labouriau 1983; Ranal and de Santana 2006).

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 Valadares 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 ($\overline{T}$).

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

`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 1994).

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

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

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 1983; 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

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

Coolbear P, Francis A, 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), 1609–1617.

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

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

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

Labouriau LG, Valadares MEB (1976). "On the germination of seeds of *Calotropis procera* (Ait.)

Ait. f." *Anais da Academia Brasileira de Ciencias*, **48**(263-284).

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

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

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

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

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 (Edmond and Drapala 1958; Czabator 1962; Ellis and Roberts 1980; Labouriau 1983; Ranal and de Santana 2006).

`VarGermTime` Variance of germination time (s_T^2) (Labouriau 1983; Ranal and de Santana 2006).

`SEGermTime` Standard error of germination time ($s_{\overline{T}}$) (Labouriau 1983; Ranal and de Santana 2006).

`CVSEGermTime` Coefficient of variation of the germination time (CV_T) (Ranal and de Santana 2006).

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 (Labouriau 1983; Ranal and de Santana 2006).

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

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 (Labouriau 1983; Ranal and de Santana 2006).

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

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

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

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

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

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

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

---

plot.FourPHFfit	*Plot the four-parameter hill function fitted cumulative germination curve from a* FourPHFfit *object*

Description

plot.FourPHFfit plots the four-parameter hill function fitted cumulative germination curve (FPHF curve) from a FourPHFfit object as an object of class ggplot. Further, the rate of germination curve (RoG curve) is plotted and different parameters annotated as specified in the different arguments.

Usage

```
## S3 method for class 'FourPHFfit'
plot(x, rog = TRUE, t50.total = TRUE,
  t50.germ = TRUE, tmgr = TRUE, mgt = TRUE, uniformity = TRUE,
  limits = TRUE, plotlabels = TRUE, ...)
```

Arguments

x	An object of class FourPHFfit obtained as output from the [FourPHFfit](#) function.
rog	If TRUE, plots the Rate of Germination curve (RoG). Default is TRUE.
t50.total	If TRUE, highlights the time required for 50% of total seeds to germinate ($t_{50_{\text{Germ}}}$) as a vertical line. Default is TRUE.
t50.germ	If TRUE, highlights the time required for 50% of viable/germinated seeds to germinate ($t_{50_{\text{Total}}}$) as a vertical line. Default is TRUE.
tmgr	If TRUE, highlights the Time at Maximum Germination Rate (TMGR) as a vertical line. Default is TRUE.
mgt	If TRUE, highlights the Mean Germination Time (MGT) as a vertical line. Default is TRUE.

uniformity	If TRUE, highlights the uniformity value ($U_{t_{max}-t_{min}}$) as a horizontal line. Default is TRUE.
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.
...	Default plot arguments.

Value

The plot of the cumulative germination curve as an object of class `ggplot`.

See Also

[FourPHFfit](#)

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
#-----------------------------------------------------------------------------
fit1 <- FourPHFfit(germ.counts = x, intervals = int,
                   total.seeds = 50, tmax = 20)

# From cumulative germination counts
#-----------------------------------------------------------------------------
fit2 <- FourPHFfit(germ.counts = y, intervals = int,
                   total.seeds = 50, tmax = 20, partial = FALSE)

# Default plots
plot(fit1)
plot(fit2)

# No labels
plot(fit1, plotlabels = FALSE)
plot(fit2, plotlabels = FALSE)

# Only the FPHF curve
plot(fit1, rog = FALSE, t50.total = FALSE, t50.germ = FALSE,
     tmgr = FALSE, mgt = FALSE, uniformity = FALSE)
plot(fit2, rog = FALSE, t50.total = FALSE, t50.germ = FALSE,
     tmgr = FALSE, mgt = FALSE, uniformity = FALSE)

# Without y axis limits adjustment
plot(fit1, limits = FALSE)
plot(fit2, limits = 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, 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), 1609–1617.

Farooq M, Basra SMA, Ahmad N, Hafeez K (2005). "Thermal hardening: A new seed vigor enhancement tool in rice." *Journal of Integrative Plant Biology*, **47**(2), 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 George (1961), Timson's index or Timson's germination velocity index (Timson 1965) and it's modifications by Labouriau (Ranal and de Santana 2006) and (Khan and Ungar 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 Ungar 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

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

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

George DW (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*, 15.

Goodchild NA, Walker MG (1971). "A method of measuring seed germination in physiological studies." *Annals of Botany*, **35**(141), 615–621.

Khan MA, 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), 481–489.

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

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

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

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

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