The `germinationmetrics` Package: A Brief Introduction

Aravind, J., Vimala Devi, S., Radhamani, J., Jacob, S. R., and Kalyani Srinivasan

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ICAR-National Bureau of Plant Genetic Resources, New Delhi.

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 0.1.5.9000


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

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

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

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

Version History

The current version of the package is 0.1.5.9000. 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

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

Germination count data

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

**Table 2 :** A typical germination count data.

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

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

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

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

plot(int, cumsum(x))
```
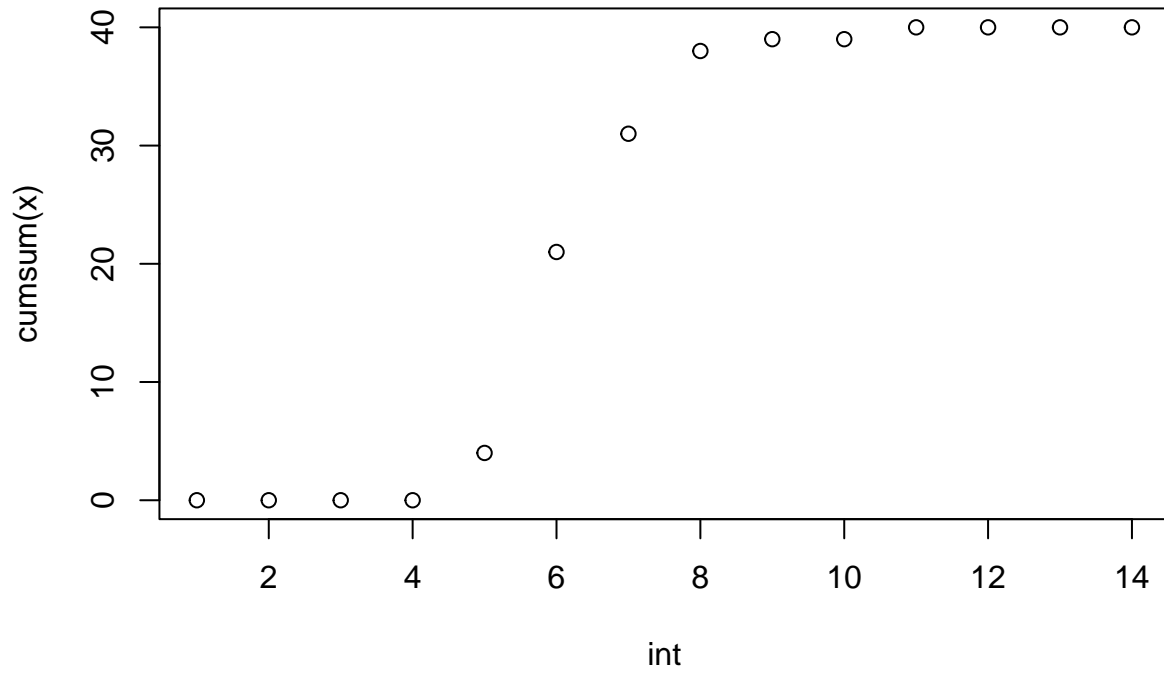
Single-value germination indices

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

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

Germination index	Function	Details	Unit	Measures	Reference
Germination percentage or Final germination percentage or Germinability (GP)	`GermPercent`	It is computed as follows. $$GP = \frac{N_g}{N_t} \times 100$$ Where, N_g is the number of germinated seeds and N_t is the total number of seeds.	Percentage (%)	Germination capacity	ISTA (2015)
Peak germination percentage (PGP)	`PeakGermPercent`	It is computed as follows. $$PGP = \frac{N_{max}}{N_t} \times 100$$ Where, N_{max} is the maximum number of seeds germinated per interval.	Percentage (%)	Germination capacity	Vallance (1950); Roh et al. (2004)
Time for the first germination or Germination time lag (t_0)	`FirstGermTime`	It is the time for first germination to occur (e.g. First day of germination). $$t_0 = \min\{T_i : N_i \neq 0\}$$ Where, T_i is the time from the start of the experiment to the ith interval and N_i is the number of seeds germinated in the ith time interval (not the accumulated number, but the number corresponding to the ith interval)	time	Germination time	Edwards (1932); Czabator (1962); Goloff and Bazzaz (1975); Labouriau (1983a); Ranal (1999); Quintanilla et al. (2000)
Time for the last germination (t_g)	`LastGermTime`	It is the time for last germination to occur (e.g. Last day of germination) $$t_g = \max\{T_i : N_i \neq 0\}$$ Where, T_i is the time from the start of the experiment to the ith interval and N_i is the number of seeds germinated in the ith time interval (not the accumulated number, but the number corresponding to the ith interval)	time	Germination time	Edwards (1932)
Time spread of germination or Germination distribution	`TimeSpreadGerm`	It is the difference between time for last germination (t_g) and time for first germination (t_0). $$Time\,spread\,of\,germination = t_g - t_0$$	time	Germination time	Al-Mudaris (1998); Schrader and Graves (2000); Kader (2005)
Peak period of germination or Modal time of germination (t_{peak})	`PeakGermTime`	It is the time in which highest frequency of germinated seeds are observed and need not be unique. $$t_{peak} = \{T_i : N_i = N_{max}\}$$ Where, T_i is the time from the start of the experiment to the ith interval, N_i is the number of seeds germinated in the ith time interval (not the accumulated number, but the number corresponding to the ith interval) and N_{max} is the maximum number of seeds germinated per interval.	time	Germination time	Ranal and Santana (2006)

Germination index	Function	Details	Unit	Measures	Reference
Median germination time (t_{50}) (Coolbear)	`t50`	It is the time to reach 50% of final/maximum germination. With argument `method` specified as `"coolbear"`, it is computed as follows. $$t_{50} = T_i + \frac{(\frac{N+1}{2} - N_i)(T_j - T_i)}{N_j - N_i}$$ Where, t_{50} is the median germination time, N is the final number of germinated seeds, and N_i and N_j are the total number of seeds germinated in adjacent counts at time T_i and T_j respectively, when $N_i < \frac{N+1}{2} < N_j$.	time	Germination time	Coolbear et al. (1984)
Median germination time (t_{50}) (Farooq)	`t50`	With argument `method` specified as `"farooq"`, it is computed as follows. $$t_{50} = T_i + \frac{(\frac{N}{2} - N_i)(T_j - T_i)}{N_j - N_i}$$ Where, t_{50} is the median germination time, N is the final number of germinated seeds, and N_i and N_j are the total number of seeds germinated in adjacent counts at time T_i and T_j respectively, when $N_i < \frac{N}{2} < N_j$.	time	Germination time	Farooq et al. (2005)
Mean germination time or Mean length of incubation time ($\overline{T}$) or Germination resistance (GR) or Sprouting index (SI) or Emergence index (EI)	`MeanGermTime`	It is the average length of time required for maximum germination of a seed lot and is estimated according to the following formula. $$\overline{T} = \frac{\sum_{i=1}^{k} N_i T_i}{\sum_{i=1}^{k} N_i}$$ Where, T_i is the time from the start of the experiment to the ith interval, N_i is the number of seeds germinated in the ith time interval (not the accumulated number, but the number corresponding to the ith interval), and k is the total number of time intervals. It is the inverse of mean germination rate ($\overline{V}$). $$\overline{T} = \frac{1}{\overline{V}}$$	time	Germination time	Edmond and Drapala (1958); Czabator (1962); Smith and Millet (1964); Gordon (1969); Gordon (1971); Mock and Eberhart (1972); Ellis and Roberts (1980) Labouriau (1983a); Ranal and Santana (2006)

Germination index	Function	Details	Unit	Measures	Reference
Variance of germination time (s_T^2)	`VarGermTime`	It is computed according to the following formula. $$s_T^2 = \frac{\sum_{i=1}^{k} N_i (T_i - \overline{T})^2}{\sum_{i=1}^{k} N_i - 1}$$ Where, T_i is the time from the start of the experiment to the ith interval, N_i is the number of seeds germinated in the ith time interval (not the accumulated number, but the number corresponding to the ith interval), and k is the total number of time intervals.	time^{-1}	Germination time	Labouriau (1983a); Ranal and Santana (2006)
Standard error of germination time $(s_{\overline{T}})$	`SEGermTime`	It signifies the accuracy of the calculation of the mean germination time. It is estimated according to the following formula: $$s_{\overline{T}} = \sqrt{\frac{s_T^2}{\sum_{i=1}^{k} N_i}}$$ Where, N_i is the number of seeds germinated in the ith time interval (not the accumulated number, but the number corresponding to the ith interval) and k is the total number of time intervals.	time	Germination time	Labouriau (1983a); Ranal and Santana (2006)
Mean germination rate $(\overline{V})$	`MeanGermRate`	It is computed according to the following formula: $$\overline{V} = \frac{\sum_{i=1}^{k} N_i}{\sum_{i=1}^{k} N_i T_i}$$ Where, T_i is the time from the start of the experiment to the ith interval, N_i is the number of seeds germinated in the ith time interval (not the accumulated number, but the number corresponding to the ith interval), and k is the total number of time intervals. It is the inverse of mean germination time $(\overline{T})$. $$\overline{V} = \frac{1}{\overline{T}}$$	time^{-1}	Germination rate	Labouriau and Valadares (1976); Labouriau (1983b); Ranal and Santana (2006)

Germination index	Function	Details	Unit	Measures	Reference
Coefficient of velocity of germination (CVG) or Coefficient of rate of germination (CRG) or Kotowski's coefficient of velocity	CVG	It is estimated according to the following formula. $$CVG = \frac{\sum_{i=1}^{k} N_i}{\sum_{i=1}^{k} N_i T_i} \times 100$$ $$CVG = \overline{V} \times 100$$ Where, T_i is the time from the start of the experiment to the ith interval, N_i is the number of seeds germinated in the ith time interval (not the accumulated number, but the number corresponding to the ith interval), and k is the total number of time intervals.	% time^{-1}	Germination rate	Kotowski ([1926](#)), Nichols and Heydecker ([1968](#)); Bewley and Black ([1994](#)); Labouriau ([1983b](#)); Scott et al. ([1984](#))
Variance of germination rate (s_V^2)	VarGermRate	It is calculated according to the following formula. $$s_V^2 = \overline{V}^4 \times s_T^2$$ Where, s_T^2 is the variance of germination time.	time^{-2}	Germination rate	Labouriau ([1983b](#)); Ranal and Santana ([2006](#))
Standard error of germination rate ($s_{\overline{V}}$)	SEGermRate	It is estimated according to the following formula. $$s_{\overline{V}} = \sqrt{\frac{s_V^2}{\sum_{i=1}^{k} N_i}}$$ Where, N_i is the number of seeds germinated in the ith time interval (not the accumulated number, but the number corresponding to the ith interval), and k is the total number of time intervals.	time^{-1}	Germination rate	Labouriau ([1983b](#)); Ranal and Santana ([2006](#))
Germination rate as the reciprocal of the median time (v_{50})	GermRateRecip	It is the reciprocal of the median germination time (t_{50}). $$v_{50} = \frac{1}{t_{50}}$$	time^{-1}	Germination rate	Went ([1957](#)); Labouriau ([1983b](#)); Ranal and Santana ([2006](#))
Speed of germination or Germination rate Index or index of velocity of germination or Emergence rate index (Allan, Vogel and Peterson; Erbach; Hsu and Nelson) or Germination index (AOSA)	GermSpeed	It is the rate of germination in terms of the total number of seeds that germinate in a time interval. It is estimated as follows. $$S = \sum_{i=1}^{k} \frac{N_i}{T_i}$$ Where, T_i is the time from the start of the experiment to the ith interval, N_i is the number of seeds germinated in the ith time interval (not the accumulated number, but the number corresponding to the ith interval), and k is the total number of time intervals. Instead of germination counts, germination percentages may also be used for computation of speed of germination.	% time^{-1} or count time^{-1}	Mixed	Throneberry and Smith ([1955](#)); Maguire ([1962](#)); Allan et al. ([1962](#)); Kendrick and Frankland ([1969](#)); Bouton et al. ([1976](#)); Erbach ([1982](#)); AOSA ([1983](#)); Khandakar and Bradbeer ([1983](#)); Hsu and Nelson ([1986](#)); Bradbeer ([1988](#)); Wardle et al. ([1991](#))

Germination index	Function	Details	Unit	Measures	Reference
Speed of accumulated germination	GermSpeedAccumulate	It is the rate of germination in terms of the accumulated/cumulative total number of seeds that germinate in a time interval. It is estimated as follows. $$S_{accumulated} = \sum_{i=1}^{k} \frac{\sum_{j=1}^{i} N_j}{T_i}$$ Where, T_i is the time from the start of the experiment to the ith interval, $\sum_{j=1}^{i} N_j$ is the cumuative/accumulated number of seeds germinated in the ith interval, and k is the total number of time intervals. Instead of germination counts, germination percentages may also be used for computation of speed of germination.	% time^{-1} or count time^{-1}	Mixed	Bradbeer ([1988]); Wardle et al. ([1991]); Haugland and Brandsaeter ([1996]); Santana and Ranal ([2004])
Corrected germination rate index	GermSpeedCorrected	It is computed as follows. $$S_{corrected} = \frac{S}{FGP}$$ Where, 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)

Germination index	Function	Details	Unit	Measures	Reference
Germination Index (GI) (Melville)	`GermIndex`	It is estimated as follows. $$GI = \sum_{i=1}^{k} \frac{|(T_k - T_i)\, N_i|}{N_t}$$ 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. $$GI_{mod} = \sum_{i=1}^{k} \frac{|(T_k - T_i)\, N_i|}{N_g}$$ 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

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

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

GermPercent()

```
[1] 80
```

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

```
[1] 34
```

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

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

```
[1] 22
```

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

```
[1] 80
```

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

```
[1] 34
```

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

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

```
[1] 22
```

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

```
[1] 80
```

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

# From partial germination counts
```

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

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

```
[1] 5
```

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

```
[1] 11
```

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

```
[1] 6
```

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

```
[1] 6
# For multiple peak germination times
PeakGermTime(germ.counts = z, intervals = int)
```

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

```
[1] 5 6
# From cumulative germination counts
#-------------------------------------------------------------------------
FirstGermTime(germ.counts = y, intervals = int, partial = FALSE)
```

```
[1] 5
```

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

```
[1] 11
```

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

```
[1] 6
```

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

```
[1] 6
# For multiple peak germination time
PeakGermTime(germ.counts = cumsum(z), intervals = int, partial = FALSE)
```

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

```
[1] 5 6
```

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

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

```
t50()
```

```
[1] 5.970588
t50(germ.counts = x, intervals = int, method = "farooq")
```

```
[1] 5.941176
# From cumulative germination counts
#-----------------------------------------------------------------------------
t50(germ.counts = y, intervals = int, partial = FALSE, method = "coolbear")
```

```
[1] 5.970588
t50(germ.counts = y, intervals = int, partial = FALSE, method = "farooq")
```

```
[1] 5.941176
```

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

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

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

```
[1] 6.7
VarGermTime(germ.counts = x, intervals = int)
```

```
[1] 1.446154
SEGermTime(germ.counts = x, intervals = int)
```

```
[1] 0.1901416
CVGermTime(germ.counts = x, intervals = int)
```

```
[1] 0.1794868
# From cumulative germination counts
#-----------------------------------------------------------------------------
MeanGermTime(germ.counts = y, intervals = int, partial = FALSE)
```

```
[1] 6.7
VarGermTime(germ.counts = y, intervals = int, partial = FALSE)
```

```
[1] 19.04012
SEGermTime(germ.counts = y, intervals = int, partial = FALSE)
```

```
[1] 0.2394781
CVGermTime(germ.counts = y, intervals = int, partial = FALSE)
```

```
[1] 0.6512685
```

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

```
int <- 1:length(x)
```

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

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

```
[1] 0.1492537
CVG(germ.counts = x, intervals = int)
```

```
[1] 14.92537
VarGermRate(germ.counts = x, intervals = int)
```

```
[1] 0.0007176543
SEGermRate(germ.counts = x, intervals = int)
```

```
[1] 0.004235724
GermRateRecip(germ.counts = x, intervals = int, method = "coolbear")
```

```
[1] 0.1674877
GermRateRecip(germ.counts = x, intervals = int, method = "farooq")
```

```
[1] 0.1683168
# From cumulative germination counts
#-------------------------------------------------------------------------
MeanGermRate(germ.counts = y, intervals = int, partial = FALSE)
```

```
[1] 0.1492537
CVG(germ.counts = y, intervals = int, partial = FALSE)
```

```
[1] 14.92537
VarGermRate(germ.counts = y, intervals = int, partial = FALSE)
```

```
[1] 0.009448666
SEGermRate(germ.counts = y, intervals = int, partial = FALSE)
```

```
[1] 0.005334776
GermRateRecip(germ.counts = y, intervals = int,
              method = "coolbear", partial = FALSE)
```

```
[1] 0.1674877
GermRateRecip(germ.counts = y, intervals = int,
              method = "farooq", partial = FALSE)
```

```
[1] 0.1683168
```

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

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

```
GermSpeed(), GermSpeedAccumulated(), GermSpeedCorrected()
```

```
[1] 6.138925
```

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

```
[1] 34.61567
```

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

```
[1] 0.07673656
```

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

```
[1] 0.4326958
```

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

```
[1] 12.27785
```

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

```
[1] 69.23134
```

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

```
[1] 6.138925
```

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

```
[1] 34.61567
```

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

```
[1] 0.07673656
```

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

```
[1] 0.4326958
```

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

```
[1] 12.27785
```

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

```
[1] 69.23134
```

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

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

GermSpeed(), GermSpeedAccumulated(), GermSpeedCorrected()

```
[1] 6.138925
```

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

```
[1] 34.61567
```

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

```
[1] 0.07673656
```

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

```
[1] 0.4326958
```

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

```
[1] 12.27785
```

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

```
[1] 69.23134
```

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

```
[1] 6.138925
```

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

```
[1] 34.61567
```

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

```
[1] 0.07673656
```

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

```
[1] 0.4326958
```

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

```
[1] 12.27785
```

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

```
[1] 69.23134
```

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

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

WeightGermPercent()

```
[1] 47.42857
```

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

```
[1] 47.42857
```

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

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

MeanGermPercent(), MeanGermNumber()

```
[1] 5.714286
```

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

```
[1] 2.857143
```

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

```
[1] 5.714286
```

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

```
[1] 2.857143
```

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

```
[1] 664
```

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

```
[1] 664
```

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

```
[1] 8.3
```

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

```
[1] 47.42857
```

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

```
[1] 332
```

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

```
[1] 344
```

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

```
[1] 344
```

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

```
[1] 4.410256
```

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

```
[1] 24.57143
```

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

```
[1] 172
GermRateGeorge(germ.counts = y, intervals = int, partial = FALSE,
               max = 14)
```

```
[1] 332
```

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

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

```
GermIndex()
```

```
[1] 5.84
GermIndex(germ.counts = x, intervals = int, total.seeds = 50,
          modification = "none")
```

```
[1] 5.84
GermIndex(germ.counts = x, intervals = int, total.seeds = 50,
          modification = "santanaranal")
```

```
[1] 7.3
# From cumulative germination counts
#-------------------------------------------------------------------------
GermIndex(germ.counts = y, intervals = int, partial = FALSE,
          total.seeds = 50)
```

```
[1] 5.84
GermIndex(germ.counts = y, intervals = int, partial = FALSE,
          total.seeds = 50,
          modification = "none")
```

```
[1] 5.84
GermIndex(germ.counts = y, intervals = int, partial = FALSE,
          total.seeds = 50,
          modification = "santanaranal")
```

```
[1] 7.3
```

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

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

```
EmergenceRateIndex()
```

```
[1] 292
EmergenceRateIndex(germ.counts = x, intervals = int,
                   method = "shmueligoldberg")
```

```
[1] 292
EmergenceRateIndex(germ.counts = x, intervals = int,
                   method = "sgsantanaranal")
```

```
[1] 7.3
EmergenceRateIndex(germ.counts = x, intervals = int,
                   method = "bilbrowanjura")
```

```
[1] 5.970149
EmergenceRateIndex(germ.counts = x, intervals = int,
                   total.seeds = 50, method = "fakorede")
```

```
[1] 8.375
# From cumulative germination counts
#-------------------------------------------------------------------------------
EmergenceRateIndex(germ.counts = y, intervals = int, partial = FALSE,)
```

```
[1] 292
EmergenceRateIndex(germ.counts = y, intervals = int, partial = FALSE,
                   method = "shmueligoldberg")
```

```
[1] 292
EmergenceRateIndex(germ.counts = y, intervals = int, partial = FALSE,
                   method = "sgsantanaranal")
```

```
[1] 7.3
EmergenceRateIndex(germ.counts = y, intervals = int, partial = FALSE,
                   method = "bilbrowanjura")
```

```
[1] 5.970149
EmergenceRateIndex(germ.counts = y, intervals = int, partial = FALSE,
                   total.seeds = 50, method = "fakorede")
```

```
[1] 8.375
```

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

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

PeakValue(), GermValue()

```
[1] 9.5
```

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

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

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

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

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

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

```
$testend
[1] 16
```

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

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

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

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

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

```
[[2]]
   germ.counts intervals Cumulative.germ.counts Cumulative.germ.percent      DGS SumDGSbyN        GV
1            0         1                      0                     0.0 0.000000  0.000000  0.000000
2            0         2                      0                     0.0 0.000000  0.000000  0.000000
3           34         3                     34                    17.0 5.666667  1.888889  3.211111
4           40         4                     74                    37.0 9.250000  3.729167 13.797917
5           21         5                     95                    47.5 9.500000  4.883333 23.195833
6           10         6                    105                    52.5 8.750000  5.527778 29.020833
7            4         7                    109                    54.5 7.785714  5.850340 31.884354
8            5         8                    114                    57.0 7.125000  6.009673 34.255134
9            3         9                    117                    58.5 6.500000  6.064153 35.475298
10           5        10                    122                    61.0 6.100000  6.067738 37.013202
11           8        11                    130                    65.0 5.909091  6.053316 39.346552
12           7        12                    137                    68.5 5.708333  6.024567 41.268285
13           7        13                    144                    72.0 5.538462  5.987174 43.107655
14           6        14                    150                    75.0 5.357143  5.942172 44.566291
```

```
15        6        15              156              78.0 5.200000  5.892694 45.963013
16        4        16              160              80.0 5.000000  5.836901 46.695205
17        0        17              160              80.0 4.705882  5.770370 46.162961
18        2        18              162              81.0 4.500000  5.699794 46.168331
19        0        19              162              81.0 4.263158  5.624182 45.555871
20        2        20              164              82.0 4.100000  5.547972 45.493374
```

```
$testend
[1] 16
```

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

```
[1] 9.5
```

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

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

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

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

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

```
[[2]]
   germ.counts intervals Cumulative.germ.counts Cumulative.germ.percent      DGS SumDGSbyN        GV
3           34         3                     34                    17.0 5.666667  5.666667  9.633333
4           40         4                     74                    37.0 9.250000  7.458333 27.595833
5           21         5                     95                    47.5 9.500000  8.138889 38.659722
6           10         6                    105                    52.5 8.750000  8.291667 43.531250
```

```
7             4          7                    109               54.5 7.785714   8.190476 44.638095
8             5          8                    114               57.0 7.125000   8.012897 45.673512
9             3          9                    117               58.5 6.500000   7.796769 45.611097
10            5          10                   122               61.0 6.100000   7.584673 46.266503
11            8          11                   130               65.0 5.909091   7.398497 48.090230
12            7          12                   137               68.5 5.708333   7.229481 49.521942
13            7          13                   144               72.0 5.538462   7.075752 50.945411
14            6          14                   150               75.0 5.357143   6.932534 51.994006
15            6          15                   156               78.0 5.200000   6.799262 53.034246
16            4          16                   160               80.0 5.000000   6.670744 53.365948
17            0          17                   160               80.0 4.705882   6.539753 52.318022
18            2          18                   162               81.0 4.500000   6.412268 51.939373
19            0          19                   162               81.0 4.263158   6.285850 50.915385
20            2          20                   164               82.0 4.100000   6.164414 50.548194
```

```
$testend
[1] 16
```

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

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

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

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

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

```
[[2]]
   germ.counts intervals Cumulative.germ.counts Cumulative.germ.percent      DGS SumDGSbyN        GV
```

```
1            0        1            0            0.0 0.000000   0.000000   0.000000
2            0        2            0            0.0 0.000000   0.000000   0.000000
3           34        3           34           17.0 5.666667   1.888889   3.211111
4           40        4           74           37.0 9.250000   3.729167  13.797917
5           21        5           95           47.5 9.500000   4.883333  23.195833
6           10        6          105           52.5 8.750000   5.527778  29.020833
7            4        7          109           54.5 7.785714   5.850340  31.884354
8            5        8          114           57.0 7.125000   6.009673  34.255134
9            3        9          117           58.5 6.500000   6.064153  35.475298
10           5       10          122           61.0 6.100000   6.067738  37.013202
11           8       11          130           65.0 5.909091   6.053316  39.346552
12           7       12          137           68.5 5.708333   6.024567  41.268285
13           7       13          144           72.0 5.538462   5.987174  43.107655
14           6       14          150           75.0 5.357143   5.942172  44.566291
15           6       15          156           78.0 5.200000   5.892694  45.963013
16           4       16          160           80.0 5.000000   5.836901  46.695205
17           0       17          160           80.0 4.705882   5.770370  46.162961
18           2       18          162           81.0 4.500000   5.699794  46.168331
19           0       19          162           81.0 4.263158   5.624182  45.555871
20           2       20          164           82.0 4.100000   5.547972  45.493374

$testend
[1] 16
```

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

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

CUGerm()

```
[1] 0.7092199
```

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

```
[1] 0.05267935
```

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

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

GermSynchrony(), GermUncertainty()

```
[1] 0.2666667
```

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

```
[1] 2.062987
```

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

```
[1] 0.2666667
```

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

```
[1] 2.062987
```

Non-linear regression analysis

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

Four-parameter hill function

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

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

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

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

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

Germination parameters	Details	Unit	Measures
y intercept (y_0)	The intercept on the y axis.		
Asymptote (a)	It is the maximum cumulative germination percentage, which is equivalent to germination capacity.	%	Germination capacity
Shape and steepness (b)	Mathematical parameter controlling the shape and steepness of the germination curve. The larger the b, the steeper the rise toward the asymptote a, and the shorter the time between germination onset and maximum germination.		Germination rate
Half-maximal activation level (c)	Time required for 50% of viable seeds to germinate.	time	Germination time

Germination parameters	Details	Unit	Measures
lag	It is the time at germination onset and is computed by solving four-parameter hill function after setting y to 0 as follows. $$lag = b\sqrt{\frac{-y_0 c^b}{a + y_0}}$$	time	Germination time
D_{lag-50}	The duration between the time at germination onset (*lag*) and that at 50% germination (*c*).	time	Germination time
$t_{50_{total}}$	Time required for 50% of total seeds to germinate.	time	Germination time
$t_{50_{germinated}}$	Time required for 50% of viable/germinated seeds to germinate	time	Germination time
$t_{x_{total}}$	Time required for $x\%$ of total seeds to germinate.	time	Germination time
$t_{x_{germinated}}$	Time required for $x\%$ of viable/germinated seeds to germinate	time	Germination time
Uniformity ($U_{t_{max}-t_{min}}$)	It is the time interval between the percentages of viable seeds specified in the arguments `umin` and `umin` to germinate.	time	Germination time
Time at maximum germination rate ($TMGR$)	The partial derivative of the four-parameter hill function gives the instantaneous rate of germination (s) as follows. $$s = \frac{\partial y}{\partial x} = \frac{abc^b x^{b-1}}{(c^b + x^b)^2}$$ From this function for instantaneous rate of germination, $TMGR$ can be estimated as follows. $$TMGR = b\sqrt{\frac{c^b(b-1)}{b+1}}$$ It represents the point in time when the instantaneous rate of germination starts to decline.	time	Germination time
Area under the curve (AUC)	It is obtained by integration of the fitted curve between time 0 and time specified in the argument `tmax`.		Mixed
MGT	Calculated by integration of the fitted curve and proper normalisation.	time	Germination time
Skewness	It is computed as follows. $$\frac{MGT}{t_{50_{germinated}}}$$		

Examples

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

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

FourPHFfit()

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

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

$Fit
```
     sigma isConv      finTol    logLik      AIC      BIC deviance df.residual nobs
1 1.769385   TRUE 1.490116e-08 -25.49868 60.99736 64.19265 31.30723          10   14
```

$a
```
[1] 80
```

$b
```
[1] 9.881947
```

$c
```
[1] 6.034954
```

$y0
```
[1] 0
```

$lag
```
[1] 0
```

```
$Dlag50
[1] 6.034954

$t50.total
[1] 6.355122

$txp.total
       10        60
4.956266 6.744598

$t50.Germinated
[1] 6.034954

$txp.Germinated
       10        60
4.831809 6.287724

$Uniformity
          90           10 uniformity
   7.537688    4.831809   2.705880

$TMGR
[1] 5.912195

$AUC
[1] 1108.975

$MGT
[1] 6.632252

$Skewness
[1] 1.098973

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

$isConv
[1] TRUE

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

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

```
$data
   gp csgp intervals
1   0    0         1
2   0    0         2
3   0    0         3
4   0    0         4
5   8    8         5
```

```
6   34    42           6
7   20    62           7
8   14    76           8
9    2    78           9
10   0    78          10
11   2    80          11
12   0    80          12
13   0    80          13
14   0    80          14


$Parameters
  term   estimate std.error statistic       p.value
1    a  80.000000 1.2415867  64.43368 1.973252e-14
2    b   9.881927 0.7077918  13.96163 6.952270e-08
3    c   6.034953 0.0495266 121.85275 3.399437e-17
4   y0   0.000000 0.9160705   0.00000 1.000000e+00


$Fit
     sigma isConv      finTol    logLik      AIC      BIC deviance df.residual nobs
1 1.769385   TRUE 1.490116e-08 -25.49868 60.99736 64.19265 31.30723          10   14


$a
[1] 80

$b
[1] 9.881927

$c
[1] 6.034953

$y0
[1] 0

$lag
[1] 0

$Dlag50
[1] 6.034953

$t50.total
[1] 6.355121

$txp.total
      10       60
4.956263 6.744599

$t50.Germinated
[1] 6.034953

$txp.Germinated
      10       60
4.831806 6.287723


$Uniformity
```

```
        90         10 uniformity
  7.537691    4.831806    2.705885


$TMGR
[1] 5.912194

$AUC
[1] 1108.976

$MGT
[1] 6.632252

$Skewness
[1] 1.098973

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

$isConv
[1] TRUE

attr(,"class")
[1] "FourPHFfit" "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)
```
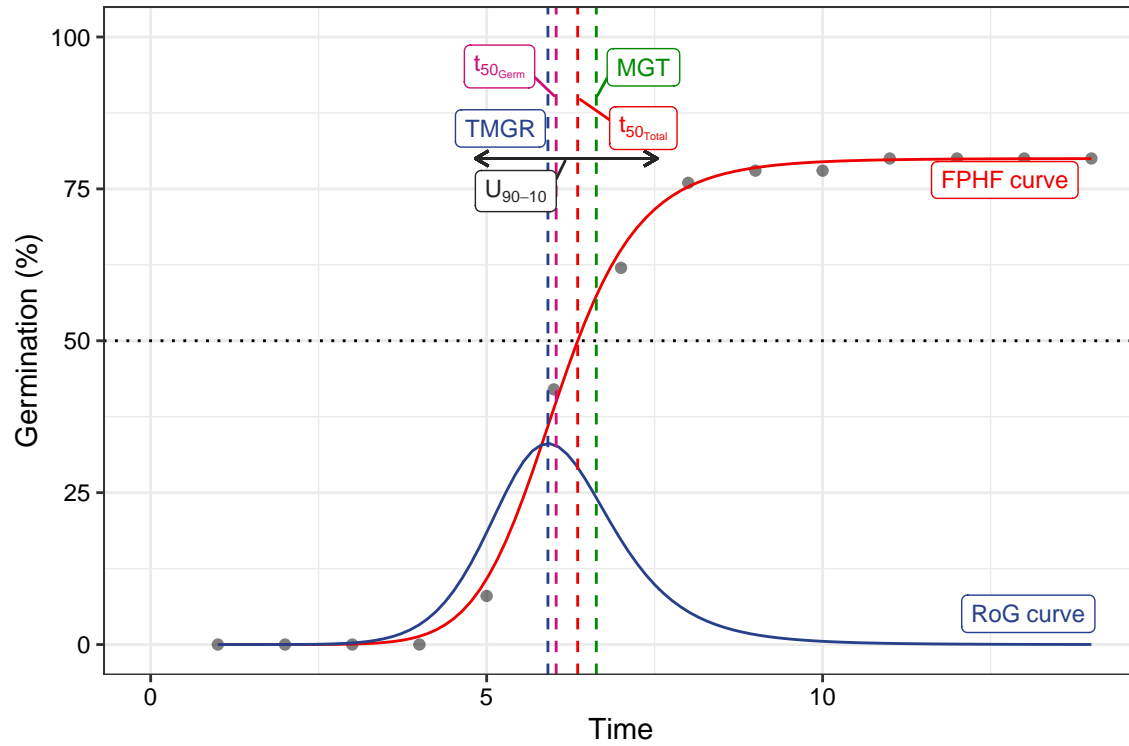
```
plot(fit2)
```
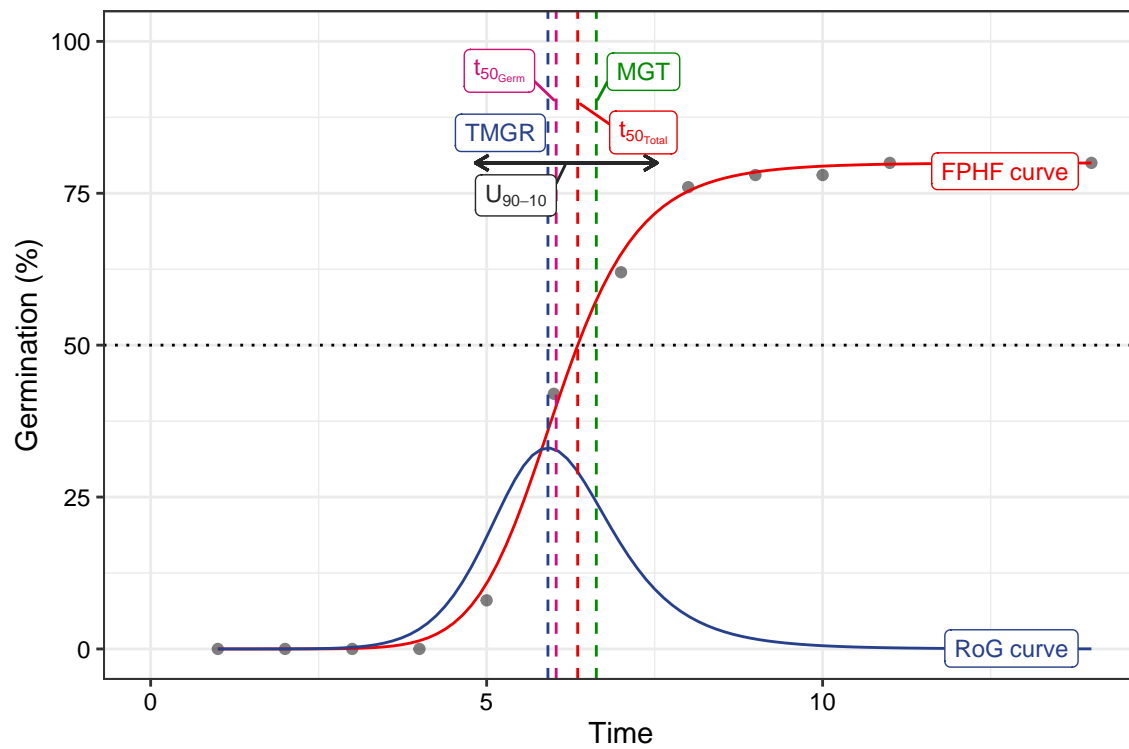


```
# No labels
plot(fit1, plotlabels = FALSE)
```
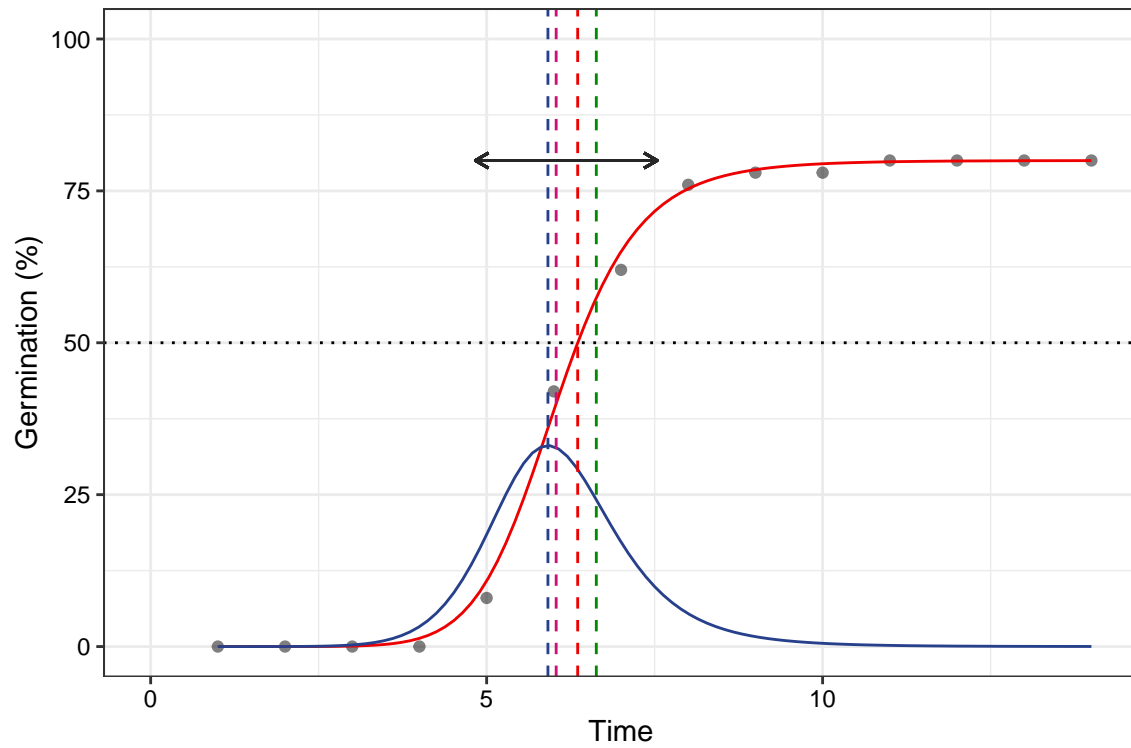
```
plot(fit2, plotlabels = FALSE)
```
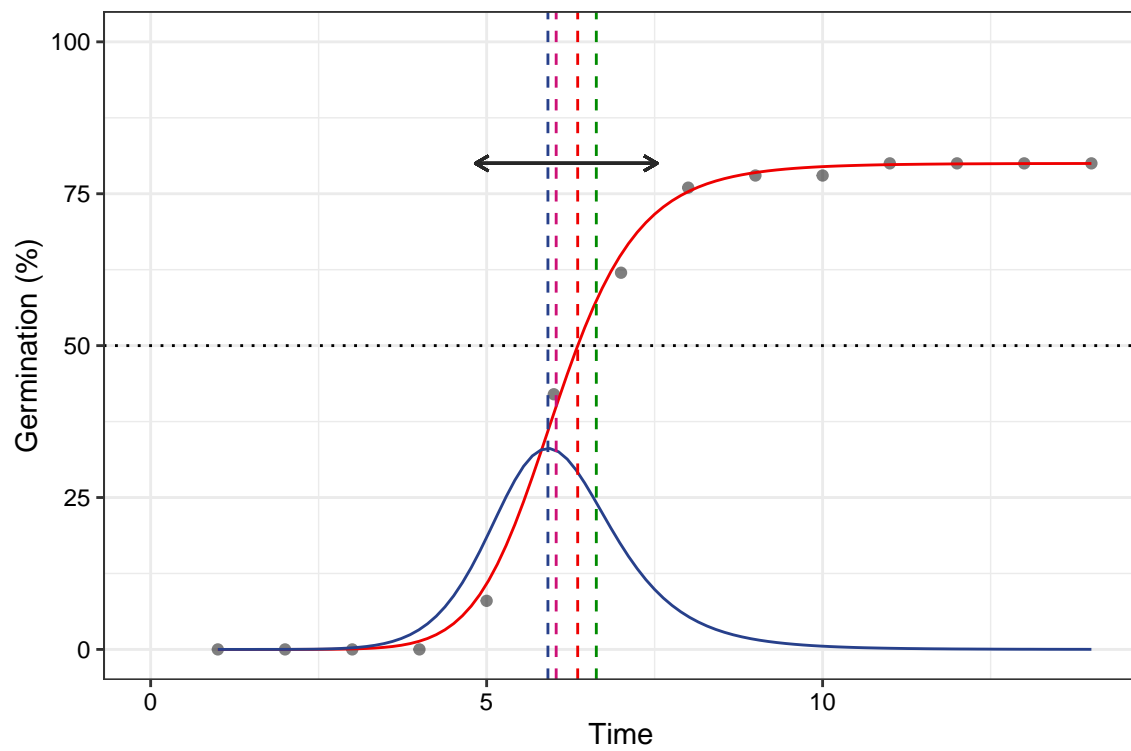


```
# Only the FPHF curve
plot(fit1, rog = FALSE, t50.total = FALSE, t50.germ = FALSE,
     tmgr = FALSE, mgt = FALSE, uniformity = FALSE)
```
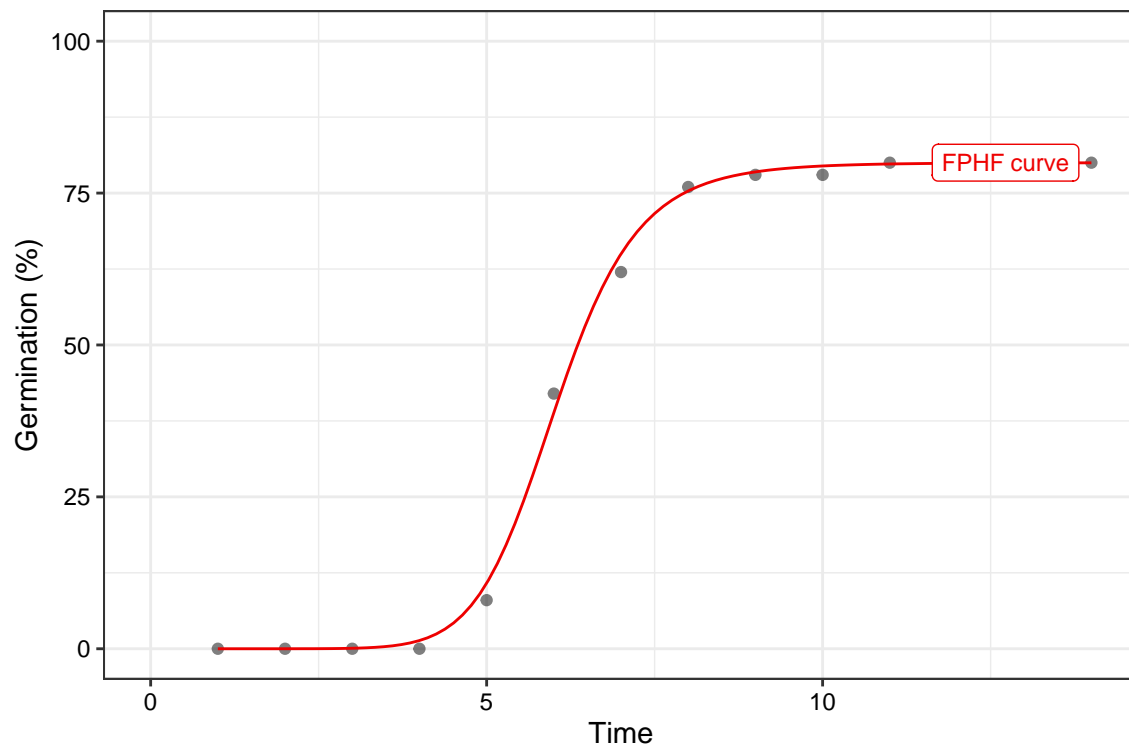
```
plot(fit2, rog = FALSE, t50.total = FALSE, t50.germ = FALSE,
     tmgr = FALSE, mgt = FALSE, uniformity = FALSE)
```
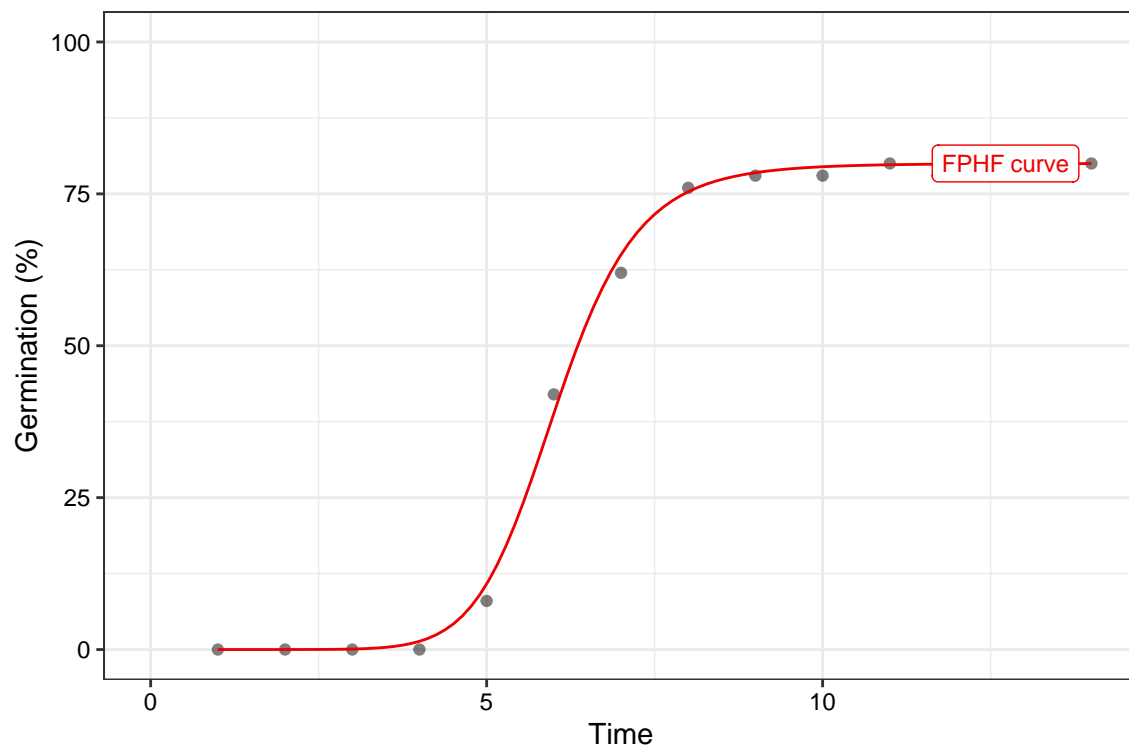
```
# Without y axis limits adjustment
plot(fit1, limits = FALSE)
```
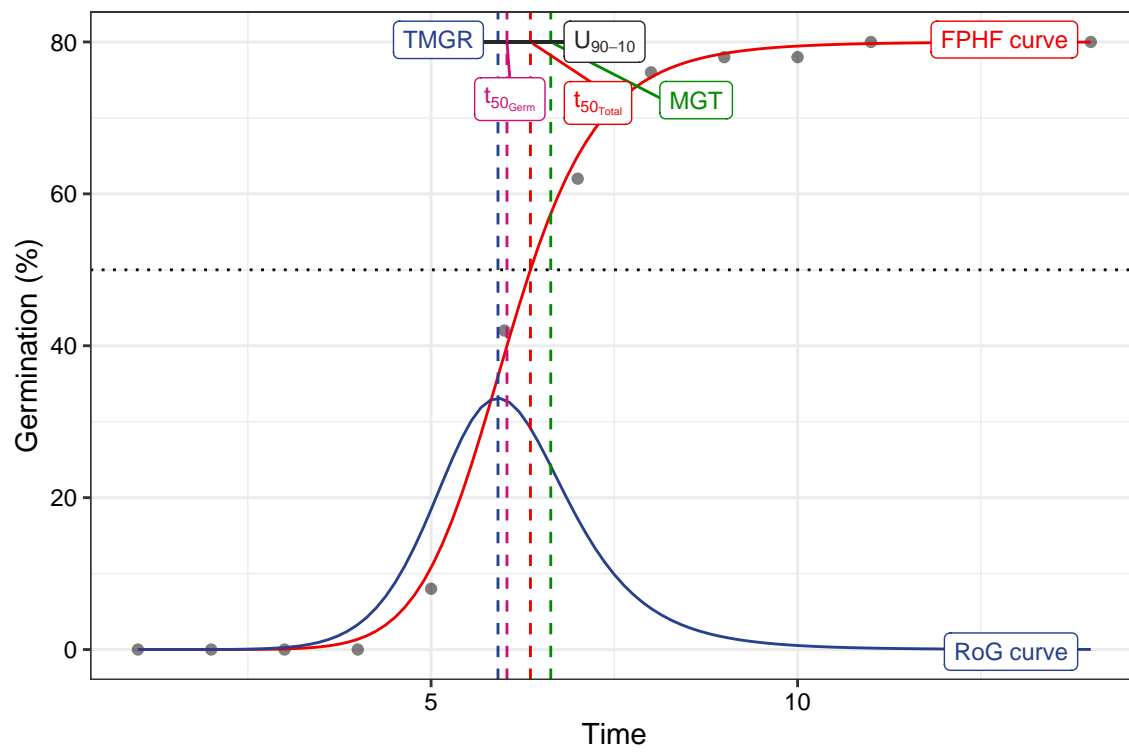


```
plot(fit2, limits = FALSE)
```
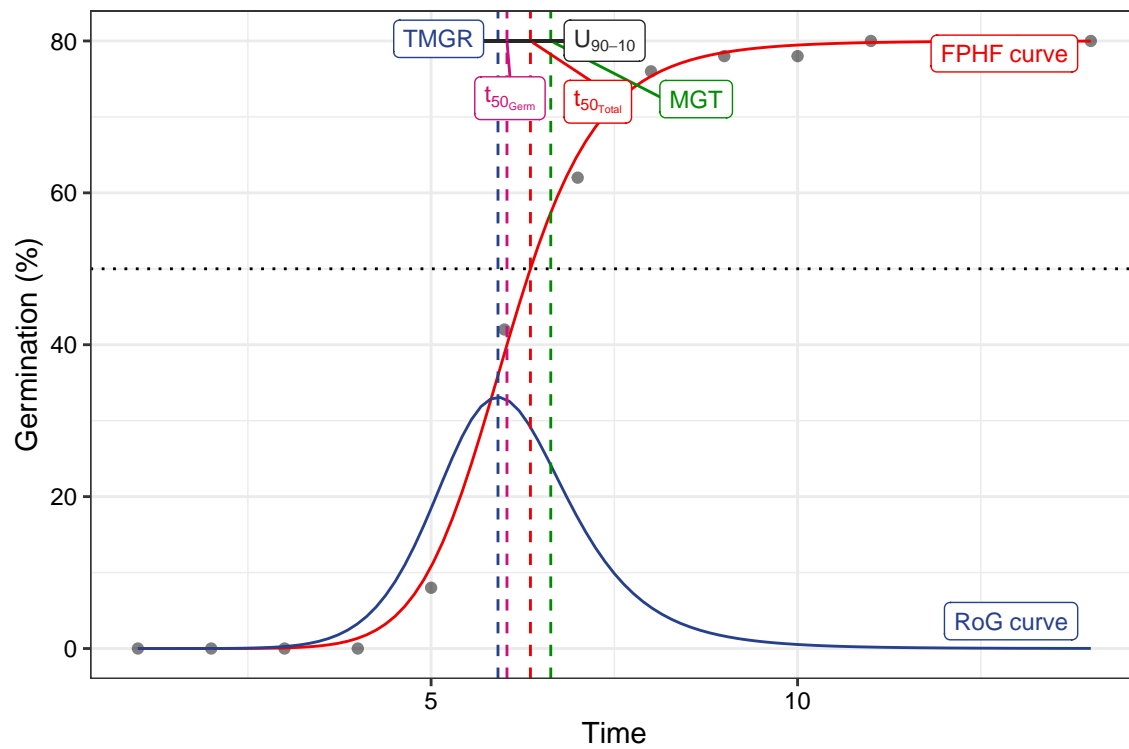
Wrapper functions

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)
```

```
Warning in EmergenceRateIndex(germ.counts = unlist(mget(counts.intervals.cols)), : Argument `method = "
Please use `method = "shmueligoldberg"` instead.

Warning in EmergenceRateIndex(germ.counts = unlist(mget(counts.intervals.cols)), : Argument `method = "
Please use `method = "shmueligoldberg"` instead.

Warning in EmergenceRateIndex(germ.counts = unlist(mget(counts.intervals.cols)), : Argument `method = "
Please use `method = "shmueligoldberg"` instead.

Warning in EmergenceRateIndex(germ.counts = unlist(mget(counts.intervals.cols)), : Argument `method = "
Please use `method = "shmueligoldberg"` instead.

Warning in EmergenceRateIndex(germ.counts = unlist(mget(counts.intervals.cols)), : Argument `method = "
Please use `method = "shmueligoldberg"` instead.

Warning in EmergenceRateIndex(germ.counts = unlist(mget(counts.intervals.cols)), : Argument `method = "
Please use `method = "shmueligoldberg"` instead.

Warning in EmergenceRateIndex(germ.counts = unlist(mget(counts.intervals.cols)), : Argument `method = "
Please use `method = "shmueligoldberg"` instead.

Warning in EmergenceRateIndex(germ.counts = unlist(mget(counts.intervals.cols)), : Argument `method = "
Please use `method = "shmueligoldberg"` instead.

Warning in EmergenceRateIndex(germ.counts = unlist(mget(counts.intervals.cols)), : Argument `method = "
Please use `method = "shmueligoldberg"` instead.

Warning in EmergenceRateIndex(germ.counts = unlist(mget(counts.intervals.cols)), : Argument `method = "
Please use `method = "shmueligoldberg"` instead.

Warning in EmergenceRateIndex(germ.counts = unlist(mget(counts.intervals.cols)), : Argument `method = "
Please use `method = "shmueligoldberg"` instead.

Warning in EmergenceRateIndex(germ.counts = unlist(mget(counts.intervals.cols)), : Argument `method = "
Please use `method = "shmueligoldberg"` instead.

Warning in EmergenceRateIndex(germ.counts = unlist(mget(counts.intervals.cols)), : Argument `method = "
```

Please use `method = "shmueligoldberg"` instead.

Warning in EmergenceRateIndex(germ.counts = unlist(mget(counts.intervals.cols)), : Argument `method = "r
Please use `method = "shmueligoldberg"` instead.

Warning in EmergenceRateIndex(germ.counts = unlist(mget(counts.intervals.cols)), : Argument `method = "r
Please use `method = "shmueligoldberg"` instead.

Warning in EmergenceRateIndex(germ.counts = unlist(mget(counts.intervals.cols)), : Argument `method = "r
Please use `method = "sgsantanaranal"` instead.

Warning in EmergenceRateIndex(germ.counts = unlist(mget(counts.intervals.cols)), : Argument `method = "r
Please use `method = "sgsantanaranal"` instead.

Warning in EmergenceRateIndex(germ.counts = unlist(mget(counts.intervals.cols)), : Argument `method = "r
Please use `method = "sgsantanaranal"` instead.

Warning in EmergenceRateIndex(germ.counts = unlist(mget(counts.intervals.cols)), : Argument `method = "r
Please use `method = "sgsantanaranal"` instead.

Warning in EmergenceRateIndex(germ.counts = unlist(mget(counts.intervals.cols)), : Argument `method = "r
Please use `method = "sgsantanaranal"` instead.

Warning in EmergenceRateIndex(germ.counts = unlist(mget(counts.intervals.cols)), : Argument `method = "r
Please use `method = "sgsantanaranal"` instead.

Warning in EmergenceRateIndex(germ.counts = unlist(mget(counts.intervals.cols)), : Argument `method = "r
Please use `method = "sgsantanaranal"` instead.

Warning in EmergenceRateIndex(germ.counts = unlist(mget(counts.intervals.cols)), : Argument `method = "r
Please use `method = "sgsantanaranal"` instead.

Warning in EmergenceRateIndex(germ.counts = unlist(mget(counts.intervals.cols)), : Argument `method = "r
Please use `method = "sgsantanaranal"` instead.

Warning in EmergenceRateIndex(germ.counts = unlist(mget(counts.intervals.cols)), : Argument `method = "r
Please use `method = "sgsantanaranal"` instead.

Warning in EmergenceRateIndex(germ.counts = unlist(mget(counts.intervals.cols)), : Argument `method = "r
Please use `method = "sgsantanaranal"` instead.

Warning in EmergenceRateIndex(germ.counts = unlist(mget(counts.intervals.cols)), : Argument `method = "r
Please use `method = "sgsantanaranal"` instead.

Warning in EmergenceRateIndex(germ.counts = unlist(mget(counts.intervals.cols)), : Argument `method = "r
Please use `method = "sgsantanaranal"` instead.

Warning in EmergenceRateIndex(germ.counts = unlist(mget(counts.intervals.cols)), : Argument `method = "r
Please use `method = "sgsantanaranal"` instead.

Genotype	Rep	Day01	Day02	Day03	Day04	Day05	Day06	Day07	Day08	Day09	Day10	Day11	Day12	Day13	Day14	Tota
1	G1	1	0	0	0	0	4	17	10	7	1	0	1	0	0	0	

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

	GermPercent	PeakGermPercent	FirstGermTime	LastGermTime	PeakGermTime	TimeSpreadGerm	t50_Coolbear	t50_
1	80.00000	34.00000	5	11	6	6	5.970588	5.9
2	82.35294	29.41176	4	12	6	8	6.192308	6.1
3	93.75000	37.50000	4	12	6	8	6.000000	5.9
4	90.19608	37.25490	5	12	6	7	6.041667	6.0
5	96.00000	40.00000	5	13	6	8	5.975000	5.9
6	93.87755	42.85714	5	12	6	7	5.976190	5.9
7	87.50000	37.50000	5	11	6	6	5.972222	5.9
8	85.10638	29.78723	4	12	6	8	6.208333	6.1
9	86.53846	36.53846	4	12	6	8	6.000000	5.9
10	90.00000	36.00000	5	12	6	7	6.076923	6.0
11	94.11765	41.17647	5	13	6	8	5.928571	5.9
12	86.27451	39.21569	5	12	6	7	5.975000	5.9
13	95.91837	38.77551	5	13	6	8	6.083333	6.0
14	91.66667	43.75000	5	12	6	7	5.928571	5.9
15	87.50000	35.41667	5	11	6	6	6.050000	6.0

	MeanGermTime	VarGermTime	SEGermTime	CVGermTime	MeanGermRate	VarGermRate	SEGermRate	CVG	GermRat
1	6.700000	1.446154	0.1901416	0.1794868	0.1492537	0.0007176543	0.004235724	14.92537	
2	6.857143	2.027875	0.2197333	0.2076717	0.1458333	0.0009172090	0.004673148	14.58333	
3	6.866667	2.572727	0.2391061	0.2335882	0.1456311	0.0011572039	0.005071059	14.56311	
4	6.891304	2.187923	0.2180907	0.2146419	0.1451104	0.0009701218	0.004592342	14.51104	
5	6.812500	2.368351	0.2221275	0.2259002	0.1467890	0.0010995627	0.004786184	14.67890	
6	6.869565	2.071498	0.2122088	0.2095140	0.1455696	0.0009301809	0.004496813	14.55696	
7	6.690476	1.389663	0.1818989	0.1761967	0.1494662	0.0006935558	0.004063648	14.94662	
8	6.875000	2.112179	0.2297923	0.2113940	0.1454545	0.0009454531	0.004861721	14.54545	
9	6.866667	2.300000	0.2260777	0.2208604	0.1456311	0.0010345321	0.004794747	14.56311	
10	6.822222	1.831313	0.2017321	0.1983606	0.1465798	0.0008453940	0.004334343	14.65798	
11	6.791667	2.381206	0.2227295	0.2272072	0.1472393	0.0011191581	0.004828643	14.72393	
12	6.886364	2.149577	0.2210295	0.2129053	0.1452145	0.0009558577	0.004660905	14.52145	
13	6.936170	2.539315	0.2324392	0.2297410	0.1441718	0.0010970785	0.004831366	14.41718	
14	6.772727	1.900634	0.2078370	0.2035568	0.1476510	0.0009033254	0.004531018	14.76510	
15	6.809524	1.670151	0.1994129	0.1897847	0.1468531	0.0007767634	0.004300508	14.68531	

	GermRateRecip_Farooq	GermSpeed_Count	GermSpeed_Percent	GermSpeedAccumulated_Count	GermSpeedAccumulate
1	0.1683168	6.138925	12.27785	34.61567	
2	0.1625000	6.362698	12.47588	35.54058	
3	0.1674419	6.882179	14.33787	38.29725	
4	0.1666667	6.927417	13.58317	38.68453	
5	0.1680672	7.318987	14.63797	41.00786	
6	0.1680000	6.931782	14.14649	38.77620	
7	0.1682243	6.448449	13.43427	36.38546	

8	0.1621622	6.053175	12.87909	33.77079
9	0.1674009	6.830592	13.13575	38.11511
10	0.1656051	6.812698	13.62540	38.19527
11	0.1693548	7.342796	14.39764	41.17452
12	0.1680672	6.622258	12.98482	37.00640
13	0.1655172	7.052320	14.39249	39.29399
14	0.1693548	6.706782	13.97246	37.69490
15	0.1666667	6.363925	13.25818	35.69697

	GermSpeedCorrected_Normal	GermSpeedCorrected_Accumulated	WeightGermPercent	MeanGermPercent	MeanGermNu
1	0.07673656	0.4326958	47.42857	5.714286	2.85
2	0.07726134	0.4315642	47.89916	5.882353	3.00
3	0.07340991	0.4085040	54.46429	6.696429	3.2
4	0.07680397	0.4288937	52.24090	6.442577	3.28
5	0.07623944	0.4271652	56.14286	6.857143	3.4
6	0.07383855	0.4130508	54.51895	6.705539	3.28
7	0.07369656	0.4158338	51.93452	6.250000	3.00
8	0.07112480	0.3968068	49.39210	6.079027	2.85
9	0.07893128	0.4404413	50.27473	6.181319	3.2
10	0.07569665	0.4243919	52.57143	6.428571	3.2
11	0.07801721	0.4374793	55.18207	6.722689	3.4
12	0.07675799	0.4289379	50.00000	6.162465	3.14
13	0.07352419	0.4096608	55.24781	6.851312	3.35
14	0.07316490	0.4112171	53.86905	6.547619	3.14
15	0.07273057	0.4079653	51.19048	6.250000	3.00

	TimsonsIndex	TimsonsIndex_Labouriau	TimsonsIndex_KhanUngar	GermRateGeorge	GermIndex	GermIndex_mod
1	8.000000	1.00	0.5714286	4	5.840000	7.300000
2	9.803922	1.25	0.7002801	5	5.882353	7.142857
3	14.583333	1.40	1.0416667	7	6.687500	7.133333
4	7.843137	1.00	0.5602241	4	6.411765	7.108696
5	10.000000	1.00	0.7142857	5	6.900000	7.187500
6	6.122449	1.00	0.4373178	3	6.693878	7.130435
7	8.333333	1.00	0.5952381	4	6.395833	7.309524
8	10.638298	1.25	0.7598784	5	6.063830	7.125000
9	9.615385	1.25	0.6868132	5	6.173077	7.133333
10	8.000000	1.00	0.5714286	4	6.460000	7.177778
11	9.803922	1.00	0.7002801	5	6.784314	7.208333
12	5.882353	1.00	0.4201681	3	6.137255	7.113636
13	8.163265	1.00	0.5830904	4	6.775510	7.063830
14	6.250000	1.00	0.4464286	3	6.625000	7.227273
15	8.333333	1.00	0.5952381	4	6.291667	7.190476

	EmergenceRateIndex_Melville	EmergenceRateIndex_Melville_mod	EmergenceRateIndex_BilbroWanjura
1	292	7.300000	5.970149
2	300	7.142857	6.125000
3	321	7.133333	6.553398
4	327	7.108696	6.675079
5	345	7.187500	7.045872
6	328	7.130435	6.696203
7	307	7.309524	6.277580
8	285	7.125000	5.818182
9	321	7.133333	6.553398
10	323	7.177778	6.596091
11	346	7.208333	7.067485
12	313	7.113636	6.389439
13	332	7.063830	6.776074

```
14                         318                    7.227273                        6.496644
15                         302                    7.190476                        6.167832
   EmergenceRateIndex_Fakorede PeakValue GermValue_Czabator GermValue_DP GermValue_Czabator_mod GermValu
1                     8.375000  9.500000           54.28571    57.93890               54.28571
2                     8.326531  9.313725           54.78662    52.58713               54.78662
3                     7.324444 10.416667           69.75446    68.62289               69.75446
4                     7.640359 10.049020           64.74158    70.43331               64.74158
5                     7.096354 11.250000           77.14286    80.16914               77.14286
6                     7.317580 10.714286           71.84506    76.51983               71.84506
7                     7.646259 10.416667           65.10417    69.41325               65.10417
8                     8.078125  9.574468           58.20345    56.00669               58.20345
9                     7.934815  9.855769           60.92165    58.13477               60.92165
10                    7.580247 10.250000           65.89286    70.91875               65.89286
11                    7.216146 11.029412           74.14731    77.39782               74.14731
12                    7.981921  9.803922           60.41632    64.44988               60.41632
13                    7.231326 10.969388           75.15470    78.16335               75.15470
14                    7.388430 10.677083           69.90947    74.40140               69.90947
15                    7.782313 10.156250           63.47656    67.62031               63.47656
      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.

```
data(gcdata)

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

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

```
  Genotype Rep Day01 Day02 Day03 Day04 Day05 Day06 Day07 Day08 Day09 Day10 Day11 Day12 Day13 Day14 Tota
1       G1   1     0     0     0     0     4    17    10     7     1     0     1     0     0     0
2       G2   1     0     0     0     1     3    15    13     6     2     1     0     1     0     0
3       G3   1     0     0     0     2     3    18     9     8     2     1     1     1     0     0
4       G4   1     0     0     0     0     4    19    12     6     2     1     1     1     0     0
```

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

	b	c	y0	lag	Dlag50	t50.total	t50.Germinated	TMGR	AUC	MGT	Skewness
1	9.881947	6.034954	0	0	6.034954	6.355122	6.034954	5.912195	1108.975	6.632252	1.098973
2	9.227667	6.175193	0	0	6.175193	6.473490	6.175193	6.031282	1128.559	6.784407	1.098655
3	7.793055	6.138110	0	0	6.138110	6.244190	6.138110	5.938179	1283.693	6.772742	1.103392
4	8.925668	6.125172	0	0	6.125172	6.276793	6.125172	5.972686	1239.887	6.739665	1.100323
5	9.419194	6.049641	0	0	6.049641	6.103433	6.049641	5.914289	1328.328	6.654980	1.100062
6	9.450187	6.097412	0	0	6.097412	6.182276	6.097412	5.961877	1294.463	6.702470	1.099232
7	10.172466	6.029851	0	0	6.029851	6.202812	6.029851	5.914057	1213.908	6.622417	1.098272
8	8.940702	6.189774	0	0	6.189774	6.439510	6.189774	6.036193	1164.346	6.804000	1.099232
9	8.617395	6.125121	0	0	6.125121	6.352172	6.125121	5.961631	1188.793	6.745241	1.101242
10	9.608849	6.109503	0	0	6.109503	6.253042	6.109503	5.978115	1240.227	6.711899	1.098600
11	9.400248	6.018759	0	0	6.018759	6.099434	6.018759	5.883558	1305.200	6.624247	1.100600
12	9.162558	6.108449	0	0	6.108449	6.326181	6.108449	5.964079	1188.021	6.718636	1.099892
13	8.995233	6.149011	0	0	6.149011	6.207500	6.149011	5.998270	1316.407	6.762272	1.099733
14	10.391898	6.015907	0	0	6.015907	6.122385	6.015907	5.905179	1273.386	6.604963	1.097916
15	9.136762	6.121580	0	0	6.121580	6.317392	6.121580	5.976088	1203.664	6.732267	1.099760

	msg	isConv	txp.total_10	txp.total_60	Uniforr
1	#1. Relative error in the sum of squares is at most `ftol`.	TRUE	4.956266	6.744598	7
2	#1. Relative error in the sum of squares is at most `ftol`.	TRUE	4.983236	6.872603	7
3	#1. Relative error in the sum of squares is at most `ftol`.	TRUE	4.673022	6.608437	8
4	#1. Relative error in the sum of squares is at most `ftol`.	TRUE	4.850876	6.614967	7
5	#1. Relative error in the sum of squares is at most `ftol`.	TRUE	4.814126	6.386788	7
6	#1. Relative error in the sum of squares is at most `ftol`.	TRUE	4.868635	6.477594	7
7	#1. Relative error in the sum of squares is at most `ftol`.	TRUE	4.930423	6.510495	7
8	#1. Relative error in the sum of squares is at most `ftol`.	TRUE	4.940058	6.823299	7
9	#1. Relative error in the sum of squares is at most `ftol`.	TRUE	4.836659	6.733275	7
10	#1. Relative error in the sum of squares is at most `ftol`.	TRUE	4.920629	6.566505	7
11	#1. Relative error in the sum of squares is at most `ftol`.	TRUE	4.798630	6.391288	7
12	#1. Relative error in the sum of squares is at most `ftol`.	TRUE	4.893597	6.684521	7
13	#1. Relative error in the sum of squares is at most `ftol`.	TRUE	4.841310	6.509952	7
14	#1. Relative error in the sum of squares is at most `ftol`.	TRUE	4.915143	6.397486	7
15	#1. Relative error in the sum of squares is at most `ftol`.	TRUE	4.892505	6.667247	7

	Uniformity_10	Uniformity
1	4.831809	2.705880
2	4.866755	2.968652
3	4.630062	3.507277
4	4.788598	3.046208
5	4.790947	2.848078
6	4.832474	2.860984
7	4.858477	2.625165
8	4.841106	3.073056
9	4.746574	3.157466
10	4.860681	2.818494

```
11        4.764249    2.839354
12        4.806015    2.957830
13        4.816395    3.033943
14        4.869401    2.562960
15        4.813086    2.972718
```

Multiple fitted curves generated in batch can also be plotted.

```
data(gcdata)

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

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

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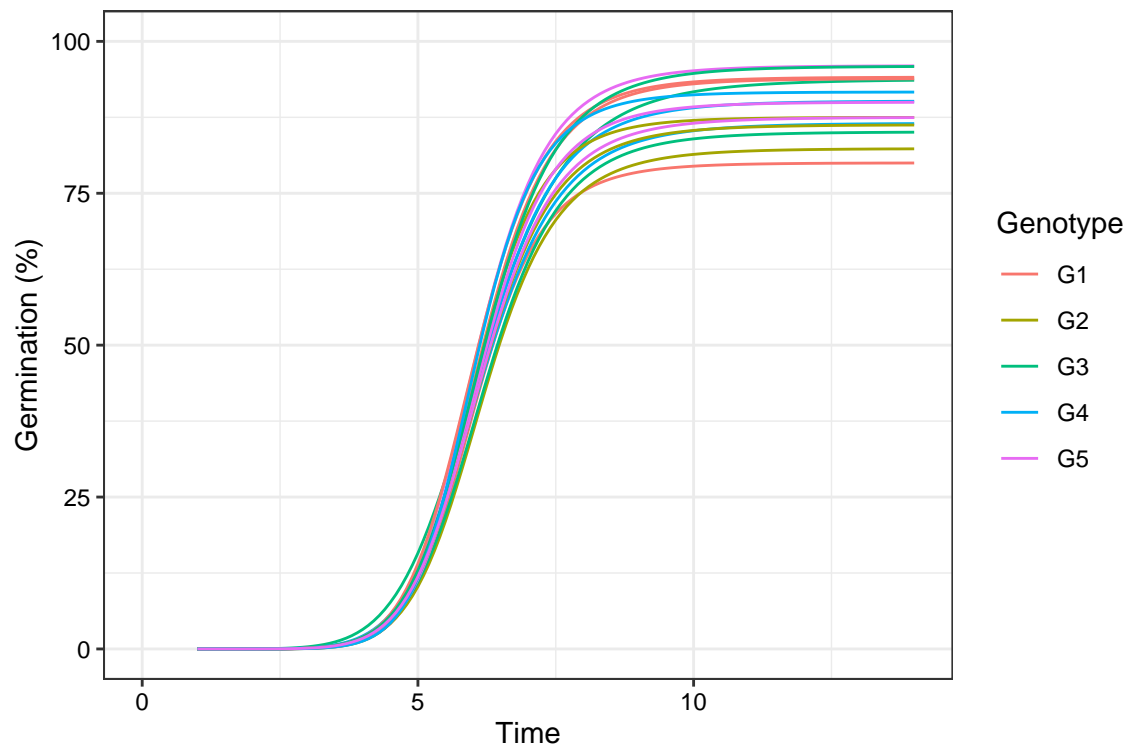


```
# Plot ROG curves
plot(fits, rog = TRUE, group.col = "Genotype")
```
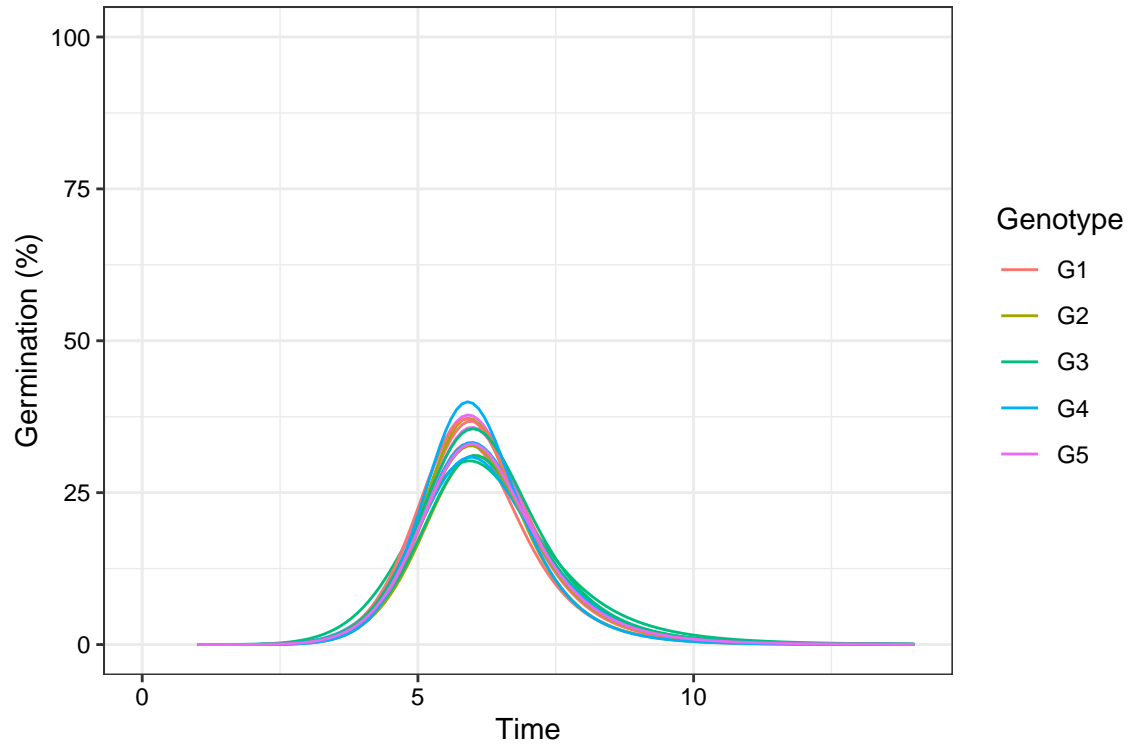
```
# Plot FPHF curves with points
plot(fits, group.col = "Genotype", show.points = TRUE)
```
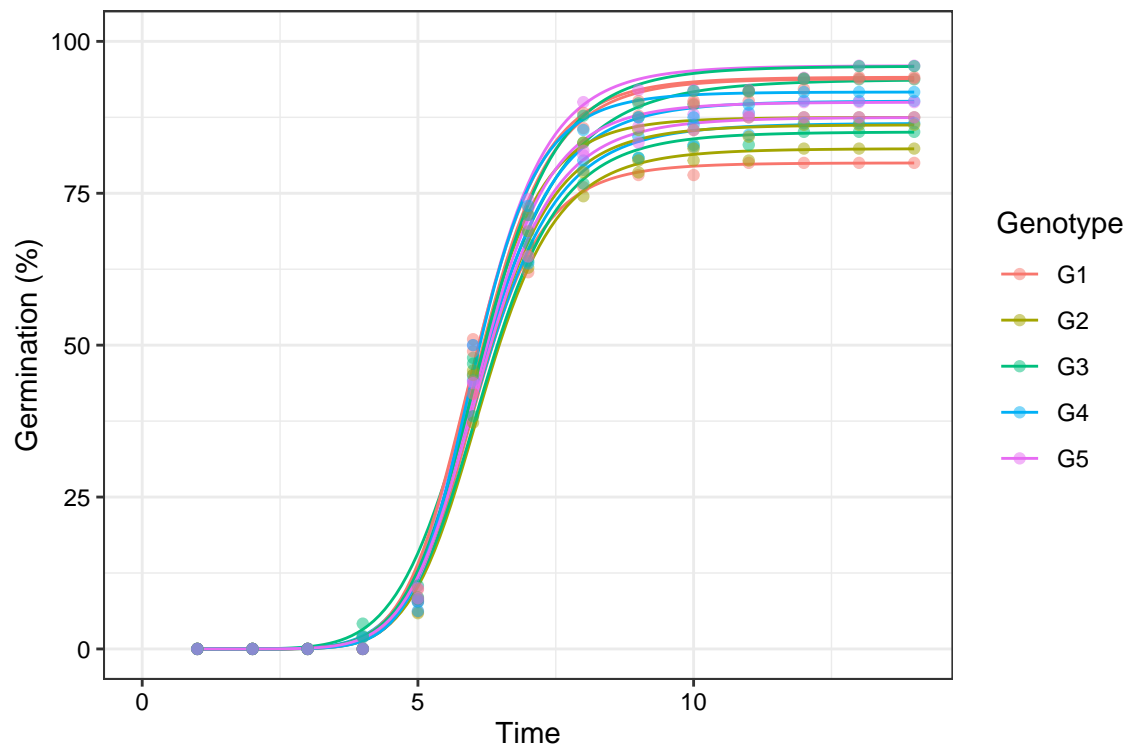


```
# Plot FPHF curves with annotations
plot(fits, group.col = "Genotype", annotate = "t50.total")
```
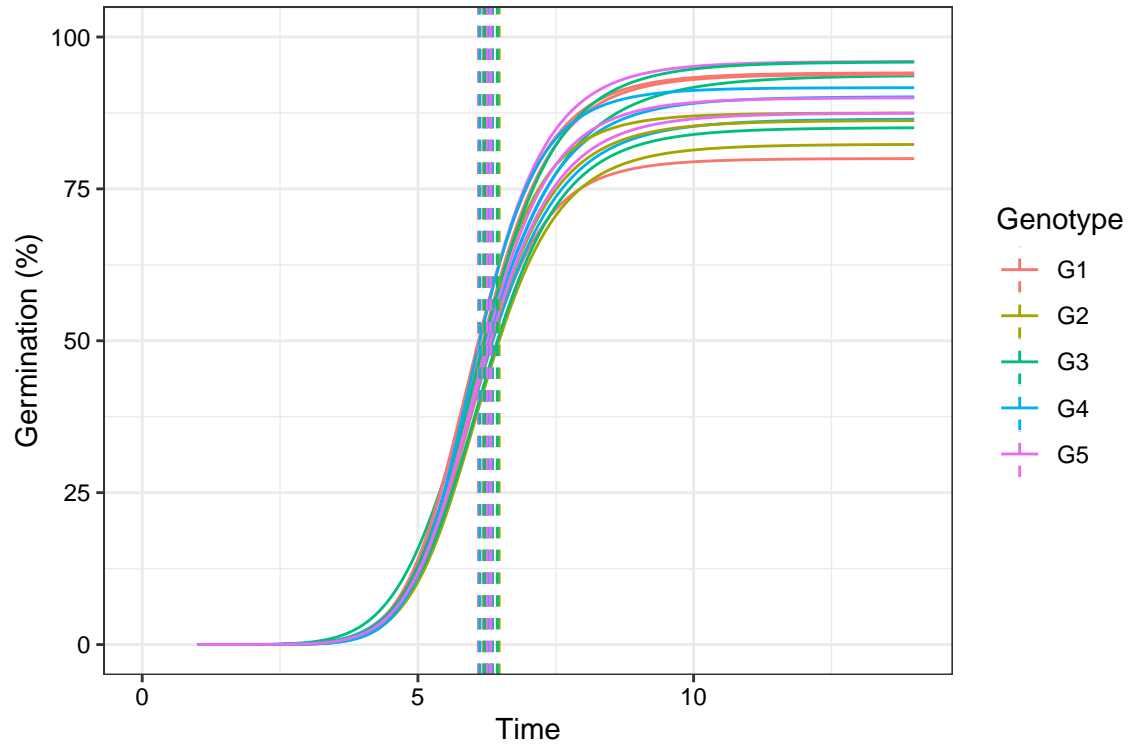
```
plot(fits, group.col = "Genotype", annotate = "t50.germ")
```
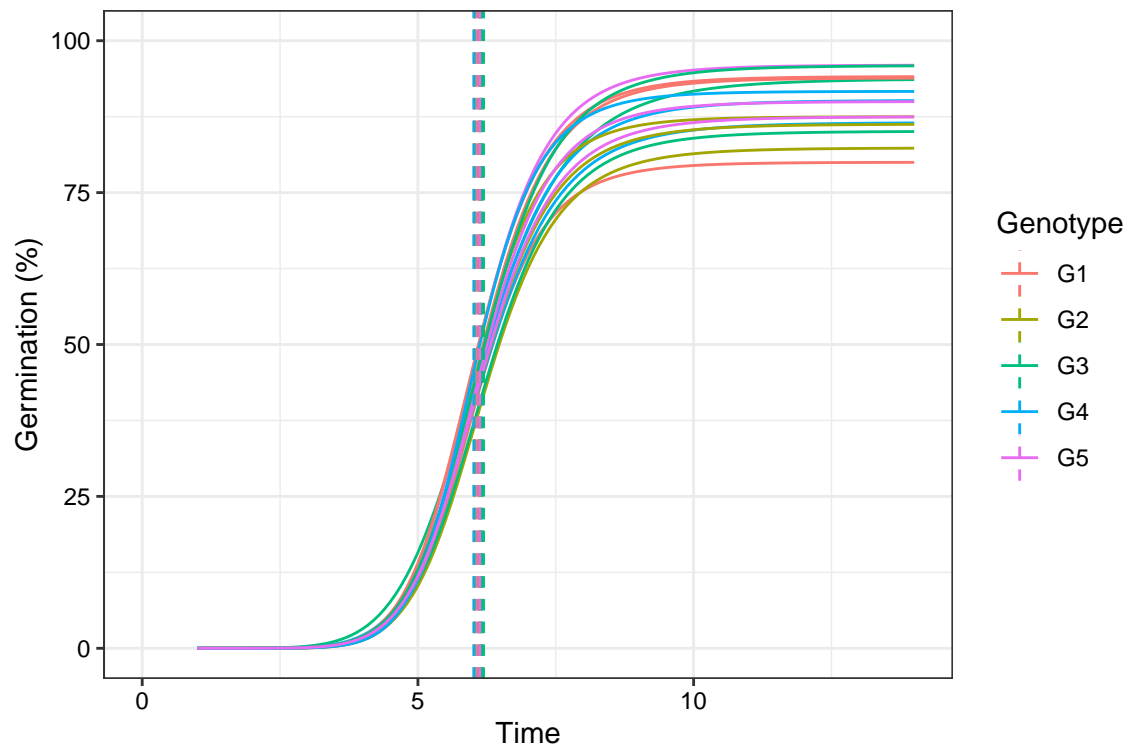


```
plot(fits, group.col = "Genotype", annotate = "tmgr")
```
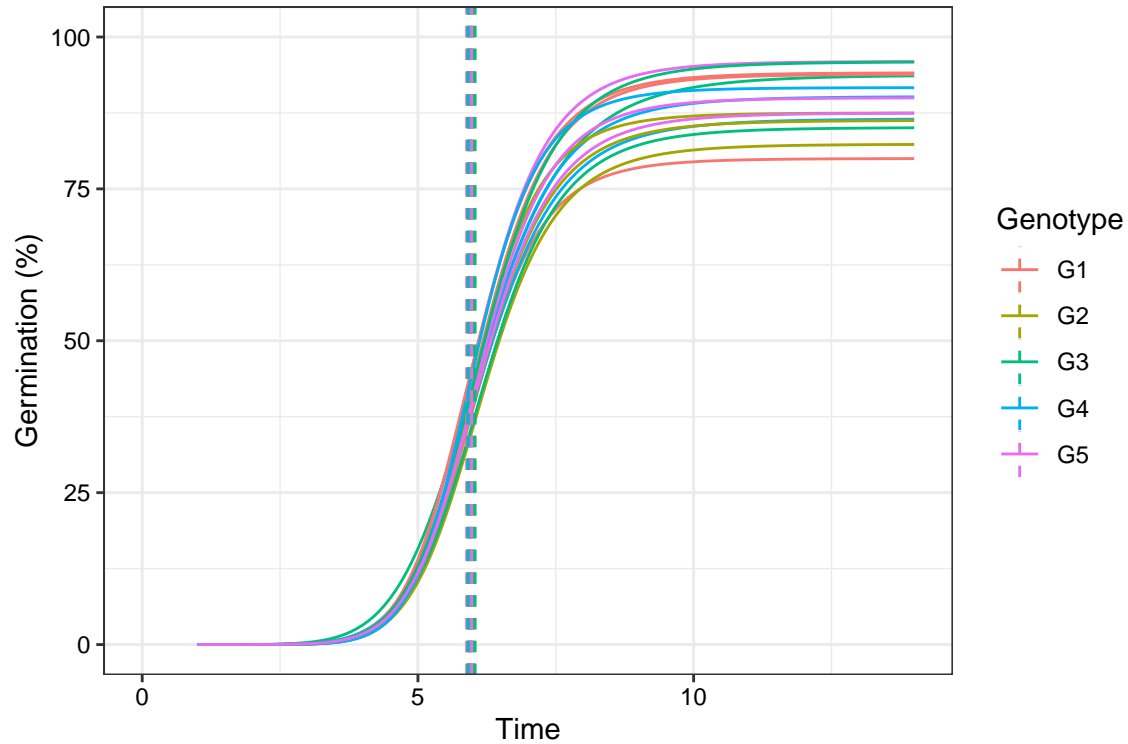
```
plot(fits, group.col = "Genotype", annotate = "mgt")
```
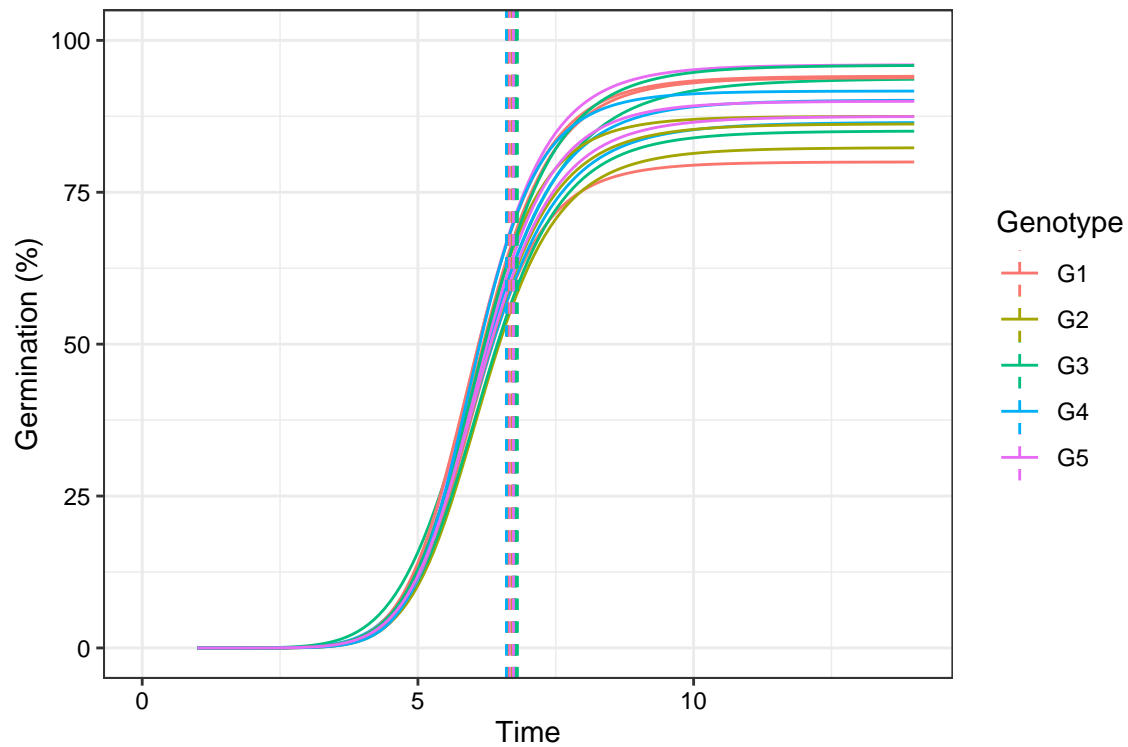


```
plot(fits, group.col = "Genotype", annotate = "uniformity")
```

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

position_dodge requires non-overlapping x intervals
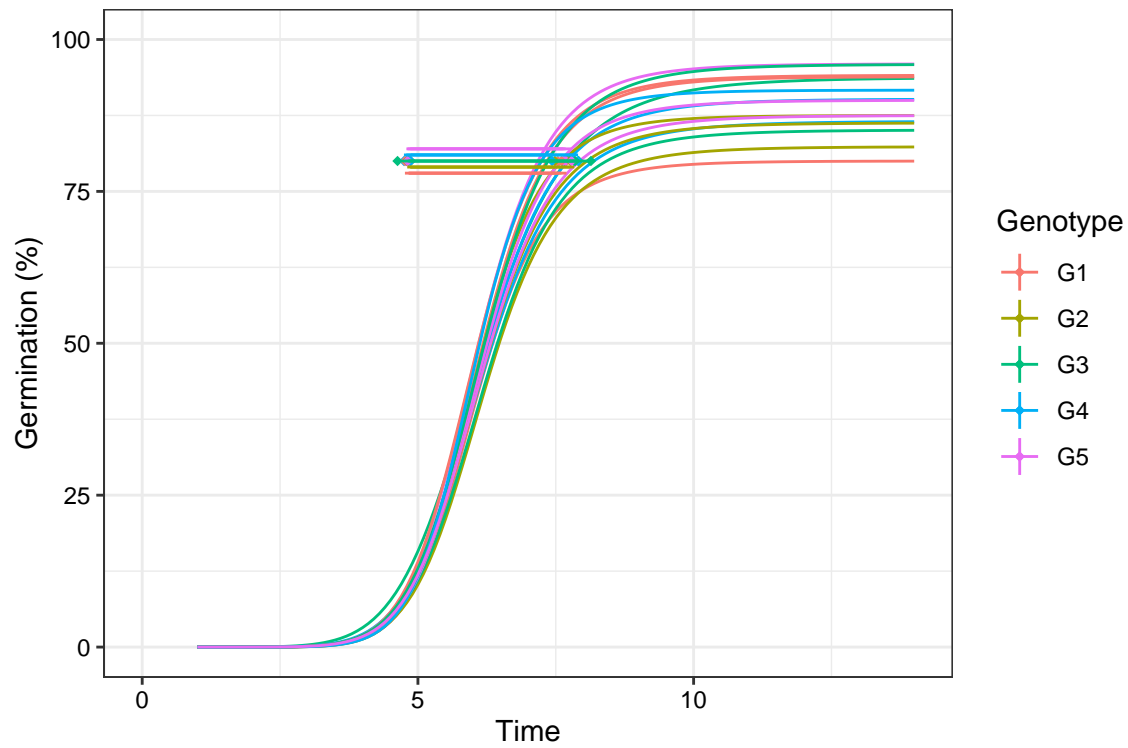

```
# Plot ROG curves with annotations
plot(fits, rog = TRUE, group.col = "Genotype", annotate = "t50.total")
```
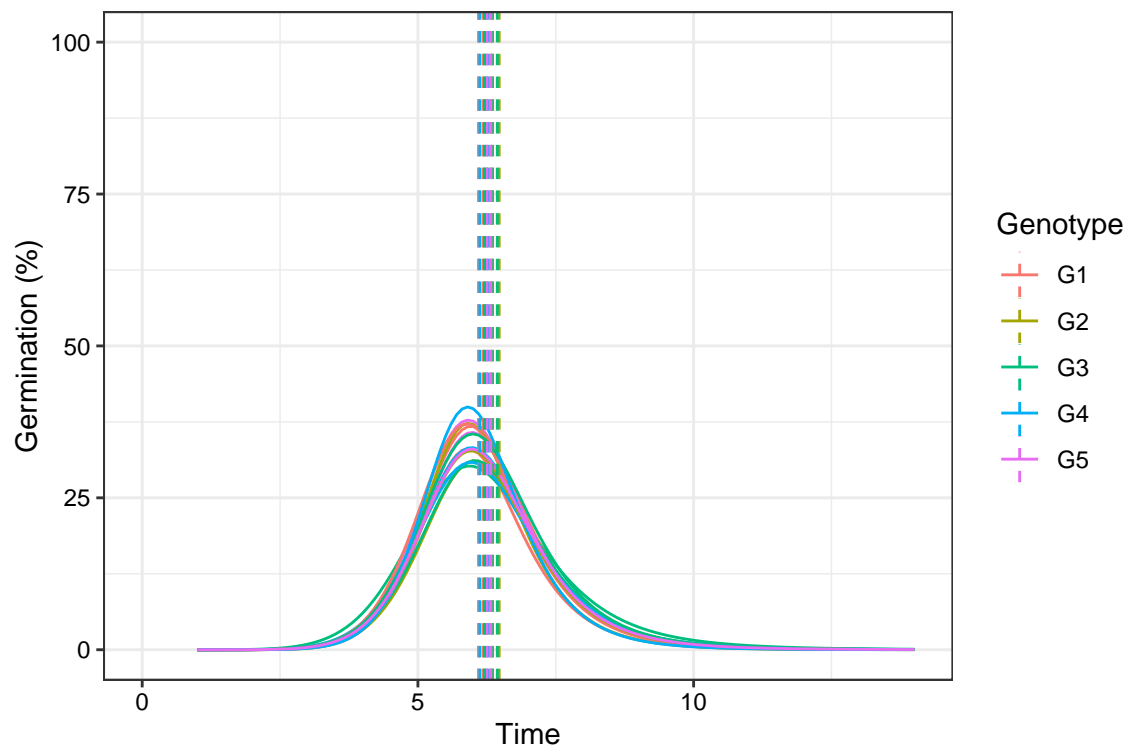
```
plot(fits, rog = TRUE, group.col = "Genotype", annotate = "t50.germ")
```
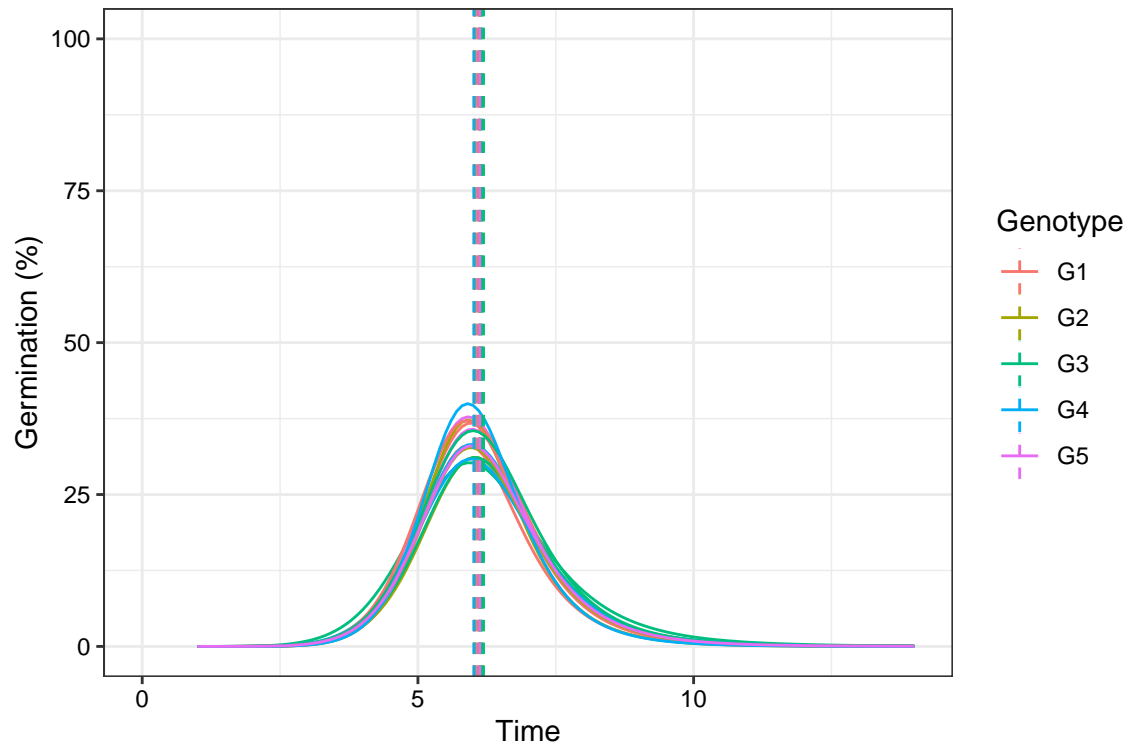


```
plot(fits, rog = TRUE, group.col = "Genotype", annotate = "tmgr")
```
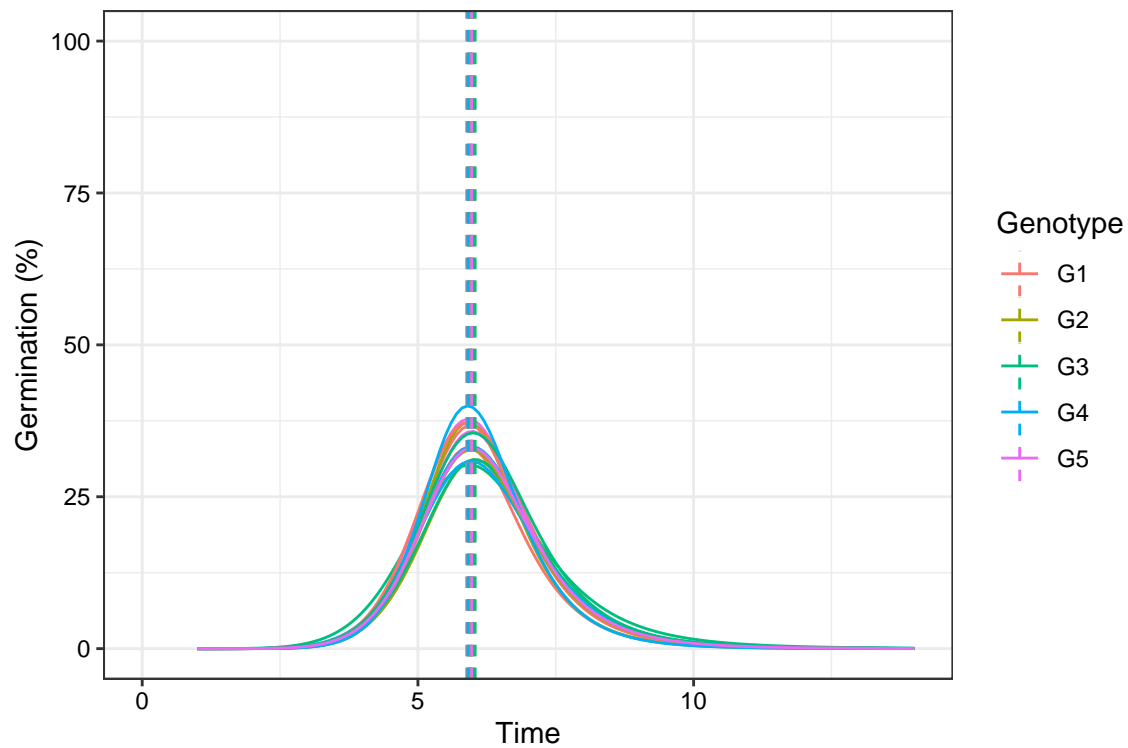
```
plot(fits, rog = TRUE, group.col = "Genotype", annotate = "mgt")
```
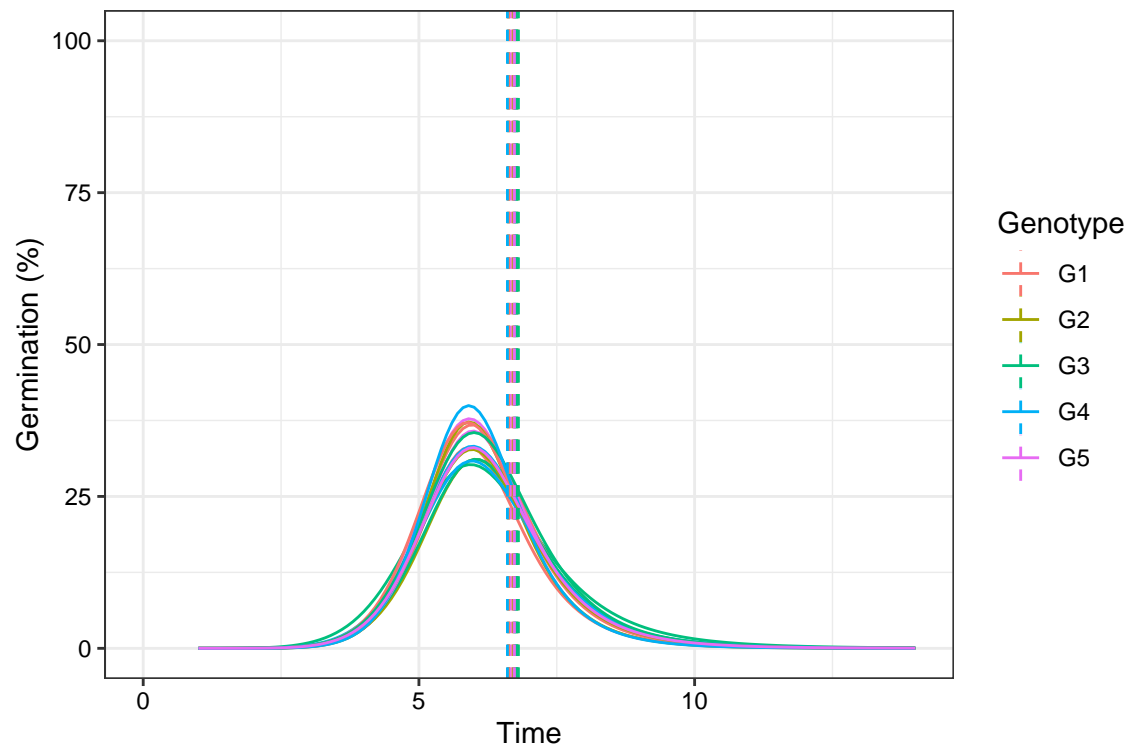


```
plot(fits, rog = TRUE, group.col = "Genotype", annotate = "uniformity")
```

```
Warning: position_dodge requires non-overlapping x intervals
position_dodge requires non-overlapping x intervals
```
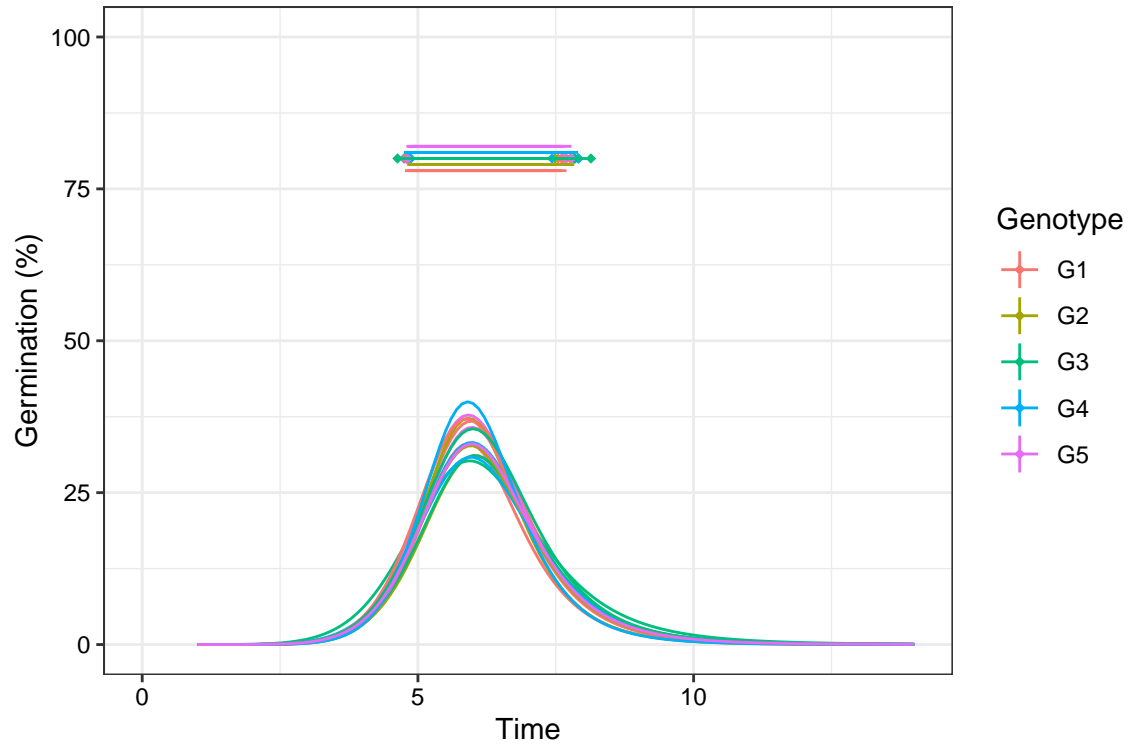
```
# Change colour of curves using ggplot2 options
library(ggplot2)
curvesplot <- plot(fits, group.col = "Genotype")

# 'Dark2' palette from RColorBrewer
curvesplot + scale_colour_brewer(palette = "Dark2")
```
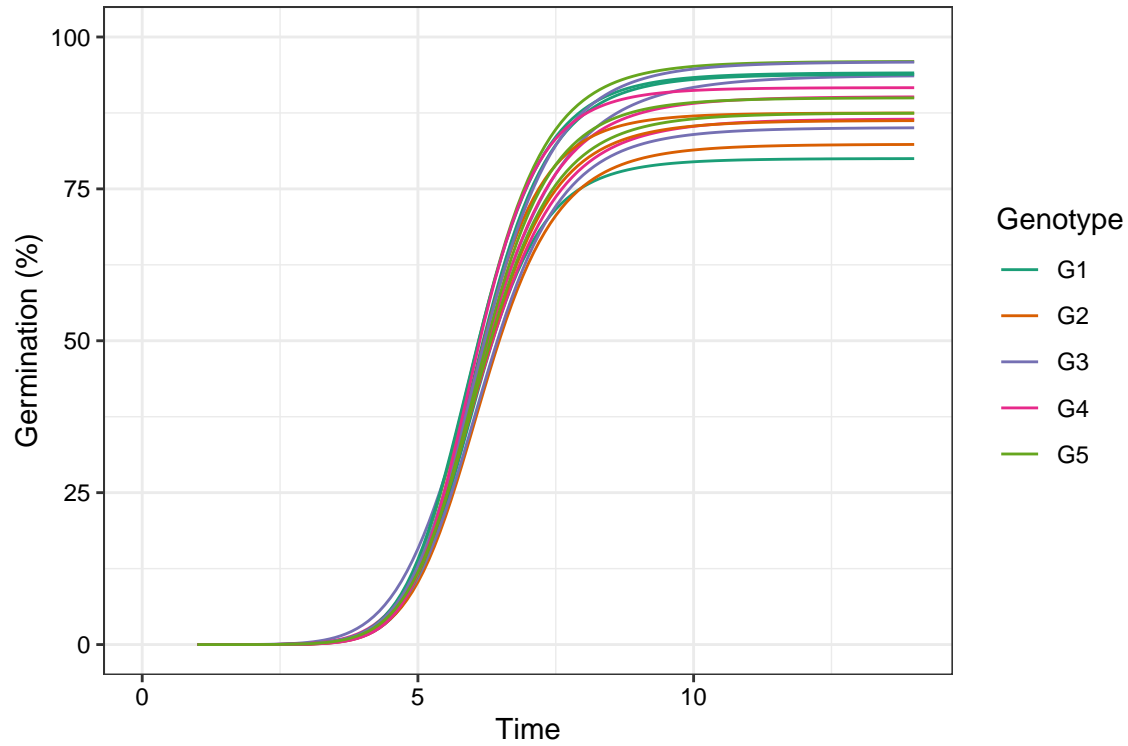
```
# Manual colours
curvesplot +
  scale_colour_manual(values = c("Coral", "Brown", "Blue",
                                 "Aquamarine", "Red"))
```
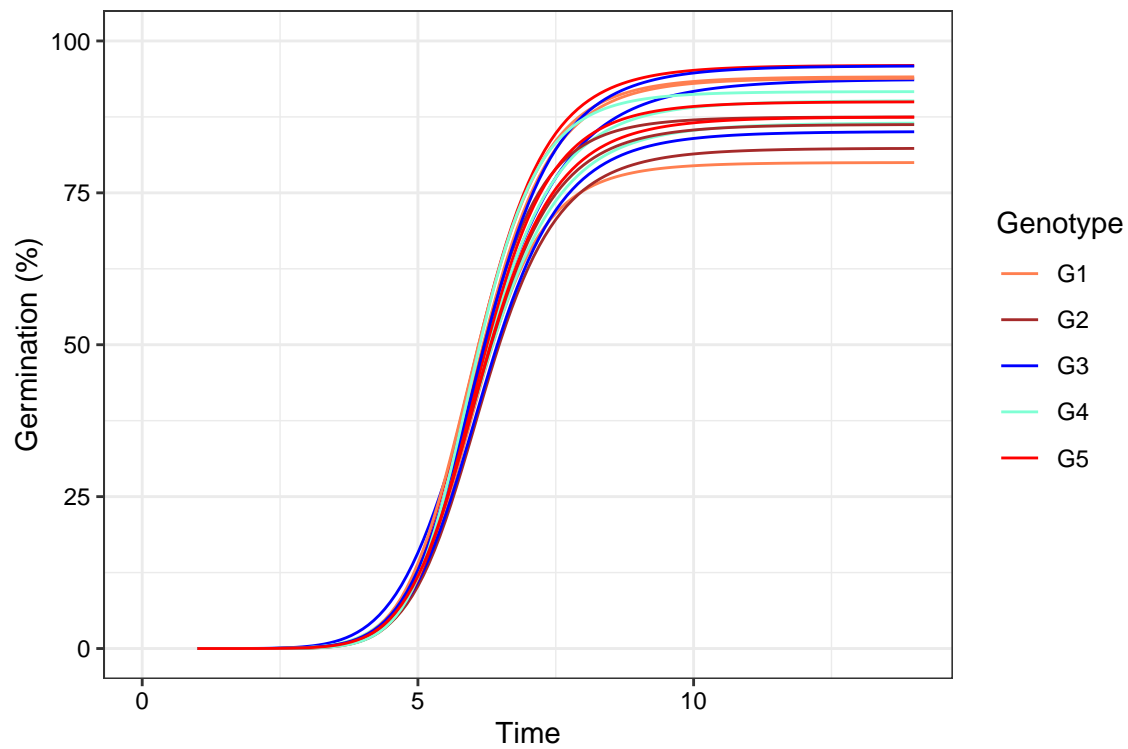
Citing germinationmetrics

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

  Aravind, J., Vimala Devi, S., Radhamani, J., Jacob, S. R., and Kalyani Srinivasan (2022).
  germinationmetrics: Seed Germination Indices and Curve Fitting. R package version 0.1.5.9000,
  https://github.com/aravind-j/germinationmetricshttps://cran.r-project.org/package=germinationmetrics.

A BibTeX entry for LaTeX users is

```
@Manual{,
  title = {germinationmetrics: Seed Germination Indices and Curve Fitting},
  author = {J. Aravind and S. {Vimala Devi} and J. Radhamani and Sherry Rachel Jacob and {Kalyani Srin
  year = {2022},
  note = {R package version 0.1.5.9000},
  note = {https://github.com/aravind-j/germinationmetrics},
  note = {https://cran.r-project.org/package=germinationmetrics},
}
```

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

Session Info

```
sessionInfo()
```

```
R Under development (unstable) (2022-06-05 r82452 ucrt)
Platform: x86_64-w64-mingw32/x64 (64-bit)
Running under: Windows 10 x64 (build 19044)

Matrix products: default

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

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

other attached packages:
[1] germinationmetrics_0.1.5.9000 ggplot2_3.3.6

loaded via a namespace (and not attached):
 [1] tidyselect_1.1.2  farver_2.1.0      dplyr_1.0.9       bitops_1.0-7      RCurl_1.98-1.6    fas
 [7] lazyeval_0.2.2    xopen_1.0.0       mathjaxr_1.6-0    XML_3.99-0.9      rex_1.2.1         dig
[13] lifecycle_1.0.1   ellipsis_0.3.2    processx_3.5.3    magrittr_2.0.3    compiler_4.3.0    rla
[19] tools_4.3.0       utf8_1.2.2        yaml_2.3.5        data.table_1.14.2 knitr_1.39        lab
[25] prettyunits_1.1.1 pkgbuild_1.3.1    curl_4.3.2        xmlparsedata_1.0.5 RColorBrewer_1.1-3 ply
[31] xml2_1.3.3        pkgload_1.2.4     covr_3.5.1        withr_2.5.0       purrr_0.3.4        des
[37] hunspell_3.0.1    grid_4.3.0        goodpractice_1.0.2 fansi_1.0.3       colorspace_2.0-3  who
[43] scales_1.2.0      cli_3.3.0         rmarkdown_2.14    crayon_1.5.1      generics_0.1.2     rem
[49] rstudioapi_0.13   reshape2_1.4.4    httr_1.4.3        sessioninfo_1.2.2 DBI_1.1.2         cac
[55] pander_0.6.5      stringr_1.4.0     assertthat_0.2.1  vctrs_0.4.1       devtools_2.4.3    jso
[61] minpack.lm_1.2-2  callr_3.7.0       rcmdcheck_1.4.0   ggrepel_0.9.1     testthat_3.1.4    cyc
```

```
[67] tidyr_1.2.0        glue_1.6.2         pkgdown_2.0.3      ps_1.7.0           stringi_1.7.6     gtal
[73] munsell_0.5.0      tibble_3.1.7       pillar_1.7.0       clisymbols_1.2.0   htmltools_0.5.2   bric
[79] praise_1.0.0       R6_2.5.1           lintr_2.0.1        Rdpack_2.3         rprojroot_2.0.3   eval
[85] highr_0.9          backports_1.4.1    rbibutils_2.2.8    memoise_2.0.1      broom_0.8.0       Rcpp
[91] xfun_0.31          fs_1.5.2           usethis_2.1.6      pkgconfig_2.0.3
```

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