The `germinationmetrics` Package: A Brief Introduction

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2023-08-13

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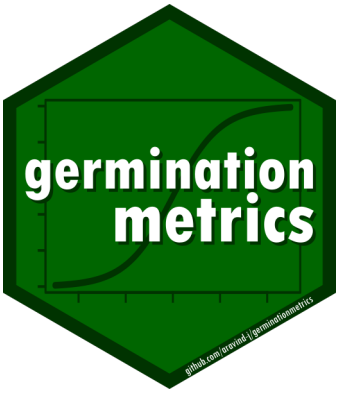
Overview



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 0.1.7.9000


# 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 0.1.7. 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
0.1.3	2019-01-19
0.1.4	2020-06-16
0.1.5	2021-02-17
0.1.6	2022-06-15

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.

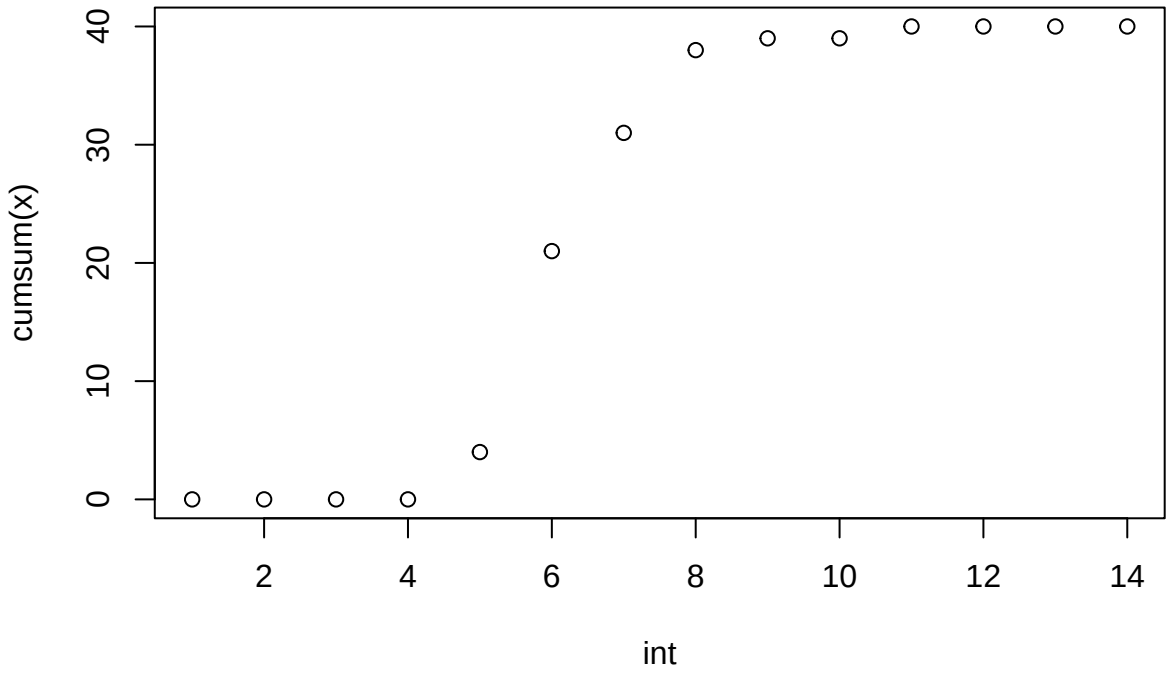
intervals	counts	cumulative.counts
1	0	0
2	0	0
3	0	0
4	0	0
5	4	4
6	17	21
7	10	31
8	7	38
9	1	39
10	0	39
11	1	40
12	0	40
13	0	40
14	0	40

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

```
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)
Peak germination percentage (PGP)	`PeakGermPercent`	It is computed as follows. $$PGP = \frac{N_{max}}{N_t} \times 100$$ Where, N_{max} is the maximum number of seeds germinated per interval.	Percentage (%)	Germination capacity	Vallance (1950); Roh et al. (2004)
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). $$t_0 = \min\{T_i : N_i \neq 0\}$$ Where, T_i is the time from the start of the experiment to the ith interval and 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)	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) $$t_g = \max\{T_i : N_i \neq 0\}$$ Where, T_i is the time from the start of the experiment to the ith interval and 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)	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 (t_{peak})	`PeakGermTime`	It is the time in which highest frequency of germinated seeds are observed and need not be unique. $$t_{peak} = \{T_i : N_i = N_{max}\}$$ 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 N_{max} is the maximum number of seeds germinated per interval.	time	Germination time	Ranal and Santana (2006)

Germination index	Function	Details	Unit	Measures	Reference
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)
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. $$\overline{T} = \frac{\sum_{i=1}^{k} N_i T_i}{\sum_{i=1}^{k} N_i}$$ 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)

Germination index	Function	Details	Unit	Measures	Reference
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^{-1}	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)
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)

Germination index	Function	Details	Unit	Measures	Reference
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.	% time^{-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)
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} or count 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)

Germination index	Function	Details	Unit	Measures	Reference
Speed of accumulated germination	`GermSpeedAccumulate`	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} or count time^{-1}	Mixed	Bradbeer (1988); Wardle et al. (1991); Haugland and Brandsaeter (1996); Santana and Ranal (2004)
Corrected germination rate index	`GermSpeedCorrected`	It is computed as follows. $$S_{corrected} = \frac{S}{FGP}$$ Where, S is the germination speed computed with germination percentage instead of counts and 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.	Percentage (%)	Mixed	Reddy et al. (1985); Reddy (1978)
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.	% time^{-1}	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.	count time^{-1}	Mixed	Khamassi et al. (2013)

Germination index	Function	Details	Unit	Measures	Reference
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 $j = i - 1$.	Percentage (%)	Mixed	Grose and Zimmer (1958); Timson (1965); (**lyonRapidMethodDetermining1966?**); 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. $$\Sigma k_{mod} = \frac{\Sigma k}{\sum_{i=1}^{k} g_i}$$	no unit	Mixed	Ranal and Santana (2006)
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). $$\Sigma k_{mod} = \frac{\Sigma k}{T_k}$$	% time^{-1}	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.	count time	Mixed	George (1961); Tucker and Wright (1965); Nichols and Heydecker (1968);Chopra and Chaudhary (1980)

Germination index	Function	Details	Unit	Measures	Reference
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.	time	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.	time	Mixed	Melville et al. (1980); Santana and Ranal (2004); Ranal and Santana (2006)
Emergence Rate Index (ERI) or Germination Rate Index (Shmueli and Goldberg)	`EmergenceRateIndex`	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.	count	Mixed	Shmueli and Goldberg (1971)
Modified Emergence Rate Index (ERI_{mod}) or Modified Germination Rate Index (Shmueli and Goldberg; Santana and Ranal)	`EmergenceRateIndex`	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.	no unit	Mixed	Shmueli and Goldberg (1971); Santana and Ranal (2004); Ranal and Santana (2006)

Germination index	Function	Details	Unit	Measures	Reference
Emergence Rate Index (ERI) or Germination Rate Index (Bilbro & Wanjura)	`EmergenceRateIndex`	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.	count time^{-1}	Mixed	Bilbro and Wanjura (1982)
Emergence Rate Index (ERI) or Germination Rate Index (Fakorede)	`EmergenceRateIndex`	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.	time count^{-1}	Mixed	Fakorede and Ayoola (1980); Fakorede and Ojo (1981); Fakorede and Agbana (1983)
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.	%^{2} time^{-2}	Mixed	Czabator (1962); Brown and Mayer (1988)

Germination index	Function	Details	Unit	Measures	Reference
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.	$\%^2$ time^{-1}	Mixed	Djavanshir and Pourbeik (1976); Brown and Mayer (1988)
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.	time^{-2}	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.	no unit	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)

Germination index	Function	Details	Unit	Measures	Reference
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.	no unit	Germination synchrony	Primack (1985); Ranal and Santana (2006)

Examples

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

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

```
GermPercent()
```

```
[1] 80
```

```
PeakGermPercent(germ.counts = x, intervals = int, total.seeds = 50)
```

```
[1] 34
```

```
# For multiple peak germination times
PeakGermPercent(germ.counts = z, intervals = int, total.seeds = 50)
```

```
Warning in PeakGermPercent(germ.counts = z, intervals = int, total.seeds = 50): Multiple peak germinati
```

```
[1] 22
```

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

```
[1] 80
```

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

```
[1] 34
```

```
# For multiple peak germination times
PeakGermPercent(germ.counts = cumsum(z), intervals = int, total.seeds = 50,
                partial = FALSE)
```

```
Warning in PeakGermPercent(germ.counts = cumsum(z), intervals = int, total.seeds = 50, : Multiple peak g
exist.
```

```
[1] 22
```

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

```
[1] 80
```

```
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
```

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

```
[1] 11
```

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

```
[1] 6
```

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

```
[1] 6
```

```
# 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
```

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

```
[1] 5
```

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

```
[1] 11
```

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

```
[1] 6
```

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

```
[1] 6
```

```
# 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 germi
exist.
```

```
[1] 5 6
```

```
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
```

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

```
[1] 5.941176
```

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

```
[1] 5.970588
```

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

```
[1] 5.941176
```

```
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
```

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

```
[1] 1.446154
```

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

```
[1] 0.1901416
```

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

```
[1] 0.1794868
```

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

```
[1] 6.7
```

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

```
[1] 19.04012
```

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

```
[1] 0.2394781
```

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

```
[1] 0.6512685
```

```
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
```

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

```
[1] 14.92537
```

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

```
[1] 0.0007176543
```

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

```
[1] 0.004235724
```

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

```
[1] 0.1674877
```

```
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] 0.1534731
```

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

```
[1] 0.8653917
```

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

```
[1] 12.27785
```

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

```
[1] 69.23134
```

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

```
[1] 6.138925
```

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

```
[1] 34.61567
```

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

```
[1] 0.1534731
```

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

```
[1] 0.8653917
```

```
# 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
```

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

```
[1] 69.23134
```

```
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
```

```
# 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
```

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

```
[1] 47.42857
```

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

```
[1] 332
```

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

```
[1] 344
```

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

```
[1] 344
```

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

```
[1] 4.410256
```

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

```
[1] 24.57143
```

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

```
[1] 172
```

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

```
[1] 332
```

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

```
[1] 664
```

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

```
[1] 664
```

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

```
[1] 8.3
```

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

```
[1] 47.42857
```

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

```
[1] 332
```

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

```
[1] 344
```

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

```
[1] 344
```

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

```
[1] 4.410256
```

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

```
[1] 24.57143
```

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

```
[1] 172
```

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

```
[1] 332
```

```
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
```

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

```
[1] 5.84
```

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

```
[1] 7.3
```

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

```
[1] 5.84
```

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

```
[1] 5.84
```

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

```
[1] 7.3
```

```
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
```

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

```
[1] 292
```

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

```
[1] 7.3
```

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

```
[1] 5.970149
```

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

```
[1] 8.375
```

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

```
[1] 292
```

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

```
[1] 292
```

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

```
[1] 7.3
```

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

```
[1] 5.970149
```

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

```
[1] 8.375
```

```
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
```

```
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
```

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

$testend
[1] 16
```

```
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 SumDGSbyN        GV
1            0         1                      0                     0.0 0.000000  0.000000  0.000000
2            0         2                      0                     0.0 0.000000  0.000000  0.000000
3           34         3                     34                    17.0 5.666667  1.888889  3.211111
4           40         4                     74                    37.0 9.250000  3.729167 13.797917
5           21         5                     95                    47.5 9.500000  4.883333 23.195833
6           10         6                    105                    52.5 8.750000  5.527778 29.020833
7            4         7                    109                    54.5 7.785714  5.850340 31.884354
8            5         8                    114                    57.0 7.125000  6.009673 34.255134
9            3         9                    117                    58.5 6.500000  6.064153 35.475298
10           5        10                    122                    61.0 6.100000  6.067738 37.013202
11           8        11                    130                    65.0 5.909091  6.053316 39.346552
12           7        12                    137                    68.5 5.708333  6.024567 41.268285
13           7        13                    144                    72.0 5.538462  5.987174 43.107655
14           6        14                    150                    75.0 5.357143  5.942172 44.566291
15           6        15                    156                    78.0 5.200000  5.892694 45.963013
16           4        16                    160                    80.0 5.000000  5.836901 46.695205
17           0        17                    160                    80.0 4.705882  5.770370 46.162961
```

```
18           2        18                   162                    81.0 4.500000  5.699794 46.168331
19           0        19                   162                    81.0 4.263158  5.624182 45.555871
20           2        20                   164                    82.0 4.100000  5.547972 45.493374

$testend
[1] 16
```

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

```
[1] 9.5
```

```
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
```

```
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 SumDGSbyN        GV
3           34         3                    34                    17.0 5.666667  5.666667  9.633333
4           40         4                    74                    37.0 9.250000  7.458333 27.595833
5           21         5                    95                    47.5 9.500000  8.138889 38.659722
6           10         6                   105                    52.5 8.750000  8.291667 43.531250
7            4         7                   109                    54.5 7.785714  8.190476 44.638095
8            5         8                   114                    57.0 7.125000  8.012897 45.673512
9            3         9                   117                    58.5 6.500000  7.796769 45.611097
```

```
10           5        10                   122                  61.0 6.100000  7.584673 46.266503
11           8        11                   130                  65.0 5.909091  7.398497 48.090230
12           7        12                   137                  68.5 5.708333  7.229481 49.521942
13           7        13                   144                  72.0 5.538462  7.075752 50.945411
14           6        14                   150                  75.0 5.357143  6.932534 51.994006
15           6        15                   156                  78.0 5.200000  6.799262 53.034246
16           4        16                   160                  80.0 5.000000  6.670744 53.365948
17           0        17                   160                  80.0 4.705882  6.539753 52.318022
18           2        18                   162                  81.0 4.500000  6.412268 51.939373
19           0        19                   162                  81.0 4.263158  6.285850 50.915385
20           2        20                   164                  82.0 4.100000  6.164414 50.548194

$testend
[1] 16
```

```
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 SumDGSbyN        GV
1            0         1                      0                     0.0 0.000000  0.000000  0.000000
2            0         2                      0                     0.0 0.000000  0.000000  0.000000
3           34         3                     34                    17.0 5.666667  1.888889  3.211111
```

```
4           40         4                74                37.0 9.250000  3.729167 13.797917
5           21         5                95                47.5 9.500000  4.883333 23.195833
6           10         6               105                52.5 8.750000  5.527778 29.020833
7            4         7               109                54.5 7.785714  5.850340 31.884354
8            5         8               114                57.0 7.125000  6.009673 34.255134
9            3         9               117                58.5 6.500000  6.064153 35.475298
10           5        10               122                61.0 6.100000  6.067738 37.013202
11           8        11               130                65.0 5.909091  6.053316 39.346552
12           7        12               137                68.5 5.708333  6.024567 41.268285
13           7        13               144                72.0 5.538462  5.987174 43.107655
14           6        14               150                75.0 5.357143  5.942172 44.566291
15           6        15               156                78.0 5.200000  5.892694 45.963013
16           4        16               160                80.0 5.000000  5.836901 46.695205
17           0        17               160                80.0 4.705882  5.770370 46.162961
18           2        18               162                81.0 4.500000  5.699794 46.168331
19           0        19               162                81.0 4.263158  5.624182 45.555871
20           2        20               164                82.0 4.100000  5.547972 45.493374

$testend
[1] 16
```

```
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
```

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

```
[1] 0.05267935
```

```
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
```

```
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".

this function can also be be reparameterized by substituting b with e^{β} to constraint b to positive values only.

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

Where, $b = e^{\beta}$ and $\beta = \log_e(b)$.

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

Germination parameters	Details	Unit	Measures
lag	It is the time at germination onset and is computed by solving four-parameter hill function after setting y to 0 as follows. $$lag = b\sqrt{\frac{-y_0 c^b}{a + y_0}}$$	time	Germination time
D_{lag-50}	The duration between the time at germination onset (lag) and that at 50% germination (c).	time	Germination time
$t_{50_{total}}$	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

```
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()

```
Warning in FourPHFfit(germ.counts = x, intervals = int, total.seeds = 50, : Convergence Error
#1. failed to evaluate 'fn' at starting values: could not find function "FourPHF_fixa_fixy0"

$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       NA        NA        NA      NA
2    b       NA        NA        NA      NA
3    c       NA        NA        NA      NA
4   y0       NA        NA        NA      NA

$Fit
  sigma isConv finTol logLik AIC BIC deviance df.residual nobs
1    NA     NA     NA     NA  NA  NA       NA          NA   NA

$a
[1] NA

$b
[1] NA

$c
[1] NA

$y0
[1] NA
```

```
$lag
[1] NA

$Dlag50
[1] NA

$t50.total
[1] NA

$txp.total
10 60
NA NA

$t50.Germinated
[1] NA

$txp.Germinated
10 60
NA NA

$Uniformity
        90         10 uniformity
        NA         NA         NA

$TMGR
[1] NA

$AUC
[1] NA

$MGT
[1] NA

$Skewness
[1] NA

$msg
[1] "#1. failed to evaluate 'fn' at starting values: could not find function \"FourPHF_fixa_fixy0\" "

$isConv
[1] NA

$model
<simpleError in gsl_nls.formula(csgp ~ FourPHF_fixa_fixy0(x = intervals, a = max(csgp),     bta, c), da

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

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

```
Warning in FourPHFfit(germ.counts = y, intervals = int, total.seeds = 50, : Convergence Error
#1. failed to evaluate 'fn' at starting values: could not find function "FourPHF_fixa_fixy0"
```

```
$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       NA        NA        NA      NA
2    b       NA        NA        NA      NA
3    c       NA        NA        NA      NA
4   y0       NA        NA        NA      NA

$Fit
  sigma isConv finTol logLik AIC BIC deviance df.residual nobs
1    NA     NA     NA     NA  NA  NA       NA          NA   NA

$a
[1] NA

$b
[1] NA

$c
[1] NA

$y0
[1] NA

$lag
[1] NA

$Dlag50
[1] NA

$t50.total
[1] NA

$txp.total
10 60
NA NA

$t50.Germinated
```

```
[1] NA

$txp.Germinated
10 60
NA NA

$Uniformity
        90         10 uniformity
        NA         NA         NA

$TMGR
[1] NA

$AUC
[1] NA

$MGT
[1] NA

$Skewness
[1] NA

$msg
[1] "#1. failed to evaluate 'fn' at starting values: could not find function \"FourPHF_fixa_fixy0\" "

$isConv
[1] NA

$model
<simpleError in gsl_nls.formula(csgp ~ FourPHF_fixa_fixy0(x = intervals, a = max(csgp),     bta, c), da

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

```
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)
```

```
Warning in FourPHFfit(germ.counts = x, intervals = int, total.seeds = 50, : Convergence Error
#1. failed to evaluate 'fn' at starting values: could not find function "FourPHF_fixa_fixy0"
```

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

```
Warning in FourPHFfit(germ.counts = y, intervals = int, total.seeds = 50, : Convergence Error
#1. failed to evaluate 'fn' at starting values: could not find function "FourPHF_fixa_fixy0"
```

```
# Default plots
plot(fit1)
```

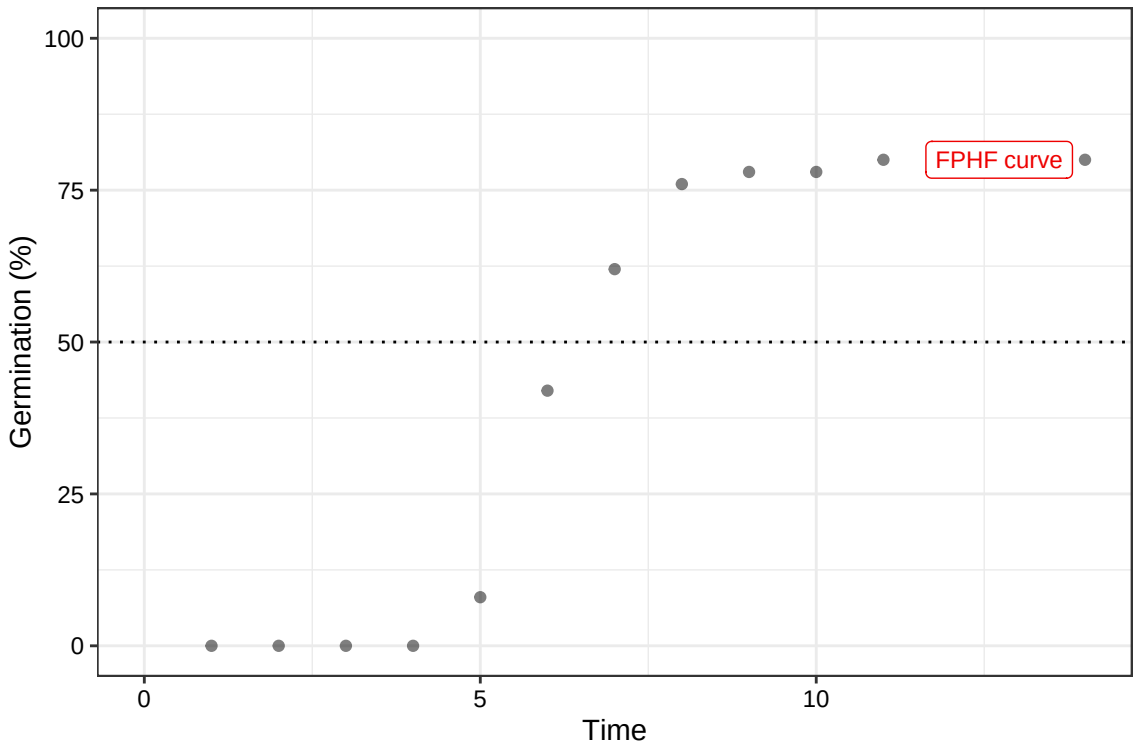
```
Warning: Removed 101 rows containing missing values (`geom_function()`).

Warning: Removed 101 rows containing missing values (`geom_function()`).

Warning: Removed 1 rows containing missing values (`geom_vline()`).
Removed 1 rows containing missing values (`geom_vline()`).

Warning: Removed 14 rows containing missing values (`geom_segment()`).
Removed 14 rows containing missing values (`geom_segment()`).

Warning: Removed 1 rows containing missing values (`geom_vline()`).
Removed 1 rows containing missing values (`geom_vline()`).
```




```
plot(fit2)
```

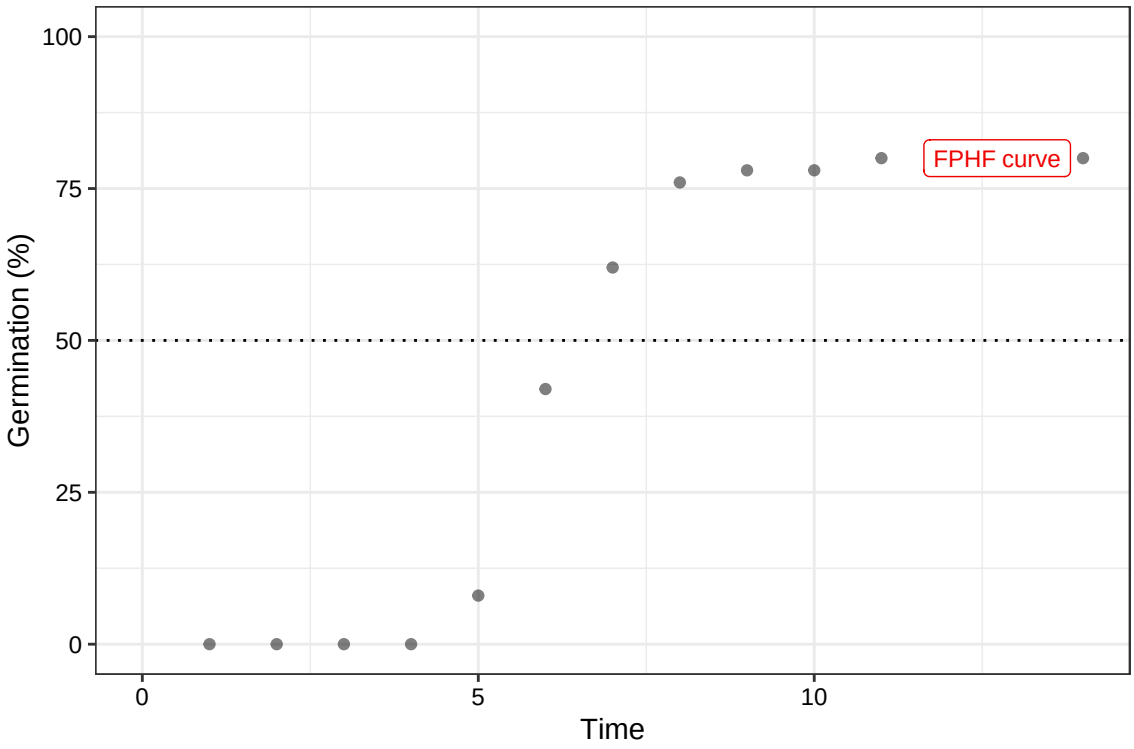
```
Warning: Removed 101 rows containing missing values (`geom_function()`).

Warning: Removed 101 rows containing missing values (`geom_function()`).

Warning: Removed 1 rows containing missing values (`geom_vline()`).
Removed 1 rows containing missing values (`geom_vline()`).

Warning: Removed 14 rows containing missing values (`geom_segment()`).
Removed 14 rows containing missing values (`geom_segment()`).

Warning: Removed 1 rows containing missing values (`geom_vline()`).
Removed 1 rows containing missing values (`geom_vline()`).
```




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

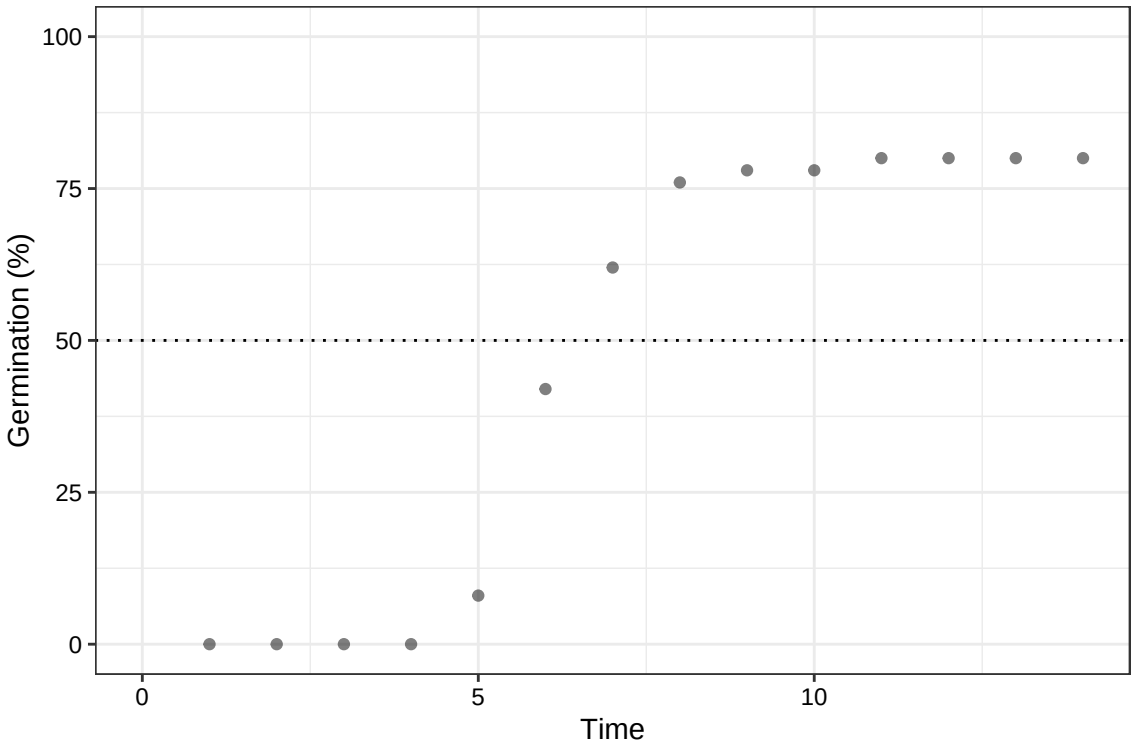
```
Warning: Removed 101 rows containing missing values (`geom_function()`).
```

```
Warning: Removed 101 rows containing missing values (`geom_function()`).
```

```
Warning: Removed 1 rows containing missing values (`geom_vline()`).
Removed 1 rows containing missing values (`geom_vline()`).
```

```
Warning: Removed 14 rows containing missing values (`geom_segment()`).
Removed 14 rows containing missing values (`geom_segment()`).
```

```
Warning: Removed 1 rows containing missing values (`geom_vline()`).
Removed 1 rows containing missing values (`geom_vline()`).
```




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

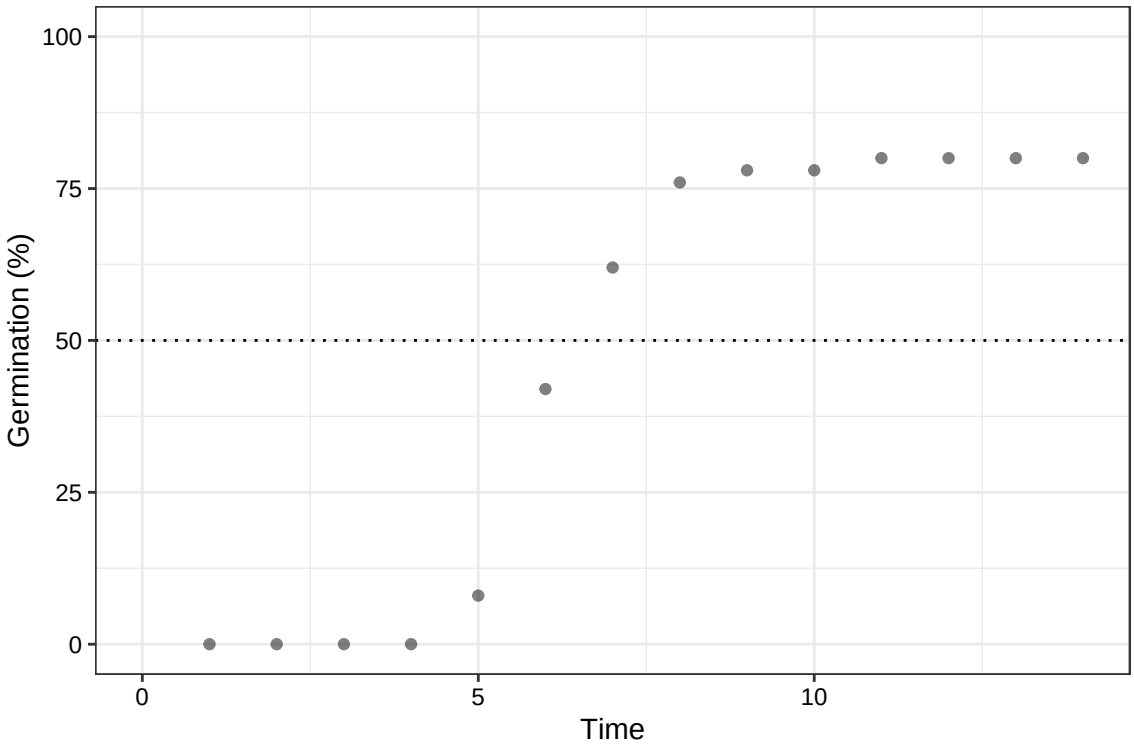
```
Warning: Removed 101 rows containing missing values (`geom_function()`).
```

```
Warning: Removed 101 rows containing missing values (`geom_function()`).
```

```
Warning: Removed 1 rows containing missing values (`geom_vline()`).
Removed 1 rows containing missing values (`geom_vline()`).
```

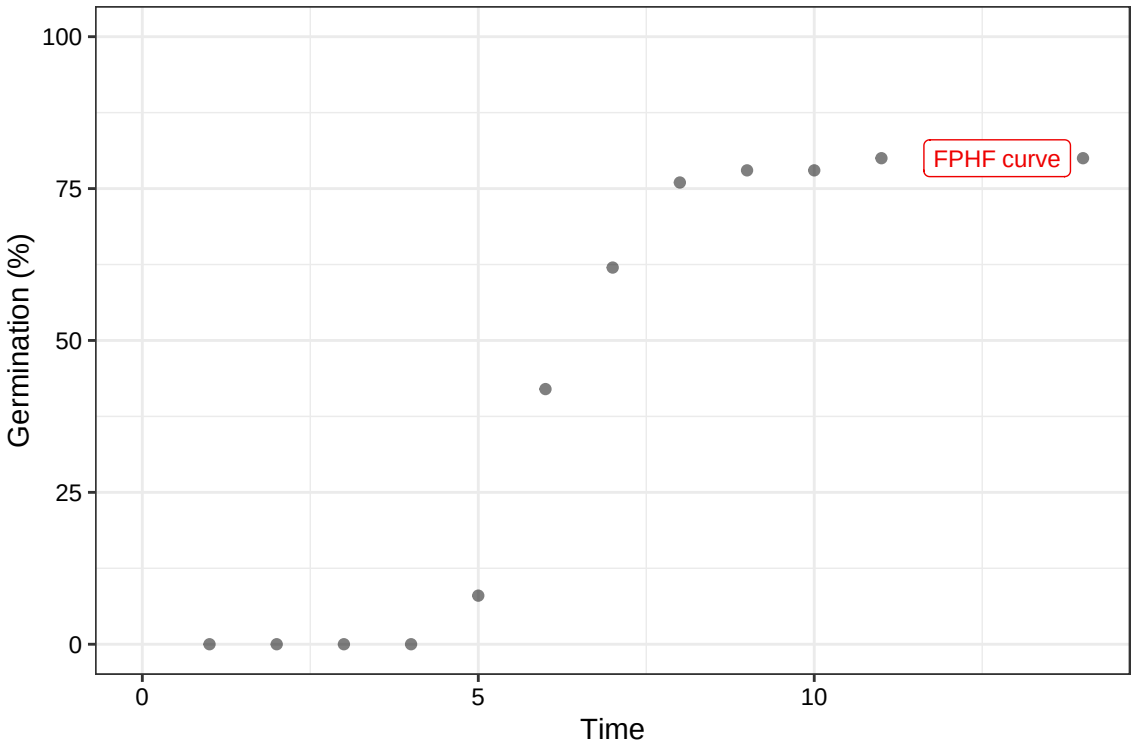
```
Warning: Removed 14 rows containing missing values (`geom_segment()`).
Removed 14 rows containing missing values (`geom_segment()`).
```

```
Warning: Removed 1 rows containing missing values (`geom_vline()`).
Removed 1 rows containing missing values (`geom_vline()`).
```



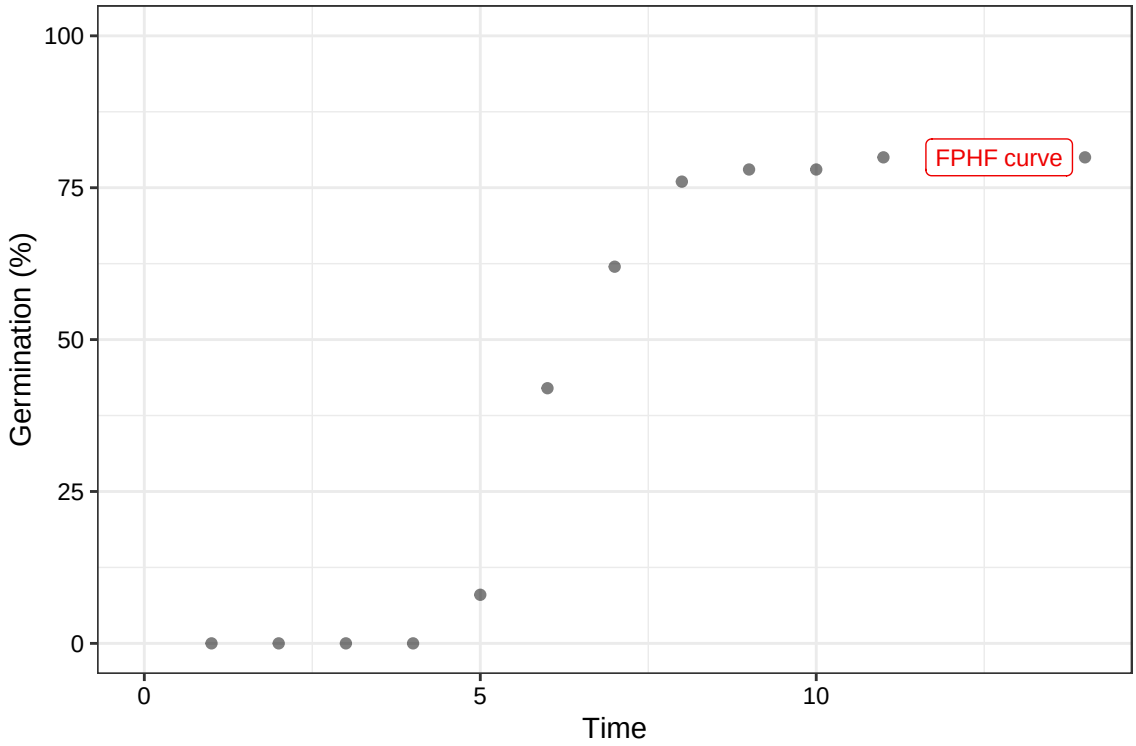

```
# Only the FPHF curve
plot(fit1, rog = FALSE, t50.total = FALSE, t50.germ = FALSE,
     tmgr = FALSE, mgt = FALSE, uniformity = FALSE)
```

```
Warning: Removed 101 rows containing missing values (`geom_function()`).
```



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

```
Warning: Removed 101 rows containing missing values (`geom_function()`).
```




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

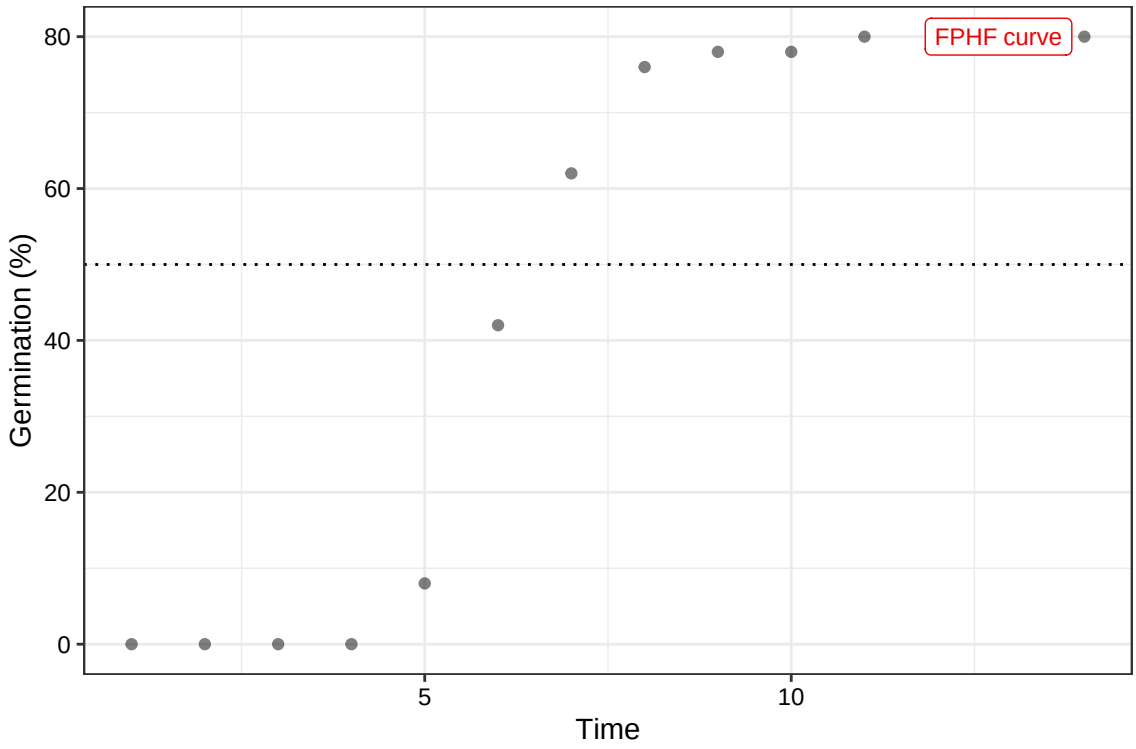
```
Warning: Removed 101 rows containing missing values (`geom_function()`).
```

```
Warning: Removed 101 rows containing missing values (`geom_function()`).
```

```
Warning: Removed 1 rows containing missing values (`geom_vline()`).
Removed 1 rows containing missing values (`geom_vline()`).
```

```
Warning: Removed 14 rows containing missing values (`geom_segment()`).
Removed 14 rows containing missing values (`geom_segment()`).
```

```
Warning: Removed 1 rows containing missing values (`geom_vline()`).
Removed 1 rows containing missing values (`geom_vline()`).
```




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

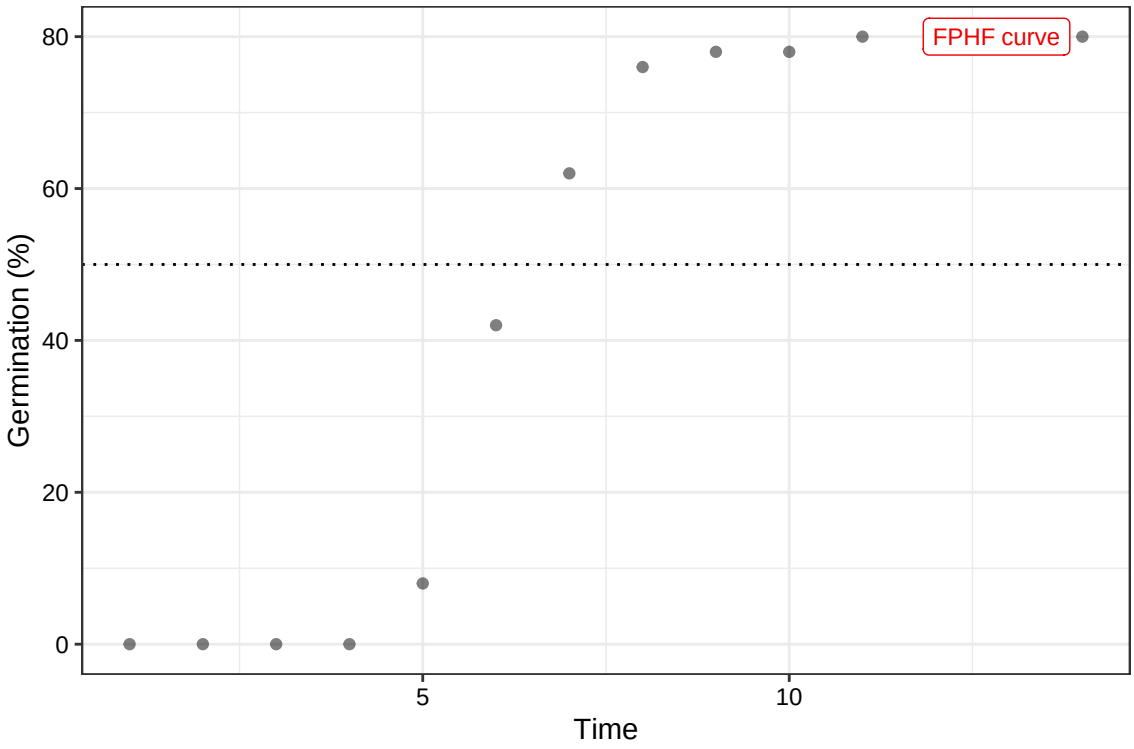
```
Warning: Removed 101 rows containing missing values (`geom_function()`).
```

```
Warning: Removed 101 rows containing missing values (`geom_function()`).
```

```
Warning: Removed 1 rows containing missing values (`geom_vline()`).
Removed 1 rows containing missing values (`geom_vline()`).
```

```
Warning: Removed 14 rows containing missing values (`geom_segment()`).
Removed 14 rows containing missing values (`geom_segment()`).
```

```
Warning: Removed 1 rows containing missing values (`geom_vline()`).
Removed 1 rows containing missing values (`geom_vline()`).
```



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	Day12	Day13	Day14	Tota
1	G1	1	0	0	0	0	4	17	10	7	1	0	1	0	0	0	
2	G2	1	0	0	0	1	3	15	13	6	2	1	0	1	0	0	
3	G3	1	0	0	0	2	3	18	9	8	2	1	1	1	0	0	
4	G4	1	0	0	0	0	4	19	12	6	2	1	1	1	0	0	
5	G5	1	0	0	0	0	5	20	12	8	1	0	0	1	1	0	
6	G1	2	0	0	0	0	3	21	11	7	1	1	1	1	0	0	
7	G2	2	0	0	0	0	4	18	11	7	1	0	1	0	0	0	
8	G3	2	0	0	0	1	3	14	12	6	2	1	0	1	0	0	
9	G4	2	0	0	0	1	3	19	10	8	1	1	1	1	0	0	
10	G5	2	0	0	0	0	4	18	13	6	2	1	0	1	0	0	
11	G1	3	0	0	0	0	5	21	11	8	1	0	0	1	1	0	

```
12       G2   3     0     0     0     0     3    20    10     7     1     1     1     1     0     0
13       G3   3     0     0     0     0     4    19    12     8     1     1     0     1     1     0
14       G4   3     0     0     0     0     3    21    11     6     1     0     1     1     0     0
15       G5   3     0     0     0     0     4    17    10     8     1     1     1     0     0     0
   GermPercent PeakGermPercent FirstGermTime LastGermTime PeakGermTime TimeSpreadGerm t50_Coolbear t50_
1     80.00000        34.00000             5            11            6              6     5.970588   5.9
2     82.35294        29.41176             4            12            6              8     6.192308   6.1
3     93.75000        37.50000             4            12            6              8     6.000000   5.9
4     90.19608        37.25490             5            12            6              7     6.041667   6.0
5     96.00000        40.00000             5            13            6              8     5.975000   5.9
6     93.87755        42.85714             5            12            6              7     5.976190   5.9
7     87.50000        37.50000             5            11            6              6     5.972222   5.9
8     85.10638        29.78723             4            12            6              8     6.208333   6.1
9     86.53846        36.53846             4            12            6              8     6.000000   5.9
10    90.00000        36.00000             5            12            6              7     6.076923   6.0
11    94.11765        41.17647             5            13            6              8     5.928571   5.9
12    86.27451        39.21569             5            12            6              7     5.975000   5.9
13    95.91837        38.77551             5            13            6              8     6.083333   6.0
14    91.66667        43.75000             5            12            6              7     5.928571   5.9
15    87.50000        35.41667             5            11            6              6     6.050000   6.0
   MeanGermTime VarGermTime SEGermTime CVGermTime MeanGermRate  VarGermRate  SEGermRate      CVG GermRa
1      6.700000    1.446154  0.1901416  0.1794868    0.1492537 0.0007176543 0.004235724 14.92537
2      6.857143    2.027875  0.2197333  0.2076717    0.1458333 0.0009172090 0.004673148 14.58333
3      6.866667    2.572727  0.2391061  0.2335882    0.1456311 0.0011572039 0.005071059 14.56311
4      6.891304    2.187923  0.2180907  0.2146419    0.1451104 0.0009701218 0.004592342 14.51104
5      6.812500    2.368351  0.2221275  0.2259002    0.1467890 0.0010995627 0.004786184 14.67890
6      6.869565    2.071498  0.2122088  0.2095140    0.1455696 0.0009301809 0.004496813 14.55696
7      6.690476    1.389663  0.1818989  0.1761967    0.1494662 0.0006935558 0.004063648 14.94662
8      6.875000    2.112179  0.2297923  0.2113940    0.1454545 0.0009454531 0.004861721 14.54545
9      6.866667    2.300000  0.2260777  0.2208604    0.1456311 0.0010345321 0.004794747 14.56311
10     6.822222    1.831313  0.2017321  0.1983606    0.1465798 0.0008453940 0.004334343 14.65798
11     6.791667    2.381206  0.2227295  0.2272072    0.1472393 0.0011191581 0.004828643 14.72393
12     6.886364    2.149577  0.2210295  0.2129053    0.1452145 0.0009558577 0.004660905 14.52145
13     6.936170    2.539315  0.2324392  0.2297410    0.1441718 0.0010970785 0.004831366 14.41718
14     6.772727    1.900634  0.2078370  0.2035568    0.1476510 0.0009033254 0.004531018 14.76510
15     6.809524    1.670151  0.1994129  0.1897847    0.1468531 0.0007767634 0.004300508 14.68531
   GermRateRecip_Farooq GermSpeed_Count GermSpeed_Percent GermSpeedAccumulated_Count GermSpeedAccumulat
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
   GermSpeedCorrected_Normal GermSpeedCorrected_Accumulated WeightGermPercent MeanGermPercent MeanGermNu
1                  0.1534731                       0.8653917          47.42857        5.714286       2.85
```

```
2                0.1514928                     0.8462043         47.89916       5.882353       3.0
3                0.1529373                     0.8510501         54.46429       6.696429       3.2
4                0.1505960                     0.8409680         52.24090       6.442577       3.2
5                0.1524789                     0.8543303         56.14286       6.857143       3.4
6                0.1506909                     0.8429608         54.51895       6.705539       3.2
7                0.1535345                     0.8663205         51.93452       6.250000       3.0
8                0.1513294                     0.8442698         49.39210       6.079027       2.8
9                0.1517909                     0.8470024         50.27473       6.181319       3.2
10               0.1513933                     0.8487837         52.57143       6.428571       3.2
11               0.1529749                     0.8578026         55.18207       6.722689       3.4
12               0.1505059                     0.8410547         50.00000       6.162465       3.1
13               0.1500494                     0.8360424         55.24781       6.851312       3.3
14               0.1524269                     0.8567022         53.86905       6.547619       3.1
15               0.1515220                     0.8499278         51.19048       6.250000       3.0
   TimsonsIndex TimsonsIndex_Labouriau TimsonsIndex_KhanUngar GermRateGeorge GermIndex GermIndex_mod
1      8.000000                  1.00             0.5714286              4  5.840000      7.300000
2      9.803922                  1.25             0.7002801              5  5.882353      7.142857
3     14.583333                  1.40             1.0416667              7  6.687500      7.133333
4      7.843137                  1.00             0.5602241              4  6.411765      7.108696
5     10.000000                  1.00             0.7142857              5  6.900000      7.187500
6      6.122449                  1.00             0.4373178              3  6.693878      7.130435
7      8.333333                  1.00             0.5952381              4  6.395833      7.309524
8     10.638298                  1.25             0.7598784              5  6.063830      7.125000
9      9.615385                  1.25             0.6868132              5  6.173077      7.133333
10     8.000000                  1.00             0.5714286              4  6.460000      7.177778
11     9.803922                  1.00             0.7002801              5  6.784314      7.208333
12     5.882353                  1.00             0.4201681              3  6.137255      7.113636
13     8.163265                  1.00             0.5830904              4  6.775510      7.063830
14     6.250000                  1.00             0.4464286              3  6.625000      7.227273
15     8.333333                  1.00             0.5952381              4  6.291667      7.190476
   EmergenceRateIndex_SG EmergenceRateIndex_SG_mod EmergenceRateIndex_BilbroWanjura EmergenceRateIndex_
1                    292                 7.300000                          5.970149                 
2                    300                 7.142857                          6.125000                 
3                    321                 7.133333                          6.553398                 
4                    327                 7.108696                          6.675079                 
5                    345                 7.187500                          7.045872                 
6                    328                 7.130435                          6.696203                 
7                    307                 7.309524                          6.277580                 
8                    285                 7.125000                          5.818182                 
9                    321                 7.133333                          6.553398                 
10                   323                 7.177778                          6.596091                 
11                   346                 7.208333                          7.067485                 
12                   313                 7.113636                          6.389439                 
13                   332                 7.063830                          6.776074                 
14                   318                 7.227273                          6.496644                 
15                   302                 7.190476                          6.167832                 
   PeakValue GermValue_Czabator GermValue_DP GermValue_Czabator_mod GermValue_DP_mod    CUGerm GermSynch
1   9.500000          54.28571     57.93890              54.28571        39.56076 0.7092199     0.260
2   9.313725          54.78662     52.58713              54.78662        40.99260 0.5051546     0.234
3  10.416667          69.75446     68.62289              69.75446        53.42809 0.3975265     0.224
4  10.049020          64.74158     70.43331              64.74158        48.86825 0.4672113     0.250
5  11.250000          77.14286     80.16914              77.14286        56.23935 0.4312184     0.260
6  10.714286          71.84506     76.51983              71.84506        53.06435 0.4934701     0.279
7  10.416667          65.10417     69.41325              65.10417        47.37690 0.7371500     0.271
```

```
8   9.574468          58.20345     56.00669          58.20345        43.67948 0.4855842     0.225
9   9.855769          60.92165     58.13477          60.92165        45.30801 0.4446640     0.249
10 10.250000          65.89286     70.91875          65.89286        49.10820 0.5584666     0.255
11 11.029412          74.14731     77.39782          74.14731        54.27520 0.4288905     0.268
12  9.803922          60.41632     64.44988          60.41632        44.71582 0.4760266     0.273
13 10.969388          75.15470     78.16335          75.15470        54.94192 0.4023679     0.250
14 10.677083          69.90947     74.40140          69.90947        51.41913 0.5383760     0.299
15 10.156250          63.47656     67.62031          63.47656        46.48043 0.6133519     0.249
   GermUncertainty
1         2.062987
2         2.321514
3         2.462012
4         2.279215
5         2.146051
6         2.160545
7         2.040796
8         2.357249
9         2.321080
10        2.187983
11        2.128670
12        2.185245
13        2.241181
14        2.037680
15        2.185028
```

FourPHFfit.bulk() This wrapper function can be used to fit the four-parameter hill function 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")

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)
```

```
Warning in FourPHFfit(germ.counts = unlist(mget(counts.intervals.cols)), : Convergence Error
#1. failed to evaluate 'fn' at starting values: could not find function "FourPHF_fixa_fixy0"

Warning in FourPHFfit(germ.counts = unlist(mget(counts.intervals.cols)), : Convergence Error
#1. failed to evaluate 'fn' at starting values: could not find function "FourPHF_fixa_fixy0"

Warning in FourPHFfit(germ.counts = unlist(mget(counts.intervals.cols)), : Convergence Error
#1. failed to evaluate 'fn' at starting values: could not find function "FourPHF_fixa_fixy0"

Warning in FourPHFfit(germ.counts = unlist(mget(counts.intervals.cols)), : Convergence Error
#1. failed to evaluate 'fn' at starting values: could not find function "FourPHF_fixa_fixy0"

Warning in FourPHFfit(germ.counts = unlist(mget(counts.intervals.cols)), : Convergence Error
#1. failed to evaluate 'fn' at starting values: could not find function "FourPHF_fixa_fixy0"
```

```
Warning in FourPHFfit(germ.counts = unlist(mget(counts.intervals.cols)), : Convergence Error
#1. failed to evaluate 'fn' at starting values: could not find function "FourPHF_fixa_fixy0"

Warning in FourPHFfit(germ.counts = unlist(mget(counts.intervals.cols)), : Convergence Error
#1. failed to evaluate 'fn' at starting values: could not find function "FourPHF_fixa_fixy0"

Warning in FourPHFfit(germ.counts = unlist(mget(counts.intervals.cols)), : Convergence Error
#1. failed to evaluate 'fn' at starting values: could not find function "FourPHF_fixa_fixy0"

Warning in FourPHFfit(germ.counts = unlist(mget(counts.intervals.cols)), : Convergence Error
#1. failed to evaluate 'fn' at starting values: could not find function "FourPHF_fixa_fixy0"

Warning in FourPHFfit(germ.counts = unlist(mget(counts.intervals.cols)), : Convergence Error
#1. failed to evaluate 'fn' at starting values: could not find function "FourPHF_fixa_fixy0"

Warning in FourPHFfit(germ.counts = unlist(mget(counts.intervals.cols)), : Convergence Error
#1. failed to evaluate 'fn' at starting values: could not find function "FourPHF_fixa_fixy0"

Warning in FourPHFfit(germ.counts = unlist(mget(counts.intervals.cols)), : Convergence Error
#1. failed to evaluate 'fn' at starting values: could not find function "FourPHF_fixa_fixy0"

Warning in FourPHFfit(germ.counts = unlist(mget(counts.intervals.cols)), : Convergence Error
#1. failed to evaluate 'fn' at starting values: could not find function "FourPHF_fixa_fixy0"

Warning in FourPHFfit(germ.counts = unlist(mget(counts.intervals.cols)), : Convergence Error
#1. failed to evaluate 'fn' at starting values: could not find function "FourPHF_fixa_fixy0"

   Genotype Rep Day01 Day02 Day03 Day04 Day05 Day06 Day07 Day08 Day09 Day10 Day11 Day12 Day13 Day14 Tota
1        G1   1     0     0     0     0     4    17    10     7     1     0     1     0     0     0
2        G2   1     0     0     0     1     3    15    13     6     2     1     0     1     0     0
3        G3   1     0     0     0     2     3    18     9     8     2     1     1     1     0     0
4        G4   1     0     0     0     0     4    19    12     6     2     1     1     1     0     0
5        G5   1     0     0     0     0     5    20    12     8     1     0     0     1     1     0
6        G1   2     0     0     0     0     3    21    11     7     1     1     1     1     0     0
7        G2   2     0     0     0     0     4    18    11     7     1     0     1     0     0     0
8        G3   2     0     0     0     1     3    14    12     6     2     1     0     1     0     0
9        G4   2     0     0     0     1     3    19    10     8     1     1     1     1     0     0
10       G5   2     0     0     0     0     4    18    13     6     2     1     0     1     0     0
11       G1   3     0     0     0     0     5    21    11     8     1     0     0     1     1     0
12       G2   3     0     0     0     0     3    20    10     7     1     1     1     1     0     0
13       G3   3     0     0     0     0     4    19    12     8     1     1     0     1     1     0
14       G4   3     0     0     0     0     3    21    11     6     1     0     1     1     0     0
15       G5   3     0     0     0     0     4    17    10     8     1     1     1     0     0     0
      b    c   y0  lag Dlag50 t50.total txp.total_10 txp.total_60 t50.Germinated txp.Germinated_10 txp.G
1  <NA> <NA> <NA> <NA>   <NA>      <NA>         <NA>         <NA>           <NA>              <NA>
2  <NA> <NA> <NA> <NA>   <NA>      <NA>         <NA>         <NA>           <NA>              <NA>
3  <NA> <NA> <NA> <NA>   <NA>      <NA>         <NA>         <NA>           <NA>              <NA>
4  <NA> <NA> <NA> <NA>   <NA>      <NA>         <NA>         <NA>           <NA>              <NA>
5  <NA> <NA> <NA> <NA>   <NA>      <NA>         <NA>         <NA>           <NA>              <NA>
6  <NA> <NA> <NA> <NA>   <NA>      <NA>         <NA>         <NA>           <NA>              <NA>
7  <NA> <NA> <NA> <NA>   <NA>      <NA>         <NA>         <NA>           <NA>              <NA>
```

```
8  <NA> <NA> <NA> <NA>   <NA>      <NA>         <NA>         <NA>           <NA>              <NA>
9  <NA> <NA> <NA> <NA>   <NA>      <NA>         <NA>         <NA>           <NA>              <NA>
10 <NA> <NA> <NA> <NA>   <NA>      <NA>         <NA>         <NA>           <NA>              <NA>
11 <NA> <NA> <NA> <NA>   <NA>      <NA>         <NA>         <NA>           <NA>              <NA>
12 <NA> <NA> <NA> <NA>   <NA>      <NA>         <NA>         <NA>           <NA>              <NA>
13 <NA> <NA> <NA> <NA>   <NA>      <NA>         <NA>         <NA>           <NA>              <NA>
14 <NA> <NA> <NA> <NA>   <NA>      <NA>         <NA>         <NA>           <NA>              <NA>
15 <NA> <NA> <NA> <NA>   <NA>      <NA>         <NA>         <NA>           <NA>              <NA>
   Uniformity_90 Uniformity_10 Uniformity TMGR  AUC  MGT Skewness
1           <NA>          <NA>       <NA> <NA> <NA> <NA>     <NA>
2           <NA>          <NA>       <NA> <NA> <NA> <NA>     <NA>
3           <NA>          <NA>       <NA> <NA> <NA> <NA>     <NA>
4           <NA>          <NA>       <NA> <NA> <NA> <NA>     <NA>
5           <NA>          <NA>       <NA> <NA> <NA> <NA>     <NA>
6           <NA>          <NA>       <NA> <NA> <NA> <NA>     <NA>
7           <NA>          <NA>       <NA> <NA> <NA> <NA>     <NA>
8           <NA>          <NA>       <NA> <NA> <NA> <NA>     <NA>
9           <NA>          <NA>       <NA> <NA> <NA> <NA>     <NA>
10          <NA>          <NA>       <NA> <NA> <NA> <NA>     <NA>
11          <NA>          <NA>       <NA> <NA> <NA> <NA>     <NA>
12          <NA>          <NA>       <NA> <NA> <NA> <NA>     <NA>
13          <NA>          <NA>       <NA> <NA> <NA> <NA>     <NA>
14          <NA>          <NA>       <NA> <NA> <NA> <NA>     <NA>
15          <NA>          <NA>       <NA> <NA> <NA> <NA>     <NA>
                                                                                                  msg Fit_sig
1  #1. failed to evaluate 'fn' at starting values: could not find function "FourPHF_fixa_fixy0"       <l
2  #1. failed to evaluate 'fn' at starting values: could not find function "FourPHF_fixa_fixy0"       <l
3  #1. failed to evaluate 'fn' at starting values: could not find function "FourPHF_fixa_fixy0"       <l
4  #1. failed to evaluate 'fn' at starting values: could not find function "FourPHF_fixa_fixy0"       <l
5  #1. failed to evaluate 'fn' at starting values: could not find function "FourPHF_fixa_fixy0"       <l
6  #1. failed to evaluate 'fn' at starting values: could not find function "FourPHF_fixa_fixy0"       <l
7  #1. failed to evaluate 'fn' at starting values: could not find function "FourPHF_fixa_fixy0"       <l
8  #1. failed to evaluate 'fn' at starting values: could not find function "FourPHF_fixa_fixy0"       <l
9  #1. failed to evaluate 'fn' at starting values: could not find function "FourPHF_fixa_fixy0"       <l
10 #1. failed to evaluate 'fn' at starting values: could not find function "FourPHF_fixa_fixy0"       <l
11 #1. failed to evaluate 'fn' at starting values: could not find function "FourPHF_fixa_fixy0"       <l
12 #1. failed to evaluate 'fn' at starting values: could not find function "FourPHF_fixa_fixy0"       <l
13 #1. failed to evaluate 'fn' at starting values: could not find function "FourPHF_fixa_fixy0"       <l
14 #1. failed to evaluate 'fn' at starting values: could not find function "FourPHF_fixa_fixy0"       <l
15 #1. failed to evaluate 'fn' at starting values: could not find function "FourPHF_fixa_fixy0"       <l
   Fit_finTol Fit_logLik Fit_AIC Fit_BIC Fit_deviance Fit_df.residual Fit_nobs
1        <NA>       <NA>    <NA>    <NA>         <NA>            <NA>     <NA>
2        <NA>       <NA>    <NA>    <NA>         <NA>            <NA>     <NA>
3        <NA>       <NA>    <NA>    <NA>         <NA>            <NA>     <NA>
4        <NA>       <NA>    <NA>    <NA>         <NA>            <NA>     <NA>
5        <NA>       <NA>    <NA>    <NA>         <NA>            <NA>     <NA>
6        <NA>       <NA>    <NA>    <NA>         <NA>            <NA>     <NA>
7        <NA>       <NA>    <NA>    <NA>         <NA>            <NA>     <NA>
8        <NA>       <NA>    <NA>    <NA>         <NA>            <NA>     <NA>
9        <NA>       <NA>    <NA>    <NA>         <NA>            <NA>     <NA>
10       <NA>       <NA>    <NA>    <NA>         <NA>            <NA>     <NA>
11       <NA>       <NA>    <NA>    <NA>         <NA>            <NA>     <NA>
12       <NA>       <NA>    <NA>    <NA>         <NA>            <NA>     <NA>
13       <NA>       <NA>    <NA>    <NA>         <NA>            <NA>     <NA>
```

```
14       <NA>       <NA>    <NA>    <NA>          <NA>            <NA>     <NA>
15       <NA>       <NA>    <NA>    <NA>          <NA>            <NA>     <NA>
```

Multiple fitted curves generated in batch can also be plotted.

```
data(gcdata)

counts.per.intervals <- c("Day01", "Day02", "Day03", "Day04", "Day05",
                          "Day06", "Day07", "Day08", "Day09", "Day10",
                          "Day11", "Day12", "Day13", "Day14")

fits <- 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)
```

```
Warning in FourPHFfit(germ.counts = unlist(mget(counts.intervals.cols)), : Convergence Error
#1. failed to evaluate 'fn' at starting values: could not find function "FourPHF_fixa_fixy0"

Warning in FourPHFfit(germ.counts = unlist(mget(counts.intervals.cols)), : Convergence Error
#1. failed to evaluate 'fn' at starting values: could not find function "FourPHF_fixa_fixy0"

Warning in FourPHFfit(germ.counts = unlist(mget(counts.intervals.cols)), : Convergence Error
#1. failed to evaluate 'fn' at starting values: could not find function "FourPHF_fixa_fixy0"

Warning in FourPHFfit(germ.counts = unlist(mget(counts.intervals.cols)), : Convergence Error
#1. failed to evaluate 'fn' at starting values: could not find function "FourPHF_fixa_fixy0"

Warning in FourPHFfit(germ.counts = unlist(mget(counts.intervals.cols)), : Convergence Error
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Warning in FourPHFfit(germ.counts = unlist(mget(counts.intervals.cols)), : Convergence Error
#1. failed to evaluate 'fn' at starting values: could not find function "FourPHF_fixa_fixy0"

Warning in FourPHFfit(germ.counts = unlist(mget(counts.intervals.cols)), : Convergence Error
#1. failed to evaluate 'fn' at starting values: could not find function "FourPHF_fixa_fixy0"

Warning in FourPHFfit(germ.counts = unlist(mget(counts.intervals.cols)), : Convergence Error
#1. failed to evaluate 'fn' at starting values: could not find function "FourPHF_fixa_fixy0"

Warning in FourPHFfit(germ.counts = unlist(mget(counts.intervals.cols)), : Convergence Error
#1. failed to evaluate 'fn' at starting values: could not find function "FourPHF_fixa_fixy0"

Warning in FourPHFfit(germ.counts = unlist(mget(counts.intervals.cols)), : Convergence Error
#1. failed to evaluate 'fn' at starting values: could not find function "FourPHF_fixa_fixy0"

Warning in FourPHFfit(germ.counts = unlist(mget(counts.intervals.cols)), : Convergence Error
#1. failed to evaluate 'fn' at starting values: could not find function "FourPHF_fixa_fixy0"
```
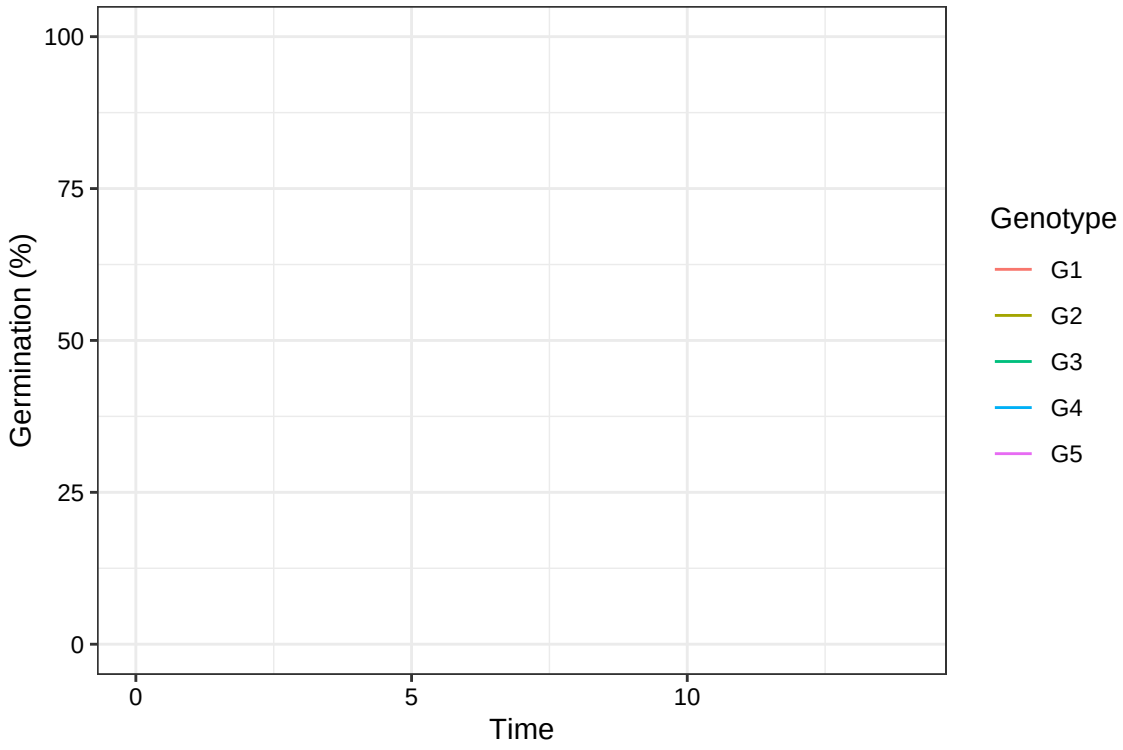

```
Warning in FourPHFfit(germ.counts = unlist(mget(counts.intervals.cols)), : Convergence Error
#1. failed to evaluate 'fn' at starting values: could not find function "FourPHF_fixa_fixy0"

Warning in FourPHFfit(germ.counts = unlist(mget(counts.intervals.cols)), : Convergence Error
#1. failed to evaluate 'fn' at starting values: could not find function "FourPHF_fixa_fixy0"
```

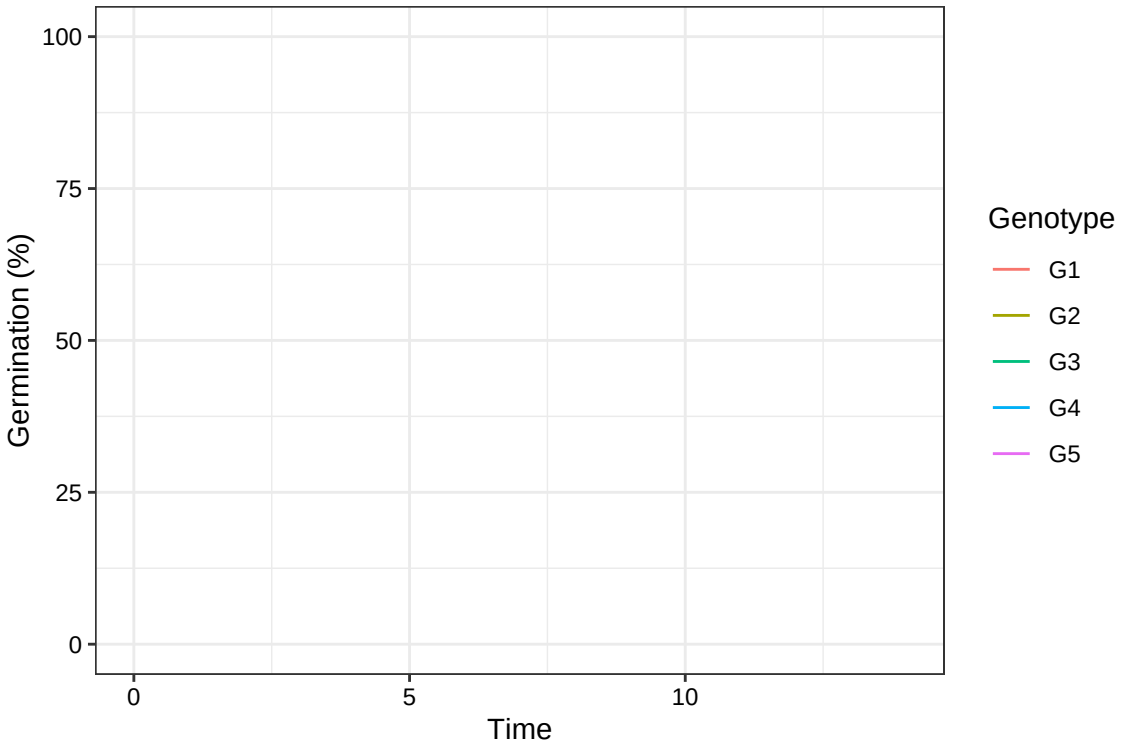
```r
# Plot FPHF curves
plot(fits, group.col = "Genotype")
```

```
Warning: Removed 1965 rows containing missing values (`geom_line()`).
```



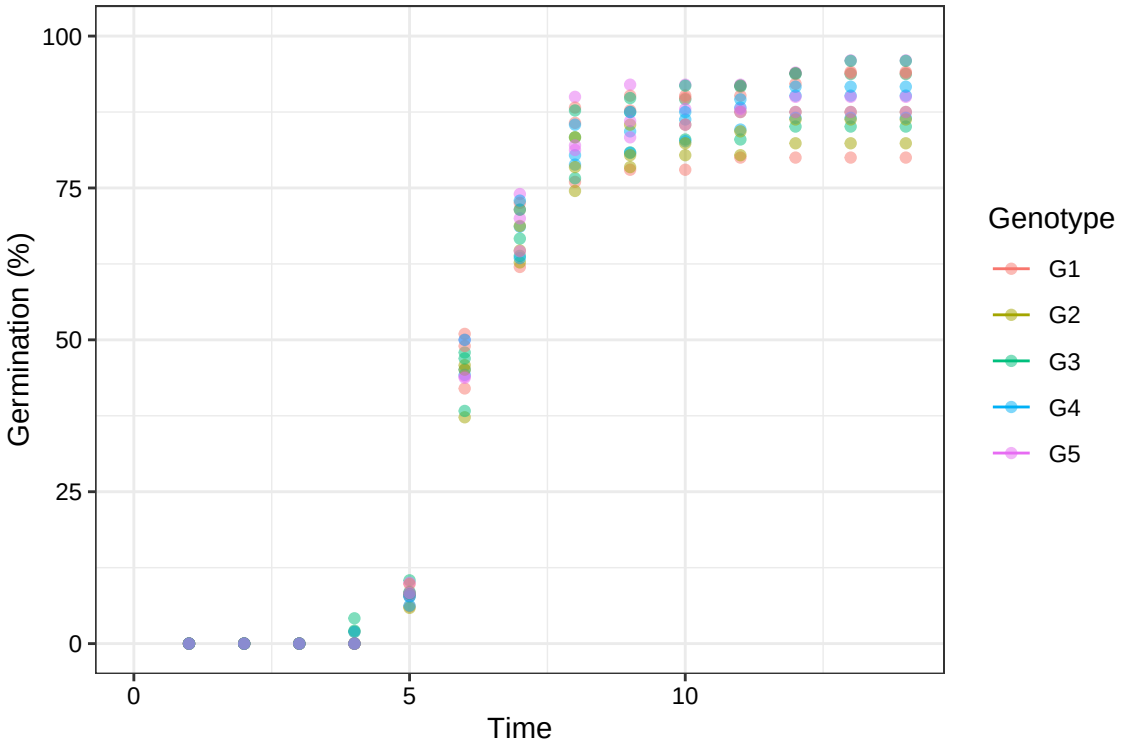

```r
# Plot ROG curves
plot(fits, rog = TRUE, group.col = "Genotype")
```

```
Warning: Removed 1965 rows containing missing values (`geom_line()`).
```




```
# Plot FPHF curves with points
plot(fits, group.col = "Genotype", show.points = TRUE)
```

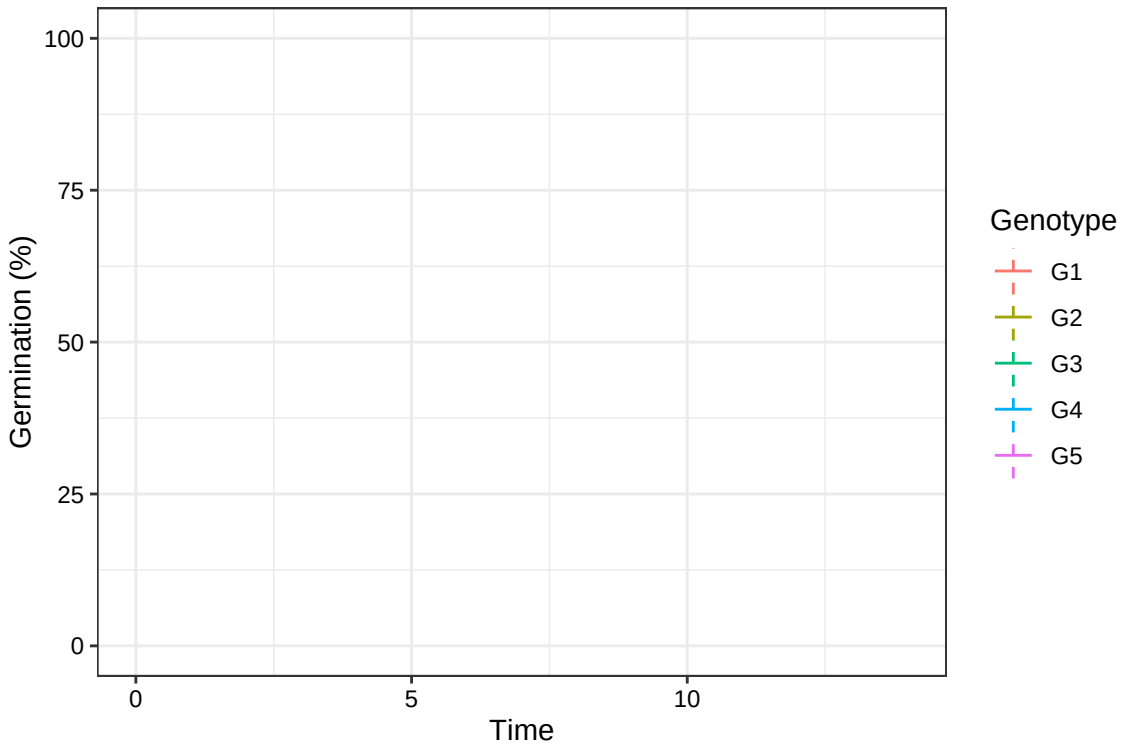
```
Warning: Removed 1965 rows containing missing values (`geom_line()`).
```




```
# Plot FPHF curves with annotations
plot(fits, group.col = "Genotype", annotate = "t50.total")
```

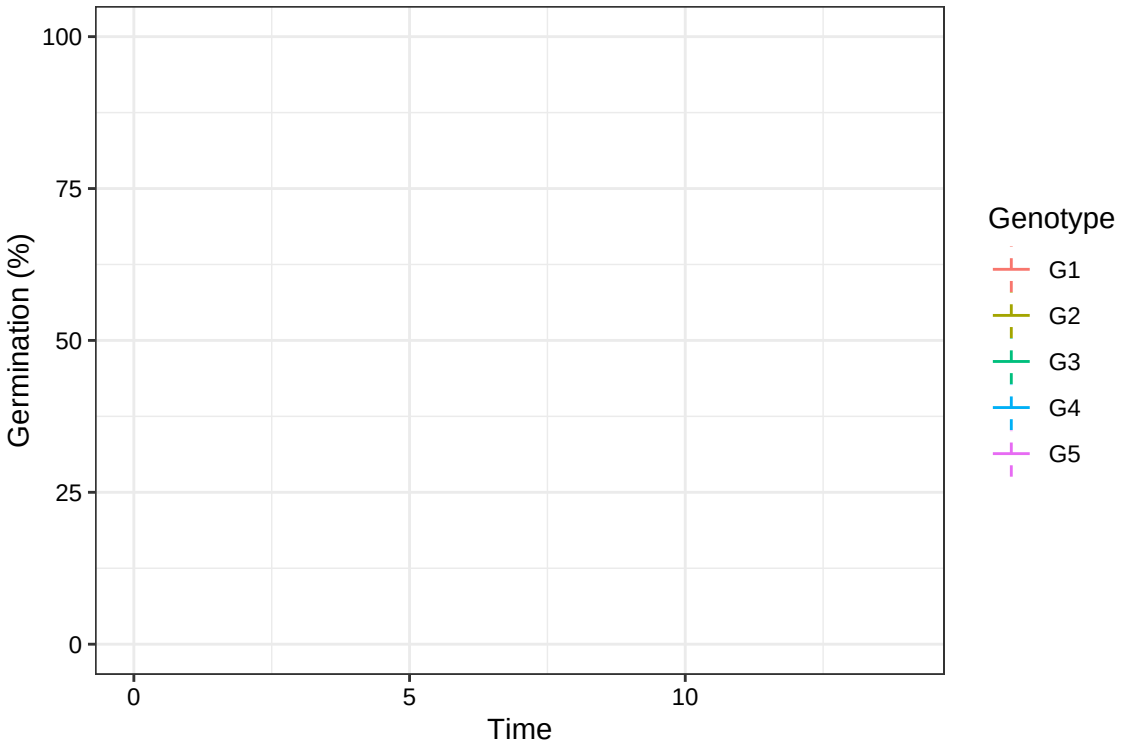
```
Warning: Removed 1965 rows containing missing values (`geom_line()`).
```

```
Warning: Removed 15 rows containing missing values (`geom_vline()`).
```



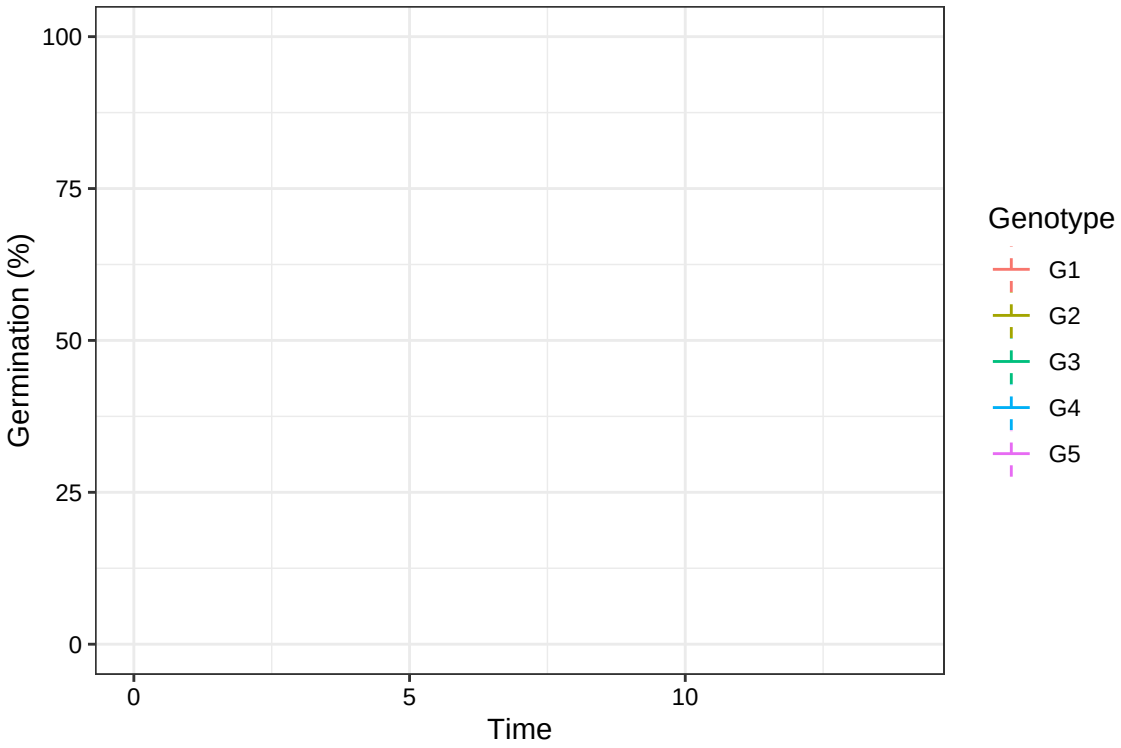

```
plot(fits, group.col = "Genotype", annotate = "t50.germ")
```

```
Warning: Removed 1965 rows containing missing values (`geom_line()`).
Removed 15 rows containing missing values (`geom_vline()`).
```



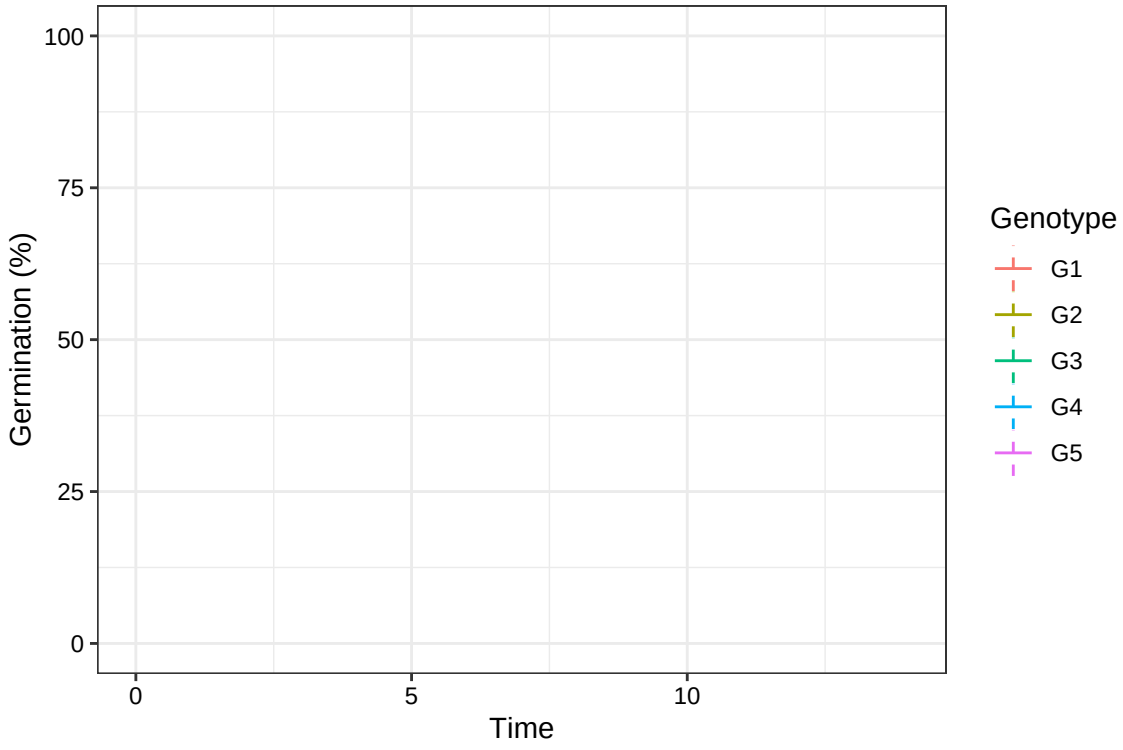

```
plot(fits, group.col = "Genotype", annotate = "tmgr")
```

```
Warning: Removed 1965 rows containing missing values (`geom_line()`).
Removed 15 rows containing missing values (`geom_vline()`).
```



```
plot(fits, group.col = "Genotype", annotate = "mgt")
```

```
Warning: Removed 1965 rows containing missing values (`geom_line()`).
Removed 15 rows containing missing values (`geom_vline()`).
```

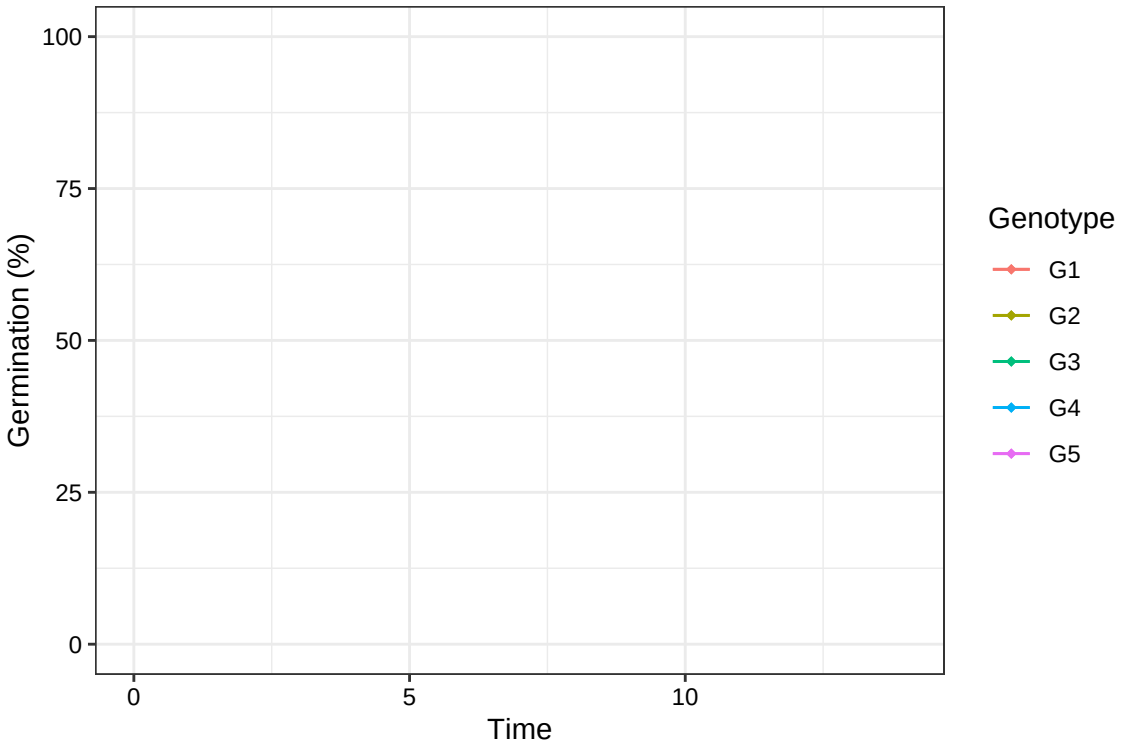



```
plot(fits, group.col = "Genotype", annotate = "uniformity")
```

```
Warning: Removed 1965 rows containing missing values (`geom_line()`).
```

```
Warning: Removed 15 rows containing missing values (`geom_point()`).
Removed 15 rows containing missing values (`geom_point()`).
```

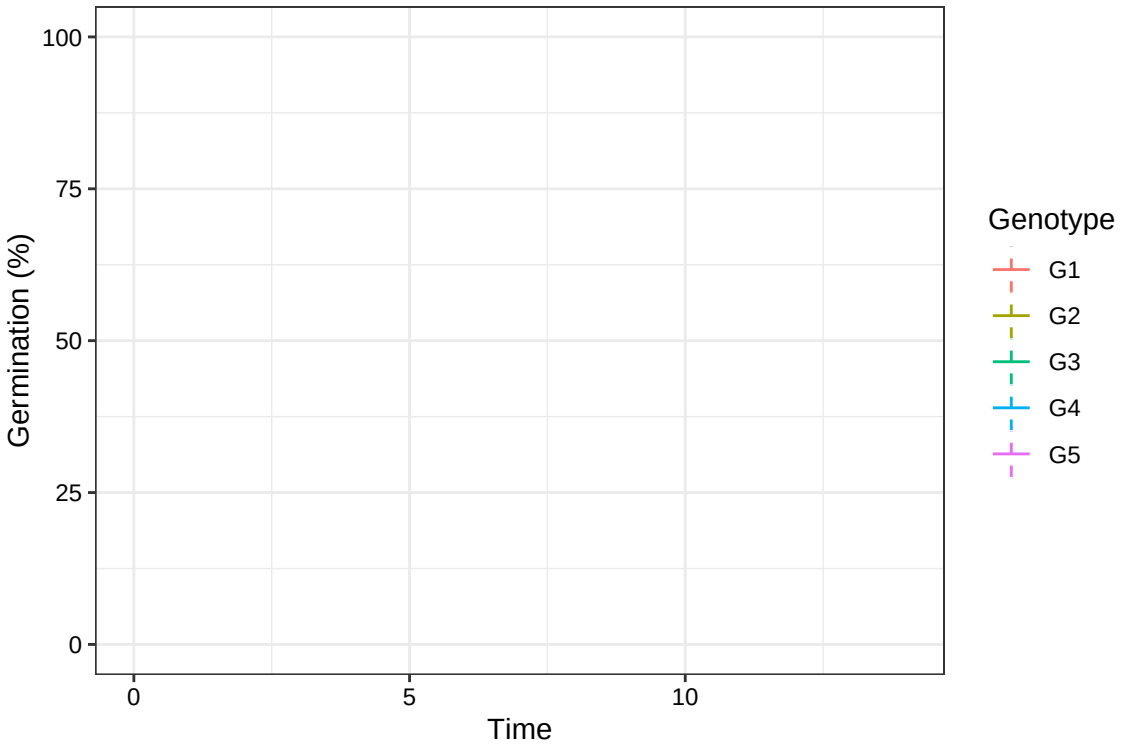
```
Warning: Removed 15 rows containing missing values (`geom_segment()`).
```




```
# Plot ROG curves with annotations
plot(fits, rog = TRUE, group.col = "Genotype", annotate = "t50.total")
```

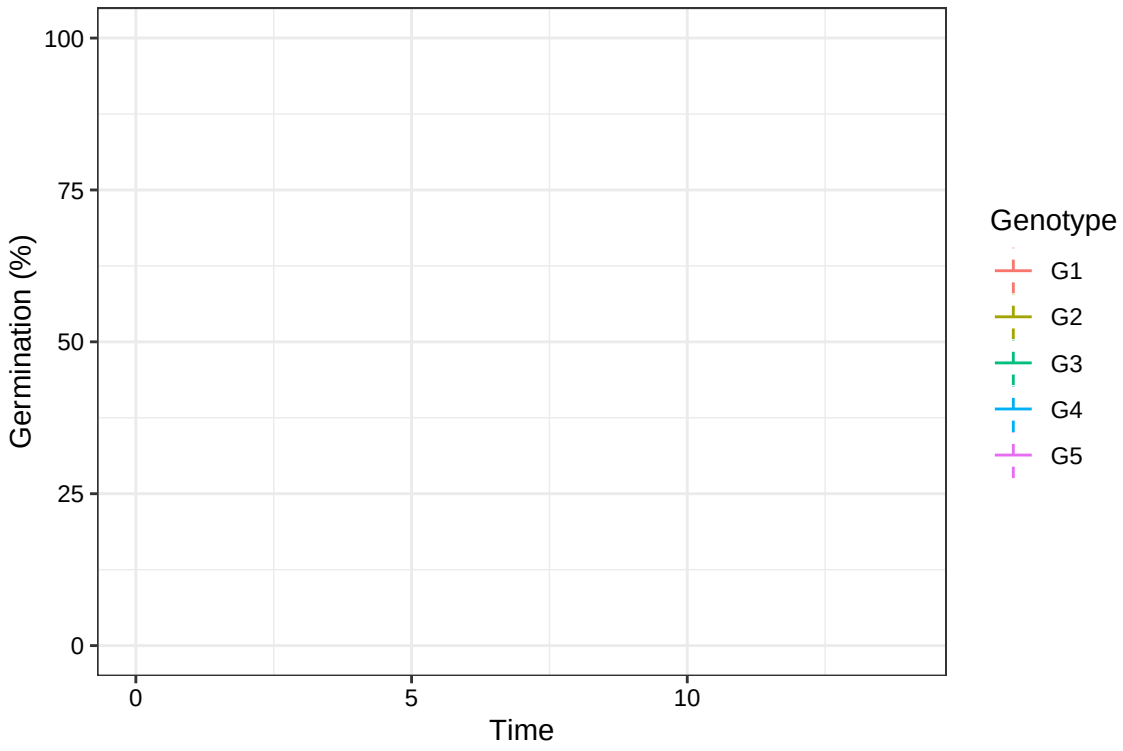
```
Warning: Removed 1965 rows containing missing values (`geom_line()`).
```

```
Warning: Removed 15 rows containing missing values (`geom_vline()`).
```



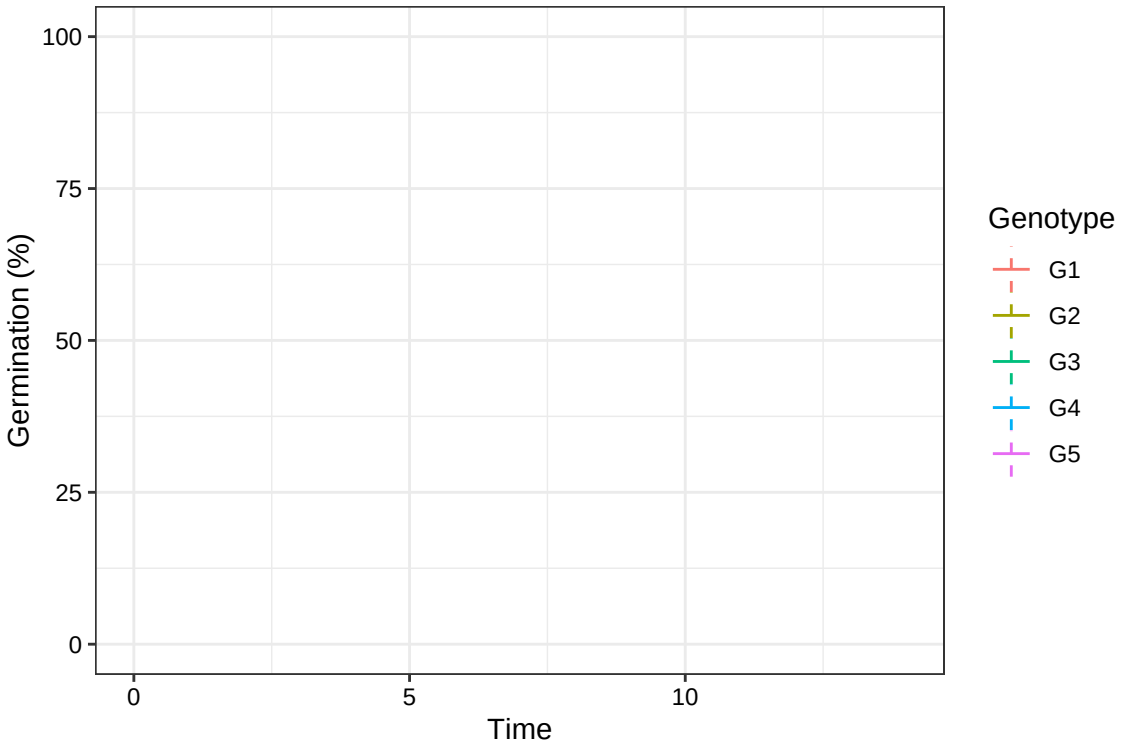
```
plot(fits, rog = TRUE, group.col = "Genotype", annotate = "t50.germ")
```

```
Warning: Removed 1965 rows containing missing values (`geom_line()`).
Removed 15 rows containing missing values (`geom_vline()`).
```



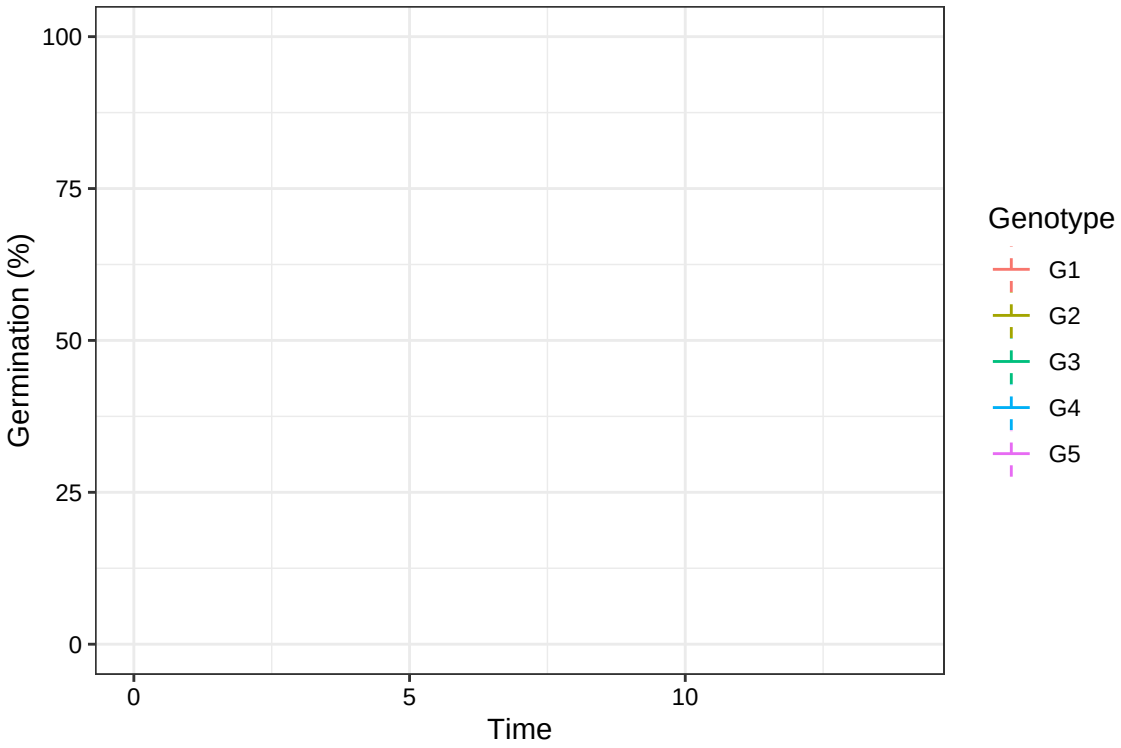

```
plot(fits, rog = TRUE, group.col = "Genotype", annotate = "tmgr")
```

```
Warning: Removed 1965 rows containing missing values (`geom_line()`).
Removed 15 rows containing missing values (`geom_vline()`).
```




```
plot(fits, rog = TRUE, group.col = "Genotype", annotate = "mgt")
```

```
Warning: Removed 1965 rows containing missing values (`geom_line()`).
Removed 15 rows containing missing values (`geom_vline()`).
```

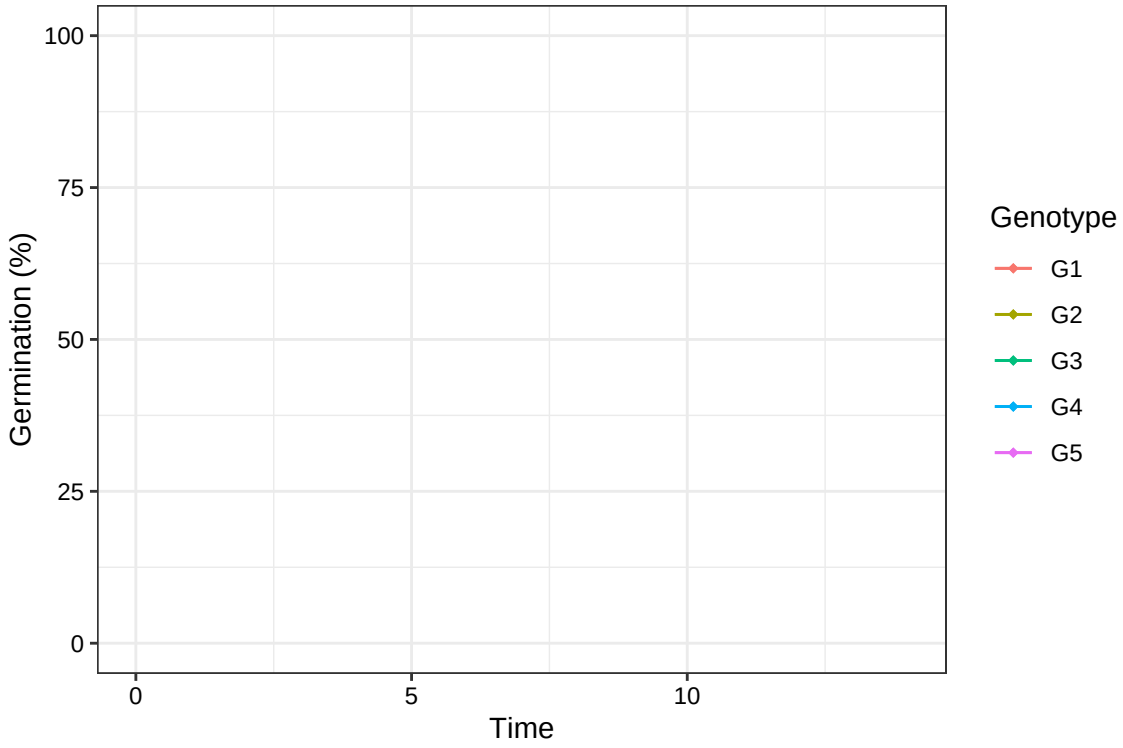


```
plot(fits, rog = TRUE, group.col = "Genotype", annotate = "uniformity")
```

```
Warning: Removed 1965 rows containing missing values (`geom_line()`).
```

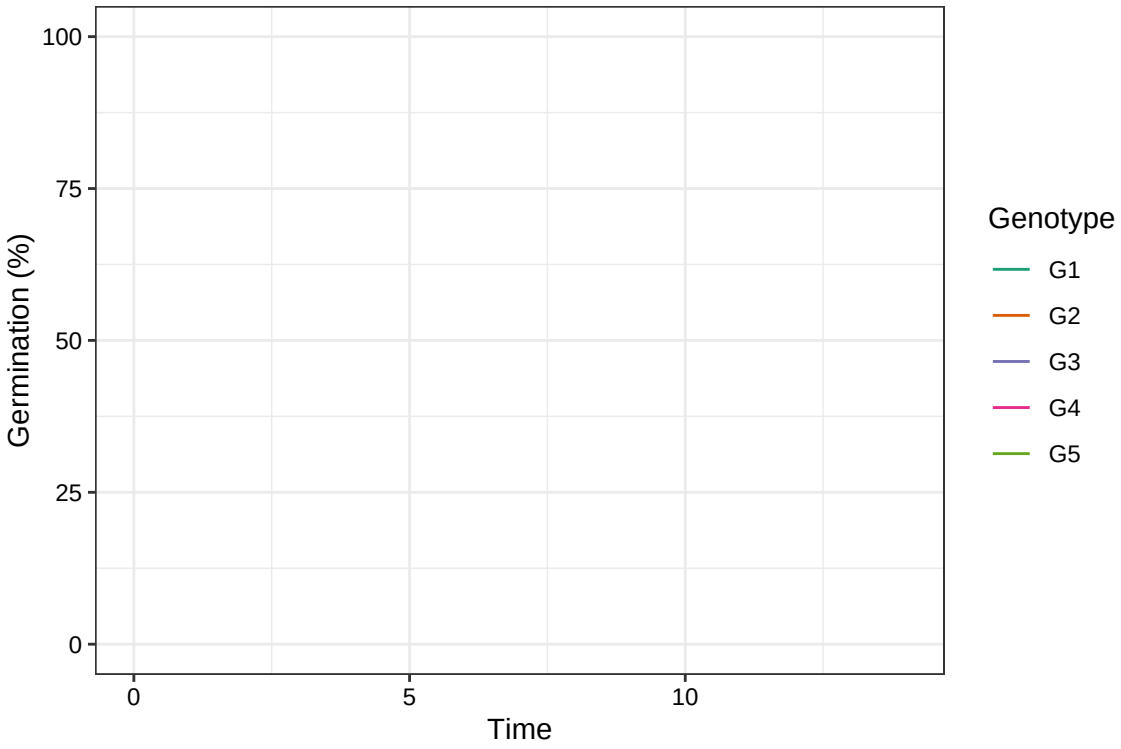
```
Warning: Removed 15 rows containing missing values (`geom_point()`).
Removed 15 rows containing missing values (`geom_point()`).
```

```
Warning: Removed 15 rows containing missing values (`geom_segment()`).
```



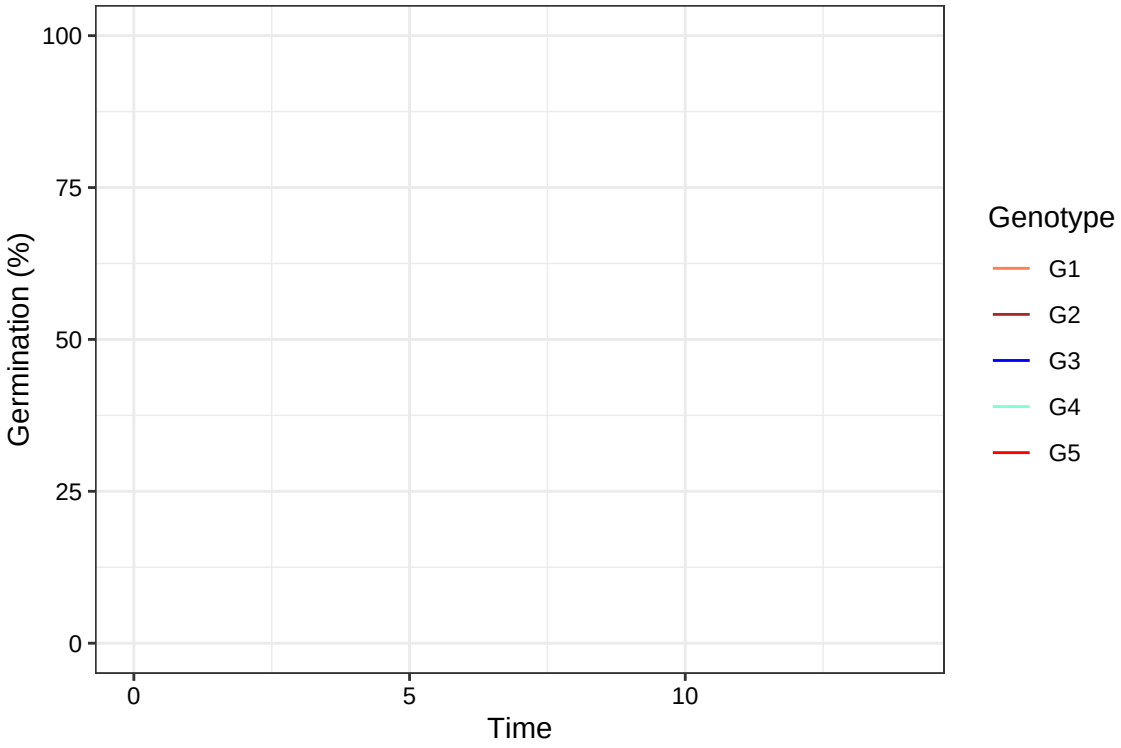

```
# Change colour of curves using ggplot2 options
library(ggplot2)
curvesplot <- plot(fits, group.col = "Genotype")

# 'Dark2' palette from RColorBrewer
curvesplot + scale_colour_brewer(palette = "Dark2")
```

```
Warning: Removed 1965 rows containing missing values (`geom_line()`).
```




```
# Manual colours
curvesplot +
  scale_colour_manual(values = c("Coral", "Brown", "Blue",
                                 "Aquamarine", "Red"))
```

```
Warning: Removed 1965 rows containing missing values (`geom_line()`).
```



Citing germinationmetrics

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

  Aravind, J., Vimala Devi, S., Radhamani, J., Jacob, S. R., and Kalyani Srinivasan ().
  germinationmetrics: Seed Germination Indices and Curve Fitting. R package version 0.1.7.9000,
  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 Srir
    note = {R package version 0.1.7.9000 https://aravind-j.github.io/germinationmetrics/ https://CRAN.R-
  }

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

Session Info

```
sessionInfo()
```

```
R Under development (unstable) (2023-08-09 r84924 ucrt)
Platform: x86_64-w64-mingw32/x64
Running under: Windows 11 x64 (build 22621)

Matrix products: default


locale:
[1] LC_COLLATE=English_India.utf8  LC_CTYPE=English_India.utf8    LC_MONETARY=English_India.utf8
[4] LC_NUMERIC=C                   LC_TIME=English_India.utf8

time zone: Asia/Calcutta
tzcode source: internal

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

other attached packages:
[1] germinationmetrics_0.1.7.9000 ggplot2_3.4.2

loaded via a namespace (and not attached):
 [1] utf8_1.2.3         generics_0.1.3     tidyr_1.3.0        bitops_1.0-7       stringi_1.7.12     lat
 [7] digest_0.6.33      magrittr_2.0.3     RColorBrewer_1.1-3 evaluate_0.21      grid_4.4.0         fas
[13] plyr_1.8.8         Matrix_1.6-0       ggrepel_0.9.3      backports_1.4.1    tinytex_0.46       htt
[19] purrr_1.0.1        fansi_1.0.4        pander_0.6.5       scales_1.2.1       XML_3.99-0.14      Rdp
[25] cli_3.6.1          rlang_1.1.1        rbibutils_2.2.14   munsell_0.5.0      withr_2.5.0        yam
[31] tools_4.4.0        parallel_4.4.0     reshape2_1.4.4     dplyr_1.1.2        colorspace_2.1-0   mat
[37] broom_1.0.5        curl_5.0.1         vctrs_0.6.3        R6_2.5.1           lifecycle_1.0.3    gsl
[43] stringr_1.5.0      pkgconfig_2.0.3    rJava_1.0-6        pillar_1.9.0       gtable_0.3.3       dat
[49] glue_1.6.2         Rcpp_1.0.11        xfun_0.40          tibble_3.2.1       tidyselect_1.2.0   hig
[55] rstudioapi_0.15.0  knitr_1.43         farver_2.1.1       htmltools_0.5.5    labeling_0.4.2     rma
```

```
[61] compiler_4.4.0     RCurl_1.98-1.12
```

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