The `germinationmetrics` Package: A Brief Introduction

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Contents

Overview

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

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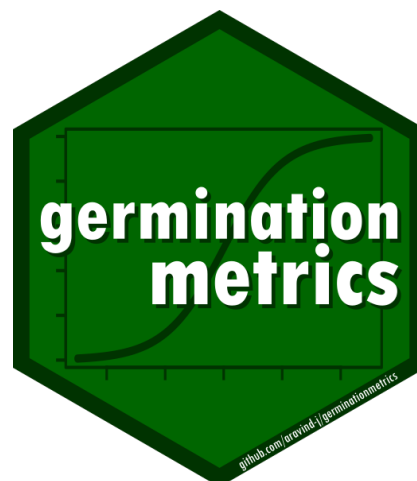
Installation

The package can be installed using the following functions:

```r
# 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

```r
library(germinationmetrics)
```

```
--------------------------------------------------------------------------------
Welcome to germinationmetrics version 0.1.9.9000


# 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 0.1.9. The previous versions are as follows.

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

Version	Date
0.1.0	2018-04-17
0.1.1	2018-07-26
0.1.1.1	2018-10-16
0.1.2	2018-10-31
0.1.3	2019-01-19
0.1.4	2020-06-16
0.1.5	2021-02-17
0.1.6	2022-06-15
0.1.7	2022-08-28
0.1.8	2023-08-18

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)
```

```r
# Time intervals of observations
int <- data$intervals

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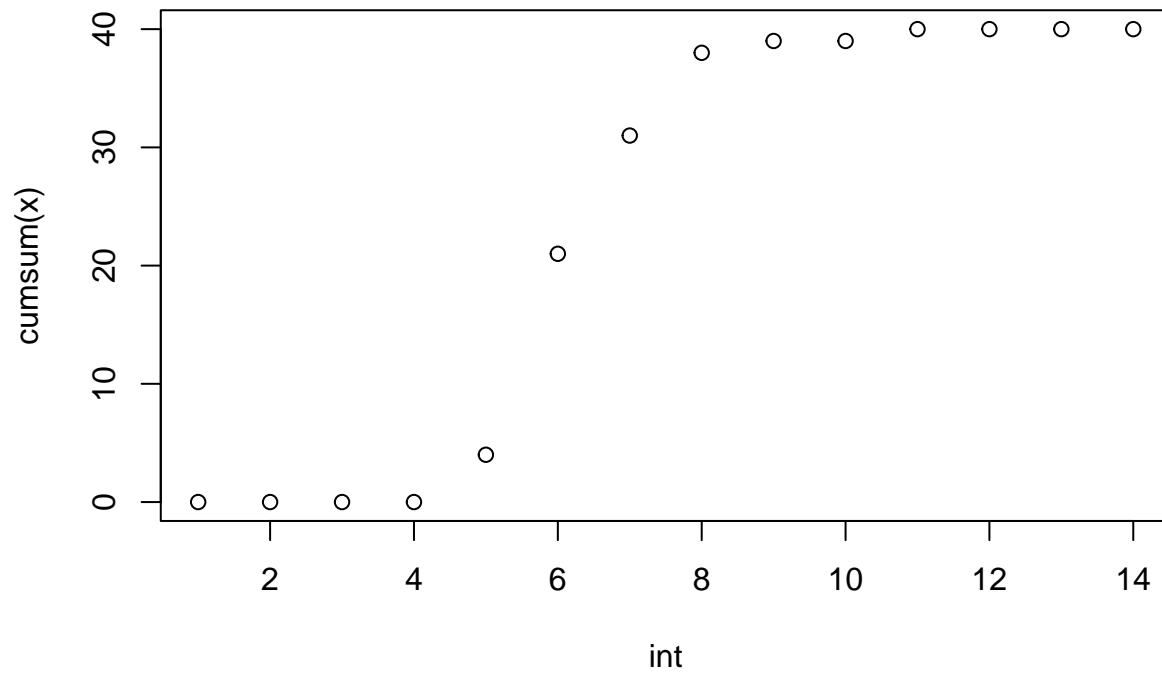

Single-value germination indices

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 (S) 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 ($S_{accumulated}$)	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 cumative/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 speed of germination or Corrected germination rate index ($\hat{S}$)	GermSpeedCorrected	It is computed as follows. $$S_{corrected} = \frac{S}{FGP}$$ Where, S is the germination speed computed with germination percentage instead of counts and FGP is the final germination percentage or germinability. It can also be computed from speed of accumulated germination (computed with germination percentage). $$\hat{S}_{accumulated} = \frac{S_{accumulated}}{FGP}$$ Where, $S_{accumulated}$ is the speed of accumulated germination computed with germination percentage instead of counts and FGP is the final germination percentage or germinability.	time^{-1}	Mixed	Evetts and Burnside (1972)
Weighted germination percentage (WGP)	WeightGermPercent	It is estimated as follows. $$WGP = \frac{\sum_{i=1}^{k}(k-i+1)N_i}{k \times N} \times 100$$ Where, N_i is the number of seeds that germinated in the time interval i (not cumulative, but partial count), N is the total number of seeds tested, and k is the total number of time intervals.	Percentage (%)	Mixed	Reddy et al. (1985); Reddy (1978)
Mean germination percentage per unit time ($\overline{GP}$)	MeanGermPercent	It is estimated as follows. $$\overline{GP} = \frac{GP}{T_k}$$ Where, GP is the final germination percentage, T_k is the time at the kth time interval, and k is the total number of time intervals required for final germination.	% time^{-1}	Mixed	Czabator (1962)

Germination index	Function	Details	Unit	Measures	Reference
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)
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)

Germination index	Function	Details	Unit	Measures	Reference
George's index (GR)	`GermRateGeorge`	It is estimated as follows. $$GR = \sum_{i=1}^{k} N_i K_i$$ Where N_i is the number of seeds germinated by ith interval and K_i is the number of intervals(eg. days) until the end of the test, and and k is the total number of time intervals.	count time	Mixed	George (1961); Tucker and Wright (1965); Nichols and Heydecker (1968);Chopra and Chaudhary (1980)
Germination Index (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)

Germination index	Function	Details	Unit	Measures	Reference
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)
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 index	Function	Details	Unit	Measures	Reference
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 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)

Germination index	Function	Details	Unit	Measures	Reference
Synchronization index ($\overline{E}$) or Uncertainty of the germination process (U) or informational entropy (H)	`GermUncertainty`	It is estimated as follows. $$\overline{E} = -\sum_{i=1}^{k} f_i \log_2 f_i$$ Where, f_i is the relative frequency of germination ($f_i = \frac{N_i}{\sum_{i=1}^{k} N_i}$), N_i is the number of seeds germinated on the ith time interval, and k is the total number of time intervals.	bit	Germination synchrony	Shannon (1948); Labouriau and Valadares (1976); Labouriau (1983b)
Synchrony of germination (Z index)	`GermSynchrony`	It is computed as follows. $$Z = \frac{\sum_{i=1}^{k} C_{N_i,2}}{C_{\Sigma N_i,2}}$$ Where, $C_{N_i,2}$ is the partial combination of the two germinated seeds from among N_i, the number of seeds germinated on the ith time interval (estimated as $C_{N_i,2} = \frac{N_i(N_i-1)}{2}$), and $C_{\Sigma N_i,2}$ is the partial combination of the two germinated seeds from among the total number of seeds germinated at the final count, assuming that all seeds that germinated did so simultaneously.	no unit	Germination synchrony	Primack (1985); Ranal and Santana (2006)

Examples

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

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

GermPercent()

```
[1] 80
```

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

```
[1] 34
```
```
# For multiple peak germination times
PeakGermPercent(germ.counts = z, intervals = int, total.seeds = 50)
```

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

```
[1] 22
```
```
# From cumulative germination counts
#-------------------------------------------------------------------------
GermPercent(germ.counts = y, total.seeds = 50, partial = FALSE)
```

```
[1] 80
```

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

```
[1] 34
```
```
# For multiple peak germination times
PeakGermPercent(germ.counts = cumsum(z), intervals = int, total.seeds = 50,
                partial = FALSE)
```

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

```
[1] 22
```
```
# From number of germinated seeds
#-------------------------------------------------------------------------
GermPercent(germinated.seeds = 40, total.seeds = 50)
```

```
[1] 80
```

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

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

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

```
[1] 5
LastGermTime(germ.counts = x, intervals = int)
```

```
[1] 11
TimeSpreadGerm(germ.counts = x, intervals = int)
```

```
[1] 6
PeakGermTime(germ.counts = x, intervals = int)
```

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

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

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

```
[1] 5
LastGermTime(germ.counts = y, intervals = int, partial = FALSE)
```

```
[1] 11
TimeSpreadGerm(germ.counts = y, intervals = int, partial = FALSE)
```

```
[1] 6
PeakGermTime(germ.counts = y, intervals = int, partial = FALSE)
```

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

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

```
[1] 5 6
```

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

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

```
t50()
```

```
[1] 5.970588
```

```
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] 1.446154
```

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

```
[1] 0.1901416
```

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

```
[1] 0.1794868
```

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

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

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

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

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

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

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

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

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

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

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

```
[1] 0.0007176543
```
```r
SEGermRate(germ.counts = y, intervals = int, partial = FALSE)
```

```
[1] 0.004235724
```
```r
GermRateRecip(germ.counts = y, intervals = int,
              method = "coolbear", partial = FALSE)
```

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

```
[1] 0.1683168
```

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

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

GermSpeed(), GermSpeedAccumulated(), GermSpeedCorrected()

```
[1] 6.138925
```

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

```
[1] 34.61567
```

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

```
[1] 0.1534731
```

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

```
[1] 0.8653917
# From partial germination counts (with percentages instead of counts)
#------------------------------------------------------------------------------
GermSpeed(germ.counts = x, intervals = int,
          percent = TRUE, total.seeds = 50)
```

```
[1] 12.27785
```

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

```
[1] 69.23134
# From cumulative germination counts
#------------------------------------------------------------------------------
GermSpeed(germ.counts = y, intervals = int, partial = FALSE)
```

```
[1] 6.138925
```

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

```
[1] 34.61567
```

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

```
[1] 0.1534731
```

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

```
[1] 0.8653917
# From cumulative germination counts (with percentages instead of counts)
#------------------------------------------------------------------------------
```

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

```
[1] 12.27785
```

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

```
[1] 69.23134
```

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

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

WeightGermPercent()

```
[1] 47.42857
```

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

```
[1] 47.42857
```

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

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

MeanGermPercent(), MeanGermNumber()

```
[1] 5.714286
```

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

```
[1] 2.857143
```

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

```
[1] 5.714286
```

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

```
[1] 2.857143
```

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

```
[1] 5.714286
```

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

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

```
TimsonsIndex(), GermRateGeorge()
```

```
[1] 664
```

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

```
[1] 664
```

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

```
[1] 8.3
```

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

```
[1] 47.42857
```

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

```
[1] 332
```

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

```
[1] 344
```

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

```
[1] 344
```

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

```
[1] 4.410256
```

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

```
[1] 24.57143
```

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

```
[1] 172
```

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

```
[1] 332
```

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

```
[1] 664
```

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

```
[1] 664
```

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

```
[1] 8.3
```

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

```
[1] 47.42857
```

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

```
[1] 332
```

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

```
[1] 344
```

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

```
[1] 344
```

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

```
[1] 4.410256
```

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

```
[1] 24.57143
```

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

```
[1] 172
```

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

```
[1] 332
```

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

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

```
GermIndex()
```

```
[1] 5.84
```

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

```
[1] 5.84
```

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

```
[1] 7.3
```

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

```
[1] 5.84
```

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

```
[1] 5.84
```

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

```
[1] 7.3
```

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

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

```
EmergenceRateIndex()
```

```
[1] 292
EmergenceRateIndex(germ.counts = x, intervals = int, total.seeds = 50,
                   method = "shmueligoldberg")
```

```
[1] 292
EmergenceRateIndex(germ.counts = x, intervals = int, total.seeds = 50,
                   method = "sgsantanaranal")
```

```
[1] 7.3
EmergenceRateIndex(germ.counts = x, intervals = int, total.seeds = 50,
                   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, total.seeds = 50,
                   partial = FALSE)
```

```
[1] 292
EmergenceRateIndex(germ.counts = y, intervals = int, total.seeds = 50,
                   partial = FALSE,
                   method = "shmueligoldberg")
```

```
[1] 292
EmergenceRateIndex(germ.counts = y, intervals = int, total.seeds = 50,
                   partial = FALSE,
                   method = "sgsantanaranal")
```

```
[1] 7.3
EmergenceRateIndex(germ.counts = y, intervals = int, total.seeds = 50,
                   partial = FALSE,
                   method = "bilbrowanjura")
```

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

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

```
[1] 9.5
```

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

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

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

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

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

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

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

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

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

```r
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] 0.7092199
```

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

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

```
GermSynchrony(), GermUncertainty()
```

```
[1] 0.2666667
```

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

```
[1] 2.062987
```

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

```
[1] 0.2666667
```

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

```
[1] 2.062987
```

Non-linear regression analysis

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

Four-parameter hill function

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

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

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

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

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

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

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

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

Germination parameters	Details	Unit	Measures
y intercept (y_0)	The intercept on the y axis.		
Asymptote (a)	It is the maximum cumulative germination percentage, which is equivalent to germination capacity.	%	Germination capacity
Shape and steepness (b)	Mathematical parameter controlling the shape and steepness of the germination curve. The larger the b, the steeper the rise toward the asymptote a, and the shorter the time between germination onset and maximum germination.		Germination rate

Germination parameters	Details	Unit	Measures
Half-maximal activation level (c)	Time required for 50% of viable seeds to germinate.	time	Germination time
lag	It is the time at germination onset and is computed by solving four-parameter hill function after setting y to 0 as follows. $$lag = b\sqrt{\frac{-y_0 c^b}{a + y_0}}$$	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. $$\frac{MGT}{t_{50_{germinated}}}$$		

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Examples

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

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

FourPHFfit()

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

```
$Parameters
  term estimate  std.error statistic      p.value
1  bta 2.290709 0.05602634  40.88628 2.965932e-14
2    c 6.034954 0.03872162 155.85488 3.270089e-21
```

```
$Fit
     sigma isConv      finTol    logLik      AIC      BIC deviance df.residual nobs
1 1.61522    TRUE 7.105427e-14 -25.49868 56.99736 58.91453 31.30723          12   14
```

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

```
$b
[1] 9.881937
```

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

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

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

```
$Dlag50
[1] 6.034954


$t50.total
[1] 6.355121


$txp.total
       10        60
4.956264 6.744598


$t50.Germinated
[1] 6.034954


$txp.Germinated
       10        60
4.831807 6.287724


$Uniformity
         90          10 uniformity
   7.537690    4.831807    2.705882


$TMGR
[1] 5.912194


$AUC
[1] 1108.976


$MGT
[1] 6.632252


$Skewness
[1] 1.098973


$msg
[1] "#1. success "


$isConv
[1] TRUE


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


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


Number of iterations to convergence: 9
Achieved convergence tolerance: 7.105e-14


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

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

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


$Parameters
  term estimate  std.error statistic      p.value
1  bta 2.290709 0.05602634  40.88628 2.965932e-14
2    c 6.034954 0.03872162 155.85488 3.270089e-21


$Fit
     sigma isConv      finTol    logLik      AIC      BIC deviance df.residual nobs
1 1.61522   TRUE 7.105427e-14 -25.49868 56.99736 58.91453 31.30723          12   14


$a
[1] 80


$b
[1] 9.881937


$c
[1] 6.034954


$y0
[1] 0


$lag
[1] 0


$Dlag50
[1] 6.034954


$t50.total
[1] 6.355121


$txp.total
      10       60
```

```
4.956264 6.744598

$t50.Germinated
[1] 6.034954

$txp.Germinated
       10        60
4.831807 6.287724

$Uniformity
         90          10 uniformity
   7.537690    4.831807    2.705882

$TMGR
[1] 5.912194

$AUC
[1] 1108.976

$MGT
[1] 6.632252

$Skewness
[1] 1.098973

$msg
[1] "#1. success "

$isConv
[1] TRUE

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

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

Number of iterations to convergence: 9
Achieved convergence tolerance: 7.105e-14

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
#-------------------------------------------------------------------------
```

```r
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)
```

Warning in geom_segment(aes(x = UfmMin, xend = UfmMax, y = ypos2, yend = ypos2), : All aesthetics have
i Please consider using `annotate()` or provide this layer with data containing a single row.

Warning in geom_segment(aes(x = UfmMax, xend = UfmMin, y = ypos2, yend = ypos2), : All aesthetics have
i Please consider using `annotate()` or provide this layer with data containing a single row.
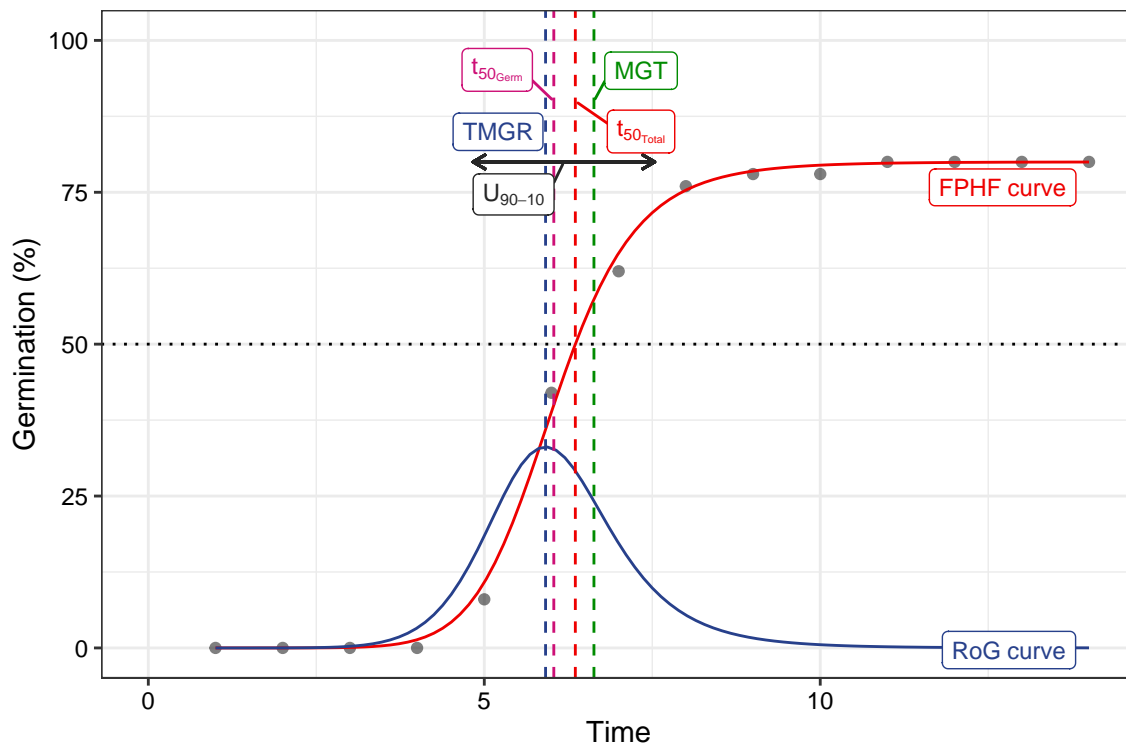

```r
plot(fit2)
```

Warning in geom_segment(aes(x = UfmMin, xend = UfmMax, y = ypos2, yend = ypos2), : All aesthetics have
i Please consider using `annotate()` or provide this layer with data containing a single row.
All aesthetics have length 1, but the data has 14 rows.
i Please consider using `annotate()` or provide this layer with data containing a single row.
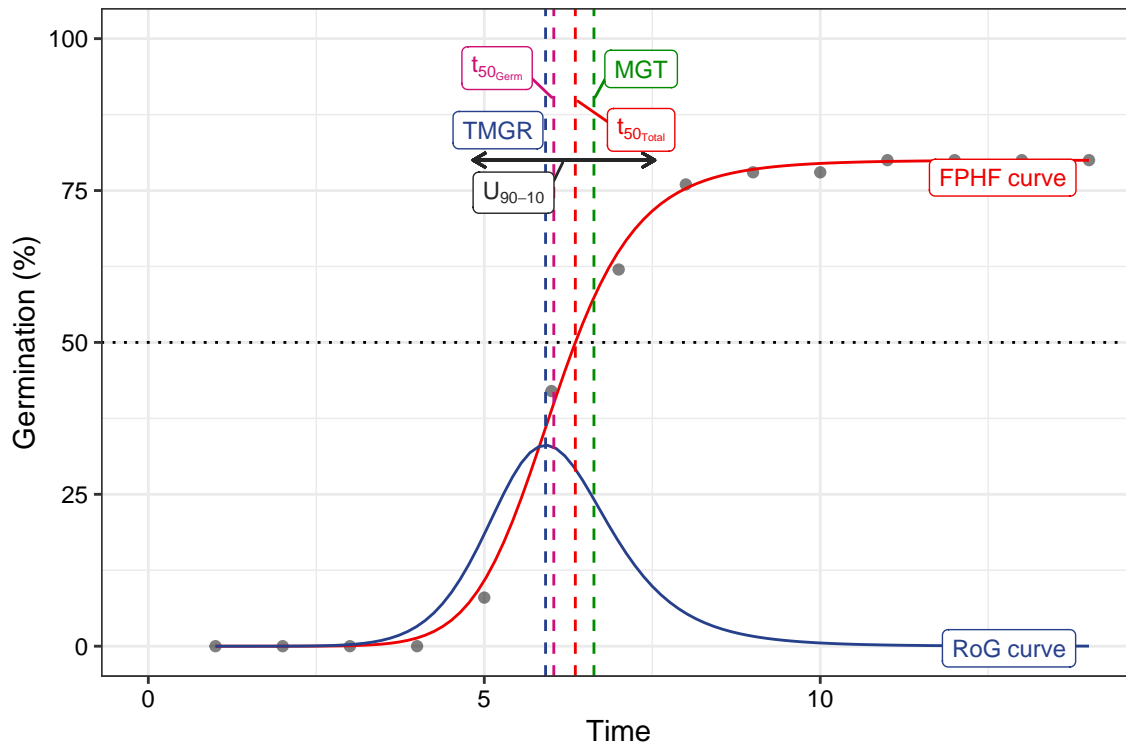
```
# No labels
plot(fit1, plotlabels = FALSE)
```

Warning in geom_segment(aes(x = UfmMin, xend = UfmMax, y = ypos2, yend = ypos2), : All aesthetics have l
i Please consider using `annotate()` or provide this layer with data containing a single row.
All aesthetics have length 1, but the data has 14 rows.
i Please consider using `annotate()` or provide this layer with data containing a single row.
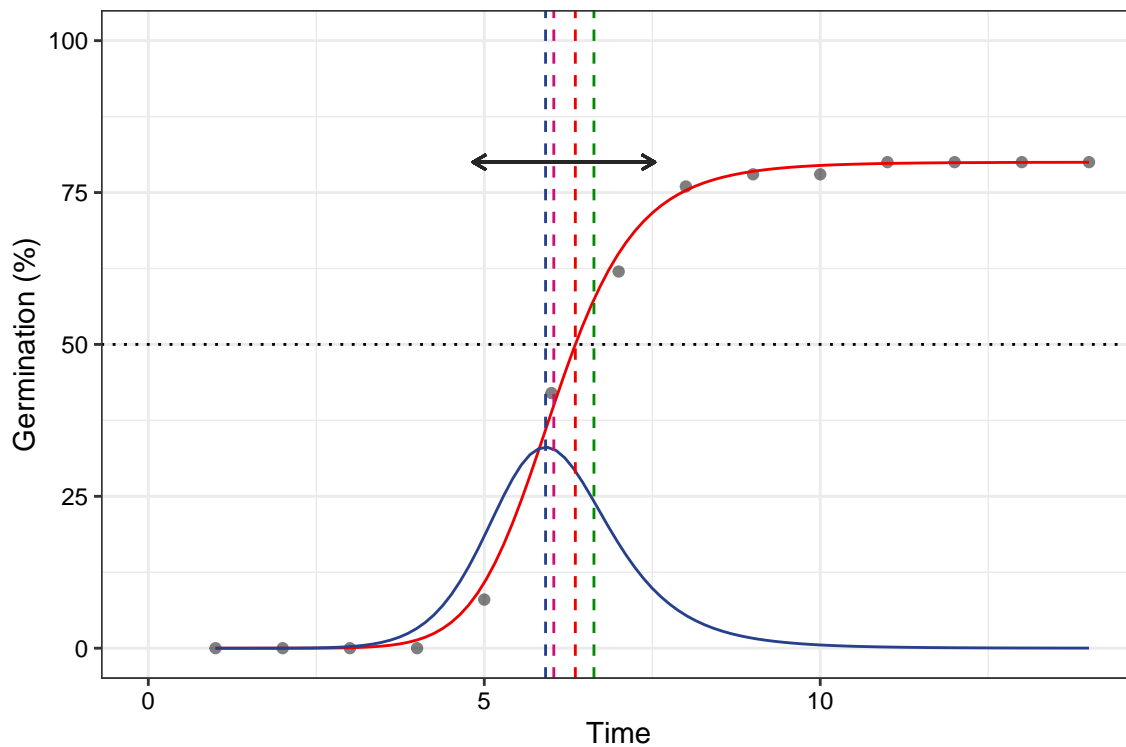
```r
plot(fit2, plotlabels = FALSE)
```

```
Warning in geom_segment(aes(x = UfmMin, xend = UfmMax, y = ypos2, yend = ypos2), : All aesthetics have
i Please consider using `annotate()` or provide this layer with data containing a single row.
All aesthetics have length 1, but the data has 14 rows.
i Please consider using `annotate()` or provide this layer with data containing a single row.
```
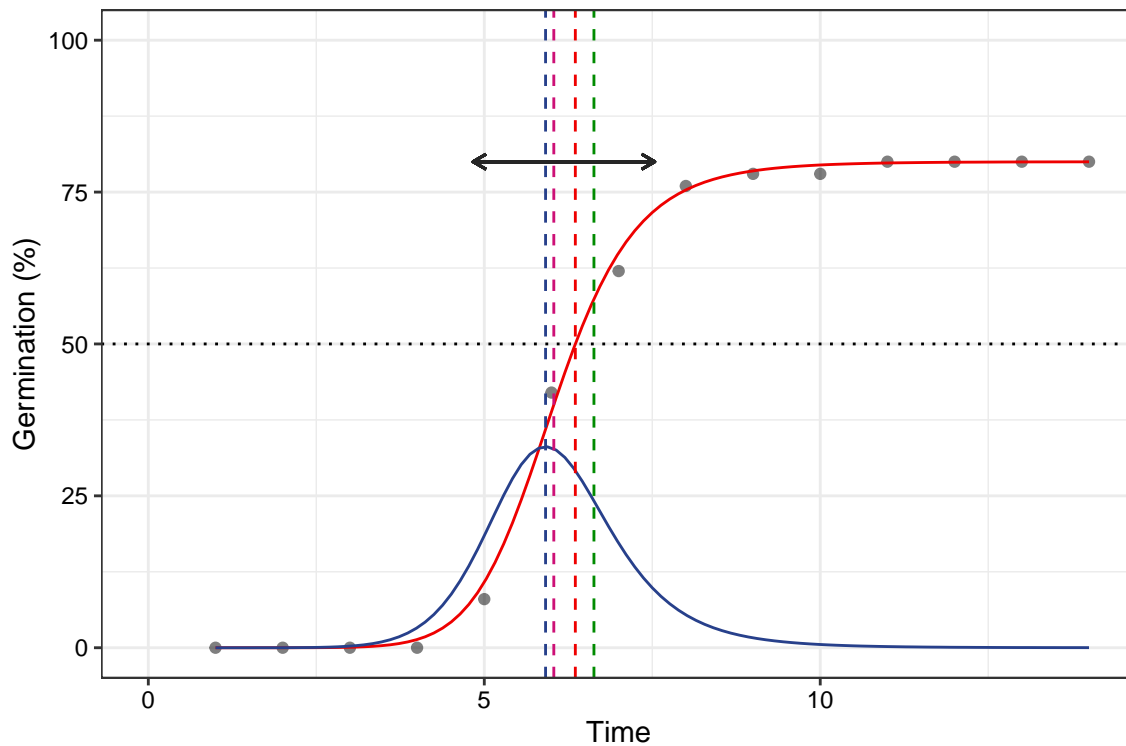


```r
# Only the FPHF curve
plot(fit1, rog = FALSE, t50.total = FALSE, t50.germ = FALSE,
     tmgr = FALSE, mgt = FALSE, uniformity = FALSE)
```
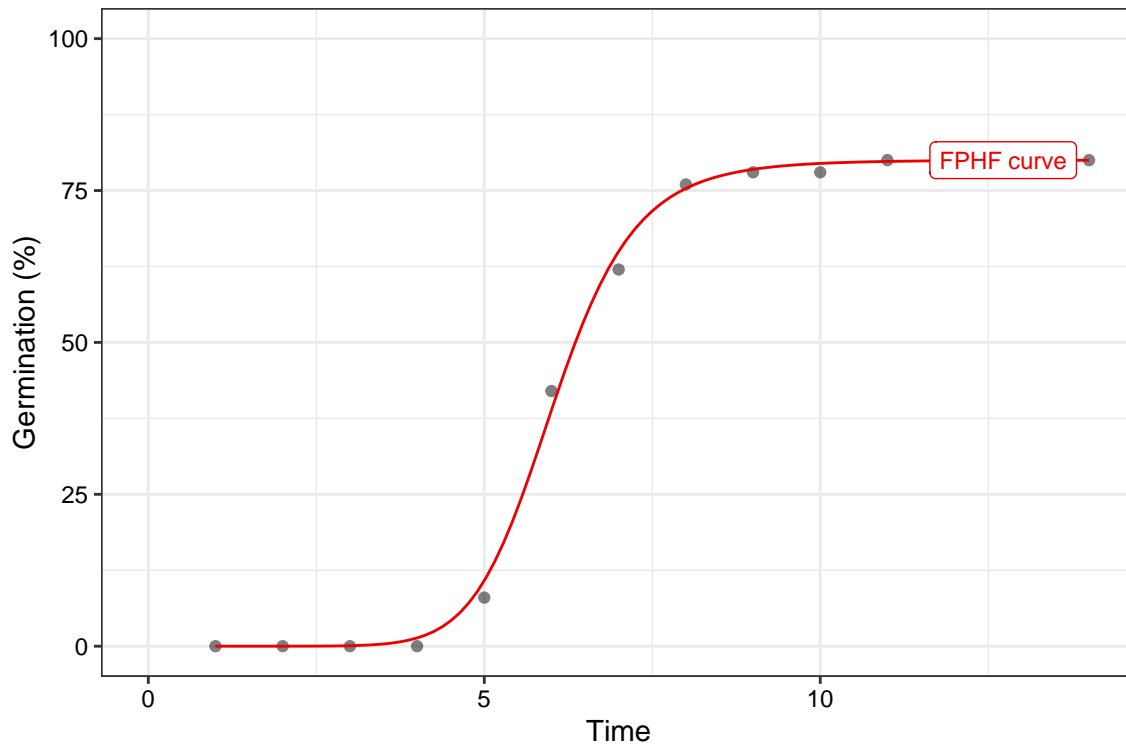
```
plot(fit2, rog = FALSE, t50.total = FALSE, t50.germ = FALSE,
     tmgr = FALSE, mgt = FALSE, uniformity = FALSE)
```
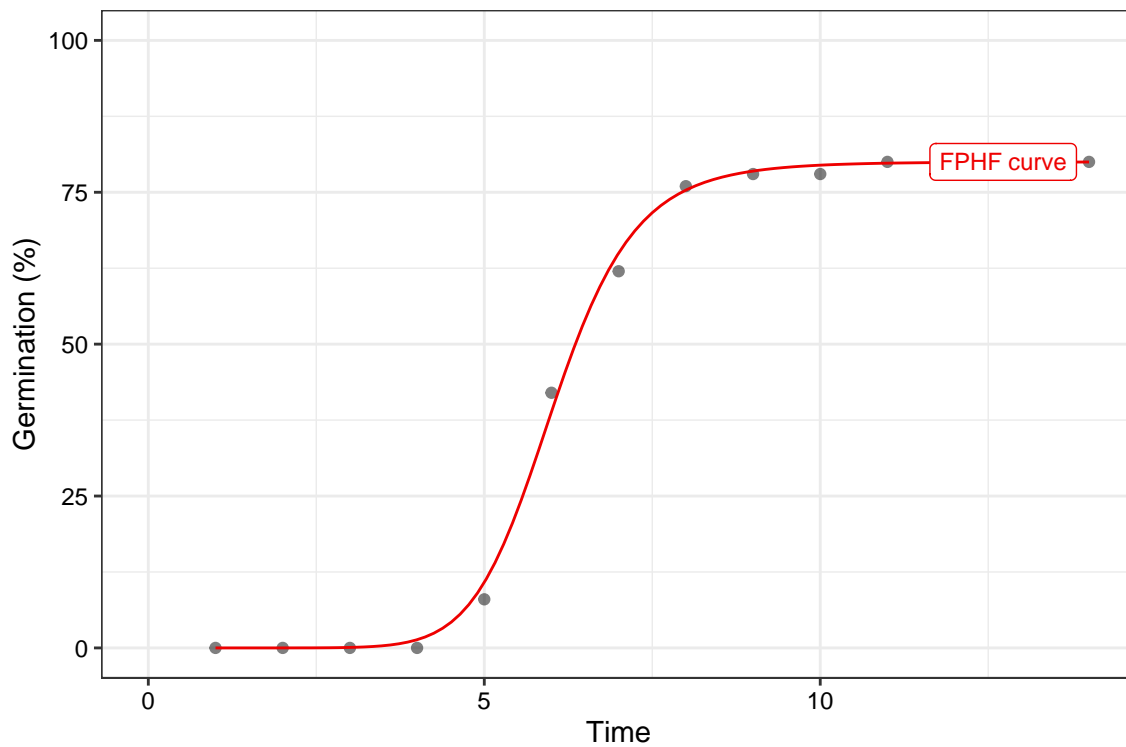


```
# Without y axis limits adjustment
plot(fit1, limits = FALSE)
```

```
Warning in geom_segment(aes(x = UfmMin, xend = UfmMax, y = ypos2, yend = ypos2), : All aesthetics have
```

```
i Please consider using `annotate()` or provide this layer with data containing a single row.
All aesthetics have length 1, but the data has 14 rows.
i Please consider using `annotate()` or provide this layer with data containing a single row.
```
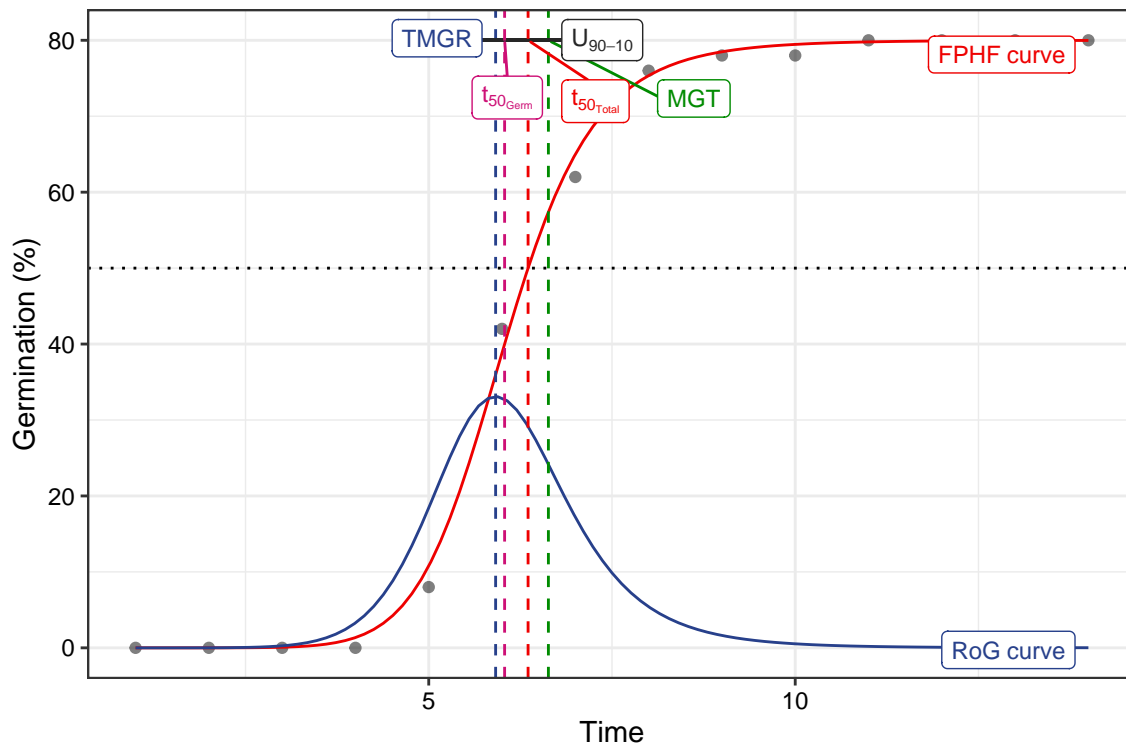


```
plot(fit2, limits = FALSE)
```

```
Warning in geom_segment(aes(x = UfmMin, xend = UfmMax, y = ypos2, yend = ypos2), : All aesthetics have
i Please consider using `annotate()` or provide this layer with data containing a single row.
All aesthetics have length 1, but the data has 14 rows.
i Please consider using `annotate()` or provide this layer with data containing a single row.
```
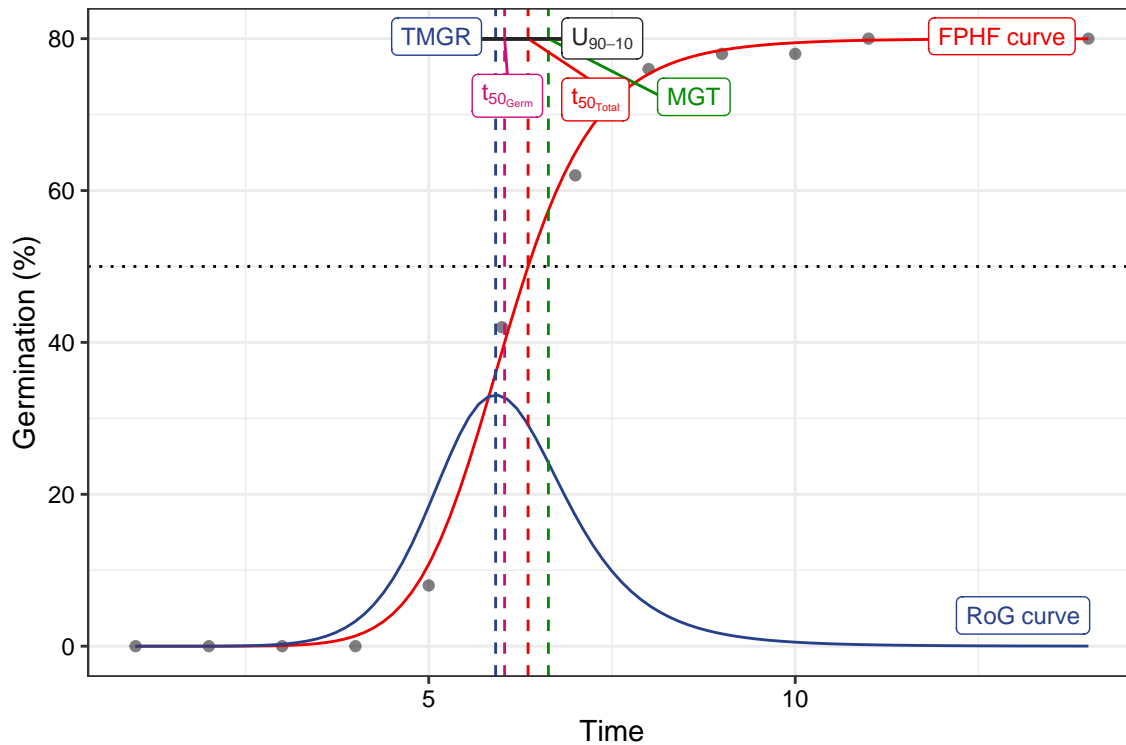
Wrapper functions

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.

```r
data(gcdata)

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

	Genotype	Rep	Day01	Day02	Day03	Day04	Day05	Day06	Day07	Day08	Day09	Day10	Day11	Day12	Day13	Day14
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

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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

	Total Seeds	GermPercent	PeakGermPercent	FirstGermTime	LastGermTime	PeakGermTime	TimeSpreadGerm	t50_C...
1	50	80.00000	34.00000	5	11	6	6	5
2	51	82.35294	29.41176	4	12	6	8	6
3	48	93.75000	37.50000	4	12	6	8	6
4	51	90.19608	37.25490	5	12	6	7	6
5	50	96.00000	40.00000	5	13	6	8	5
6	49	93.87755	42.85714	5	12	6	7	5
7	48	87.50000	37.50000	5	11	6	6	5
8	47	85.10638	29.78723	4	12	6	8	6
9	52	86.53846	36.53846	4	12	6	8	6
10	50	90.00000	36.00000	5	12	6	7	6
11	51	94.11765	41.17647	5	13	6	8	5
12	51	86.27451	39.21569	5	12	6	7	5
13	49	95.91837	38.77551	5	13	6	8	6
14	48	91.66667	43.75000	5	12	6	7	5
15	48	87.50000	35.41667	5	11	6	6	6

	t50_Farooq	MeanGermTime	VarGermTime	SEGermTime	CVGermTime	MeanGermRate	VarGermRate	SEGermRate	
1	5.941176	6.700000	1.446154	0.1901416	0.1794868	0.1492537	0.0007176543	0.004235724	14.9...
2	6.153846	6.857143	2.027875	0.2197333	0.2076717	0.1458333	0.0009172090	0.004673148	14.58...
3	5.972222	6.866667	2.572727	0.2391061	0.2335882	0.1456311	0.0011572039	0.005071059	14.56...
4	6.225806	6.891304	2.187923	0.2180907	0.2146419	0.1451104	0.0009701218	0.004592342	14.51...
5	5.950000	6.812500	2.368351	0.2221275	0.2259002	0.1467890	0.0010995627	0.004786184	14.67...
6	5.952381	6.869565	2.071498	0.2122088	0.2095140	0.1455696	0.0009301809	0.004496813	14.55...
7	5.944444	6.690476	1.389663	0.1818989	0.1761967	0.1494662	0.0006935558	0.004063648	14.94...
8	6.166667	6.875000	2.112179	0.2297923	0.2113940	0.1454545	0.0009454531	0.004861721	14.54...
9	5.973684	6.866667	2.300000	0.2260777	0.2208604	0.1456311	0.0010345321	0.004794747	14.56...
10	6.038462	6.822222	1.831313	0.2017321	0.1983606	0.1465798	0.0008453940	0.004334343	14.65...
11	5.904762	6.791667	2.381206	0.2227295	0.2272072	0.1472393	0.0011191581	0.004828643	14.72...
12	5.950000	6.886364	2.149577	0.2210295	0.2129053	0.1452145	0.0009558577	0.004660905	14.51...
13	6.041667	6.936170	2.539315	0.2324392	0.2297410	0.1441718	0.0010970785	0.004831366	14.41...
14	5.904762	6.772727	1.900634	0.2078370	0.2035568	0.1476510	0.0009033254	0.004531018	14.76...
15	6.259259	6.809524	1.670151	0.1994129	0.1897847	0.1468531	0.0007767634	0.004300508	14.68...

	GermRateRecip_Coolbear	GermRateRecip_Farooq	GermSpeed_Count	GermSpeed_Percent	GermSpeedAccumulated_C...
1	0.1674877	0.1683168	6.138925	12.27785	34.6...
2	0.1614907	0.1625000	6.362698	12.47588	35.54...
3	0.1578947	0.1674419	6.882179	14.33787	38.29...
4	0.1655172	0.1606218	6.927417	13.58317	38.68...
5	0.1673640	0.1680672	7.318987	14.63797	41.00...
6	0.1673307	0.1680000	6.931782	14.14649	38.77...
7	0.1674419	0.1682243	6.448449	13.43427	36.38...
8	0.1610738	0.1621622	6.053175	12.87909	33.77...
9	0.1584699	0.1674009	6.830592	13.13575	38.11...
10	0.1645570	0.1656051	6.812698	13.62540	38.19...
11	0.1686747	0.1693548	7.342796	14.39764	41.17...
12	0.1673640	0.1680672	6.622258	12.98482	37.00...
13	0.1643836	0.1655172	7.052320	14.39249	39.29...
14	0.1686747	0.1693548	6.706782	13.97246	37.69...
15	0.1652893	0.1597633	6.363925	13.25818	35.69...

	GermSpeedAccumulated_Percent	GermSpeedCorrected_Normal	GermSpeedCorrected_Accumulated	WeightGermPerc...
1	69.23134	0.1534731	0.8653917	47.428...

2	69.68741	0.1514928	0.8462043	47.899
3	79.78594	0.1529373	0.8510501	54.464
4	75.85202	0.1505960	0.8409680	52.240
5	82.01571	0.1524789	0.8543303	56.142
6	79.13509	0.1506909	0.8429608	54.518
7	75.80304	0.1535345	0.8663205	51.934
8	71.85275	0.1513294	0.8442698	49.392
9	73.29829	0.1517909	0.8470024	50.274
10	76.39054	0.1513933	0.8487837	52.571
11	80.73436	0.1529749	0.8578026	55.182
12	72.56158	0.1505059	0.8410547	50.000
13	80.19182	0.1500494	0.8360424	55.241
14	78.53103	0.1524269	0.8567022	53.869
15	74.36868	0.1515220	0.8499278	51.190

	MeanGermPercent	MeanGermNumber	TimsonsIndex	TimsonsIndex_Labouriau	TimsonsIndex_KhanUngar	GermRateGeo
1	5.714286	2.857143	8.000000	1.00	0.5714286	
2	5.882353	3.000000	9.803922	1.25	0.7002801	
3	6.696429	3.214286	14.583333	1.40	1.0416667	
4	6.442577	3.285714	7.843137	1.00	0.5602241	
5	6.857143	3.428571	10.000000	1.00	0.7142857	
6	6.705539	3.285714	6.122449	1.00	0.4373178	
7	6.250000	3.000000	8.333333	1.00	0.5952381	
8	6.079027	2.857143	10.638298	1.25	0.7598784	
9	6.181319	3.214286	9.615385	1.25	0.6868132	
10	6.428571	3.214286	8.000000	1.00	0.5714286	
11	6.722689	3.428571	9.803922	1.00	0.7002801	
12	6.162465	3.142857	5.882353	1.00	0.4201681	
13	6.851312	3.357143	8.163265	1.00	0.5830904	
14	6.547619	3.142857	6.250000	1.00	0.4464286	
15	6.250000	3.000000	8.333333	1.00	0.5952381	

	GermIndex	GermIndex_mod	EmergenceRateIndex_SG	EmergenceRateIndex_SG_mod	EmergenceRateIndex_BilbroWan
1	5.840000	7.300000	292	7.300000	5.970
2	5.882353	7.142857	300	7.142857	6.125
3	6.687500	7.133333	321	7.133333	6.553
4	6.411765	7.108696	327	7.108696	6.675
5	6.900000	7.187500	345	7.187500	7.045
6	6.693878	7.130435	328	7.130435	6.690
7	6.395833	7.309524	307	7.309524	6.277
8	6.063830	7.125000	285	7.125000	5.818
9	6.173077	7.133333	321	7.133333	6.553
10	6.460000	7.177778	323	7.177778	6.590
11	6.784314	7.208333	346	7.208333	7.067
12	6.137255	7.113636	313	7.113636	6.389
13	6.775510	7.063830	332	7.063830	6.770
14	6.625000	7.227273	318	7.227273	6.490
15	6.291667	7.190476	302	7.190476	6.167

	EmergenceRateIndex_Fakorede	PeakValue	GermValue_Czabator	GermValue_DP	GermValue_Czabator_mod
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
   GermValue_DP_mod    CUGerm GermSynchrony GermUncertainty
1         39.56076 0.7092199     0.2666667        2.062987
2         40.99260 0.5051546     0.2346109        2.321514
3         53.42809 0.3975265     0.2242424        2.462012
4         48.86825 0.4672113     0.2502415        2.279215
5         56.23935 0.4312184     0.2606383        2.146051
6         53.06435 0.4934701     0.2792271        2.160545
7         47.37690 0.7371500     0.2729384        2.040796
8         43.67948 0.4855842     0.2256410        2.357249
9         45.30801 0.4446640     0.2494949        2.321080
10        49.10820 0.5584666     0.2555556        2.187983
11        54.27520 0.4288905     0.2686170        2.128670
12        44.71582 0.4760266     0.2737844        2.185245
13        54.94192 0.4023679     0.2506938        2.241181
14        51.41913 0.5383760     0.2991543        2.037680
15        46.48043 0.6133519     0.2497096        2.185028
```

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

```r
data(gcdata)

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

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

	Genotype	Rep	Day01	Day02	Day03	Day04	Day05	Day06	Day07	Day08	Day09	Day10	Day11	Day12	Day13	Day14
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
```

	Total Seeds	a	b	c	y0	lag	Dlag50	t50.total	t10.total	t60.total	t50.Germinated
1	50	80.00000	9.881937	6.034954	0	0	6.034954	6.355121	4.956264	6.744598	6.034954
2	51	82.35294	9.227666	6.175193	0	0	6.175193	6.473490	4.983236	6.872603	6.175193
3	48	93.75000	7.793051	6.138110	0	0	6.138110	6.244191	4.673022	6.608438	6.138110
4	51	90.19608	8.925655	6.125173	0	0	6.125173	6.276794	4.850875	6.614968	6.125173
5	50	96.00000	9.419181	6.049642	0	0	6.049642	6.103433	4.814125	6.386789	6.049642
6	49	93.87755	9.450149	6.097415	0	0	6.097415	6.182279	4.868632	6.477599	6.097415
7	48	87.50000	10.172459	6.029851	0	0	6.029851	6.202812	4.930422	6.510495	6.029851
8	47	85.10638	8.940696	6.189774	0	0	6.189774	6.439510	4.940057	6.823299	6.189774
9	52	86.53846	8.617391	6.125122	0	0	6.125122	6.352172	4.836658	6.733276	6.125122
10	50	90.00000	9.608844	6.109504	0	0	6.109504	6.253043	4.920629	6.566506	6.109504
11	51	94.11765	9.400212	6.018760	0	0	6.018760	6.099435	4.798627	6.391291	6.018760
12	51	86.27451	9.162526	6.108452	0	0	6.108452	6.326184	4.893596	6.684526	6.108452
13	49	95.91837	8.995210	6.149012	0	0	6.149012	6.207501	4.841308	6.509954	6.149012
14	48	91.66667	10.391845	6.015910	0	0	6.015910	6.122389	4.915140	6.397491	6.015910
15	48	87.50000	9.136744	6.121579	0	0	6.121579	6.317392	4.892502	6.667247	6.121579

	t10.Germinated	t60.Germinated	Uniformity_90	Uniformity_10	Uniformity	TMGR	AUC	MGT	Skew
1	4.831807	6.287724	7.537690	4.831807	2.705882	5.912194	1108.976	6.632252	1.098
2	4.866755	6.452582	7.835407	4.866755	2.968652	6.031282	1128.559	6.784407	1.098
3	4.630062	6.465924	8.137342	4.630062	3.507280	5.938180	1283.693	6.772742	1.103
4	4.788597	6.409838	7.834810	4.788597	3.046213	5.972686	1239.887	6.739666	1.100
5	4.790946	6.315746	7.639028	4.790946	2.848083	5.914289	1328.328	6.654981	1.100
6	4.832471	6.364722	7.693469	4.832471	2.860997	5.961879	1294.463	6.702473	1.099
7	4.858476	6.275050	7.483643	4.858476	2.625166	5.914057	1213.908	6.622417	1.098
8	4.841105	6.476945	7.914163	4.841105	3.073058	6.036192	1164.346	6.804000	1.099
9	4.746573	6.420208	7.904041	4.746573	3.157468	5.961631	1188.793	6.745241	1.10
10	4.860681	6.372823	7.679177	4.860681	2.818496	5.978115	1240.227	6.711900	1.098
11	4.764246	6.284051	7.603611	4.764246	2.839365	5.883557	1305.200	6.624248	1.100
12	4.806013	6.384836	7.763854	4.806013	2.957841	5.964080	1188.021	6.718639	1.099
13	4.816393	6.432524	7.850345	4.816393	3.033952	5.998270	1316.407	6.762274	1.099
14	4.869398	6.255276	7.432372	4.869398	2.562974	5.905180	1273.385	6.604967	1.097
15	4.813083	6.399357	7.785806	4.813083	2.972723	5.976087	1203.664	6.732266	1.099

	msg	sigma	finTol	logLik	AIC	BIC	deviance	df.residual	nobs
1	#1. success	1.615220	7.105427e-14	-25.49868	56.99736	58.91453	31.30723	12	14
2	#1. success	1.115372	2.309264e-14	-20.31471	46.62943	48.54660	14.92865	12	14
3	#1. success	2.432704	9.947598e-14	-31.23213	68.46426	70.38143	71.01658	12	14
4	#1. success	2.396582	5.684342e-14	-31.02269	68.04538	69.96256	68.92324	12	14
5	#1. success	2.399662	1.094236e-12	-31.04067	68.08135	69.99852	69.10052	12	14
6	#1. success	3.034962	1.563194e-13	-34.32887	74.65774	76.57491	110.53195	12	14
7	#1. success	1.663019	1.421085e-13	-25.90697	57.81395	59.73112	33.18760	12	14
8	#1. success	1.120704	4.327205e-12	-20.38149	46.76298	48.68015	15.07174	12	14
9	#1. success	2.429960	7.958079e-13	-31.21633	68.43266	70.34984	70.85647	12	14
10	#1. success	1.686656	8.142820e-12	-26.10456	58.20911	60.12629	34.13771	12	14
11	#1. success	2.628113	1.989520e-13	-32.31381	70.62762	72.54479	82.88372	12	14
12	#1. success	2.878146	1.151079e-12	-33.58613	73.17227	75.08944	99.40469	12	14
13	#1. success	2.604588	2.984279e-13	-32.18793	70.37586	72.29303	81.40654	12	14
14	#1. success	2.764756	9.805490e-13	-33.02342	72.04684	73.96401	91.72652	12	14
15	#1. success	1.954008	8.739676e-13	-28.16444	62.32888	64.24606	45.81777	12	14

Multiple fitted curves generated in batch can also be plotted.

```r
data(gcdata)
```

```r
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")
```
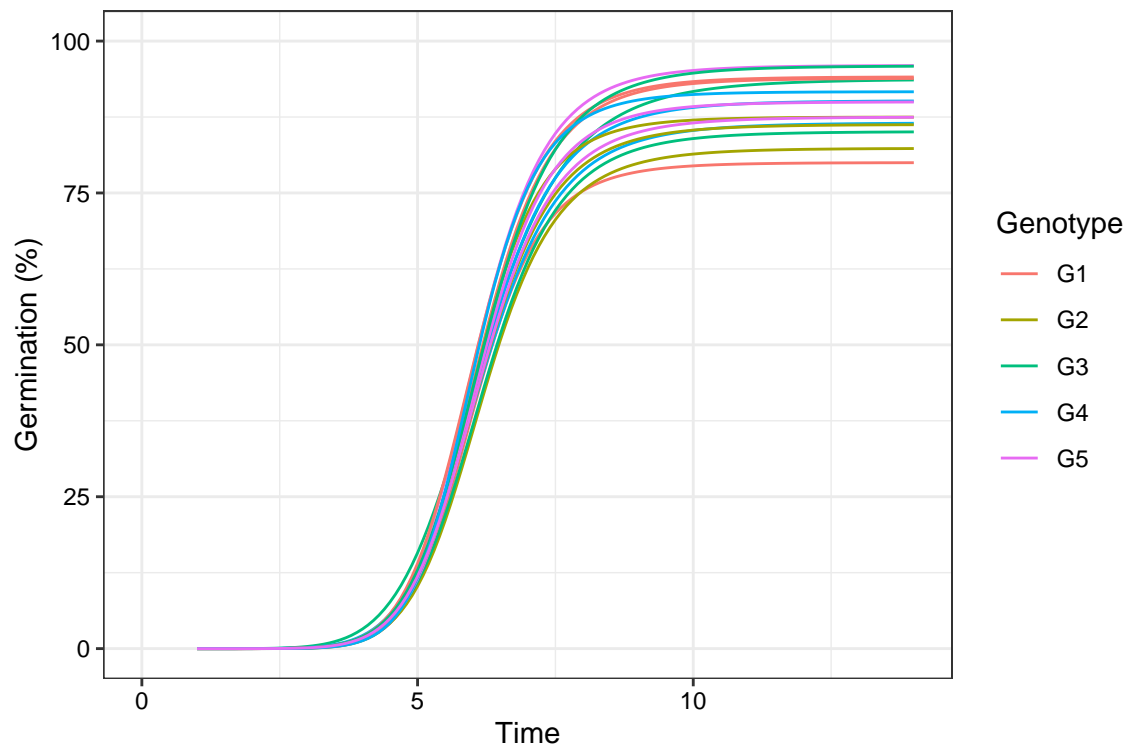


```
# Plot ROG curves
plot(fits, rog = TRUE, group.col = "Genotype")
```
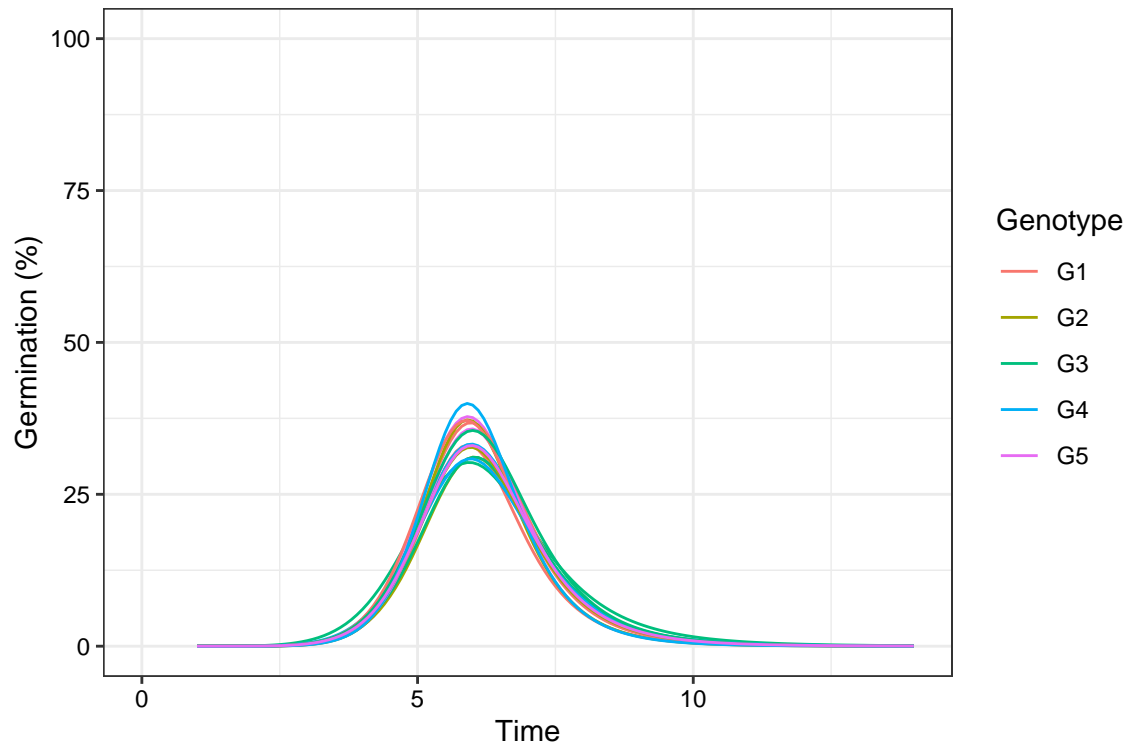
```
# Plot FPHF curves with points
plot(fits, group.col = "Genotype", show.points = TRUE)
```
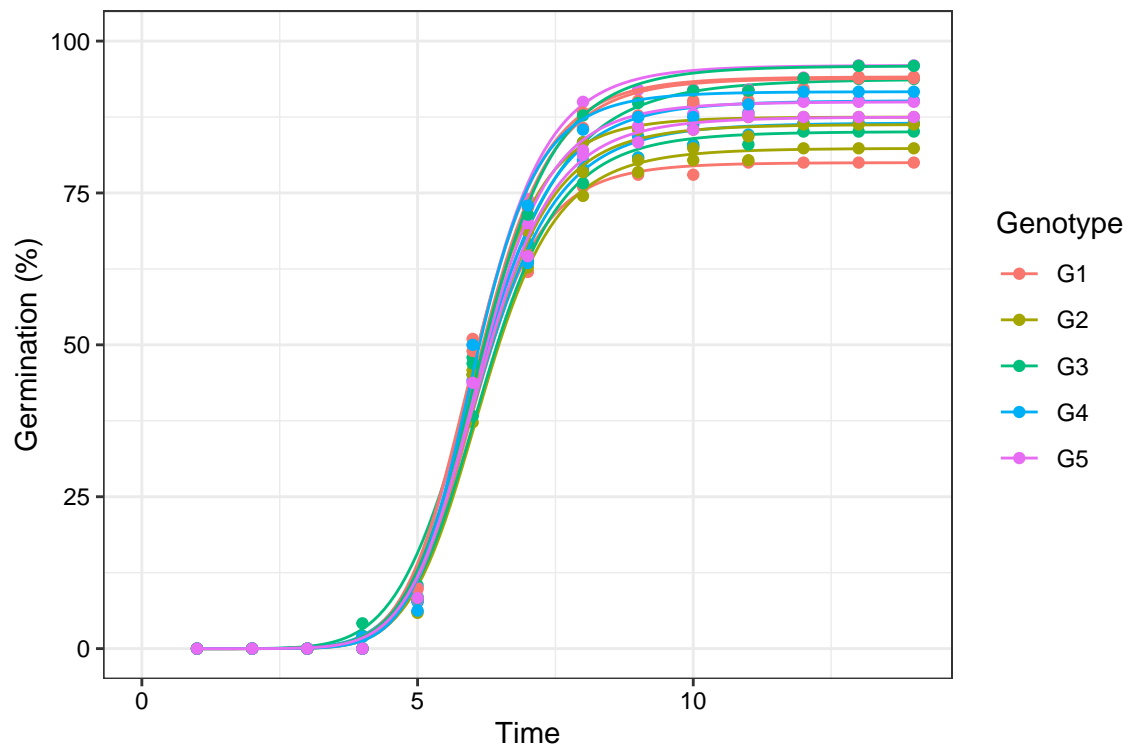


```
# Plot FPHF curves with annotations
plot(fits, group.col = "Genotype", annotate = "t50.total")
```
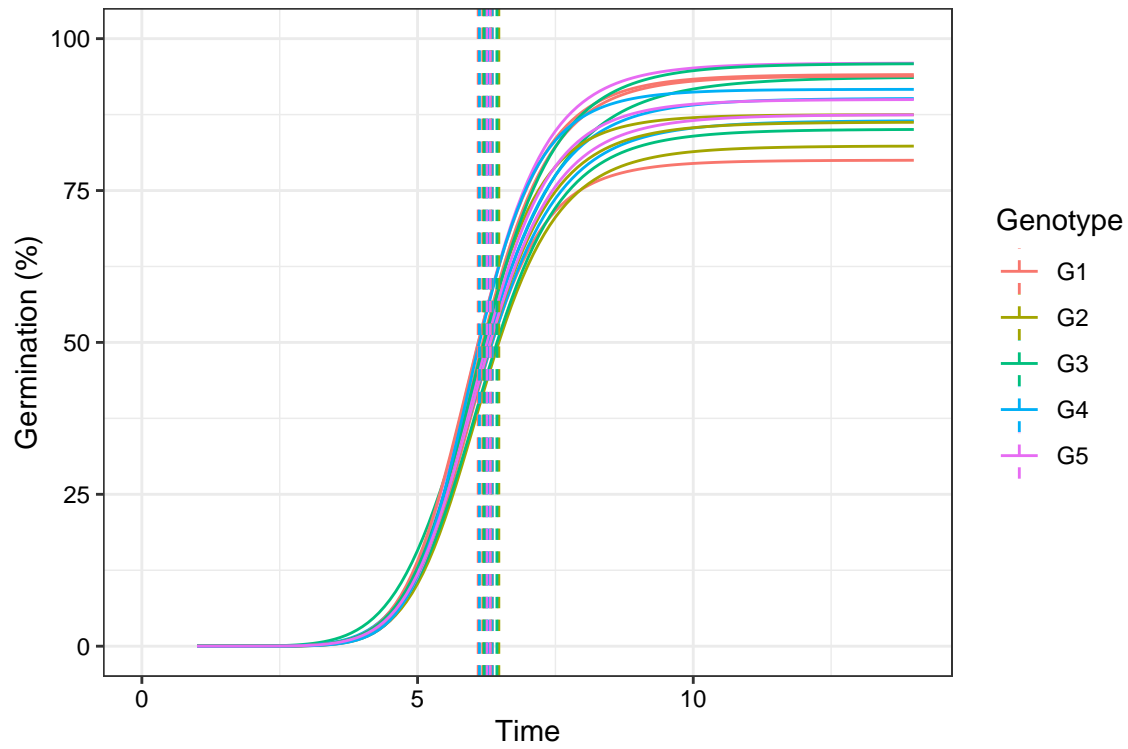
```
plot(fits, group.col = "Genotype", annotate = "t50.germ")
```
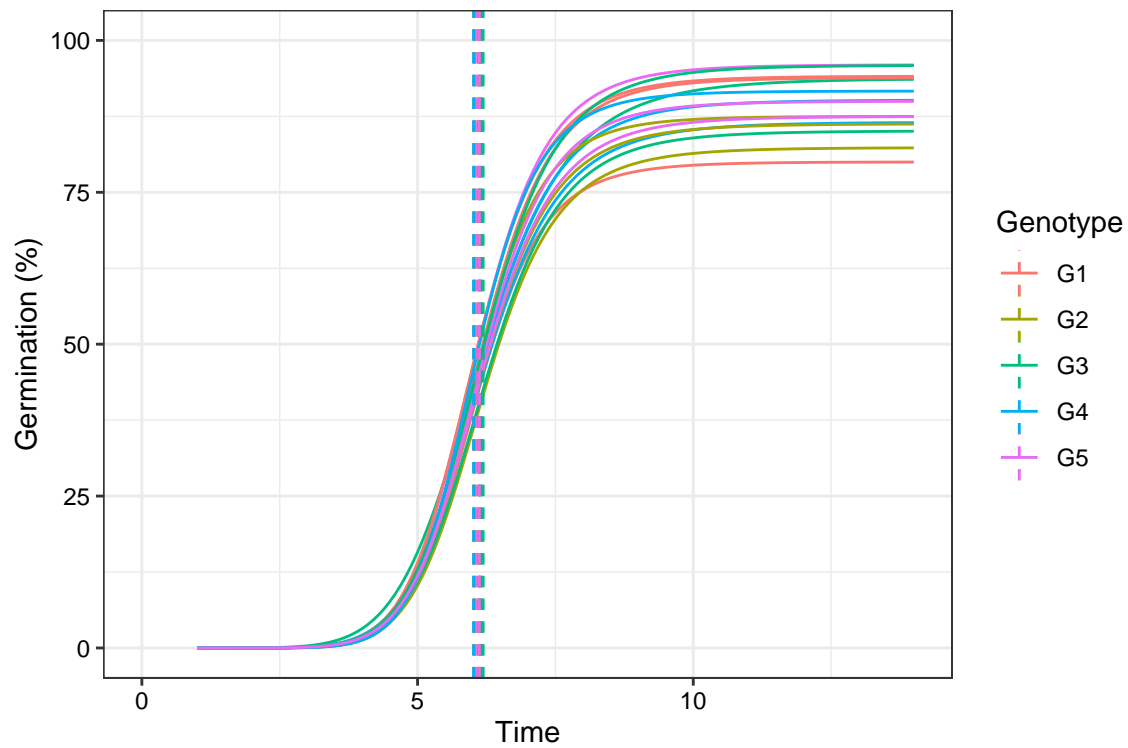


```
plot(fits, group.col = "Genotype", annotate = "tmgr")
```
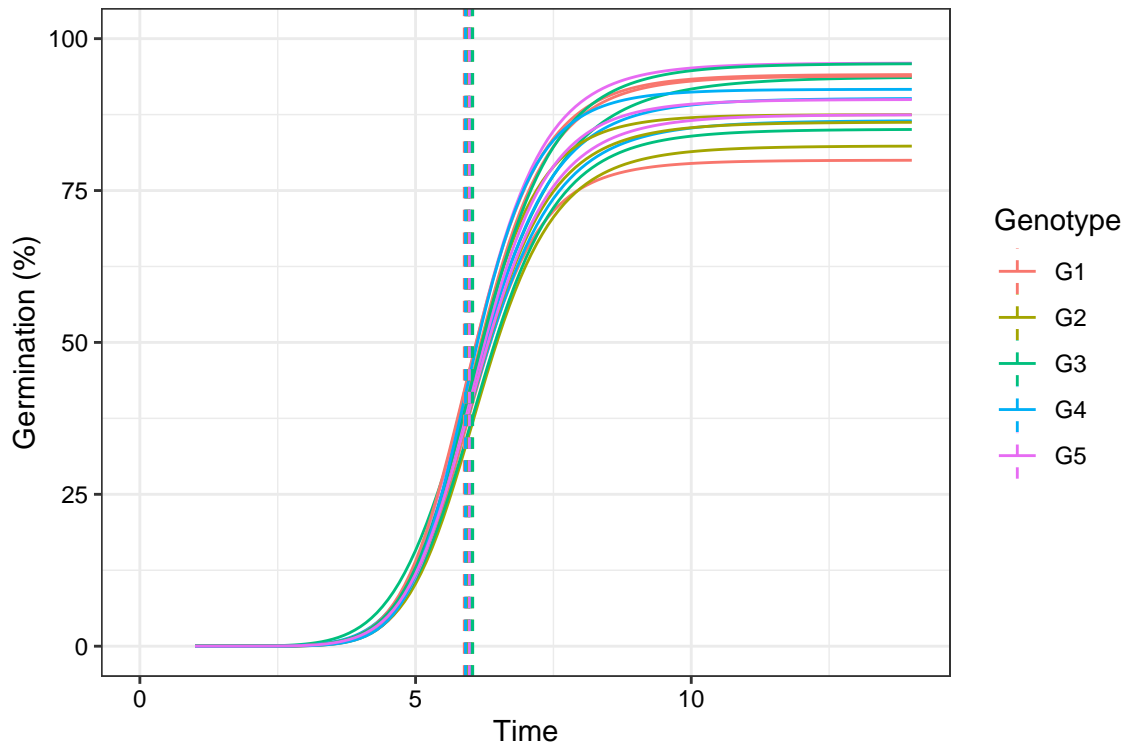
```r
plot(fits, group.col = "Genotype", annotate = "mgt")
```



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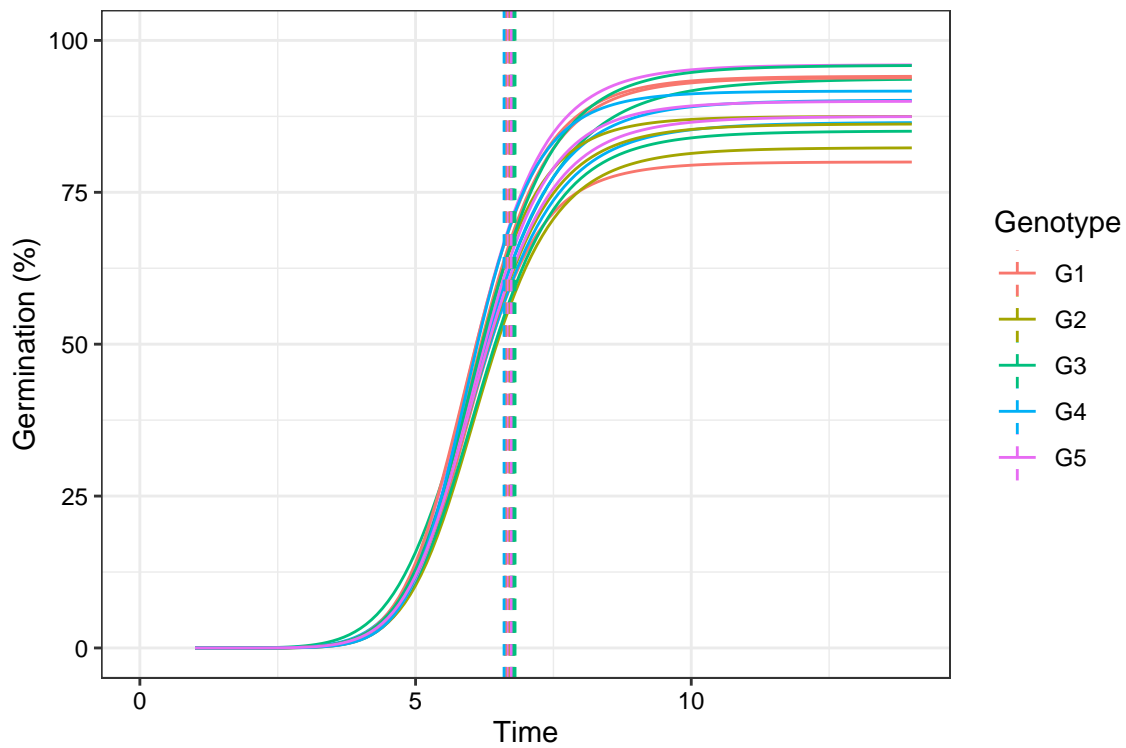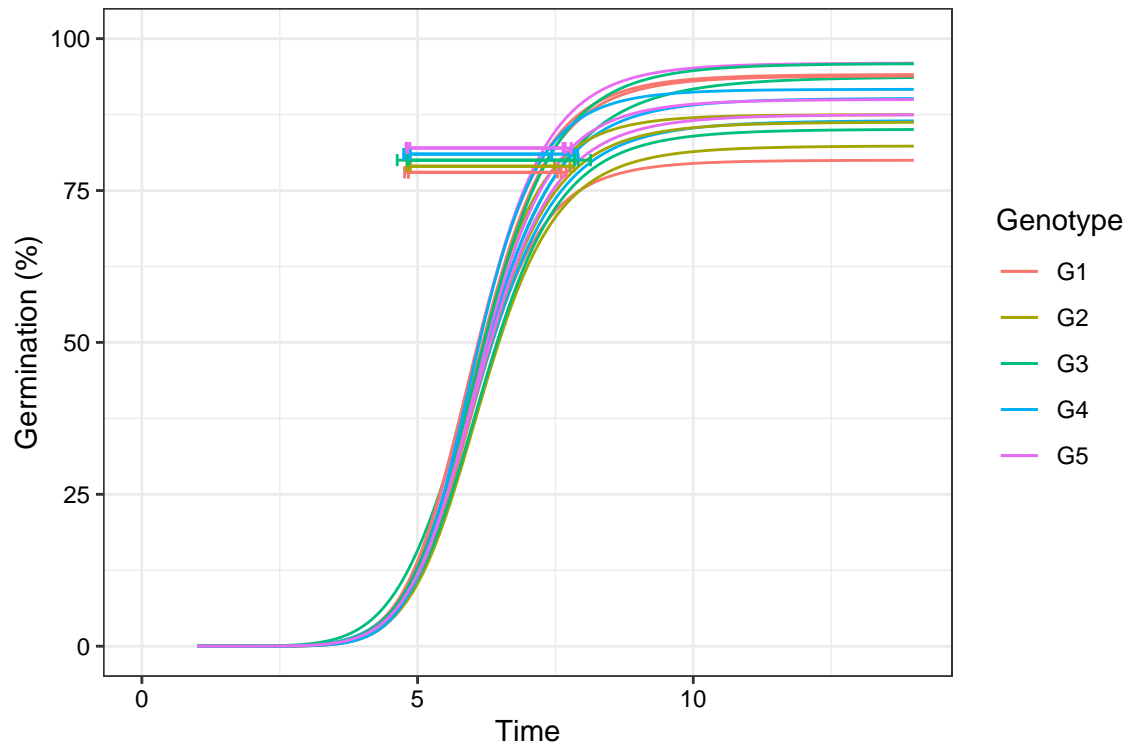
```r
# Plot ROG curves with annotations
plot(fits, rog = TRUE, group.col = "Genotype", annotate = "t50.total")
```



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

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



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

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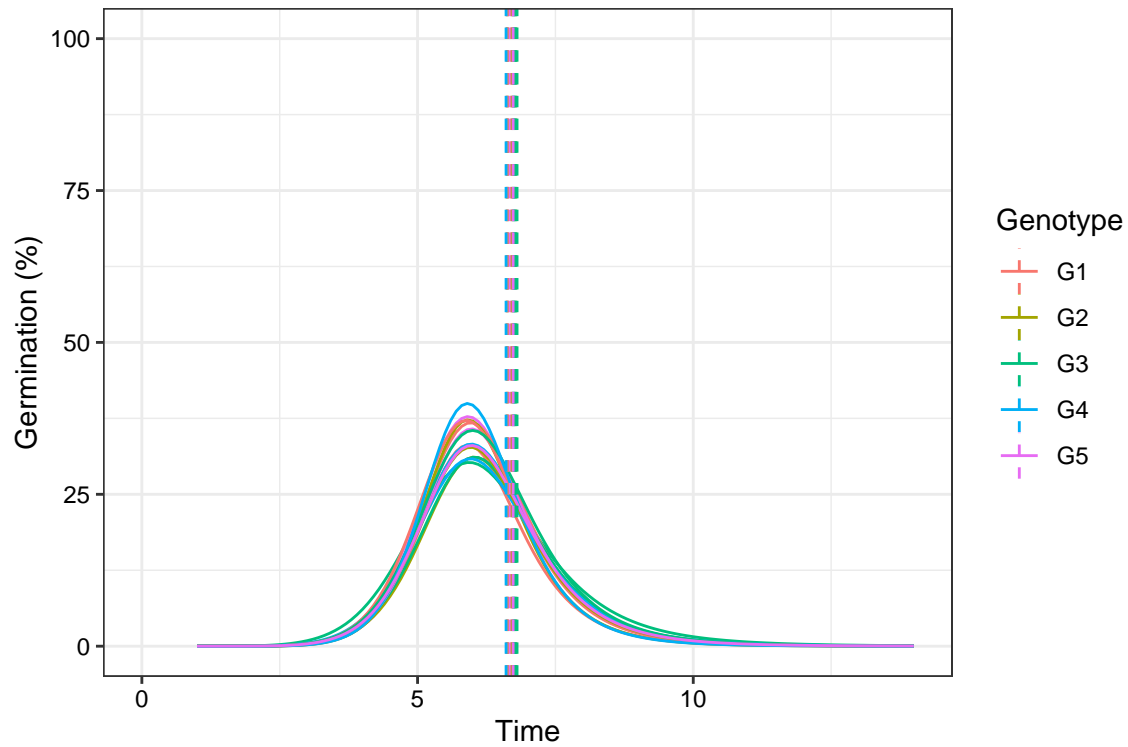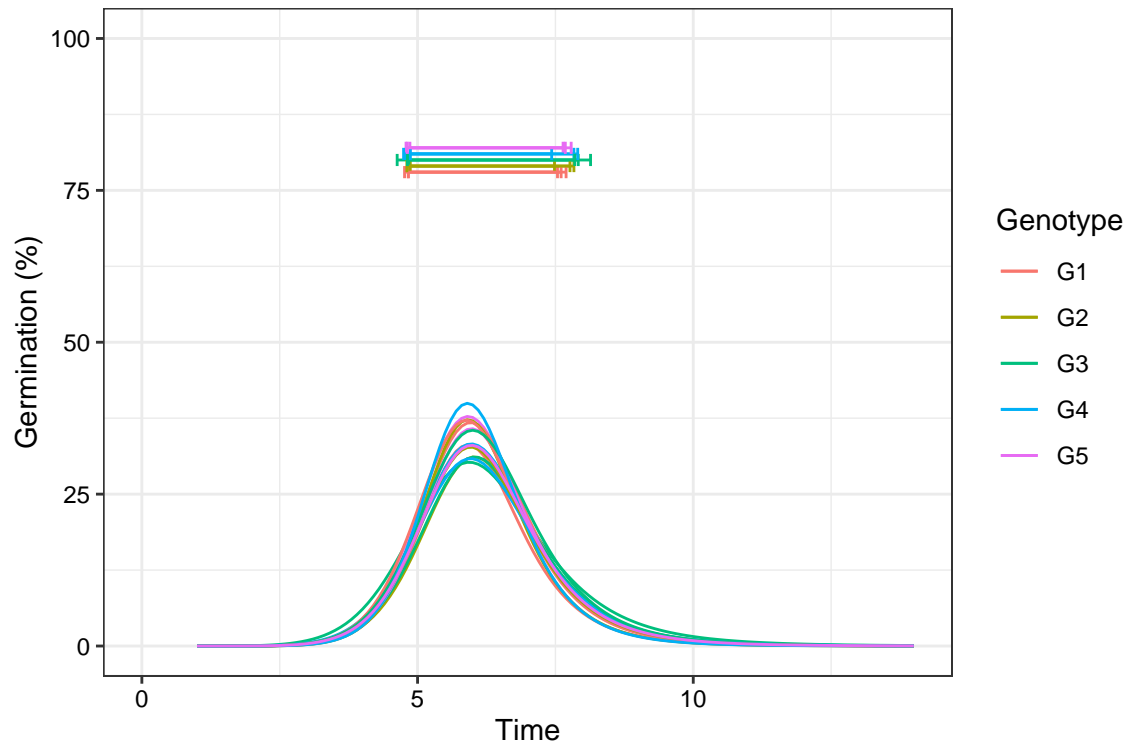


```r
# Change colour of curves using ggplot2 options
library(ggplot2)
curvesplot <- plot(fits, group.col = "Genotype")

# 'Dark2' palette from RColorBrewer
```

```r
curvesplot + scale_colour_brewer(palette = "Dark2")
```
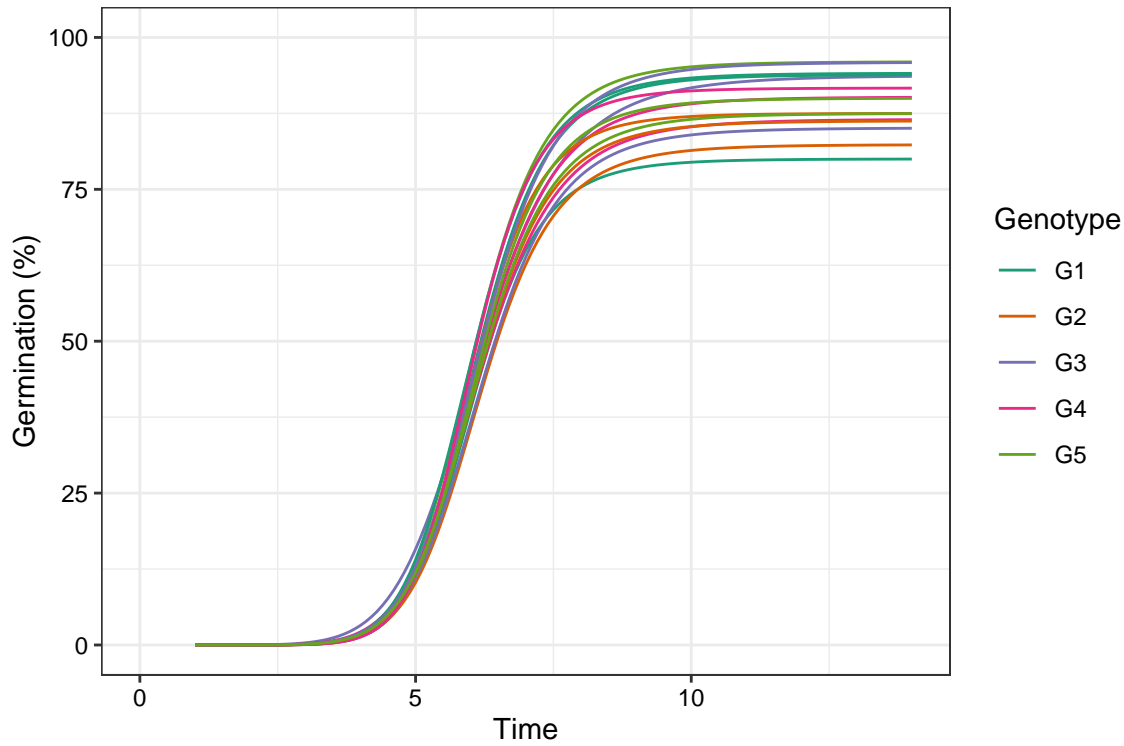


```r
# Manual colours
curvesplot +
  scale_colour_manual(values = c("Coral", "Brown", "Blue",
                                 "Aquamarine", "Red"))
```
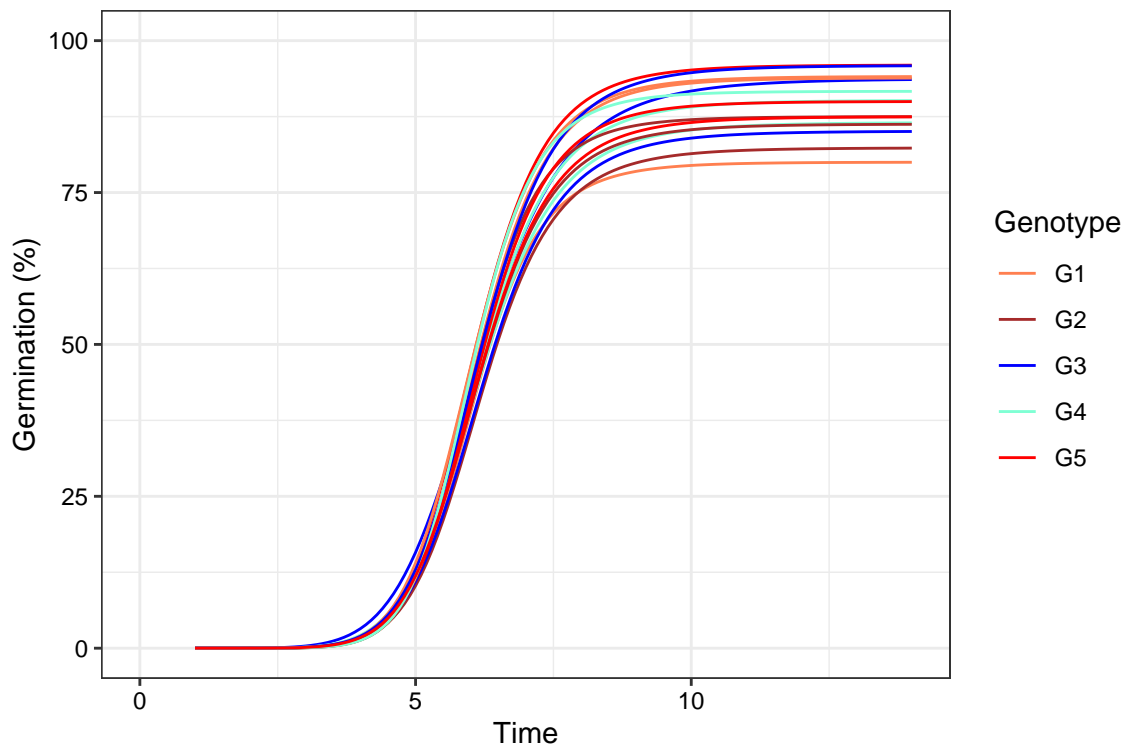
Citing `germinationmetrics`

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

  Aravind, J., Vimala Devi, S., Radhamani, J., Jacob, S. R., and Kalyani Srinivasan (2025).
  germinationmetrics: Seed Germination Indices and Curve Fitting. R package version 0.1.9.9000,
  https://github.com/aravind-j/germinationmetrics
  https://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
  note = {R package version 0.1.9.9000 https://aravind-j.github.io/germinationmetrics/ https://CRAN.R-
  year = {2025},
}
```

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

Session Info

```r
sessionInfo()
```

```
R Under development (unstable) (2025-12-09 r89129 ucrt)
Platform: x86_64-w64-mingw32/x64
Running under: Windows 11 x64 (build 26200)

Matrix products: default
  LAPACK version 3.12.1

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

time zone: Asia/Calcutta
tzcode source: internal

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

other attached packages:
[1] germinationmetrics_0.1.9.9000 ggplot2_4.0.1

loaded via a namespace (and not attached):
 [1] generics_0.1.4    tidyr_1.3.2       stringi_1.8.7     lattice_0.22-7    digest_0.6.39
 [6] magrittr_2.0.4    evaluate_1.0.5    grid_4.6.0        RColorBrewer_1.1-3 fastmap_1.2.0
[11] plyr_1.8.9        Matrix_1.7-4      ggrepel_0.9.6     backports_1.5.0   tinytex_0.58
[16] httr_1.4.7        purrr_1.2.0       pander_0.6.6      scales_1.4.0      XML_3.99-0.20
[21] Rdpack_2.6.4      cli_3.6.5         rlang_1.1.6       rbibutils_2.4     withr_3.0.2
[26] yaml_2.3.12       tools_4.6.0       parallel_4.6.0    reshape2_1.4.5    dplyr_1.1.4
[31] mathjaxr_2.0-0    broom_1.0.11      curl_7.0.0        vctrs_0.6.5       R6_2.6.1
[36] stats4_4.6.0      lifecycle_1.0.4   gslnls_1.4.2      stringr_1.6.0     pkgconfig_2.0.3
```

```
[41] rJava_1.0-11      pillar_1.11.1    gtable_0.3.6     rsconnect_1.7.0  data.table_1.17.8
[46] glue_1.8.0        Rcpp_1.1.0.8.1   xfun_0.55        tibble_3.3.0     tidyselect_1.2.1
[51] rstudioapi_0.17.1 knitr_1.50       dichromat_2.0-0.1 farver_2.1.2    htmltools_0.5.9
[56] labeling_0.4.3    rmarkdown_2.30   compiler_4.6.0   S7_0.2.1
```

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25_2_79.pdf.

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