

# The `germinationmetrics` Package: A Brief Introduction

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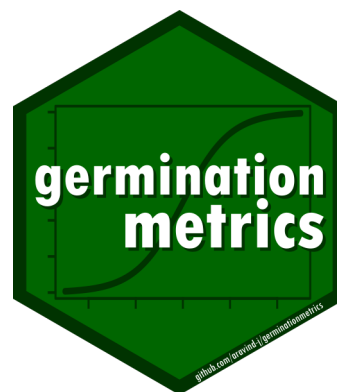
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## Overview

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

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



## Installation

The package can be installed using the following functions:

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

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

Then the package can be loaded using the function

```
library(germinationmetrics)
```

Welcome to `germinationmetrics` version 0.1.5.9000

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

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

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

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

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## Version History

The current version of the package is 0.1.5.9000. The previous versions are as follows.

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

Version	Date
0.1.0	2018-04-17
0.1.1	2018-07-26
0.1.1.1	2018-10-16
0.1.2	2018-10-31
0.1.3	2019-01-19
0.1.4	2020-06-16
0.1.5	2021-02-17

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

## Germination count data

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

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

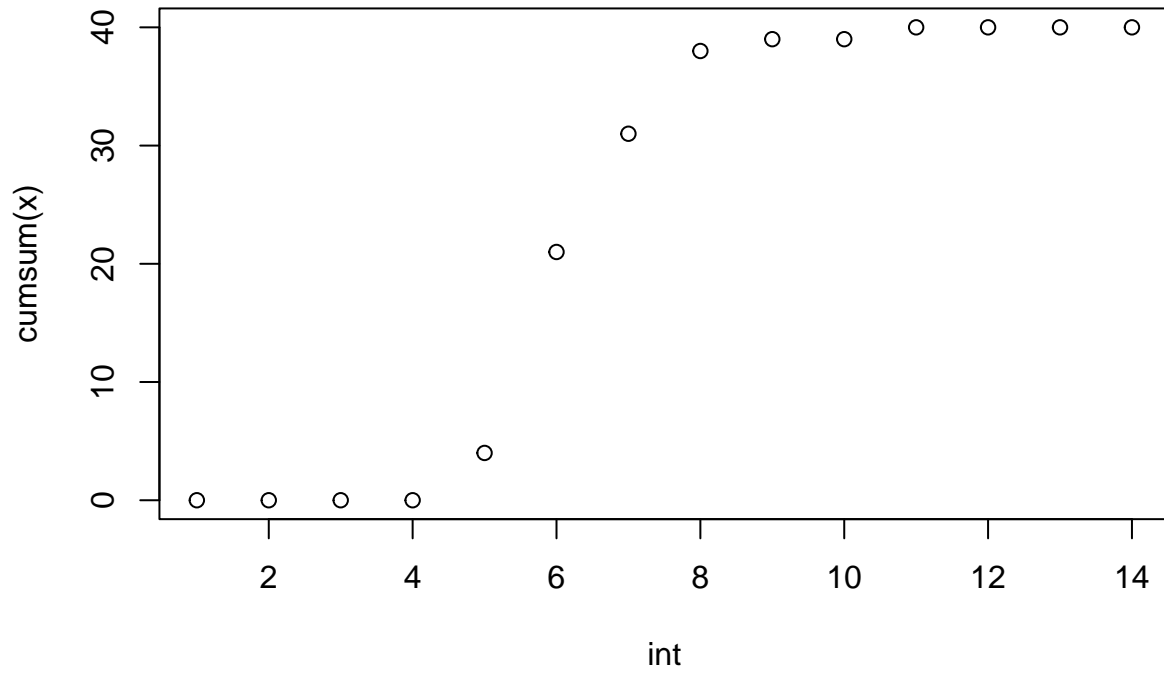
intervals	counts	cumulative.counts
1	0	0
2	0	0
3	0	0
4	0	0
5	4	4
6	17	21
7	10	31
8	7	38
9	1	39
10	0	39
11	1	40
12	0	40
13	0	40
14	0	40

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

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

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

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



### Single-value germination indices

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

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

Germination index	Function	Details	Unit	Measures	Reference
Germination percentage or Final germination percentage or Germinability ( $GP$ )	<b>GermPercent</b>	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 ( $PGP$ )	<b>PeakGermPercent</b>	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 ( $t_0$ )	<b>FirstGermTime</b>	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 $i$ th interval and $N_i$ is the number of seeds germinated in the $i$ th time interval (not the accumulated number, but the number corresponding to the $i$ th 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 ( $t_g$ )	<b>LastGermTime</b>	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 $i$ th interval and $N_i$ is the number of seeds germinated in the $i$ th time interval (not the accumulated number, but the number corresponding to the $i$ th interval)	time	Germination time	Edwards (1932)
Time spread of germination or Germination distribution	<b>TimeSpreadGerm</b>	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 ( $t_{peak}$ )	<b>PeakGermTime</b>	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 $i$ th interval, $N_i$ is the number of seeds germinated in the $i$ th time interval (not the accumulated number, but the number corresponding to the $i$ th 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)	<b>t50</b>	<p>It is the time to reach 50% of final/maximum germination. With argument <b>method</b> specified as "coolbear", it is computed as follows.</p> $t_{50} = T_i + \frac{(\frac{N+1}{2} - N_i)(T_j - T_i)}{N_j - N_i}$ <p>Where, <math>t_{50}</math> is the median germination time, <math>N</math> is the final number of germinated seeds, and <math>N_i</math> and <math>N_j</math> are the total number of seeds germinated in adjacent counts at time <math>T_i</math> and <math>T_j</math> respectively, when <math>N_i &lt; \frac{N+1}{2} &lt; N_j</math>.</p>	time	Germination time	Coolbear et al. (1984)
Median germination time ( $t_{50}$ ) (Farooq)	<b>t50</b>	<p>With argument <b>method</b> specified as "farooq", it is computed as follows.</p> $t_{50} = T_i + \frac{(\frac{N}{2} - N_i)(T_j - T_i)}{N_j - N_i}$ <p>Where, <math>t_{50}</math> is the median germination time, <math>N</math> is the final number of germinated seeds, and <math>N_i</math> and <math>N_j</math> are the total number of seeds germinated in adjacent counts at time <math>T_i</math> and <math>T_j</math> respectively, when <math>N_i &lt; \frac{N}{2} &lt; N_j</math>.</p>	time	Germination time	Farooq et al. (2005)
Mean germination time or Mean length of incubation time ( $\bar{T}$ ) or Germination resistance ( $GR$ ) or Sprouting index ( $SI$ ) or Emergence index ( $EI$ )	<b>MeanGermTime</b>	<p>It is the average length of time required for maximum germination of a seed lot and is estimated according to the following formula.</p> $\bar{T} = \frac{\sum_{i=1}^k N_i T_i}{\sum_{i=1}^k N_i}$ <p>Where, <math>T_i</math> is the time from the start of the experiment to the <math>i</math>th interval, <math>N_i</math> is the number of seeds germinated in the <math>i</math>th time interval (not the accumulated number, but the number corresponding to the <math>i</math>th interval), and <math>k</math> is the total number of time intervals.</p> <p>It is the inverse of mean germination rate (<math>\bar{V}</math>).</p> $\bar{T} = \frac{1}{\bar{V}}$	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 ( $s_T^2$ )	<b>VarGermTime</b>	<p>It is computed according to the following formula.</p> $s_T^2 = \frac{\sum_{i=1}^k N_i (T_i - \bar{T})^2}{\sum_{i=1}^k N_i - 1}$ <p>Where, <math>T_i</math> is the time from the start of the experiment to the <math>i</math>th interval, <math>N_i</math> is the number of seeds germinated in the <math>i</math>th time interval (not the accumulated number, but the number corresponding to the <math>i</math>th interval), and <math>k</math> is the total number of time intervals.</p>	time <sup>-1</sup>	Germination time	Labouriau (1983a); Ranal and Santana (2006)
Standard error of germination time ( $s_{\bar{T}}$ )	<b>SEGermTime</b>	<p>It signifies the accuracy of the calculation of the mean germination time.</p> <p>It is estimated according to the following formula:</p> $s_{\bar{T}} = \sqrt{\frac{s_T^2}{\sum_{i=1}^k N_i}}$ <p>Where, <math>N_i</math> is the number of seeds germinated in the <math>i</math>th time interval (not the accumulated number, but the number corresponding to the <math>i</math>th interval) and <math>k</math> is the total number of time intervals.</p>	time	Germination time	Labouriau (1983a); Ranal and Santana (2006)
Mean germination rate ( $\bar{V}$ )	<b>MeanGermRate</b>	<p>It is computed according to the following formula:</p> $\bar{V} = \frac{\sum_{i=1}^k N_i}{\sum_{i=1}^k N_i T_i}$ <p>Where, <math>T_i</math> is the time from the start of the experiment to the <math>i</math>th interval, <math>N_i</math> is the number of seeds germinated in the <math>i</math>th time interval (not the accumulated number, but the number corresponding to the <math>i</math>th interval), and <math>k</math> is the total number of time intervals.</p> <p>It is the inverse of mean germination time (<math>\bar{T}</math>).</p> $\bar{V} = \frac{1}{\bar{T}}$	time <sup>-1</sup>	Germination rate	Labouriau and Valadares (1976); Labouriau (1983b); Ranal and Santana (2006)

Germination index	Function	Details	Unit	Measures	Reference
Coefficient of velocity of germination ( <i>CVG</i> ) or Coefficient of rate of germination ( <i>CRG</i> ) or Kotowski's coefficient of velocity	<b>CVG</b>	<p>It is estimated according to the following formula.</p> $CVG = \frac{\sum_{i=1}^k N_i}{\sum_{i=1}^k N_i T_i} \times 100$ $CVG = \bar{V} \times 100$ <p>Where, <math>T_i</math> is the time from the start of the experiment to the <math>i</math>th interval, <math>N_i</math> is the number of seeds germinated in the <math>i</math>th time interval (not the accumulated number, but the number corresponding to the <math>i</math>th interval), and <math>k</math> is the total number of time intervals.</p>	% time <sup>-1</sup>	Germination rate	Kotowski (1926), Nichols and Heydecker (1968); Bewley and Black (1994); Labouriau (1983b); Scott et al. (1984)
Variance of germination rate ( $s_V^2$ )	<b>VarGermRate</b>	<p>It is calculated according to the following formula.</p> $s_V^2 = \bar{V}^4 \times s_T^2$ <p>Where, <math>s_T^2</math> is the variance of germination time.</p>	time <sup>-2</sup>	Germination rate	Labouriau (1983b); Ranal and Santana (2006)
Standard error of germination rate ( $s_{\bar{V}}$ )	<b>SEGermRate</b>	<p>It is estimated according to the following formula.</p> $s_{\bar{V}} = \sqrt{\frac{s_V^2}{\sum_{i=1}^k N_i}}$ <p>Where, <math>N_i</math> is the number of seeds germinated in the <math>i</math>th time interval (not the accumulated number, but the number corresponding to the <math>i</math>th interval), and <math>k</math> is the total number of time intervals.</p>	time <sup>-1</sup>	Germination rate	Labouriau (1983b); Ranal and Santana (2006)
Germination rate as the reciprocal of the median time ( $v_{50}$ )	<b>GermRateRecip</b>	<p>It is the reciprocal of the median germination time (<math>t_{50}</math>).</p> $v_{50} = \frac{1}{t_{50}}$	time <sup>-1</sup>	Germination rate	Went (1957); Labouriau (1983b); Ranal and Santana (2006)
Speed of germination or Germination rate Index or index of velocity of germination or Emergence rate index (Allan, Vogel and Peterson; Erbach; Hsu and Nelson) or Germination index (AOSA)	<b>GermSpeed</b>	<p>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.</p> $S = \sum_{i=1}^k \frac{N_i}{T_i}$ <p>Where, <math>T_i</math> is the time from the start of the experiment to the <math>i</math>th interval, <math>N_i</math> is the number of seeds germinated in the <math>i</math>th time interval (not the accumulated number, but the number corresponding to the <math>i</math>th interval), and <math>k</math> is the total number of time intervals.</p> <p>Instead of germination counts, germination percentages may also be used for computation of speed of germination.</p>	% time <sup>-1</sup> or count time <sup>-1</sup>	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	<b>GermSpeedAccumulate</b>	<p>It is the rate of germination in terms of the accumulated/cumulative total number of seeds that germinate in a time interval.</p> <p>It is estimated as follows.</p> $S_{accumulated} = \sum_{i=1}^k \frac{\sum_{j=1}^i N_j}{T_i}$ <p>Where, <math>T_i</math> is the time from the start of the experiment to the <math>i</math>th interval, <math>\sum_{j=1}^i N_j</math> is the cumulative/accumulated number of seeds germinated in the <math>i</math>th interval, and <math>k</math> is the total number of time intervals.</p> <p>Instead of germination counts, germination percentages may also be used for computation of speed of germination.</p>	% time <sup>-1</sup> or count time <sup>-1</sup>	Mixed	Bradbeer (1988); Wardle et al. (1991); Haugland and Brandsaeter (1996); Santana and Ranal (2004)
Corrected germination rate index	<b>GermSpeedCorrected</b>	<p>It is computed as follows.</p> $S_{corrected} = \frac{S}{FGP}$ <p>Where, <math>S</math> is the germination speed computed with germination percentage instead of counts and <math>FGP</math> is the final germination percentage or germinability.</p>	time <sup>-1</sup>	Mixed	Evetts and Burnside (1972)
Weighted germination percentage ( <i>WGP</i> )	<b>WeightGermPercent</b>	<p>It is estimated as follows.</p> $WGP = \frac{\sum_{i=1}^k (k - i + 1) N_i}{k \times N} \times 100$ <p>Where, <math>N_i</math> is the number of seeds that germinated in the time interval <math>i</math> (not cumulative, but partial count), <math>N</math> is the total number of seeds tested, and <math>k</math> is the total number of time intervals.</p>	Percentage (%)	Mixed	Reddy et al. (1985); Reddy (1978)
Mean germination percentage per unit time ( <i>GP</i> )	<b>MeanGermPercent</b>	<p>It is estimated as follows.</p> $\overline{GP} = \frac{GP}{T_k}$ <p>Where, <math>GP</math> is the final germination percentage, <math>T_k</math> is the time at the <math>k</math>th time interval, and <math>k</math> is the total number of time intervals required for final germination.</p>	% time <sup>-1</sup>	Mixed	Czabator (1962)
Number of seeds germinated per unit time $\overline{N}$	<b>MeanGermNumber</b>	<p>It is estimated as follows.</p> $\overline{N} = \frac{N_g}{T_k}$ <p>Where, <math>N_g</math> is the number of germinated seeds at the end of the germination test, <math>T_k</math> is the time at the <math>k</math>th time interval, and <math>k</math> is the total number of time intervals required for final germination.</p>	count time <sup>-1</sup>	Mixed	Khamassi et al. (2013)

Germination index	Function	Details	Unit	Measures	Reference
Timson's index [ $\sum 10$ (Ten summation), $\sum 5$ or $\sum 20$ ] or Germination energy index ( <i>GEI</i> )	<b>TimsonsIndex</b>	<p>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 (<math>G_i</math>) as follows.</p> $\Sigma k = \sum_{i=1}^k G_i$ <p>Where, <math>G_i</math> is the cumulative germination percentage in time interval <math>i</math>, and <math>k</math> is the total number of time intervals. It also estimated in terms of partial germination percentage as follows.</p> $\Sigma k = \sum_{i=1}^k g_i(k-j)$ <p>Where, <math>g_i</math> is the germination (not cumulative, but partial germination) in time interval <math>i</math> (<math>i</math> varying from 0 to <math>k</math>), <math>k</math> is the total number of time intervals, and <math>j = i - 1</math>.</p>	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 ( $\Sigma k_{mod}$ ) (Labouriau)	<b>TimsonsIndex</b>	<p>It is estimated as Timson's index <math>\Sigma k</math> divided by the sum of partial germination percentages.</p> $\Sigma k_{mod} = \frac{\Sigma k}{\sum_{i=1}^k g_i}$	no unit	Mixed	Ranal and Santana (2006)
Modified Timson's index ( $\Sigma k_{mod}$ ) (Khan and Unger)	<b>TimsonsIndex</b>	<p>It is estimated as Timson's index (<math>\Sigma k</math>) divided by the total time period of germination (<math>T_k</math>).</p> $\Sigma k_{mod} = \frac{\Sigma k}{T_k}$	% time <sup>-1</sup>	Mixed	Khan and Ungar (1984)
George's index ( <i>GR</i> )	<b>GermRateGeorge</b>	<p>It is estimated as follows.</p> $GR = \sum_{i=1}^k N_i K_i$ <p>Where <math>N_i</math> is the number of seeds germinated by <math>i</math>th interval and <math>K_i</math> is the number of intervals(eg. days) until the end of the test, and and <math>k</math> is the total number of time intervals.</p>	count time	Mixed	George (1961); Tucker and Wright (1965); Nichols and Heydecker (1968)

Germination index	Function	Details	Unit	Measures	Reference
Germination Index ( $GI$ ) (Melville)	<b>GermIndex</b>	<p>It is estimated as follows.</p> $GI = \sum_{i=1}^k \frac{ (T_k - T_i) N_i }{N_t}$ <p>Where, <math>T_i</math> is the time from the start of the experiment to the <math>i</math>th interval (day for the example), <math>N_i</math> is the number of seeds germinated in the <math>i</math>th time interval (not the accumulated number, but the number corresponding to the <math>i</math>th interval), <math>N_t</math> is the total number of seeds used in the test, and <math>k</math> is the total number of time intervals.</p>	time	Mixed	Melville et al. (1980)
Germination Index ( $GI_{mod}$ ) (Melville; Santana and Ranal)	<b>GermIndex</b>	<p>It is estimated as follows.</p> $GI_{mod} = \sum_{i=1}^k \frac{ (T_k - T_i) N_i }{N_g}$ <p>Where, <math>T_i</math> is the time from the start of the experiment to the <math>i</math>th interval (day for the example), <math>N_i</math> is the number of seeds germinated in the <math>i</math>th time interval (not the accumulated number, but the number corresponding to the <math>i</math>th interval), <math>N_g</math> is the total number of germinated seeds at the end of the test, and <math>k</math> is the total number of time intervals.</p>	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)	<b>EmergenceRateIndex</b>	<p>It is estimated as follows.</p> $ERI = \sum_{i=i_0}^{k-1} N_i(k-i)$ <p>Where, <math>N_i</math> is the number of seeds germinated in the <math>i</math>th time interval (not the accumulated number, but the number corresponding to the <math>i</math>th interval), <math>i_0</math> is the time interval when emergence/germination started, and <math>k</math> is the total number of time intervals.</p>	count	Mixed	Shmueli and Goldberg (1971)
Modified Emergence Rate Index ( $ERI_{mod}$ ) or Modified Germination Rate Index (Shmueli and Goldberg; Santana and Ranal)	<b>EmergenceRateIndex</b>	<p>It is estimated by dividing Emergence rate index (<math>ERI</math>) by total number of emerged seedlings (or germinated seeds).</p> $ERI_{mod} = \frac{\sum_{i=i_0}^{k-1} N_i(k-i)}{N_g} = \frac{ERI}{N_g}$ <p>Where, <math>N_g</math> is the total number of germinated seeds at the end of the test, <math>N_i</math> is the number of seeds germinated in the <math>i</math>th time interval (not the accumulated number, but the number corresponding to the <math>i</math>th interval), <math>i_0</math> is the time interval when emergence/germination started, and <math>k</math> is the total number of time intervals.</p>	no unit	Mixed	Shmueli and Goldberg (1971); Santana and Ranal (2004); Ranal and Santana (2006)

Germination index	Function	Details	Unit	Measures	Reference
Emergence Rate Index ( <i>ERI</i> ) or Germination Rate Index (Bilbro & Wanjura)	<b>EmergenceRateIndex</b>	<p>It is the estimated as follows.</p> $ERI = \frac{\sum_{i=1}^k N_i}{\bar{T}} = \frac{N_g}{\bar{T}}$ <p>Where, <math>N_g</math> is the total number of germinated seeds at the end of the test, <math>N_i</math> is the number of seeds germinated in the <math>i</math>th time interval (not the accumulated number, but the number corresponding to the <math>i</math>th interval), and <math>\bar{T}</math> is the mean germination time or mean emergence time.</p>	count time <sup>-1</sup>	Mixed	Bilbro and Wanjura (1982)
Emergence Rate Index ( <i>ERI</i> ) or Germination Rate Index (Fakorede)	<b>EmergenceRateIndex</b>	<p>It is estimated as follows.</p> $ERI = \frac{\bar{T}}{FGP/100}$ <p>Where, <math>\bar{T}</math> is the Mean germination time and <math>FGP</math> is the final germination time.</p>	time count <sup>-1</sup>	Mixed	Fakorede and Ayoola (1980); Fakorede and Ojo (1981); Fakorede and Agbana (1983)
Peak value( <i>PV</i> ) (Czabator) or Emergence Energy ( <i>EE</i> )	<b>PeakValue</b>	<p>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.</p> $PV = \max \left( \frac{G_1}{T_1}, \frac{G_2}{T_2}, \dots, \frac{G_k}{T_k} \right)$ <p>Where, <math>T_i</math> is the time from the start of the experiment to the <math>i</math>th interval, <math>G_i</math> is the cumulative germination percentage in the <math>i</math>th time interval, and <math>k</math> is the total number of time intervals.</p>	% time <sup>-1</sup>	Mixed	Czabator (1962); Bonner (1967)
Germination value ( <i>GV</i> ) (Czabator)	<b>GermValue</b>	<p>It is computed as follows.</p> $GV = PV \times MDG$ <p>Where, <math>PV</math> is the peak value and <math>MDG</math> 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 <math>MDG</math> with the mean germination percentage per unit time (<math>GP</math>). <math>GV</math> value can be modified (<math>GV_{mod}</math>), to consider the entire duration from the beginning of the test instead of just from the onset of germination.</p>	% <sup>2</sup> time <sup>-2</sup>	Mixed	Czabator (1962); Brown and Mayer (1988)

Germination index	Function	Details	Unit	Measures	Reference
Germination value (GV) (Diavanshir and Pourbiek)	<b>GermValue</b>	<p>It is computed as follows.</p> $GV = \frac{\sum DGS}{N} \times GP \times c$ <p>Where, <math>DGS</math> is the daily germination speed computed by dividing cumulative germination percentage by the number of days since the onset of germination, <math>N</math> is the frequency or number of DGS calculated during the test, <math>GP</math> is the germination percentage expressed over 100, and <math>c</math> is a constant. The value of <math>c</math> is decided on the basis of average daily speed of germination (<math>\frac{\sum DGS}{N}</math>). If it is less than 10, then <math>c</math> value of 10 can be used and if it is more than 10, then value of 7 or 8 can be used for <math>c</math>.  <math>GV</math> value can be modified (<math>GV_{mod}</math>), to consider the entire duration from the beginning of the test instead of just from the onset of germination.</p>	% <sup>2</sup> time <sup>-1</sup>	Mixed	Djavanshir and Pourbeik (1976); Brown and Mayer (1988)
Coefficient of uniformity of germination (CUG)	<b>CUGerm</b>	<p>It is computed as follows.</p> $CUG = \frac{\sum_{i=1}^k N_i}{\sum_{i=1}^k (\bar{T} - T_i)^2 N_i}$ <p>Where, <math>\bar{T}</math> is the the mean germination time, <math>T_i</math> is the time from the start of the experiment to the <math>i</math>th interval (day for the example), <math>N_i</math> is the number of seeds germinated in the <math>i</math>th time interval (not the accumulated number, but the number corresponding to the <math>i</math>th interval), and <math>k</math> is the total number of time intervals.</p>	time <sup>-2</sup>	Germination unifromity	Heydecker (1972); Bewley and Black (1994)
Coefficient of variation of the germination time (CV <sub>T</sub> )	<b>CVGermTime</b>	<p>It is estimated as follows.</p> $CV_T = \sqrt{\frac{s_T^2}{\bar{T}}}$ <p>Where, <math>s_T^2</math> is the variance of germination time and <math>\bar{T}</math> is the mean germination time.</p>	no unit	Germination unifromity	Gomes (1960); Ranal and Santana (2006)
Synchronization index ( $\bar{E}$ ) or Uncertainty of the germination process ( $U$ ) or informational entropy ( $H$ )	<b>GermUncertainty</b>	<p>It is estimated as follows.</p> $\bar{E} = - \sum_{i=1}^k f_i \log_2 f_i$ <p>Where, <math>f_i</math> is the relative frequency of germination (<math>f_i = \frac{N_i}{\sum_{i=1}^k N_i}</math>), <math>N_i</math> is the number of seeds germinated on the <math>i</math>th time interval, and <math>k</math> is the total number of time intervals.</p>	bit	Germination synchrony	Shannon (1948); Labouriau and Valadares (1976); Labouriau (1983b)

Germination index	Function	Details	Unit	Measures	Reference
Synchrony of germination ( $Z$ index)	<b>GermSynchrony</b>	<p>It is computed as follows.</p> $Z = \frac{\sum_{i=1}^k C_{N_i,2}}{C_{\Sigma N_i,2}}$ <p>Where, <math>C_{N_i,2}</math> is the partial combination of the two germinated seeds from among <math>N_i</math>, the number of seeds germinated on the <math>i</math>th time interval (estimated as <math>C_{N_i,2} = \frac{N_i(N_i-1)}{2}</math>), and <math>C_{\Sigma N_i,2}</math> 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.</p>	no unit	Germination synchrony	Primack ( <a href="#">1985</a> ); Ranal and Santana ( <a href="#">2006</a> )

## Examples

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

```
# From partial germination counts
```

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

```
GermPercent(germ.counts = x, total.seeds = 50)
```

```
GermPercent()
```

```
[1] 80
```

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

```
[1] 34
```

```
# For multiple peak germination times
```

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

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

```
[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 exist.`

```
[1] 22
```

```
# From number of germinated seeds
```

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

```
GermPercent(germinated.seeds = 40, total.seeds = 50)
```

```
[1] 80
```

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

```
# From partial germination counts
```

```

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

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

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

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

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

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

Warning in PeakGermTime(germ.counts = z, intervals = int): Multiple peak germination times exist.
[1] 5 6
# From cumulative germination counts
#-----
FirstGermTime(germ.counts = y, intervals = int, partial = FALSE)

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

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

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

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

Warning in PeakGermTime(germ.counts = cumsum(z), intervals = int, partial = FALSE): Multiple peak germination times exist.
[1] 5 6

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

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

t50()

```



```
[1] 5.970588
```

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

```
[1] 5.941176
```

```
# From cumulative germination counts
```

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

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

```
[1] 5.970588
```

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

```
[1] 5.941176
```

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

```
# From partial germination counts
```

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

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

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

```
[1] 6.7
```

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

```
[1] 1.446154
```

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

```
[1] 0.1901416
```

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

```
[1] 0.1794868
```

```
# From cumulative germination counts
```

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

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

```
[1] 6.7
```

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

```
[1] 19.04012
```

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

```
[1] 0.2394781
```

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

```
[1] 0.6512685
```

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

```

int <- 1:length(x)

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

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

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

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

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

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

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

[1] 0.1683168

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

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

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

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

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

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

[1] 0.1683168

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

```

```

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

GermSpeed(), GermSpeedAccumulated(), GermSpeedCorrected()

[1] 6.138925
GermSpeedAccumulated(germ.counts = x, intervals = int)

[1] 34.61567
GermSpeedCorrected(germ.counts = x, intervals = int, total.seeds = 50,
                    method = "normal")

[1] 0.1534731
GermSpeedCorrected(germ.counts = x, intervals = int, total.seeds = 50,
                    method = "accumulated")

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

[1] 12.27785
GermSpeedAccumulated(germ.counts = x, intervals = int,
                     percent = TRUE, total.seeds = 50)

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

[1] 6.138925
GermSpeedAccumulated(germ.counts = y, intervals = int, partial = FALSE)

[1] 34.61567
GermSpeedCorrected(germ.counts = y, intervals = int,
                   partial = FALSE, total.seeds = 50, method = "normal")

[1] 0.1534731
GermSpeedCorrected(germ.counts = y, intervals = int,
                   partial = FALSE, total.seeds = 50, method = "accumulated")

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

[1] 12.27785

```

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

```
[1] 69.23134
```

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

```
# From partial germination counts
```

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

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

```
[1] 6.138925
```

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

```
[1] 34.61567
```

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

```
[1] 0.1534731
```

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

```
[1] 0.8653917
```

```
# From partial germination counts (with percentages instead of counts)
```

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

```
[1] 12.27785
```

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

```
[1] 69.23134
```

```
# From cumulative germination counts
```

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

```
[1] 6.138925
```

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

```
[1] 34.61567
```

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

```
[1] 0.1534731
```

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

```
[1] 0.8653917
```

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

```
[1] 12.27785
```

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

```
[1] 69.23134
```

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

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

```
WeightGermPercent()
```

```
[1] 47.42857
```

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

```
[1] 47.42857
```

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

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

```
MeanGermPercent(), MeanGermNumber()
```

```
[1] 5.714286
```

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

```
[1] 2.857143
```

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

```
[1] 5.714286
```

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

```
[1] 2.857143
```

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

```
[1] 5.714286
```

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

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

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

```
[1] 664
```

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

```
[1] 664
```

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

```
[1] 8.3
```

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

```
[1] 47.42857
```

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

```
[1] 332
```

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

```
[1] 344
```

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

```
[1] 344
```

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

```
[1] 4.410256
```

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

```
[1] 24.57143
```

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

[1] 172

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

[1] 332

```
# From cumulative germination counts
#-----
# 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)
```

```
EmergenceRateIndex()
```



```
[1] 292
```

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

```
[1] 292
```

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

```
[1] 7.3
```

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

```
[1] 5.970149
```

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

```
[1] 8.375
```

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

```
[1] 292
```

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

```
[1] 292
```

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

```
[1] 7.3
```

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

```
[1] 5.970149
```

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

```
[1] 8.375
```

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

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

```
PeakValue(), GermValue()
```

```
[1] 9.5
```

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

```
$`Germination Value`
```

```
[1] 38.95
```

```
[[2]]
```

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

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

```
$`Germination Value`
```

```
[1] 53.36595
```

```
[[2]]
```

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

```
$testend
```

```
[1] 16
```

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

```
$`Germination Value`
```

```
[1] 38.95
```

```
[[2]]
```

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

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

```
$`Germination Value`
```

```
[1] 46.6952
```

```
[[2]]
```

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

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

```
$testend
```

```
[1] 16
```

```
# From cumulative germination counts
```

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

```
PeakValue(germ.counts = y, interval = int, total.seeds = 200,
           partial = FALSE)
```

```
[1] 9.5
```

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

```
$`Germination Value`
```

```
[1] 38.95
```

```
[[2]]
```

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

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

```
$`Germination Value`
```

```
[1] 53.36595
```

```
[[2]]
```

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

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

```
$testend
```

```
[1] 16
```

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

```
$`Germination Value`
```

```
[1] 38.95
```

```
[[2]]
```

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

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

```
$`Germination Value`
```

```
[1] 46.6952
```

```
[[2]]
```

	germ.counts	intervals	Cumulative.germ.counts	Cumulative.germ.percent	DGS	SumDGSbyN	GV
--	-------------	-----------	------------------------	-------------------------	-----	-----------	----

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

```
$testend
```

```
[1] 16
```

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

```
# From partial germination counts
```

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

```
CUGerm()
```

```
[1] 0.7092199
```

```
# From cumulative germination counts
```

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

```
[1] 0.05267935
```

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

```
# From partial germination counts
```

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

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

```
[1] 0.2666667
```

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

[1] 2.062987

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

[1] 0.2666667

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

[1] 2.062987
```

## Non-linear regression analysis

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

### Four-parameter hill function

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

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

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

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

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

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

Germination parameters	Details	Unit	Measures
<i>lag</i>	It is the time at germination onset and is computed by solving four-parameter hill function after setting $y$ to 0 as follows. $lag = b\sqrt{\frac{-y_0c^b}{a + y_0}}$	time	Germination time
$D_{lag-50}$	The duration between the time at germination onset ( <i>lag</i> ) and that at 50% germination ( $c$ ).	time	Germination time
$t_{50total}$	Time required for 50% of total seeds to germinate.	time	Germination time
$t_{50germinated}$	Time required for 50% of viable/germinated seeds to germinate	time	Germination time
$t_{xtotal}$	Time required for $x\%$ of total seeds to germinate.	time	Germination time
$t_{xgerminated}$	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 <b>umin</b> and <b>umax</b> to germinate.	time	Germination time
Time at maximum germination rate ( <i>TMGR</i> )	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, <i>TMGR</i> 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 ( <i>AUC</i> )	It is obtained by integration of the fitted curve between time 0 and time specified in the argument <b>tmax</b> .		Mixed
<i>MGT</i>	Calculated by integration of the fitted curve and proper normalisation.	time	Germination time
<i>Skewness</i>	It is computed as follows. $\frac{MGT}{t_{50germinated}}$		

## Examples



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

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

```
FourPHFfit()
```

```
$data
```

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

```
$Parameters
```

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

```
$Fit
```

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

```
$a
```

```
[1] 80
```

```
$b
```

```
[1] 9.881947
```

```
$c
```

```
[1] 6.034954
```

```
$y0
```

```
[1] 0
```

```
$lag
```

```
[1] 0
```

```

$Dlag50
[1] 6.034954

$t50.total
[1] 6.355122

$txp.total
      10      60
4.956266 6.744598

$t50.Germinated
[1] 6.034954

$txp.Germinated
      10      60
4.831809 6.287724

$Uniformity
      90      10 uniformity
7.537688 4.831809 2.705880

$TMGR
[1] 5.912195

$AUC
[1] 1108.975

$MGT
[1] 6.632252

$Skewness
[1] 1.098973

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

$isConv
[1] TRUE

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

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

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

```

```

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

```

`$Parameters`

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

`$Fit`

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

`$a`

```
[1] 80
```

`$b`

```
[1] 9.881927
```

`$c`

```
[1] 6.034953
```

`$y0`

```
[1] 0
```

`$lag`

```
[1] 0
```

`$Dlag50`

```
[1] 6.034953
```

`$t50.total`

```
[1] 6.355121
```

`$txp.total`

```

      10      60
4.956263 6.744599

```

`$t50.Germinated`

```
[1] 6.034953
```

`$txp.Germinated`

```

      10      60
4.831806 6.287723

```

`$Uniformity`

```

          90          10 uniformity
7.537691  4.831806  2.705885

$TMGR
[1] 5.912194

$AUC
[1] 1108.976

$MGT
[1] 6.632252

$Skewness
[1] 1.098973

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

$isConv
[1] TRUE

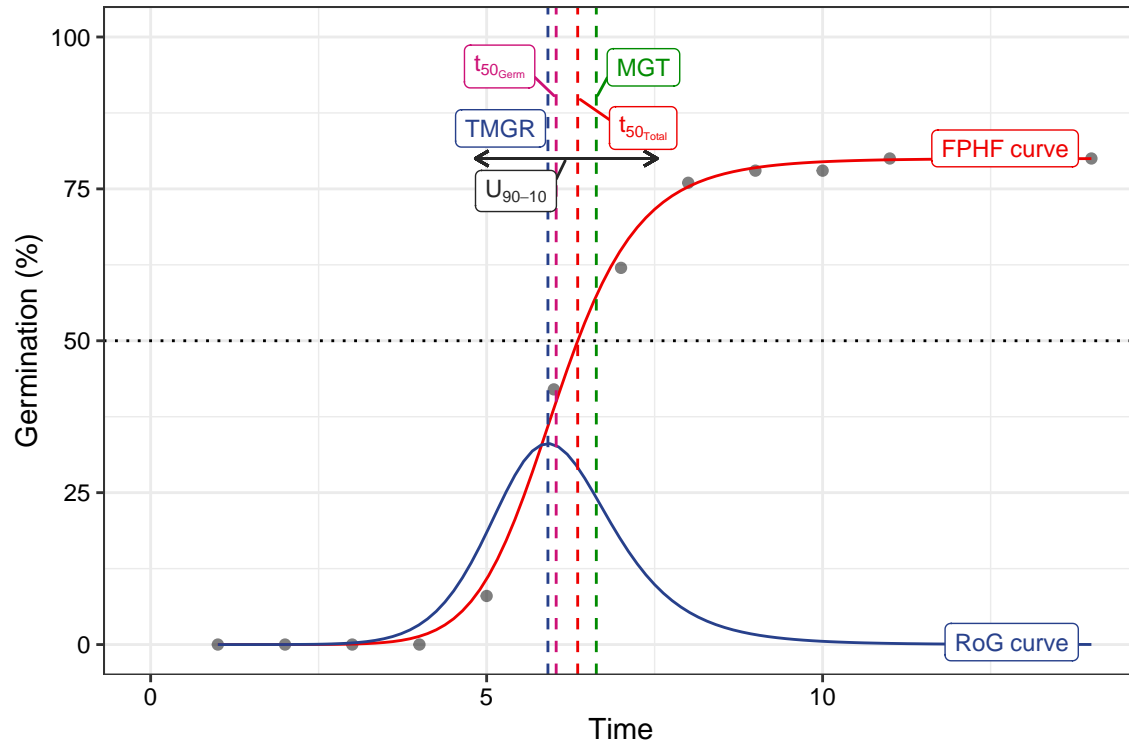
attr("class")
[1] "FourPHFfit" "list"
x <- c(0, 0, 0, 0, 4, 17, 10, 7, 1, 0, 1, 0, 0, 0)
y <- c(0, 0, 0, 0, 4, 21, 31, 38, 39, 39, 40, 40, 40, 40)
int <- 1:length(x)
total.seeds = 50

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

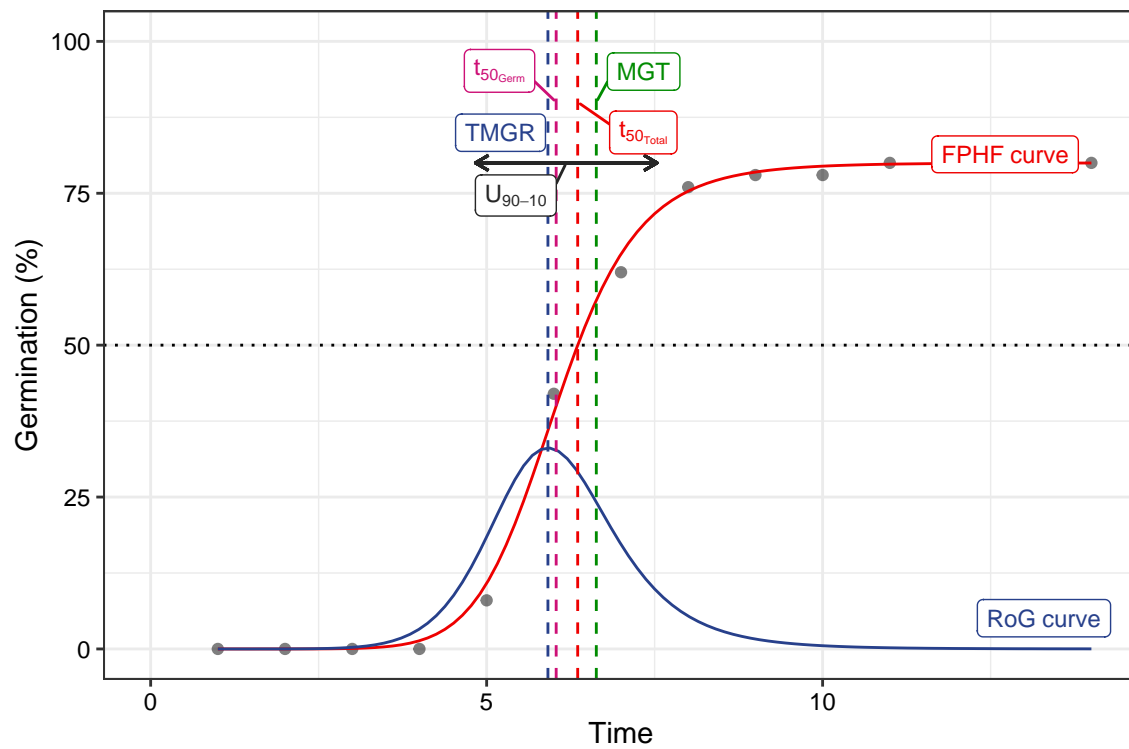
# From cumulative germination counts
#-----
fit2 <- FourPHFfit(germ.counts = y, intervals = int,
                  total.seeds = 50, tmax = 20, partial = FALSE)

# Default plots
plot(fit1)

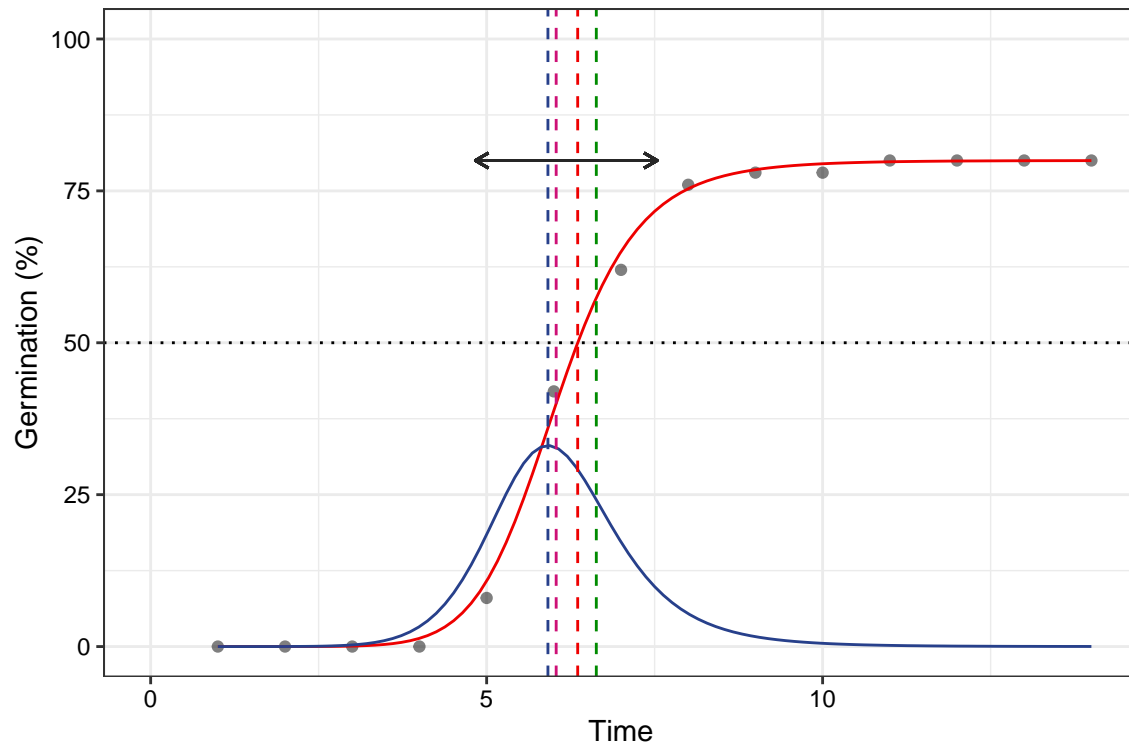
```



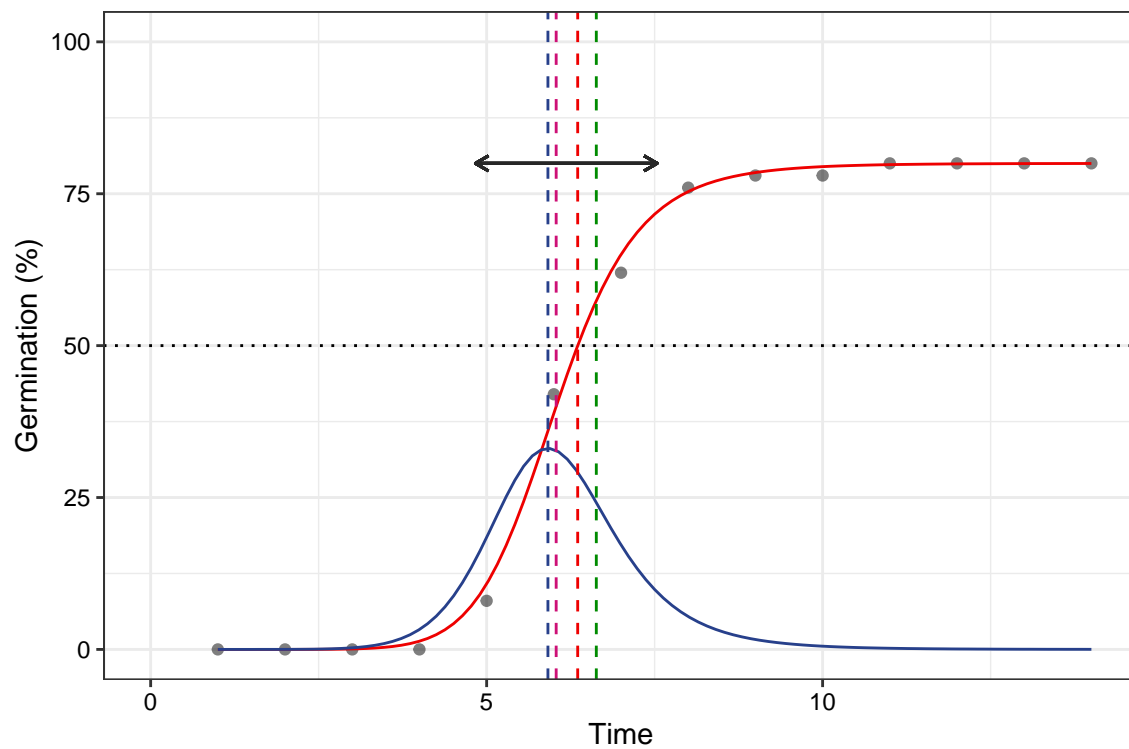
```
plot(fit2)
```



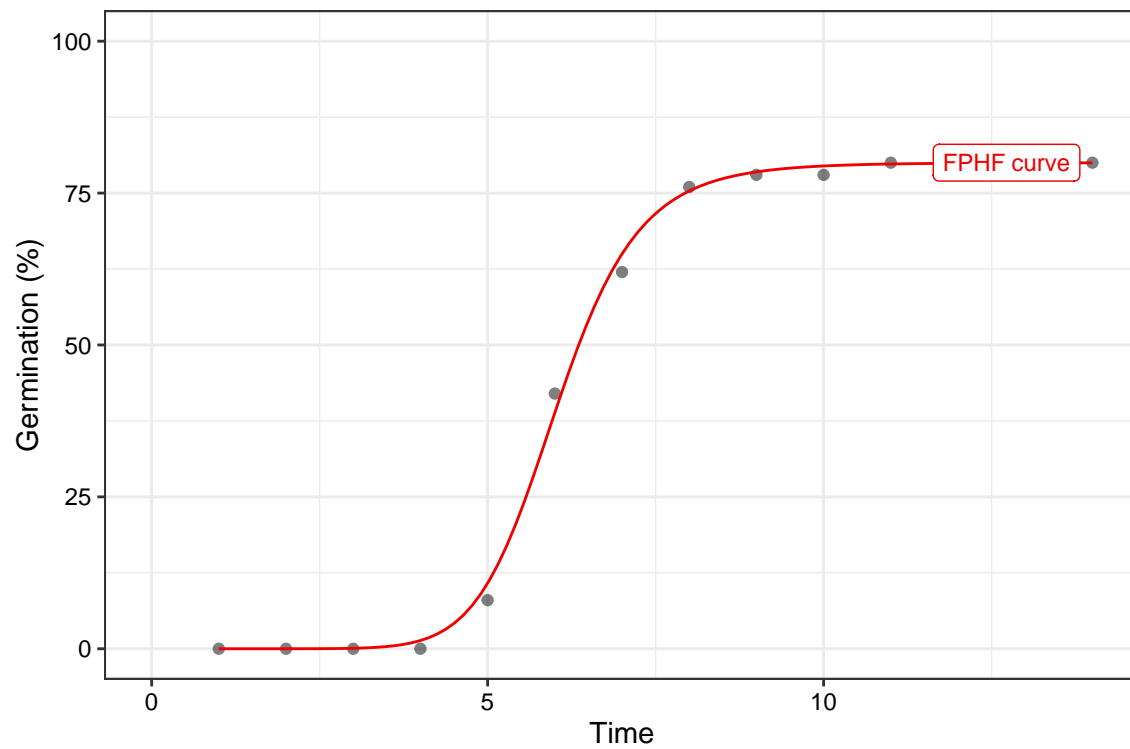
```
# No labels
plot(fit1, plotlabels = FALSE)
```



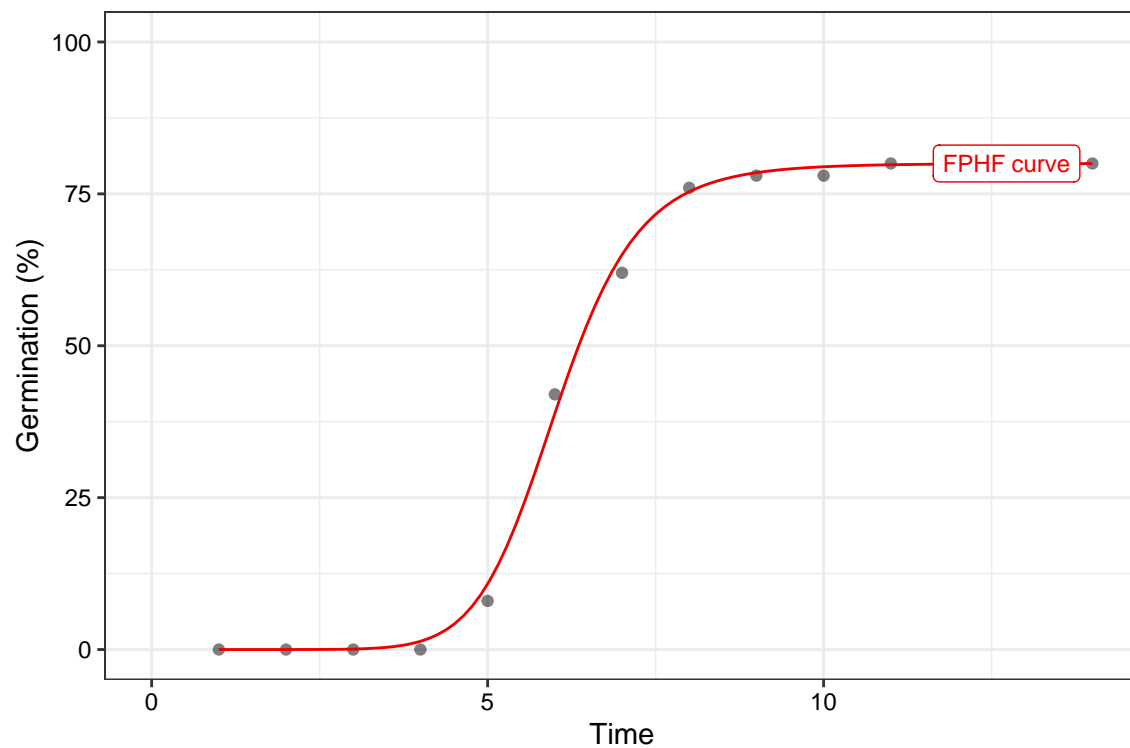
```
plot(fit2, plotlabels = FALSE)
```



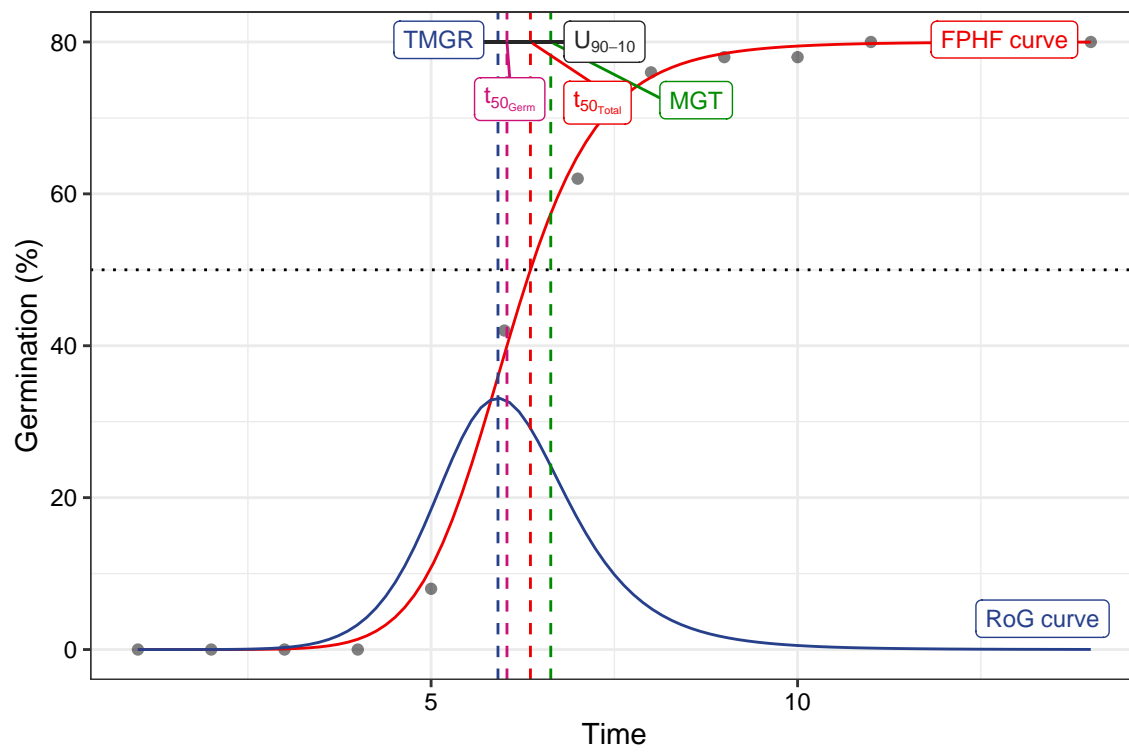
```
# Only the FPGHF curve
plot(fit1, rog = FALSE, t50.total = FALSE, t50.germ = FALSE,
     tmgr = FALSE, mgt = FALSE, uniformity = FALSE)
```



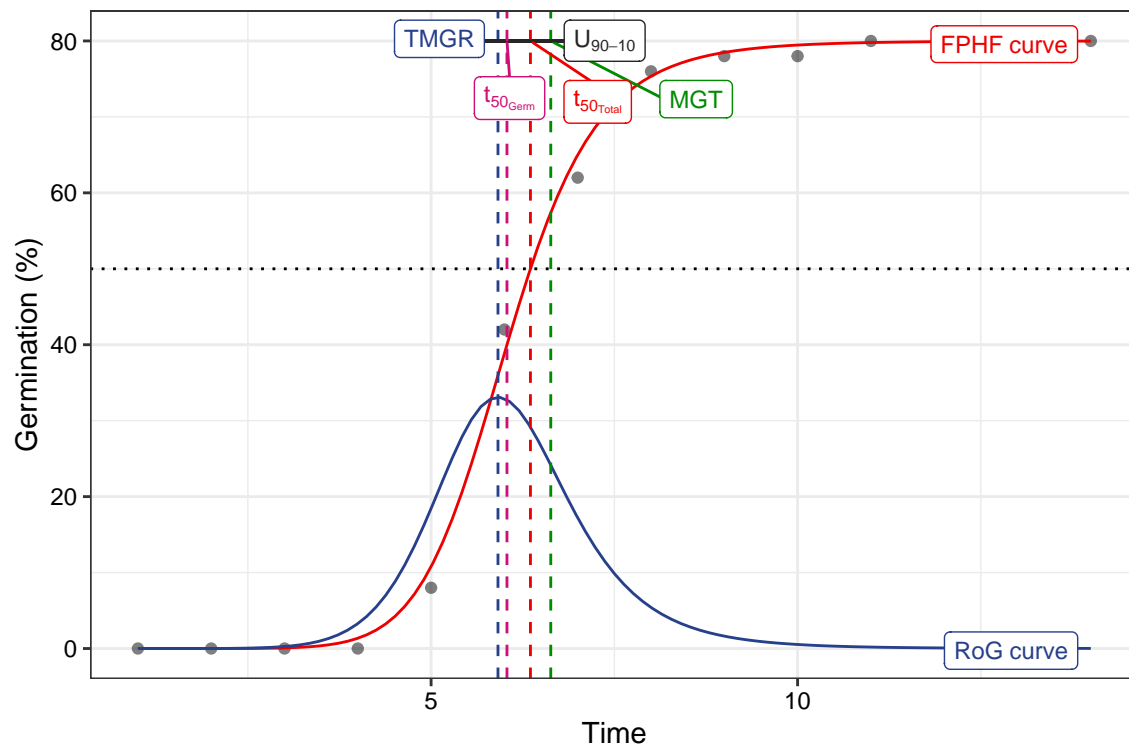
```
plot(fit2, rog = FALSE, t50.total = FALSE, t50.germ = FALSE,  
     tmgr = FALSE, mgt = FALSE, uniformity = FALSE)
```



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



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





## Wrapper functions

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

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

```
data(gcdata)

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

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

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

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

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

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

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

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

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

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

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

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

Please use ``method = "shmueligoldberg"`` instead.

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

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

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

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

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

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

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

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

2	G2	1	0	0	0	1	3	15	13	6	2	1	0	1	0	0
3	G3	1	0	0	0	2	3	18	9	8	2	1	1	1	0	0
4	G4	1	0	0	0	0	4	19	12	6	2	1	1	1	0	0
5	G5	1	0	0	0	0	5	20	12	8	1	0	0	1	1	0
6	G1	2	0	0	0	0	3	21	11	7	1	1	1	1	0	0
7	G2	2	0	0	0	0	4	18	11	7	1	0	1	0	0	0
8	G3	2	0	0	0	1	3	14	12	6	2	1	0	1	0	0
9	G4	2	0	0	0	1	3	19	10	8	1	1	1	1	0	0
10	G5	2	0	0	0	0	4	18	13	6	2	1	0	1	0	0
11	G1	3	0	0	0	0	5	21	11	8	1	0	0	1	1	0
12	G2	3	0	0	0	0	3	20	10	7	1	1	1	1	0	0
13	G3	3	0	0	0	0	4	19	12	8	1	1	0	1	1	0
14	G4	3	0	0	0	0	3	21	11	6	1	0	1	1	0	0
15	G5	3	0	0	0	0	4	17	10	8	1	1	1	0	0	0
	GermPercent	PeakGermPercent	FirstGermTime	LastGermTime	PeakGermTime	TimeSpreadGerm	t50_Coolbear	t50_Lowbear								
1	80.00000	34.00000	5	11	6	6	5.970588	5.970588								
2	82.35294	29.41176	4	12	6	8	6.192308	6.192308								
3	93.75000	37.50000	4	12	6	8	6.000000	5.970588								
4	90.19608	37.25490	5	12	6	7	6.041667	6.041667								
5	96.00000	40.00000	5	13	6	8	5.975000	5.975000								
6	93.87755	42.85714	5	12	6	7	5.976190	5.976190								
7	87.50000	37.50000	5	11	6	6	5.972222	5.972222								
8	85.10638	29.78723	4	12	6	8	6.208333	6.208333								
9	86.53846	36.53846	4	12	6	8	6.000000	5.970588								
10	90.00000	36.00000	5	12	6	7	6.076923	6.076923								
11	94.11765	41.17647	5	13	6	8	5.928571	5.928571								
12	86.27451	39.21569	5	12	6	7	5.975000	5.975000								
13	95.91837	38.77551	5	13	6	8	6.083333	6.083333								
14	91.66667	43.75000	5	12	6	7	5.928571	5.928571								
15	87.50000	35.41667	5	11	6	6	6.050000	6.050000								
	MeanGermTime	VarGermTime	SEGermTime	CVGermTime	MeanGermRate	VarGermRate	SEGermRate	CVGermRate								
1	6.700000	1.446154	0.1901416	0.1794868	0.1492537	0.0007176543	0.004235724	14.92537								
2	6.857143	2.027875	0.2197333	0.2076717	0.1458333	0.0009172090	0.004673148	14.58333								
3	6.866667	2.572727	0.2391061	0.2335882	0.1456311	0.0011572039	0.005071059	14.56311								
4	6.891304	2.187923	0.2180907	0.2146419	0.1451104	0.0009701218	0.004592342	14.51104								
5	6.812500	2.368351	0.2221275	0.2259002	0.1467890	0.0010995627	0.004786184	14.67890								
6	6.869565	2.071498	0.2122088	0.2095140	0.1455696	0.0009301809	0.004496813	14.55696								
7	6.690476	1.389663	0.1818989	0.1761967	0.1494662	0.0006935558	0.004063648	14.94662								
8	6.875000	2.112179	0.2297923	0.2113940	0.1454545	0.0009454531	0.004861721	14.54545								
9	6.866667	2.300000	0.2260777	0.2208604	0.1456311	0.0010345321	0.004794747	14.56311								
10	6.822222	1.831313	0.2017321	0.1983606	0.1465798	0.0008453940	0.004334343	14.65798								
11	6.791667	2.381206	0.2227295	0.2272072	0.1472393	0.0011191581	0.004828643	14.72393								
12	6.886364	2.149577	0.2210295	0.2129053	0.1452145	0.0009558577	0.004660905	14.52145								
13	6.936170	2.539315	0.2324392	0.2297410	0.1441718	0.0010970785	0.004831366	14.41718								
14	6.772727	1.900634	0.2078370	0.2035568	0.1476510	0.0009033254	0.004531018	14.76510								
15	6.809524	1.670151	0.1994129	0.1897847	0.1468531	0.0007767634	0.004300508	14.68531								
	GermRateRecip_Farooq	GermSpeed_Count	GermSpeed_Percent	GermSpeedAccumulated_Count	GermSpeedAccumulated_Percent											
1	0.1683168	6.138925	12.27785	34.61567												
2	0.1625000	6.362698	12.47588	35.54058												
3	0.1674419	6.882179	14.33787	38.29725												
4	0.1666667	6.927417	13.58317	38.68453												
5	0.1680672	7.318987	14.63797	41.00786												
6	0.1680000	6.931782	14.14649	38.77620												
7	0.1682243	6.448449	13.43427	36.38546												

8	0.1621622	6.053175	12.87909	33.77079		
9	0.1674009	6.830592	13.13575	38.11511		
10	0.1656051	6.812698	13.62540	38.19527		
11	0.1693548	7.342796	14.39764	41.17452		
12	0.1680672	6.622258	12.98482	37.00640		
13	0.1655172	7.052320	14.39249	39.29399		
14	0.1693548	6.706782	13.97246	37.69490		
15	0.1666667	6.363925	13.25818	35.69697		
	GermSpeedCorrected_Normal	GermSpeedCorrected_Accumulated	WeightGermPercent	MeanGermPercent	MeanGermN	
1	0.1534731	0.8653917	47.42857	5.714286	2.8	
2	0.1514928	0.8462043	47.89916	5.882353	3.0	
3	0.1529373	0.8510501	54.46429	6.696429	3.2	
4	0.1505960	0.8409680	52.24090	6.442577	3.2	
5	0.1524789	0.8543303	56.14286	6.857143	3.4	
6	0.1506909	0.8429608	54.51895	6.705539	3.2	
7	0.1535345	0.8663205	51.93452	6.250000	3.0	
8	0.1513294	0.8442698	49.39210	6.079027	2.8	
9	0.1517909	0.8470024	50.27473	6.181319	3.2	
10	0.1513933	0.8487837	52.57143	6.428571	3.2	
11	0.1529749	0.8578026	55.18207	6.722689	3.4	
12	0.1505059	0.8410547	50.00000	6.162465	3.1	
13	0.1500494	0.8360424	55.24781	6.851312	3.3	
14	0.1524269	0.8567022	53.86905	6.547619	3.1	
15	0.1515220	0.8499278	51.19048	6.250000	3.0	
	TimsonsIndex	TimsonsIndex_Labouriau	TimsonsIndex_KhanUngar	GermRateGeorge	GermIndex	GermIndex_mod
1	8.000000	1.00	0.5714286	4	5.840000	7.300000
2	9.803922	1.25	0.7002801	5	5.882353	7.142857
3	14.583333	1.40	1.0416667	7	6.687500	7.133333
4	7.843137	1.00	0.5602241	4	6.411765	7.108696
5	10.000000	1.00	0.7142857	5	6.900000	7.187500
6	6.122449	1.00	0.4373178	3	6.693878	7.130435
7	8.333333	1.00	0.5952381	4	6.395833	7.309524
8	10.638298	1.25	0.7598784	5	6.063830	7.125000
9	9.615385	1.25	0.6868132	5	6.173077	7.133333
10	8.000000	1.00	0.5714286	4	6.460000	7.177778
11	9.803922	1.00	0.7002801	5	6.784314	7.208333
12	5.882353	1.00	0.4201681	3	6.137255	7.113636
13	8.163265	1.00	0.5830904	4	6.775510	7.063830
14	6.250000	1.00	0.4464286	3	6.625000	7.227273
15	8.333333	1.00	0.5952381	4	6.291667	7.190476
	EmergenceRateIndex_Melville	EmergenceRateIndex_Melville_mod	EmergenceRateIndex_BilbroWanjura			
1		292	7.300000		5.970149	
2		300	7.142857		6.125000	
3		321	7.133333		6.553398	
4		327	7.108696		6.675079	
5		345	7.187500		7.045872	
6		328	7.130435		6.696203	
7		307	7.309524		6.277580	
8		285	7.125000		5.818182	
9		321	7.133333		6.553398	
10		323	7.177778		6.596091	
11		346	7.208333		7.067485	
12		313	7.113636		6.389439	
13		332	7.063830		6.776074	

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

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

```
data(gcdata)

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

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

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

5	G5	1	0	0	0	0	5	20	12	8	1	0	0	1	1	0
6	G1	2	0	0	0	0	3	21	11	7	1	1	1	1	0	0
7	G2	2	0	0	0	0	4	18	11	7	1	0	1	0	0	0
8	G3	2	0	0	0	1	3	14	12	6	2	1	0	1	0	0
9	G4	2	0	0	0	1	3	19	10	8	1	1	1	1	0	0
10	G5	2	0	0	0	0	4	18	13	6	2	1	0	1	0	0
11	G1	3	0	0	0	0	5	21	11	8	1	0	0	1	1	0
12	G2	3	0	0	0	0	3	20	10	7	1	1	1	1	0	0
13	G3	3	0	0	0	0	4	19	12	8	1	1	0	1	1	0
14	G4	3	0	0	0	0	3	21	11	6	1	0	1	1	0	0
15	G5	3	0	0	0	0	4	17	10	8	1	1	1	0	0	0
b c y0 lag Dlag50 t50.total t50.Germinated TMGR AUC MGT Skewness																
1	9.881947	6.034954	0	0	6.034954	6.355122	6.034954	5.912195	1108.975	6.632252	1.098973					
2	9.227667	6.175193	0	0	6.175193	6.473490	6.175193	6.031282	1128.559	6.784407	1.098655					
3	7.793055	6.138110	0	0	6.138110	6.244190	6.138110	5.938179	1283.693	6.772742	1.103392					
4	8.925668	6.125172	0	0	6.125172	6.276793	6.125172	5.972686	1239.887	6.739665	1.100323					
5	9.419194	6.049641	0	0	6.049641	6.103433	6.049641	5.914289	1328.328	6.654980	1.100062					
6	9.450187	6.097412	0	0	6.097412	6.182276	6.097412	5.961877	1294.463	6.702470	1.099232					
7	10.172466	6.029851	0	0	6.029851	6.202812	6.029851	5.914057	1213.908	6.622417	1.098272					
8	8.940702	6.189774	0	0	6.189774	6.439510	6.189774	6.036193	1164.346	6.804000	1.099232					
9	8.617395	6.125121	0	0	6.125121	6.352172	6.125121	5.961631	1188.793	6.745241	1.101242					
10	9.608849	6.109503	0	0	6.109503	6.253042	6.109503	5.978115	1240.227	6.711899	1.098600					
11	9.400248	6.018759	0	0	6.018759	6.099434	6.018759	5.883558	1305.200	6.624247	1.100600					
12	9.162558	6.108449	0	0	6.108449	6.326181	6.108449	5.964079	1188.021	6.718636	1.099892					
13	8.995233	6.149011	0	0	6.149011	6.207500	6.149011	5.998270	1316.407	6.762272	1.099733					
14	10.391898	6.015907	0	0	6.015907	6.122385	6.015907	5.905179	1273.386	6.604963	1.097916					
15	9.136762	6.121580	0	0	6.121580	6.317392	6.121580	5.976088	1203.664	6.732267	1.099760					
msg isConv txp.total_10 txp.total_60 Uniformity																
1	#1. Relative error in the sum of squares is at most `ftol'.	TRUE	4.956266	6.744598	7											
2	#1. Relative error in the sum of squares is at most `ftol'.	TRUE	4.983236	6.872603	7											
3	#1. Relative error in the sum of squares is at most `ftol'.	TRUE	4.673022	6.608437	8											
4	#1. Relative error in the sum of squares is at most `ftol'.	TRUE	4.850876	6.614967	7											
5	#1. Relative error in the sum of squares is at most `ftol'.	TRUE	4.814126	6.386788	7											
6	#1. Relative error in the sum of squares is at most `ftol'.	TRUE	4.868635	6.477594	7											
7	#1. Relative error in the sum of squares is at most `ftol'.	TRUE	4.930423	6.510495	7											
8	#1. Relative error in the sum of squares is at most `ftol'.	TRUE	4.940058	6.823299	7											
9	#1. Relative error in the sum of squares is at most `ftol'.	TRUE	4.836659	6.733275	7											
10	#1. Relative error in the sum of squares is at most `ftol'.	TRUE	4.920629	6.566505	7											
11	#1. Relative error in the sum of squares is at most `ftol'.	TRUE	4.798630	6.391288	7											
12	#1. Relative error in the sum of squares is at most `ftol'.	TRUE	4.893597	6.684521	7											
13	#1. Relative error in the sum of squares is at most `ftol'.	TRUE	4.841310	6.509952	7											
14	#1. Relative error in the sum of squares is at most `ftol'.	TRUE	4.915143	6.397486	7											
15	#1. Relative error in the sum of squares is at most `ftol'.	TRUE	4.892505	6.667247	7											
Uniformity_10 Uniformity																
1	4.831809	2.705880														
2	4.866755	2.968652														
3	4.630062	3.507277														
4	4.788598	3.046208														
5	4.790947	2.848078														
6	4.832474	2.860984														
7	4.858477	2.625165														
8	4.841106	3.073056														
9	4.746574	3.157466														
10	4.860681	2.818494														

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

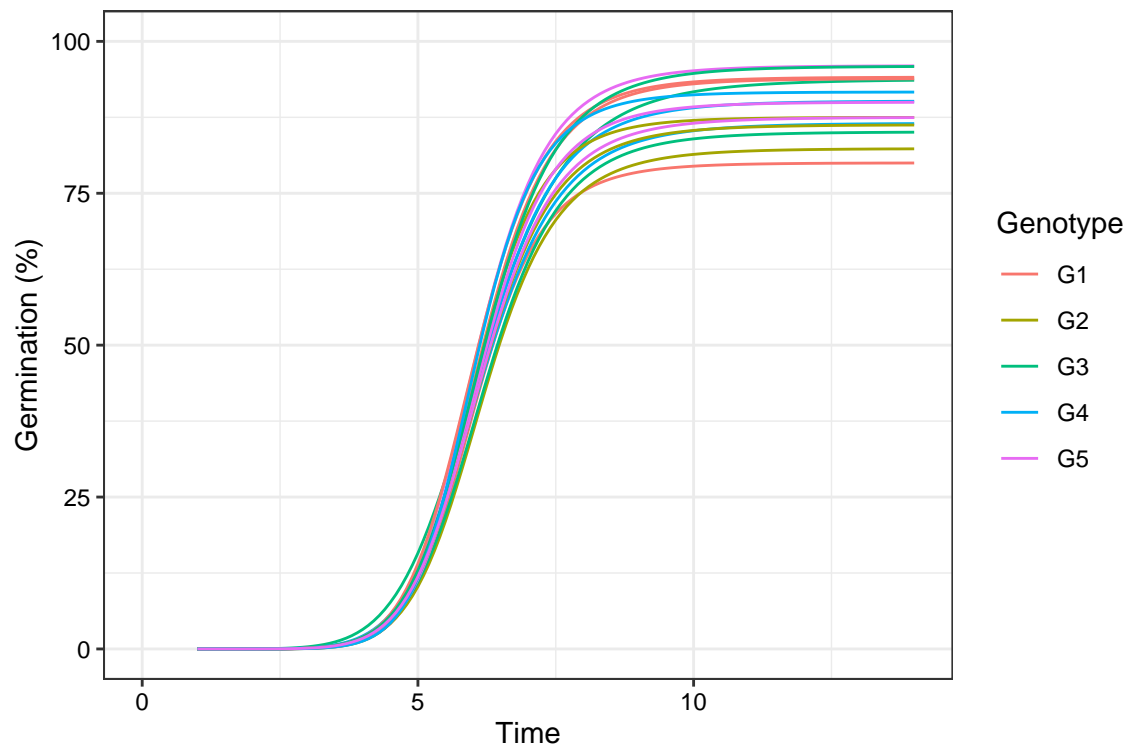
Multiple fitted curves generated in batch can also be plotted.

```
data(gcdata)

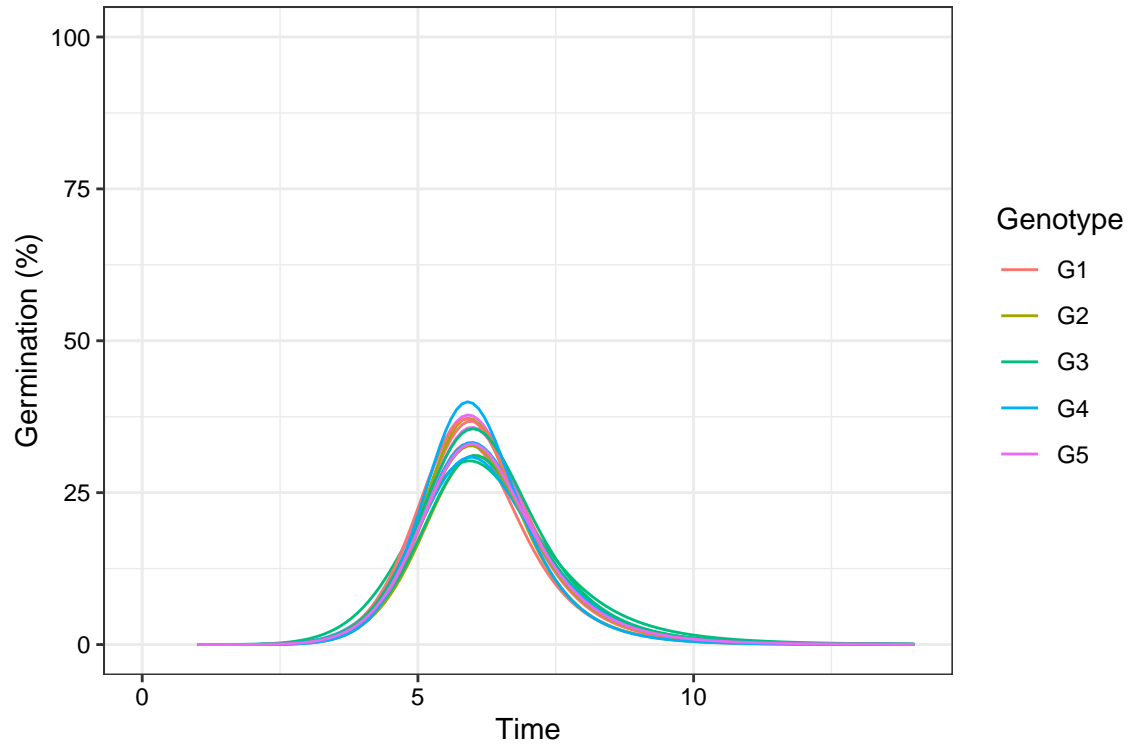
counts.per.intervals <- c("Day01", "Day02", "Day03", "Day04", "Day05",
                          "Day06", "Day07", "Day08", "Day09", "Day10",
                          "Day11", "Day12", "Day13", "Day14")

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

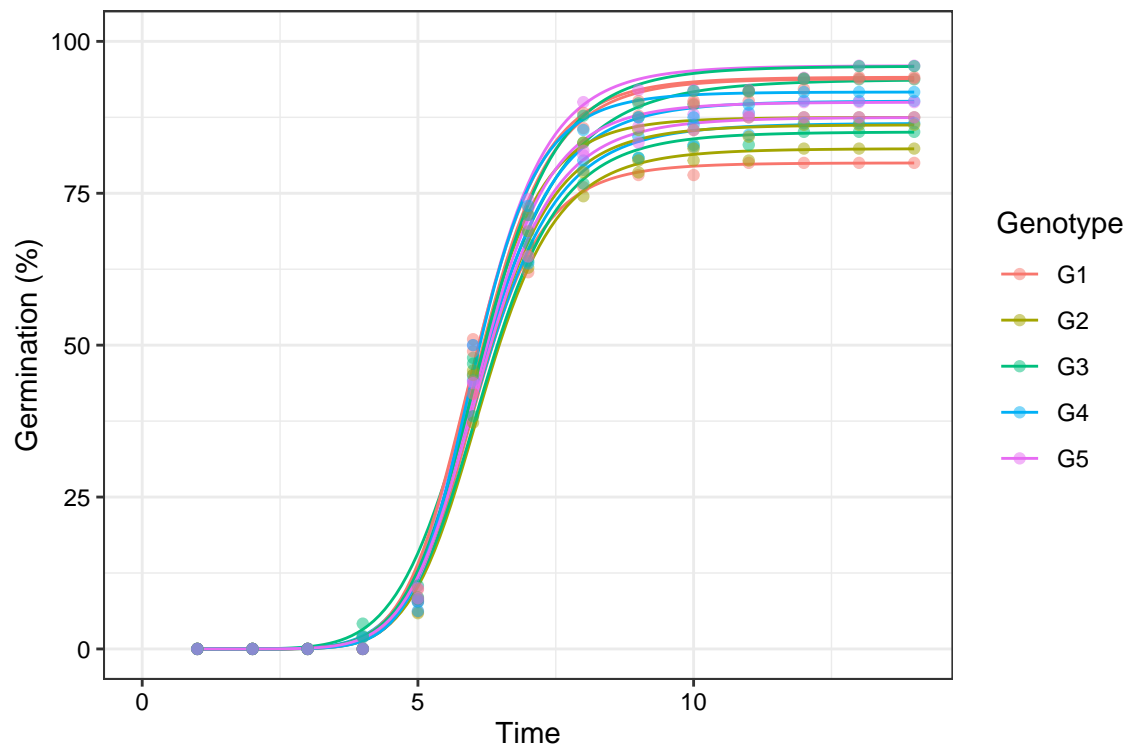
# Plot FPHF curves
plot(fits, group.col = "Genotype")
```



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

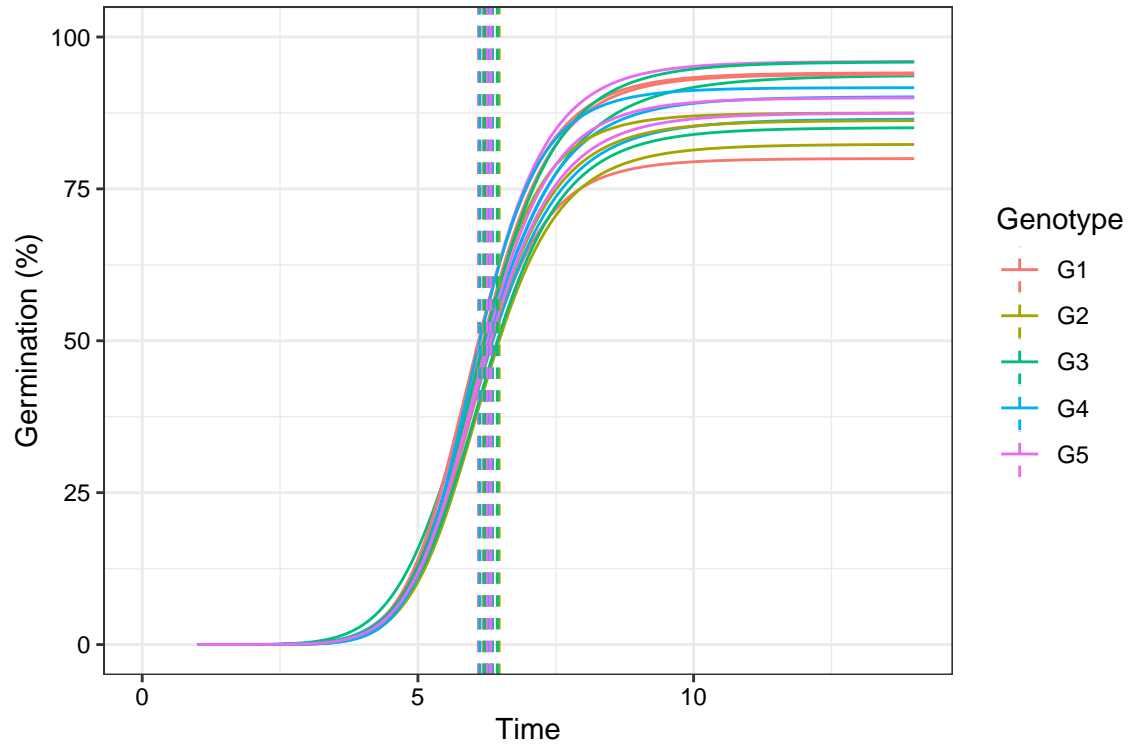


```
# Plot FPHF curves with points
plot(fits, group.col = "Genotype", show.points = TRUE)
```

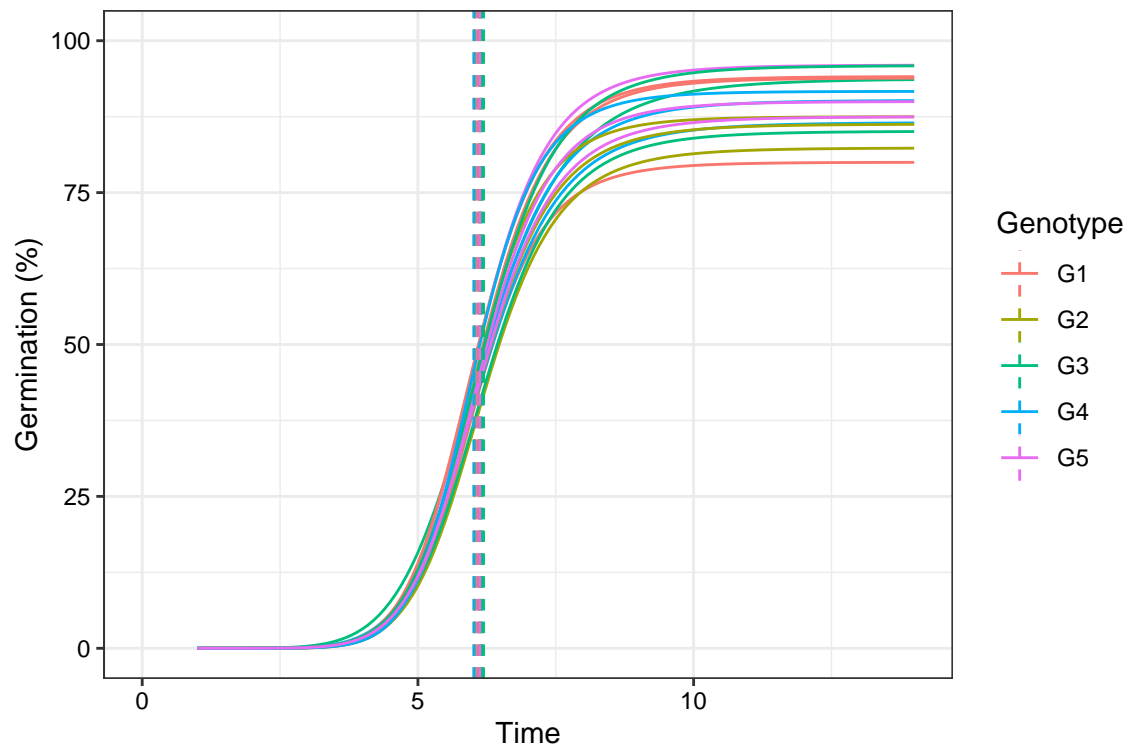


```
# Plot FPHF curves with annotations
plot(fits, group.col = "Genotype", annotate = "t50.total")
```

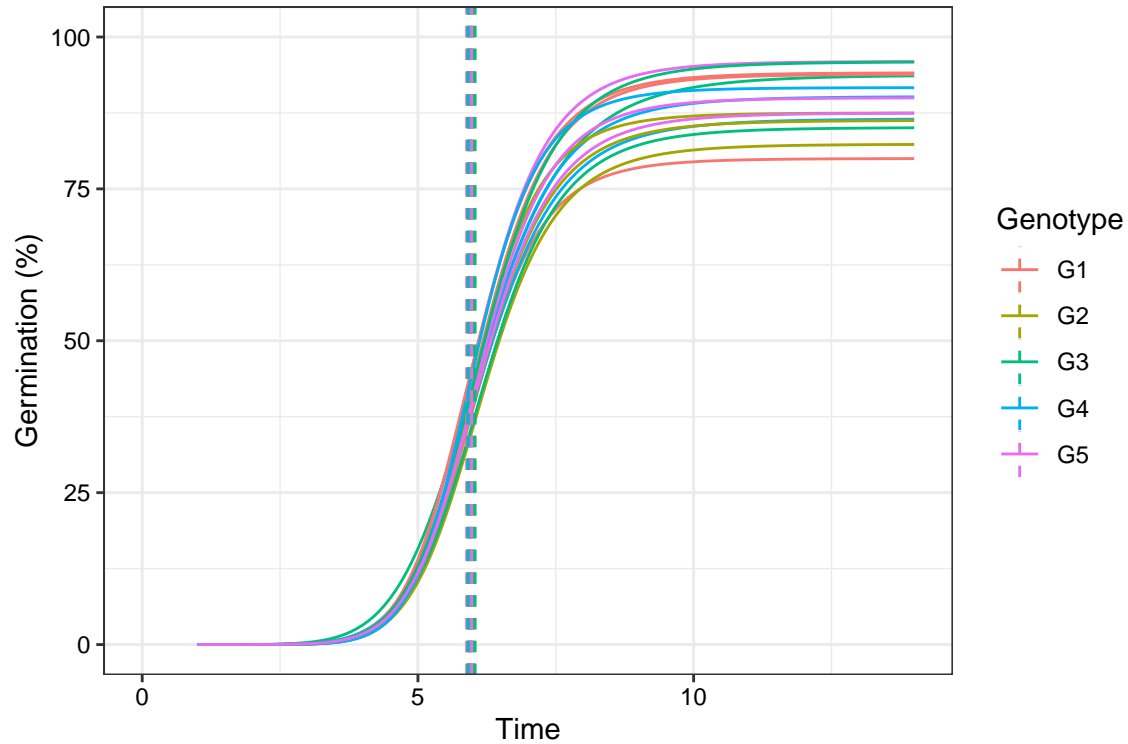




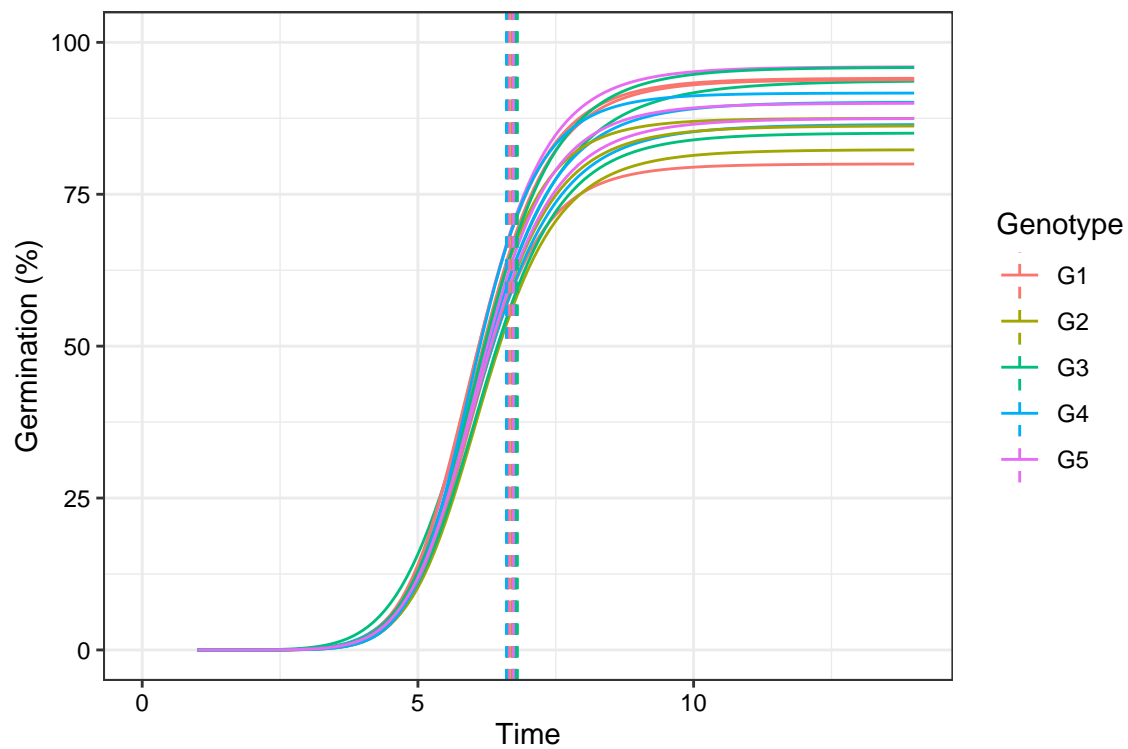
```
plot(fits, group.col = "Genotype", annotate = "t50.germ")
```



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



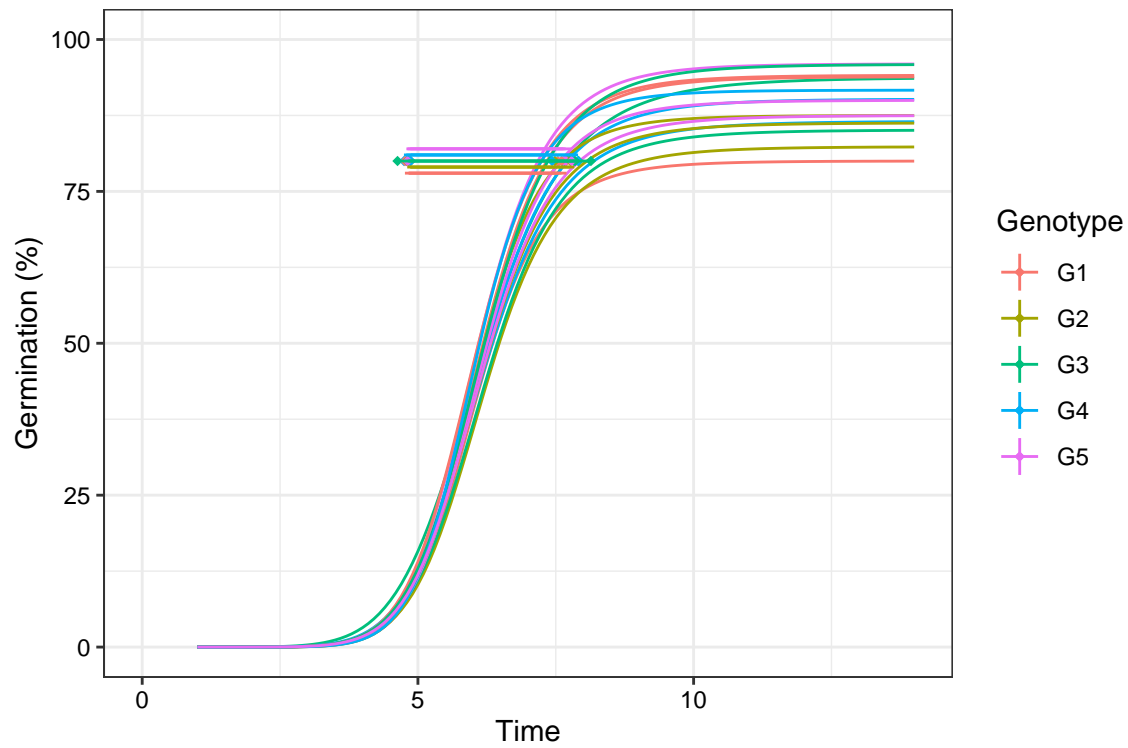
```
plot(fits, group.col = "Genotype", annotate = "mgt")
```



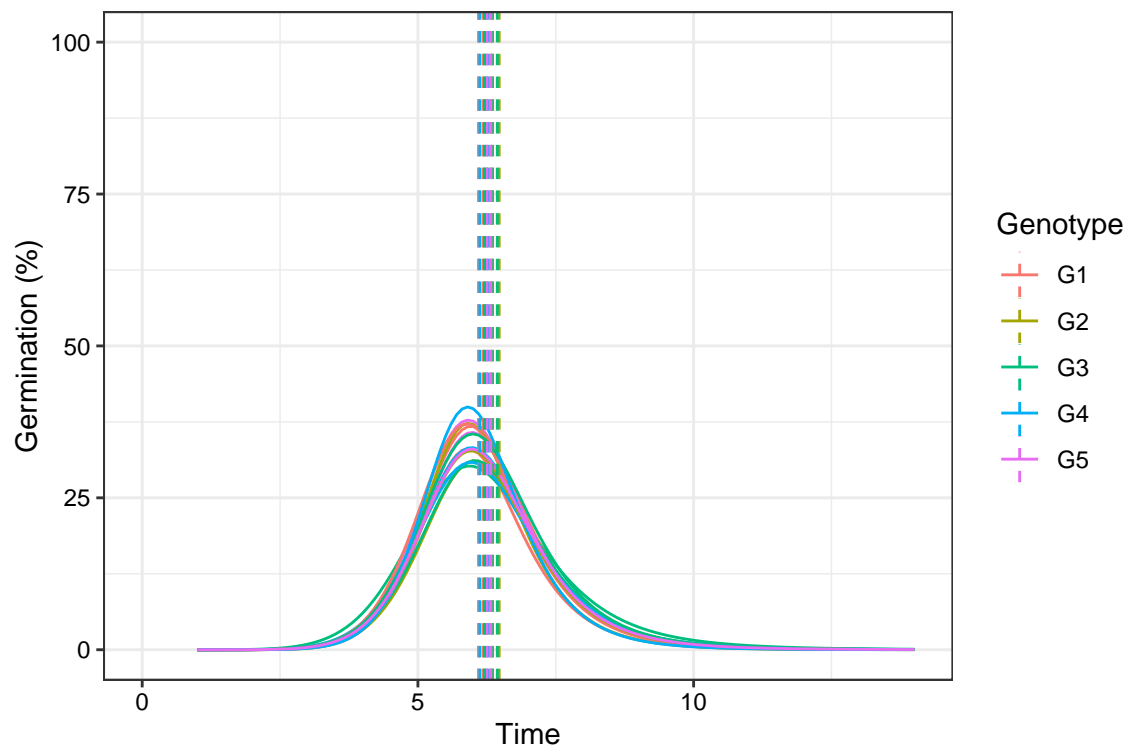
```
plot(fits, group.col = "Genotype", annotate = "uniformity")
```

Warning: position\_dodge requires non-overlapping x intervals

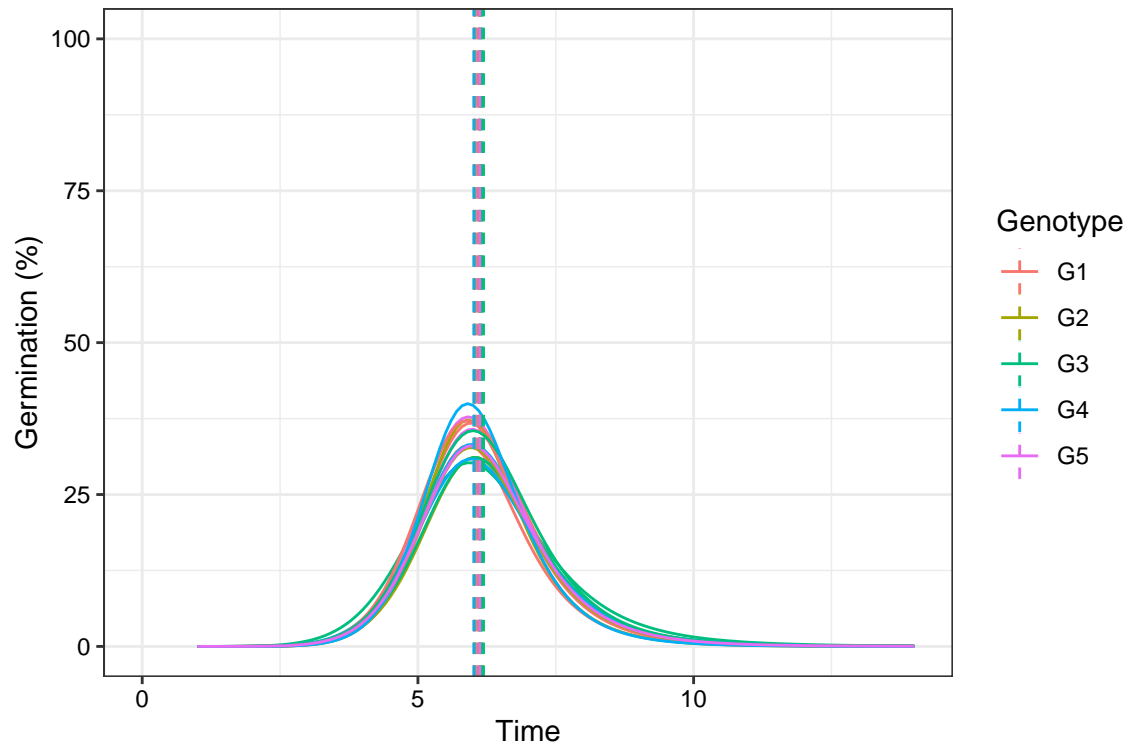
`position_dodge` requires non-overlapping x intervals



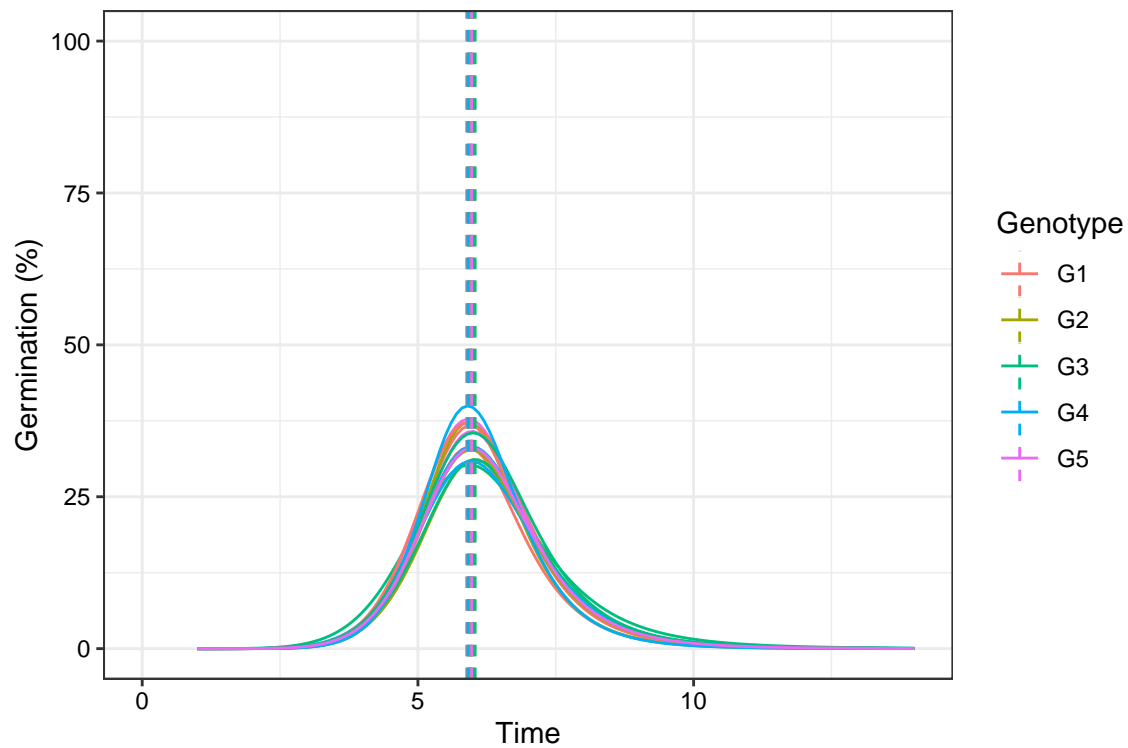
```
# Plot ROG curves with annotations
plot(fits, rog = TRUE, group.col = "Genotype", annotate = "t50.total")
```



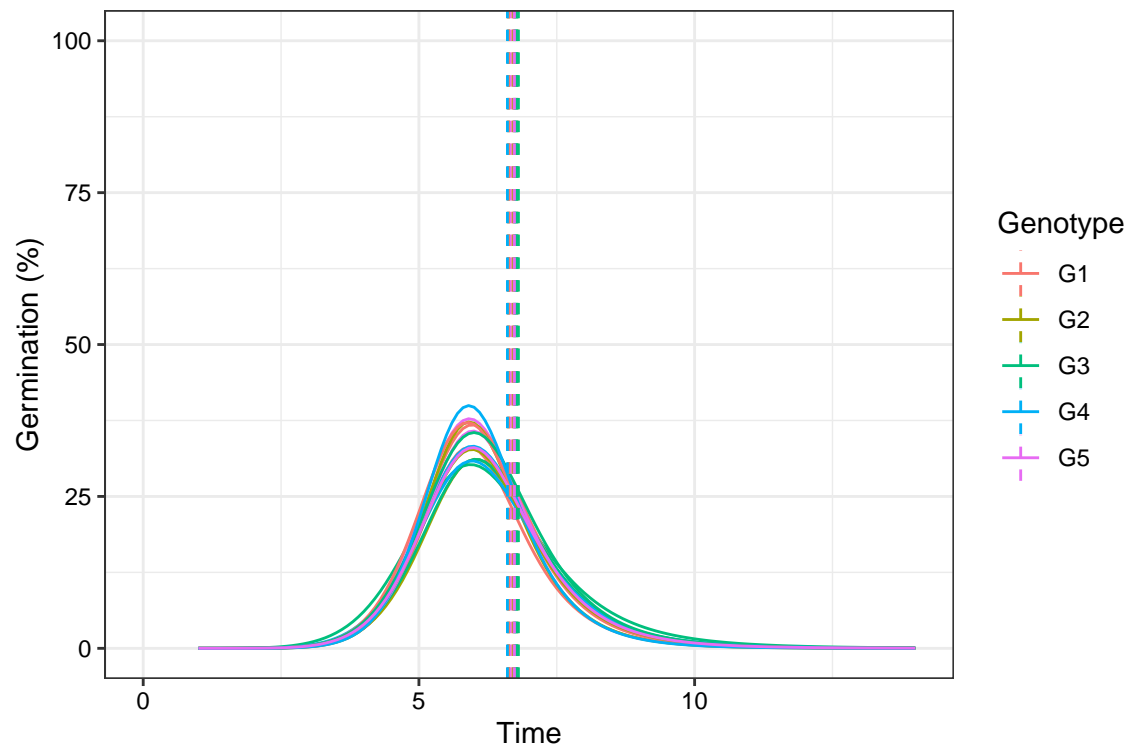
```
plot(fits, rog = TRUE, group.col = "Genotype", annotate = "t50.germ")
```



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

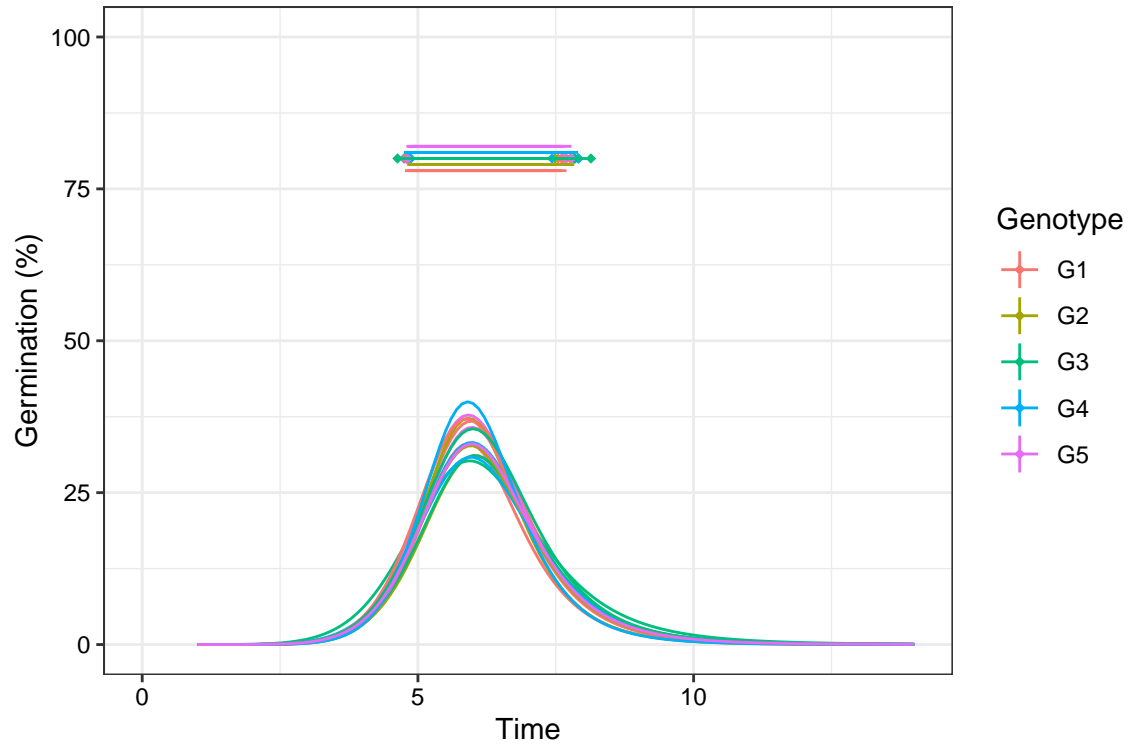


```
plot(fits, rog = TRUE, group.col = "Genotype", annotate = "mgt")
```



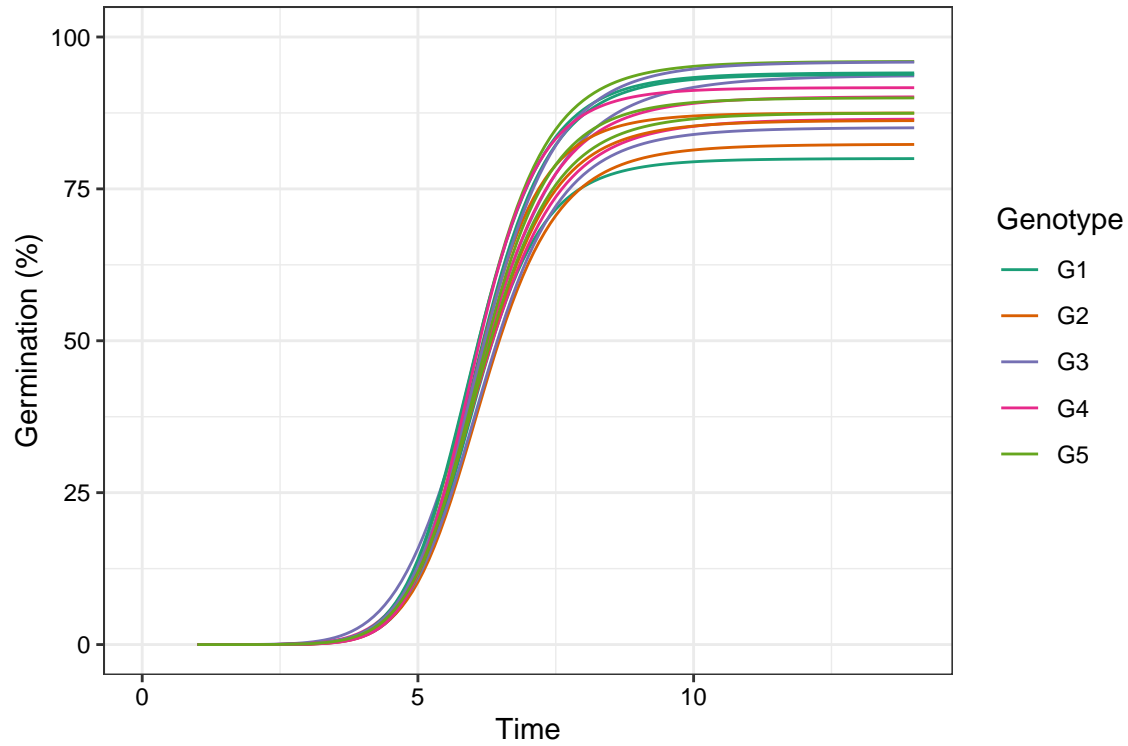
```
plot(fits, rog = TRUE, group.col = "Genotype", annotate = "uniformity")
```

Warning: position\_dodge requires non-overlapping x intervals  
position\_dodge requires non-overlapping x intervals

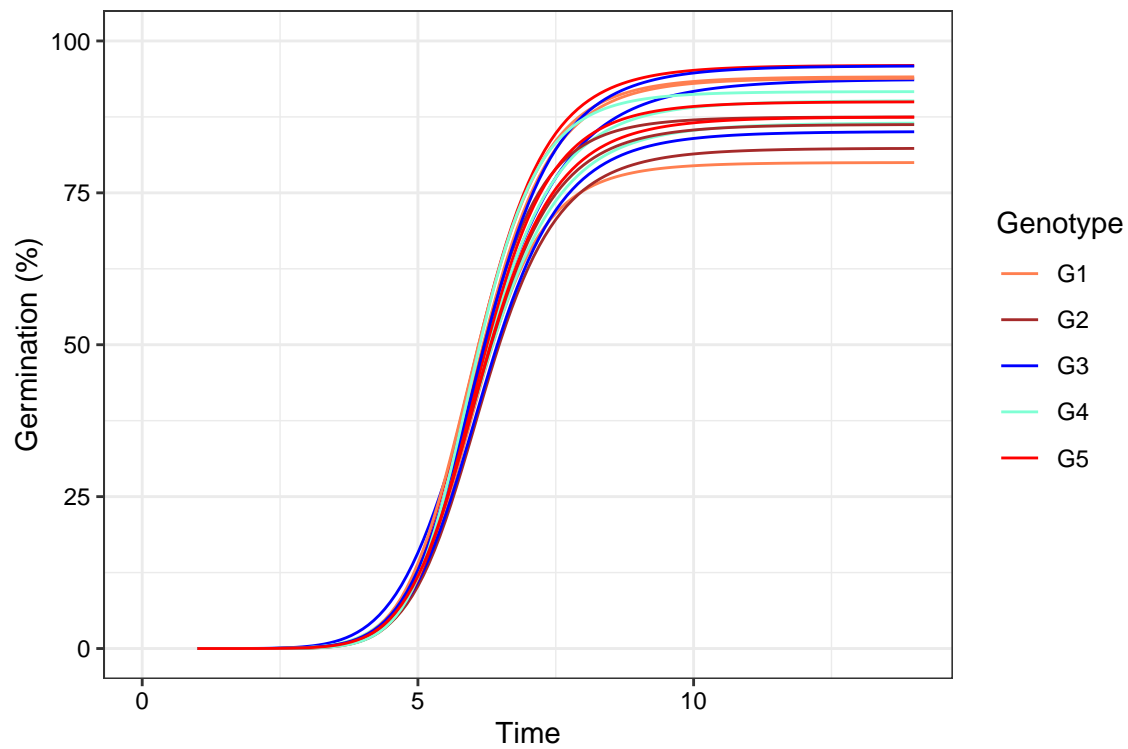


```
# Change colour of curves using ggplot2 options
library(ggplot2)
curvesplot <- plot(fits, group.col = "Genotype")

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



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



## Citing *germinationmetrics*

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

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

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

## Session Info

```
sessionInfo()
```

R Under development (unstable) (2022-06-05 r82452 ucrt)

Platform: x86\_64-w64-mingw32/x64 (64-bit)

Running under: Windows 10 x64 (build 19044)

Matrix products: default

locale:

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

attached base packages:

```
[1] stats      graphics  grDevices  utils      datasets  methods   base
```

other attached packages:

```
[1] germinationmetrics_0.1.5.9000 ggplot2_3.3.6
```

loaded via a namespace (and not attached):

```
[1] tidyselect_1.1.2  farver_2.1.0      dplyr_1.0.9       bitops_1.0-7      RCurl_1.98-1.6    fast_0.1.1
[7] lazyeval_0.2.2    xopen_1.0.0       mathjaxr_1.6-0    XML_3.99-0.9      rex_1.2.1         digits_0.1.1
[13] lifecycle_1.0.1   ellipsis_0.3.2    processx_3.5.3    magrittr_2.0.3    compiler_4.3.0    rlang_0.4.10
[19] tools_4.3.0       utf8_1.2.2        yaml_2.3.5        data.table_1.14.2 knitr_1.39         labels_0.4.2
[25] prettyunits_1.1.1 pkgbuild_1.3.1     curl_4.3.2        xmlparsedata_1.0.5 RColorBrewer_1.1-3 plyr_1.8.6
[31] xml2_1.3.3         pkgload_1.2.4     covr_3.5.1        withr_2.5.0       purrr_0.3.4       desc_1.4.1
[37] hunspell_3.0.1     grid_4.3.0        goodpractice_1.0.2 fansi_1.0.3        colorspace_2.0-3  who_0.1.1
[43] scales_1.2.0       cli_3.3.0          rmarkdown_2.14    crayon_1.5.1       generics_0.1.2    remotes_0.4.1
[49] rstudioapi_0.13    reshape2_1.4.4    httr_1.4.3        sessioninfo_1.2.2 DBI_1.1.2          cachem_1.0.6
[55] pander_0.6.5       stringr_1.4.0     assertthat_0.2.1  vctrs_0.4.1       devtools_2.4.3    jsonlite_1.8.4
[61] minpack.lm_1.2-2   callr_3.7.0       rcmdcheck_1.4.0   ggrepel_0.9.1     testthat_3.1.4    cyclops_0.1.1
```



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

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