# The `germinationmetrics` Package: A Brief Introduction

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## Contents



### Overview

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

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

### Installation

The package can be installed using the following functions:

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

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

Then the package can be loaded using the function

```r
library(germinationmetrics)
```

## 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).

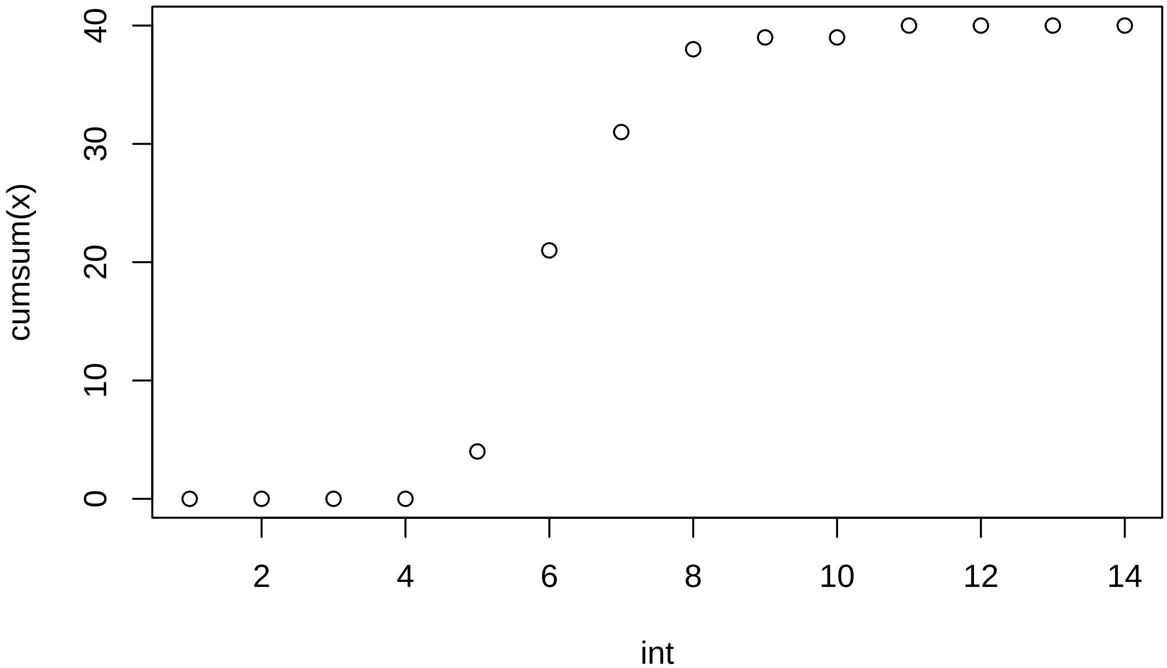
**Table 2 :** A typical germination count data.

| 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.

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

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

```
int <- data$intervals

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




## Single-value germination indices

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

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

| Germination index | Function | Details | Unit | Measures | Reference |
|---|---|---|---|---|---|
| Germination percentage or Final germination percentage or Germinability ($GP$) | `GermPercent` | It is computed as follows. $$GP = \frac{N_g}{N_t} \times 100$$ Where, $N_g$ is the number of germinated seeds and $N_t$ is the total number of seeds. | Percentage (%) | Germination capacity | ISTA (2015) |
| Peak germination percentage ($PGP$) | `PeakGermPercent` | It is computed as follows. $$PGP = \frac{N_{max}}{N_t} \times 100$$ Where, $N_{max}$ is the maximum number of seeds germinated per interval. | Percentage (%) | Germination capacity | Vallance (1950); Roh et al. (2004) |
| Time for the first germination or Germination time lag ($t_0$) | `FirstGermTime` | It is the time for first germination to occur (e.g. First day of germination). $$t_0 = \min\{T_i : N_i \neq 0\}$$ Where, $T_i$ is the time from the start of the experiment to the $i$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 ($t_g$) | `LastGermTime` | It is the time for last germination to occur (e.g. Last day of germination) $$t_g = \max\{T_i : N_i \neq 0\}$$ Where, $T_i$ is the time from the start of the experiment to the $i$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 | `TimeSpreadGerm` | It is the difference between time for last germination ($t_g$) and time for first germination ($t_0$). $$Time\,spread\,of\,germination = t_g - t_0$$ | time | Germination time | Al-Mudaris (1998); Schrader and Graves (2000); Kader (2005) |
| Peak period of germination or Modal time of germination ($t_{peak}$) | `PeakGermTime` | It is the time in which highest frequency of germinated seeds are observed and need not be unique. $$t_{peak} = \{T_i : N_i = N_{max}\}$$ Where, $T_i$ is the time from the start of the experiment to the $i$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) | `t50` | It is the time to reach 50% of final/maximum germination. With argument `method` specified as `"coolbear"`, it is computed as follows.<br>$$t_{50} = T_i + \frac{(\frac{N+1}{2} - N_i)(T_j - T_i)}{N_j - N_i}$$<br>Where, $t_{50}$ is the median germination time, $N$ is the final number of germinated seeds, and $N_i$ and $N_j$ are the total number of seeds germinated in adjacent counts at time $T_i$ and $T_j$ respectively, when $N_i < \frac{N+1}{2} < N_j$. | time | Germination time | Coolbear et al. (1984) |
| Median germination time ($t_{50}$) (Farooq) | `t50` | With argument `method` specified as `"farooq"`, it is computed as follows.<br>$$t_{50} = T_i + \frac{(\frac{N}{2} - N_i)(T_j - T_i)}{N_j - N_i}$$<br>Where, $t_{50}$ is the median germination time, $N$ is the final number of germinated seeds, and $N_i$ and $N_j$ are the total number of seeds germinated in adjacent counts at time $T_i$ and $T_j$ respectively, when $N_i < \frac{N}{2} < N_j$. | time | Germination time | Farooq et al. (2005) |
| Mean germination time or Mean length of incubation time ($\overline{T}$) or Germination resistance ($GR$) or Sprouting index ($SI$) or Emergence index ($EI$) | `MeanGermTime` | It is the average length of time required for maximum germination of a seed lot and is estimated according to the following formula.<br>$$\overline{T} = \frac{\sum_{i=1}^{k} N_i T_i}{\sum_{i=1}^{k} N_i}$$<br>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 $k$ is the total number of time intervals.<br>It is the inverse of mean germination rate ($\overline{V}$).<br>$$\overline{T} = \frac{1}{\overline{V}}$$ | time | Germination time | Edmond and Drapala (1958); Czabator (1962); Smith and Millet (1964); Gordon (1969); Gordon (1971); Mock and Eberhart (1972); Ellis and Roberts (1980) Labouriau (1983a); Ranal and Santana (2006) |

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

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

| Germination index | Function | Details | Unit | Measures | Reference |
|---|---|---|---|---|---|
| Speed of accumulated germination ($S_{accumulated}$) | `GermSpeedAccumulate` | It is the rate of germination in terms of the accumulated/cumulative total number of seeds that germinate in a time interval.<br>It is estimated as follows.<br>$S_{accumulated} = \sum_{i=1}^{k} \frac{\sum_{j=1}^{i} N_j}{T_i}$<br>Where, $T_i$ is the time from the start of the experiment to the $i$th interval, $\sum_{j=1}^{i} N_j$ is the cumuative/accumulated number of seeds germinated in the $i$th interval, and $k$ is the total number of time intervals.<br>Instead of germination counts, germination percentages may also be used for computation of speed of germination. | % time$^{-1}$ or count time$^{-1}$ | Mixed | Bradbeer (1988); Wardle et al. (1991); Haugland and Brandsaeter (1996); Santana and Ranal (2004) |
| Corrected speed of germination or Corrected germination rate index ($\hat{S}$) | `GermSpeedCorrected` | It is computed as follows.<br>$S_{corrected} = \frac{S}{FGP}$<br>Where, $S$ is the germination speed computed with germination percentage instead of counts and $FGP$ is the final germination percentage or germinability.<br>It can also be computed from speed of accumulated germination (computed with germination percentage).<br>$\hat{S}_{accumulated} = \frac{S_{accumulated}}{FGP}$<br>Where, $S_{accumulated}$ is the speed of accumulated germination computed with germination percentage instead of counts and $FGP$ is the final germination percentage or germinability. | time$^{-1}$ | Mixed | Evetts and Burnside (1972) |
| Weighted germination percentage ($WGP$) | `WeightGermPercent` | It is estimated as follows.<br>$WGP = \frac{\sum_{i=1}^{k}(k-i+1)N_i}{k \times N} \times 100$<br>Where, $N_i$ is the number of seeds that germinated in the time interval $i$ (not cumulative, but partial count), $N$ is the total number of seeds tested, and $k$ is the total number of time intervals. | Percentage (%) | Mixed | Reddy et al. (1985); Reddy (1978) |
| Mean germination percentage per unit time ($\overline{GP}$) | `MeanGermPercent` | It is estimated as follows.<br>$\overline{GP} = \frac{GP}{T_k}$<br>Where, $GP$ is the final germination percentage, $T_k$ is the time at the $k$th time interval, and $k$ is the total number of time intervals required for final germination. | % time$^{-1}$ | Mixed | Czabator (1962) |

| Germination index | Function | Details | Unit | Measures | Reference |
| --- | --- | --- | --- | --- | --- |
| Number of seeds germinated per unit time $\overline{N}$ | `MeanGermNumber` | It is estimated as follows. $$\overline{N} = \frac{N_g}{T_k}$$ Where, $N_g$ is the number of germinated seeds at the end of the germination test, $T_k$ is the time at the $k$th time interval, and $k$ is the total number of time intervals required for final germination. | count time$^{-1}$ | Mixed | Khamassi et al. (2013) |
| Timson's index [$\sum 10$ (Ten summation), $\sum 5$ or $\sum 20$] or Germination energy index ($GEI$) | `TimsonsIndex` | It is the progressive total of cumulative germination percentage recorded at specific intervals for a set period of time and is estimated in terms of cumulative germination percentage ($G_i$) as follows. $$\Sigma k = \sum_{i=1}^{k} G_i$$ Where, $G_i$ is the cumulative germination percentage in time interval $i$, and $k$ is the total number of time intervals.<br>It also estimated in terms of partial germination percentage as follows. $$\Sigma k = \sum_{i=1}^{k} g_i(k-j)$$ Where, $g_i$ is the germination (not cumulative, but partial germination) in time interval $i$ ($i$ varying from 0 to $k$), $k$ is the total number of time intervals, and $j = i - 1$. | Percentage (%) | Mixed | Grose and Zimmer (1958); Timson (1965); Lyon and Coffelt (1966); Chaudhary and Ghildyal (1970); Negm and Smith (1978); Brown and Mayer (1988); Baskin and Baskin (1998); Goodchild and Walker (1971) |
| Modified Timson's index ($\Sigma k_{mod}$) (Labouriau) | `TimsonsIndex` | It is estimated as Timson's index $\Sigma k$ divided by the sum of partial germination percentages. $$\Sigma k_{mod} = \frac{\Sigma k}{\sum_{i=1}^{k} g_i}$$ | no unit | Mixed | Ranal and Santana (2006) |
| Modified Timson's index ($\Sigma k_{mod}$) (Khan and Unger) | `TimsonsIndex` | It is estimated as Timson's index ($\Sigma k$) divided by the total time period of germination ($T_k$). $$\Sigma k_{mod} = \frac{\Sigma k}{T_k}$$ | % time$^{-1}$ | Mixed | Khan and Ungar (1984) |

| Germination index | Function | Details | Unit | Measures | Reference |
|---|---|---|---|---|---|
| George's index ($GR$) | `GermRateGeorge` | It is estimated as follows. $$GR = \sum_{i=1}^{k} N_i K_i$$ Where $N_i$ is the number of seeds germinated by $i$th interval and $K_i$ is the number of intervals(eg. days) until the end of the test, and and $k$ is the total number of time intervals. | count time | Mixed | George (1961); Tucker and Wright (1965); Nichols and Heydecker (1968);Chopra and Chaudhary (1980) |
| Germination Index ($GI$) (Melville) | `GermIndex` | It is estimated as follows. $$GI = \sum_{i=1}^{k} \frac{\lvert (T_k - T_i)\, N_i \rvert}{N_t}$$ Where, $T_i$ is the time from the start of the experiment to the $i$th interval (day for the example), $N_i$ 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), $N_t$ is the total number of seeds used in the test, and $k$ is the total number of time intervals. | time | Mixed | Melville et al. (1980) |
| Germination Index ($GI_{mod}$) (Melville; Santana and Ranal) | `GermIndex` | It is estimated as follows. $$GI_{mod} = \sum_{i=1}^{k} \frac{\lvert (T_k - T_i)\, N_i \rvert}{N_g}$$ Where, $T_i$ is the time from the start of the experiment to the $i$th interval (day for the example), $N_i$ 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), $N_g$ is the total number of germinated seeds at the end of the test, and $k$ is the total number of time intervals. | time | Mixed | Melville et al. (1980); Santana and Ranal (2004); Ranal and Santana (2006) |
| Emergence Rate Index ($ERI$) or Germination Rate Index (Shmueli and Goldberg) | `EmergenceRateIndex` | It is estimated as follows. $$ERI = \sum_{i=i_0}^{k-1} N_i (k - i)$$ Where, $N_i$ is the number of seeds germinated in the $i$th time interval (not the accumulated number, but the number corresponding to the $i$th interval), $i_0$ is the time interval when emergence/germination started, and $k$ is the total number of time intervals. | count | Mixed | Shmueli and Goldberg (1971) |

| Germination index | Function | Details | Unit | Measures | Reference |
|---|---|---|---|---|---|
| Modified Emergence Rate Index ($ERI_{mod}$) or Modified Germination Rate Index (Shmueli and Goldberg; Santana and Ranal) | `EmergenceRateIndex` | It is estimated by dividing Emergence rate index ($ERI$) by total number of emerged seedlings (or germinated seeds). $$ERI_{mod} = \frac{\sum_{i=i_0}^{k-1} N_i(k-i)}{N_g} = \frac{ERI}{N_g}$$ Where, $N_g$ is the total number of germinated seeds at the end of the test, $N_i$ is the number of seeds germinated in the $i$th time interval (not the accumulated number, but the number corresponding to the $i$th interval), $i_0$ is the time interval when emergence/germination started, and $k$ is the total number of time intervals. | no unit | Mixed | Shmueli and Goldberg (1971); Santana and Ranal (2004); Ranal and Santana (2006) |
| Emergence Rate Index ($ERI$) or Germination Rate Index (Bilbro & Wanjura) | `EmergenceRateIndex` | It is the estimated as follows. $$ERI = \frac{\sum_{i=1}^{k} N_i}{\overline{T}} = \frac{N_g}{\overline{T}}$$ Where, $N_g$ is the total number of germinated seeds at the end of the test, $N_i$ is the number of seeds germinated in the $i$th time interval (not the accumulated number, but the number corresponding to the $i$th interval), and $\overline{T}$ is the mean germination time or mean emergence time. | count time$^{-1}$ | Mixed | Bilbro and Wanjura (1982) |
| Emergence Rate Index ($ERI$) or Germination Rate Index (Fakorede) | `EmergenceRateIndex` | It is estimated as follows. $$ERI = \frac{\overline{T}}{FGP/100}$$ Where, $\overline{T}$ is the Mean germination time and $FGP$ is the final germination time. | time count$^{-1}$ | Mixed | Fakorede and Ayoola (1980); Fakorede and Ojo (1981); Fakorede and Agbana (1983) |
| Peak value($PV$) (Czabator) or Emergence Energy ($EE$) | `PeakValue` | It is the accumulated number of seeds germinated at the point on the germination curve at which the rate of germination starts to decrease. It is computed as the maximum quotient obtained by dividing successive cumulative germination values by the relevant incubation time. $$PV = \max\left(\frac{G_1}{T_1}, \frac{G_2}{T_2}, \cdots \frac{G_k}{T_k}\right)$$ Where, $T_i$ is the time from the start of the experiment to the $i$th interval, $G_i$ is the cumulative germination percentage in the $i$th time interval, and $k$ is the total number of time intervals. | % time$^{-1}$ | Mixed | Czabator (1962); Bonner (1967) |

| Germination index | Function | Details | Unit | Measures | Reference |
|---|---|---|---|---|---|
| Germination value ($GV$) (Czabator) | `GermValue` | It is computed as follows.<br>$GV = PV \times MDG$<br>Where, $PV$ is the peak value and $MDG$ is the mean daily germination percentage from the onset of germination.<br>It can also be computed for other time intervals of successive germination counts, by replacing $MDG$ with the mean germination percentage per unit time ($\overline{GP}$).<br>$GV$ value can be modified ($GV_{mod}$), to consider the entire duration from the beginning of the test instead of just from the onset of germination. | $\%^2$ time$^{-2}$ | Mixed | Czabator (1962); Brown and Mayer (1988) |
| Germination value ($GV$) (Diavanshir and Pourbiek) | `GermValue` | It is computed as follows.<br>$GV = \frac{\sum DGS}{N} \times GP \times c$<br>Where, $DGS$ is the daily germination speed computed by dividing cumulative germination percentage by the number of days since the since the onset of germination, $N$ is the frequency or number of DGS calculated during the test, $GP$ is the germination percentage expressed over 100, and $c$ is a constant. The value of $c$ is decided on the basis of average daily speed of germination ($\frac{\sum DGS}{N}$). If it is less than 10, then $c$ value of 10 can be used and if it is more than 10, then value of 7 or 8 can be used for $c$.<br>$GV$ value can be modified ($GV_{mod}$), to consider the entire duration from the beginning of the test instead of just from the onset of germination. | $\%^2$ time$^{-1}$ | Mixed | Djavanshir and Pourbeik (1976); Brown and Mayer (1988) |
| Coefficient of uniformity of germination ($CUG$) | `CUGerm` | It is computed as follows.<br>$CUG = \frac{\sum_{i=1}^{k} N_i}{\sum_{i=1}^{k} (\overline{T} - T_i)^2 N_i}$<br>Where, $\overline{T}$ is the the mean germination time, $T_i$ is the time from the start of the experiment to the $i$th interval (day for the example), $N_i$ 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 $k$ is the total number of time intervals. | time$^{-2}$ | Germination unifromity | Heydecker (1972); Bewley and Black (1994) |
| Coefficient of variation of the germination time ($CV_T$) | `CVGermTime` | It is estimated as follows.<br>$CV_T = \sqrt{\frac{s_T^2}{\overline{T}}}$<br>Where, $s_T^2$ is the variance of germination time and $\overline{T}$ is the mean germination time. | no unit | Germination unifromity | Gomes (1960); Ranal and Santana (2006) |

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

### Examples

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

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

**GermPercent()**

```
[1] 80
```

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

```
[1] 34
```

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

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

```
[1] 22
```

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

```
[1] 80
```

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

```
[1] 34
```

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

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

```
[1] 22
```

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

```
[1] 80
```

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

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

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

```
[1] 5
```

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

```
[1] 11
```

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

```
[1] 6
```

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

```
[1] 6
```

```r
# 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
```

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

```
[1] 5
```

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

```
[1] 11
```

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

```
[1] 6
```

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

```
[1] 6
```

```r
# 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
```

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

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

**t50()**

```
[1] 5.970588
```

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

```
[1] 5.941176
```

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

```
[1] 5.970588
```

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

```
[1] 5.941176
```

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

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

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

```
[1] 6.7
```

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

```
[1] 1.446154
```

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

```
[1] 0.1901416
```

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

```
[1] 0.1794868
```

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

```
[1] 6.7
```

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

```
[1] 1.446154
```

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

```
[1] 0.1901416
```

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

```
[1] 0.1794868
```

```
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
```

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

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

**GermSpeed(), GermSpeedAccumulated(), GermSpeedCorrected()**

```
[1] 6.138925
```

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

```
[1] 34.61567
```

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

```
[1] 0.1534731
```

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

```
[1] 0.8653917
```

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

```
[1] 12.27785
```

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

```
[1] 69.23134
```

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

```
[1] 6.138925
```

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

```
[1] 34.61567
```

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

```
[1] 0.1534731
```

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

```
[1] 0.8653917
```

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

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

```
[1] 12.27785
```

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

```
[1] 69.23134
```

```r

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

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

**WeightGermPercent()**

```
[1] 47.42857
```

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

```
[1] 47.42857
```

```r

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

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

**MeanGermPercent(), MeanGermNumber()**

```
[1] 5.714286
```

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

```
[1] 2.857143
```

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

```
[1] 5.714286
```

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

```
[1] 2.857143
```

```
# 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
```

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

```
[1] 332
```

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

```
[1] 664
```

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

```
[1] 664
```

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

```
[1] 8.3
```

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

```
[1] 47.42857
```

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

```
[1] 332
```

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

```
[1] 344
```

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

```
[1] 344
```

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

```
[1] 4.410256
```

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

```
[1] 24.57143
```

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

```
[1] 172
```

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

```
[1] 332
```

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

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

**GermIndex()**

```
[1] 5.84
```

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

```
[1] 5.84
```

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

```
[1] 7.3
```

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

```
[1] 5.84
```

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

```
[1] 5.84
```

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

```
[1] 7.3
```

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

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

**EmergenceRateIndex()**

```
[1] 292
```

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

```
[1] 292
```

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

```
[1] 7.3
```

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

```
[1] 5.970149
```

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

```
[1] 8.375
```

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

```
[1] 292
```

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

```
[1] 292
```

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

```
[1] 7.3
```

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

```
[1] 5.970149
```

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

```
[1] 8.375
```

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

# From partial germination counts
```

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

**PeakValue(), GermValue()**

```
[1] 9.5
```

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

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

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

```r
GermValue(germ.counts = 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
```

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

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

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

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

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

[[2]]
   germ.counts intervals Cumulative.germ.counts Cumulative.germ.percent      DGS SumDGSbyN        GV
1            0         1                      0                      0.0 0.000000  0.000000  0.000000
2            0         2                      0                      0.0 0.000000  0.000000  0.000000
3           34         3                     34                     17.0 5.666667  1.888889  3.211111
4           40         4                     74                     37.0 9.250000  3.729167 13.797917
5           21         5                     95                     47.5 9.500000  4.883333 23.195833
6           10         6                    105                     52.5 8.750000  5.527778 29.020833
7            4         7                    109                     54.5 7.785714  5.850340 31.884354
8            5         8                    114                     57.0 7.125000  6.009673 34.255134
9            3         9                    117                     58.5 6.500000  6.064153 35.475298
10           5        10                    122                     61.0 6.100000  6.067738 37.013202
```

```
11             8         11                      130                     65.0 5.909091  6.053316 39.346552
12             7         12                      137                     68.5 5.708333  6.024567 41.268285
13             7         13                      144                     72.0 5.538462  5.987174 43.107655
14             6         14                      150                     75.0 5.357143  5.942172 44.566291
15             6         15                      156                     78.0 5.200000  5.892694 45.963013
16             4         16                      160                     80.0 5.000000  5.836901 46.695205
17             0         17                      160                     80.0 4.705882  5.770370 46.162961
18             2         18                      162                     81.0 4.500000  5.699794 46.168331
19             0         19                      162                     81.0 4.263158  5.624182 45.555871
20             2         20                      164                     82.0 4.100000  5.547972 45.493374

$testend
[1] 16
```

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

```
[1] 9.5
```

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

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

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

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

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

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

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

$testend
[1] 16
```

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

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

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

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

```
$`Germination Value`
```

```
[1] 46.6952

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

$testend
[1] 16
```

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

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

**CUGerm()**

```
[1] 0.7092199
```

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

```
[1] 0.7092199
```

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

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

**GermSynchrony(), GermUncertainty()**

```
[1] 0.2666667
```

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

```
[1] 2.062987
```

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

```
[1] 0.2666667
```

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

```
[1] 2.062987
```

## Non-linear regression analysis

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

### Four-parameter hill function

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

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

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

this function can also be be reparameterized by substituting $b$ with $e^\beta$ 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 |

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

### Examples

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

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

**FourPHFfit()**

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

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

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

$a
[1] 80

$b
[1] 9.881937

$c
[1] 6.034954

$y0
[1] 0

$lag
[1] 0
```

```
$Dlag50
[1] 6.034954

$t50.total
[1] 6.355121

$txp.total
      10       60
4.956264 6.744598

$t50.Germinated
[1] 6.034954

$txp.Germinated
      10       60
4.831807 6.287724

$Uniformity
        90         10 uniformity
  7.537690   4.831807   2.705882

$TMGR
[1] 5.912194

$AUC
[1] 1108.976

$MGT
[1] 6.632252

$Skewness
[1] 1.098973

$msg
[1] "#1. success "

$isConv
[1] TRUE

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

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

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

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

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

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

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

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

$a
[1] 80

$b
[1] 9.881937

$c
[1] 6.034954

$y0
[1] 0

$lag
[1] 0

$Dlag50
[1] 6.034954

$t50.total
[1] 6.355121

$txp.total
      10       60
```

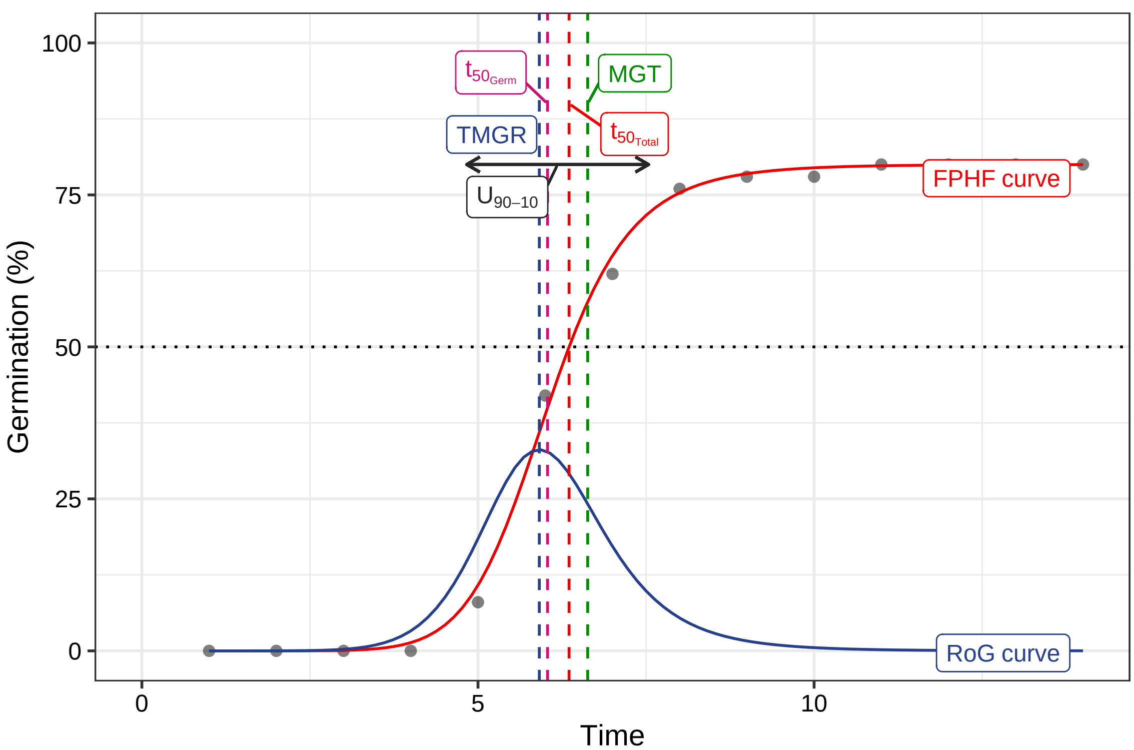
```
4.956264 6.744598

$t50.Germinated
[1] 6.034954

$txp.Germinated
      10       60 
4.831807 6.287724 

$Uniformity
        90         10 uniformity 
  7.537690   4.831807   2.705882 

$TMGR
[1] 5.912194

$AUC
[1] 1108.976

$MGT
[1] 6.632252

$Skewness
[1] 1.098973

$msg
[1] "#1. success "

$isConv
[1] TRUE

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

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

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

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

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

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

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

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

# Default plots
plot(fit1)
```

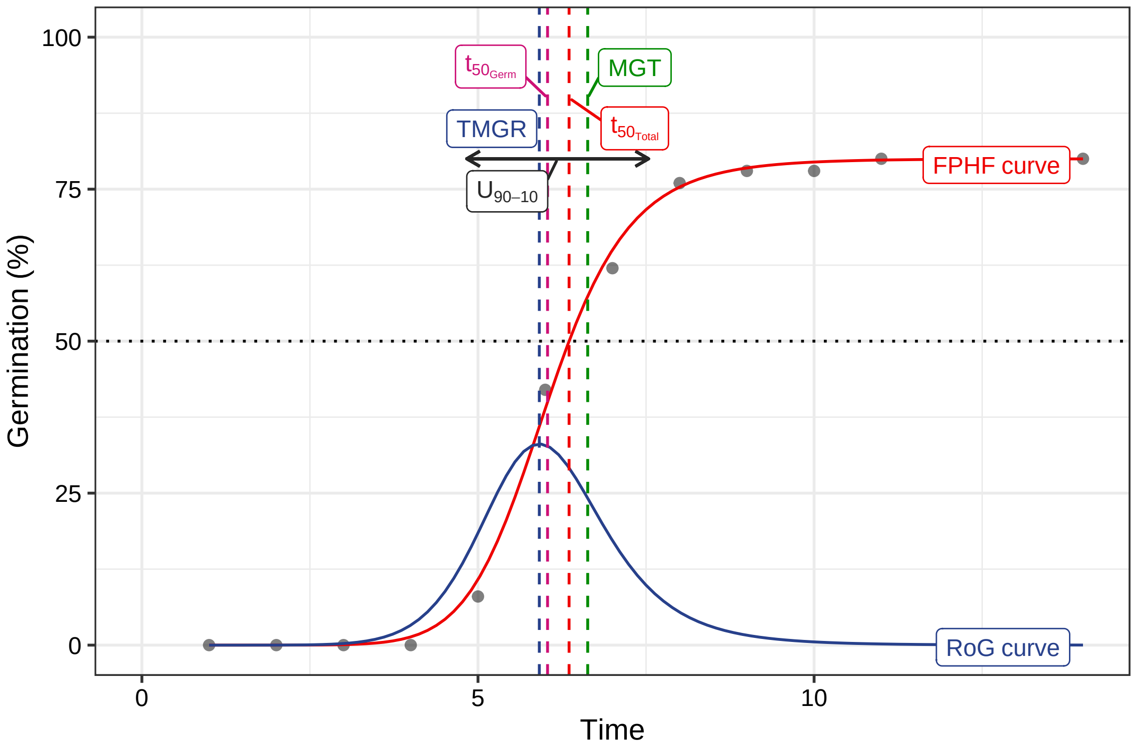
```
Warning in geom_segment(aes(x = UfmMin, xend = UfmMax, y = ypos2, yend = ypos2), : All aesthetics have l
i Please consider using `annotate()` or provide this layer with data containing a single row.
```

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



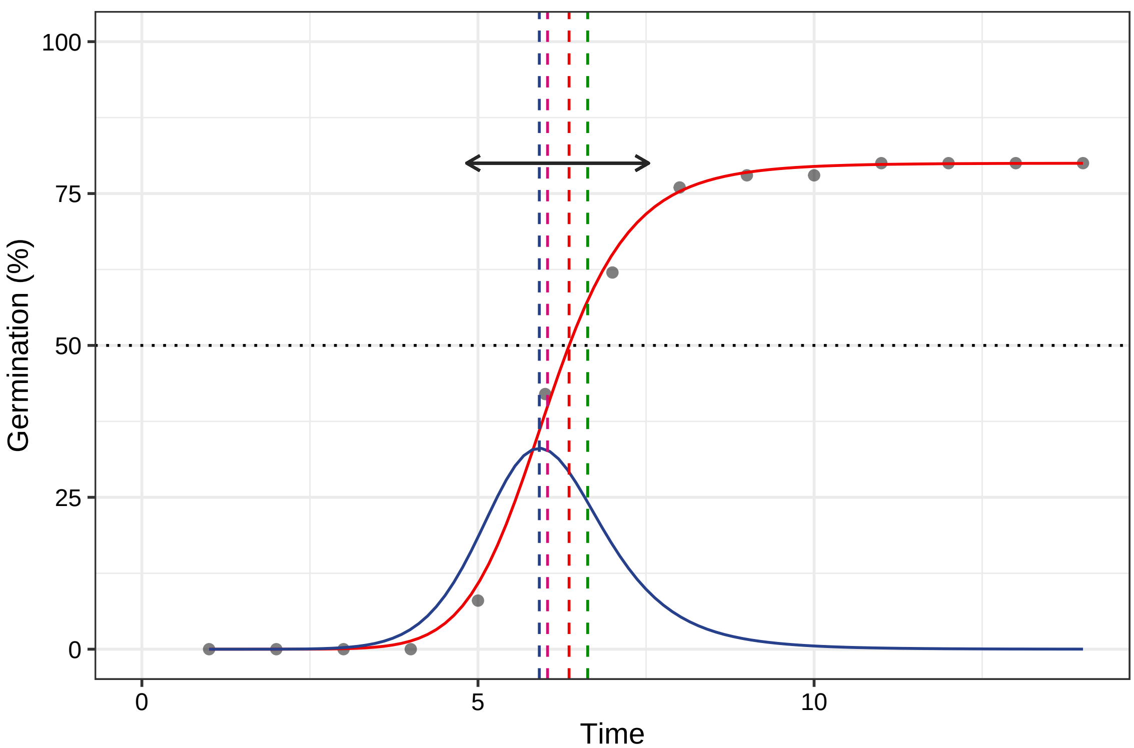

```
plot(fit2)
```

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



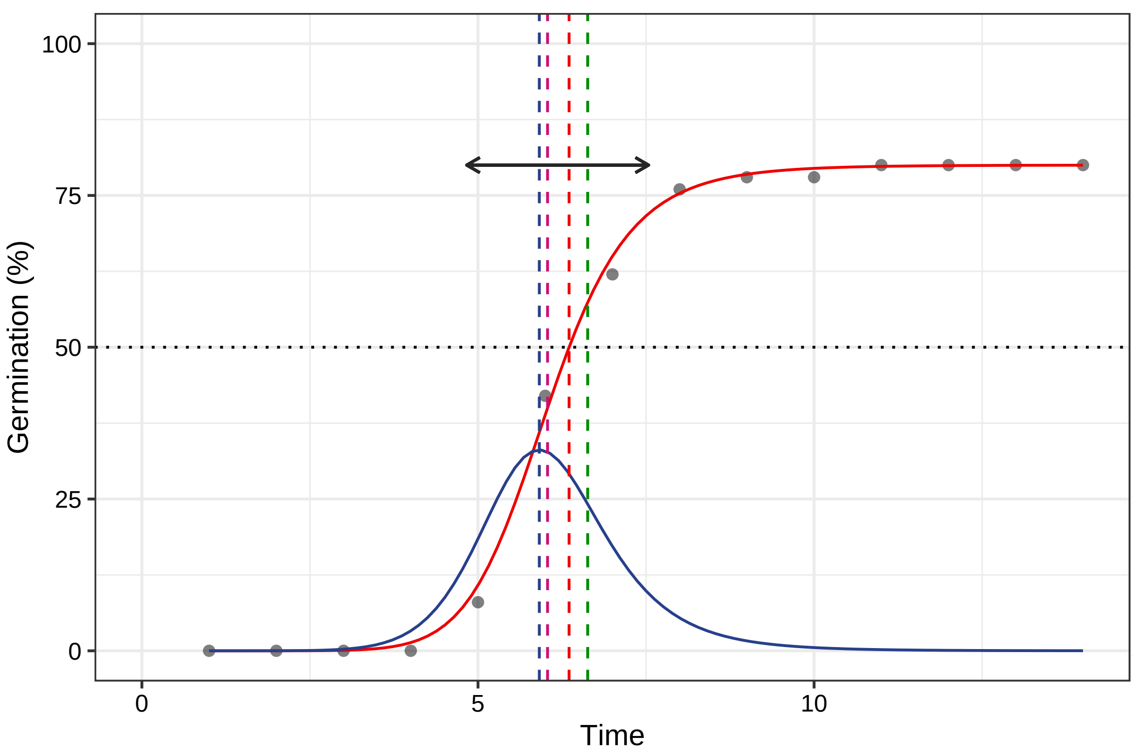

```
# No labels
plot(fit1, plotlabels = FALSE)
```

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

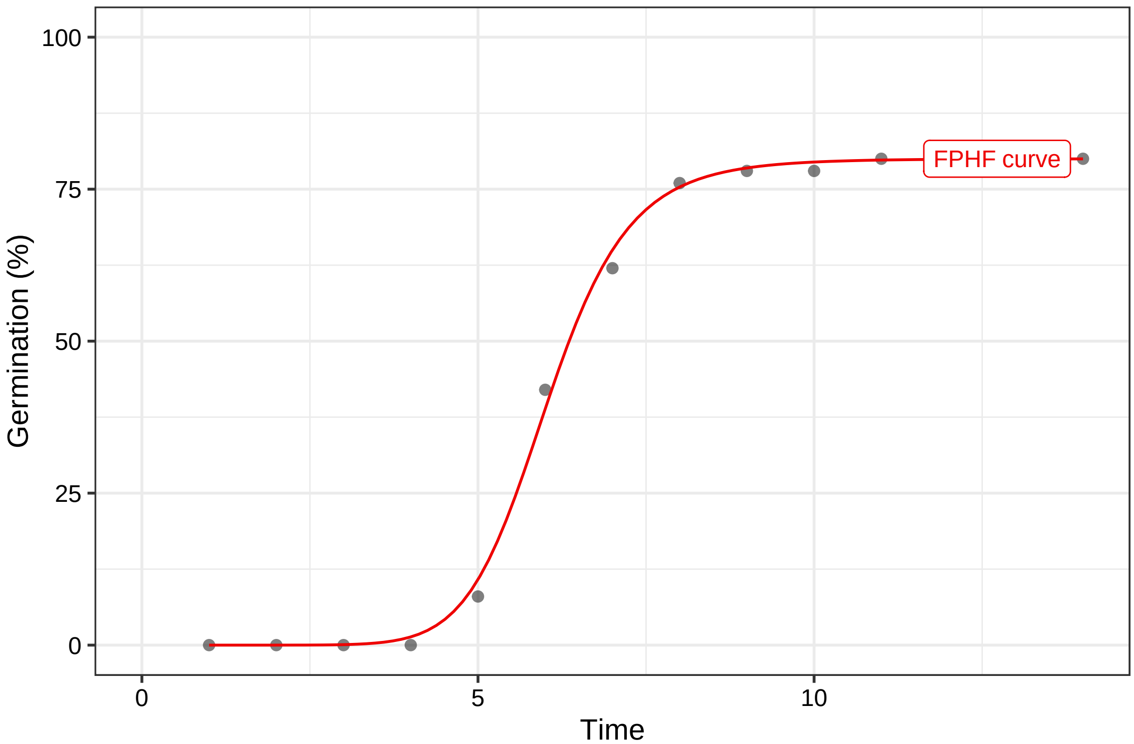


```r
plot(fit2, plotlabels = FALSE)
```

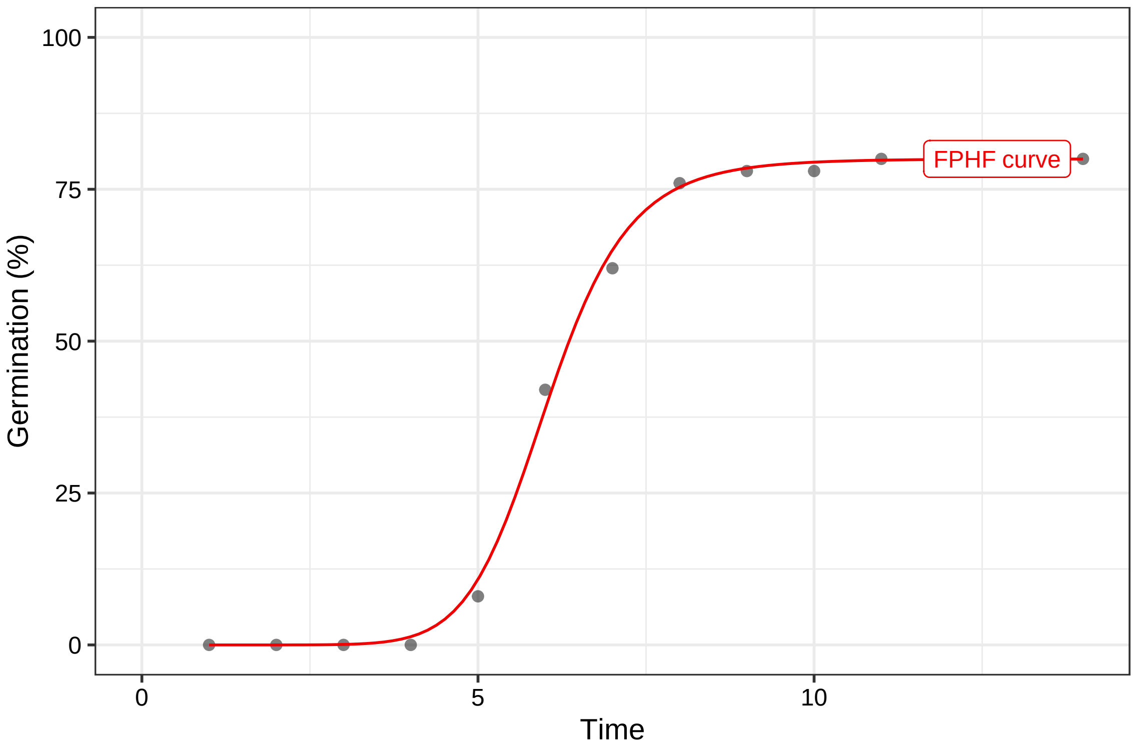
```
Warning in geom_segment(aes(x = UfmMin, xend = UfmMax, y = ypos2, yend = ypos2), : All aesthetics have l
i Please consider using `annotate()` or provide this layer with data containing a single row.
All aesthetics have length 1, but the data has 14 rows.
i Please consider using `annotate()` or provide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




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



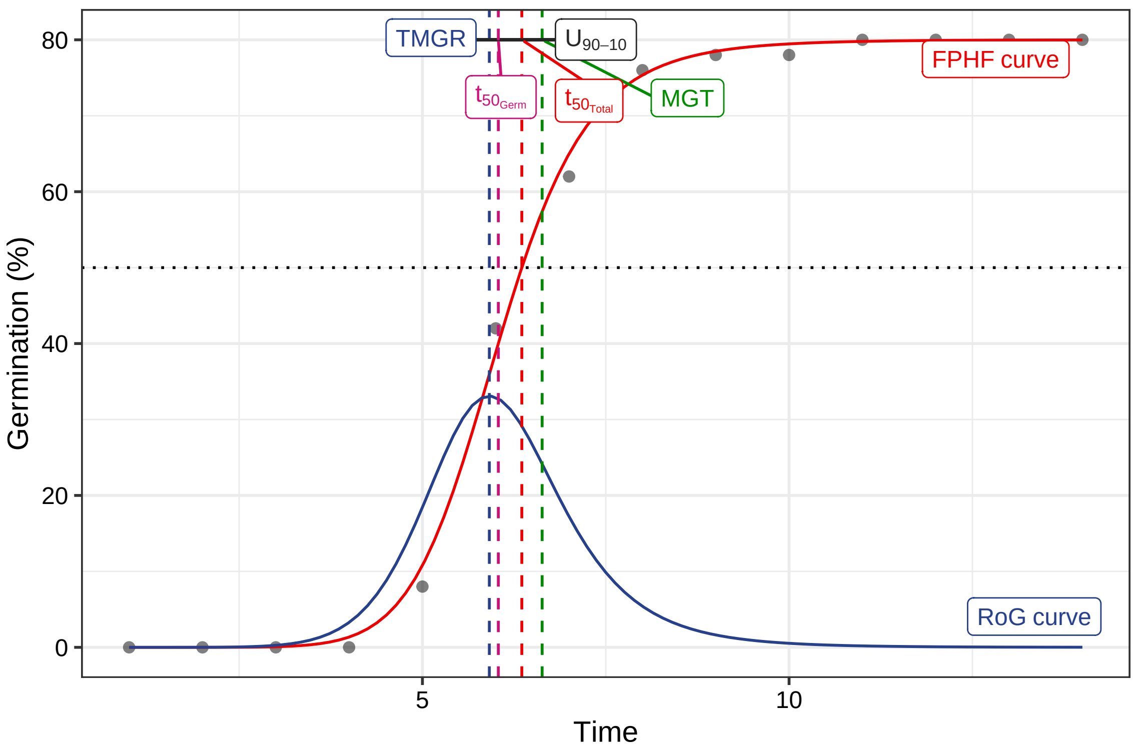

```
plot(fit2, rog = FALSE, t50.total = FALSE, t50.germ = FALSE,
     tmgr = FALSE, mgt = FALSE, uniformity = FALSE)
```




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

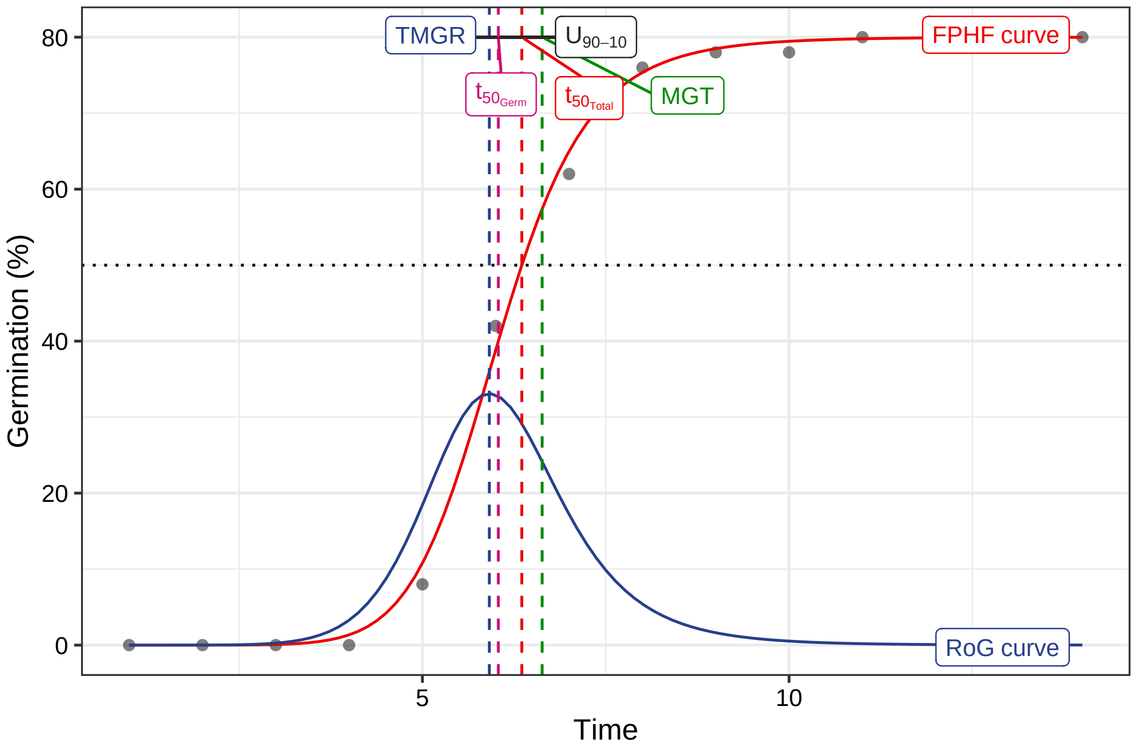
```
Warning in geom_segment(aes(x = UfmMin, xend = UfmMax, y = ypos2, yend = ypos2), : All aesthetics have l
```

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




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

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




## Wrapper functions

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

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

```r
data(gcdata)

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

```
   Genotype Rep Day01 Day02 Day03 Day04 Day05 Day06 Day07 Day08 Day09 Day10 Day11 Day12 Day13 Day14
1        G1   1     0     0     0     0     4    17    10     7     1     0     1     0     0     0
2        G2   1     0     0     0     1     3    15    13     6     2     1     0     1     0     0
3        G3   1     0     0     0     2     3    18     9     8     2     1     1     1     0     0
4        G4   1     0     0     0     0     4    19    12     6     2     1     1     1     0     0
5        G5   1     0     0     0     0     5    20    12     8     1     0     0     1     1     0
6        G1   2     0     0     0     0     3    21    11     7     1     1     1     1     0     0
7        G2   2     0     0     0     0     4    18    11     7     1     0     1     0     0     0
8        G3   2     0     0     0     1     3    14    12     6     2     1     0     1     0     0
9        G4   2     0     0     0     1     3    19    10     8     1     1     1     1     0     0
10       G5   2     0     0     0     0     4    18    13     6     2     1     0     1     0     0
11       G1   3     0     0     0     0     5    21    11     8     1     0     0     1     1     0
```

```
12      G2   3    0    0    0    0    3   20   10    7    1    1    1    1    0    0
13      G3   3    0    0    0    0    4   19   12    8    1    1    0    1    1    0
14      G4   3    0    0    0    0    3   21   11    6    1    0    1    1    0    0
15      G5   3    0    0    0    0    4   17   10    8    1    1    1    0    0    0
   Total Seeds GermPercent PeakGermPercent FirstGermTime LastGermTime PeakGermTime TimeSpreadGerm
1           50    80.00000        34.00000             5           11            6              6
2           51    82.35294        29.41176             4           12            6              8
3           48    93.75000        37.50000             4           12            6              8
4           51    90.19608        37.25490             5           12            6              7
5           50    96.00000        40.00000             5           13            6              8
6           49    93.87755        42.85714             5           12            6              7
7           48    87.50000        37.50000             5           11            6              6
8           47    85.10638        29.78723             4           12            6              8
9           52    86.53846        36.53846             4           12            6              8
10          50    90.00000        36.00000             5           12            6              7
11          51    94.11765        41.17647             5           13            6              8
12          51    86.27451        39.21569             5           12            6              7
13          49    95.91837        38.77551             5           13            6              8
14          48    91.66667        43.75000             5           12            6              7
15          48    87.50000        35.41667             5           11            6              6
   t50_Coolbear t50_Farooq MeanGermTime VarGermTime SEGermTime CVGermTime MeanGermRate  VarGermRate
1      5.970588   5.941176     6.700000    1.446154  0.1901416  0.1794868    0.1492537 0.0007176543
2      6.192308   6.153846     6.857143    2.027875  0.2197333  0.2076717    0.1458333 0.0009172090
3      6.333333   5.972222     6.866667    2.572727  0.2391061  0.2335882    0.1456311 0.0011572039
4      6.041667   6.225806     6.891304    2.187923  0.2180907  0.2146419    0.1451104 0.0009701218
5      5.975000   5.950000     6.812500    2.368351  0.2221275  0.2259002    0.1467890 0.0010995627
6      5.976190   5.952381     6.869565    2.071498  0.2122088  0.2095140    0.1455696 0.0009301809
7      5.972222   5.944444     6.690476    1.389663  0.1818989  0.1761967    0.1494662 0.0006935558
8      6.208333   6.166667     6.875000    2.112179  0.2297923  0.2113940    0.1454545 0.0009454531
9      6.310345   5.973684     6.866667    2.300000  0.2260777  0.2208604    0.1456311 0.0010345321
10     6.076923   6.038462     6.822222    1.831313  0.2017321  0.1983606    0.1465798 0.0008453940
11     5.928571   5.904762     6.791667    2.381206  0.2227295  0.2272072    0.1472393 0.0011191581
12     5.975000   5.950000     6.886364    2.149577  0.2210295  0.2129053    0.1452145 0.0009558577
13     6.083333   6.041667     6.936170    2.539315  0.2324392  0.2297410    0.1441718 0.0010970785
14     5.928571   5.904762     6.772727    1.900634  0.2078370  0.2035568    0.1476510 0.0009033254
15     6.050000   6.259259     6.809524    1.670151  0.1994129  0.1897847    0.1468531 0.0007767634
    SEGermRate      CVG GermRateRecip_Coolbear GermRateRecip_Farooq GermSpeed_Count GermSpeed_Percent
1  0.004235724 14.92537              0.1674877            0.1683168        6.138925          12.27785
2  0.004673148 14.58333              0.1614907            0.1625000        6.362698          12.47588
3  0.005071059 14.56311              0.1578947            0.1674419        6.882179          14.33787
4  0.004592342 14.51104              0.1655172            0.1606218        6.927417          13.58317
5  0.004786184 14.67890              0.1673640            0.1680672        7.318987          14.63797
6  0.004496813 14.55696              0.1673307            0.1680000        6.931782          14.14649
7  0.004063648 14.94662              0.1674419            0.1682243        6.448449          13.43427
8  0.004861721 14.54545              0.1610738            0.1621622        6.053175          12.87909
9  0.004794747 14.56311              0.1584699            0.1674009        6.830592          13.13575
10 0.004334343 14.65798              0.1645570            0.1656051        6.812698          13.62540
11 0.004828643 14.72393              0.1686747            0.1693548        7.342796          14.39764
12 0.004660905 14.52145              0.1673640            0.1680672        6.622258          12.98482
13 0.004831366 14.41718              0.1643836            0.1655172        7.052320          14.39249
14 0.004531018 14.76510              0.1686747            0.1693548        6.706782          13.97246
15 0.004300508 14.68531              0.1652893            0.1597633        6.363925          13.25818
   GermSpeedAccumulated_Count GermSpeedAccumulated_Percent GermSpeedCorrected_Normal
1                    34.61567                     69.23134                 0.1534731
```

```
2                    35.54058                     69.68741                 0.1514928
3                    38.29725                     79.78594                 0.1529373
4                    38.68453                     75.85202                 0.1505960
5                    41.00786                     82.01571                 0.1524789
6                    38.77620                     79.13509                 0.1506909
7                    36.38546                     75.80304                 0.1535345
8                    33.77079                     71.85275                 0.1513294
9                    38.11511                     73.29829                 0.1517909
10                   38.19527                     76.39054                 0.1513933
11                   41.17452                     80.73436                 0.1529749
12                   37.00640                     72.56158                 0.1505059
13                   39.29399                     80.19182                 0.1500494
14                   37.69490                     78.53103                 0.1524269
15                   35.69697                     74.36868                 0.1515220
   GermSpeedCorrected_Accumulated WeightGermPercent MeanGermPercent MeanGermNumber TimsonsIndex
1                       0.8653917          47.42857        5.714286       2.857143     8.000000
2                       0.8462043          47.89916        5.882353       3.000000     9.803922
3                       0.8510501          54.46429        6.696429       3.214286    14.583333
4                       0.8409680          52.24090        6.442577       3.285714     7.843137
5                       0.8543303          56.14286        6.857143       3.428571    10.000000
6                       0.8429608          54.51895        6.705539       3.285714     6.122449
7                       0.8663205          51.93452        6.250000       3.000000     8.333333
8                       0.8442698          49.39210        6.079027       2.857143    10.638298
9                       0.8470024          50.27473        6.181319       3.214286     9.615385
10                      0.8487837          52.57143        6.428571       3.214286     8.000000
11                      0.8578026          55.18207        6.722689       3.428571     9.803922
12                      0.8410547          50.00000        6.162465       3.142857     5.882353
13                      0.8360424          55.24781        6.851312       3.357143     8.163265
14                      0.8567022          53.86905        6.547619       3.142857     6.250000
15                      0.8499278          51.19048        6.250000       3.000000     8.333333
   TimsonsIndex_Labouriau TimsonsIndex_KhanUngar GermRateGeorge GermIndex GermIndex_mod
1                    1.00              0.5714286              4  5.840000      7.300000
2                    1.25              0.7002801              5  5.882353      7.142857
3                    1.40              1.0416667              7  6.687500      7.133333
4                    1.00              0.5602241              4  6.411765      7.108696
5                    1.00              0.7142857              5  6.900000      7.187500
6                    1.00              0.4373178              3  6.693878      7.130435
7                    1.00              0.5952381              4  6.395833      7.309524
8                    1.25              0.7598784              5  6.063830      7.125000
9                    1.25              0.6868132              5  6.173077      7.133333
10                   1.00              0.5714286              4  6.460000      7.177778
11                   1.00              0.7002801              5  6.784314      7.208333
12                   1.00              0.4201681              3  6.137255      7.113636
13                   1.00              0.5830904              4  6.775510      7.063830
14                   1.00              0.4464286              3  6.625000      7.227273
15                   1.00              0.5952381              4  6.291667      7.190476
   EmergenceRateIndex_SG EmergenceRateIndex_SG_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
1                     8.375000  9.500000          54.28571     57.93890               54.28571
2                     8.326531  9.313725          54.78662     52.58713               54.78662
3                     7.324444 10.416667          69.75446     68.62289               69.75446
4                     7.640359 10.049020          64.74158     70.43331               64.74158
5                     7.096354 11.250000          77.14286     80.16914               77.14286
6                     7.317580 10.714286          71.84506     76.51983               71.84506
7                     7.646259 10.416667          65.10417     69.41325               65.10417
8                     8.078125  9.574468          58.20345     56.00669               58.20345
9                     7.934815  9.855769          60.92165     58.13477               60.92165
10                    7.580247 10.250000          65.89286     70.91875               65.89286
11                    7.216146 11.029412          74.14731     77.39782               74.14731
12                    7.981921  9.803922          60.41632     64.44988               60.41632
13                    7.231326 10.969388          75.15470     78.16335               75.15470
14                    7.388430 10.677083          69.90947     74.40140               69.90947
15                    7.782313 10.156250          63.47656     67.62031               63.47656
   GermValue_DP_mod    CUGerm GermSynchrony GermUncertainty
1          39.56076 0.7092199     0.2666667        2.062987
2          40.99260 0.5051546     0.2346109        2.321514
3          53.42809 0.3975265     0.2242424        2.462012
4          48.86825 0.4672113     0.2502415        2.279215
5          56.23935 0.4312184     0.2606383        2.146051
6          53.06435 0.4934701     0.2792271        2.160545
7          47.37690 0.7371500     0.2729384        2.040796
8          43.67948 0.4855842     0.2256410        2.357249
9          45.30801 0.4446640     0.2494949        2.321080
10         49.10820 0.5584666     0.2555556        2.187983
11         54.27520 0.4288905     0.2686170        2.128670
12         44.71582 0.4760266     0.2737844        2.185245
13         54.94192 0.4023679     0.2506938        2.241181
14         51.41913 0.5383760     0.2991543        2.037680
15         46.48043 0.6133519     0.2497096        2.185028
```

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

```r
data(gcdata)

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

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

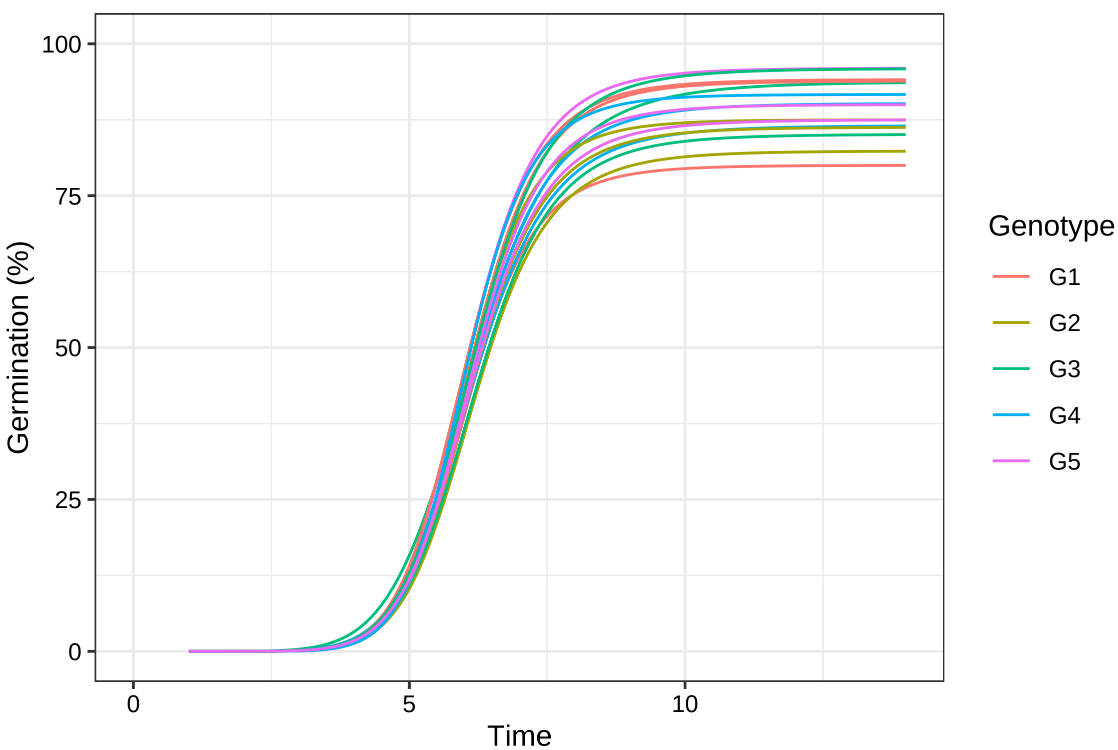
```
                         tmax = 20, tries = 3, umax = 90, umin = 10)
```

```
   Genotype Rep Day01 Day02 Day03 Day04 Day05 Day06 Day07 Day08 Day09 Day10 Day11 Day12 Day13 Day14
1        G1   1     0     0     0     0     4    17    10     7     1     0     1     0     0     0
2        G2   1     0     0     0     1     3    15    13     6     2     1     0     1     0     0
3        G3   1     0     0     0     2     3    18     9     8     2     1     1     1     0     0
4        G4   1     0     0     0     0     4    19    12     6     2     1     1     1     0     0
5        G5   1     0     0     0     0     5    20    12     8     1     0     0     1     1     0
6        G1   2     0     0     0     0     3    21    11     7     1     1     1     1     0     0
7        G2   2     0     0     0     0     4    18    11     7     1     0     1     0     0     0
8        G3   2     0     0     0     1     3    14    12     6     2     1     0     1     0     0
9        G4   2     0     0     0     1     3    19    10     8     1     1     1     1     0     0
10       G5   2     0     0     0     0     4    18    13     6     2     1     0     1     0     0
11       G1   3     0     0     0     0     5    21    11     8     1     0     0     1     1     0
12       G2   3     0     0     0     0     3    20    10     7     1     1     1     1     0     0
13       G3   3     0     0     0     0     4    19    12     8     1     1     0     1     1     0
14       G4   3     0     0     0     0     3    21    11     6     1     0     1     1     0     0
15       G5   3     0     0     0     0     4    17    10     8     1     1     1     0     0     0
   Total Seeds        a         b        c y0 lag   Dlag50 t50.total t10.total t60.total t50.Germinated
1           50 80.00000  9.881937 6.034954  0   0 6.034954  6.355121  4.956264  6.744598       6.034954
2           51 82.35294  9.227666 6.175193  0   0 6.175193  6.473490  4.983236  6.872603       6.175193
3           48 93.75000  7.793051 6.138110  0   0 6.138110  6.244191  4.673022  6.608438       6.138110
4           51 90.19608  8.925655 6.125173  0   0 6.125173  6.276794  4.850875  6.614968       6.125173
5           50 96.00000  9.419181 6.049642  0   0 6.049642  6.103433  4.814125  6.386789       6.049642
6           49 93.87755  9.450149 6.097415  0   0 6.097415  6.182279  4.868632  6.477599       6.097415
7           48 87.50000 10.172459 6.029851  0   0 6.029851  6.202812  4.930422  6.510495       6.029851
8           47 85.10638  8.940696 6.189774  0   0 6.189774  6.439510  4.940057  6.823299       6.189774
9           52 86.53846  8.617391 6.125122  0   0 6.125122  6.352172  4.836658  6.733276       6.125122
10          50 90.00000  9.608844 6.109504  0   0 6.109504  6.253043  4.920629  6.566506       6.109504
11          51 94.11765  9.400212 6.018760  0   0 6.018760  6.099435  4.798627  6.391291       6.018760
12          51 86.27451  9.162526 6.108452  0   0 6.108452  6.326184  4.893596  6.684526       6.108452
13          49 95.91837  8.995210 6.149012  0   0 6.149012  6.207501  4.841308  6.509954       6.149012
14          48 91.66667 10.391845 6.015910  0   0 6.015910  6.122389  4.915140  6.397491       6.015910
15          48 87.50000  9.136744 6.121579  0   0 6.121579  6.317392  4.892502  6.667247       6.121579
   t10.Germinated t60.Germinated Uniformity_90 Uniformity_10 Uniformity     TMGR      AUC      MGT Skewn
1        4.831807       6.287724      7.537690      4.831807   2.705882 5.912194 1108.976 6.632252 1.098
2        4.866755       6.452582      7.835407      4.866755   2.968652 6.031282 1128.559 6.784407 1.098
3        4.630062       6.465924      8.137342      4.630062   3.507280 5.938180 1283.693 6.772742 1.103
4        4.788597       6.409838      7.834810      4.788597   3.046213 5.972686 1239.887 6.739666 1.100
5        4.790946       6.315746      7.639028      4.790946   2.848083 5.914289 1328.328 6.654981 1.100
6        4.832471       6.364722      7.693469      4.832471   2.860997 5.961879 1294.463 6.702473 1.099
7        4.858476       6.275050      7.483643      4.858476   2.625166 5.914057 1213.908 6.622417 1.098
8        4.841105       6.476945      7.914163      4.841105   3.073058 6.036192 1164.346 6.804000 1.099
9        4.746573       6.420208      7.904041      4.746573   3.157468 5.961631 1188.793 6.745241 1.101
10       4.860681       6.372823      7.679177      4.860681   2.818496 5.978115 1240.227 6.711900 1.098
11       4.764246       6.284051      7.603611      4.764246   2.839365 5.883557 1305.200 6.624248 1.100
12       4.806013       6.384836      7.763854      4.806013   2.957841 5.964080 1188.021 6.718639 1.099
13       4.816393       6.432524      7.850345      4.816393   3.033952 5.998270 1316.407 6.762274 1.099
14       4.869398       6.255276      7.432372      4.869398   2.562974 5.905180 1273.385 6.604967 1.097
15       4.813083       6.399357      7.785806      4.813083   2.972723 5.976087 1203.664 6.732266 1.099
           msg    sigma       finTol    logLik      AIC      BIC  deviance df.residual nobs
1  #1. success  1.615220 7.105427e-14 -25.49868 56.99736 58.91453  31.30723          12   14
2  #1. success  1.115372 2.309264e-14 -20.31471 46.62943 48.54660  14.92865          12   14
3  #1. success  2.432704 9.947598e-14 -31.23213 68.46426 70.38143  71.01658          12   14
```

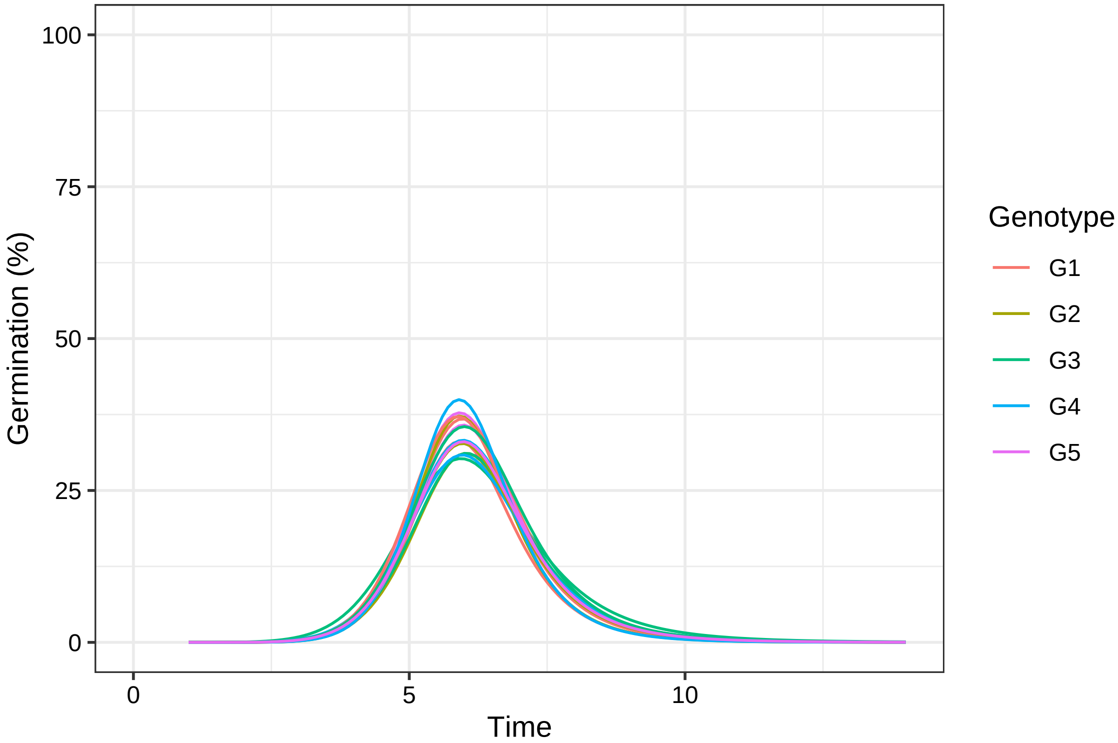
```
4  #1. success  2.396582 5.684342e-14 -31.02269 68.04538 69.96256  68.92324          12    14
5  #1. success  2.399662 1.094236e-12 -31.04067 68.08135 69.99852  69.10052          12    14
6  #1. success  3.034962 1.563194e-13 -34.32887 74.65774 76.57491 110.53195          12    14
7  #1. success  1.663019 1.421085e-13 -25.90697 57.81395 59.73112  33.18760          12    14
8  #1. success  1.120704 4.327205e-12 -20.38149 46.76298 48.68015  15.07174          12    14
9  #1. success  2.429960 7.958079e-13 -31.21633 68.43266 70.34984  70.85647          12    14
10 #1. success  1.686656 8.142820e-12 -26.10456 58.20911 60.12629  34.13771          12    14
11 #1. success  2.628113 1.989520e-13 -32.31381 70.62762 72.54479  82.88372          12    14
12 #1. success  2.878146 1.151079e-12 -33.58613 73.17227 75.08944  99.40469          12    14
13 #1. success  2.604588 2.984279e-13 -32.18793 70.37586 72.29303  81.40654          12    14
14 #1. success  2.764756 9.805490e-13 -33.02342 72.04684 73.96401  91.72652          12    14
15 #1. success  1.954008 8.739676e-13 -28.16444 62.32888 64.24606  45.81777          12    14
```

Multiple fitted curves generated in batch can also be plotted.

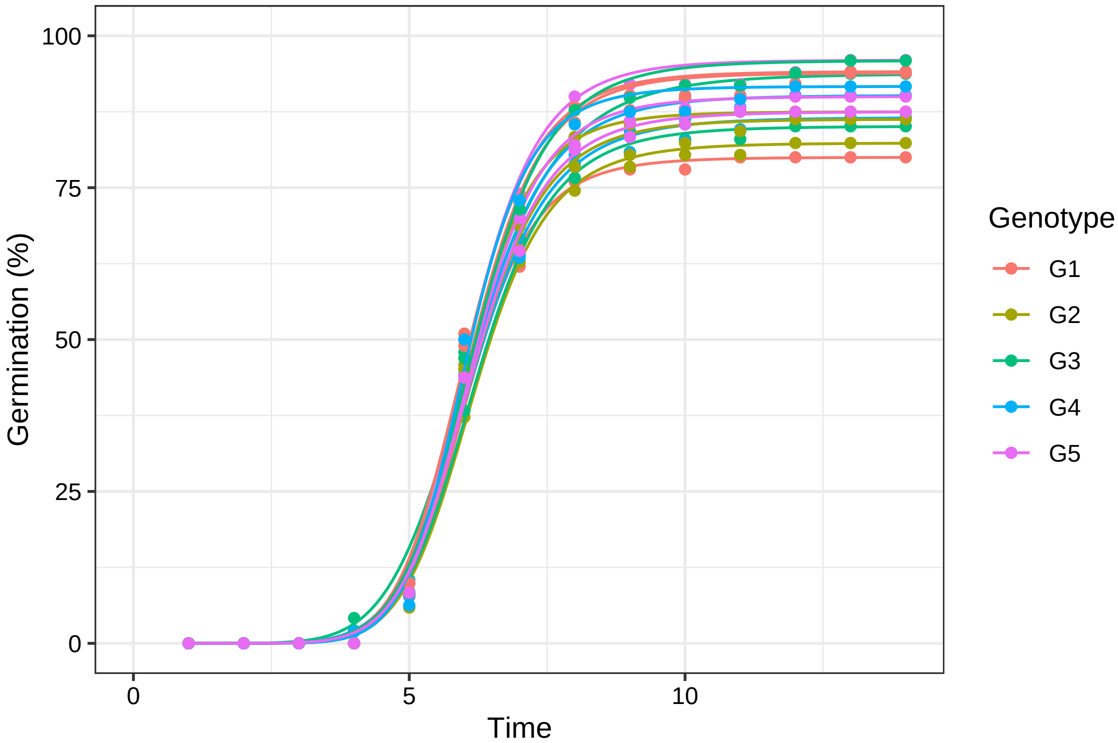
```r
data(gcdata)

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

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

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



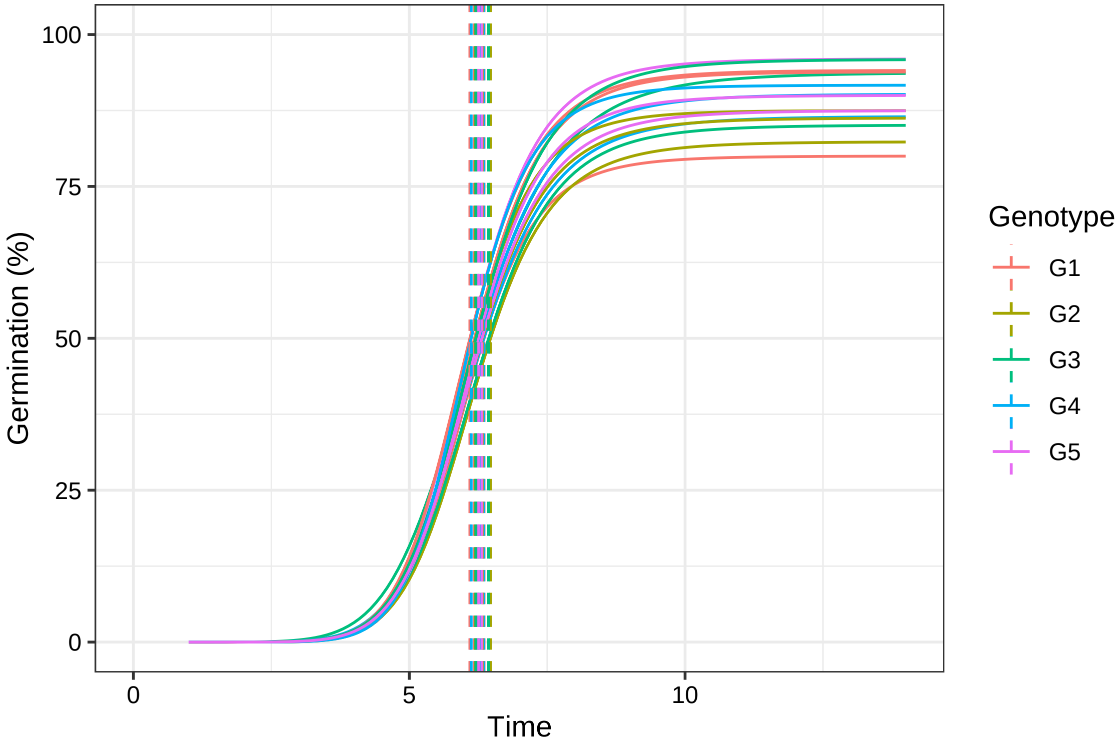
```r
# Plot ROG curves
plot(fits, rog = TRUE, group.col = "Genotype")
```



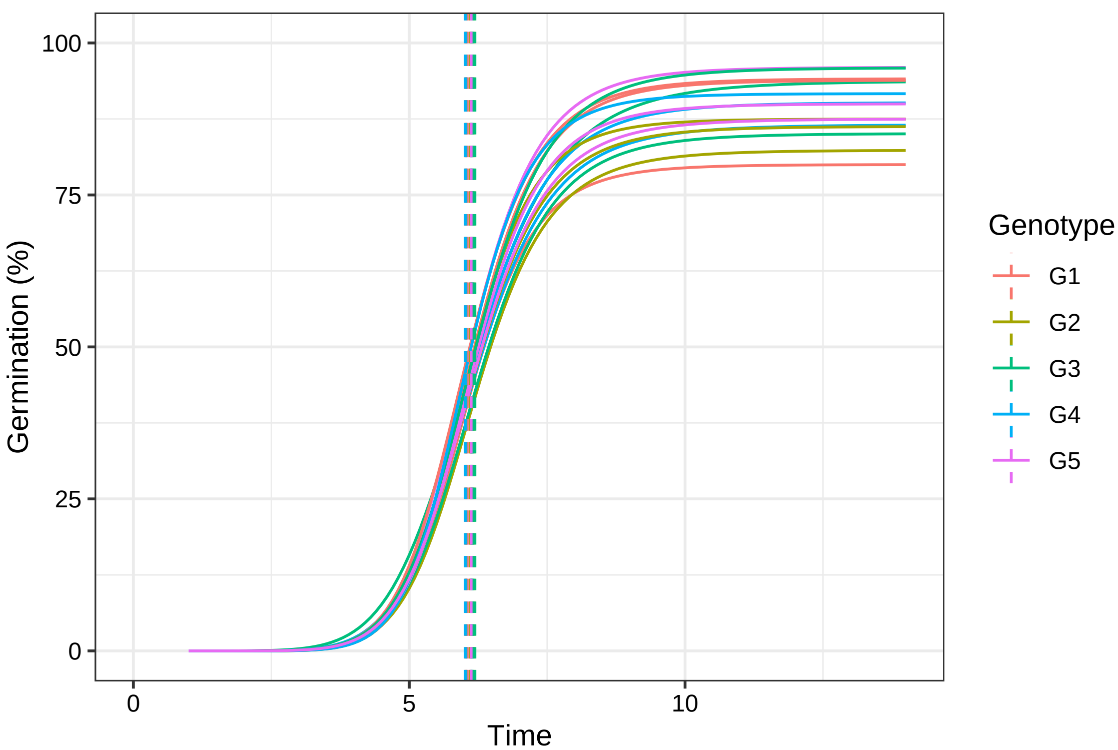

```r
# Plot FPHF curves with points
plot(fits, group.col = "Genotype", show.points = TRUE)
```



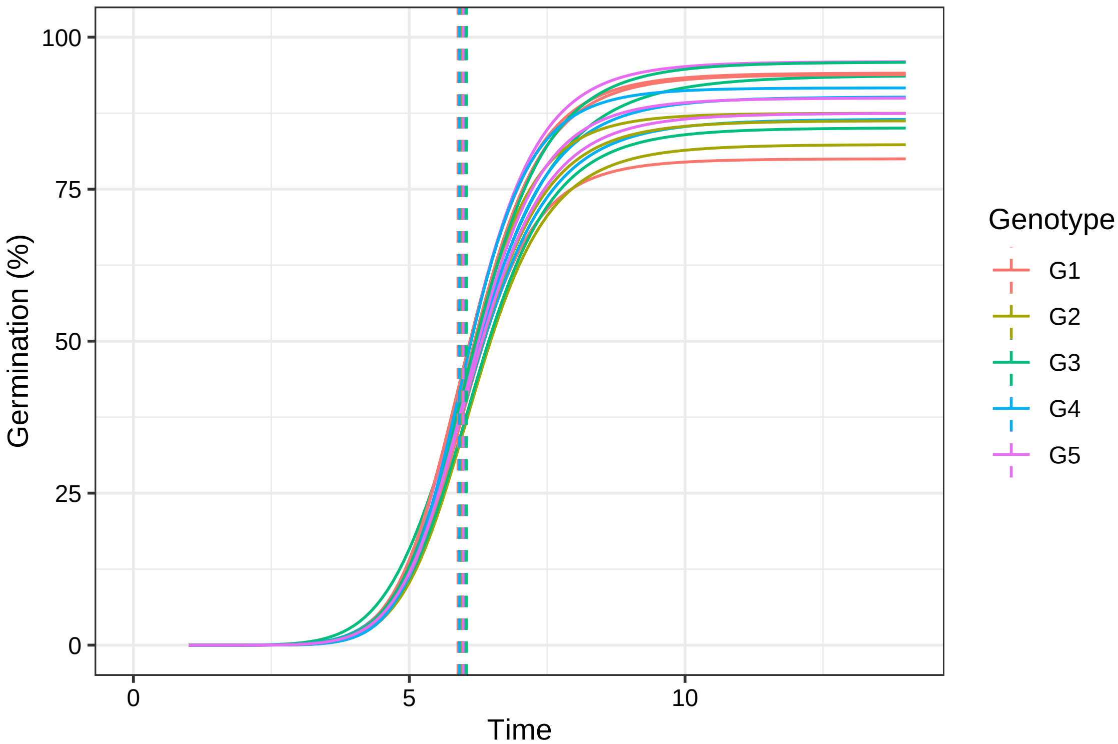
```
# Plot FPHF curves with annotations
plot(fits, group.col = "Genotype", annotate = "t50.total")
```



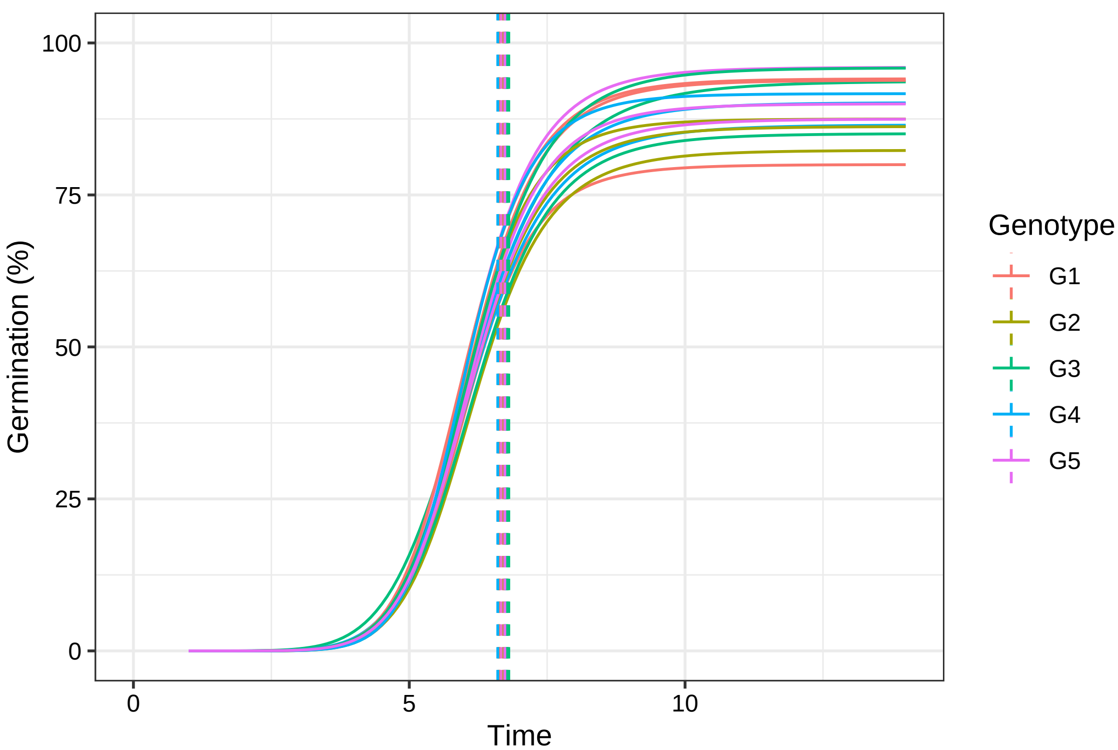

```
plot(fits, group.col = "Genotype", annotate = "t50.germ")
```



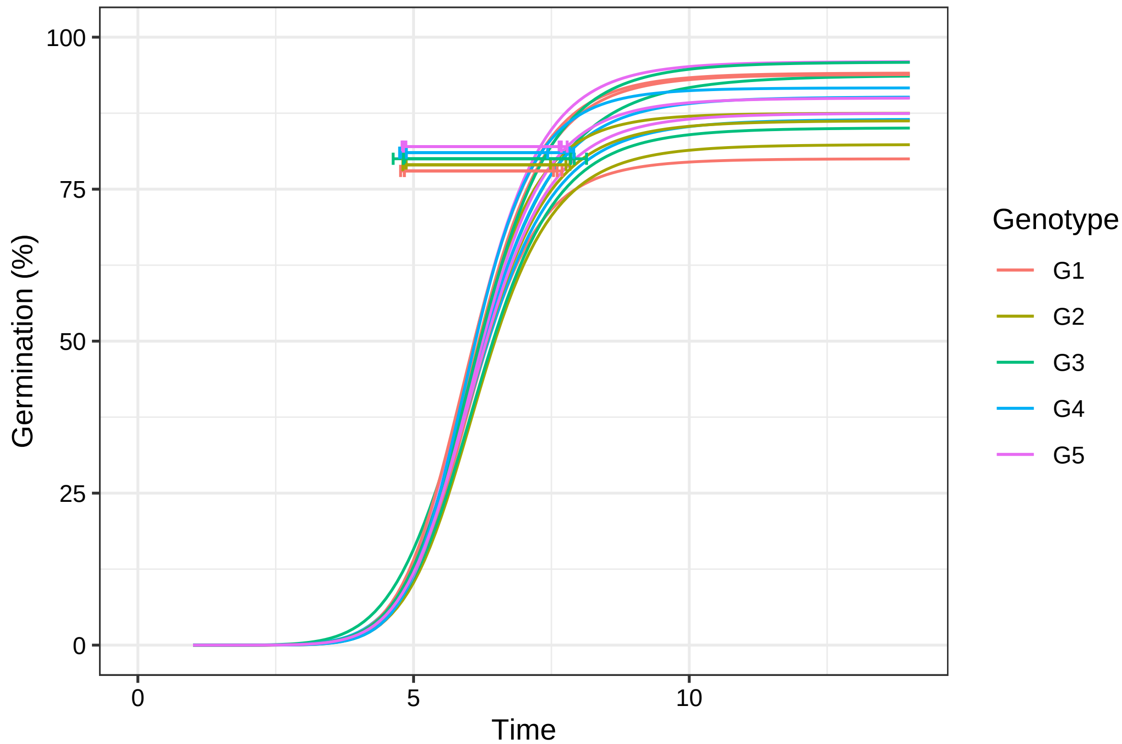

```
plot(fits, group.col = "Genotype", annotate = "tmgr")
```



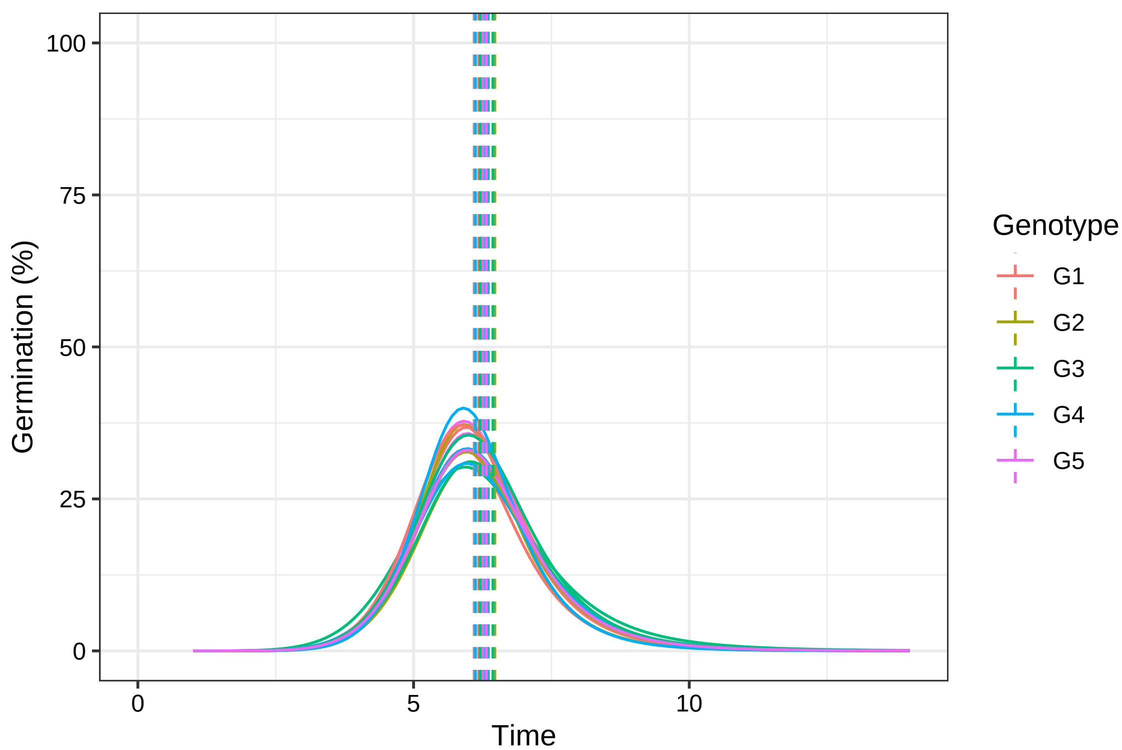

```r
plot(fits, group.col = "Genotype", annotate = "mgt")
```



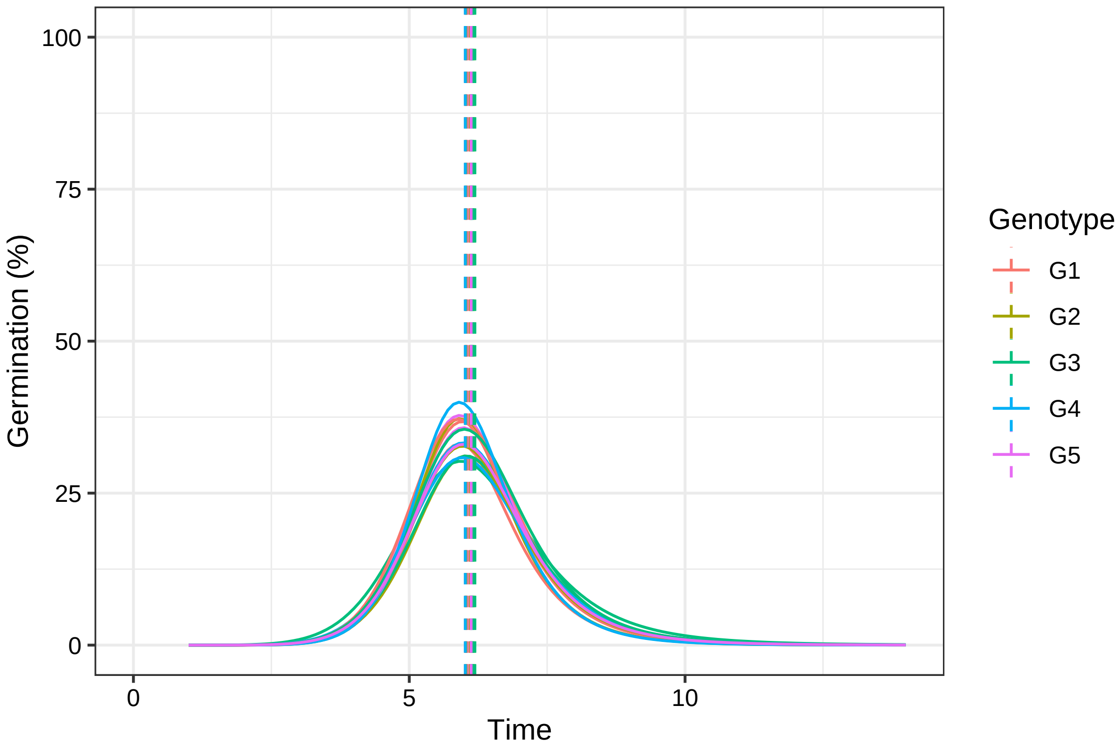

```r
plot(fits, group.col = "Genotype", annotate = "uniformity")
```



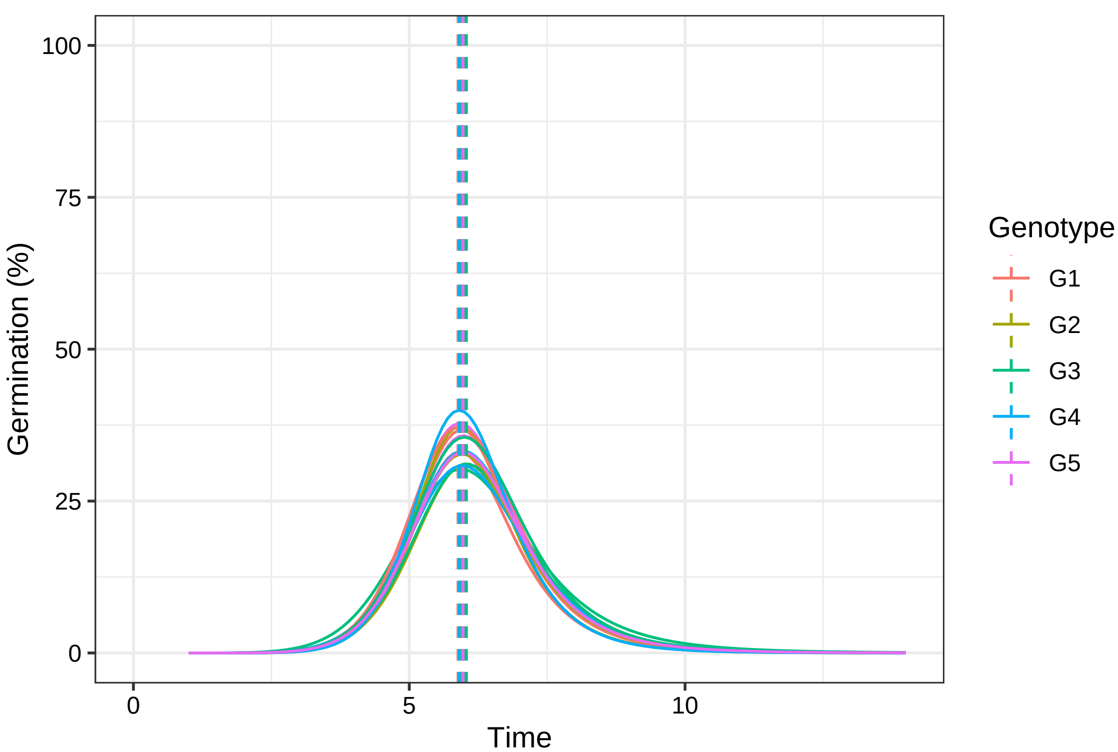

```r
# Plot ROG curves with annotations
plot(fits, rog = TRUE, group.col = "Genotype", annotate = "t50.total")
```



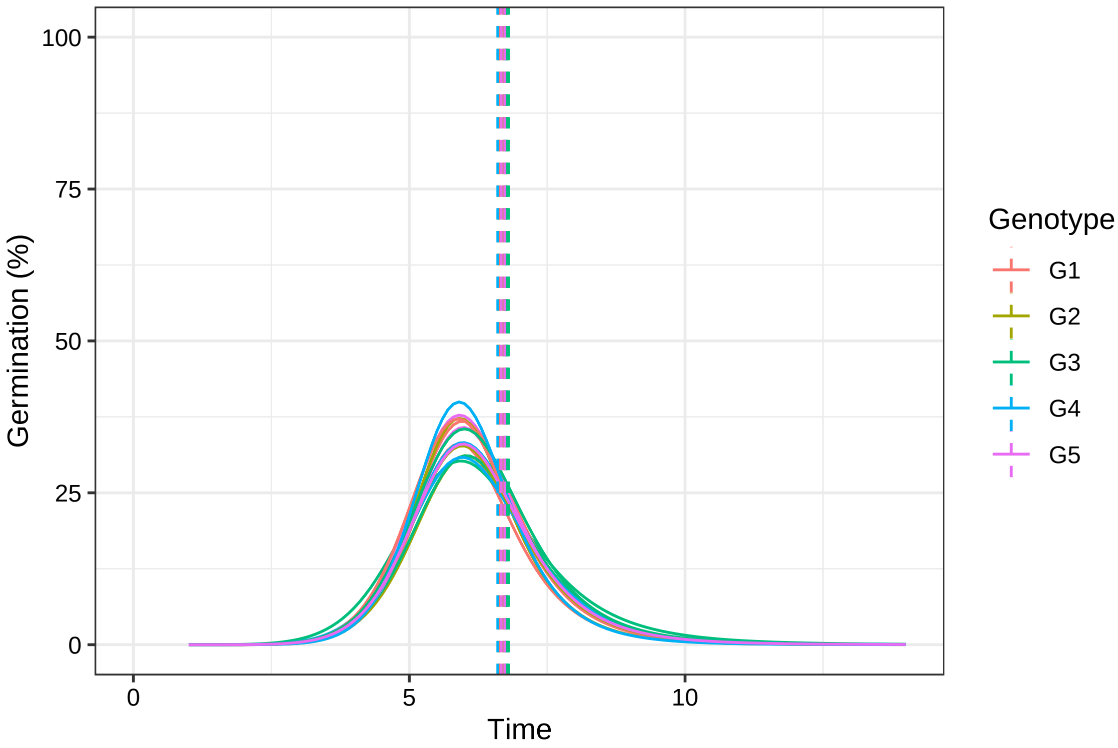

```r
plot(fits, rog = TRUE, group.col = "Genotype", annotate = "t50.germ")
```



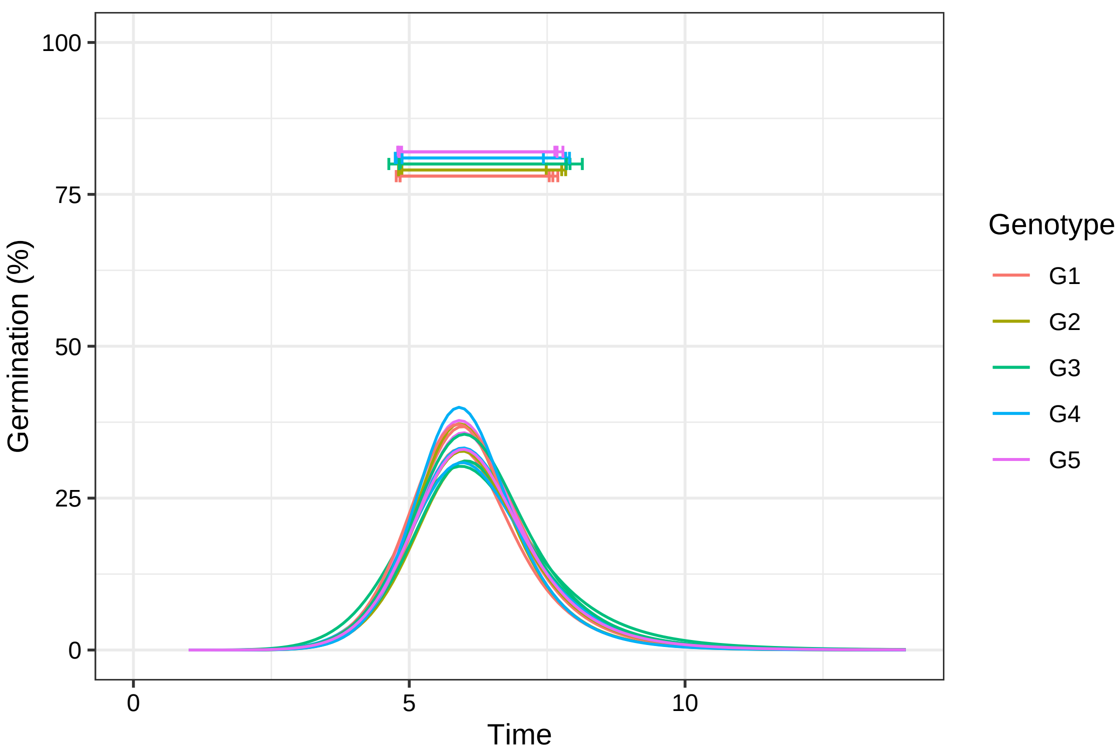

```
plot(fits, rog = TRUE, group.col = "Genotype", annotate = "tmgr")
```




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



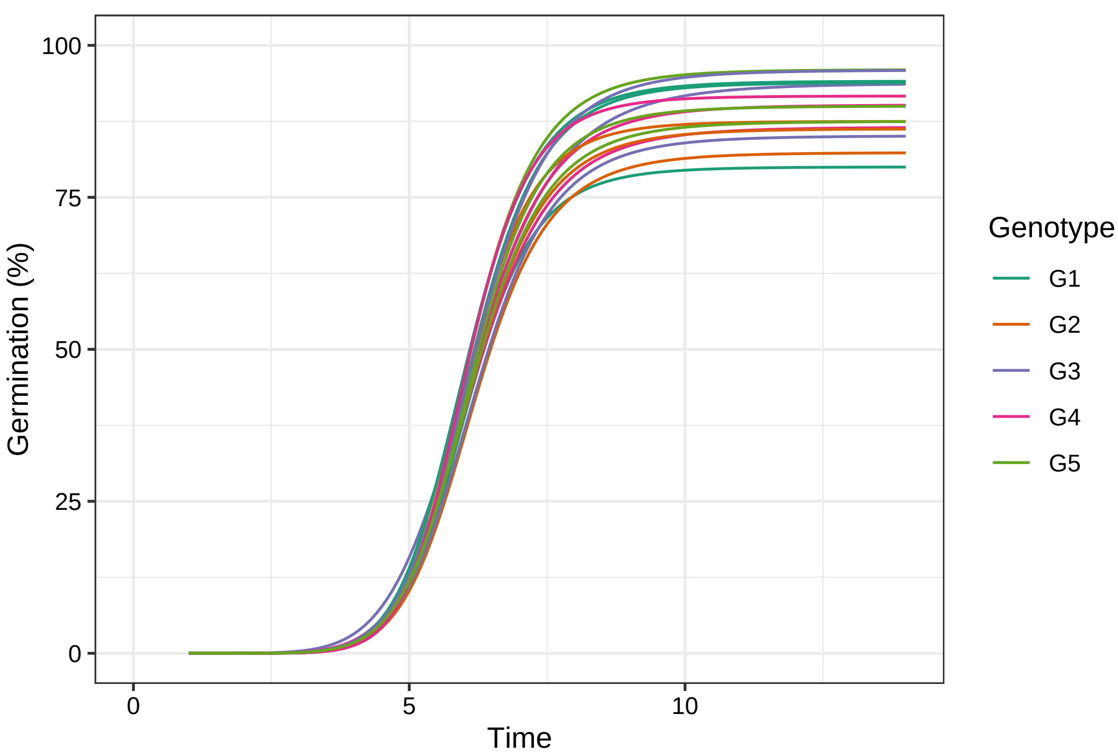

```r
plot(fits, rog = TRUE, group.col = "Genotype", annotate = "uniformity")
```



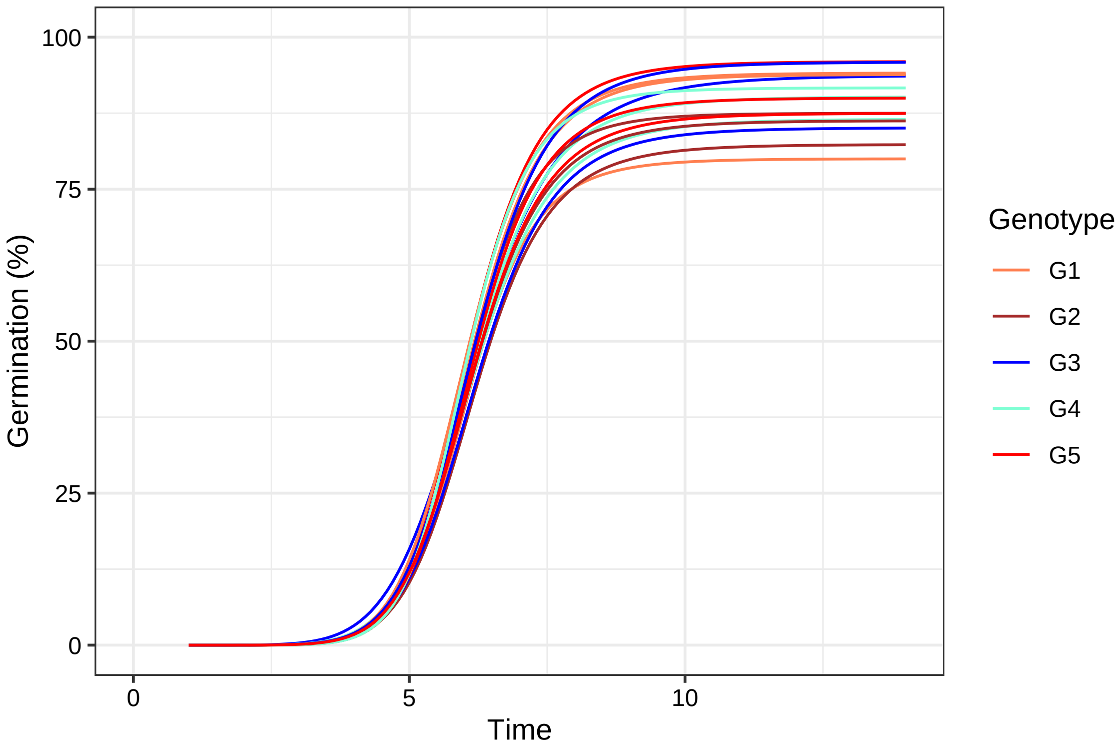

```r
# Change colour of curves using ggplot2 options
library(ggplot2)
```

```
Posit Community (formerly RStudio Community) is a great place to get help:
https://forum.posit.co/c/tidyverse
```

```
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 (2025).
  germinationmetrics: Seed Germination Indices and 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 Sri
    note = {R package version 0.1.8.9000 https://aravind-j.github.io/germinationmetrics/ https://CRAN.R
    year = {2025},
  }

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

## Session Info

```r
sessionInfo()
```

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

Matrix products: default
```

```
 LAPACK version 3.12.1

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

time zone: Asia/Calcutta
tzcode source: internal

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

other attached packages:
[1] germinationmetrics_0.1.8.9000 ggplot2_4.0.1                 readxl_1.4.5                 
[4] RCurl_1.98-1.17               testthat_3.3.1               

loaded via a namespace (and not attached):
 [1] gtable_0.3.6       xfun_0.54          devtools_2.4.6     remotes_2.5.0.9000 processx_3.8.6    
 [6] ggrepel_0.9.6      rJava_1.0-11       lattice_0.22-7     callr_3.7.6        mathjaxr_2.0-0    
[11] bitops_1.0-9       vctrs_0.6.5        tools_4.6.0        Rdpack_2.6.4       ps_1.9.1          
[16] generics_0.1.4     stats4_4.6.0       curl_7.0.0         parallel_4.6.0     tibble_3.3.0      
[21] pkgconfig_2.0.3    gslnls_1.4.2       Matrix_1.7-4       data.table_1.17.8  RColorBrewer_1.1-3
[26] S7_0.2.1           desc_1.4.3         lifecycle_1.0.4    compiler_4.6.0     farver_2.1.2      
[31] stringr_1.6.0      brio_1.1.5         tinytex_0.58       htmltools_0.5.9    usethis_3.2.1     
[36] yaml_2.3.12        pillar_1.11.1      tidyr_1.3.1        ellipsis_0.3.2     rsconnect_1.7.0   
[41] cachem_1.1.0       sessioninfo_1.2.3  tidyselect_1.2.1   digest_0.6.39      stringi_1.8.7     
[46] reshape2_1.4.5     pander_0.6.6       dplyr_1.1.4        purrr_1.2.0        labeling_0.4.3    
[51] rprojroot_2.1.1    fastmap_1.2.0      grid_4.6.0         cli_3.6.5          magrittr_2.0.4    
[56] XML_3.99-0.20      dichromat_2.0-0.1  pkgbuild_1.4.8     broom_1.0.11       withr_3.0.2       
[61] scales_1.4.0       backports_1.5.0    httr_1.4.7         roxygen2_7.3.3     rmarkdown_2.30    
[66] cellranger_1.1.0   memoise_2.0.1      evaluate_1.0.5     knitr_1.50         rbibutils_2.4     
[71] rlang_1.1.6        Rcpp_1.1.0.8.1     glue_1.8.0         xml2_1.5.1         pkgload_1.4.1     
[76] rstudioapi_0.17.1  R6_2.6.1           plyr_1.8.9         fs_1.6.6          
```

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