

# The `germinationmetrics` Package: A Brief Introduction

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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)
```

## Version History

The current version of the package is 0.1.8. The previous versions are as follows.

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

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

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

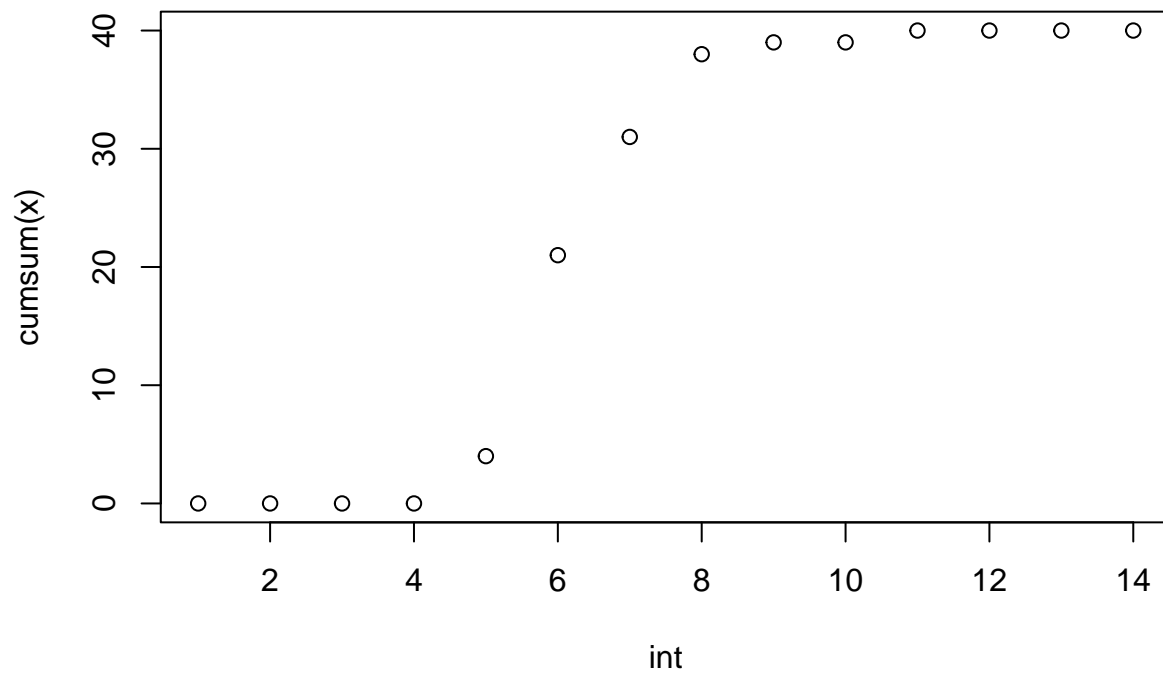
The time-course of germination can be plotted as follows.

```
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 <code>method</code> 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 <code>method</code> 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> $s_T^2 = \frac{\sum_{i=1}^k N_i (T_i - \overline{T})^2}{\sum_{i=1}^k N_i - 1}$ <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 ( $s_{\overline{T}}$ )	<b>SEGermTime</b>	<p>It signifies the accuracy of the calculation of the mean germination time. It is estimated according to the following formula:</p> $s_{\overline{T}} = \sqrt{\frac{s_T^2}{\sum_{i=1}^k N_i}}$ <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 ( $\overline{V}$ )	<b>MeanGermRate</b>	<p>It is computed according to the following formula:</p> $\overline{V} = \frac{\sum_{i=1}^k N_i}{\sum_{i=1}^k N_i T_i}$ <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. It is the inverse of mean germination time (<math>\overline{T}</math>).</p> $\overline{V} = \frac{1}{\overline{T}}$	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. 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 ( $WGP$ )	<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 ( $\overline{GP}$ )	<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 <math>k</math> is the total number of time intervals.</p>	count time	Mixed	George (1961); Tucker and Wright (1965); Nichols and Heydecker (1968); Chopra and Chaudhary (1980)

Germination index	Function	Details	Unit	Measures	Reference
Germination Index ( $GI$ ) (Melville)	<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 ( <i>GV</i> ) (Diavanshir and Pourbiek)	<b>GermValue</b>	<p>It is computed as follows.</p> $GV = \frac{\sum DGS}{N} \times GP \times c$ <p>Where, <i>DGS</i> is the daily germination speed computed by dividing cumulative germination percentage by the number of days since the onset of germination, <i>N</i> is the frequency or number of DGS calculated during the test, <i>GP</i> is the germination percentage expressed over 100, and <i>c</i> is a constant. The value of <i>c</i> is decided on the basis of average daily speed of germination (<math>\frac{\sum DGS}{N}</math>). If it is less than 10, then <i>c</i> value of 10 can be used and if it is more than 10, then value of 7 or 8 can be used for <i>c</i>.  <i>GV</i> value can be modified (<i>GV<sub>mod</sub></i>), 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 ( <i>CUG</i> )	<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, <i>T<sub>i</sub></i> is the time from the start of the experiment to the <i>i</i>th interval (day for the example), <i>N<sub>i</sub></i> is the number of seeds germinated in the <i>i</i>th time interval (not the accumulated number, but the number corresponding to the <i>i</i>th interval), and <i>k</i> 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 ( <i>CV<sub>T</sub></i> )	<b>CVGermTime</b>	<p>It is estimated as follows.</p> $CV_T = \sqrt{\frac{s_T^2}{\bar{T}}}$ <p>Where, <i>s<sub>T</sub><sup>2</sup></i> 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 ( <i>U</i> ) or informational entropy ( <i>H</i> )	<b>GermUncertainty</b>	<p>It is estimated as follows.</p> $\bar{E} = - \sum_{i=1}^k f_i \log_2 f_i$ <p>Where, <i>f<sub>i</sub></i> is the relative frequency of germination (<math>f_i = \frac{N_i}{\sum_{i=1}^k N_i}</math>), <i>N<sub>i</sub></i> is the number of seeds germinated on the <i>i</i>th time interval, and <i>k</i> 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 (1985); Rana1 and Santana (2006)

## Examples

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

```
# From partial germination counts
```

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

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

```
GermPercent()
```

```
[1] 80
```

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

```
[1] 34
```

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

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

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

```
[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
```

```
[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] 1.446154
```

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

```
[1] 0.1901416
```

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

```
[1] 0.1794868
```

```
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] 0.0007176543

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

[1] 0.004235724

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

[1] 0.1674877

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

[1] 0.1683168

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

# From partial germination counts

```

```

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

GermSpeed(), GermSpeedAccumulated(), GermSpeedCorrected()

[1] 6.138925

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

[1] 34.61567

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

[1] 0.1534731

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

[1] 0.8653917

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

[1] 12.27785

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

[1] 69.23134

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

[1] 6.138925

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

[1] 34.61567

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

[1] 0.1534731

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

[1] 0.8653917

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

[1] 12.27785

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

```

```
[1] 69.23134
```

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

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

```
WeightGermPercent()
```

```
[1] 47.42857
```

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

```
[1] 47.42857
```

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

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

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

```
[1] 5.714286
```

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

```
[1] 2.857143
```

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

```
[1] 5.714286
```

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

```
[1] 2.857143
```

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

```
[1] 5.714286
```

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

```

# From partial germination counts
#-----
# 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] 0.7092199
```

```
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 reparameterized by substituting  $b$  with  $e^\beta$  to constraint  $b$  to positive values only.

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

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

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

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

Germination parameters	Details	Unit	Measures
y intercept ( $y_0$ )	The intercept on the y axis.		
Asymptote ( $a$ )	It is the maximum cumulative germination percentage, which is equivalent to germination capacity.	%	Germination capacity
Shape and steepness ( $b$ )	Mathematical parameter controlling the shape and steepness of the germination curve. The larger the $b$ , the steeper the rise toward the asymptote $a$ , and the shorter the time between germination onset and maximum germination.		Germination rate
Half-maximal activation level ( $c$ )	Time required for 50% of viable seeds to germinate.	time	Germination time
$lag$	It is the time at germination onset and is computed by solving four-parameter hill function after setting $y$ to 0 as follows.	time	Germination time
$lag = b \sqrt{\frac{-y_0 c^b}{a + y_0}}$			

Germination parameters	Details	Unit	Measures
$D_{lag-50}$	The duration between the time at germination onset ( <i>lag</i> ) and that at 50% germination ( <i>c</i> ).	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 <b>umin</b> and <b>umin</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 ( <i>s</i> ) 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. $\frac{MGT}{t_{50_{germinated}}}$		

## Examples

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

# From partial germination counts
#-----
```

```
FourPHFfit(germ.counts = x, intervals = int, total.seeds = 50, tmax = 20)
```

```
FourPHFfit()
```

```
$data
```

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

```
$Parameters
```

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

```
$Fit
```

	sigma	isConv	finTol	logLik	AIC	BIC	deviance	df.residual	nobs
1	1.61522	TRUE	2.884804e-12	-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: df
    bta      c
2.291 6.035
residual sum-of-squares: 31.31

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

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

attr("class")
[1] "FourPHFfit" "list"
# From cumulative germination counts
#-----
FourPHFfit(germ.counts = y, intervals = int, total.seeds = 50, tmax = 20,
           partial = FALSE)

$data
      gp csgp intervals
1    0    0          1
2    0    0          2

```



```

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

```

```
$Parameters
```

```

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

```

```
$Fit
```

```

      sigma isConv      finTol    logLik      AIC      BIC deviance df.residual nobs
1 1.61522  TRUE 2.884804e-12 -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: df
    bta      c
2.291 6.035
residual sum-of-squares: 31.31

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

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

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

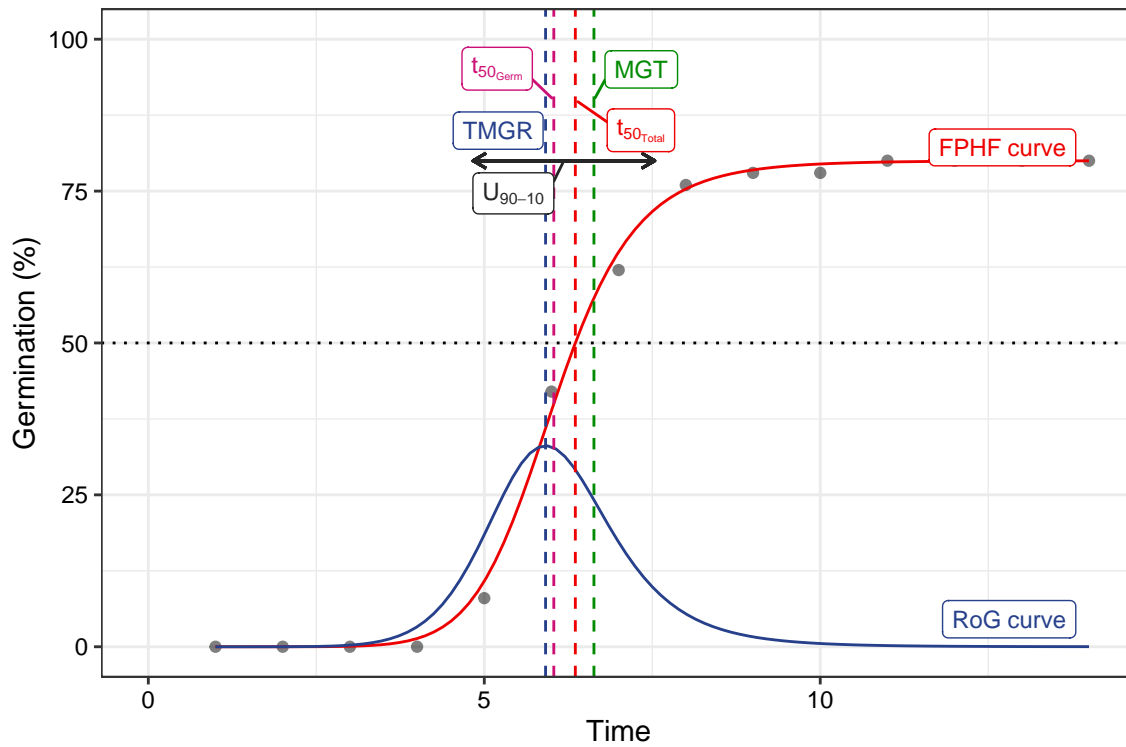
# From partial germination counts
#-----
fit1 <- FourPHFfit(germ.counts = x, intervals = int,
                  total.seeds = 50, tmax = 20)

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

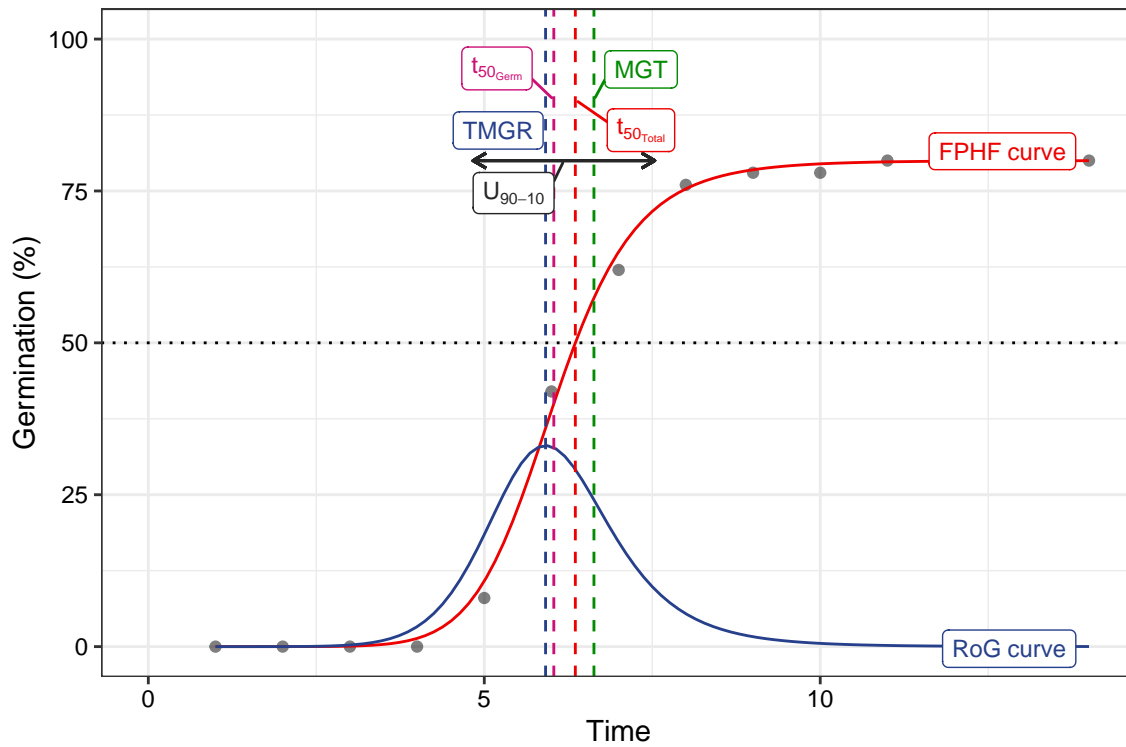
# Default plots

```

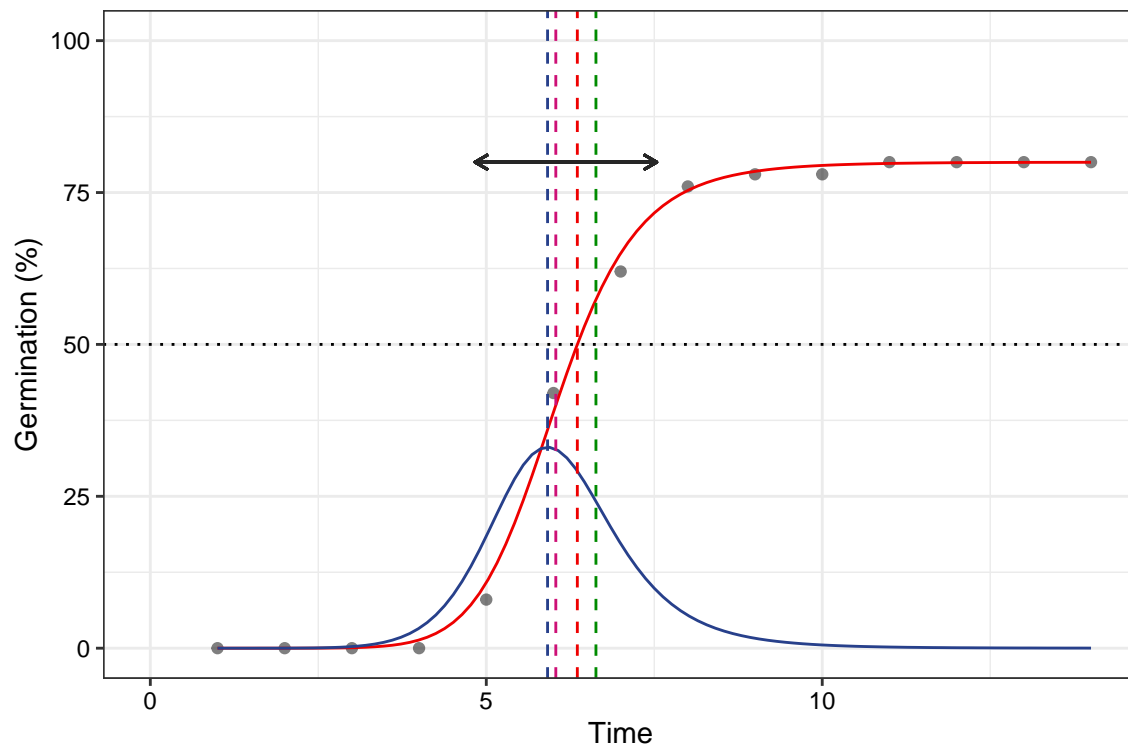
```
plot(fit1)
```



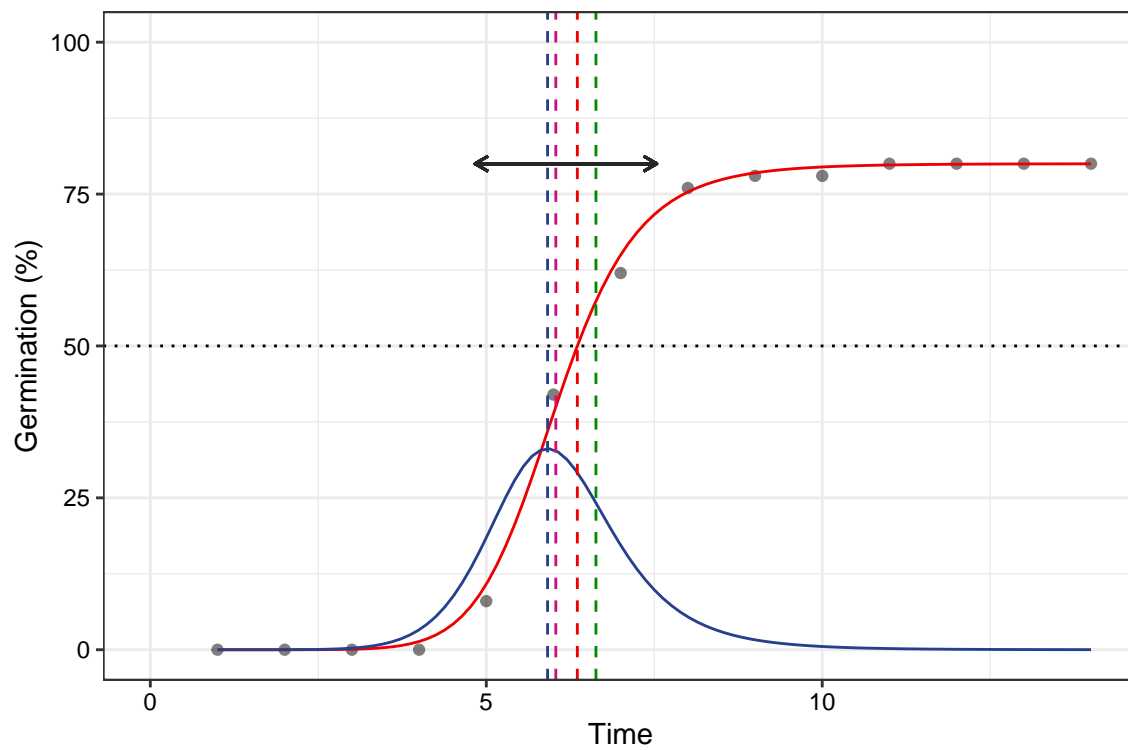
```
plot(fit2)
```



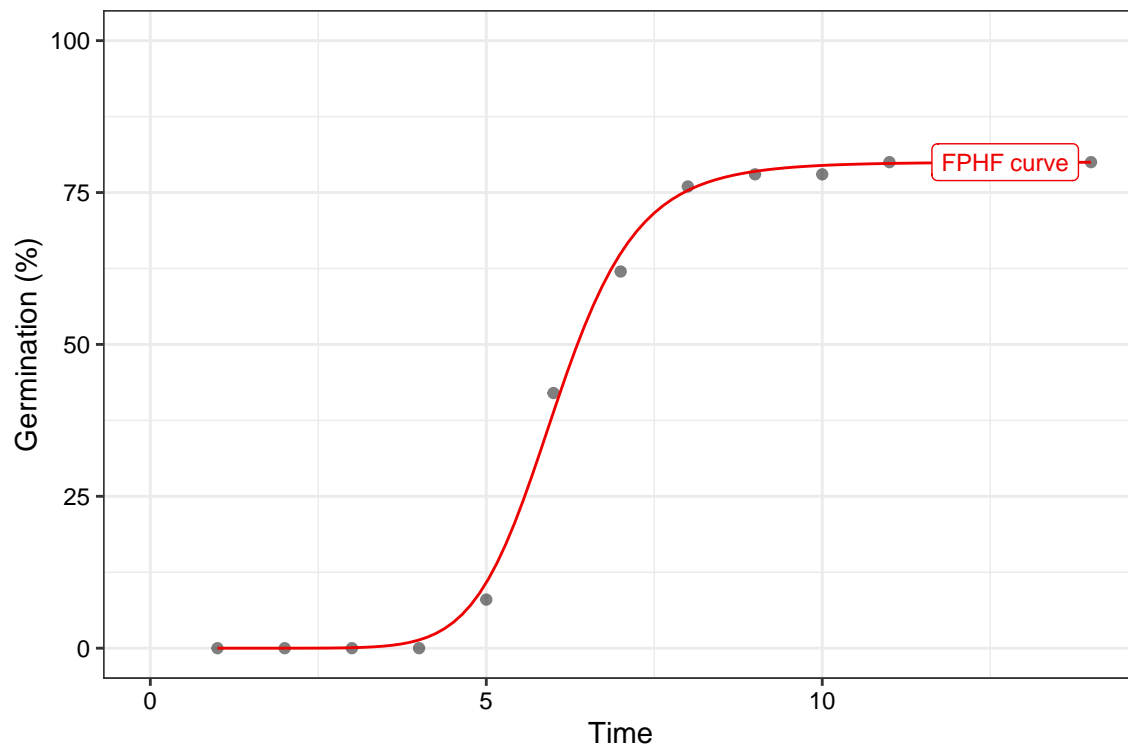
```
# No labels
plot(fit1, plotlabels = FALSE)
```



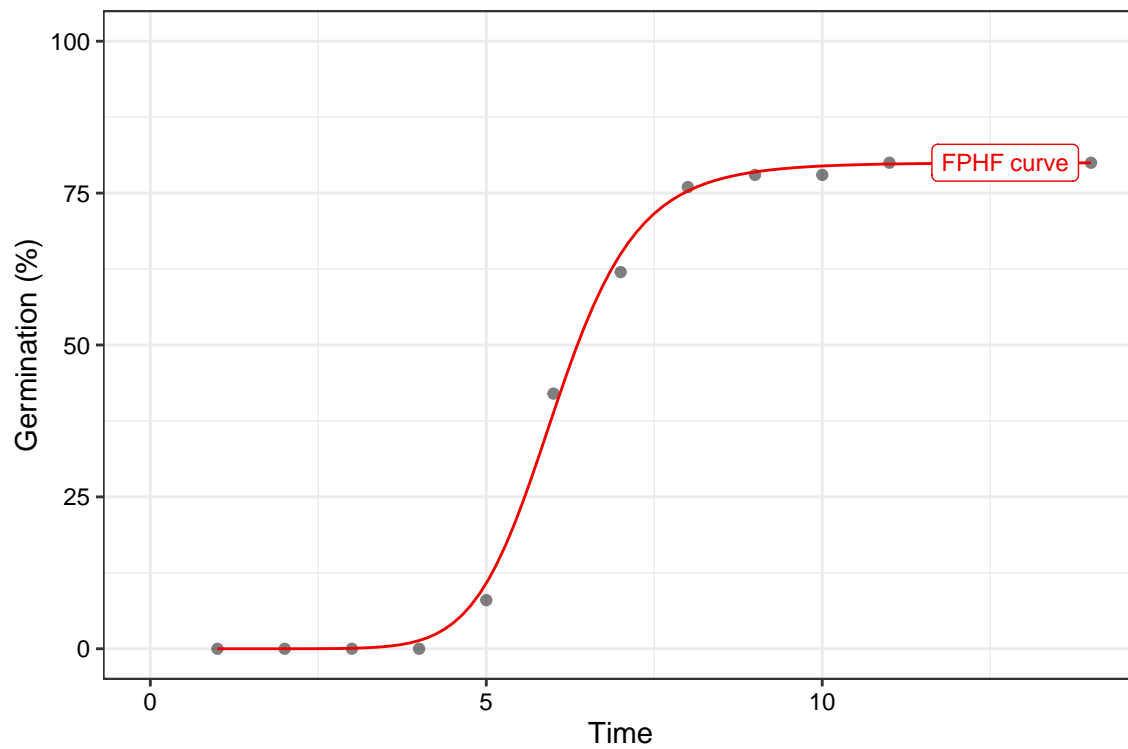
```
plot(fit2, plotlabels = FALSE)
```



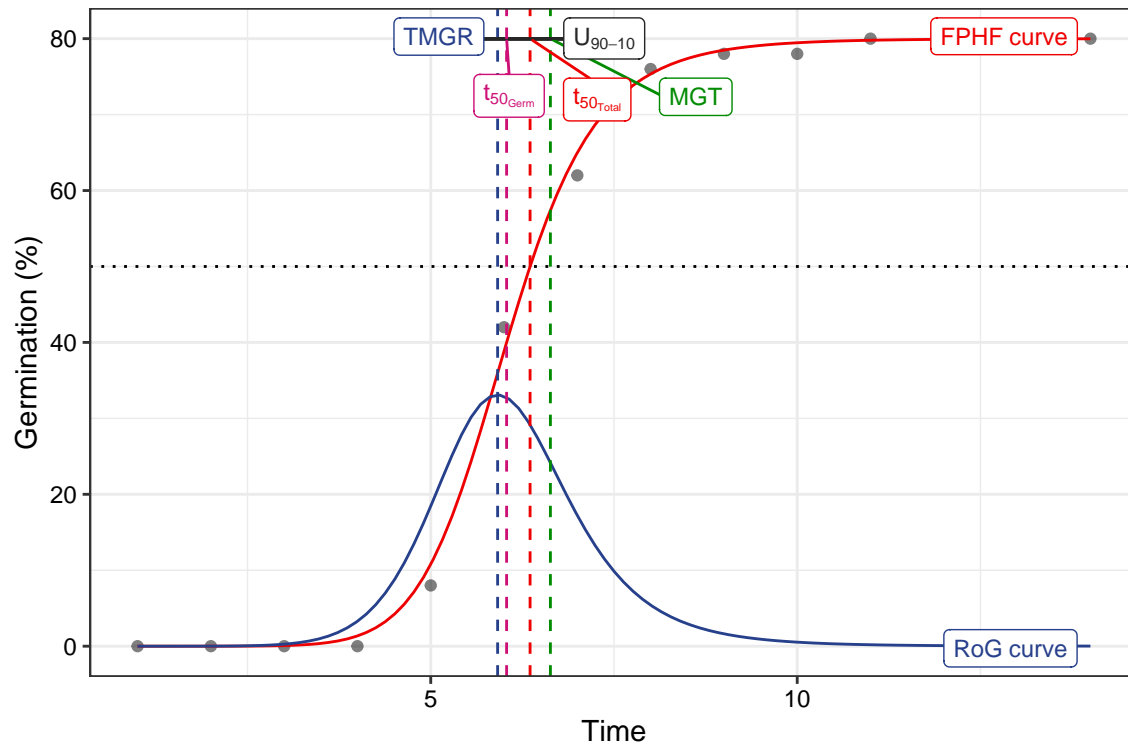
```
# Only the FPGH curve
plot(fit1, rog = FALSE, t50.total = FALSE, t50.germ = FALSE,
     tmgr = FALSE, mgt = FALSE, uniformity = FALSE)
```



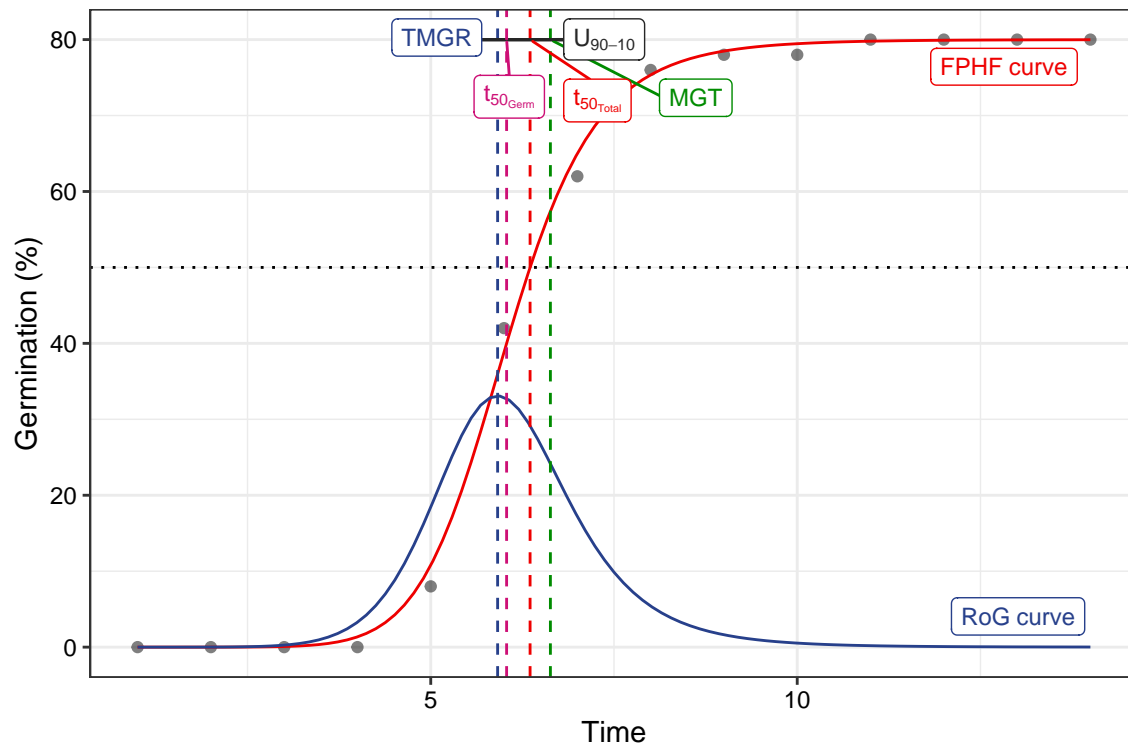
```
plot(fit2, rog = FALSE, t50.total = FALSE, t50.germ = FALSE,
     tmgr = FALSE, mgt = FALSE, uniformity = FALSE)
```



```
# 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)
```

	Genotype	Rep	Day01	Day02	Day03	Day04	Day05	Day06	Day07	Day08	Day09	Day10	Day11	Day12	Day13	Day14	Tot
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	
	LastGermTime		PeakGermTime		TimeSpreadGerm		t50_Coolbear		t50_Farooq		MeanGermTime		VarGermTime		SEGermTime		
1		11		6		6	5.970588		5.941176		6.700000		1.446154		0.1901416		
2		12		6		8	6.192308		6.153846		6.857143		2.027875		0.2197333		
3		12		6		8	6.000000		5.972222		6.866667		2.572727		0.2391061		
4		12		6		7	6.041667		6.000000		6.891304		2.187923		0.2180907		
5		13		6		8	5.975000		5.950000		6.812500		2.368351		0.2221275		
6		12		6		7	5.976190		5.952381		6.869565		2.071498		0.2122088		
7		11		6		6	5.972222		5.944444		6.690476		1.389663		0.1818989		
8		12		6		8	6.208333		6.166667		6.875000		2.112179		0.2297923		
9		12		6		8	6.000000		5.973684		6.866667		2.300000		0.2260777		
10		12		6		7	6.076923		6.038462		6.822222		1.831313		0.2017321		
11		13		6		8	5.928571		5.904762		6.791667		2.381206		0.2227295		
12		12		6		7	5.975000		5.950000		6.886364		2.149577		0.2210295		
13		13		6		8	6.083333		6.041667		6.936170		2.539315		0.2324392		
14		12		6		7	5.928571		5.904762		6.772727		1.900634		0.2078370		
15		11		6		6	6.050000		6.000000		6.809524		1.670151		0.1994129		
	CVG		GermRateRecip_Coolbear		GermRateRecip_Farooq		GermSpeed_Count		GermSpeed_Percent		GermSpeedAccur						
1	14.92537		0.1674877		0.1683168		6.138925		12.27785								
2	14.58333		0.1614907		0.1625000		6.362698		12.47588								
3	14.56311		0.1666667		0.1674419		6.882179		14.33787								
4	14.51104		0.1655172		0.1666667		6.927417		13.58317								
5	14.67890		0.1673640		0.1680672		7.318987		14.63797								
6	14.55696		0.1673307		0.1680000		6.931782		14.14649								
7	14.94662		0.1674419		0.1682243		6.448449		13.43427								
8	14.54545		0.1610738		0.1621622		6.053175		12.87909								

9	14.56311	0.1666667	0.1674009	6.830592	13.13575	
10	14.65798	0.1645570	0.1656051	6.812698	13.62540	
11	14.72393	0.1686747	0.1693548	7.342796	14.39764	
12	14.52145	0.1673640	0.1680672	6.622258	12.98482	
13	14.41718	0.1643836	0.1655172	7.052320	14.39249	
14	14.76510	0.1686747	0.1693548	6.706782	13.97246	
15	14.68531	0.1652893	0.1666667	6.363925	13.25818	
	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_KhanUngar	GermRateGeorge	GermIndex	GermIndex_mod	EmergenceRateIndex_SG	EmergenceRateInd
1	0.5714286	4	5.840000	7.300000	292	
2	0.7002801	5	5.882353	7.142857	300	
3	1.0416667	7	6.687500	7.133333	321	
4	0.5602241	4	6.411765	7.108696	327	
5	0.7142857	5	6.900000	7.187500	345	
6	0.4373178	3	6.693878	7.130435	328	
7	0.5952381	4	6.395833	7.309524	307	
8	0.7598784	5	6.063830	7.125000	285	
9	0.6868132	5	6.173077	7.133333	321	
10	0.5714286	4	6.460000	7.177778	323	
11	0.7002801	5	6.784314	7.208333	346	
12	0.4201681	3	6.137255	7.113636	313	
13	0.5830904	4	6.775510	7.063830	332	
14	0.4464286	3	6.625000	7.227273	318	
15	0.5952381	4	6.291667	7.190476	302	
	EmergenceRateIndex_Fakorede	PeakValue	GermValue_Czabator	GermValue_DP	GermValue_Czabator_mod	GermVal
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

**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	
			c y0 lag	Dlag50			t50.total			txp.total_10			txp.total_60			t50.Ge	
1	6.03495355423453		0	0	6.03495355423453		6.3551214973865			4.95626430994715			6.7445983463311			6.03495355423453	
2	6.17519294911323		0	0	6.17519294911323		6.47349044022769			4.98323617967833			6.8726033802361			6.17519294911323	
3	6.13811027378334		0	0	6.13811027378334		6.24419103019226			4.67302155573313			6.60843809234118			6.13811027378334	
4	6.12517308176588		0	0	6.12517308176588		6.27679437746254			4.85087548237175			6.61496814302537			6.12517308176588	
5	6.04964210720327		0	0	6.04964210720327		6.10343321091848			4.81412549010201			6.38678874941426			6.04964210720327	
6	6.0974148527557		0	0	6.0974148527557		6.18227860798315			4.86863251633358			6.477598609442			6.0974148527557	
7	6.02985089631599		0	0	6.02985089631599		6.20281219696422			4.93042184740182			6.51049505523			6.02985089631599	
8	6.18977354961439		0	0	6.18977354961439		6.43951015764455			4.94005695310539			6.82329908278267			6.18977354961439	
9	6.12512151399929		0	0	6.12512151399929		6.35217197764166			4.83665841861718			6.73327569782723			6.12512151399929	
10	6.10950363596761		0	0	6.10950363596761		6.2530432080492			4.92062915320932			6.56650619550494			6.10950363596761	
11	6.01875974061195		0	0	6.01875974061195		6.09943499335382			4.79862683383817			6.3912906236839			6.01875974061195	
12	6.1084516820797		0	0	6.1084516820797		6.32618435705024			4.89359557090626			6.68452626570581			6.1084516820797	
13	6.14901168717124		0	0	6.14901168717124		6.20750091190278			4.84130798420802			6.50995386860368			6.14901168717124	
14	6.01591019490093		0	0	6.01591019490093		6.12238872875573			4.91514013437311			6.39749098023249			6.01591019490093	
15	6.12157936163499		0	0	6.12157936163499		6.31739163301497			4.89250226946576			6.66724718740801			6.12157936163499	
			Uniformity_90		Uniformity_10		Uniformity			TMGR			AUC			MG	
1	7.53768963497883		4.83180737938015		2.70588225559868		5.91219440464896			1108.97550938733			6.6322519662728				
2	7.83540706385743		4.86675518553144		2.96865187832599		6.03128155445793			1128.55880085138			6.7844073567977				
3	8.13734180246507		4.63006208264611		3.50727971981896		5.93817948943725			1283.69307344081			6.7727423283087				
4	7.83480960415051		4.78859693817119		3.04621266597932		5.97268622562109			1239.88674124826			6.7396659272138				
5	7.63902819750811		4.79094574322756		2.84808245428055		5.91428884333636			1328.32820017628			6.6549807574810				

6	7.69346877523834	4.83247140825032	2.86099736698802	5.96187868660636	1294.46271441017	6.7024731263246
7	7.48364280989593	4.85847638047658	2.62516642941935	5.91405695229978	1213.90764565674	6.6224170854824
8	7.91416293168472	4.84110536088622	3.07305757079851	6.03619216805867	1164.34586106316	6.8040002121391
9	7.90404141879274	4.74657350251934	3.1574679162734	5.9616310497804	1188.79304149759	6.745241086306
10	7.67917745255724	4.8606813566304	2.81849609592684	5.97811533043387	1240.22733172402	6.7118999882487
11	7.60361082322955	4.76424552194859	2.83936530128096	5.88355748786772	1305.20007906005	6.6242481763091
12	7.76385405638773	4.80601279742022	2.95784125896751	5.9640804983933	1188.0211599463	6.7186389364901
13	7.85034473566269	4.81639291039067	3.03395182527202	5.99827012362062	1316.40687308654	6.7622736053089
14	7.4323719910534	4.86939775305615	2.56297423799725	5.9051804897395	1273.38526597411	6.604966788205
15	7.78580612916975	4.81308335438754	2.97272277478221	5.97608676470078	1203.66421628837	6.7322657904219
	Fit_isConv	Fit_finTol	Fit_logLik	Fit_AIC	Fit_BIC	Fit_deviance
1	TRUE	2.88480350718601e-12	-25.498681342686	56.9973626853719	58.9145346742177	31.3072289092405
2	TRUE	5.15498754793953e-12	-20.3147146781893	46.6294293563786	48.5466013452244	14.9286526064903
3	TRUE	8.43840552988695e-11	-31.2321314996742	68.4642629993484	70.3814349881942	71.0165774207971
4	TRUE	3.38218342221808e-12	-31.0226924019787	68.0453848039574	69.9625567928032	68.923242888336
5	TRUE	6.74447164783487e-11	-31.0406736477542	68.0813472955084	69.9985192843541	69.1005170158358
6	TRUE	3.97619714931352e-11	-34.328870450832	74.6577409016639	76.5749128905097	110.531949324479
7	TRUE	3.90798504668055e-12	-25.9069727183683	57.8139454367367	59.7311174255824	33.1876017805038
8	TRUE	4.32720526077901e-12	-20.3814877326307	46.7629754652615	48.6801474541073	15.0717385035725
9	TRUE	1.77209358298569e-11	-31.2163324798379	68.4326649596759	70.3498369485217	70.8564735497253
10	TRUE	8.14281975181075e-12	-26.1045565628368	58.2091131256735	60.1262851145193	34.1377096911127
11	TRUE	1.32729383039987e-11	-32.3138085946749	70.6276171893498	72.5447891781956	82.8837176958294
12	TRUE	3.51434437106946e-11	-33.5861335093548	73.1722670187096	75.0894390075554	99.4046940082808
13	TRUE	1.10560449684272e-11	-32.1879276469568	70.3758552939135	72.2930272827593	81.406542245287
14	TRUE	9.80548975348938e-13	-33.023419198233	72.046838396466	73.9640103853118	91.726523289527
15	TRUE	8.73967564984923e-13	-28.1644422917083	62.3288845834165	64.2460565722623	45.8177705510444

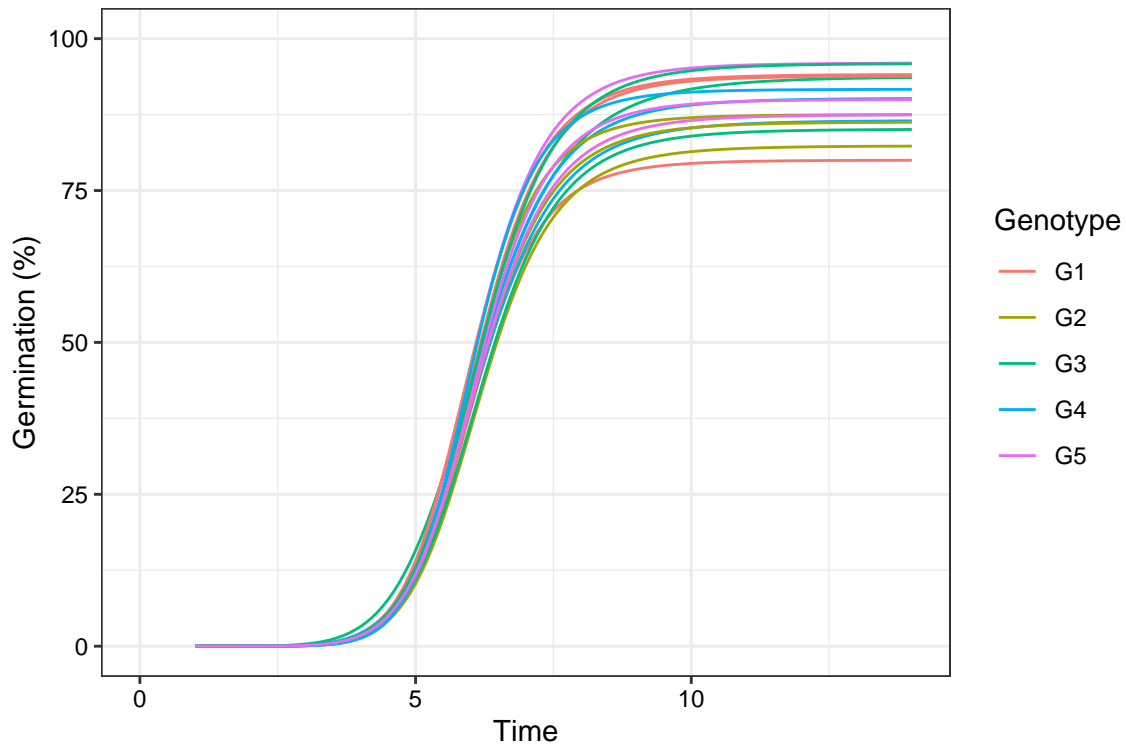
Multiple fitted curves generated in batch can also be plotted.

```
data(gcdata)

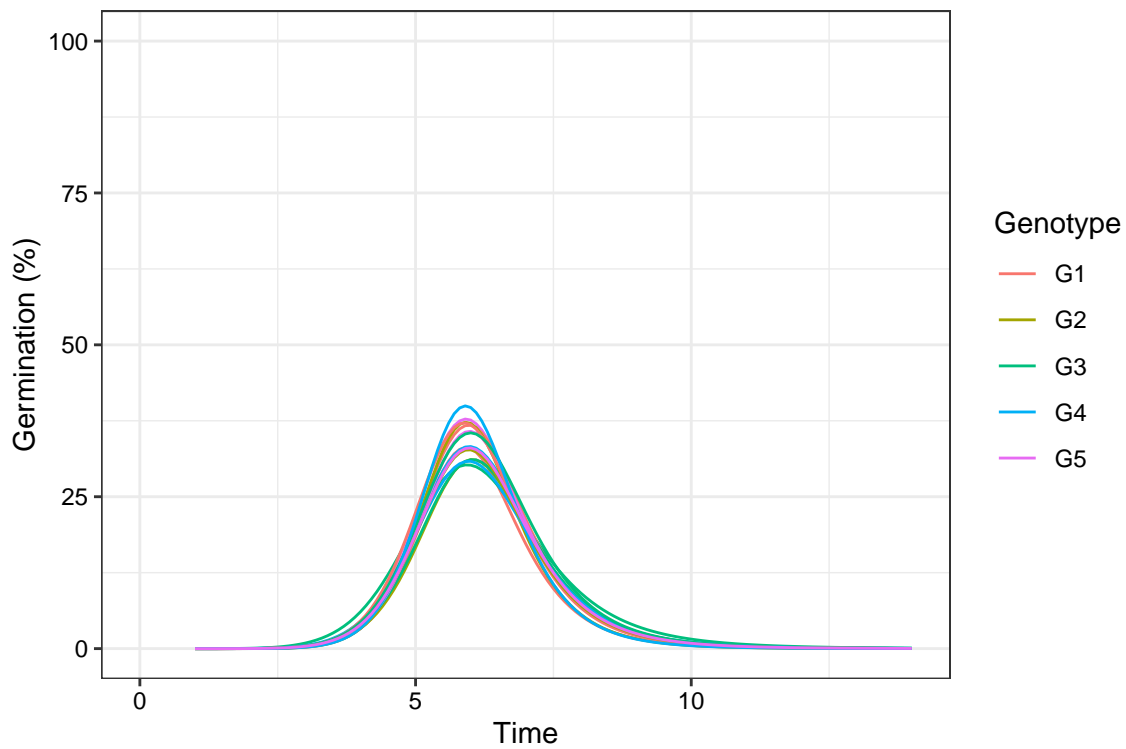
counts.per.intervals <- c("Day01", "Day02", "Day03", "Day04", "Day05",
                          "Day06", "Day07", "Day08", "Day09", "Day10",
                          "Day11", "Day12", "Day13", "Day14")

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)

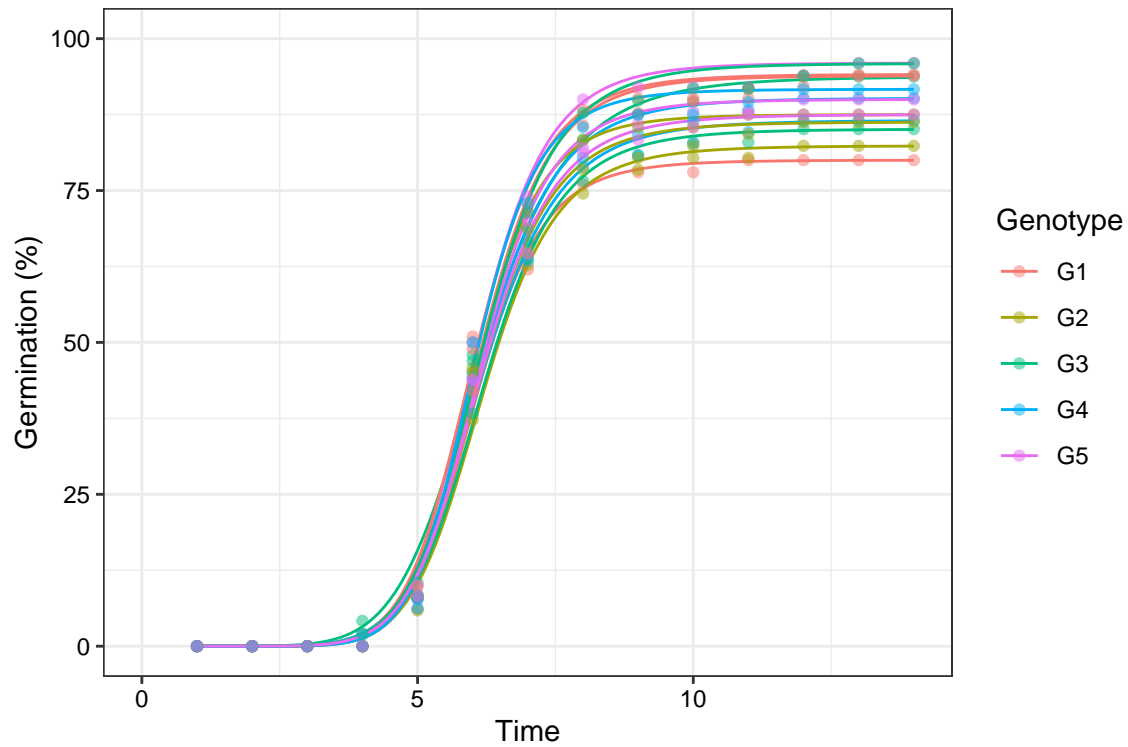
# Plot FPHF curves
plot(fits, group.col = "Genotype")
```



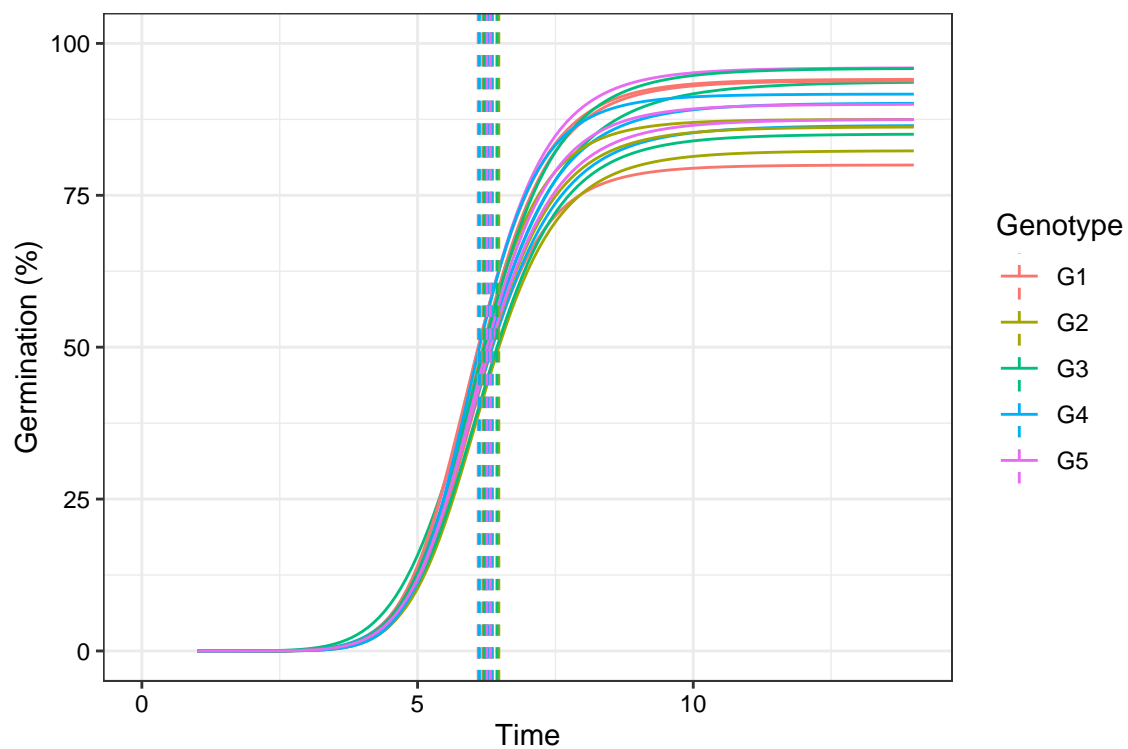
```
# Plot ROG curves
plot(fits, rog = TRUE, group.col = "Genotype")
```



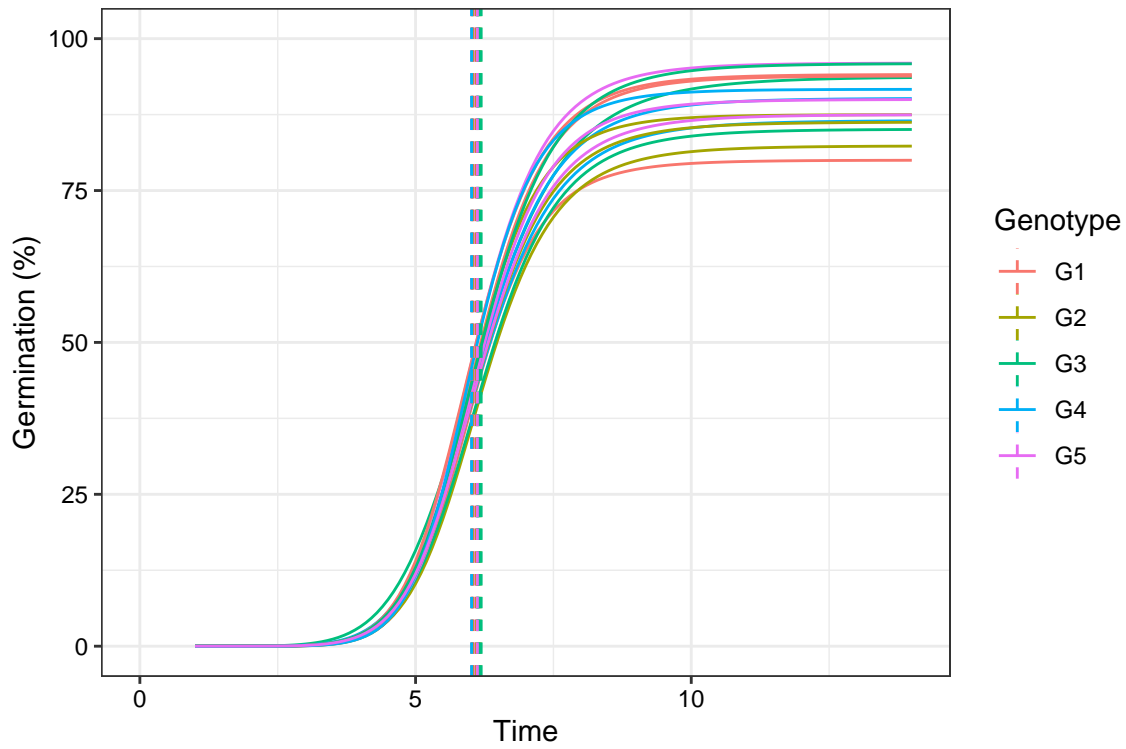
```
# Plot FPHF curves with points
plot(fits, group.col = "Genotype", show.points = TRUE)
```



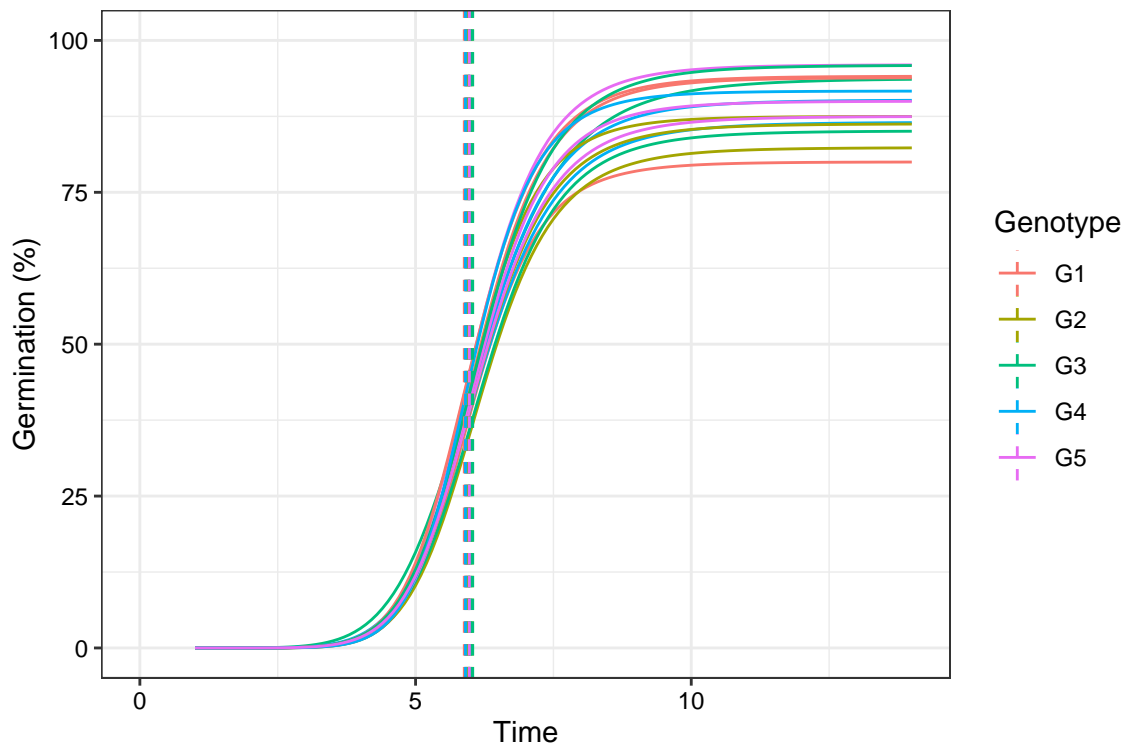
```
# Plot FPHF curves with annotations
plot(fits, group.col = "Genotype", annotate = "t50.total")
```



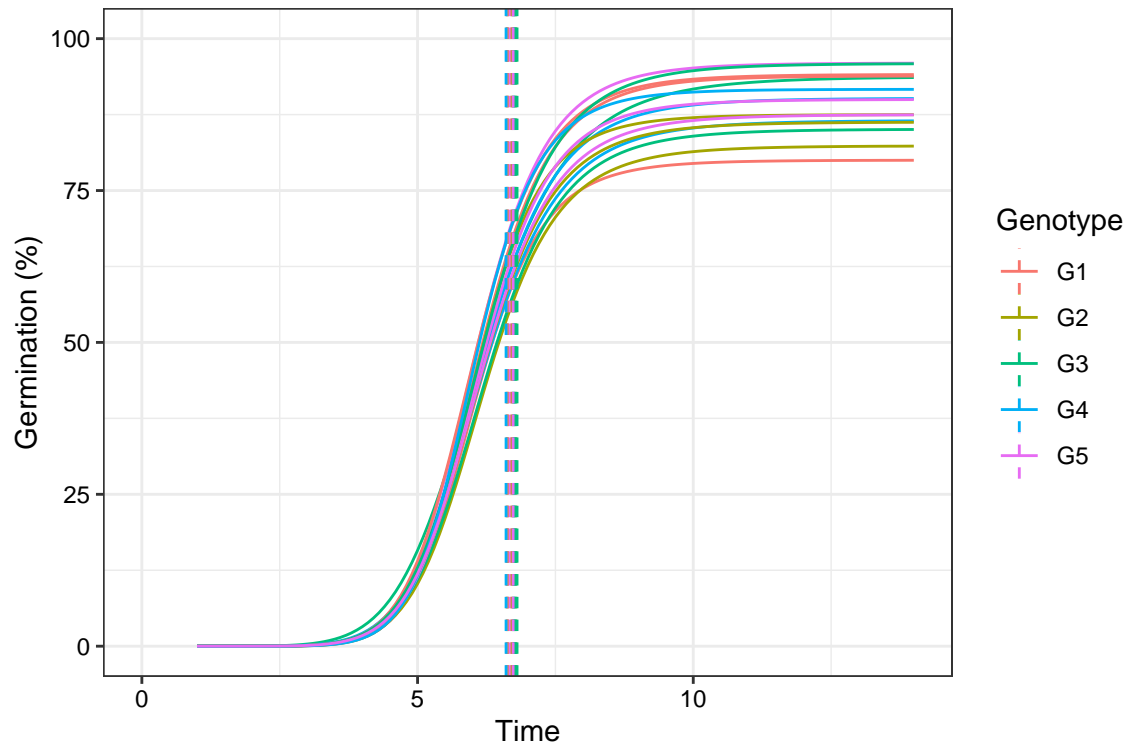
```
plot(fits, group.col = "Genotype", annotate = "t50.germ")
```



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

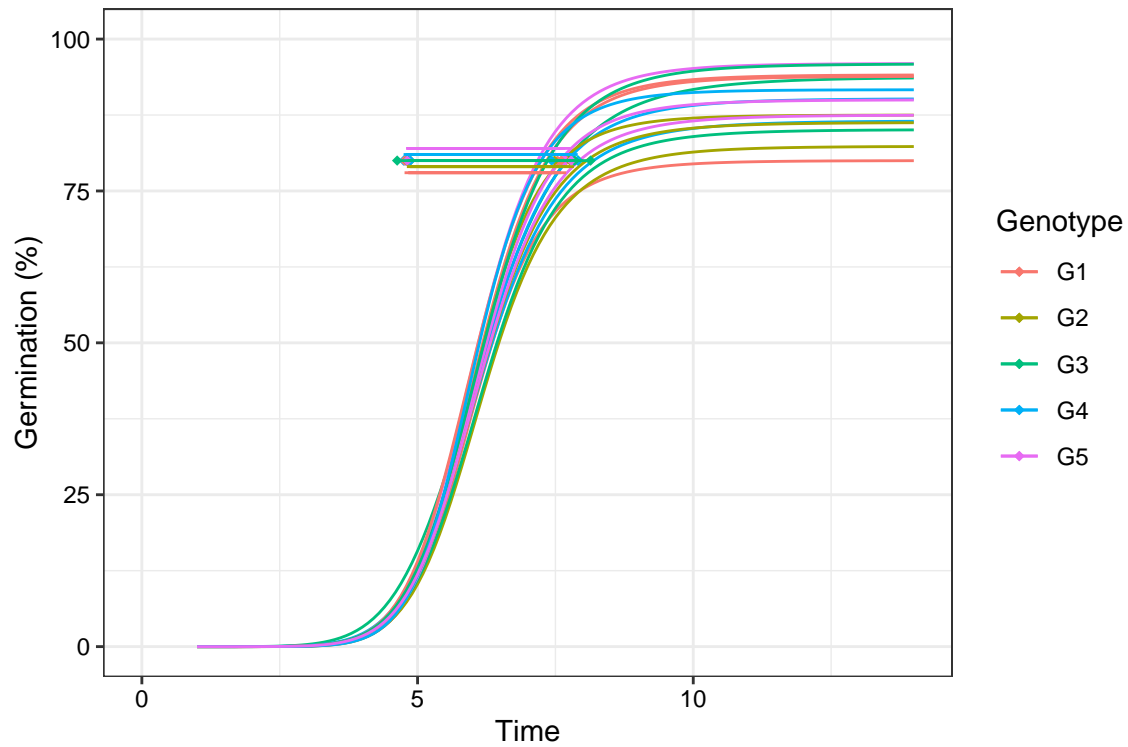


```
plot(fits, group.col = "Genotype", annotate = "mgt")
```

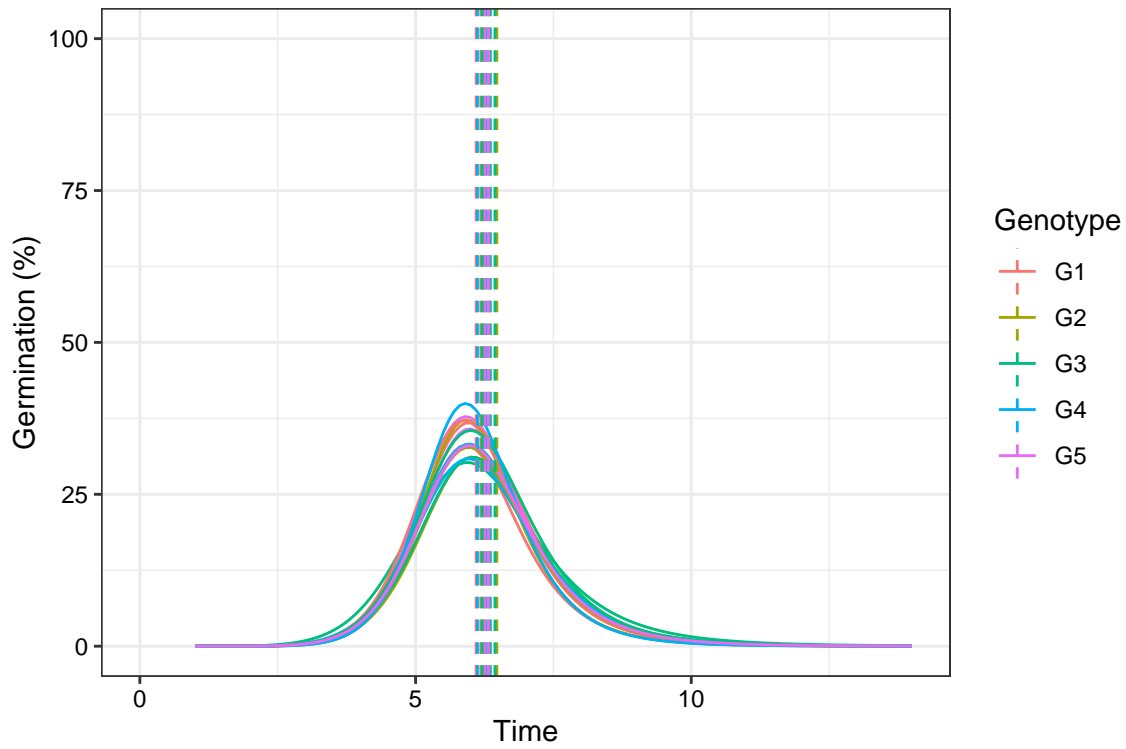


```
plot(fits, group.col = "Genotype", annotate = "uniformity")
```

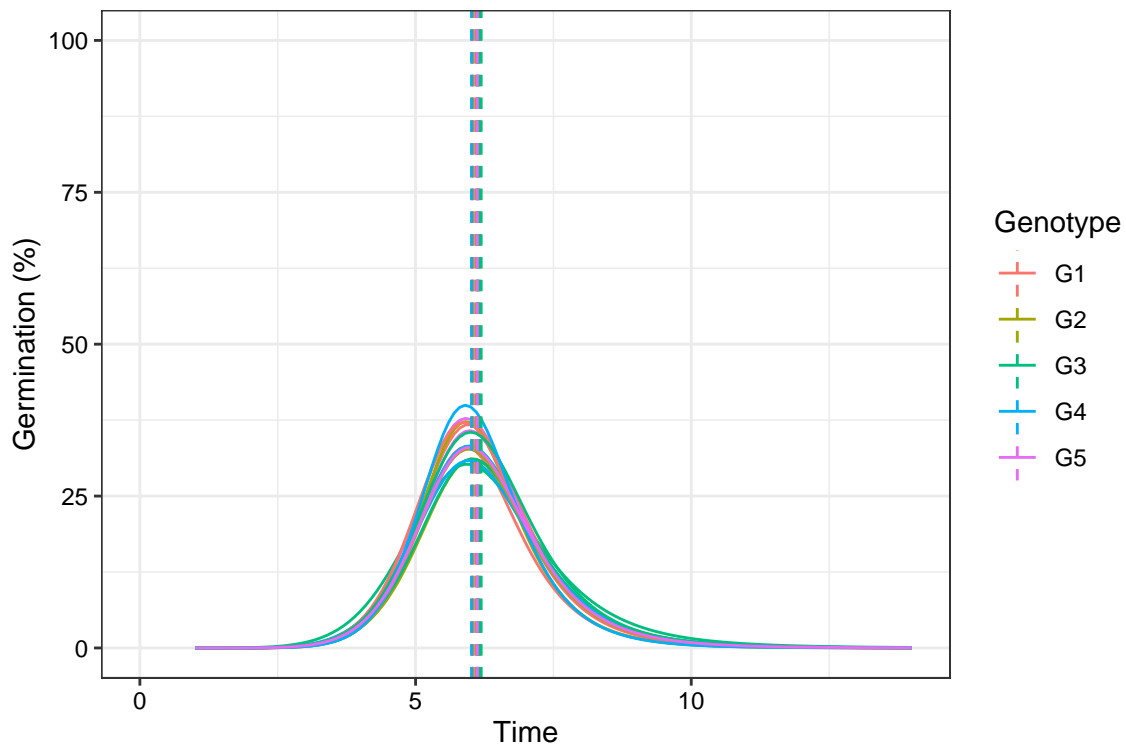
Warning: `position\_dodge()` requires non-overlapping x intervals  
 `position\_dodge()` requires non-overlapping x intervals



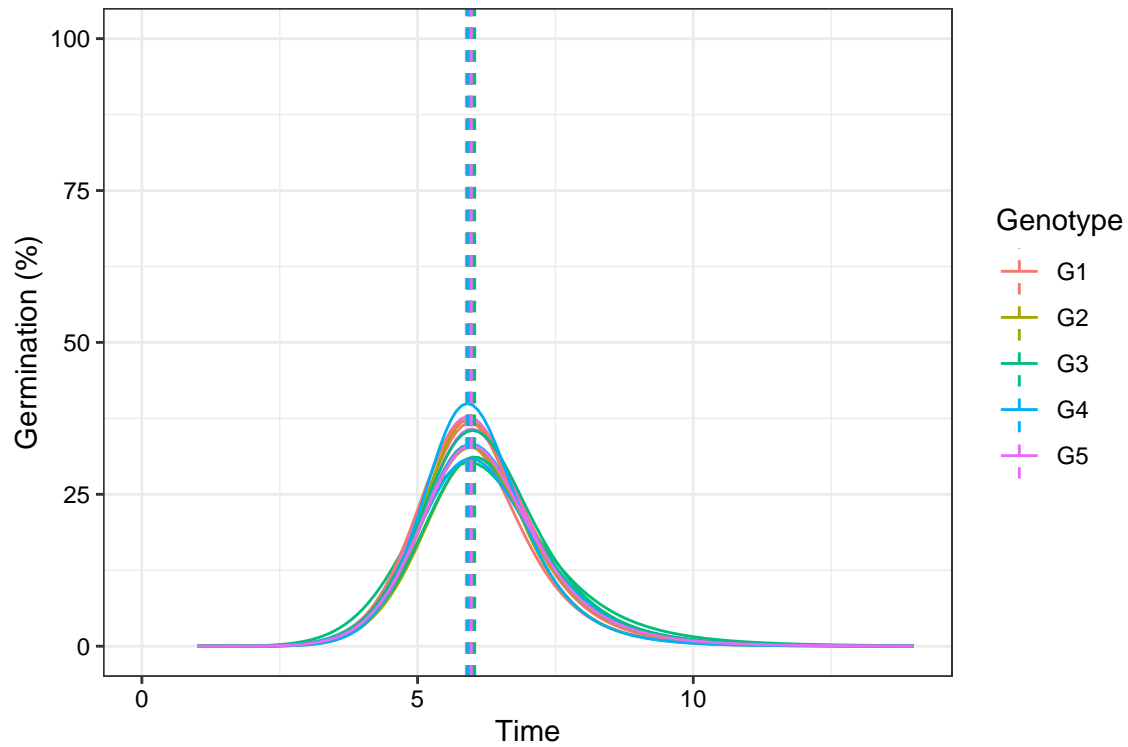
```
# Plot ROG curves with annotations
plot(fits, rog = TRUE, group.col = "Genotype", annotate = "t50.total")
```



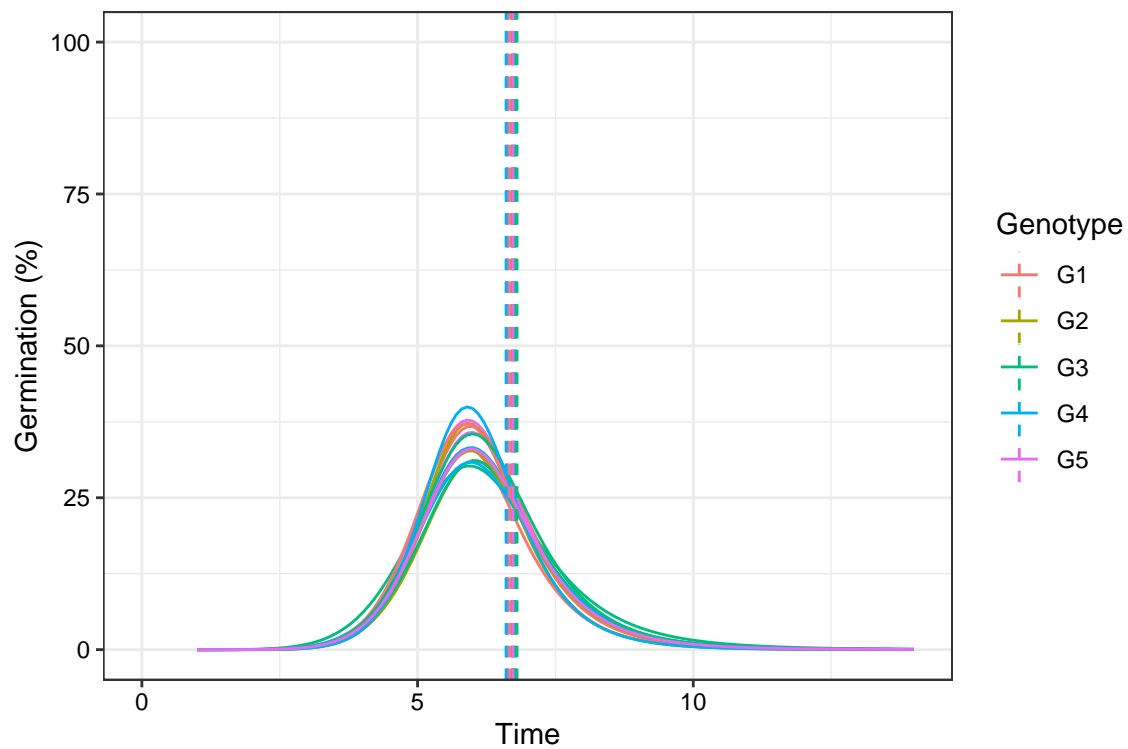
```
plot(fits, rog = TRUE, group.col = "Genotype", annotate = "t50.germ")
```



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



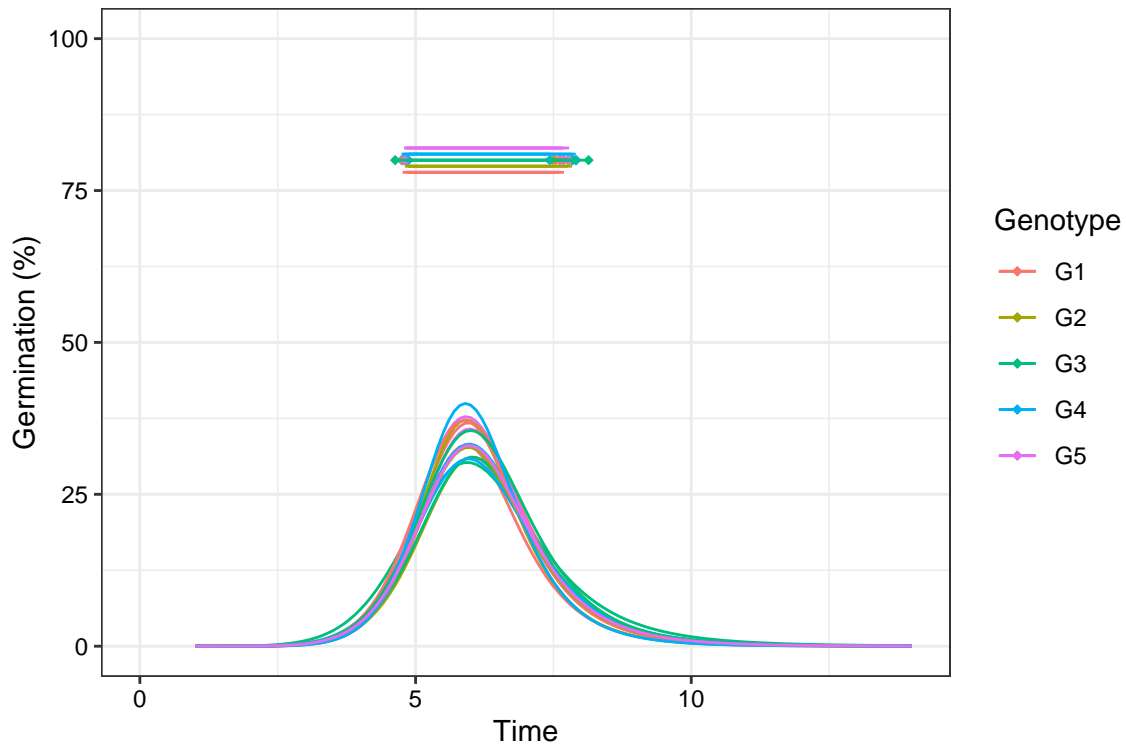
```
plot(fits, rog = TRUE, group.col = "Genotype", annotate = "mgt")
```



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

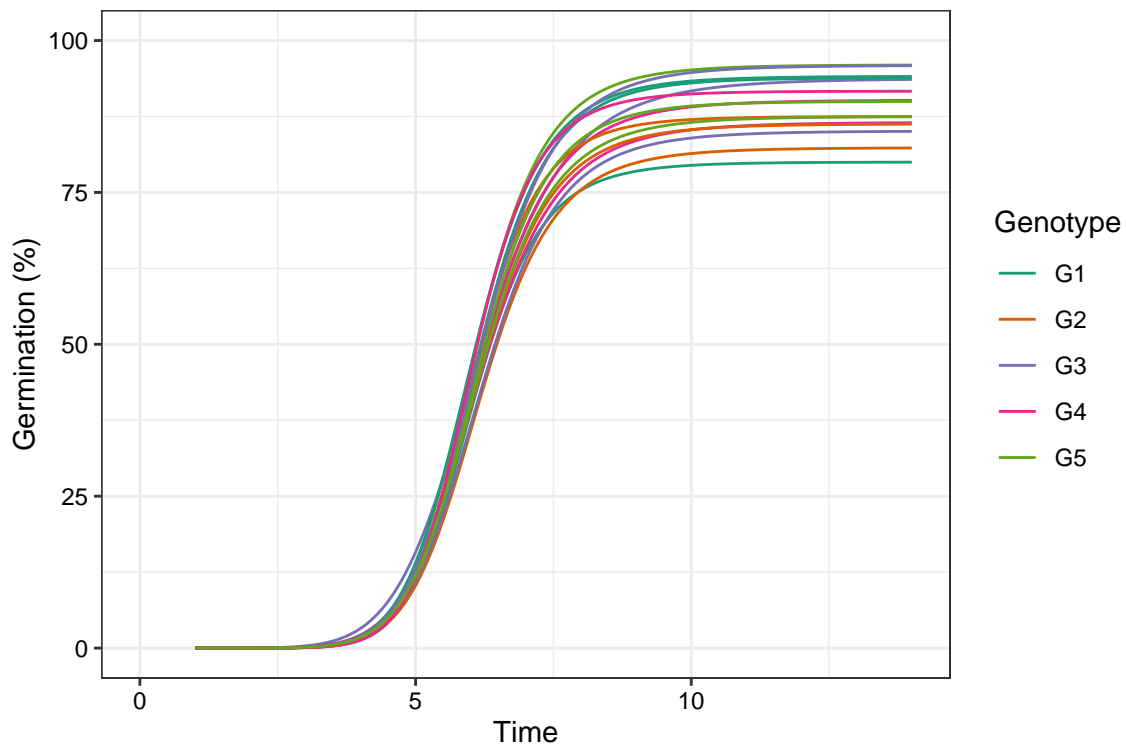
Warning: `position\_dodge()` requires non-overlapping x intervals  
 `position\_dodge()` requires non-overlapping x intervals



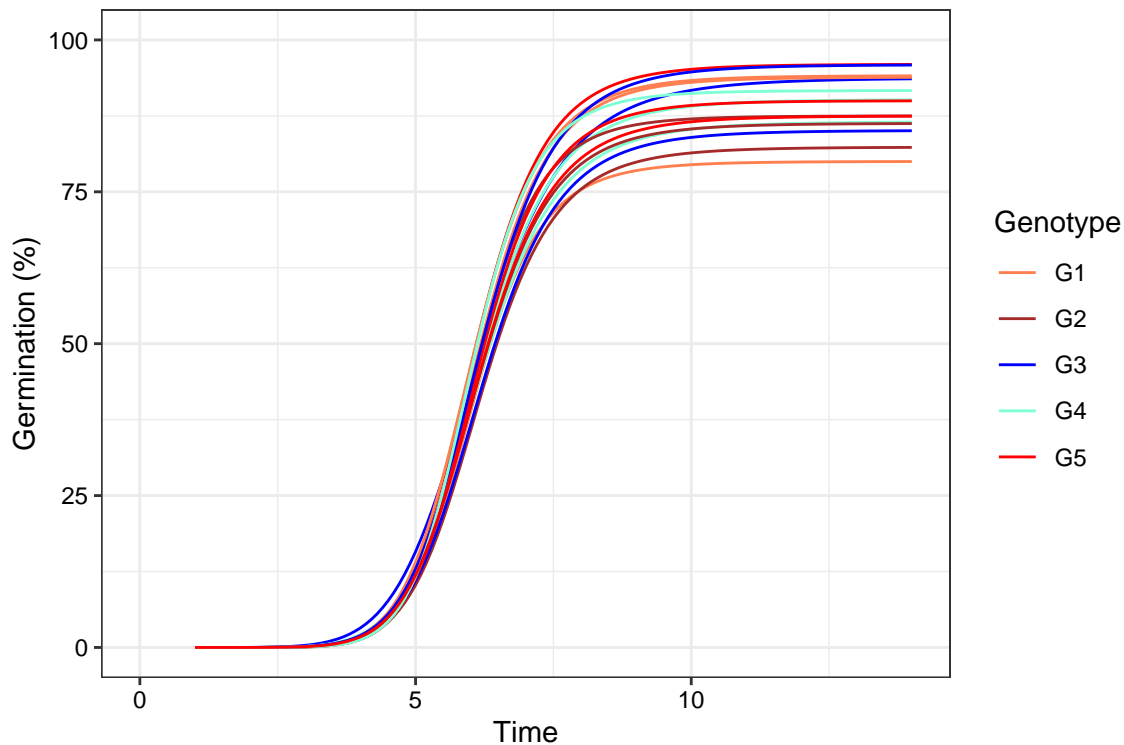


```
# Change colour of curves using ggplot2 options
library(ggplot2)
curvesplot <- plot(fits, group.col = "Genotype")

# '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 (). *germinationmetrics*: Curve Fitting. R package version 0.1.8.9000,  
<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}},
  note = {R package version 0.1.8.9000 https://aravind-j.github.io/germinationmetrics/ 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 cite it by citing the package.

## Session Info

```
sessionInfo()
```

```
R Under development (unstable) (2023-08-09 r84924 ucrt)
Platform: x86_64-w64-mingw32/x64
```

Running under: Windows 11 x64 (build 22621)

Matrix products: default

locale:

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

time zone: Asia/Calcutta

tzcode source: internal

attached base packages:

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

other attached packages:

```
[1] germinationmetrics_0.1.8.9000 ggplot2_3.4.2                RCurl_1.98-1.12              testthat_3.1.1
```

loaded via a namespace (and not attached):

```
[1] bitops_1.0-7      Rdpack_2.4        remotes_2.4.2.1   rlang_1.1.1       magrittr_2.0.3    hun
[8] roxygen2_7.2.3    reshape2_1.4.4    png_0.1-8         callr_3.7.3       vctrs_0.6.3       st
[15] pkgconfig_2.0.3   crayon_1.5.2      fastmap_1.1.1     backports_1.4.1   ellipsis_0.3.2    lab
[22] utf8_1.2.3        promises_1.2.0.1  rmarkdown_2.23    sessioninfo_1.2.2 ps_1.7.5          tim
[29] xfun_0.40         gsinls_1.1.2      cachem_1.0.8      covr_3.6.2        jsonlite_1.8.7    hig
[36] broom_1.0.5       parallel_4.4.0    prettyunits_1.1.1 R6_2.5.1          RColorBrewer_1.1-3 st
[43] brio_1.1.3        Rcpp_1.0.11       knitr_1.43        usethis_2.2.2     clisymbols_1.2.0  ht
[50] tidyselect_1.2.0  yaml_2.3.7        rstudioapi_0.15.0 miniUI_0.1.1.1    curl_5.0.1        pr
[57] lattice_0.21-8    tibble_3.2.1      plyr_1.8.8        shiny_1.7.4.1     withr_2.5.0       eva
[64] rJava_1.0-6       urlchecker_1.0.1  whoami_1.3.0      xml2_1.3.5        pillar_1.9.0      res
[71] pingr_2.0.2       generics_0.1.3    rprojroot_2.0.3   mathjaxr_1.6-0    xopen_1.0.0       mur
[78] scales_1.2.1      xtable_1.8-4      glue_1.6.2        clipr_0.8.0       lazyeval_0.2.2    too
[85] goodpractice_1.0.4 XML_3.99-0.14     fs_1.6.3          grid_4.4.0        tidyr_1.3.0       cy
[92] lintr_3.1.0       devtools_2.4.5    colorspace_2.1-0  cli_3.6.1         rcmdcheck_1.4.0   far
[99] praise_1.0.0      gtable_0.3.3      digest_0.6.33     ggrepel_0.9.3     farver_2.1.1      xml
[106] memoise_2.0.1     htmltools_0.5.5   pkgdown_2.0.7     lifecycle_1.0.3   httr_1.4.6        min
```

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