The `germinationmetrics` Package: A Brief Introduction

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2020-02-09

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Contents

Overview

The package `germinationmetrics` is a collection of functions which implements various methods for describing the time-course of germination in terms of single-value germination indices as well as fitted curves.

The goal of this vignette is to introduce the users to these functions and get started in describing sequentially recorded germination count data. This document assumes a basic knowledge of `R` programming language.

Installation

The package can be installed using the following functions:

```
# Install from CRAN
install.packages('germinationmetrics', dependencies=TRUE)

# Install development version from Github
devtools::install_github("aravind-j/germinationmetrics")
```

Then the package can be loaded using the function

```
library(germinationmetrics)
```

```
Welcome to germinationmetrics version 0.1.3.9000


# To know how to use this package type:
  browseVignettes(package = 'germinationmetrics')
  for the package vignette.

# To know whats new in this version type:
  news(package='germinationmetrics')
  for the NEWS file.

# To cite the methods in the package type:
  citation(package='germinationmetrics')

# To suppress this message use:
  suppressPackageStartupMessages(library(germinationmetrics))
--------------------------------------------------------------------------------
```

Version History

The current version of the package is 0.1.3. The previous versions are as follows.

Table 1. Version history of `germinationmetrics` `R` package.

Version	Date
0.1.0	2018-04-17
0.1.1	2018-07-26
0.1.1.1	2018-10-16
0.1.2	2018-10-31

To know detailed history of changes use `news(package='germinationmetrics')`.

Germination count data

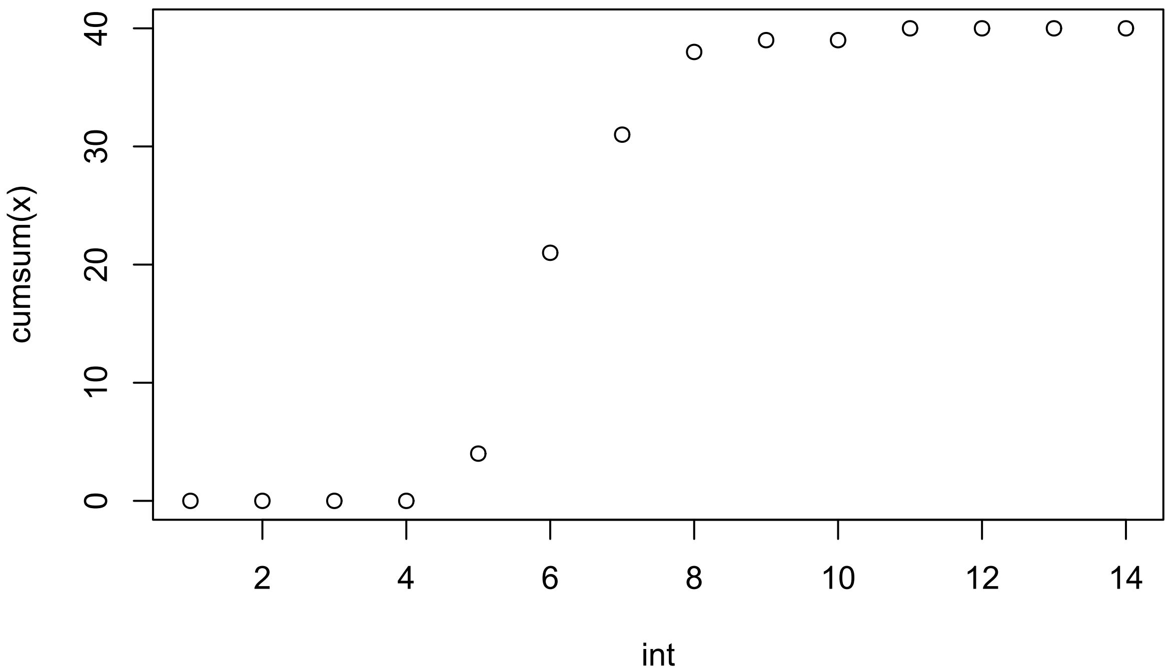
Typically in a germination test, the germination count data of a fixed number of seeds is recorded at regular intervals for a definite period of time or until all the seeds have germinated. These germination count data can be either partial or cumulative (Table 2).

Table 2 : A typical germination count data.

intervals	counts	cumulative.counts
1	0	0
2	0	0
3	0	0
4	0	0
5	4	4
6	17	21
7	10	31
8	7	38
9	1	39
10	0	39
11	1	40
12	0	40
13	0	40
14	0	40

The time-course of germination can be plotted as follows.

```r
data <- data.frame(intervals = 1:14,
                   counts = c(0, 0, 0, 0, 4, 17, 10, 7, 1, 0, 1, 0, 0, 0))

# Partial germination counts
x <- data$counts
# Cumulative germination counts
y <- cumsum(x)
# Time intervals of observations
int <- data$intervals

plot(int, cumsum(x))
```



Single-value germination indices

The details about the single-value germination indices implemented in `germinationmetrics` are described in Table 3.

Table 3 : Single-value germination indices implemented in `germinationmetrics`.

Germination index	Function	Details	Unit	Measures	Reference
Germination percentage or Final germination percentage or Germinability (GP)	`GermPercent`	It 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.	Percentage (%)	Germination capacity	ISTA (2015)
Time for the first germination or Germination time lag (t_0)	`FirstGermTime`	It is the time for first germination to occur (e.g. First day of germination)	time	Germination time	Edwards (1932); Czabator (1962); Goloff and Bazzaz (1975); Labouriau (1983a); Ranal (1999); Quintanilla et al. (2000)
Time for the last germination (t_g)	`LastGermTime`	It is the time for last germination to occur (e.g. Last day of germination)	time	Germination time	Edwards (1932)
Time spread of germination or Germination distribution	`TimeSpreadGerm`	It is the difference between time for last germination (t_g) and time for first germination (t_0). $$Time\,spread\,of\,germination = t_g - t_0$$	time	Germination time	Al-Mudaris (1998); Schrader and Graves (2000); Kader (2005)
Peak period of germination or Modal time of germination	`PeakGermTime`	It is the time in which highest frequency of germinated seeds are observed and need not be unique.	time	Germination time	Ranal and Santana (2006)
Median germination time (t_{50}) (Coolbear)	`t50`	It is the time to reach 50% of final/maximum germination. With argument `method` specified as `"coolbear"`, it is computed 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 $N_i < \frac{N+1}{2} < N_j$.	time	Germination time	Coolbear et al. (1984)
Median germination time (t_{50}) (Farooq)	`t50`	With argument `method` specified as `"farooq"`, it is computed 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 $N_i < \frac{N}{2} < N_j$.	time	Germination time	Farooq et al. (2005)

Germination index	Function	Details	Unit	Measures	Reference
Mean germination time or Mean length of incubation time ($\overline{T}$) or Germination resistance (GR) or Sprouting index (SI) or Emergence index (EI)	`MeanGermTime`	It is the average length of time required for maximum germination of a seed lot and is estimated according to the following formula. $$\overline{T} = \frac{\sum_{i=1}^{k} N_iT_i}{\sum_{i=1}^{k} N_i}$$ Where, T_i is the time from the start of the experiment to the ith interval, N_i is the number of seeds germinated in the ith time interval (not the accumulated number, but the number corresponding to the ith interval), and k is the total number of time intervals. It is the inverse of mean germination rate ($\overline{V}$). $$\overline{T} = \frac{1}{\overline{V}}$$	time	Germination time	Edmond and Drapala (1958); Czabator (1962); Smith and Millet (1964); Gordon (1969); Gordon (1971); Mock and Eberhart (1972); Ellis and Roberts (1980) Labouriau (1983a); Ranal and Santana (2006)
Variance of germination time (s_{T}^{2})	`VarGermTime`	It is computed 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 interval, N_i is the number of seeds germinated in the ith time interval (not the accumulated number, but the number corresponding to the ith interval), and k is the total number of time intervals.	time	Germination time	Labouriau (1983a); Ranal and Santana (2006)
Standard error of germination time ($s_{\overline{T}}$)	`SEGermTime`	It signifies the accuracy of the calculation of the mean germination time. It is estimated 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 interval (not the accumulated number, but the number corresponding to the ith interval) and k is the total number of time intervals.	time	Germination time	Labouriau (1983a); Ranal and Santana (2006)

Germination index	Function	Details	Unit	Measures	Reference
Mean germination rate ($\overline{V}$)	`MeanGermRate`	It is computed according to the following formula: $$\overline{V} = \frac{\sum_{i=1}^{k} N_i}{\sum_{i=1}^{k} N_i T_i}$$ Where, T_i is the time from the start of the experiment to the ith interval, N_i is the number of seeds germinated in the ith time interval (not the accumulated number, but the number corresponding to the ith interval), and k is the total number of time intervals. It is the inverse of mean germination time ($\overline{T}$). $$\overline{V} = \frac{1}{\overline{T}}$$	time^{-1}	Germination rate	Labouriau and Valadares (1976); Labouriau (1983b); Ranal and Santana (2006)
Coefficient of velocity of germination (CVG) or Coefficient of rate of germination (CRG) or Kotowski's coefficient of velocity	`CVG`	It is estimated according to the following formula. $$CVG = \frac{\sum_{i=1}^{k} N_i}{\sum_{i=1}^{k} N_i T_i} \times 100$$ $$CVG = \overline{V} \times 100$$ Where, T_i is the time from the start of the experiment to the ith interval, N_i is the number of seeds germinated in the ith time interval (not the accumulated number, but the number corresponding to the ith interval), and k is the total number of time intervals.	% day $^{-1}$	Germination rate	Kotowski (1926), Nichols and Heydecker (1968); Bewley and Black (1994); Labouriau (1983b); Scott et al. (1984)
Variance of germination rate (s_{V}^{2})	`VarGermRate`	It is calculated according to the following formula. $$s_{V}^{2} = \overline{V}^{4} \times s_{T}^{2}$$ Where, s_{T}^{2} is the variance of germination time.	time^{-2}	Germination rate	Labouriau (1983b); Ranal and Santana (2006)
Standard error of germination rate ($s_{\overline{V}}$)	`SEGermRate`	It is estimated according to the following formula. $$s_{\overline{V}} = \sqrt{\frac{s_{V}^{2}}{\sum_{i=1}^{k} N_i}}$$ Where, N_i is the number of seeds germinated in the ith time interval (not the accumulated number, but the number corresponding to the ith interval), and k is the total number of time intervals.	time^{-1}	Germination rate	Labouriau (1983b); Ranal and Santana (2006)
Germination rate as the reciprocal of the median time (v_{50})	`GermRateRecip`	It is the reciprocal of the median germination time (t_{50}). $$v_{50} = \frac{1}{t_{50}}$$	time^{-1}	Germination rate	Went (1957); Labouriau (1983b); Ranal and Santana (2006)

Germination index	Function	Details	Unit	Measures	Reference
Speed of germination or Germination rate Index or index of velocity of germination or Emergence rate index (Allan, Vogel and Peterson; Erbach; Hsu and Nelson) or Germination index (AOSA)	`GermSpeed`	It is the rate of germination in terms of the total number of seeds that germinate in a time interval. It is estimated as follows. $$S = \sum_{i=1}^{k} \frac{N_i}{T_i}$$ Where, T_i is the time from the start of the experiment to the ith interval, N_i is the number of seeds germinated in the ith time interval (not the accumulated number, but the number corresponding to the ith interval), and k is the total number of time intervals. Instead of germination counts, germination percentages may also be used for computation of speed of germination.	% time^{-1}	Mixed	Throneberry and Smith (1955); Maguire (1962); Allan et al. (1962); Kendrick and Frankland (1969); Bouton et al. (1976); Erbach (1982); AOSA (1983); Khandakar and Bradbeer (1983); Hsu and Nelson (1986); Bradbeer (1988); Wardle et al. (1991)
Speed of accumulated germination	`GermSpeedAccumula`	It is the rate of germination in terms of the accumulated/cumulative total number of seeds that germinate in a time interval. It is estimated as follows. $$S_{accumulated} = \sum_{i=1}^{k} \frac{\sum_{j=1}^{i} N_j}{T_i}$$ Where, T_i is the time from the start of the experiment to the ith interval, $\sum_{j=1}^{i} N_j$ is the cumuative/accumulated number of seeds germinated in the ith interval, and k is the total number of time intervals. Instead of germination counts, germination percentages may also be used for computation of speed of germination.	% time^{-1}	Mixed	Bradbeer (1988); Wardle et al. (1991); Haugland and Brandsaeter (1996); Santana and Ranal (2004)
Corrected germination rate index	`GermSpeedCorrecte`	It is computed as follows. $$S_{corrected} = \frac{S}{FGP}$$ Where, FGP is the final germination percentage or germinability.	time^{-1}	Mixed	Evetts and Burnside (1972)
Weighted germination percentage (WGP)	`WeightGermPercent`	It is estimated as follows. $$WGP = \frac{\sum_{i=1}^{k}(k-i+1)N_i}{k \times N} \times 100$$ Where, N_i is the number of seeds that germinated in the time interval i (not cumulative, but partial count), N is the total number of seeds tested, and k is the total number of time intervals.		Mixed	Reddy et al. (1985); Reddy (1978)

Germination index	Function	Details	Unit	Measures	Reference
Mean germination percentage per unit time ($\overline{GP}$)	`MeanGermPercent`	It is estimated as follows. $$\overline{GP} = \frac{GP}{T_k}$$ Where, GP is the final germination percentage, T_k is the time at the kth time interval, and k is the total number of time intervals required for final germination.		Mixed	Czabator (1962)
Number of seeds germinated per unit time $\overline{N}$	`MeanGermNumber`	It is estimated as follows. $$\overline{N} = \frac{N_g}{T_k}$$ Where, N_g is the number of germinated seeds at the end of the germination test, T_k is the time at the kth time interval, and k is the total number of time intervals required for final germination.		Mixed	Khamassi et al. (2013)
Timson's index [$\sum 10$ (Ten summation), $\sum 5$ or $\sum 20$] or Germination energy index (GEI)	`TimsonsIndex`	It is the progressive total of cumulative germination percentage recorded at specific intervals for a set period of time and is estimated in terms of cumulative germination percentage (G_i) as follows. $$\Sigma k = \sum_{i=1}^{k} G_i$$ Where, G_i is the cumulative germination percentage in time interval i, and k is the total number of time intervals. It also estimated in terms of partial germination percentage as follows. $$\Sigma k = \sum_{i=1}^{k} g_i(k-j)$$ Where, g_i is the germination (not cumulative, but partial germination) in time interval i (i varying from 0 to k), k is the total number of time intervals, and $j = i - 1$.		Mixed	Grose and Zimmer (1958); Timson (1965); Lyon and Coffelt (1966); Chaudhary and Ghildyal (1970); Negm and Smith (1978); Brown and Mayer (1988); Baskin and Baskin (1998); Goodchild and Walker (1971)
Modified Timson's index (Σk_{mod}) (Labouriau)	`TimsonsIndex`	It is estimated as Timson's index Σk divided by the sum of partial germination percentages. $$\Sigma k_{mod} = \frac{\Sigma k}{\sum_{i=1}^{k} g_i}$$		Mixed	Ranal and Santana (2006)

Germination index	Function	Details	Unit	Measures	Reference
Modified Timson's index (Σk_{mod}) (Khan and Unger)	`TimsonsIndex`	It is estimated as Timson's index (Σk) divided by the total time period of germination (T_k). $$\Sigma k_{mod} = \frac{\Sigma k}{T_k}$$		Mixed	Khan and Ungar (1984)
George's index (GR)	`GermRateGeorge`	It is estimated as follows. $$GR = \sum_{i=1}^{k} N_i K_i$$ Where N_i is the number of seeds germinated by ith interval and K_i is the number of intervals(eg. days) until the end of the test, and and k is the total number of time intervals.		Mixed	George (1961); Tucker and Wright (1965); Nichols and Heydecker (1968)
Germination Index (GI) (Melville)	`GermIndex`	It is estimated as follows. $$GI = \sum_{i=1}^{k} \frac{\lvert (T_k - T_i)\, N_i \rvert}{N_t}$$ Where, T_i is the time from the start of the experiment to the ith interval (day for the example), N_i is the number of seeds germinated in the ith time interval (not the accumulated number, but the number corresponding to the ith interval), N_t is the total number of seeds used in the test, and k is the total number of time intervals.		Mixed	Melville et al. (1980)
Germination Index (GI_{mod}) (Melville; Santana and Ranal)	`GermIndex`	It is estimated as follows. $$GI_{mod} = \sum_{i=1}^{k} \frac{\lvert (T_k - T_i)\, N_i \rvert}{N_g}$$ Where, T_i is the time from the start of the experiment to the ith interval (day for the example), N_i is the number of seeds germinated in the ith time interval (not the accumulated number, but the number corresponding to the ith interval), N_g is the total number of germinated seeds at the end of the test, and k is the total number of time intervals.		Mixed	Melville et al. (1980); Santana and Ranal (2004); Ranal and Santana (2006)

Germination index	Function	Details	Unit	Measures	Reference
Emergence Rate Index (ERI) or Germination Rate Index (Shmueli and Goldberg)	`EmergenceRateInde`	It is estimated as follows. $$ERI = \sum_{i=i_0}^{k-1} N_i(k-i)$$ Where, N_i is the number of seeds germinated in the ith time interval (not the accumulated number, but the number corresponding to the ith interval), i_0 is the time interval when emergence/germination started, and k is the total number of time intervals.		Mixed	Shmueli and Goldberg (1971)
Modified Emergence Rate Index (ERI_{mod}) or Modified Germination Rate Index (Shmueli and Goldberg; Santana and Ranal)	`EmergenceRateInde`	It is estimated by dividing Emergence rate index (ERI) by total number of emerged seedlings (or germinated seeds). $$ERI_{mod} = \frac{\sum_{i=i_0}^{k-1} N_i(k-i)}{N_g} = \frac{ERI}{N_g}$$ Where, N_g is the total number of germinated seeds at the end of the test, N_i is the number of seeds germinated in the ith time interval (not the accumulated number, but the number corresponding to the ith interval), i_0 is the time interval when emergence/germination started, and k is the total number of time intervals.		Mixed	Shmueli and Goldberg (1971); Santana and Ranal (2004); Ranal and Santana (2006)
Emergence Rate Index (ERI) or Germination Rate Index (Bilbro & Wanjura)	`EmergenceRateInde`	It is the estimated as follows. $$ERI = \frac{\sum_{i=1}^{k} N_i}{\overline{T}} = \frac{N_g}{\overline{T}}$$ Where, N_g is the total number of germinated seeds at the end of the test, N_i is the number of seeds germinated in the ith time interval (not the accumulated number, but the number corresponding to the ith interval), and $\overline{T}$ is the mean germination time or mean emergence time.		Mixed	Bilbro and Wanjura (1982)
Emergence Rate Index (ERI) or Germination Rate Index (Fakorede)	`EmergenceRateInde`	It is estimated as follows. $$ERI = \frac{\overline{T}}{FGP/100}$$ Where, $\overline{T}$ is the Mean germination time and FGP is the final germination time.		Mixed	Fakorede and Ayoola (1980); Fakorede and Ojo (1981); Fakorede and Agbana (1983)

Germination index	Function	Details	Unit	Measures	Reference
Peak value(PV) (Czabator) or Emergence Energy (EE)	`PeakValue`	It is the accumulated number of seeds germinated at the point on the germination curve at which the rate of germination starts to decrease. It is computed as the maximum quotient obtained by dividing successive cumulative germination values by the relevant incubation time. $$PV = \max\left(\frac{G_1}{T_1}, \frac{G_2}{T_2}, \cdots \frac{G_k}{T_k}\right)$$ Where, T_i is the time from the start of the experiment to the ith interval, G_i is the cumulative germination percentage in the ith time interval, and k is the total number of time intervals.	% time^{-1}	Mixed	Czabator (1962); Bonner (1967)
Germination value (GV) (Czabator)	`GermValue`	It is computed as follows. $$GV = PV \times MDG$$ Where, PV is the peak value and MDG is the mean daily germination percentage from the onset of germination. It can also be computed for other time intervals of successive germination counts, by replacing MDG with the mean germination percentage per unit time ($\overline{GP}$). GV value can be modified (GV_{mod}), to consider the entire duration from the beginning of the test instead of just from the onset of germination.		Mixed	Czabator (1962); Brown and Mayer (1988)
Germination value (GV) (Diavanshir and Pourbiek)	`GermValue`	It is computed as follows. $$GV = \frac{\sum DGS}{N} \times GP \times c$$ Where, DGS is the daily germination speed computed by dividing cumulative germination percentage by the number of days since the since the onset of germination, N is the frequency or number of DGS calculated during the test, GP is the germination percentage expressed over 100, and c is a constant. The value of c is decided on the basis of average daily speed of germination ($\frac{\sum DGS}{N}$). If it is less than 10, then c value of 10 can be used and if it is more than 10, then value of 7 or 8 can be used for c. GV value can be modified (GV_{mod}), to consider the entire duration from the beginning of the test instead of just from the onset of germination.		Mixed	Djavanshir and Pourbeik (1976); Brown and Mayer (1988)

Germination index	Function	Details	Unit	Measures	Reference
Coefficient of uniformity of germination (CUG)	`CUGerm`	It is computed as follows. $$CUG = \frac{\sum_{i=1}^{k} N_i}{\sum_{i=1}^{k}(\overline{T} - T_i)^2 N_i}$$ Where, $\overline{T}$ is the the mean germination time, T_i is the time from the start of the experiment to the ith interval (day for the example), N_i is the number of seeds germinated in the ith time interval (not the accumulated number, but the number corresponding to the ith interval), and k is the total number of time intervals.		Germination unifromity	Heydecker (1972); Bewley and Black (1994)
Coefficient of variation of the germination time (CV_T)	`CVGermTime`	It is estimated as follows. $$CV_T = \sqrt{\frac{s_T^2}{\overline{T}}}$$ Where, s_T^2 is the variance of germination time and $\overline{T}$ is the mean germination time.		Germination unifromity	Gomes (1960); Ranal and Santana (2006)
Synchronization index ($\overline{E}$) or Uncertainty of the germination process (U) or informational entropy (H)	`GermUncertainty`	It is estimated as follows. $$\overline{E} = -\sum_{i=1}^{k} f_i \log_2 f_i$$ Where, f_i is the relative frequency of germination ($f_i = \frac{N_i}{\sum_{i=1}^{k} N_i}$), N_i is the number of seeds germinated on the ith time interval, and k is the total number of time intervals.	bit	Germination synchrony	Shannon (1948); Labouriau and Valadares (1976); Labouriau (1983b)
Synchrony of germination (Z index)	`GermSynchrony`	It is computed as follows. $$Z = \frac{\sum_{i=1}^{k} C_{N_i,2}}{C_{\Sigma N_i,2}}$$ 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 interval (estimated as $C_{N_i,2} = \frac{N_i(N_i-1)}{2}$), 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.		Germination synchrony	Primack (1985); Ranal and Santana (2006)

Examples

```r
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)
```

GermPercent()

```
[1] 80
```

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

```
[1] 80
```

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

```
[1] 80
```

```r
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)
```

FirstGermTime(), LastGermTime(), PeakGermTime(), TimeSpreadGerm()

```
[1] 5
```

```r
LastGermTime(germ.counts = x, intervals = int)
```

```
[1] 11
```

```r
TimeSpreadGerm(germ.counts = x, intervals = int)
```

```
[1] 6
```

```r
PeakGermTime(germ.counts = x, intervals = int)
```

```
[1] 6
```

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

```
Warning in PeakGermTime(germ.counts = z, intervals = int): Multiple peak germination
times exist.
```

```
[1] 5 6
```

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

```
[1] 5
```

```r
LastGermTime(germ.counts = y, intervals = int, partial = FALSE)
```

```
[1] 11
```

```r
TimeSpreadGerm(germ.counts = y, intervals = int, partial = FALSE)
```

```
[1] 6
```

```r
PeakGermTime(germ.counts = y, intervals = int, partial = FALSE)
```

```
[1] 6
```

```r
# For multiple peak germination time
PeakGermTime(germ.counts = cumsum(z), intervals = int, partial = FALSE)
```

```
Warning in PeakGermTime(germ.counts = cumsum(z), intervals = int, partial = FALSE):
Multiple peak germination times exist.
```

```
[1] 5 6
```

```r

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()`

```
[1] 5.970588
```

```r
t50(germ.counts = x, intervals = int, method = "farooq")
```

```
[1] 5.941176
```

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

```
[1] 5.970588
```

```r
t50(germ.counts = y, intervals = int, partial = FALSE, method = "farooq")
```

```
[1] 5.941176
```

```r

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)
```

`MeanGermTime(), VarGermTime(), SEGermTime(), CVGermTime()`

```
[1] 6.7
```

```r
VarGermTime(germ.counts = x, intervals = int)
```

```
[1] 1.446154
```

```r
SEGermTime(germ.counts = x, intervals = int)
```

```
[1] 0.1901416
```

```r
CVGermTime(germ.counts = x, intervals = int)
```

```
[1] 0.1794868
```

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

```
[1] 6.7
```

```r
VarGermTime(germ.counts = y, intervals = int, partial = FALSE)
```

```
[1] 19.04012
```

```r
SEGermTime(germ.counts = y, intervals = int, partial = FALSE)
```

```
[1] 0.2394781
```

```r
CVGermTime(germ.counts = y, intervals = int, partial = FALSE)
```

```
[1] 0.6512685
```

```r
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)
```

MeanGermRate(), CVG(), VarGermRate(), SEGermRate(), GermRateRecip()

```
[1] 0.1492537
```

```r
CVG(germ.counts = x, intervals = int)
```

```
[1] 14.92537
```

```r
VarGermRate(germ.counts = x, intervals = int)
```

```
[1] 0.0007176543
```

```r
SEGermRate(germ.counts = x, intervals = int)
```

```
[1] 0.004235724
```

```r
GermRateRecip(germ.counts = x, intervals = int, method = "coolbear")
```

```
[1] 0.1674877
```

```r
GermRateRecip(germ.counts = x, intervals = int, method = "farooq")
```

```
[1] 0.1683168
```

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

```
[1] 0.1492537
```

```
CVG(germ.counts = y, intervals = int, partial = FALSE)
```

```
[1] 14.92537
```

```
VarGermRate(germ.counts = y, intervals = int, partial = FALSE)
```

```
[1] 0.009448666
```

```
SEGermRate(germ.counts = y, intervals = int, partial = FALSE)
```

```
[1] 0.005334776
```

```
GermRateRecip(germ.counts = y, intervals = int,
              method = "coolbear", partial = FALSE)
```

```
[1] 0.1674877
```

```
GermRateRecip(germ.counts = y, intervals = int,
              method = "farooq", partial = FALSE)
```

```
[1] 0.1683168
```

```

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)
```

GermSpeed(), GermSpeedAccumulated(), GermSpeedCorrected()

```
[1] 6.138925
```

```
GermSpeedAccumulated(germ.counts = x, intervals = int)
```

```
[1] 34.61567
```

```
GermSpeedCorrected(germ.counts = x, intervals = int, total.seeds = 50,
                   method = "normal")
```

```
[1] 0.07673656
```

```
GermSpeedCorrected(germ.counts = x, intervals = int, total.seeds = 50,
                   method = "accumulated")
```

```
[1] 0.4326958
```

```
# From partial germination counts (with percentages instead of counts)
#----------------------------------------------------------------------------
GermSpeed(germ.counts = x, intervals = int,
          percent = TRUE, total.seeds = 50)
```

```
[1] 12.27785
```

```r
GermSpeedAccumulated(germ.counts = x, intervals = int,
                     percent = TRUE, total.seeds = 50)
```

```
[1] 69.23134
```

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

```
[1] 6.138925
```

```r
GermSpeedAccumulated(germ.counts = y, intervals = int, partial = FALSE)
```

```
[1] 34.61567
```

```r
GermSpeedCorrected(germ.counts = y, intervals = int,
                   partial = FALSE, total.seeds = 50, method = "normal")
```

```
[1] 0.07673656
```

```r
GermSpeedCorrected(germ.counts = y, intervals = int,
                   partial = FALSE, total.seeds = 50, method = "accumulated")
```

```
[1] 0.4326958
```

```r
# From cumulative germination counts (with percentages instead of counts)
#----------------------------------------------------------------------------
GermSpeed(germ.counts = y, intervals = int, partial = FALSE,
          percent = TRUE, total.seeds = 50)
```

```
[1] 12.27785
```

```r
GermSpeedAccumulated(germ.counts = y, intervals = int, partial = FALSE,
                     percent = TRUE, total.seeds = 50)
```

```
[1] 69.23134
```

```r
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)
```

GermSpeed(), GermSpeedAccumulated(), GermSpeedCorrected()

```
[1] 6.138925
```

```r
GermSpeedAccumulated(germ.counts = x, intervals = int)
```

```
[1] 34.61567
```

```r
GermSpeedCorrected(germ.counts = x, intervals = int, total.seeds = 50,
                   method = "normal")
```

```
[1] 0.07673656
```

```r
GermSpeedCorrected(germ.counts = x, intervals = int, total.seeds = 50,
                   method = "accumulated")
```

```
[1] 0.4326958
```

```r
# From partial germination counts (with percentages instead of counts)
#----------------------------------------------------------------------------
GermSpeed(germ.counts = x, intervals = int,
          percent = TRUE, total.seeds = 50)
```

```
[1] 12.27785
```

```r
GermSpeedAccumulated(germ.counts = x, intervals = int,
                     percent = TRUE, total.seeds = 50)
```

```
[1] 69.23134
```

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

```
[1] 6.138925
```

```r
GermSpeedAccumulated(germ.counts = y, intervals = int, partial = FALSE)
```

```
[1] 34.61567
```

```r
GermSpeedCorrected(germ.counts = y, intervals = int,
                   partial = FALSE, total.seeds = 50, method = "normal")
```

```
[1] 0.07673656
```

```r
GermSpeedCorrected(germ.counts = y, intervals = int,
                   partial = FALSE, total.seeds = 50, method = "accumulated")
```

```
[1] 0.4326958
```

```r
# From cumulative germination counts (with percentages instead of counts)
#----------------------------------------------------------------------------
GermSpeed(germ.counts = y, intervals = int, partial = FALSE,
          percent = TRUE, total.seeds = 50)
```

```
[1] 12.27785
```

```r
GermSpeedAccumulated(germ.counts = y, intervals = int, partial = FALSE,
                     percent = TRUE, total.seeds = 50)
```

```
[1] 69.23134
```

```r
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
#----------------------------------------------------------------------------
WeightGermPercent(germ.counts = x, total.seeds = 50, intervals = int)
```

WeightGermPercent()

```
[1] 47.42857
```

```r
# From cumulative germination counts
#----------------------------------------------------------------------------
```

```
WeightGermPercent(germ.counts = y, total.seeds = 50, intervals = int,
                  partial = FALSE)
```

```
[1] 47.42857
```

```
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)
```

MeanGermPercent(), MeanGermNumber()

```
[1] 5.714286
```

```
MeanGermNumber(germ.counts = x, intervals = int)
```

```
[1] 2.857143
```

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

```
[1] 5.714286
```

```
MeanGermNumber(germ.counts = y, intervals = int, partial = FALSE)
```

```
[1] 2.857143
```

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

```
[1] 5.714286
```

```
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(), GermRateGeorge()

```
[1] 664
```

```
TimsonsIndex(germ.counts = x, intervals = int, total.seeds = 50,
             modification = "none")
```

```
[1] 664
```

```
TimsonsIndex(germ.counts = x, intervals = int, total.seeds = 50,
             modification = "labouriau")
```

```
[1] 8.3
```

```r
TimsonsIndex(germ.counts = x, intervals = int, total.seeds = 50,
             modification = "khanungar")
```

```
[1] 47.42857
```

```r
GermRateGeorge(germ.counts = x, intervals = int)
```

```
[1] 332
```

```r
# With max specified
TimsonsIndex(germ.counts = x, intervals = int, total.seeds = 50, max = 10)
```

```
[1] 344
```

```r
TimsonsIndex(germ.counts = x, intervals = int, total.seeds = 50,
             max = 10, modification = "none")
```

```
[1] 344
```

```r
TimsonsIndex(germ.counts = x, intervals = int, total.seeds = 50,
             max = 10, modification = "labouriau")
```

```
[1] 4.410256
```

```r
TimsonsIndex(germ.counts = x, intervals = int, total.seeds = 50,
             max = 10, modification = "khanungar")
```

```
[1] 24.57143
```

```r
GermRateGeorge(germ.counts = x, intervals = int, max = 10)
```

```
[1] 172
```

```r
GermRateGeorge(germ.counts = x, intervals = int, max = 14)
```

```
[1] 332
```

```r
# From cumulative germination counts
#----------------------------------------------------------------------------
# Wihout max specified
TimsonsIndex(germ.counts = y, intervals = int, partial = FALSE,
             total.seeds = 50)
```

```
[1] 664
```

```r
TimsonsIndex(germ.counts = y, intervals = int, partial = FALSE,
             total.seeds = 50,
             modification = "none")
```

```
[1] 664
```

```r
TimsonsIndex(germ.counts = y, intervals = int, partial = FALSE,
             total.seeds = 50,
             modification = "labouriau")
```

```
[1] 8.3
```

```r
TimsonsIndex(germ.counts = y, intervals = int, partial = FALSE,
             total.seeds = 50,
             modification = "khanungar")
```

```
[1] 47.42857
```

```r
GermRateGeorge(germ.counts = y, intervals = int, partial = FALSE,)
```

```
[1] 332
```

```r
# With max specified
TimsonsIndex(germ.counts = y, intervals = int, partial = FALSE,
             total.seeds = 50, max = 10)
```

```
[1] 344
```

```r
TimsonsIndex(germ.counts = y, intervals = int, partial = FALSE,
             total.seeds = 50,
             max = 10, modification = "none")
```

```
[1] 344
```

```r
TimsonsIndex(germ.counts = y, intervals = int, partial = FALSE,
             total.seeds = 50,
             max = 10, modification = "labouriau")
```

```
[1] 4.410256
```

```r
TimsonsIndex(germ.counts = y, intervals = int, partial = FALSE,
             total.seeds = 50,
             max = 10, modification = "khanungar")
```

```
[1] 24.57143
```

```r
GermRateGeorge(germ.counts = y, intervals = int, partial = FALSE,
               max = 10)
```

```
[1] 172
```

```r
GermRateGeorge(germ.counts = y, intervals = int, partial = FALSE,
               max = 14)
```

```
[1] 332
```

```r
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
#----------------------------------------------------------------------------
GermIndex(germ.counts = x, intervals = int, total.seeds = 50)
```

GermIndex()

```
[1] 5.84
```

```r
GermIndex(germ.counts = x, intervals = int, total.seeds = 50,
          modification = "none")
```

```
[1] 5.84
```

```r
GermIndex(germ.counts = x, intervals = int, total.seeds = 50,
          modification = "santanaranal")
```

```
[1] 7.3
```

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

```
[1] 5.84
```

```r
GermIndex(germ.counts = y, intervals = int, partial = FALSE,
          total.seeds = 50,
          modification = "none")
```

```
[1] 5.84
```

```r
GermIndex(germ.counts = y, intervals = int, partial = FALSE,
          total.seeds = 50,
          modification = "santanaranal")
```

```
[1] 7.3
```

```r
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
#----------------------------------------------------------------------------
EmergenceRateIndex(germ.counts = x, intervals = int)
```

EmergenceRateIndex()

```
[1] 292
```

```r
EmergenceRateIndex(germ.counts = x, intervals = int,
                   method = "melville")
```

```
[1] 292
```

```r
EmergenceRateIndex(germ.counts = x, intervals = int,
                   method = "melvillesantanaranal")
```

```
[1] 7.3
```

```r
EmergenceRateIndex(germ.counts = x, intervals = int,
                   method = "bilbrowanjura")
```

```
[1] 5.970149
```

```r
EmergenceRateIndex(germ.counts = x, intervals = int,
                   total.seeds = 50, method = "fakorede")
```

```
[1] 8.375
```

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

```
[1] 292
```

```r
EmergenceRateIndex(germ.counts = y, intervals = int, partial = FALSE,
                   method = "melville")
```

```
[1] 292
```

```r
EmergenceRateIndex(germ.counts = y, intervals = int, partial = FALSE,
                   method = "melvillesantanaranal")
```

```
[1] 7.3
```

```r
EmergenceRateIndex(germ.counts = y, intervals = int, partial = FALSE,
                   method = "bilbrowanjura")
```

```
[1] 5.970149
```

```r
EmergenceRateIndex(germ.counts = y, intervals = int, partial = FALSE,
                   total.seeds = 50, method = "fakorede")
```

```
[1] 8.375
```

```r
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)
```

PeakValue(), GermValue()

```
[1] 9.5
```

```r
GermValue(germ.counts = x, intervals = int, total.seeds = 200,
          method = "czabator")
```

```
$`Germination Value`
[1] 38.95

[[2]]
   germ.counts intervals Cumulative.germ.counts Cumulative.germ.percent      DGS
3           34         3                     34                    17.0 5.666667
4           40         4                     74                    37.0 9.250000
5           21         5                     95                    47.5 9.500000
6           10         6                    105                    52.5 8.750000
7            4         7                    109                    54.5 7.785714
8            5         8                    114                    57.0 7.125000
9            3         9                    117                    58.5 6.500000
10           5        10                    122                    61.0 6.100000
11           8        11                    130                    65.0 5.909091
12           7        12                    137                    68.5 5.708333
13           7        13                    144                    72.0 5.538462
14           6        14                    150                    75.0 5.357143
15           6        15                    156                    78.0 5.200000
16           4        16                    160                    80.0 5.000000
17           0        17                    160                    80.0 4.705882
18           2        18                    162                    81.0 4.500000
19           0        19                    162                    81.0 4.263158
20           2        20                    164                    82.0 4.100000
```

```r
GermValue(germ.counts = x, intervals = int, total.seeds = 200,
          method = "dp", k = 10)
```

```
$`Germination Value`
[1] 53.36595

[[2]]
   germ.counts intervals Cumulative.germ.counts Cumulative.germ.percent       DGS
3           34         3                     34                    17.0 5.666667
4           40         4                     74                    37.0 9.250000
5           21         5                     95                    47.5 9.500000
6           10         6                    105                    52.5 8.750000
7            4         7                    109                    54.5 7.785714
8            5         8                    114                    57.0 7.125000
9            3         9                    117                    58.5 6.500000
10           5        10                    122                    61.0 6.100000
11           8        11                    130                    65.0 5.909091
12           7        12                    137                    68.5 5.708333
13           7        13                    144                    72.0 5.538462
14           6        14                    150                    75.0 5.357143
15           6        15                    156                    78.0 5.200000
16           4        16                    160                    80.0 5.000000
17           0        17                    160                    80.0 4.705882
18           2        18                    162                    81.0 4.500000
19           0        19                    162                    81.0 4.263158
20           2        20                    164                    82.0 4.100000
   SumDGSbyN        GV
3   5.666667  9.633333
4   7.458333 27.595833
5   8.138889 38.659722
6   8.291667 43.531250
7   8.190476 44.638095
8   8.012897 45.673512
9   7.796769 45.611097
10  7.584673 46.266503
11  7.398497 48.090230
12  7.229481 49.521942
13  7.075752 50.945411
14  6.932534 51.994006
15  6.799262 53.034246
16  6.670744 53.365948
17  6.539753 52.318022
18  6.412268 51.939373
19  6.285850 50.915385
20  6.164414 50.548194

$testend
[1] 16
```

```r
GermValue(germ.counts = x, intervals = int, total.seeds = 200,
          method = "czabator", from.onset = FALSE)
```

```
$`Germination Value`
[1] 38.95
```

```
[[2]]
   germ.counts intervals Cumulative.germ.counts Cumulative.germ.percent      DGS
1            0         1                      0                     0.0 0.000000
2            0         2                      0                     0.0 0.000000
3           34         3                     34                    17.0 5.666667
4           40         4                     74                    37.0 9.250000
5           21         5                     95                    47.5 9.500000
6           10         6                    105                    52.5 8.750000
7            4         7                    109                    54.5 7.785714
8            5         8                    114                    57.0 7.125000
9            3         9                    117                    58.5 6.500000
10           5        10                    122                    61.0 6.100000
11           8        11                    130                    65.0 5.909091
12           7        12                    137                    68.5 5.708333
13           7        13                    144                    72.0 5.538462
14           6        14                    150                    75.0 5.357143
15           6        15                    156                    78.0 5.200000
16           4        16                    160                    80.0 5.000000
17           0        17                    160                    80.0 4.705882
18           2        18                    162                    81.0 4.500000
19           0        19                    162                    81.0 4.263158
20           2        20                    164                    82.0 4.100000
```

```
GermValue(germ.counts = x, intervals = int, total.seeds = 200,
          method = "dp", k = 10, from.onset = FALSE)
```

```
$`Germination Value`
[1] 46.6952

[[2]]
   germ.counts intervals Cumulative.germ.counts Cumulative.germ.percent      DGS
1            0         1                      0                     0.0 0.000000
2            0         2                      0                     0.0 0.000000
3           34         3                     34                    17.0 5.666667
4           40         4                     74                    37.0 9.250000
5           21         5                     95                    47.5 9.500000
6           10         6                    105                    52.5 8.750000
7            4         7                    109                    54.5 7.785714
8            5         8                    114                    57.0 7.125000
9            3         9                    117                    58.5 6.500000
10           5        10                    122                    61.0 6.100000
11           8        11                    130                    65.0 5.909091
12           7        12                    137                    68.5 5.708333
13           7        13                    144                    72.0 5.538462
14           6        14                    150                    75.0 5.357143
15           6        15                    156                    78.0 5.200000
16           4        16                    160                    80.0 5.000000
17           0        17                    160                    80.0 4.705882
18           2        18                    162                    81.0 4.500000
19           0        19                    162                    81.0 4.263158
20           2        20                    164                    82.0 4.100000
   SumDGSbyN        GV
1   0.000000  0.000000
2   0.000000  0.000000
```

```
3   1.888889  3.211111
4   3.729167 13.797917
5   4.883333 23.195833
6   5.527778 29.020833
7   5.850340 31.884354
8   6.009673 34.255134
9   6.064153 35.475298
10  6.067738 37.013202
11  6.053316 39.346552
12  6.024567 41.268285
13  5.987174 43.107655
14  5.942172 44.566291
15  5.892694 45.963013
16  5.836901 46.695205
17  5.770370 46.162961
18  5.699794 46.168331
19  5.624182 45.555871
20  5.547972 45.493374

$testend
[1] 16
```

```r
# From cumulative germination counts
#----------------------------------------------------------------------------
PeakValue(germ.counts = y, interval = int, total.seeds = 200,
          partial = FALSE)
```

```
[1] 9.5
```

```r
GermValue(germ.counts = y, intervals = int, total.seeds = 200,
          partial = FALSE, method = "czabator")
```

```
$`Germination Value`
[1] 38.95

[[2]]
   germ.counts intervals Cumulative.germ.counts Cumulative.germ.percent      DGS
3           34         3                     34                    17.0 5.666667
4           40         4                     74                    37.0 9.250000
5           21         5                     95                    47.5 9.500000
6           10         6                    105                    52.5 8.750000
7            4         7                    109                    54.5 7.785714
8            5         8                    114                    57.0 7.125000
9            3         9                    117                    58.5 6.500000
10           5        10                    122                    61.0 6.100000
11           8        11                    130                    65.0 5.909091
12           7        12                    137                    68.5 5.708333
13           7        13                    144                    72.0 5.538462
14           6        14                    150                    75.0 5.357143
15           6        15                    156                    78.0 5.200000
16           4        16                    160                    80.0 5.000000
17           0        17                    160                    80.0 4.705882
18           2        18                    162                    81.0 4.500000
19           0        19                    162                    81.0 4.263158
20           2        20                    164                    82.0 4.100000
```

```r
GermValue(germ.counts = y, intervals = int, total.seeds = 200,
          partial = FALSE, method = "dp", k = 10)
```

```
$`Germination Value`
[1] 53.36595

[[2]]
   germ.counts intervals Cumulative.germ.counts Cumulative.germ.percent      DGS
3           34         3                     34                    17.0 5.666667
4           40         4                     74                    37.0 9.250000
5           21         5                     95                    47.5 9.500000
6           10         6                    105                    52.5 8.750000
7            4         7                    109                    54.5 7.785714
8            5         8                    114                    57.0 7.125000
9            3         9                    117                    58.5 6.500000
10           5        10                    122                    61.0 6.100000
11           8        11                    130                    65.0 5.909091
12           7        12                    137                    68.5 5.708333
13           7        13                    144                    72.0 5.538462
14           6        14                    150                    75.0 5.357143
15           6        15                    156                    78.0 5.200000
16           4        16                    160                    80.0 5.000000
17           0        17                    160                    80.0 4.705882
18           2        18                    162                    81.0 4.500000
19           0        19                    162                    81.0 4.263158
20           2        20                    164                    82.0 4.100000
   SumDGSbyN        GV
3   5.666667  9.633333
4   7.458333 27.595833
5   8.138889 38.659722
6   8.291667 43.531250
7   8.190476 44.638095
8   8.012897 45.673512
9   7.796769 45.611097
10  7.584673 46.266503
11  7.398497 48.090230
12  7.229481 49.521942
13  7.075752 50.945411
14  6.932534 51.994006
15  6.799262 53.034246
16  6.670744 53.365948
17  6.539753 52.318022
18  6.412268 51.939373
19  6.285850 50.915385
20  6.164414 50.548194

$testend
[1] 16
```

```r
GermValue(germ.counts = y, intervals = int, total.seeds = 200,
          partial = FALSE, method = "czabator", from.onset = FALSE)
```

```
$`Germination Value`
[1] 38.95
```

```
[[2]]
   germ.counts intervals Cumulative.germ.counts Cumulative.germ.percent      DGS
1            0         1                      0                     0.0 0.000000
2            0         2                      0                     0.0 0.000000
3           34         3                     34                    17.0 5.666667
4           40         4                     74                    37.0 9.250000
5           21         5                     95                    47.5 9.500000
6           10         6                    105                    52.5 8.750000
7            4         7                    109                    54.5 7.785714
8            5         8                    114                    57.0 7.125000
9            3         9                    117                    58.5 6.500000
10           5        10                    122                    61.0 6.100000
11           8        11                    130                    65.0 5.909091
12           7        12                    137                    68.5 5.708333
13           7        13                    144                    72.0 5.538462
14           6        14                    150                    75.0 5.357143
15           6        15                    156                    78.0 5.200000
16           4        16                    160                    80.0 5.000000
17           0        17                    160                    80.0 4.705882
18           2        18                    162                    81.0 4.500000
19           0        19                    162                    81.0 4.263158
20           2        20                    164                    82.0 4.100000
```

```
GermValue(germ.counts = y, intervals = int, total.seeds = 200,
          partial = FALSE, method = "dp", k = 10, from.onset = FALSE)
```

```
$`Germination Value`
[1] 46.6952

[[2]]
   germ.counts intervals Cumulative.germ.counts Cumulative.germ.percent      DGS
1            0         1                      0                     0.0 0.000000
2            0         2                      0                     0.0 0.000000
3           34         3                     34                    17.0 5.666667
4           40         4                     74                    37.0 9.250000
5           21         5                     95                    47.5 9.500000
6           10         6                    105                    52.5 8.750000
7            4         7                    109                    54.5 7.785714
8            5         8                    114                    57.0 7.125000
9            3         9                    117                    58.5 6.500000
10           5        10                    122                    61.0 6.100000
11           8        11                    130                    65.0 5.909091
12           7        12                    137                    68.5 5.708333
13           7        13                    144                    72.0 5.538462
14           6        14                    150                    75.0 5.357143
15           6        15                    156                    78.0 5.200000
16           4        16                    160                    80.0 5.000000
17           0        17                    160                    80.0 4.705882
18           2        18                    162                    81.0 4.500000
19           0        19                    162                    81.0 4.263158
20           2        20                    164                    82.0 4.100000
   SumDGSbyN        GV
1   0.000000  0.000000
2   0.000000  0.000000
```

```
3   1.888889  3.211111
4   3.729167 13.797917
5   4.883333 23.195833
6   5.527778 29.020833
7   5.850340 31.884354
8   6.009673 34.255134
9   6.064153 35.475298
10  6.067738 37.013202
11  6.053316 39.346552
12  6.024567 41.268285
13  5.987174 43.107655
14  5.942172 44.566291
15  5.892694 45.963013
16  5.836901 46.695205
17  5.770370 46.162961
18  5.699794 46.168331
19  5.624182 45.555871
20  5.547972 45.493374

$testend
[1] 16
```

```r
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)
```

CUGerm()

```
[1] 0.7092199
```

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

```
[1] 0.05267935
```

```r
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)
```

GermSynchrony(), GermUncertainty()

```
[1] 0.2666667
```

```r
GermUncertainty(germ.counts = x, intervals = int)
```

```
[1] 2.062987
```

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

```
[1] 0.2666667
```

```
GermUncertainty(germ.counts = y, intervals = int, partial = FALSE)
```

```
[1] 2.062987
```

Non-linear regression analysis

Several mathematical functions have been used to fit the cumulative germination count data and describe the germination process by non-linear regression analysis. They include functions such as Richard's, Weibull, logistic, log-logistic, gaussian, four-parameter hill function etc. Currently `germinationmetrics` implements the four-parameter hill function to fit the count data and computed various associated metrics.

Four-parameter hill function

The four-parameter hill function defined as follows (El-Kassaby et al., 2008).

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

Where, y is the cumulative germination percentage at time x, y_0 is the intercept on the y axis, a is the asymptote, b is a mathematical parameter controlling the shape and steepness of the germination curve and c is the "half-maximal activation level".

The details of various parameters that are computed from this function are given in Table 4.

Table 4 Germination parameters estimated from the four-parameter hill function.

Germination parameters	Details	Unit	Measures
y intercept (y_0)	The intercept on the y axis.		
Asymptote (a)	It is the maximum cumulative germination percentage, which is equivalent to germination capacity.	%	Germination capacity
Shape and steepness (b)	Mathematical parameter controlling the shape and steepness of the germination curve. The larger the b , the steeper the rise toward the asymptote a, and the shorter the time between germination onset and maximum germination.		Germination rate
Half-maximal activation level (c)	Time required for 50% of viable seeds to germinate.	time	Germination time
lag	It is the time at germination onset and is computed by solving four-parameter hill function after setting y to 0 as follows. $$lag = b\sqrt{\frac{-y_0c^b}{a+y_0}}$$	time	Germination time
D_{lag-50}	The duration between the time at germination onset (lag) and that at 50% germination (c).	time	Germination time

Germination parameters	Details	Unit	Measures
$t_{50_{total}}$	Time required for 50% of total seeds to germinate.	time	Germination time
$t_{50_{germinated}}$	Time required for 50% of viable/germinated seeds to germinate	time	Germination time
$t_{x_{total}}$	Time required for x% of total seeds to germinate.	time	Germination time
$t_{x_{germinated}}$	Time required for x% of viable/germinated seeds to germinate	time	Germination time
Uniformity ($U_{t_{max}-t_{min}}$)	It is the time interval between the percentages of viable seeds specified in the arguments `umin` and `umin` to germinate.	time	Germination time
Time at maximum germination rate ($TMGR$)	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, $TMGR$ can be estimated as follows. $$TMGR = b\sqrt{\frac{c^b(b-1)}{b+1}}$$ It represents the point in time when the instantaneous rate of germination starts to decline.	time	Germination time
Area under the curve (AUC)	It is obtained by integration of the fitted curve between time 0 and time specified in the argument `tmax`.		Mixed
MGT	Calculated by integration of the fitted curve and proper normalisation.	time	Germination time
$Skewness$	It is computed as follows. $$\frac{MGT}{t_{50_{germinated}}}$$		

Examples

```r
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)
```

```
FourPHFfit()
```

```
$data
   gp csgp intervals
1   0    0         1
2   0    0         2
3   0    0         3
4   0    0         4
5   8    8         5
6  34   42         6
7  20   62         7
8  14   76         8
9   2   78         9
10  0   78        10
11  2   80        11
12  0   80        12
13  0   80        13
14  0   80        14

$Parameters
  term  estimate  std.error statistic      p.value
1    a 80.000000 1.24158595  64.43372 1.973240e-14
2    b  9.881947 0.70779379  13.96162 6.952322e-08
3    c  6.034954 0.04952654 121.85294 3.399385e-17
4   y0  0.000000 0.91607007   0.00000 1.000000e+00

$Fit
     sigma isConv       finTol    logLik      AIC      BIC deviance df.residual
1 1.769385   TRUE 1.490116e-08 -25.49868 60.99736 64.19265 31.30723          10

$a
[1] 80

$b
[1] 9.881947

$c
[1] 6.034954

$y0
[1] 0

$lag
[1] 0

$Dlag50
[1] 6.034954

$t50.total
[1] 6.355122

$txp.total
      10       60
4.956266 6.744598

$t50.Germinated
```

```
[1] 6.034954

$txp.Germinated
      10       60 
4.831809 6.287724 

$Uniformity
        90         10 uniformity 
  7.537688   4.831809   2.705880 

$TMGR
[1] 5.912195

$AUC
[1] 1108.975

$MGT
[1] 6.632252

$Skewness
[1] 1.098973

$msg
[1] "#1. Relative error in the sum of squares is at most `ftol'. "

$isConv
[1] TRUE

attr(,"class")
[1] "FourPHFfit"
```

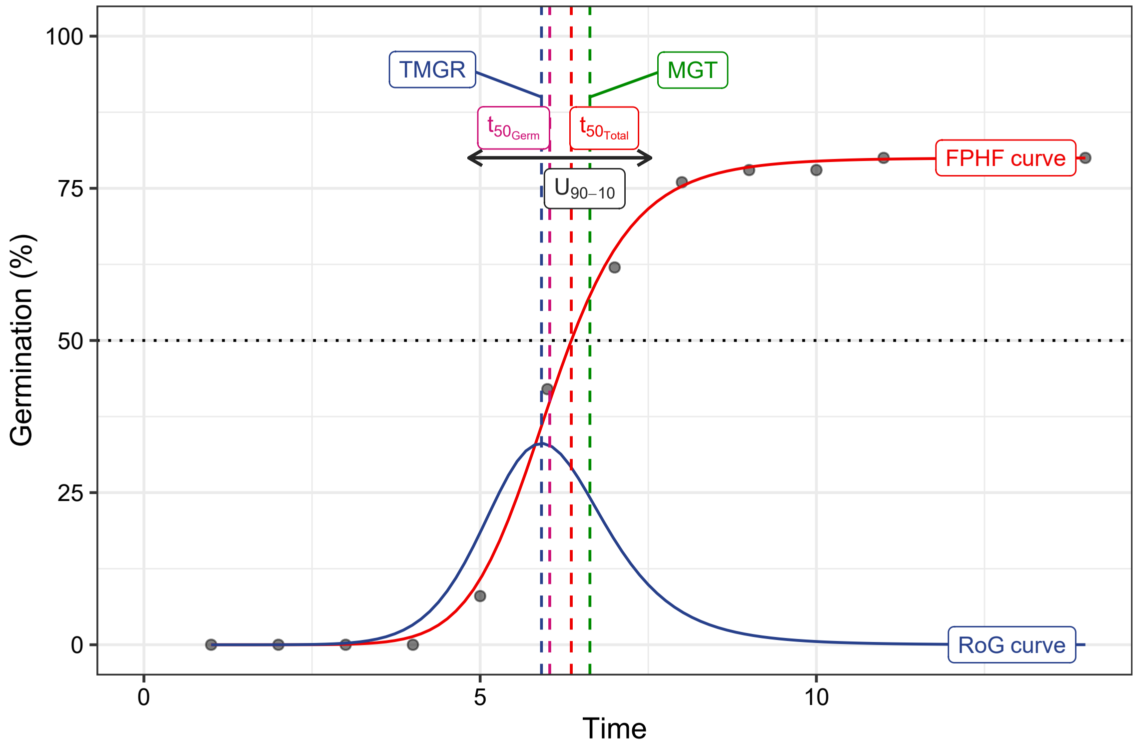
```
# From cumulative germination counts
#----------------------------------------------------------------------------
FourPHFfit(germ.counts = y, intervals = int, total.seeds = 50, tmax = 20,
partial = FALSE)
```

```
$data
   gp csgp intervals
1   0    0         1
2   0    0         2
3   0    0         3
4   0    0         4
5   8    8         5
6  34   42         6
7  20   62         7
8  14   76         8
9   2   78         9
10  0   78        10
11  2   80        11
12  0   80        12
13  0   80        13
14  0   80        14

$Parameters
  term   estimate std.error statistic      p.value
```

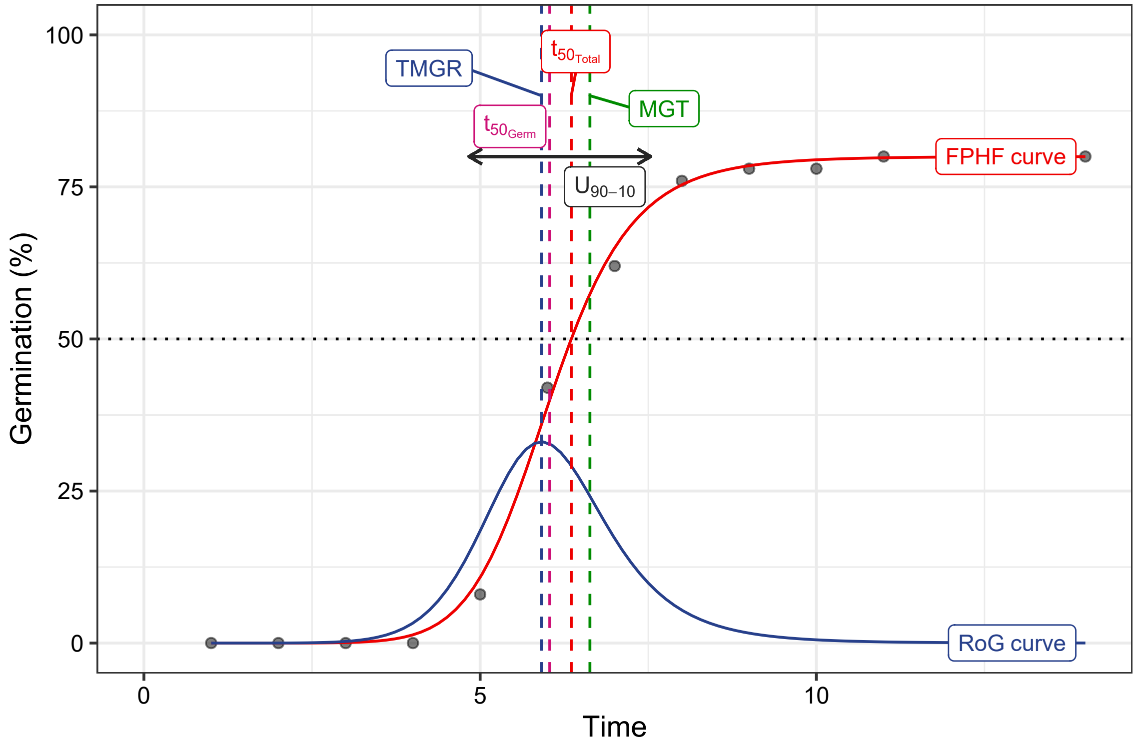
```
1     a 80.000000 1.2415867  64.43368 1.973252e-14
2     b  9.881927 0.7077918  13.96163 6.952270e-08
3     c  6.034953 0.0495266 121.85275 3.399437e-17
4    y0  0.000000 0.9160705   0.00000 1.000000e+00

$Fit
     sigma isConv       finTol    logLik      AIC      BIC deviance df.residual
1 1.769385   TRUE 1.490116e-08 -25.49868 60.99736 64.19265 31.30723          10

$a
[1] 80

$b
[1] 9.881927

$c
[1] 6.034953

$y0
[1] 0

$lag
[1] 0

$Dlag50
[1] 6.034953

$t50.total
[1] 6.355121

$txp.total
      10       60
4.956263 6.744599

$t50.Germinated
[1] 6.034953

$txp.Germinated
      10       60
4.831806 6.287723

$Uniformity
        90         10 uniformity
  7.537691   4.831806   2.705885

$TMGR
[1] 5.912194

$AUC
[1] 1108.976

$MGT
[1] 6.632252
```

```
$Skewness
[1] 1.098973

$msg
[1] "#1. Relative error in the sum of squares is at most `ftol'. "

$isConv
[1] TRUE

attr(,"class")
[1] "FourPHFfit"
```

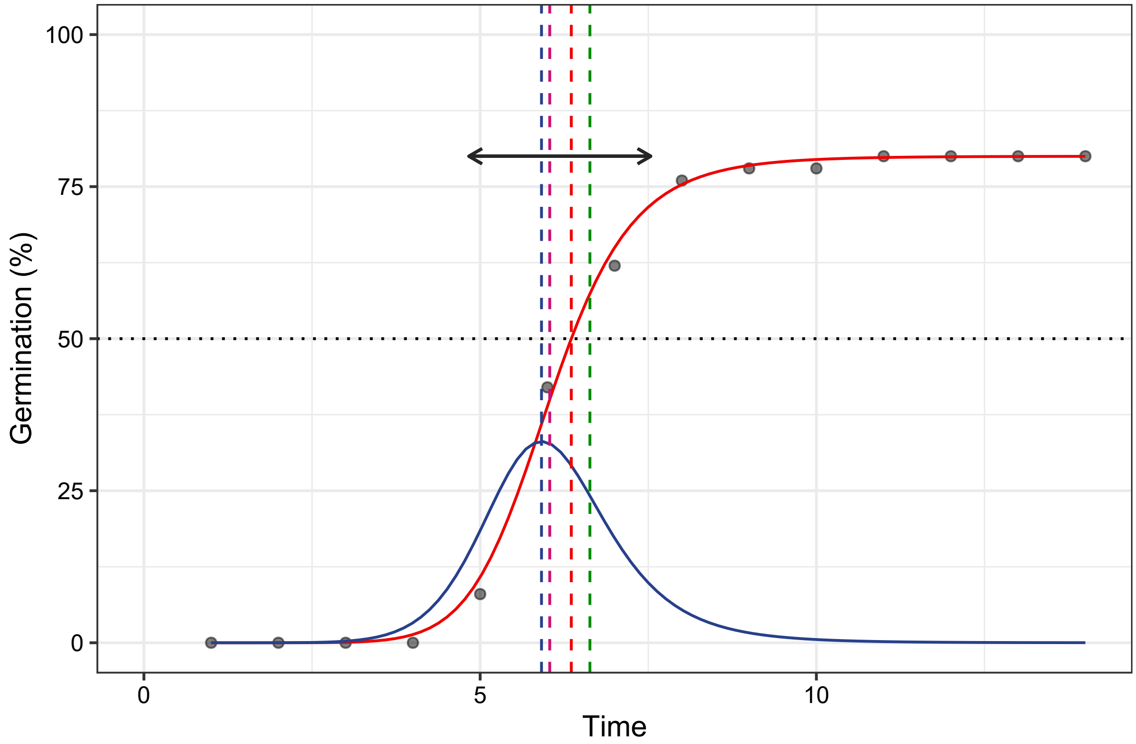
```r
x <- c(0, 0, 0, 0, 4, 17, 10, 7, 1, 0, 1, 0, 0, 0)
y <- c(0, 0, 0, 0, 4, 21, 31, 38, 39, 39, 40, 40, 40, 40)
int <- 1:length(x)
total.seeds = 50

# 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)
```



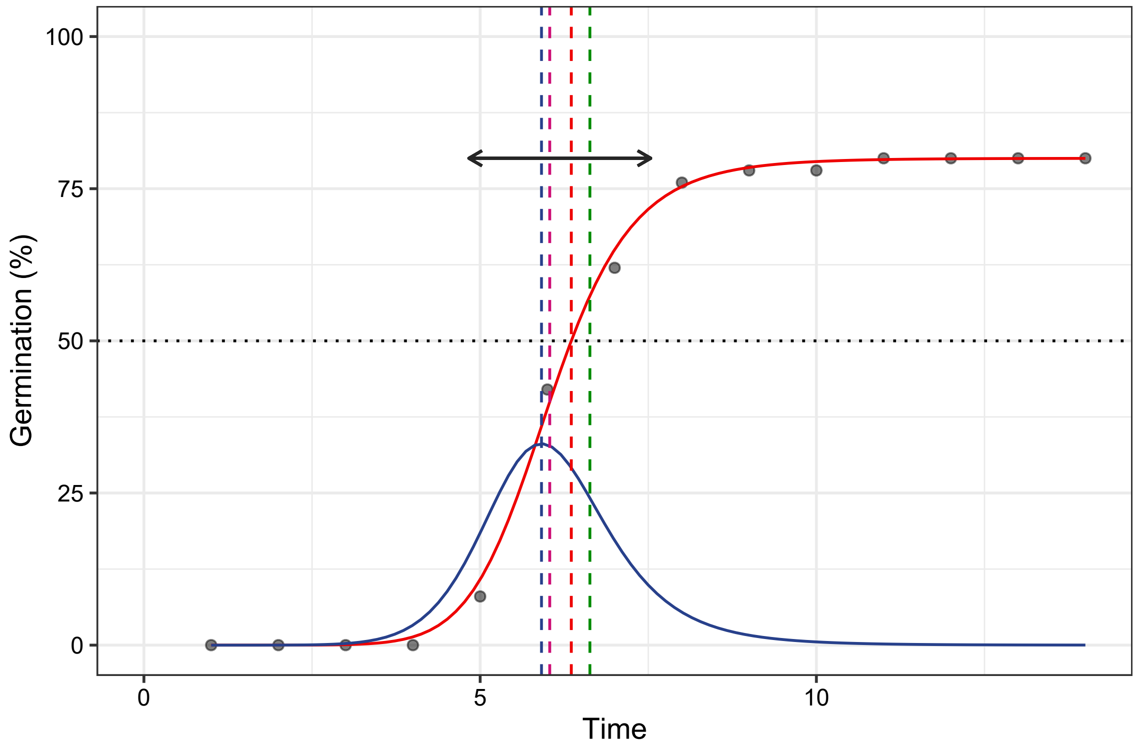
```r
plot(fit2)
```



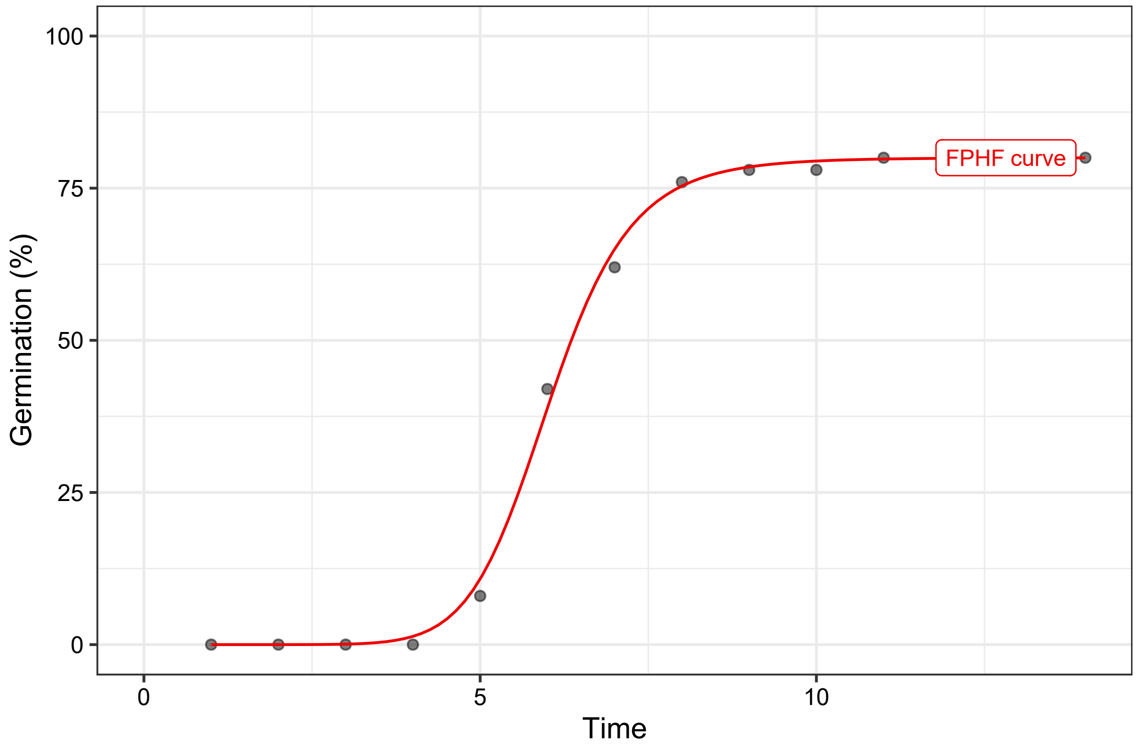

```r
# No labels
plot(fit1, plotlabels = FALSE)
```



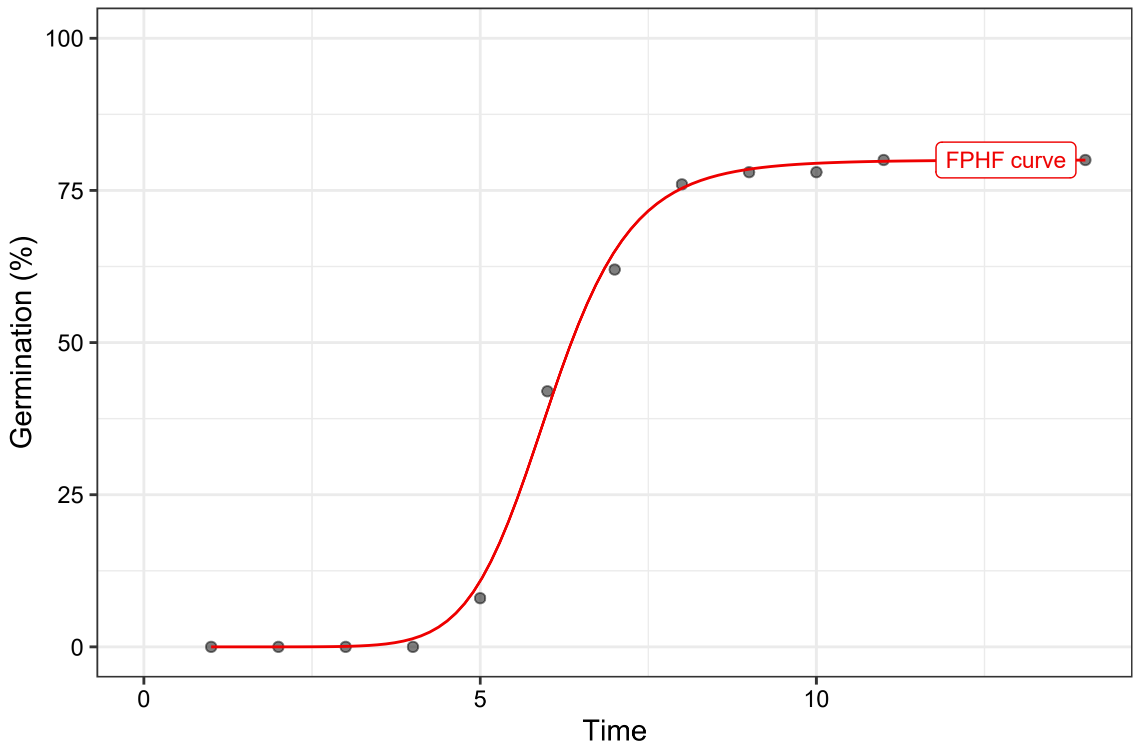
```r
plot(fit2, plotlabels = FALSE)
```



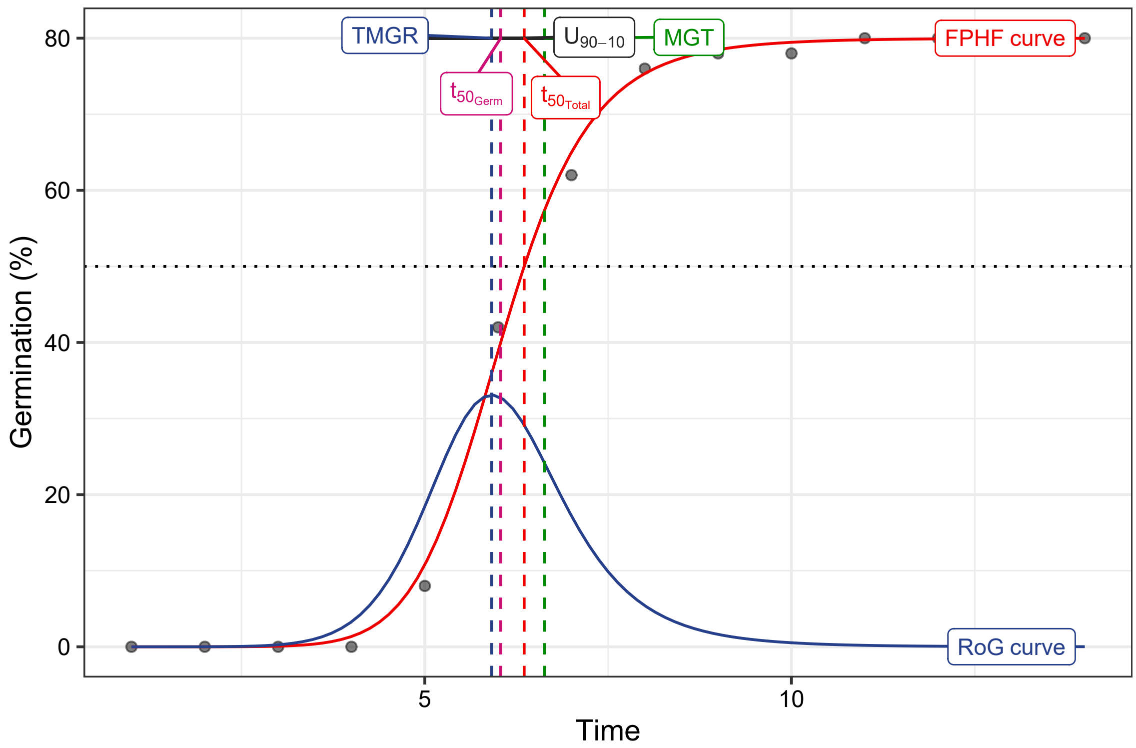

```r
# Only the FPHF curve
plot(fit1, rog = FALSE, t50.total = FALSE, t50.germ = FALSE,
     tmgr = FALSE, mgt = FALSE, uniformity = FALSE)
```



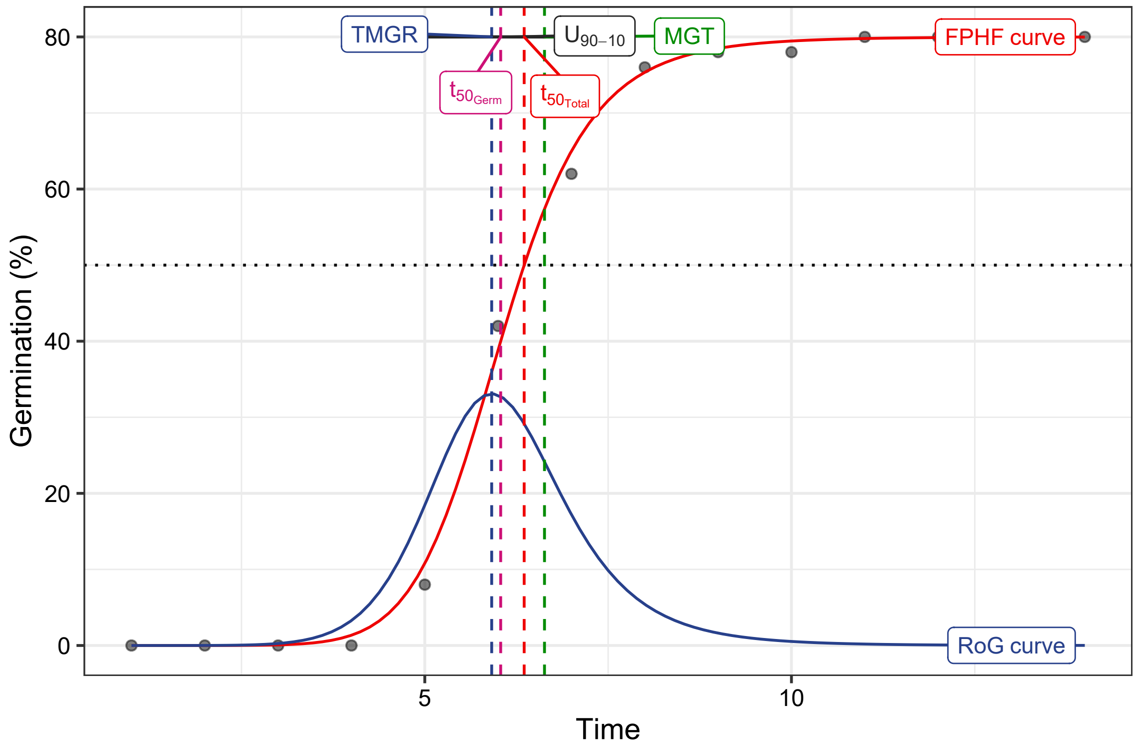

```
plot(fit2, rog = FALSE, t50.total = FALSE, t50.germ = FALSE,
     tmgr = FALSE, mgt = FALSE, uniformity = FALSE)
```




```
# Without y axis limits adjustment
plot(fit1, limits = FALSE)
```




```r
plot(fit2, limits = FALSE)
```



Wrapper functions

Wrapper functions `germination.indices()` and `FourPHFfit.bulk()` are available in the package for computing results for multiple samples in batch from a data frame of germination counts recorded at specific time intervals.

germination.indices() This wrapper function can be used to compute several germination indices simultaneously for multiple samples in batch.

```
data(gcdata)

counts.per.intervals <- c("Day01", "Day02", "Day03", "Day04", "Day05",
                          "Day06", "Day07", "Day08", "Day09", "Day10",
                          "Day11", "Day12", "Day13", "Day14")
germination.indices(gcdata, total.seeds.col = "Total Seeds",
                    counts.intervals.cols = counts.per.intervals,
                    intervals = 1:14, partial = TRUE, max.int = 5)
```

```
   Genotype Rep Day01 Day02 Day03 Day04 Day05 Day06 Day07 Day08 Day09 Day10 Day11
1        G1   1     0     0     0     0     4    17    10     7     1     0     1
2        G2   1     0     0     0     1     3    15    13     6     2     1     0
3        G3   1     0     0     0     2     3    18     9     8     2     1     1
4        G4   1     0     0     0     0     4    19    12     6     2     1     1
5        G5   1     0     0     0     0     5    20    12     8     1     0     0
6        G1   2     0     0     0     0     3    21    11     7     1     1     1
7        G2   2     0     0     0     0     4    18    11     7     1     0     1
8        G3   2     0     0     0     1     3    14    12     6     2     1     0
9        G4   2     0     0     0     1     3    19    10     8     1     1     1
10       G5   2     0     0     0     0     4    18    13     6     2     1     0
11       G1   3     0     0     0     0     5    21    11     8     1     0     0
12       G2   3     0     0     0     0     3    20    10     7     1     1     1
13       G3   3     0     0     0     0     4    19    12     8     1     1     0
14       G4   3     0     0     0     0     3    21    11     6     1     0     1
15       G5   3     0     0     0     0     4    17    10     8     1     1     1
   Day12 Day13 Day14 Total Seeds GermPercent FirstGermTime LastGermTime PeakGermTime
1      0     0     0          50    80.00000             5           11            6
2      1     0     0          51    82.35294             4           12            6
3      1     0     0          48    93.75000             4           12            6
4      1     0     0          51    90.19608             5           12            6
5      1     1     0          50    96.00000             5           13            6
6      1     0     0          49    93.87755             5           12            6
7      0     0     0          48    87.50000             5           11            6
8      1     0     0          47    85.10638             4           12            6
9      1     0     0          52    86.53846             4           12            6
10     1     0     0          50    90.00000             5           12            6
11     1     1     0          51    94.11765             5           13            6
12     1     0     0          51    86.27451             5           12            6
13     1     1     0          49    95.91837             5           13            6
14     1     0     0          48    91.66667             5           12            6
15     0     0     0          48    87.50000             5           11            6
   TimeSpreadGerm t50_Coolbear t50_Farooq MeanGermTime VarGermTime SEGermTime
1               6     5.970588   5.941176     6.700000    1.446154  0.1901416
2               8     6.192308   6.153846     6.857143    2.027875  0.2197333
3               8     6.000000   5.972222     6.866667    2.572727  0.2391061
4               7     6.041667   6.000000     6.891304    2.187923  0.2180907
```

```
5               8      5.975000   5.950000     6.812500    2.368351  0.2221275
6               7      5.976190   5.952381     6.869565    2.071498  0.2122088
7               6      5.972222   5.944444     6.690476    1.389663  0.1818989
8               8      6.208333   6.166667     6.875000    2.112179  0.2297923
9               8      6.000000   5.973684     6.866667    2.300000  0.2260777
10              7      6.076923   6.038462     6.822222    1.831313  0.2017321
11              8      5.928571   5.904762     6.791667    2.381206  0.2227295
12              7      5.975000   5.950000     6.886364    2.149577  0.2210295
13              8      6.083333   6.041667     6.936170    2.539315  0.2324392
14              7      5.928571   5.904762     6.772727    1.900634  0.2078370
15              6      6.050000   6.000000     6.809524    1.670151  0.1994129
   CVGermTime MeanGermRate  VarGermRate  SEGermRate      CVG GermRateRecip_Coolbear
1   0.1794868    0.1492537 0.0007176543 0.004235724 14.92537              0.1674877
2   0.2076717    0.1458333 0.0009172090 0.004673148 14.58333              0.1614907
3   0.2335882    0.1456311 0.0011572039 0.005071059 14.56311              0.1666667
4   0.2146419    0.1451104 0.0009701218 0.004592342 14.51104              0.1655172
5   0.2259002    0.1467890 0.0010995627 0.004786184 14.67890              0.1673640
6   0.2095140    0.1455696 0.0009301809 0.004496813 14.55696              0.1673307
7   0.1761967    0.1494662 0.0006935558 0.004063648 14.94662              0.1674419
8   0.2113940    0.1454545 0.0009454531 0.004861721 14.54545              0.1610738
9   0.2208604    0.1456311 0.0010345321 0.004794747 14.56311              0.1666667
10  0.1983606    0.1465798 0.0008453940 0.004334343 14.65798              0.1645570
11  0.2272072    0.1472393 0.0011191581 0.004828643 14.72393              0.1686747
12  0.2129053    0.1452145 0.0009558577 0.004660905 14.52145              0.1673640
13  0.2297410    0.1441718 0.0010970785 0.004831366 14.41718              0.1643836
14  0.2035568    0.1476510 0.0009033254 0.004531018 14.76510              0.1686747
15  0.1897847    0.1468531 0.0007767634 0.004300508 14.68531              0.1652893
   GermRateRecip_Farooq GermSpeed_Count GermSpeed_Percent GermSpeedAccumulated_Count
1             0.1683168        6.138925          12.27785                   34.61567
2             0.1625000        6.362698          12.47588                   35.54058
3             0.1674419        6.882179          14.33787                   38.29725
4             0.1666667        6.927417          13.58317                   38.68453
5             0.1680672        7.318987          14.63797                   41.00786
6             0.1680000        6.931782          14.14649                   38.77620
7             0.1682243        6.448449          13.43427                   36.38546
8             0.1621622        6.053175          12.87909                   33.77079
9             0.1674009        6.830592          13.13575                   38.11511
10            0.1656051        6.812698          13.62540                   38.19527
11            0.1693548        7.342796          14.39764                   41.17452
12            0.1680672        6.622258          12.98482                   37.00640
13            0.1655172        7.052320          14.39249                   39.29399
14            0.1693548        6.706782          13.97246                   37.69490
15            0.1666667        6.363925          13.25818                   35.69697
   GermSpeedAccumulated_Percent GermSpeedCorrected_Normal
1                      69.23134                0.07673656
2                      69.68741                0.07726134
3                      79.78594                0.07340991
4                      75.85202                0.07680397
5                      82.01571                0.07623944
6                      79.13509                0.07383855
7                      75.80304                0.07369656
8                      71.85275                0.07112480
9                      73.29829                0.07893128
10                     76.39054                0.07569665
```

```
11                  80.73436              0.07801721
12                  72.56158              0.07675799
13                  80.19182              0.07352419
14                  78.53103              0.07316490
15                  74.36868              0.07273057
   GermSpeedCorrected_Accumulated WeightGermPercent MeanGermPercent MeanGermNumber
1                       0.4326958          47.42857        5.714286       2.857143
2                       0.4315642          47.89916        5.882353       3.000000
3                       0.4085040          54.46429        6.696429       3.214286
4                       0.4288937          52.24090        6.442577       3.285714
5                       0.4271652          56.14286        6.857143       3.428571
6                       0.4130508          54.51895        6.705539       3.285714
7                       0.4158338          51.93452        6.250000       3.000000
8                       0.3968068          49.39210        6.079027       2.857143
9                       0.4404413          50.27473        6.181319       3.214286
10                      0.4243919          52.57143        6.428571       3.214286
11                      0.4374793          55.18207        6.722689       3.428571
12                      0.4289379          50.00000        6.162465       3.142857
13                      0.4096608          55.24781        6.851312       3.357143
14                      0.4112171          53.86905        6.547619       3.142857
15                      0.4079653          51.19048        6.250000       3.000000
   TimsonsIndex TimsonsIndex_Labouriau TimsonsIndex_KhanUngar GermRateGeorge
1      8.000000                   1.00              0.5714286              4
2      9.803922                   1.25              0.7002801              5
3     14.583333                   1.40              1.0416667              7
4      7.843137                   1.00              0.5602241              4
5     10.000000                   1.00              0.7142857              5
6      6.122449                   1.00              0.4373178              3
7      8.333333                   1.00              0.5952381              4
8     10.638298                   1.25              0.7598784              5
9      9.615385                   1.25              0.6868132              5
10     8.000000                   1.00              0.5714286              4
11     9.803922                   1.00              0.7002801              5
12     5.882353                   1.00              0.4201681              3
13     8.163265                   1.00              0.5830904              4
14     6.250000                   1.00              0.4464286              3
15     8.333333                   1.00              0.5952381              4
   GermIndex GermIndex_mod EmergenceRateIndex_Melville
1   5.840000      7.300000                         292
2   5.882353      7.142857                         300
3   6.687500      7.133333                         321
4   6.411765      7.108696                         327
5   6.900000      7.187500                         345
6   6.693878      7.130435                         328
7   6.395833      7.309524                         307
8   6.063830      7.125000                         285
9   6.173077      7.133333                         321
10  6.460000      7.177778                         323
11  6.784314      7.208333                         346
12  6.137255      7.113636                         313
13  6.775510      7.063830                         332
14  6.625000      7.227273                         318
15  6.291667      7.190476                         302
   EmergenceRateIndex_Melville_mod EmergenceRateIndex_BilbroWanjura
```

```
1                           7.300000                         5.970149
2                           7.142857                         6.125000
3                           7.133333                         6.553398
4                           7.108696                         6.675079
5                           7.187500                         7.045872
6                           7.130435                         6.696203
7                           7.309524                         6.277580
8                           7.125000                         5.818182
9                           7.133333                         6.553398
10                          7.177778                         6.596091
11                          7.208333                         7.067485
12                          7.113636                         6.389439
13                          7.063830                         6.776074
14                          7.227273                         6.496644
15                          7.190476                         6.167832
   EmergenceRateIndex_Fakorede PeakValue GermValue_Czabator GermValue_DP
1                     8.375000  9.500000          54.28571     57.93890
2                     8.326531  9.313725          54.78662     52.58713
3                     7.324444 10.416667          69.75446     68.62289
4                     7.640359 10.049020          64.74158     70.43331
5                     7.096354 11.250000          77.14286     80.16914
6                     7.317580 10.714286          71.84506     76.51983
7                     7.646259 10.416667          65.10417     69.41325
8                     8.078125  9.574468          58.20345     56.00669
9                     7.934815  9.855769          60.92165     58.13477
10                    7.580247 10.250000          65.89286     70.91875
11                    7.216146 11.029412          74.14731     77.39782
12                    7.981921  9.803922          60.41632     64.44988
13                    7.231326 10.969388          75.15470     78.16335
14                    7.388430 10.677083          69.90947     74.40140
15                    7.782313 10.156250          63.47656     67.62031
   GermValue_Czabator_mod GermValue_DP_mod    CUGerm GermSynchrony GermUncertainty
1                54.28571         39.56076 0.7092199     0.2666667        2.062987
2                54.78662         40.99260 0.5051546     0.2346109        2.321514
3                69.75446         53.42809 0.3975265     0.2242424        2.462012
4                64.74158         48.86825 0.4672113     0.2502415        2.279215
5                77.14286         56.23935 0.4312184     0.2606383        2.146051
6                71.84506         53.06435 0.4934701     0.2792271        2.160545
7                65.10417         47.37690 0.7371500     0.2729384        2.040796
8                58.20345         43.67948 0.4855842     0.2256410        2.357249
9                60.92165         45.30801 0.4446640     0.2494949        2.321080
10               65.89286         49.10820 0.5584666     0.2555556        2.187983
11               74.14731         54.27520 0.4288905     0.2686170        2.128670
12               60.41632         44.71582 0.4760266     0.2737844        2.185245
13               75.15470         54.94192 0.4023679     0.2506938        2.241181
14               69.90947         51.41913 0.5383760     0.2991543        2.037680
15               63.47656         46.48043 0.6133519     0.2497096        2.185028
```

FourPHFfit.bulk() This wrapper function can be used to fit the four-parameter hill function for multiple samples in batch.

```r
data(gcdata)

counts.per.intervals <- c("Day01", "Day02", "Day03", "Day04", "Day05",
```

```
                            "Day06", "Day07", "Day08", "Day09", "Day10",
                            "Day11", "Day12", "Day13", "Day14")

FourPHFfit.bulk(gcdata, total.seeds.col = "Total Seeds",
                    counts.intervals.cols = counts.per.intervals,
                    intervals = 1:14, partial = TRUE,
                    fix.y0 = TRUE, fix.a = TRUE, xp = c(10, 60),
                    tmax = 20, tries = 3, umax = 90, umin = 10)
```

```
    Genotype Rep Day01 Day02 Day03 Day04 Day05 Day06 Day07 Day08 Day09 Day10 Day11
 1:       G1   1     0     0     0     0     4    17    10     7     1     0     1
 2:       G2   1     0     0     0     1     3    15    13     6     2     1     0
 3:       G3   1     0     0     0     2     3    18     9     8     2     1     1
 4:       G4   1     0     0     0     0     4    19    12     6     2     1     1
 5:       G5   1     0     0     0     0     5    20    12     8     1     0     0
 6:       G1   2     0     0     0     0     3    21    11     7     1     1     1
 7:       G2   2     0     0     0     0     4    18    11     7     1     0     1
 8:       G3   2     0     0     0     1     3    14    12     6     2     1     0
 9:       G4   2     0     0     0     1     3    19    10     8     1     1     1
10:       G5   2     0     0     0     0     4    18    13     6     2     1     0
11:       G1   3     0     0     0     0     5    21    11     8     1     0     0
12:       G2   3     0     0     0     0     3    20    10     7     1     1     1
13:       G3   3     0     0     0     0     4    19    12     8     1     1     0
14:       G4   3     0     0     0     0     3    21    11     6     1     0     1
15:       G5   3     0     0     0     0     4    17    10     8     1     1     1
    Day12 Day13 Day14 Total Seeds        a         b        c y0 lag   Dlag50
 1:     0     0     0          50 80.00000  9.881947 6.034954  0   0 6.034954
 2:     1     0     0          51 82.35294  9.227667 6.175193  0   0 6.175193
 3:     1     0     0          48 93.75000  7.793055 6.138110  0   0 6.138110
 4:     1     0     0          51 90.19608  8.925668 6.125172  0   0 6.125172
 5:     1     1     0          50 96.00000  9.419194 6.049641  0   0 6.049641
 6:     1     0     0          49 93.87755  9.450187 6.097412  0   0 6.097412
 7:     0     0     0          48 87.50000 10.172466 6.029851  0   0 6.029851
 8:     1     0     0          47 85.10638  8.940702 6.189774  0   0 6.189774
 9:     1     0     0          52 86.53846  8.617395 6.125121  0   0 6.125121
10:     1     0     0          50 90.00000  9.608849 6.109503  0   0 6.109503
11:     1     1     0          51 94.11765  9.400248 6.018759  0   0 6.018759
12:     1     0     0          51 86.27451  9.162558 6.108449  0   0 6.108449
13:     1     1     0          49 95.91837  8.995233 6.149011  0   0 6.149011
14:     1     0     0          48 91.66667 10.391898 6.015907  0   0 6.015907
15:     0     0     0          48 87.50000  9.136762 6.121580  0   0 6.121580
    t50.total t50.Germinated     TMGR      AUC      MGT Skewness
 1:  6.355122       6.034954 5.912195 1108.975 6.632252 1.098973
 2:  6.473490       6.175193 6.031282 1128.559 6.784407 1.098655
 3:  6.244190       6.138110 5.938179 1283.693 6.772742 1.103392
 4:  6.276793       6.125172 5.972686 1239.887 6.739665 1.100323
 5:  6.103433       6.049641 5.914289 1328.328 6.654980 1.100062
 6:  6.182276       6.097412 5.961877 1294.463 6.702470 1.099232
 7:  6.202812       6.029851 5.914057 1213.908 6.622417 1.098272
 8:  6.439510       6.189774 6.036193 1164.346 6.804000 1.099232
 9:  6.352172       6.125121 5.961631 1188.793 6.745241 1.101242
10:  6.253042       6.109503 5.978115 1240.227 6.711899 1.098600
11:  6.099434       6.018759 5.883558 1305.200 6.624247 1.100600
12:  6.326181       6.108449 5.964079 1188.021 6.718636 1.099892
```

```
13:  6.207500       6.149011 5.998270 1316.407 6.762272 1.099733
14:  6.122385       6.015907 5.905179 1273.386 6.604963 1.097916
15:  6.317392       6.121580 5.976088 1203.664 6.732267 1.099760
                                                             msg isConv txp.total_10
 1: #1. Relative error in the sum of squares is at most `ftol'.   TRUE     4.956266
 2: #1. Relative error in the sum of squares is at most `ftol'.   TRUE     4.983236
 3: #1. Relative error in the sum of squares is at most `ftol'.   TRUE     4.673022
 4: #1. Relative error in the sum of squares is at most `ftol'.   TRUE     4.850876
 5: #1. Relative error in the sum of squares is at most `ftol'.   TRUE     4.814126
 6: #1. Relative error in the sum of squares is at most `ftol'.   TRUE     4.868635
 7: #1. Relative error in the sum of squares is at most `ftol'.   TRUE     4.930423
 8: #1. Relative error in the sum of squares is at most `ftol'.   TRUE     4.940058
 9: #1. Relative error in the sum of squares is at most `ftol'.   TRUE     4.836659
10: #1. Relative error in the sum of squares is at most `ftol'.   TRUE     4.920629
11: #1. Relative error in the sum of squares is at most `ftol'.   TRUE     4.798630
12: #1. Relative error in the sum of squares is at most `ftol'.   TRUE     4.893597
13: #1. Relative error in the sum of squares is at most `ftol'.   TRUE     4.841310
14: #1. Relative error in the sum of squares is at most `ftol'.   TRUE     4.915143
15: #1. Relative error in the sum of squares is at most `ftol'.   TRUE     4.892505
    txp.total_60 Uniformity_90 Uniformity_10 Uniformity
 1:     6.744598      7.537688      4.831809   2.705880
 2:     6.872603      7.835407      4.866755   2.968652
 3:     6.608437      8.137340      4.630062   3.507277
 4:     6.614967      7.834806      4.788598   3.046208
 5:     6.386788      7.639025      4.790947   2.848078
 6:     6.477594      7.693458      4.832474   2.860984
 7:     6.510495      7.483642      4.858477   2.625165
 8:     6.823299      7.914162      4.841106   3.073056
 9:     6.733275      7.904040      4.746574   3.157466
10:     6.566505      7.679176      4.860681   2.818494
11:     6.391288      7.603603      4.764249   2.839354
12:     6.684521      7.763844      4.806015   2.957830
13:     6.509952      7.850339      4.816395   3.033943
14:     6.397486      7.432360      4.869401   2.562960
15:     6.667247      7.785804      4.813086   2.972718
```

Citing germinationmetrics

```
To cite the R package 'germinationmetrics' in publications use:

  Aravind, J., Vimala Devi, S., Radhamani, J., Jacob, S. R., and Kalyani
  Srinivasan (2020).  germinationmetrics: Seed Germination Indices and Curve
  Fitting. R package version 0.1.3.9000,
  https://github.com/aravind-j/germinationmetricshttps://cran.r-project.org/package=germinationmetrics.

A BibTeX entry for LaTeX users is

  @Manual{,
    title = {germinationmetrics: Seed Germination Indices and Curve Fitting},
    author = {J. Aravind and S. {Vimala Devi} and J. Radhamani and Sherry Rachel Jacob and {Kalyani Sri
    year = {2020},
    note = {R package version 0.1.3.9000},
    note = {https://github.com/aravind-j/germinationmetrics},
```

```
    note = {https://cran.r-project.org/package=germinationmetrics},
  }
```

```
This free and open-source software implements academic research by the
authors and co-workers. If you use it, please support the project by citing
the package.
```

Session Info

```r
sessionInfo()
```

```
R Under development (unstable) (2019-11-08 r77393)
Platform: x86_64-w64-mingw32/x64 (64-bit)
Running under: Windows 10 x64 (build 18362)

Matrix products: default

locale:
[1] LC_COLLATE=English_India.1252  LC_CTYPE=English_India.1252
[3] LC_MONETARY=English_India.1252 LC_NUMERIC=C
[5] LC_TIME=English_India.1252

attached base packages:
[1] stats     graphics  grDevices utils     datasets  methods   base

other attached packages:
[1] germinationmetrics_0.1.3.9000

loaded via a namespace (and not attached):
 [1] minpack.lm_1.2-1  tidyselect_0.2.5  xfun_0.12         purrr_0.3.3
 [5] pander_0.6.3      lattice_0.20-38   colorspace_1.4-1  generics_0.0.2
 [9] vctrs_0.2.2       htmltools_0.4.0   yaml_2.2.0        XML_3.99-0.3
[13] rlang_0.4.3       pillar_1.4.3      glue_1.3.1        lifecycle_0.1.0
[17] plyr_1.8.5        stringr_1.4.0     munsell_0.5.0     gtable_0.3.0
[21] evaluate_0.14     labeling_0.3      knitr_1.28        gbRd_0.4-11
[25] curl_4.3          highr_0.8         broom_0.5.3       Rcpp_1.0.3
[29] scales_1.1.0      backports_1.1.5   farver_2.0.3      ggplot2_3.2.1
[33] packrat_0.5.0     digest_0.6.23     stringi_1.4.5     dplyr_0.8.3
[37] ggrepel_0.8.1     grid_4.0.0        bibtex_0.4.2.2    Rdpack_0.11-1
[41] tools_4.0.0       bitops_1.0-6      magrittr_1.5      lazyeval_0.2.2
[45] RCurl_1.95-4.12   tibble_2.1.3      crayon_1.3.4      tidyr_1.0.2
[49] pkgconfig_2.0.3   data.table_1.12.8 assertthat_0.2.1  rmarkdown_2.1
[53] httr_1.4.1        R6_2.4.1          nlme_3.1-143      compiler_4.0.0
```

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