The `germinationmetrics` Package: A Brief Introduction

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2023-08-18

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Contents

Overview

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

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

Installation

The package can be installed using the following functions:

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

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

Then the package can be loaded using the function

```
library(germinationmetrics)
```

```
--------------------------------------------------------------------------------
Welcome to germinationmetrics version 0.1.8


# 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 0.1.8. 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).

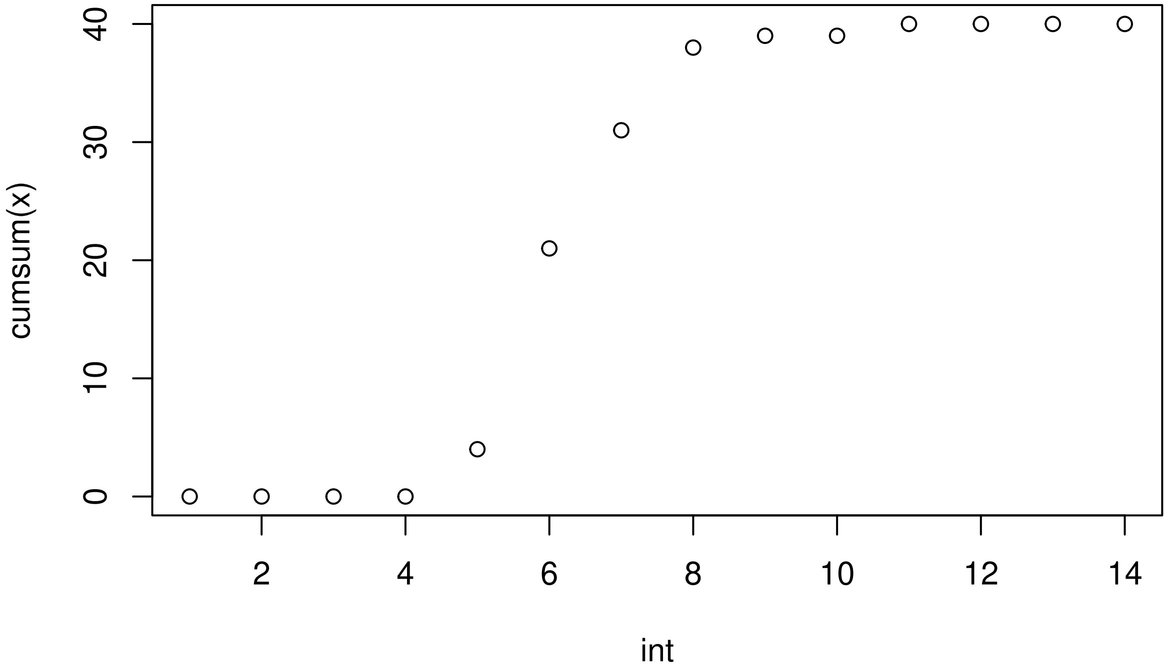
Table 2 : A typical germination count data.

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^2_T)	`VarGermTime`	It is computed according to the following formula. $$s^2_T = \frac{\sum_{i=1}^{k} N_i(T_i - \overline{T})^2}{\sum_{i=1}^{k} N_i - 1}$$ 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: $$s_{\overline{T}} = \sqrt{\frac{s^2_T}{\sum_{i=1}^{k} N_i}}$$ 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); Lyon and Coffelt (1966); Chaudhary and Ghildyal (1970); Negm and Smith (1978); Brown and Mayer (1988); Baskin and Baskin (1998); Goodchild and Walker (1971)
Modified Timson's index (Σk_{mod}) (Labouriau)	`TimsonsIndex`	It is estimated as Timson's index Σk divided by the sum of partial germination percentages. $$\Sigma k_{mod} = \frac{\Sigma k}{\sum_{i=1}^{k} g_i}$$	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 germination times exist.

[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 germination times 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 germination times 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
```

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

```
[1] 5.941176
```

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

```
[1] 5.970588
```

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

```
[1] 5.941176
```

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

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

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

```
[1] 6.7
```

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

```
[1] 1.446154
```

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

```
[1] 0.1901416
```

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

```
[1] 0.1794868
```

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

```
[1] 6.7
```

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

```
[1] 1.446154
```

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

```
[1] 0.1901416
```

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

```
[1] 0.1794868
```

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

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

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

```
[1] 0.1492537
```

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

```
[1] 14.92537
```

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

```
[1] 0.0007176543
```

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

```
[1] 0.004235724
```

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

```
[1] 0.1674877
```

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

```
[1] 0.1683168
```

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

```
[1] 0.1492537
```

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

```
[1] 14.92537
```

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

```
[1] 0.0007176543
```

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

```
[1] 0.004235724
```

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

```
[1] 0.1674877
```

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

```
[1] 0.1683168
```

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

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

GermSpeed(), GermSpeedAccumulated(), GermSpeedCorrected()

```
[1] 6.138925
```

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

```
[1] 34.61567
```

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

```
[1] 0.1534731
```

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

```
[1] 0.8653917
```

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

```
[1] 12.27785
```

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

```
[1] 69.23134
```

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

```
[1] 6.138925
```

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

```
[1] 34.61567
```

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

```
[1] 0.1534731
```

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

```
[1] 0.8653917
```

```r
# From cumulative germination counts (with percentages instead of counts)
#----------------------------------------------------------------------------
```

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

```
[1] 12.27785
```

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

```
[1] 69.23134
```

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

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

WeightGermPercent()

```
[1] 47.42857
```

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

```
[1] 47.42857
```

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

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

MeanGermPercent(), MeanGermNumber()

```
[1] 5.714286
```

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

```
[1] 2.857143
```

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

```
[1] 5.714286
```

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

```
[1] 2.857143
```

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

```
[1] 5.714286
```

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

# From partial germination counts
#----------------------------------------------------------------------------
# Without max specified
TimsonsIndex(germ.counts = x, intervals = int, total.seeds = 50)
```

TimsonsIndex(), GermRateGeorge()

```
[1] 664
```

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

```
[1] 664
```

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

```
[1] 8.3
```

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

```
[1] 47.42857
```

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

```
[1] 332
```

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

```
[1] 344
```

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

```
[1] 344
```

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

```
[1] 4.410256
```

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

```
[1] 24.57143
```

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

```
[1] 172
```

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

```
[1] 332
```

```r
# From cumulative germination counts
#----------------------------------------------------------------------------
# Without max specified
TimsonsIndex(germ.counts = y, intervals = int, partial = FALSE,
             total.seeds = 50)
```

```
[1] 664
```

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

```
[1] 664
```

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

```
[1] 8.3
```

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

```
[1] 47.42857
```

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

```
[1] 332
```

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

```
[1] 344
```

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

```
[1] 344
```

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

```
[1] 4.410256
```

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

```
[1] 24.57143
```

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

```
[1] 172
```

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

```
[1] 332
```

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

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

GermIndex()

```
[1] 5.84
```

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

```
[1] 5.84
```

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

```
[1] 7.3
```

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

```
[1] 5.84
```

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

```
[1] 5.84
```

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

```
[1] 7.3
```

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

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

EmergenceRateIndex()

```
[1] 292
```

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

```
[1] 292
```

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

```
[1] 7.3
```

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

```
[1] 5.970149
```

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

```
[1] 8.375
```

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

```
[1] 292
```

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

```
[1] 292
```

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

```
[1] 7.3
```

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

```
[1] 5.970149
```

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

```
[1] 8.375
```

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

# From partial germination counts
#----------------------------------------------------------------------------
PeakValue(germ.counts = x, intervals = int, total.seeds = 200)
```

PeakValue(), GermValue()

```
[1] 9.5
```

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

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

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

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

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

[[2]]
```

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

$testend
[1] 16
```

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

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

[[2]]
   germ.counts intervals Cumulative.germ.counts Cumulative.germ.percent
1            0         1                      0                     0.0
2            0         2                      0                     0.0
3           34         3                     34                    17.0
4           40         4                     74                    37.0
5           21         5                     95                    47.5
```

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

```
11          8       11                     130                    65.0
12          7       12                     137                    68.5
13          7       13                     144                    72.0
14          6       14                     150                    75.0
15          6       15                     156                    78.0
16          4       16                     160                    80.0
17          0       17                     160                    80.0
18          2       18                     162                    81.0
19          0       19                     162                    81.0
20          2       20                     164                    82.0
        DGS SumDGSbyN        GV
1  0.000000  0.000000  0.000000
2  0.000000  0.000000  0.000000
3  5.666667  1.888889  3.211111
4  9.250000  3.729167 13.797917
5  9.500000  4.883333 23.195833
6  8.750000  5.527778 29.020833
7  7.785714  5.850340 31.884354
8  7.125000  6.009673 34.255134
9  6.500000  6.064153 35.475298
10 6.100000  6.067738 37.013202
11 5.909091  6.053316 39.346552
12 5.708333  6.024567 41.268285
13 5.538462  5.987174 43.107655
14 5.357143  5.942172 44.566291
15 5.200000  5.892694 45.963013
16 5.000000  5.836901 46.695205
17 4.705882  5.770370 46.162961
18 4.500000  5.699794 46.168331
19 4.263158  5.624182 45.555871
20 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
3          34         3                     34                    17.0
4          40         4                     74                    37.0
5          21         5                     95                    47.5
6          10         6                    105                    52.5
7           4         7                    109                    54.5
```

```
8            5          8                      114                     57.0
9            3          9                      117                     58.5
10           5         10                      122                     61.0
11           8         11                      130                     65.0
12           7         12                      137                     68.5
13           7         13                      144                     72.0
14           6         14                      150                     75.0
15           6         15                      156                     78.0
16           4         16                      160                     80.0
17           0         17                      160                     80.0
18           2         18                      162                     81.0
19           0         19                      162                     81.0
20           2         20                      164                     82.0
        DGS
3  5.666667
4  9.250000
5  9.500000
6  8.750000
7  7.785714
8  7.125000
9  6.500000
10 6.100000
11 5.909091
12 5.708333
13 5.538462
14 5.357143
15 5.200000
16 5.000000
17 4.705882
18 4.500000
19 4.263158
20 4.100000
```

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

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

[[2]]
   germ.counts intervals Cumulative.germ.counts Cumulative.germ.percent
3           34         3                     34                    17.0
4           40         4                     74                    37.0
5           21         5                     95                    47.5
6           10         6                    105                    52.5
7            4         7                    109                    54.5
8            5         8                    114                    57.0
9            3         9                    117                    58.5
10           5        10                    122                    61.0
11           8        11                    130                    65.0
12           7        12                    137                    68.5
13           7        13                    144                    72.0
14           6        14                    150                    75.0
15           6        15                    156                    78.0
16           4        16                    160                    80.0
```

```
17           0        17                         160                      80.0
18           2        18                         162                      81.0
19           0        19                         162                      81.0
20           2        20                         164                      82.0
        DGS SumDGSbyN        GV
3  5.666667  5.666667  9.633333
4  9.250000  7.458333 27.595833
5  9.500000  8.138889 38.659722
6  8.750000  8.291667 43.531250
7  7.785714  8.190476 44.638095
8  7.125000  8.012897 45.673512
9  6.500000  7.796769 45.611097
10 6.100000  7.584673 46.266503
11 5.909091  7.398497 48.090230
12 5.708333  7.229481 49.521942
13 5.538462  7.075752 50.945411
14 5.357143  6.932534 51.994006
15 5.200000  6.799262 53.034246
16 5.000000  6.670744 53.365948
17 4.705882  6.539753 52.318022
18 4.500000  6.412268 51.939373
19 4.263158  6.285850 50.915385
20 4.100000  6.164414 50.548194

$testend
[1] 16
```

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

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

[[2]]
   germ.counts intervals Cumulative.germ.counts Cumulative.germ.percent
1            0         1                      0                     0.0
2            0         2                      0                     0.0
3           34         3                     34                    17.0
4           40         4                     74                    37.0
5           21         5                     95                    47.5
6           10         6                    105                    52.5
7            4         7                    109                    54.5
8            5         8                    114                    57.0
9            3         9                    117                    58.5
10           5        10                    122                    61.0
11           8        11                    130                    65.0
12           7        12                    137                    68.5
13           7        13                    144                    72.0
14           6        14                    150                    75.0
15           6        15                    156                    78.0
16           4        16                    160                    80.0
17           0        17                    160                    80.0
18           2        18                    162                    81.0
19           0        19                    162                    81.0
20           2        20                    164                    82.0
```

```
        DGS
1  0.000000
2  0.000000
3  5.666667
4  9.250000
5  9.500000
6  8.750000
7  7.785714
8  7.125000
9  6.500000
10 6.100000
11 5.909091
12 5.708333
13 5.538462
14 5.357143
15 5.200000
16 5.000000
17 4.705882
18 4.500000
19 4.263158
20 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
1            0         1                      0                     0.0
2            0         2                      0                     0.0
3           34         3                     34                    17.0
4           40         4                     74                    37.0
5           21         5                     95                    47.5
6           10         6                    105                    52.5
7            4         7                    109                    54.5
8            5         8                    114                    57.0
9            3         9                    117                    58.5
10           5        10                    122                    61.0
11           8        11                    130                    65.0
12           7        12                    137                    68.5
13           7        13                    144                    72.0
14           6        14                    150                    75.0
15           6        15                    156                    78.0
16           4        16                    160                    80.0
17           0        17                    160                    80.0
18           2        18                    162                    81.0
19           0        19                    162                    81.0
20           2        20                    164                    82.0
        DGS SumDGSbyN        GV
1  0.000000  0.000000  0.000000
2  0.000000  0.000000  0.000000
3  5.666667  1.888889  3.211111
4  9.250000  3.729167 13.797917
```

```
5   9.500000   4.883333 23.195833
6   8.750000   5.527778 29.020833
7   7.785714   5.850340 31.884354
8   7.125000   6.009673 34.255134
9   6.500000   6.064153 35.475298
10  6.100000   6.067738 37.013202
11  5.909091   6.053316 39.346552
12  5.708333   6.024567 41.268285
13  5.538462   5.987174 43.107655
14  5.357143   5.942172 44.566291
15  5.200000   5.892694 45.963013
16  5.000000   5.836901 46.695205
17  4.705882   5.770370 46.162961
18  4.500000   5.699794 46.168331
19  4.263158   5.624182 45.555871
20  4.100000   5.547972 45.493374

$testend
[1] 16
```

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

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

CUGerm()

```
[1] 0.7092199
```

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

```
[1] 0.7092199
```

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

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

GermSynchrony(), GermUncertainty()

```
[1] 0.2666667
```

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

```
[1] 2.062987
```

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

```
[1] 0.2666667
```

```r
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. $$lag = b\sqrt{\frac{-y_0c^b}{a+y_0}}$$	time	Germination time
D_{lag-50}	The duration between the time at germination onset (lag) and that at 50% germination (c).	time	Germination time
$t_{50_{total}}$	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. $$s = \frac{\partial y}{\partial x} = \frac{abc^bx^{b-1}}{(c^b+x^b)^2}$$ 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()

$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  bta 2.290709 0.05602634  40.88628 2.965932e-14
2    c 6.034954 0.03872162 155.85488 3.270090e-21

$Fit
    sigma isConv       finTol    logLik      AIC      BIC deviance df.residual
1 1.61522   TRUE 2.884804e-12 -25.49868 56.99736 58.91453 31.30723          12
  nobs
1   14

$a
[1] 80

$b
[1] 9.881937

$c
[1] 6.034954

$y0
[1] 0

$lag
[1] 0
```

```
$Dlag50
[1] 6.034954

$t50.total
[1] 6.355121

$txp.total
      10       60
4.956264 6.744598

$t50.Germinated
[1] 6.034954

$txp.Germinated
      10       60
4.831807 6.287724

$Uniformity
        90         10 uniformity
  7.537690   4.831807   2.705882

$TMGR
[1] 5.912194

$AUC
[1] 1108.976

$MGT
[1] 6.632252

$Skewness
[1] 1.098973

$msg
[1] "#1. success "

$isConv
[1] TRUE

$model
Nonlinear regression model
  model: csgp ~ FourPHF_fixa_fixy0(x = intervals, a = max(csgp), bta,     c)
   data: df
  bta     c
2.291 6.035
 residual sum-of-squares: 31.31

Algorithm: multifit/levenberg-marquardt, (scaling: levenberg, solver: qr)

Number of iterations to convergence: 8
Achieved convergence tolerance: 2.885e-12

attr(,"class")
```

```
[1] "FourPHFfit" "list"
```

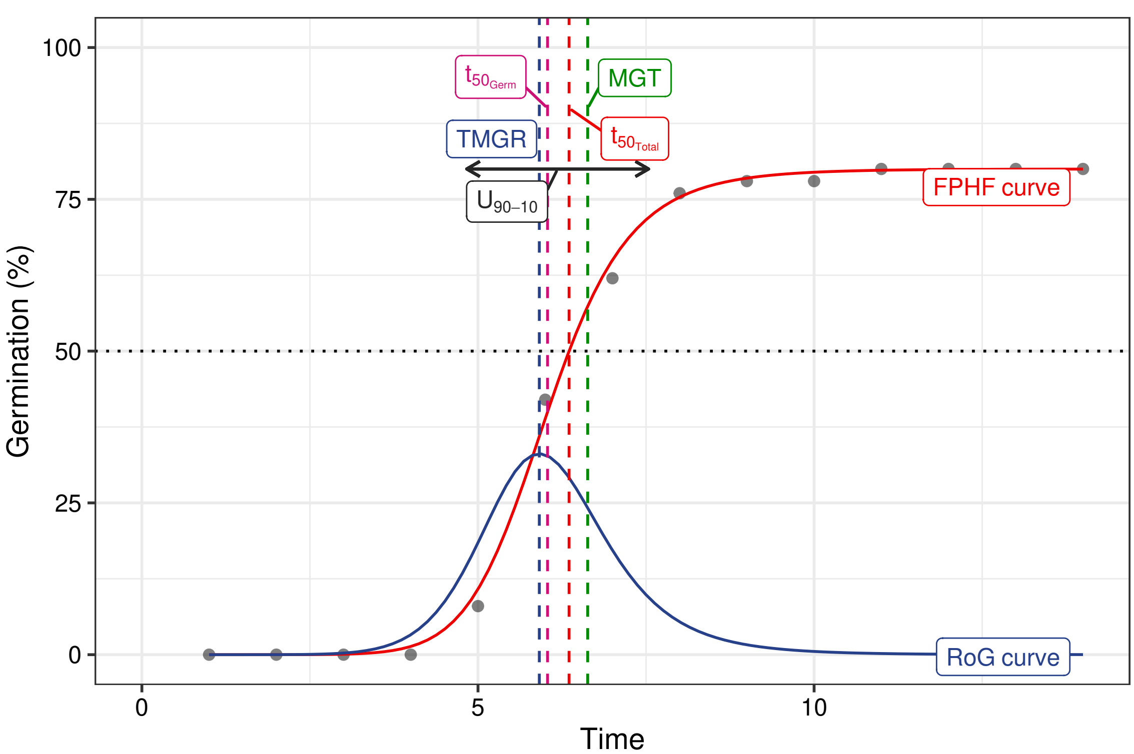
```
# From cumulative germination counts
#----------------------------------------------------------------------------
FourPHFfit(germ.counts = y, intervals = int, total.seeds = 50, tmax = 20,
           partial = FALSE)
```

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

$Parameters
  term estimate  std.error statistic      p.value
1  bta 2.290709 0.05602634  40.88628 2.965932e-14
2    c 6.034954 0.03872162 155.85488 3.270090e-21

$Fit
    sigma isConv       finTol    logLik      AIC      BIC deviance df.residual
1 1.61522   TRUE 2.884804e-12 -25.49868 56.99736 58.91453 31.30723          12
  nobs
1   14

$a
[1] 80

$b
[1] 9.881937

$c
[1] 6.034954

$y0
[1] 0

$lag
[1] 0

$Dlag50
[1] 6.034954

$t50.total
[1] 6.355121
```

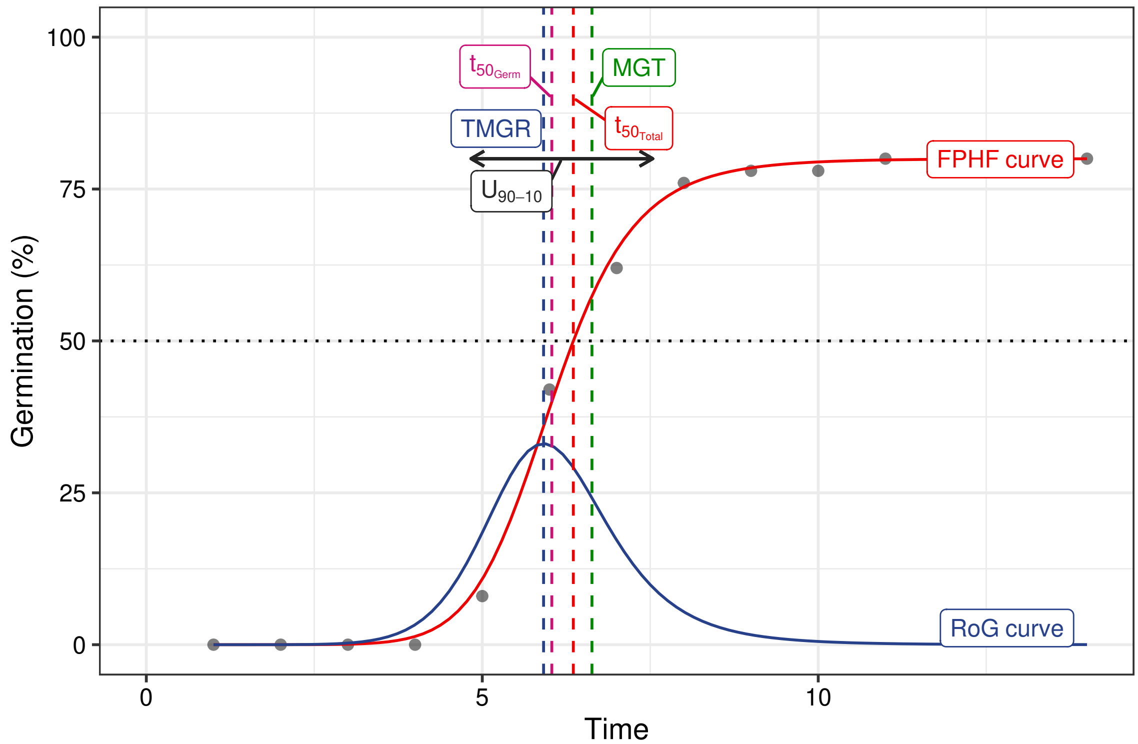
```
$txp.total
      10       60 
4.956264 6.744598 

$t50.Germinated
[1] 6.034954

$txp.Germinated
      10       60 
4.831807 6.287724 

$Uniformity
        90         10 uniformity 
  7.537690   4.831807   2.705882 

$TMGR
[1] 5.912194

$AUC
[1] 1108.976

$MGT
[1] 6.632252

$Skewness
[1] 1.098973

$msg
[1] "#1. success "

$isConv
[1] TRUE

$model
Nonlinear regression model
  model: csgp ~ FourPHF_fixa_fixy0(x = intervals, a = max(csgp), bta,      c)
   data: df
  bta     c 
2.291 6.035 
 residual sum-of-squares: 31.31

Algorithm: multifit/levenberg-marquardt, (scaling: levenberg, solver: qr)

Number of iterations to convergence: 8 
Achieved convergence tolerance: 2.885e-12

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

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

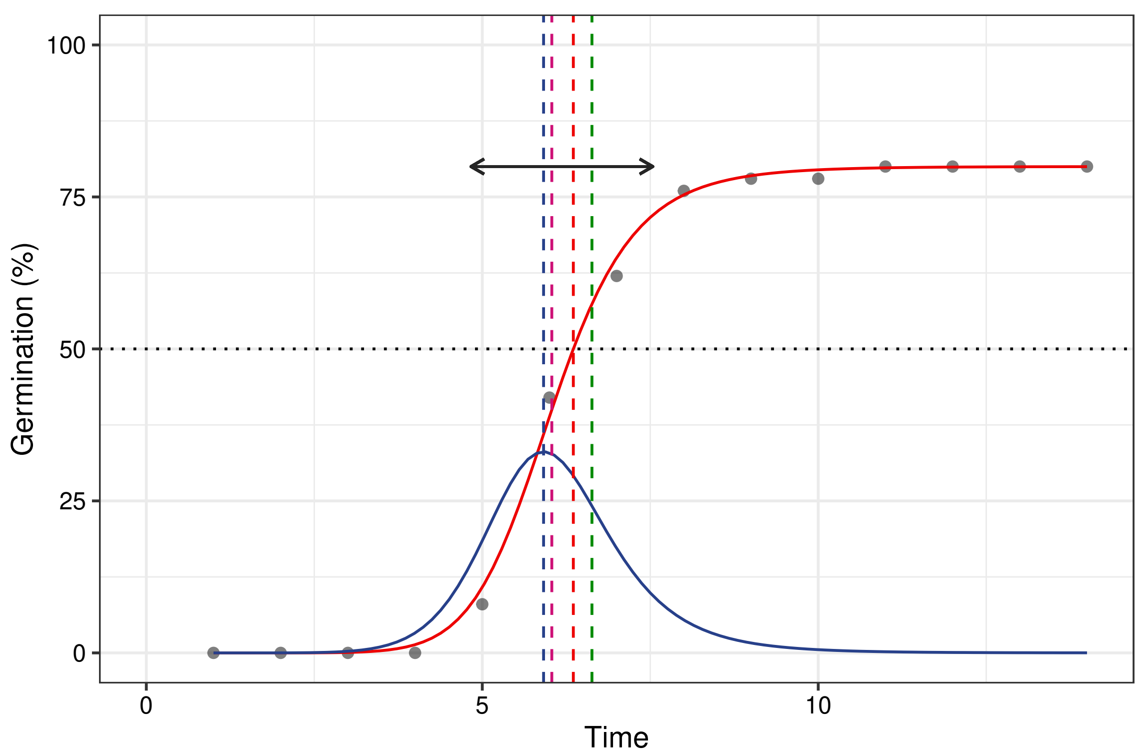
```
# From partial germination counts
#----------------------------------------------------------------------------
fit1 <- FourPHFfit(germ.counts = x, intervals = int,
                   total.seeds = 50, tmax = 20)

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

# Default plots
plot(fit1)
```



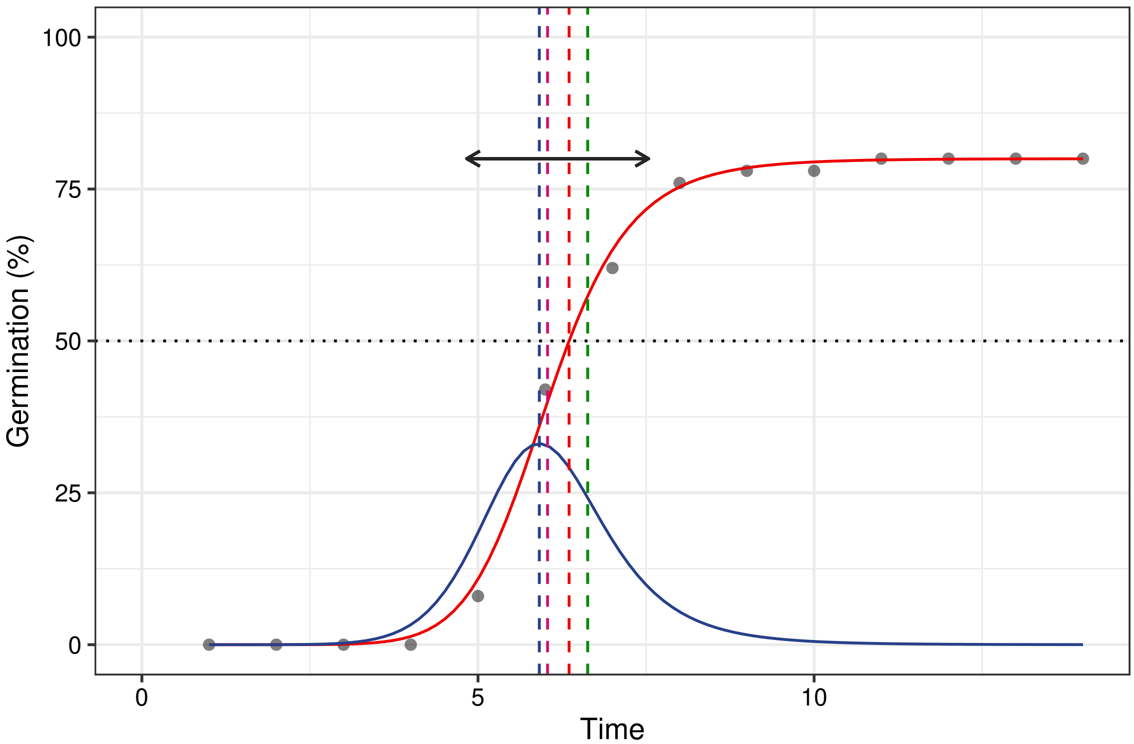

```
plot(fit2)
```



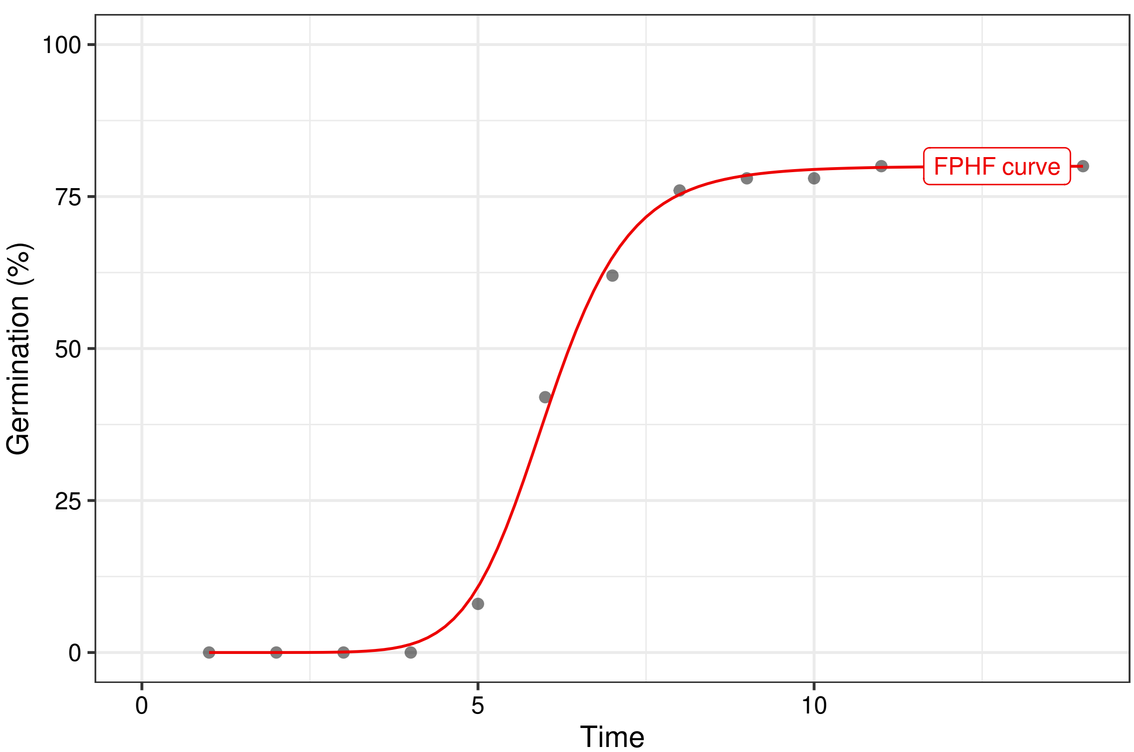

```
# No labels
plot(fit1, plotlabels = FALSE)
```



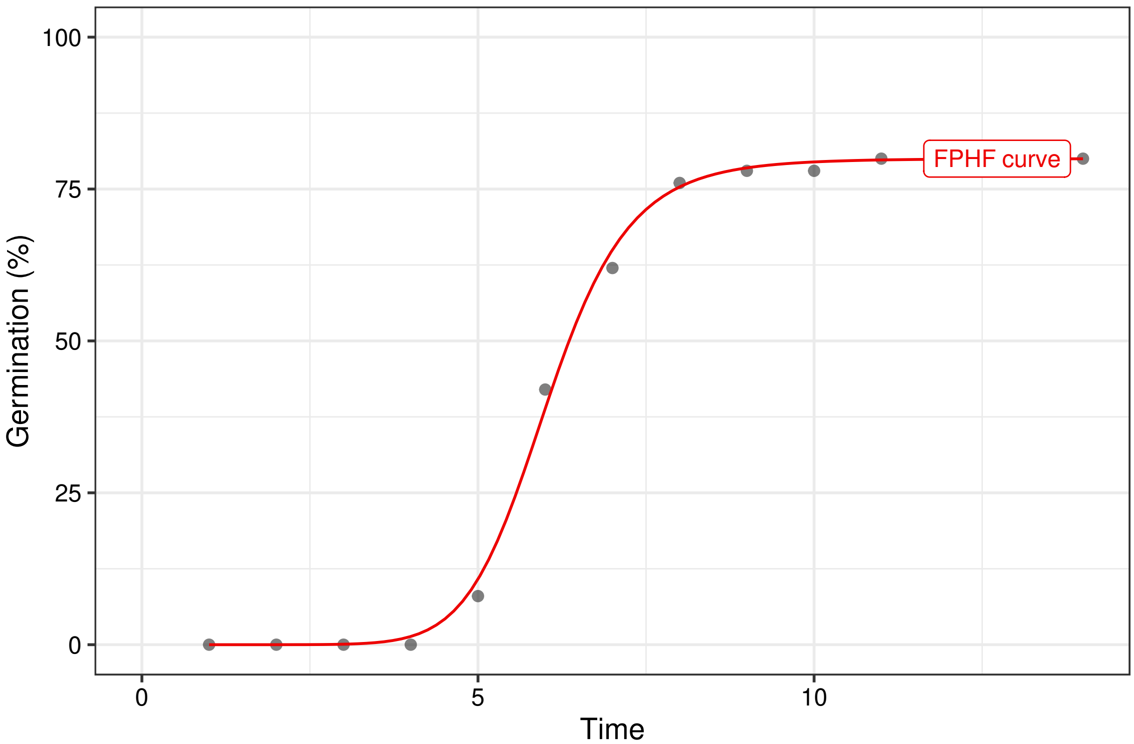

```
plot(fit2, plotlabels = FALSE)
```



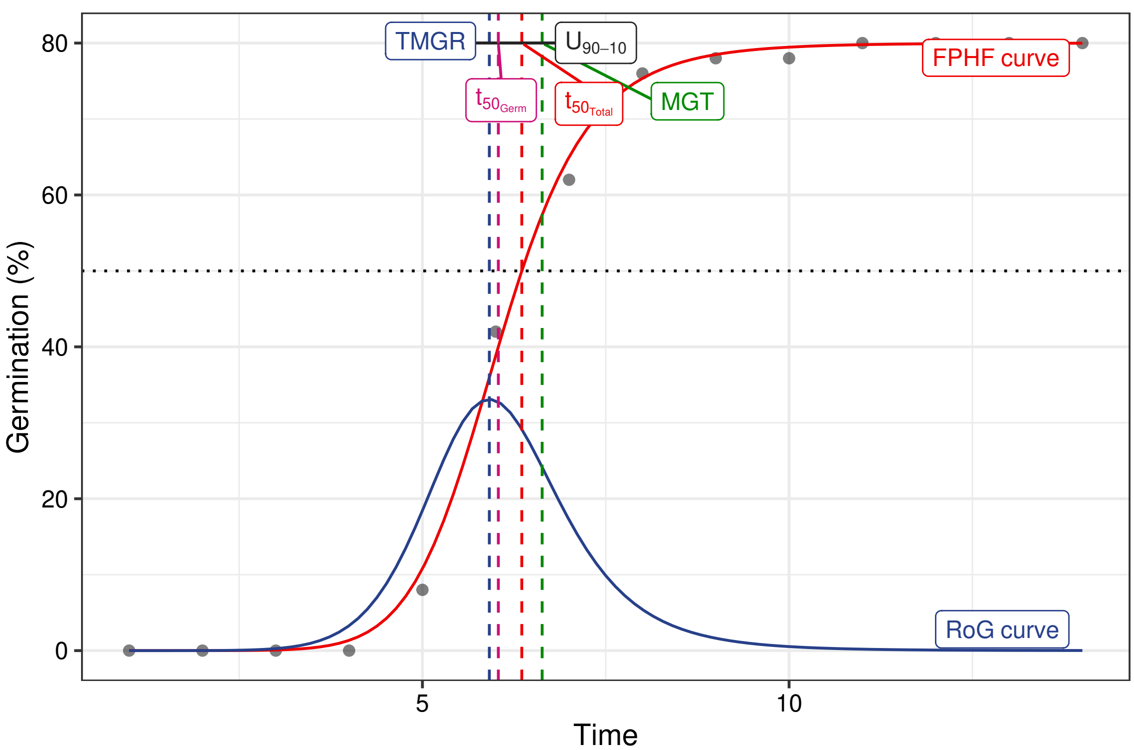

```
# Only the FPHF curve
plot(fit1, rog = FALSE, t50.total = FALSE, t50.germ = FALSE,
     tmgr = FALSE, mgt = FALSE, uniformity = FALSE)
```



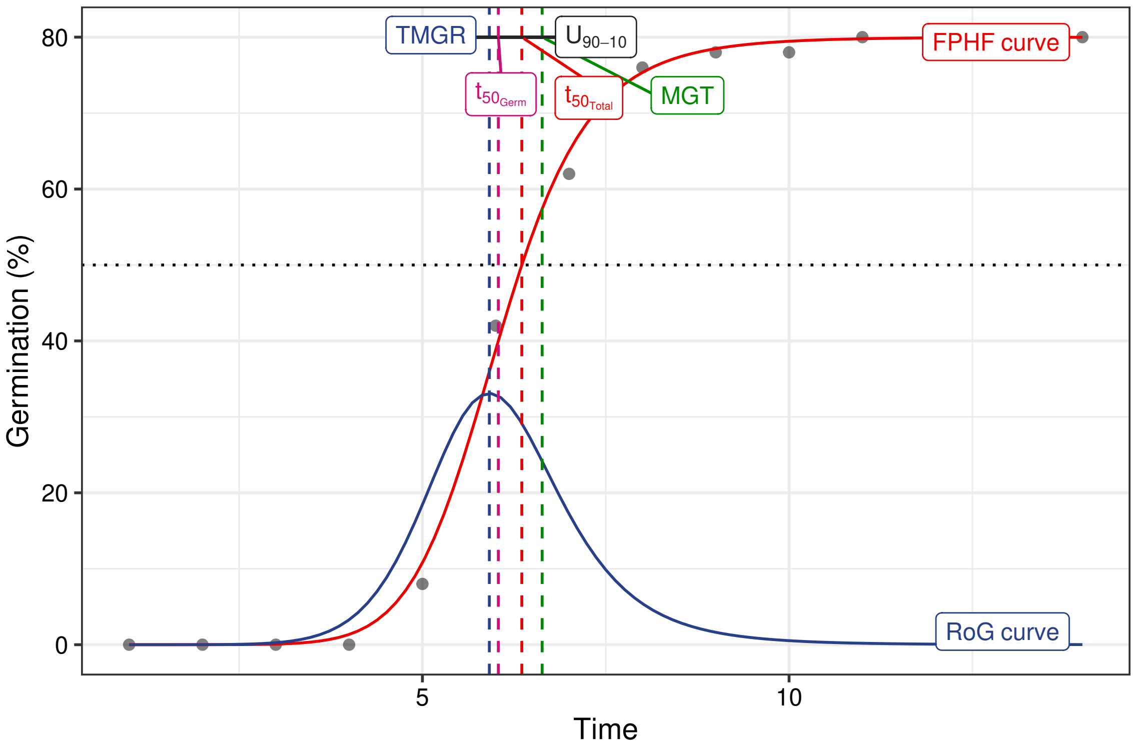

```
plot(fit2, rog = FALSE, t50.total = FALSE, t50.germ = FALSE,
     tmgr = FALSE, mgt = FALSE, uniformity = FALSE)
```




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




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



Wrapper functions

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

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

```
data(gcdata)

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

```
   Genotype Rep Day01 Day02 Day03 Day04 Day05 Day06 Day07 Day08 Day09 Day10
1        G1   1     0     0     0     0     4    17    10     7     1     0
2        G2   1     0     0     0     1     3    15    13     6     2     1
3        G3   1     0     0     0     2     3    18     9     8     2     1
4        G4   1     0     0     0     0     4    19    12     6     2     1
5        G5   1     0     0     0     0     5    20    12     8     1     0
6        G1   2     0     0     0     0     3    21    11     7     1     1
7        G2   2     0     0     0     0     4    18    11     7     1     0
8        G3   2     0     0     0     1     3    14    12     6     2     1
9        G4   2     0     0     0     1     3    19    10     8     1     1
10       G5   2     0     0     0     0     4    18    13     6     2     1
11       G1   3     0     0     0     0     5    21    11     8     1     0
```

```
12       G2   3     0     0     0     0     3    20    10     7     1     1
13       G3   3     0     0     0     0     4    19    12     8     1     1
14       G4   3     0     0     0     0     3    21    11     6     1     0
15       G5   3     0     0     0     0     4    17    10     8     1     1
   Day11 Day12 Day13 Day14 Total Seeds GermPercent PeakGermPercent
1      1     0     0     0          50    80.00000        34.00000
2      0     1     0     0          51    82.35294        29.41176
3      1     1     0     0          48    93.75000        37.50000
4      1     1     0     0          51    90.19608        37.25490
5      0     1     1     0          50    96.00000        40.00000
6      1     1     0     0          49    93.87755        42.85714
7      1     0     0     0          48    87.50000        37.50000
8      0     1     0     0          47    85.10638        29.78723
9      1     1     0     0          52    86.53846        36.53846
10     0     1     0     0          50    90.00000        36.00000
11     0     1     1     0          51    94.11765        41.17647
12     1     1     0     0          51    86.27451        39.21569
13     0     1     1     0          49    95.91837        38.77551
14     1     1     0     0          48    91.66667        43.75000
15     1     0     0     0          48    87.50000        35.41667
   FirstGermTime LastGermTime PeakGermTime TimeSpreadGerm t50_Coolbear
1              5           11            6              6     5.970588
2              4           12            6              8     6.192308
3              4           12            6              8     6.000000
4              5           12            6              7     6.041667
5              5           13            6              8     5.975000
6              5           12            6              7     5.976190
7              5           11            6              6     5.972222
8              4           12            6              8     6.208333
9              4           12            6              8     6.000000
10             5           12            6              7     6.076923
11             5           13            6              8     5.928571
12             5           12            6              7     5.975000
13             5           13            6              8     6.083333
14             5           12            6              7     5.928571
15             5           11            6              6     6.050000
   t50_Farooq MeanGermTime VarGermTime SEGermTime CVGermTime MeanGermRate
1    5.941176     6.700000    1.446154  0.1901416  0.1794868    0.1492537
2    6.153846     6.857143    2.027875  0.2197333  0.2076717    0.1458333
3    5.972222     6.866667    2.572727  0.2391061  0.2335882    0.1456311
4    6.000000     6.891304    2.187923  0.2180907  0.2146419    0.1451104
5    5.950000     6.812500    2.368351  0.2221275  0.2259002    0.1467890
6    5.952381     6.869565    2.071498  0.2122088  0.2095140    0.1455696
7    5.944444     6.690476    1.389663  0.1818989  0.1761967    0.1494662
8    6.166667     6.875000    2.112179  0.2297923  0.2113940    0.1454545
9    5.973684     6.866667    2.300000  0.2260777  0.2208604    0.1456311
10   6.038462     6.822222    1.831313  0.2017321  0.1983606    0.1465798
11   5.904762     6.791667    2.381206  0.2227295  0.2272072    0.1472393
12   5.950000     6.886364    2.149577  0.2210295  0.2129053    0.1452145
13   6.041667     6.936170    2.539315  0.2324392  0.2297410    0.1441718
14   5.904762     6.772727    1.900634  0.2078370  0.2035568    0.1476510
15   6.000000     6.809524    1.670151  0.1994129  0.1897847    0.1468531
    VarGermRate  SEGermRate      CVG GermRateRecip_Coolbear
1  0.0007176543 0.004235724 14.92537              0.1674877
```

```
2  0.0009172090 0.004673148 14.58333            0.1614907
3  0.0011572039 0.005071059 14.56311            0.1666667
4  0.0009701218 0.004592342 14.51104            0.1655172
5  0.0010995627 0.004786184 14.67890            0.1673640
6  0.0009301809 0.004496813 14.55696            0.1673307
7  0.0006935558 0.004063648 14.94662            0.1674419
8  0.0009454531 0.004861721 14.54545            0.1610738
9  0.0010345321 0.004794747 14.56311            0.1666667
10 0.0008453940 0.004334343 14.65798            0.1645570
11 0.0011191581 0.004828643 14.72393            0.1686747
12 0.0009558577 0.004660905 14.52145            0.1673640
13 0.0010970785 0.004831366 14.41718            0.1643836
14 0.0009033254 0.004531018 14.76510            0.1686747
15 0.0007767634 0.004300508 14.68531            0.1652893
   GermRateRecip_Farooq GermSpeed_Count GermSpeed_Percent
1             0.1683168        6.138925          12.27785
2             0.1625000        6.362698          12.47588
3             0.1674419        6.882179          14.33787
4             0.1666667        6.927417          13.58317
5             0.1680672        7.318987          14.63797
6             0.1680000        6.931782          14.14649
7             0.1682243        6.448449          13.43427
8             0.1621622        6.053175          12.87909
9             0.1674009        6.830592          13.13575
10            0.1656051        6.812698          13.62540
11            0.1693548        7.342796          14.39764
12            0.1680672        6.622258          12.98482
13            0.1655172        7.052320          14.39249
14            0.1693548        6.706782          13.97246
15            0.1666667        6.363925          13.25818
   GermSpeedAccumulated_Count GermSpeedAccumulated_Percent
1                    34.61567                     69.23134
2                    35.54058                     69.68741
3                    38.29725                     79.78594
4                    38.68453                     75.85202
5                    41.00786                     82.01571
6                    38.77620                     79.13509
7                    36.38546                     75.80304
8                    33.77079                     71.85275
9                    38.11511                     73.29829
10                   38.19527                     76.39054
11                   41.17452                     80.73436
12                   37.00640                     72.56158
13                   39.29399                     80.19182
14                   37.69490                     78.53103
15                   35.69697                     74.36868
   GermSpeedCorrected_Normal GermSpeedCorrected_Accumulated WeightGermPercent
1                  0.1534731                      0.8653917          47.42857
2                  0.1514928                      0.8462043          47.89916
3                  0.1529373                      0.8510501          54.46429
4                  0.1505960                      0.8409680          52.24090
5                  0.1524789                      0.8543303          56.14286
6                  0.1506909                      0.8429608          54.51895
7                  0.1535345                      0.8663205          51.93452
```

```
8                 0.1513294                     0.8442698          49.39210
9                 0.1517909                     0.8470024          50.27473
10                0.1513933                     0.8487837          52.57143
11                0.1529749                     0.8578026          55.18207
12                0.1505059                     0.8410547          50.00000
13                0.1500494                     0.8360424          55.24781
14                0.1524269                     0.8567022          53.86905
15                0.1515220                     0.8499278          51.19048
   MeanGermPercent MeanGermNumber TimsonsIndex TimsonsIndex_Labouriau
1         5.714286       2.857143     8.000000                   1.00
2         5.882353       3.000000     9.803922                   1.25
3         6.696429       3.214286    14.583333                   1.40
4         6.442577       3.285714     7.843137                   1.00
5         6.857143       3.428571    10.000000                   1.00
6         6.705539       3.285714     6.122449                   1.00
7         6.250000       3.000000     8.333333                   1.00
8         6.079027       2.857143    10.638298                   1.25
9         6.181319       3.214286     9.615385                   1.25
10        6.428571       3.214286     8.000000                   1.00
11        6.722689       3.428571     9.803922                   1.00
12        6.162465       3.142857     5.882353                   1.00
13        6.851312       3.357143     8.163265                   1.00
14        6.547619       3.142857     6.250000                   1.00
15        6.250000       3.000000     8.333333                   1.00
   TimsonsIndex_KhanUngar GermRateGeorge GermIndex GermIndex_mod
1               0.5714286              4  5.840000      7.300000
2               0.7002801              5  5.882353      7.142857
3               1.0416667              7  6.687500      7.133333
4               0.5602241              4  6.411765      7.108696
5               0.7142857              5  6.900000      7.187500
6               0.4373178              3  6.693878      7.130435
7               0.5952381              4  6.395833      7.309524
8               0.7598784              5  6.063830      7.125000
9               0.6868132              5  6.173077      7.133333
10              0.5714286              4  6.460000      7.177778
11              0.7002801              5  6.784314      7.208333
12              0.4201681              3  6.137255      7.113636
13              0.5830904              4  6.775510      7.063830
14              0.4464286              3  6.625000      7.227273
15              0.5952381              4  6.291667      7.190476
   EmergenceRateIndex_SG EmergenceRateIndex_SG_mod
1                    292                  7.300000
2                    300                  7.142857
3                    321                  7.133333
4                    327                  7.108696
5                    345                  7.187500
6                    328                  7.130435
7                    307                  7.309524
8                    285                  7.125000
9                    321                  7.133333
10                   323                  7.177778
11                   346                  7.208333
12                   313                  7.113636
13                   332                  7.063830
```

```
14                  318                  7.227273
15                  302                  7.190476
   EmergenceRateIndex_BilbroWanjura EmergenceRateIndex_Fakorede PeakValue
1                          5.970149                    8.375000  9.500000
2                          6.125000                    8.326531  9.313725
3                          6.553398                    7.324444 10.416667
4                          6.675079                    7.640359 10.049020
5                          7.045872                    7.096354 11.250000
6                          6.696203                    7.317580 10.714286
7                          6.277580                    7.646259 10.416667
8                          5.818182                    8.078125  9.574468
9                          6.553398                    7.934815  9.855769
10                         6.596091                    7.580247 10.250000
11                         7.067485                    7.216146 11.029412
12                         6.389439                    7.981921  9.803922
13                         6.776074                    7.231326 10.969388
14                         6.496644                    7.388430 10.677083
15                         6.167832                    7.782313 10.156250
   GermValue_Czabator GermValue_DP GermValue_Czabator_mod GermValue_DP_mod
1            54.28571     57.93890               54.28571         39.56076
2            54.78662     52.58713               54.78662         40.99260
3            69.75446     68.62289               69.75446         53.42809
4            64.74158     70.43331               64.74158         48.86825
5            77.14286     80.16914               77.14286         56.23935
6            71.84506     76.51983               71.84506         53.06435
7            65.10417     69.41325               65.10417         47.37690
8            58.20345     56.00669               58.20345         43.67948
9            60.92165     58.13477               60.92165         45.30801
10           65.89286     70.91875               65.89286         49.10820
11           74.14731     77.39782               74.14731         54.27520
12           60.41632     64.44988               60.41632         44.71582
13           75.15470     78.16335               75.15470         54.94192
14           69.90947     74.40140               69.90947         51.41913
15           63.47656     67.62031               63.47656         46.48043
      CUGerm GermSynchrony GermUncertainty
1  0.7092199     0.2666667        2.062987
2  0.5051546     0.2346109        2.321514
3  0.3975265     0.2242424        2.462012
4  0.4672113     0.2502415        2.279215
5  0.4312184     0.2606383        2.146051
6  0.4934701     0.2792271        2.160545
7  0.7371500     0.2729384        2.040796
8  0.4855842     0.2256410        2.357249
9  0.4446640     0.2494949        2.321080
10 0.5584666     0.2555556        2.187983
11 0.4288905     0.2686170        2.128670
12 0.4760266     0.2737844        2.185245
13 0.4023679     0.2506938        2.241181
14 0.5383760     0.2991543        2.037680
15 0.6133519     0.2497096        2.185028
```

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

```r
data(gcdata)

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

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

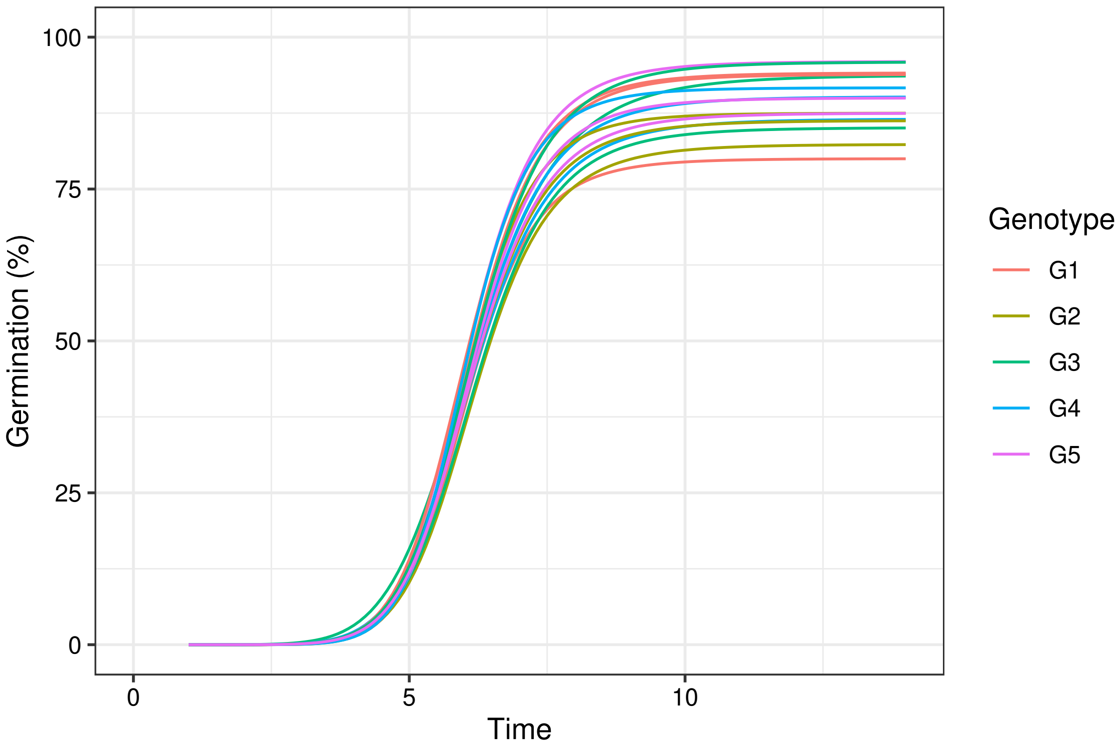
```
   Genotype Rep Day01 Day02 Day03 Day04 Day05 Day06 Day07 Day08 Day09 Day10
1        G1   1     0     0     0     0     4    17    10     7     1     0
2        G2   1     0     0     0     1     3    15    13     6     2     1
3        G3   1     0     0     0     2     3    18     9     8     2     1
4        G4   1     0     0     0     0     4    19    12     6     2     1
5        G5   1     0     0     0     0     5    20    12     8     1     0
6        G1   2     0     0     0     0     3    21    11     7     1     1
7        G2   2     0     0     0     0     4    18    11     7     1     0
8        G3   2     0     0     0     1     3    14    12     6     2     1
9        G4   2     0     0     0     1     3    19    10     8     1     1
10       G5   2     0     0     0     0     4    18    13     6     2     1
11       G1   3     0     0     0     0     5    21    11     8     1     0
12       G2   3     0     0     0     0     3    20    10     7     1     1
13       G3   3     0     0     0     0     4    19    12     8     1     1
14       G4   3     0     0     0     0     3    21    11     6     1     0
15       G5   3     0     0     0     0     4    17    10     8     1     1
   Day11 Day12 Day13 Day14 Total Seeds                a                b
1      1     0     0     0          50               80 9.88193689219798
2      0     1     0     0          51 82.3529411764706 9.22766646166019
3      1     1     0     0          48            93.75 7.79305097718417
4      1     1     0     0          51 90.1960784313725 8.92565503394839
5      0     1     1     0          50               96  9.4191816695981
6      1     1     0     0          49 93.8775510204082 9.45014900441008
7      1     0     0     0          48             87.5 10.1724586100529
8      0     1     0     0          47 85.1063829787234 8.94069602989349
9      1     1     0     0          52 86.5384615384615  8.6173913532163
10     0     1     0     0          50               90 9.60884373831177
11     0     1     1     0          51 94.1176470588235 9.40021183872586
12     1     1     0     0          51 86.2745098039216 9.16252658054406
13     0     1     1     0          49 95.9183673469388 8.99520960996306
14     1     1     0     0          48 91.6666666666667 10.3918447690499
15     1     0     0     0          48             87.5 9.13674439831543
                  c y0 lag           Dlag50        t50.total     txp.total_10
1  6.03495355423453  0   0 6.03495355423453  6.3551214973865 4.95626430994715
2  6.17519294911323  0   0 6.17519294911323 6.47349044022769 4.98323617967833
3  6.13811027378334  0   0 6.13811027378334 6.24419103019226 4.67302155573313
4  6.12517308176588  0   0 6.12517308176588 6.27679437746254 4.85087548237175
5  6.04964210720327  0   0 6.04964210720327 6.10343321091848 4.81412549010201
6   6.0974148527557  0   0  6.0974148527557 6.18227860798315 4.86863251633358
7  6.02985089631599  0   0 6.02985089631599 6.20281219696422 4.93042184740182
8  6.18977354961439  0   0 6.18977354961439 6.43951015764455 4.94005695310539
9  6.12512151399929  0   0 6.12512151399929 6.35217197764166 4.83665841861718
```

```
10 6.10950363596761  0    0 6.10950363596761  6.2530432080492 4.92062915320932
11 6.01875974061195  0    0 6.01875974061195 6.09943499335382 4.79862683383817
12  6.1084516820797  0    0  6.1084516820797 6.32618435705024 4.89359557090626
13 6.14901168717124  0    0 6.14901168717124 6.20750091190278 4.84130798420802
14 6.01591019490093  0    0 6.01591019490093 6.12238872875573 4.91514013437311
15 6.12157936163499  0    0 6.12157936163499 6.31739163301497 4.89250226946576
       txp.total_60   t50.Germinated txp.Germinated_10 txp.Germinated_60
1   6.7445983463311 6.03495355423453  4.83180737938015  6.28772357367537
2   6.8726033802361 6.17519294911323  4.86675518553144  6.45258151299607
3  6.60843809234118 6.13811027378334  4.63006208264611  6.46592435703346
4  6.61496814302537 6.12517308176588  4.78859693817119  6.40983765941072
5  6.38678874941426 6.04964210720327  4.79094574322756  6.31574586639992
6    6.477598609442  6.0974148527557  4.83247140825032  6.36472210276664
7     6.51049505523 6.02985089631599  4.85847638047658   6.2750496018235
8  6.82329908278267 6.18977354961439  4.84110536088622  6.47694540370958
9  6.73327569782723 6.12512151399929  4.74657350251934  6.42020821882777
10 6.56650619550494 6.10950363596761   4.8606813566304  6.37282341573569
11  6.3912906236839 6.01875974061195  4.76424552194859   6.2840509537431
12 6.68452626570581  6.1084516820797  4.80601279742022  6.38483647023757
13 6.50995386860368 6.14901168717124  4.81639291039067   6.4325242722081
14 6.39749098023249 6.01591019490093  4.86939775305615  6.25527610473983
15 6.66724718740801 6.12157936163499  4.81308335438754  6.39935718177504
      Uniformity_90    Uniformity_10       Uniformity             TMGR
1  7.53768963497883 4.83180737938015 2.70588225559868 5.91219440464896
2  7.83540706385743 4.86675518553144 2.96865187832599 6.03128155445793
3  8.13734180246507 4.63006208264611 3.50727971981896 5.93817948943725
4  7.83480960415051 4.78859693817119 3.04621266597932 5.97268622562109
5  7.63902819750811 4.79094574322756 2.84808245428055 5.91428884333636
6  7.69346877523834 4.83247140825032 2.86099736698802 5.96187868660636
7  7.48364280989593 4.85847638047658 2.62516642941935 5.91405695229978
8  7.91416293168472 4.84110536088622 3.07305757079851 6.03619216805867
9  7.90404141879274 4.74657350251934  3.1574679162734  5.9616310497804
10 7.67917745255724  4.8606813566304 2.81849609592684 5.97811533043387
11 7.60361082322955 4.76424552194859 2.83936530128096 5.88355748786772
12 7.76385405638773 4.80601279742022 2.95784125896751  5.9640804983933
13 7.85034473566269 4.81639291039067 3.03395182527202 5.99827012362062
14  7.4323719910534 4.86939775305615 2.56297423799725  5.9051804897395
15 7.78580612916975 4.81308335438754 2.97272277478221 5.97608676470078
                AUC              MGT         Skewness          msg
1  1108.97550938733 6.63225196627282 1.09897315806502 #1. success
2  1128.55880085138 6.78440735679779 1.09865512101481 #1. success
3  1283.69307344081 6.77274232830874 1.10339209076057 #1. success
4  1239.88674124826 6.73966592721389 1.10032252758331 #1. success
5  1328.32820017628 6.65498075748102 1.10006189449736 #1. success
6  1294.46271441017 6.70247312632466 1.09923193487409 #1. success
7  1213.90764565674 6.62241708548249 1.09827211308468 #1. success
8  1164.34586106316 6.80400021213917 1.09923249333783 #1. success
9  1188.79304149759  6.7452410863068 1.10124200326315 #1. success
10 1240.22733172402 6.71189998824877 1.09859988440546 #1. success
11 1305.20007906005 6.62424817630914 1.10060020033889 #1. success
12  1188.0211599463 6.71863893649018 1.09989229450739 #1. success
13 1316.40687308654 6.76227360530894 1.09973341234936 #1. success
14 1273.38526597411  6.6049667882059 1.09791645390655 #1. success
15 1203.66421628837 6.73226579042194 1.09975961965212 #1. success
```

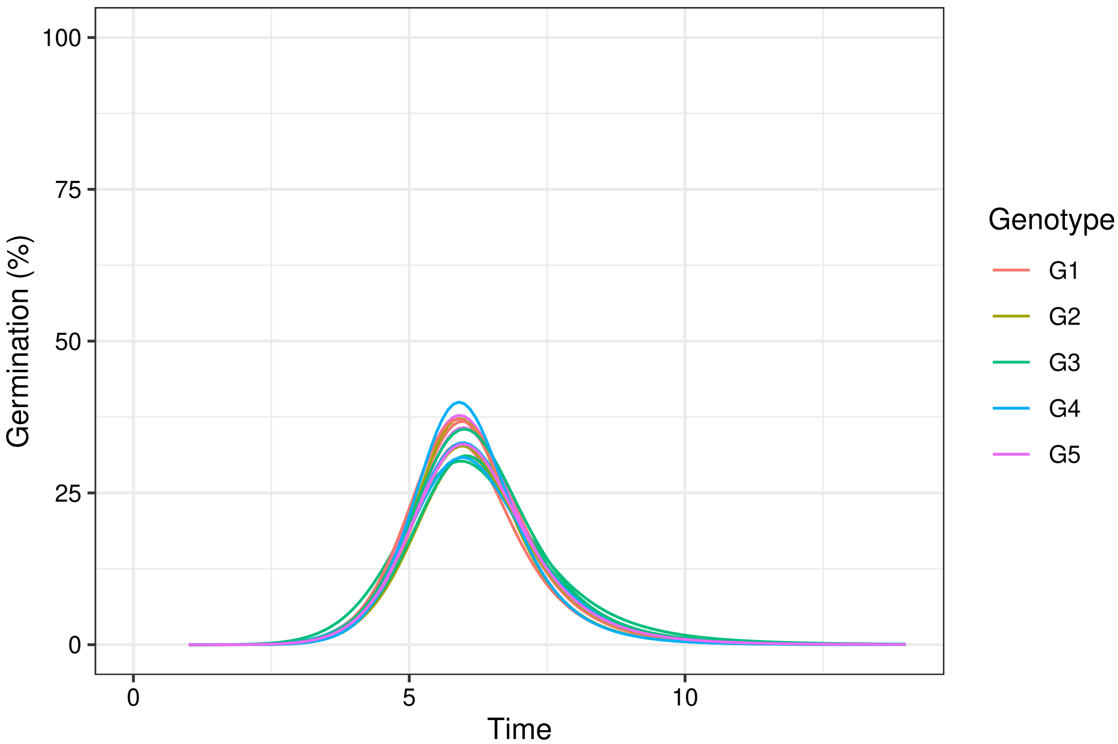
```
          Fit_sigma Fit_isConv           Fit_finTol        Fit_logLik
1  1.61522002910957       TRUE 2.88480350718601e-12  -25.498681342686
2  1.11537185901124       TRUE 5.15498754793953e-12 -20.3147146781893
3  2.43270386985341       TRUE 8.43840552988695e-11 -31.2321314996742
4  2.39658164351394       TRUE 3.38218342221808e-12 -31.0226924019787
5  2.39966172990826       TRUE 6.74447164783487e-11 -31.0406736477542
6   3.0349622365097       TRUE 3.97619714931352e-11  -34.328870450832
7  1.66301938705135       TRUE 3.90798504668055e-12 -25.9069727183683
8  1.12070433595621       TRUE 4.32720526077901e-12 -20.3814877326307
9  2.42996010854989       TRUE 1.77209358298569e-11 -31.2163324798379
10 1.68665620116432       TRUE 8.14281975181075e-12 -26.1045565628368
11 2.62811272107047       TRUE 1.32729383039987e-11 -32.3138085946749
12 2.87814601795845       TRUE 3.51434437106946e-11 -33.5861335093548
13 2.60458797517776       TRUE 1.10560449684272e-11 -32.1879276469568
14 2.76475621724483       TRUE 9.80548975348938e-13  -33.023419198233
15 1.95400807212262       TRUE 8.73967564984923e-13 -28.1644422917083
            Fit_AIC          Fit_BIC     Fit_deviance Fit_df.residual Fit_nobs
1  56.9973626853719 58.9145346742177 31.3072289092405              12       14
2  46.6294293563786 48.5466013452244 14.9286526064903              12       14
3  68.4642629993484 70.3814349881942 71.0165774207971              12       14
4  68.0453848039574 69.9625567928032  68.923242888336              12       14
5  68.0813472955084 69.9985192843541 69.1005170158358              12       14
6  74.6577409016639 76.5749128905097 110.531949324479              12       14
7  57.8139454367367 59.7311174255824 33.1876017805038              12       14
8  46.7629754652615 48.6801474541073 15.0717385035725              12       14
9  68.4326649596759 70.3498369485217 70.8564735497253              12       14
10 58.2091131256735 60.1262851145193 34.1377096911127              12       14
11 70.6276171893498 72.5447891781956 82.8837176958294              12       14
12 73.1722670187096 75.0894390075554 99.4046940082808              12       14
13 70.3758552939135 72.2930272827593  81.406542245287              12       14
14  72.046838396466 73.9640103853118  91.726523289527              12       14
15 62.3288845834165 64.2460565722623 45.8177705510444              12       14
```

Multiple fitted curves generated in batch can also be plotted.

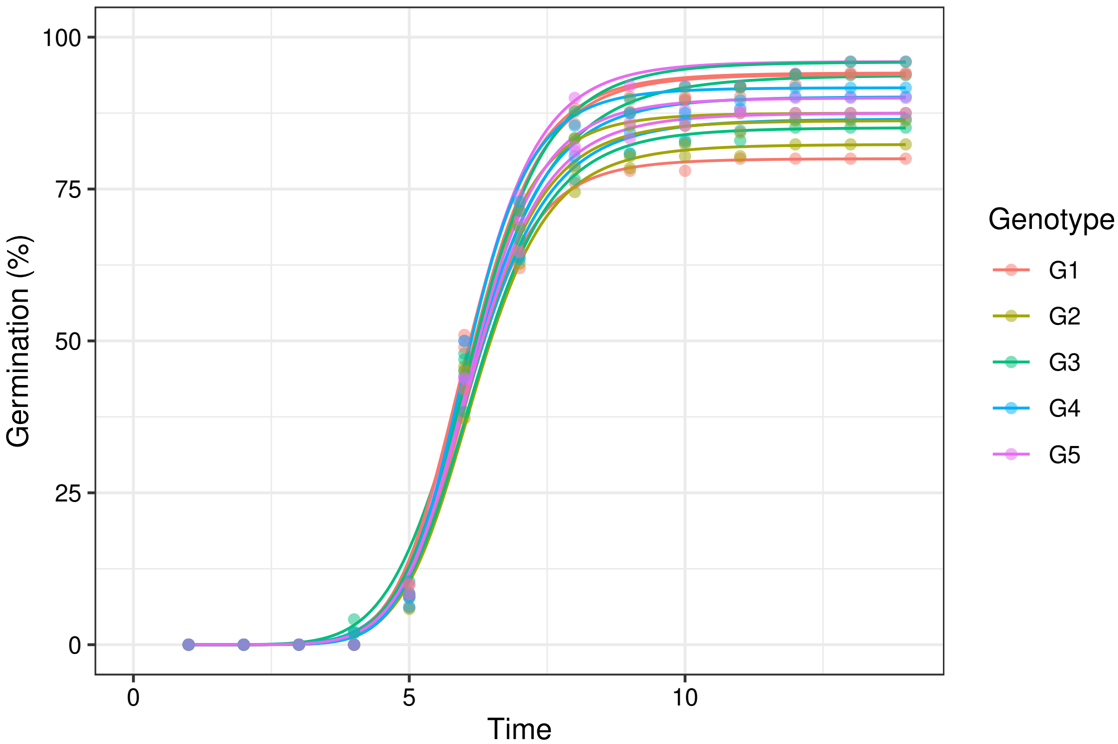
```r
data(gcdata)

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)

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



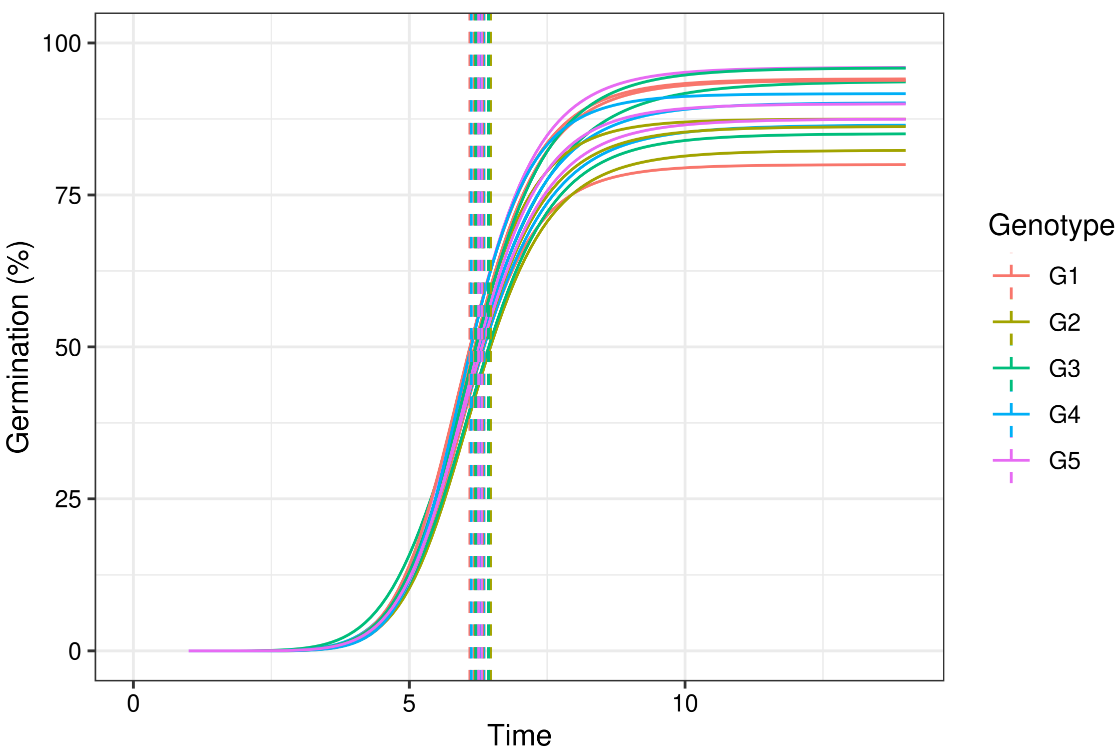

```r
# Plot ROG curves
plot(fits, rog = TRUE, group.col = "Genotype")
```



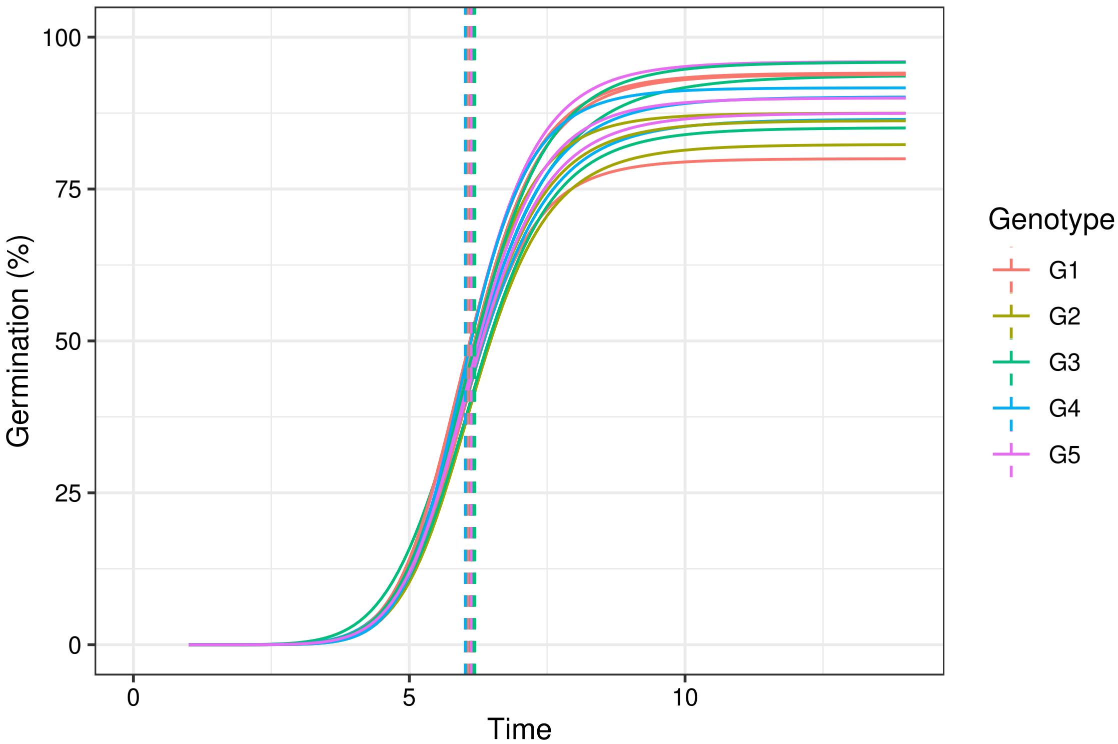

```r
# Plot FPHF curves with points
plot(fits, group.col = "Genotype", show.points = TRUE)
```



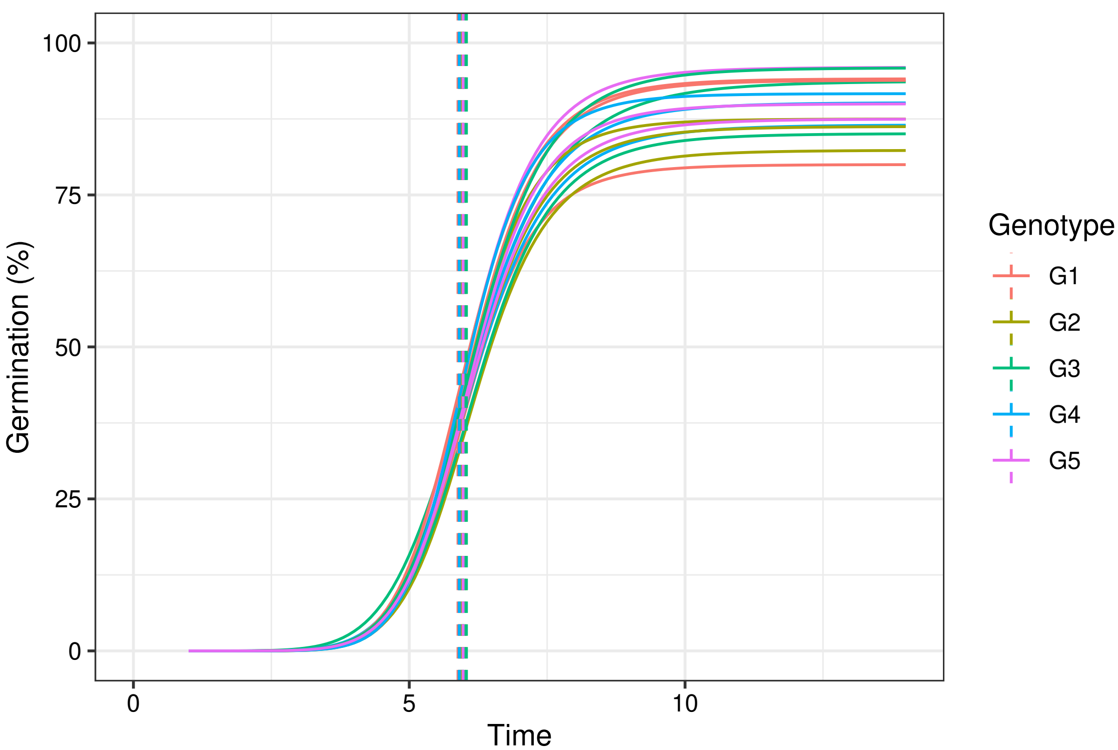

```r
# Plot FPHF curves with annotations
plot(fits, group.col = "Genotype", annotate = "t50.total")
```



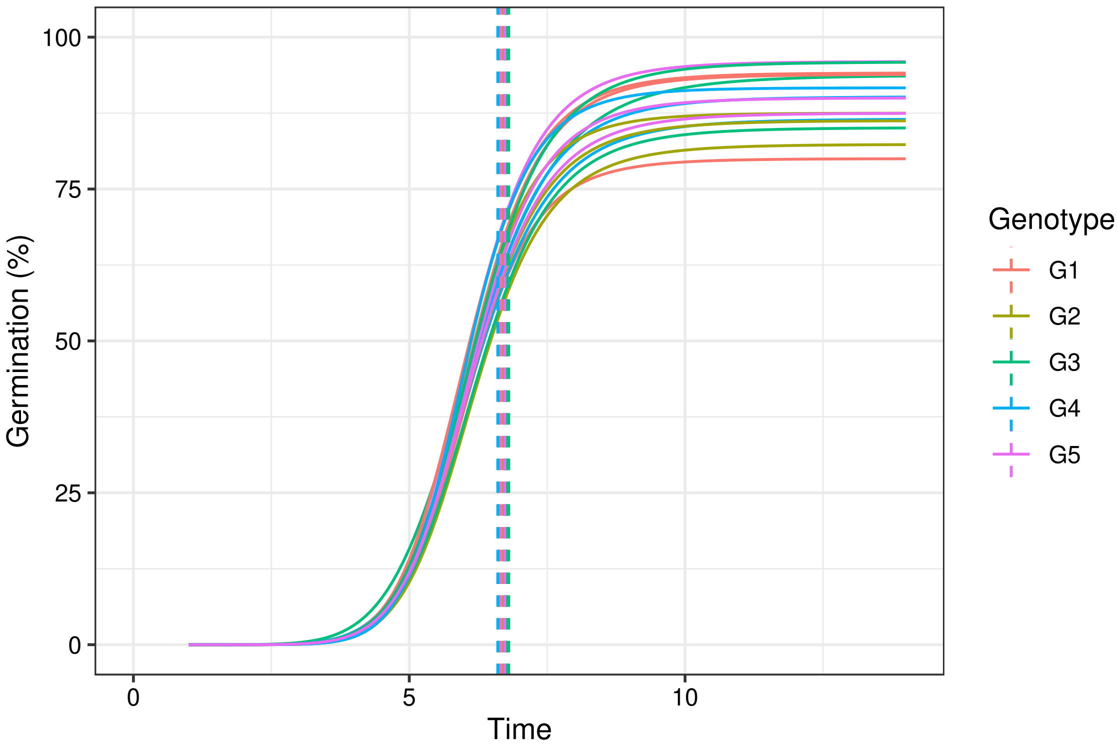

```r
plot(fits, group.col = "Genotype", annotate = "t50.germ")
```




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

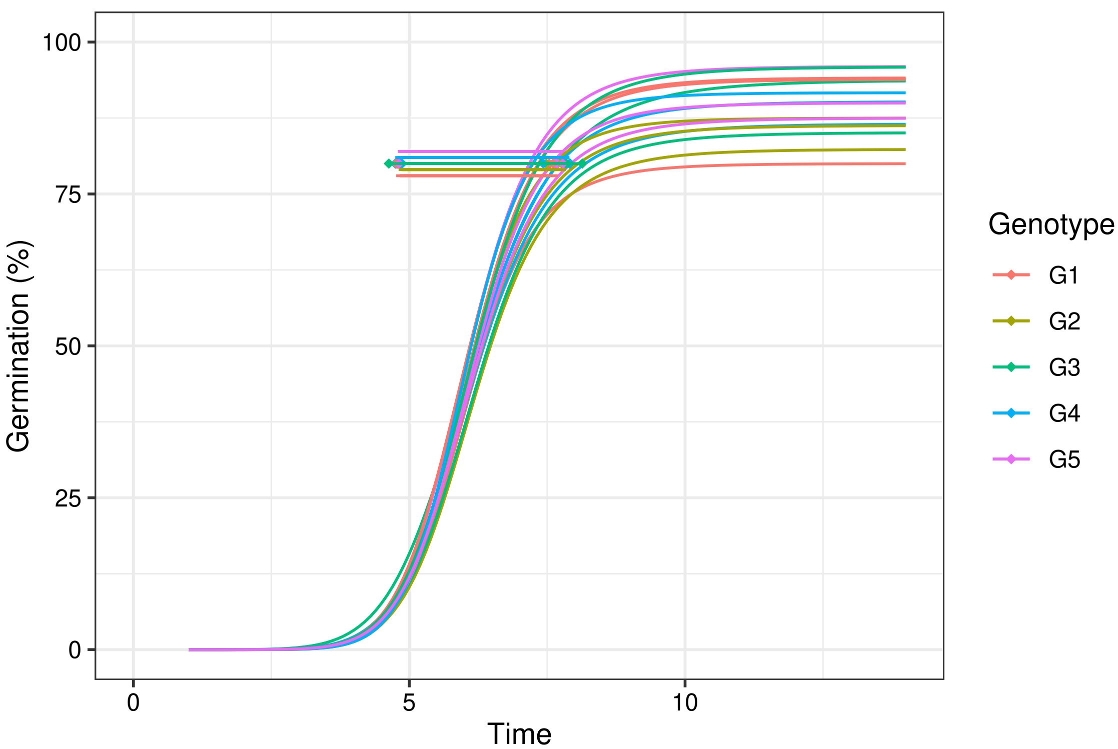



```r
plot(fits, group.col = "Genotype", annotate = "mgt")
```

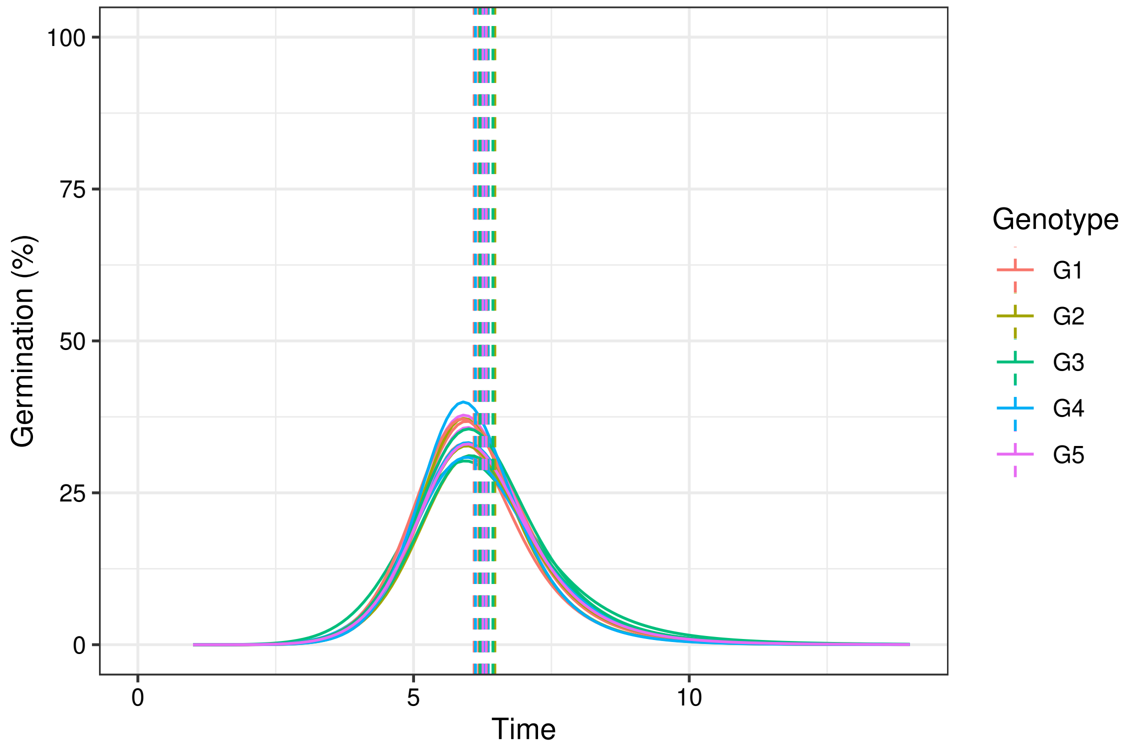



```r
plot(fits, group.col = "Genotype", annotate = "uniformity")
```

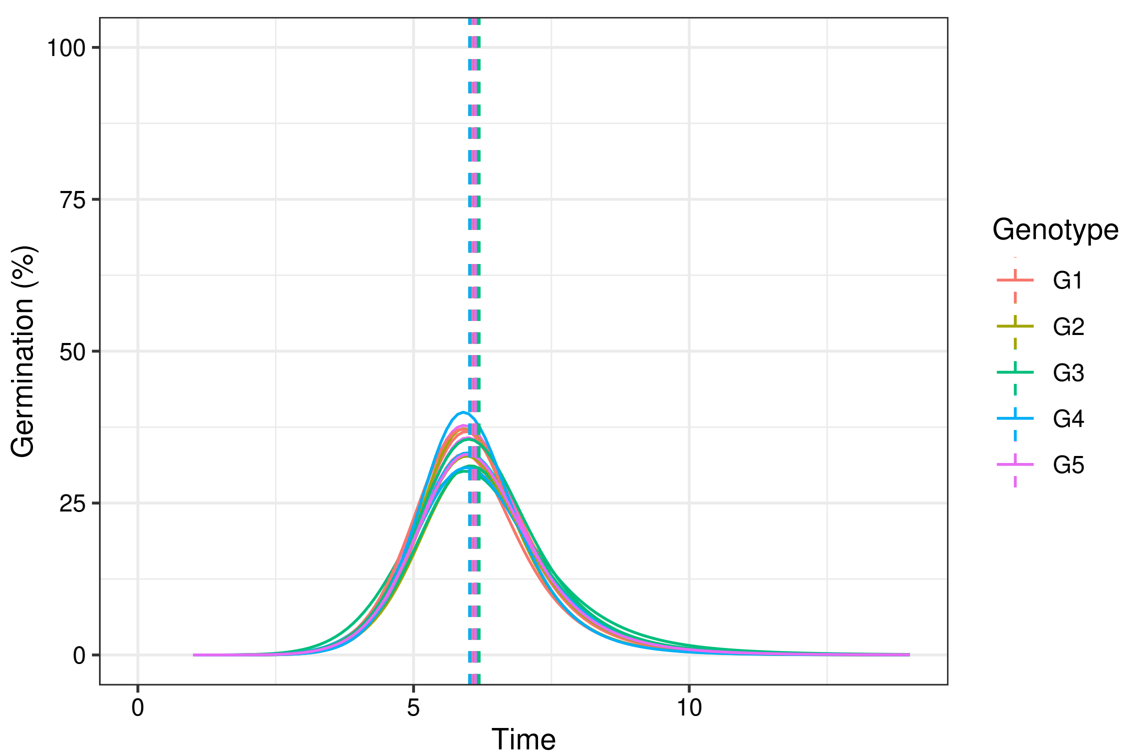
```
Warning: `position_dodge()` requires non-overlapping x intervals
`position_dodge()` requires non-overlapping x intervals
```



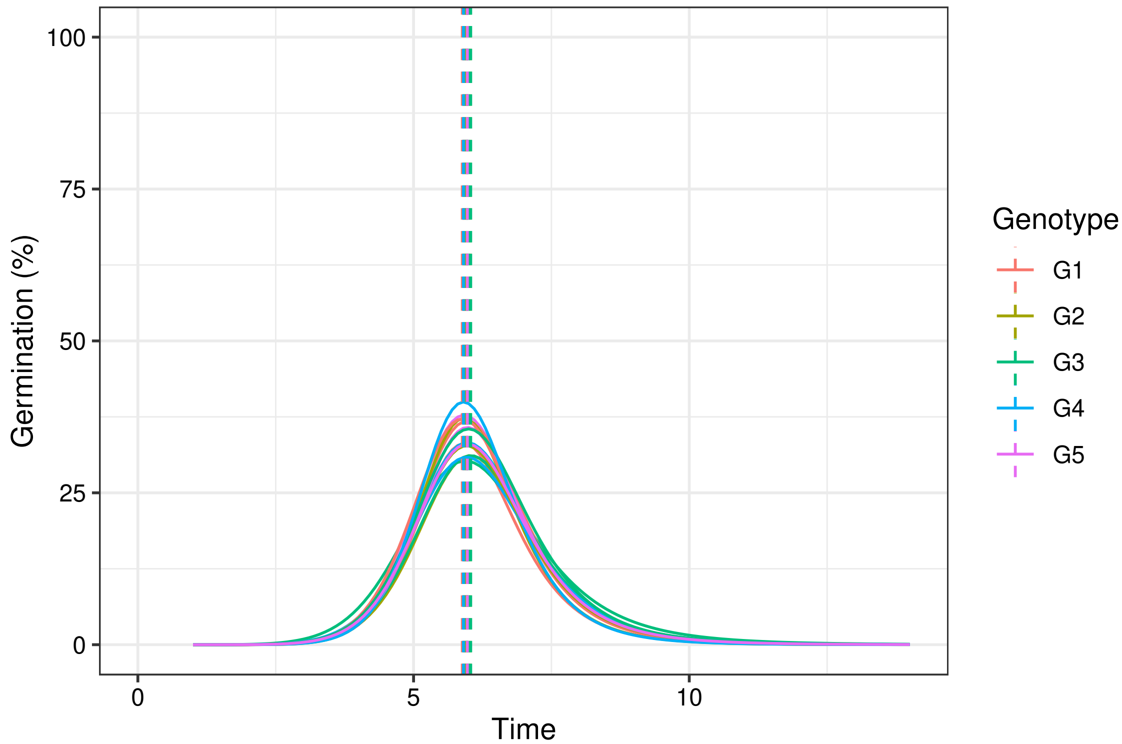

```r
# Plot ROG curves with annotations
plot(fits, rog = TRUE, group.col = "Genotype", annotate = "t50.total")
```



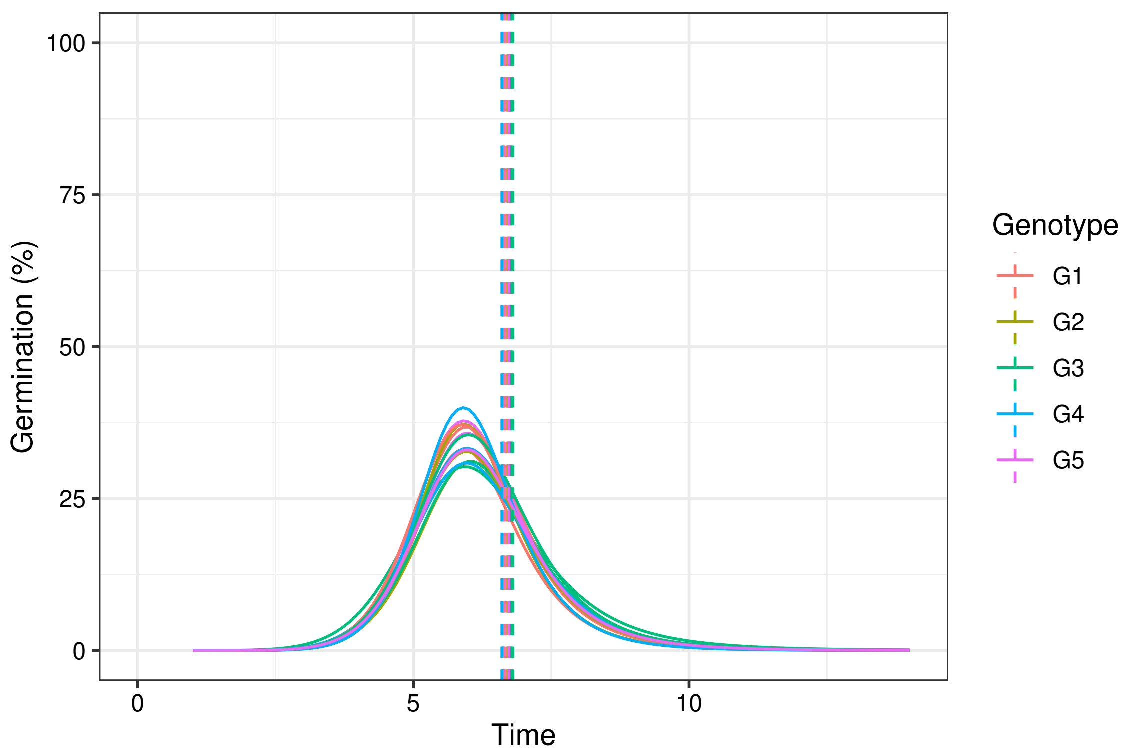

```
plot(fits, rog = TRUE, group.col = "Genotype", annotate = "t50.germ")
```




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

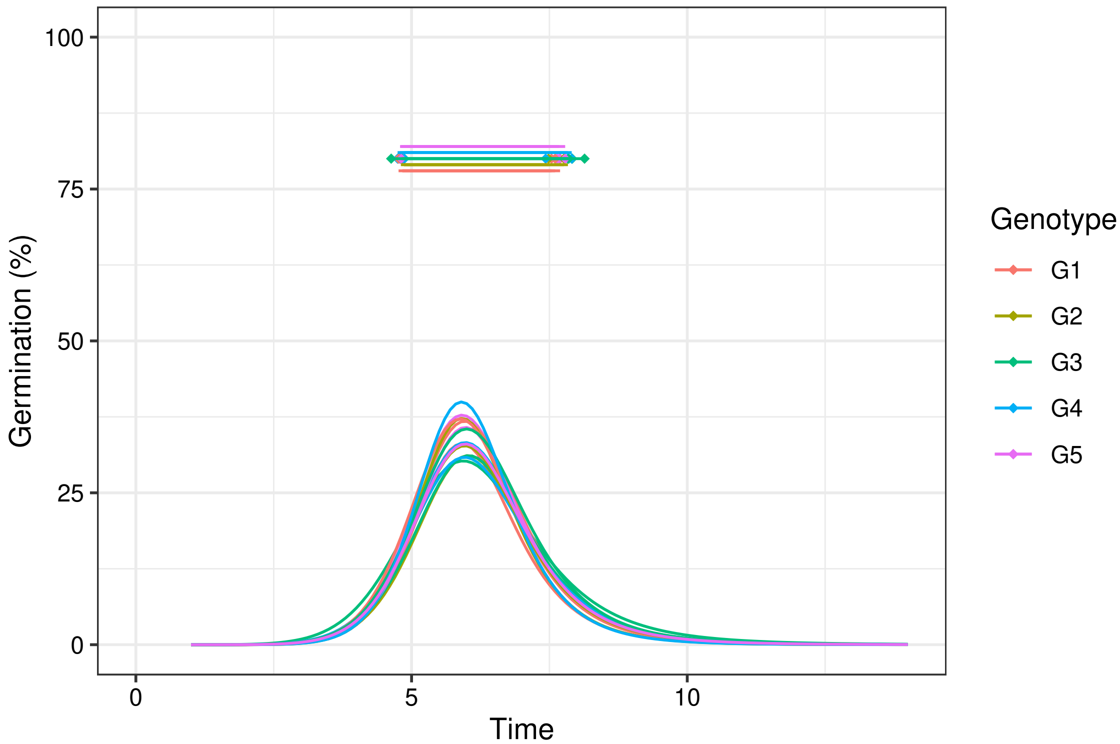



```
plot(fits, rog = TRUE, group.col = "Genotype", annotate = "mgt")
```

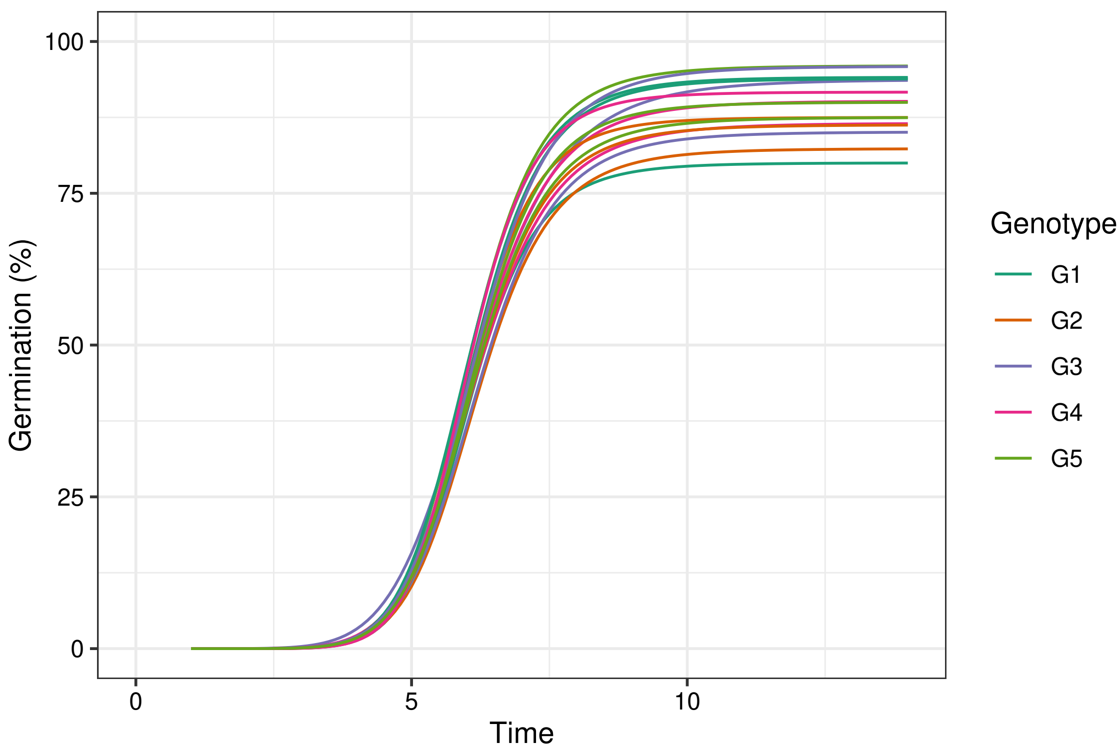



```
plot(fits, rog = TRUE, group.col = "Genotype", annotate = "uniformity")
```

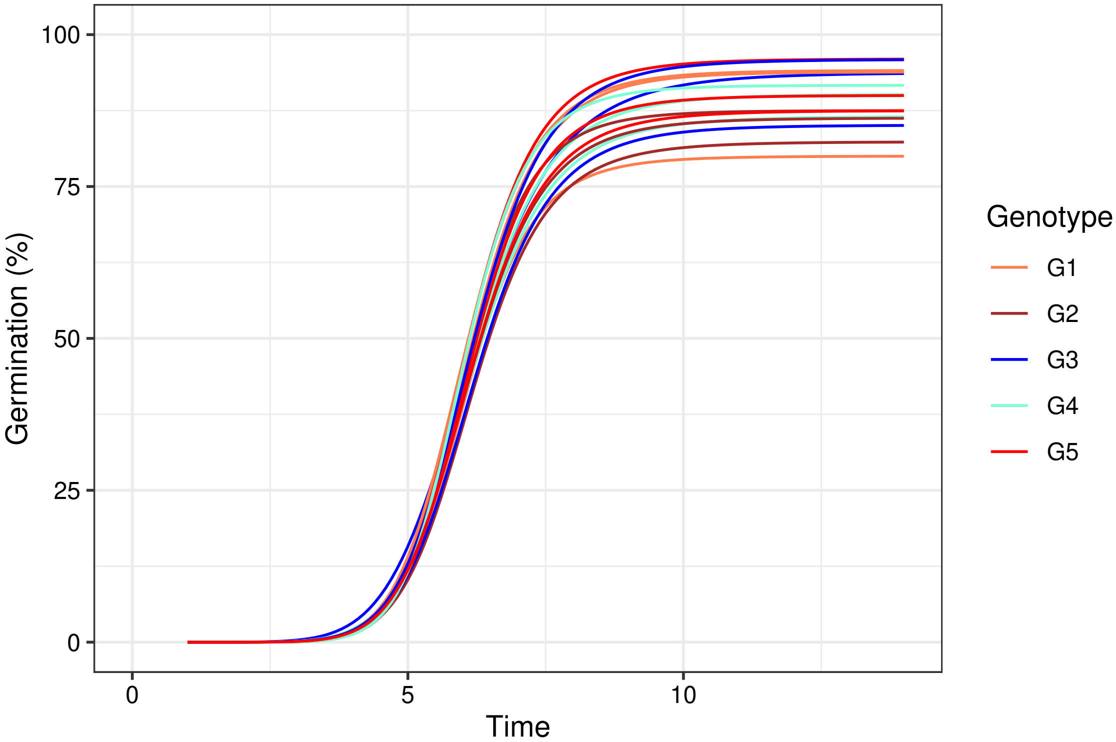
```
Warning: `position_dodge()` requires non-overlapping x intervals
`position_dodge()` requires non-overlapping x intervals
```




```
# 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")
```



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



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 0.1.8,
  https://github.com/aravind-j/germinationmetricshttps://cran.r-project.org/package=germinationmetrics.

A BibTeX entry for LaTeX users is

  @Manual{,
    title = {germinationmetrics: Seed Germination Indices and Curve Fitting},
    author = {J. Aravind and S. {Vimala Devi} and J. Radhamani and Sherry Rachel Jacob and {Kalyani Sri
    note = {R package version 0.1.8 https://aravind-j.github.io/germinationmetrics/ https://CRAN.R-proj
  }

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

Session Info

```r
sessionInfo()
```

```
R Under development (unstable) (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=C                   LC_CTYPE=English_India.utf8
[3] LC_MONETARY=English_India.utf8 LC_NUMERIC=C
[5] 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_0.1.8 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
 [5] stringi_1.7.12     lattice_0.21-8     digest_0.6.33      magrittr_2.0.3
 [9] RColorBrewer_1.1-3 evaluate_0.21      grid_4.4.0         fastmap_1.1.1
[13] plyr_1.8.8         Matrix_1.6-0       ggrepel_0.9.3      backports_1.4.1
[17] tinytex_0.46       httr_1.4.6         purrr_1.0.1        fansi_1.0.4
[21] pander_0.6.5       scales_1.2.1       XML_3.99-0.14      Rdpack_2.4
[25] cli_3.6.1          rlang_1.1.1        rbibutils_2.2.14   munsell_0.5.0
[29] withr_2.5.0        yaml_2.3.7         tools_4.4.0        reshape2_1.4.4
[33] dplyr_1.1.2        colorspace_2.1-0   mathjaxr_1.6-0     broom_1.0.5
[37] curl_5.0.1         vctrs_0.6.3        R6_2.5.1           lifecycle_1.0.3
[41] gslnls_1.1.2       stringr_1.5.0      pkgconfig_2.0.3    pillar_1.9.0
[45] gtable_0.3.3       data.table_1.14.8  glue_1.6.2         Rcpp_1.0.11
[49] xfun_0.40          tibble_3.2.1       tidyselect_1.2.0   highr_0.10
[53] rstudioapi_0.15.0  knitr_1.43         farver_2.1.1       htmltools_0.5.5
[57] labeling_0.4.2     rmarkdown_2.23     compiler_4.4.0     RCurl_1.98-1.12
```

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