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)
```

Germination count data

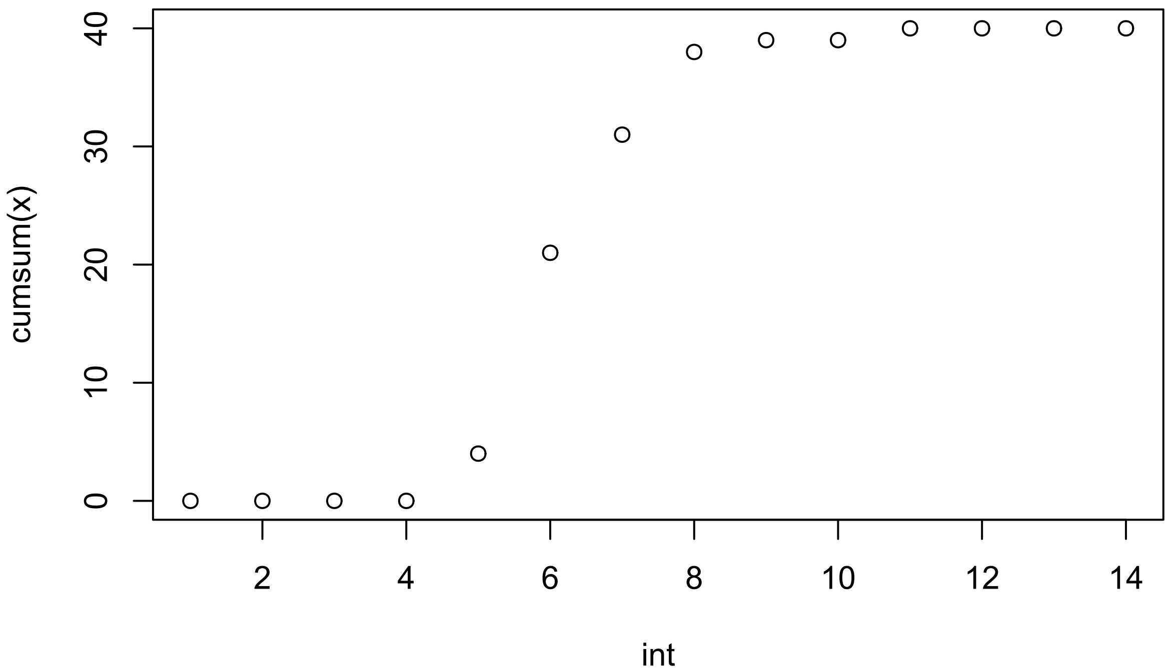
Typically in a germination test, the germination count data of a fixed number of seeds is recorded at regular intervals for a definite period of time or until all the seeds have germinated. These germination count data can be either partial or cumulative (Table 1).

Table 1 : A typical germination count data.

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

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

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

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

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



Single-value germination indices

The details about the single-value germination indices implemented in `germinationmetrics` are described in Table 2.

Table 2 : Single-value germination indices implemented in `germinationmetrics`.

Germination index	function	Details	Unit	Measures	Reference
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)
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)	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)	time	Germination time	Edwards (1932)
Time spread of germination	`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); Kader (2005)
Peak period of germination or Modal time of germination	`PeakGermTime`	It is the time in which highest frequency of germinated seeds are observed and need not be unique.	time	Germination time	Ranal and Santana (2006)
Median germination time (Coolbear)	`t50`	It is the time to reach 50% of final/maximum germination. With argument method specified as `"coolbear"`, it is computed according to the formula by (Coolbear et al., 1984) as follows: $$t_{50} = T_i + \frac{(\frac{N+1}{2} - N_i)(T_j - T_i)}{N_j - N_i}$$ Where, t_{50} is the median germination time, N is the final number of germinated seeds and N_i and N_j are the total number of seeds germinated in adjacent counts at time T_i and T_j respectively, when $N_i < \frac{N+1}{2} < N_j$.	time	Germination time	Coolbear et al. (1984)
Median germination time (Farooq)	`t50`	With argument method specified as `"farooq"`, it is computed according to the formula by (Coolbear et al., 1984) as follows: $$t_{50} = T_i + \frac{(\frac{N}{2} - N_i)(T_j - T_i)}{N_j - N_i}$$ Where, t_{50} is the median germination time, N is the final number of germinated seeds and N_i and N_j are the total number of seeds germinated in adjacent counts at time T_i and T_j respectively, when $N_i < \frac{N}{2} < N_j$.	time	Germination time	Farooq et al. (2005)

Germination index	function	Details	Unit	Measures	Reference
Mean germination time or Mean length of incubation time ($\overline{T}$)	`MeanGermTime`	It is the average length of time required for maximum germination of a seed lot and is estimated according to the following formula. $\overline{T} = \frac{\sum_{i=1}^{k} N_i T_i}{\sum_{i=1}^{k} N_i}$ Where, T_i is the time from the start of the experiment to the ith observation, N_i is the number of seeds germinated in the ith time (not the accumulated number, but the number correspondent to the ith observation) and k is the last time of germination. It is the inverse of mean germination rate ($\overline{V}$). $\overline{T} = \frac{1}{\overline{V}}$	time	Germination time	Edmond and Drapala (1958); Czabator (1962); Ellis and Roberts (1980) Labouriau (1983a); Ranal and Santana (2006)
Variance of germination time (s_{T}^{2})	`VarGermTime`	It is computed according to the following formula. $s_{T}^{2} = \frac{\sum_{i=1}^{k} N_i (T_i - \overline{T})^2}{\sum_{i=1}^{k} N_i - 1}$ Where, T_i is the time from the start of the experiment to the ith observation, N_i is the number of seeds germinated in the ith time (not the accumulated number, but the number correspondent to the ith observation) and k is the last time of germination.	time	Germination time	Labouriau (1983a); Ranal and Santana (2006)
Standard error of germination time ($s_{\overline{T}}$)	`SEGermTime`	It signifies the accuracy of the calculation of the mean germination time. It is estimated according to the following formula: $s_{\overline{T}} = \sqrt{\frac{s_{T}^{2}}{\sum_{i=1}^{k} N_i}}$ Where, N_i is the number of seeds germinated in the ith time (not the accumulated number, but the number correspondent to the ith observation) and k is the last time of germination.	time	Germination time	Labouriau (1983a); Ranal and Santana (2006)

Germination index	function	Details	Unit	Measures	Reference
Mean germination rate ($\overline{V}$)	`MeanGermRate`	It is computed according to the following formula: $$\overline{V} = \frac{\sum_{i=1}^{k} N_i}{\sum_{i=1}^{k} N_i T_i}$$ Where, T_i is the time from the start of the experiment to the ith observation, N_i is the number of seeds germinated in the ith time (not the accumulated number, but the number correspondent to the ith observation) and k is the last time of germination. It is the inverse of mean germination rate ($\overline{V}$). $$\overline{V} = \frac{1}{\overline{T}}$$	time^{-1}	Germination rate	Labouriau and Viladares (1976); Labouriau (1983b); Ranal and Santana (2006)
Coefficient of velocity/rate of germination or Kotowski's coefficient of velocity (CVG)	`CVG`	It is estimated according to the following formula. $$CVG = \frac{\sum_{i=1}^{k} N_i}{\sum_{i=1}^{k} N_i T_i} \times 100$$ $$CVG = \overline{V} \times 100$$ Where, T_i is the time from the start of the experiment to the ith observation, N_i is the number of seeds germinated in the ith time (not the accumulated number, but the number correspondent to the ith observation) and k is the last time of germination.	% day $^{-1}$	Germination rate	Kotowski (1926), Nichols and Heydecker (1968); Bewley and Black (1994); Labouriau (1983b); Scott et al. (1984)
Variance of germination rate (s_{V}^{2})	`VarGermRate`	It is calculated according to the following formula. $$s_{V}^{2} = \overline{V}^{4} \times s_{T}^{2}$$ Where, s_{T}^{2} is the variance of germination time.	time^{-2}	Germination rate	Labouriau (1983b); Ranal and Santana (2006)
Standard error of germination rate ($s_{\overline{V}}$)	`SEGermRate`	It is estimated according to the following formula. $$s_{\overline{V}} = \sqrt{\frac{s_{V}^{2}}{\sum_{i=1}^{k} N_i}}$$ Where, N_i is the number of seeds germinated in the ith time (not the accumulated number, but the number correspondent to the ith observation) and k is the last time of germination.	time^{-1}	Germination rate	Labouriau (1983b); Ranal and Santana (2006)
Germination rate as the reciprocal of the median time (v_{50})	`GermRateRecip`	It is the reciprocal of the median germination time (t_{50}). $$v_{50} = \frac{1}{t_{50}}$$	time^{-1}	Germination rate	Went (1957); Labouriau (1983b); Ranal and Santana (2006)

Germination index	function	Details	Unit	Measures	Reference
Speed of germination or Germination rate Index or Index of velocity of germination (Germination Index according to AOSA)	`GermSpeed`	It is the rate of germination in terms of the total number of seeds that germinate in a time interval. It is estimated as follows: $S = \frac{N_1}{T_1} + \frac{N_2}{T_2} + \frac{N_3}{T_3} + \cdots + \frac{N_n}{T_n}$ Where, N_1, N_2, N_3, $\cdots$, N_n are the number of germinated seeds observed at time (days or hours) T_1, T_2, T_3, $\cdots$, T_n after sowing. (Not accumulated/cumulative number, but the number of seeds that germinated at the specific time).	% time^{-1}	Mixed	Throneberry and Smith (1955); Maguire (1962); Kendrick and Frankland (1969); AOSA (1983); Khandakar and Bradbeer (1983); Bradbeer (1988); Wardle et al. (1991)
Speed of accumulated germination	`GermSpeedAccumulat`	It is estimated as follows: $S_{accumulated} = \frac{N_1}{T_1} + \frac{N_1 + N_2}{T_2} + \frac{N_1 + N_2 + N_3}{T_3} + \cdots + \frac{N_1 + N_2 +}{T}$ Where, N_1, N_2, N_3, $\cdots$, N_n are the number of germinated seeds observed at time (days or hours) T_1, T_2, T_3, $\cdots$, T_n after sowing. (Not accumulated/cumulative number, but the number of seeds that germinated at the specific time).	% time^{-1}	Mixed	Bradbeer (1988); Wardle et al. (1991); Haugland and Brandsaeter (1996); Santana and Ranal (2004)
Corrected germination rate index	`GermSpeedCorrected`	It is computed as follows: $S_{corrected} = \frac{S}{FGP}$ Where, FGP: the final germination percentage or germinability.	time^{-1}	Mixed	Evetts and Burnside (1972)
Mean germination percentage per unit time $\overline{GP}$	`MeanGermPercent`	It is estimated as follows: $\overline{G} = \frac{GP}{T_n}$ Where, GP is the final germination percentage and T_n is the total number of intervals(e.g. days) required for final germination.		Mixed	Czabator (1962)
Number of seeds germinated per unit time $\overline{N}$	`MeanGermNumber`	It is estimated as follows: $\overline{N} = \frac{N_g}{T_n}$ Where, N_g is the number of germinated seeds and $T_n$is the total number of intervals (e.g. days) required for final germination.		Mixed	Khamassi et al. (2013)

Germination index	function	Details	Unit	Measures	Reference
Timson's index ($\sum 10$ (Ten summation), $\sum 5$ or $\sum 20$)	`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: $$\sum n = \sum_{i=1}^{t} G_i$$ Where, G_i is the cumulative germination percentage in time interval i and t is the total number of time intervals. It also estimated in terms of partial germination percentage as follows: $$\sum n = \sum_{i=1}^{t} g_i(t-j)$$ Where, g_i is the germination (not cumulative, but partial germination) in time interval i (i varying from 0 to t) and t is the total number of time intervals and $j = i - 1$.		Mixed	Timson (1965); Brown and Mayer (1988); Baskin and Baskin (1998); Goodchild and Walker (1971)
Modified Timson's Index (Labouriau)	`TimsonsIndex`	It is estimated as Timson's index T divided by the sum of partial germination percentages. $$T_{mod} = \frac{T}{\sum_{i=1}^{t} g_i}$$		Mixed	Ranal and Santana (2006)
Modified Timson's Index (Khan and Unger)	`TimsonsIndex`	It is estimated as Timson's index (T) divided by the number of intervals (t). $$T_{mod} = \frac{T}{t}$$		Mixed	Khan and Ungar (1984)
George's index	`GermRateGeorge`	It is estimated as follows: $$GR = \sum_{i=1}^{t} N_i K_i$$ Where N_i is the number of seeds germinated by ith interval and K_i is the number of intervals(eg. days) until the end of the test.		Mixed	George (1961); Tucker and Wright (1965); Nichols and Heydecker (1968)
Peak value (Czabator)	`PeakValue`	It is the maximum quotient obtained by dividing successive cumulative germination values by the relevant incubation time.		Mixed	Czabator (1962)

Germination index	function	Details	Unit	Measures	Reference
Germination value (Czabator)	`GermValue`	It is computed as follows: $$GV = PV \times MDG$$ Where, PV is the peak value and MDG is the mean daily germination percentage. It can also be computed for other time intervals of successive germination counts, by replacing MDG with the mean germination percentage per unit time ($\overline{GP}$).		Mixed	Czabator (1962)
Germination value (Diavanshir and Pourbiek)	`GermValue`	It is computed as follows: $$GV = \frac{\sum DGS}{N} \times GP \times k$$ Where, DGS is the daily germination speed computed by dividing cumulative germination percentage by the number of days since the beginning of the test, N is the frequency or number of DGS calculated during the test, GP is the germination percentage expressed over 100 and k is a constant. The value of k is decided on the basis of average daily speed of germination ($\frac{\sum DGS}{N}$). If it is less than 10, then k value of 10 can be used and if it is more than 10, then value of 7 or 8 can be used for k.		Mixed	Djavanshir and Pourbeik (1976)
Coefficient of uniformity of germination	`CUGerm`	It is computed as follows: $$CUG = \frac{\sum_{i=1}^{k} N_i}{\sum_{i=1}^{k} (\overline{T} - T_i)^2 N_i}$$ Where, $\overline{T}$ is the the mean germination time, T_i is the time from the start of the experiment to the ith observation (day for the example); N_i is the number of seeds germinated in the ith time (not the accumulated number, but the number correspondent to the ith observation), and k is the last time of germination.		Germinatin unifromity	Heydecker (1972); Bewley and Black (1994)
Coefficient of variation of the germination time	`CVSEGermTime`	It is estimated as follows: $$CV_T = \sqrt{\frac{s_T^2}{\overline{T}}}$$ Where, s_T^2 is the variance of germination time and $\overline{T}$ is the mean germination time.		Germinatin unifromity	Ranal and Santana (2006)

Germination index	function	Details	Unit	Measures	Reference
Synchronization index ($\overline{E}$) or Uncertainty of the germination process (U) or informational entropy (H)	`GermUncertainty`	It is estimated as follows: $$\overline{E} = -\sum_{i=1}^{k} f_i \log_2 f_i$$ Where, f_i is the relative frequency of germination ($f_i = \frac{N_i}{\sum_{i=1}^{k} N_i}$), N_i is the number of seeds germinated on the ith time and k is the last day of observation.	bit	Germination synchrony	Shannon (1948); Labouriau and Viladares (1976); Labouriau (1983b)
Synchrony of germination (Z index)	`GermSynchrony`	It is computed as follows: $$Z = \frac{\sum_{i=1}^{k} C_{N_i,2}}{C_{\Sigma N_i,2}}$$ Where, $C_{N_i,2}$ is the partial combination of the two germinated seeds from among N_i, the number of seeds germinated on the ith time (estimated as $C_{N_i,2} = \frac{Ni(Ni-1)}{2}$) 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.		Germination synchrony	Primack (1985); Ranal and Santana (2006)

Examples

GermPercent()

```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)

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

```
[1] 80
```

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

```
[1] 80
```

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

```
[1] 80
```

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

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

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

```
[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
```

t50()

```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")
```

```
[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
```

MeanGermTime(), VarGermTime(), SEGermTime(), CVSEGermTime()

```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)
```

```
[1] 6.7
```

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

```
[1] 1.446154
```

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

```
[1] 0.1901416
```

```r
CVSEGermTime(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] 19.04012
```

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

```
[1] 0.2394781
```

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

```
[1] 0.6512685
```

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

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

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

```
[1] 0.1492537
```

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

```
[1] 14.92537
```

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

```
[1] 0.0007176543
```

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

```
[1] 0.004235724
```

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

```
[1] 0.1674877
```

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

```
[1] 0.1683168
```

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

```
[1] 0.1492537
```

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

```
[1] 14.92537
```

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

```
[1] 0.009448666
```

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

```
[1] 0.005334776
```

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

```
[1] 0.1674877
```

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

```
[1] 0.1683168
```

GermSpeed(), GermSpeedAccumulated(), GermSpeedCorrected()

```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)
```

```
[1] 6.138925
```

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

```
[1] 34.61567
```

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

```
[1] 0.07673656
```

```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)
```

```
[1] 0.009245369
```

GermSpeed(), GermSpeedAccumulated(), GermSpeedCorrected()

```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)
```

```
[1] 6.138925
```

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

```
[1] 34.61567
```

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

```
[1] 0.07673656
```

```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)
```

```
[1] 0.009245369
```

MeanGermPercent(), MeanGermNumber()

```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)
```

```
[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
```

```
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
```

TimsonsIndex(), GermRateGeorge()

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

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

```
[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 = "khanunger")
```

```
[1] 47.42857
```

```
# 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 = "khanunger")
```

```
[1] 24.57143
```

```
# Wihout max specified
GermRateGeorge(germ.counts = x, intervals = int)
```

```
[1] 332
```

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

```
[1] 172
```

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

```
[1] 332
```

```r
# From cumulative germination counts
#----------------------------------------------------------------------------


# Wihout max specified
GermRateGeorge(germ.counts = x, intervals = int, partial = TRUE)
```

```
[1] 332
```

```r
# With max specified
GermRateGeorge(germ.counts = x, intervals = int, partial = TRUE, max = 10)
```

```
[1] 172
```

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

```
[1] 332
```

PeakValue(), GermValue()

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

```
[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
3           34         3                     34                    17.0
4           40         4                     74                    37.0
5           21         5                     95                    47.5
6           10         6                    105                    52.5
7            4         7                    109                    54.5
8            5         8                    114                    57.0
9            3         9                    117                    58.5
10           5        10                    122                    61.0
```

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

```
20           2        20                    164                    82.0
        DGS SumDGSbyN        GV
3  5.666667  5.666667  9.633333
4  9.250000  7.458333 27.595833
5  9.500000  8.138889 38.659722
6  8.750000  8.291667 43.531250
7  7.785714  8.190476 44.638095
8  7.125000  8.012897 45.673512
9  6.500000  7.796769 45.611097
10 6.100000  7.584673 46.266503
11 5.909091  7.398497 48.090230
12 5.708333  7.229481 49.521942
13 5.538462  7.075752 50.945411
14 5.357143  6.932534 51.994006
15 5.200000  6.799262 53.034246
16 5.000000  6.670744 53.365948
17 4.705882  6.539753 52.318022
18 4.500000  6.412268 51.939373
19 4.263158  6.285850 50.915385
20 4.100000  6.164414 50.548194

$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
3           34         3                     34                    17.0
4           40         4                     74                    37.0
5           21         5                     95                    47.5
6           10         6                    105                    52.5
7            4         7                    109                    54.5
8            5         8                    114                    57.0
9            3         9                    117                    58.5
10           5        10                    122                    61.0
11           8        11                    130                    65.0
12           7        12                    137                    68.5
13           7        13                    144                    72.0
14           6        14                    150                    75.0
15           6        15                    156                    78.0
16           4        16                    160                    80.0
17           0        17                    160                    80.0
18           2        18                    162                    81.0
```

```
19           0        19                     162                    81.0
20           2        20                     164                    82.0
        DGS
3  5.666667
4  9.250000
5  9.500000
6  8.750000
7  7.785714
8  7.125000
9  6.500000
10 6.100000
11 5.909091
12 5.708333
13 5.538462
14 5.357143
15 5.200000
16 5.000000
17 4.705882
18 4.500000
19 4.263158
20 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
3           34         3                     34                    17.0
4           40         4                     74                    37.0
5           21         5                     95                    47.5
6           10         6                    105                    52.5
7            4         7                    109                    54.5
8            5         8                    114                    57.0
9            3         9                    117                    58.5
10           5        10                    122                    61.0
11           8        11                    130                    65.0
12           7        12                    137                    68.5
13           7        13                    144                    72.0
14           6        14                    150                    75.0
15           6        15                    156                    78.0
16           4        16                    160                    80.0
17           0        17                    160                    80.0
18           2        18                    162                    81.0
19           0        19                    162                    81.0
20           2        20                    164                    82.0
        DGS SumDGSbyN        GV
3  5.666667  5.666667  9.633333
4  9.250000  7.458333 27.595833
5  9.500000  8.138889 38.659722
6  8.750000  8.291667 43.531250
7  7.785714  8.190476 44.638095
8  7.125000  8.012897 45.673512
```

```
9   6.500000  7.796769 45.611097
10  6.100000  7.584673 46.266503
11  5.909091  7.398497 48.090230
12  5.708333  7.229481 49.521942
13  5.538462  7.075752 50.945411
14  5.357143  6.932534 51.994006
15  5.200000  6.799262 53.034246
16  5.000000  6.670744 53.365948
17  4.705882  6.539753 52.318022
18  4.500000  6.412268 51.939373
19  4.263158  6.285850 50.915385
20  4.100000  6.164414 50.548194

$testend
[1] 16
```

CUGerm()

```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)
```

```
[1] 0.7092199
```

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

```
[1] 0.05267935
```

GermSynchrony(), GermUncertainty()

```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)
```

```
[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
```

Curve fitting

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

Four-parameter hill function

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

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

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

The details of various parameters that are computed from this function are given in Table 3.

Table 3 Germination parameters estimated from the four-parameter hill function.

Germination parameters	Details	Unit	Measures
y intercept (y_0)	The intercept on the y axis.		
Asymptote (a)	It is the maximum cumulative germination percentage, which is equivalent to germination capacity.	%	Germination capacity
Shape and steepness (b)	Mathematical parameter controlling the shape and steepness of the germination curve. The larger the b , the steeper the rise toward the asymptote a, and the shorter the time between germination onset and maximum germination.		Germination rate
Half-maximal activation level (c)	Time required for 50% of viable seeds to germinate.	time	Germination time
lag	It is the time at germination onset and is computed by solving four-parameter hill function after setting y to 0 as follows: $$lag = b\sqrt{\frac{-y_0c^b}{a+y_0}}$$	time	Germination time
D_{lag-50}	The duration between the time at germination onset (lag) and that at 50% germination (c).	time	Germination time
$t50_{total}$	Time required for 50% of total seeds to germinate.	time	Germination time

Germination parameters	Details	Unit	Measures
$t_{50_{germinated}}$	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

`FourPHFfit()`

```
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)
```

```
$data
   gp csgp intervals
```

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

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

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

$a
[1] 80

$b
[1] 9.881947

$c
[1] 6.034954

$y0
[1] 0

$lag
[1] 0

$Dlag50
[1] 6.034954

$t50.total
[1] 6.355122

$txp.total
[1] 4.956266 6.744598

$t50.Germinated
[1] 6.034954
```

```
$txp.Germinated
[1] 4.831809 6.287724

$Uniformity
       90         10 uniformity
 7.537688   4.831809   2.705880

$TMGR
[1] 5.912195

$AUC
[1] 1108.975

$MGT
[1] 6.632252

$Skewness
[1] 1.098973

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

$isConv
[1] TRUE

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

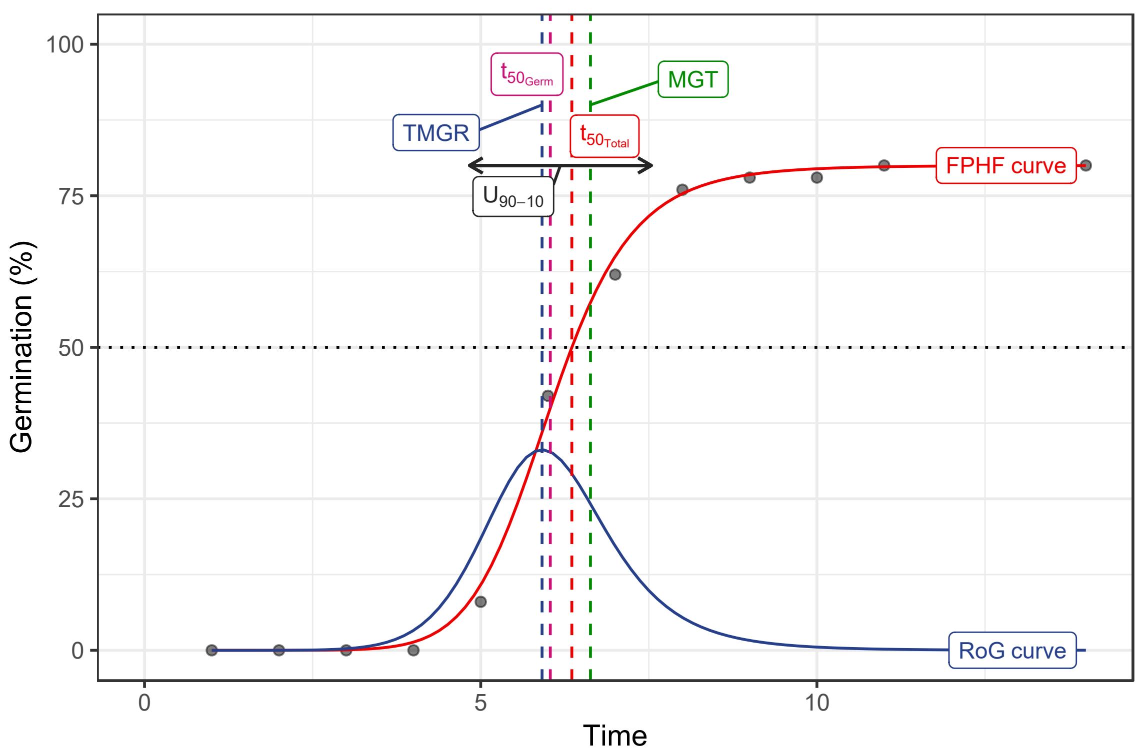
```
# From cumulative germination counts
#----------------------------------------------------------------------------
FourPHFfit(germ.counts = y, intervals = int, total.seeds = 50, tmax = 20,
partial = FALSE)
```

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

$Parameters
  term  estimate std.error statistic      p.value
1    a 80.000000 1.2415867  64.43368 1.973252e-14
2    b  9.881927 0.7077918  13.96163 6.952270e-08
```

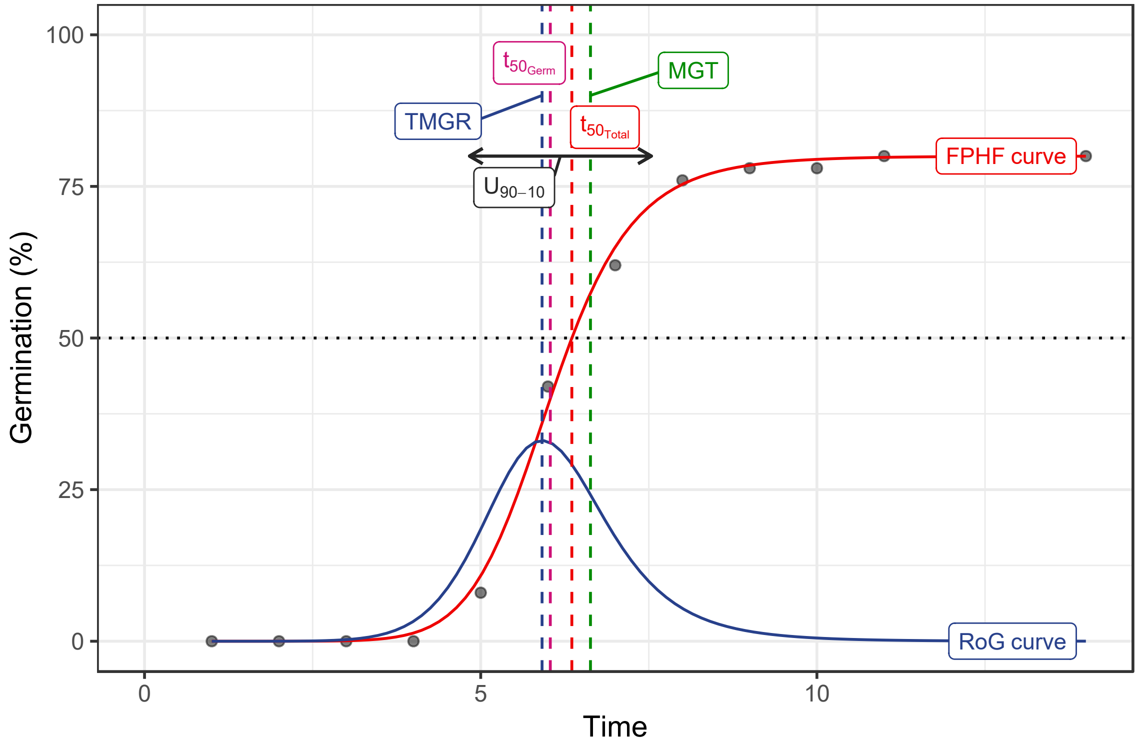
```
3    c  6.034953 0.0495266 121.85275 3.399437e-17
4   y0  0.000000 0.9160705   0.00000 1.000000e+00

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

$a
[1] 80

$b
[1] 9.881927

$c
[1] 6.034953

$y0
[1] 0

$lag
[1] 0

$Dlag50
[1] 6.034953

$t50.total
[1] 6.355121

$txp.total
[1] 4.956263 6.744599

$t50.Germinated
[1] 6.034953

$txp.Germinated
[1] 4.831806 6.287723

$Uniformity
        90         10 uniformity
  7.537691   4.831806   2.705885

$TMGR
[1] 5.912194

$AUC
[1] 1108.976

$MGT
[1] 6.632252

$Skewness
[1] 1.098973
```

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

$isConv
[1] TRUE

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

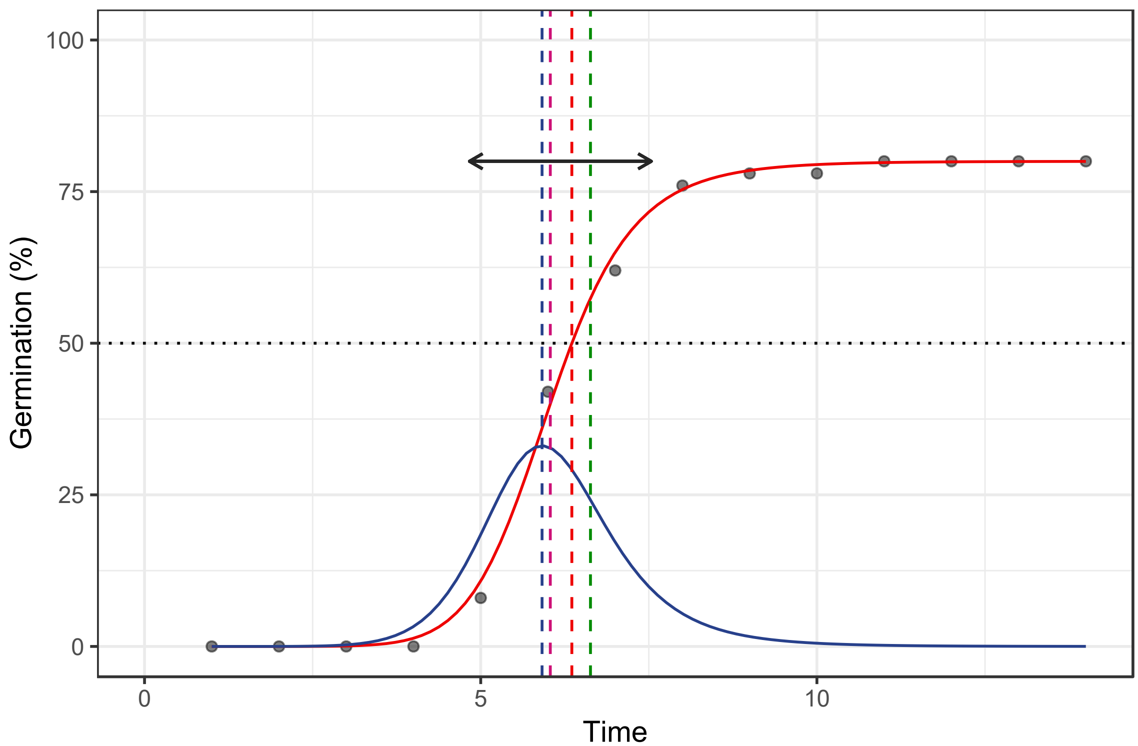
```
x <- c(0, 0, 0, 0, 4, 17, 10, 7, 1, 0, 1, 0, 0, 0)
y <- c(0, 0, 0, 0, 4, 21, 31, 38, 39, 39, 40, 40, 40, 40)
int <- 1:length(x)
total.seeds = 50

# 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)
```



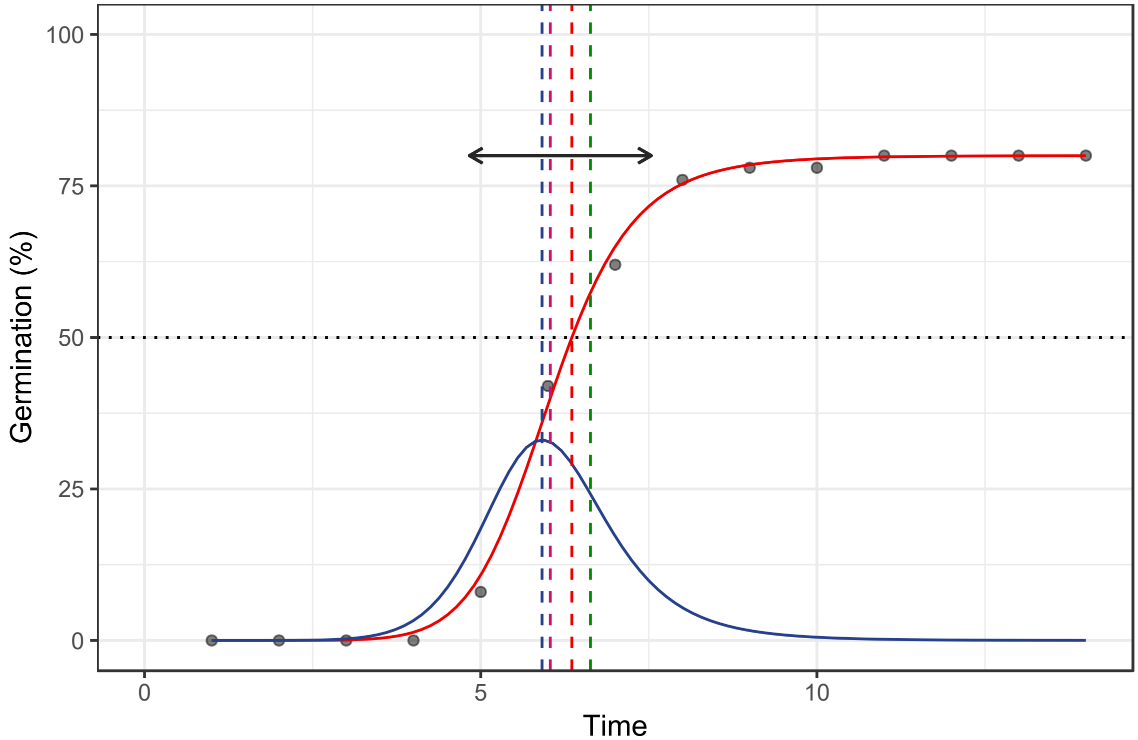
```r
plot(fit2)
```



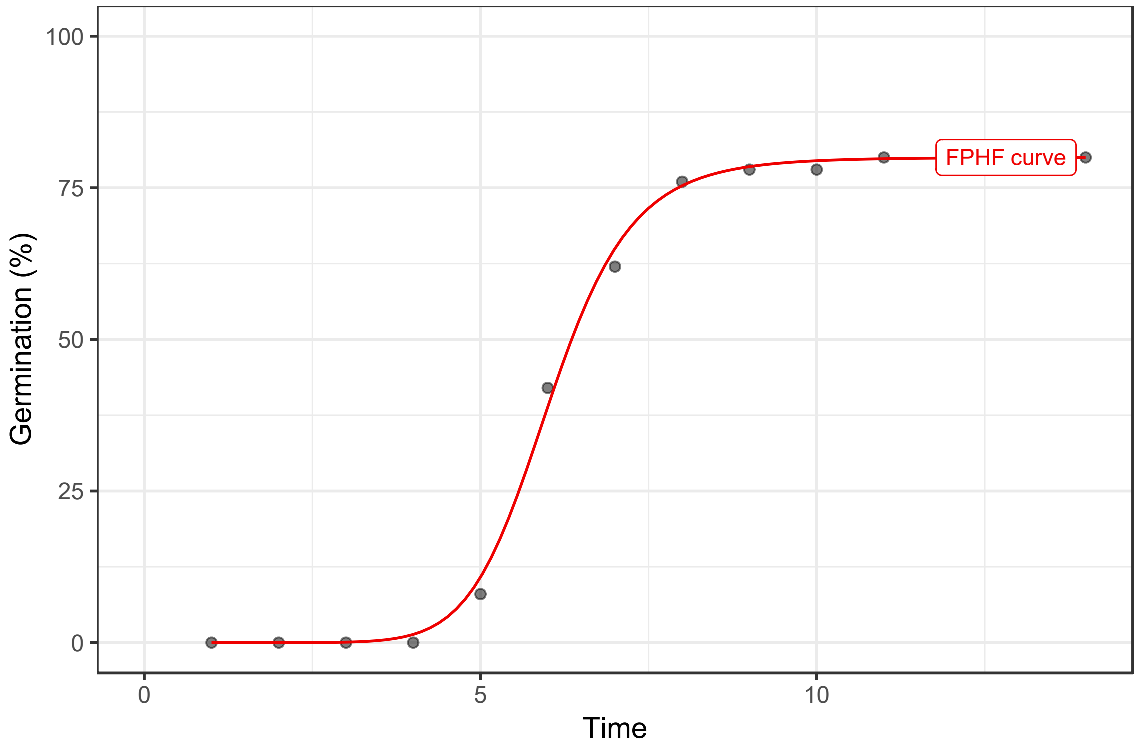

```r
# No labels
plot(fit1, plotlabels = FALSE)
```



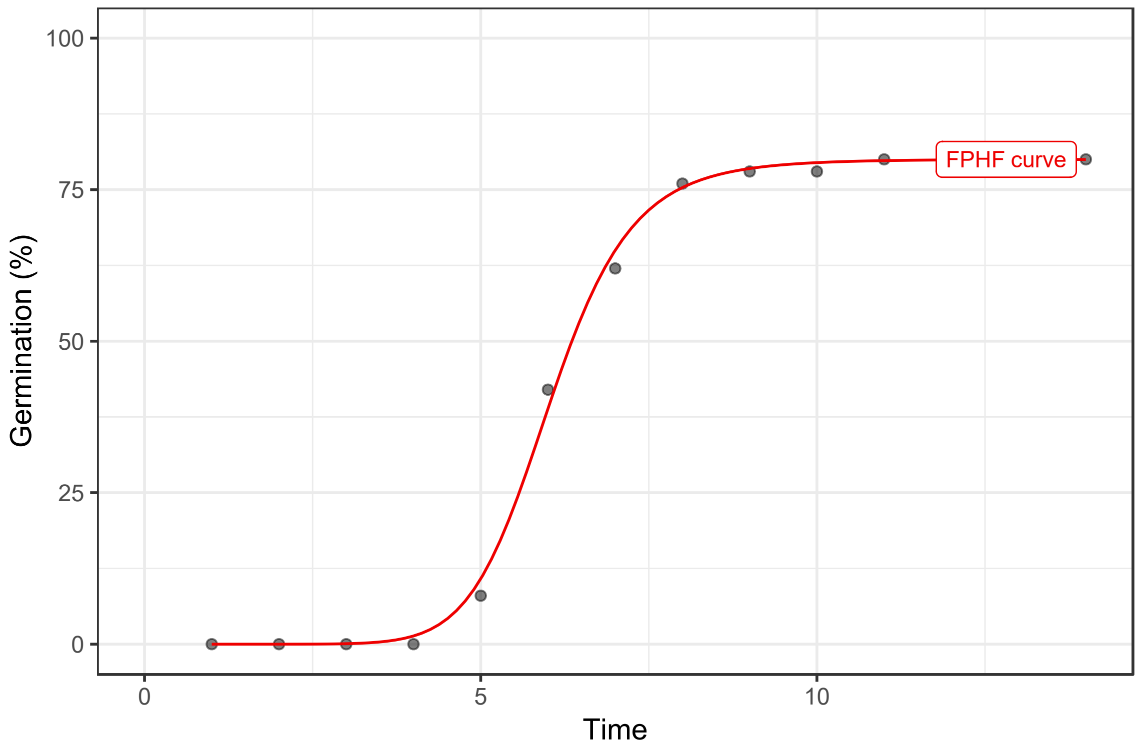
```r
plot(fit2, plotlabels = FALSE)
```



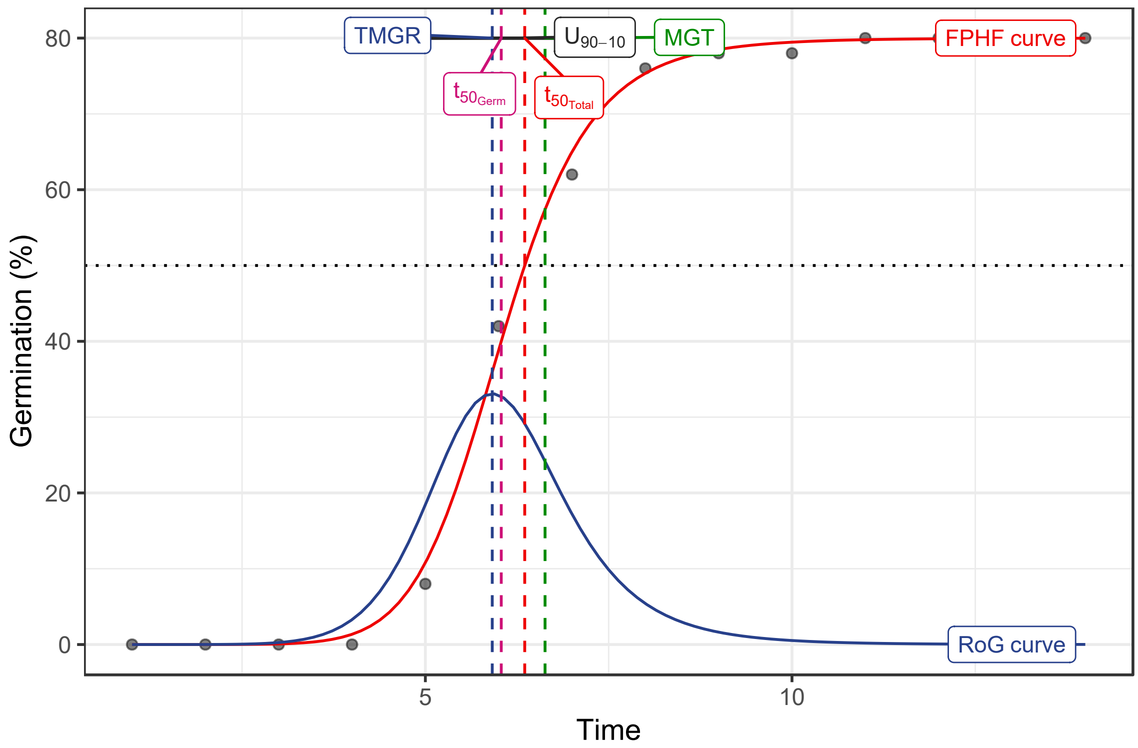

```r
# Only the FPHF curve
plot(fit1, rog = FALSE, t50.total = FALSE, t50.germ = FALSE,
     tmgr = FALSE, mgt = FALSE, uniformity = FALSE)
```



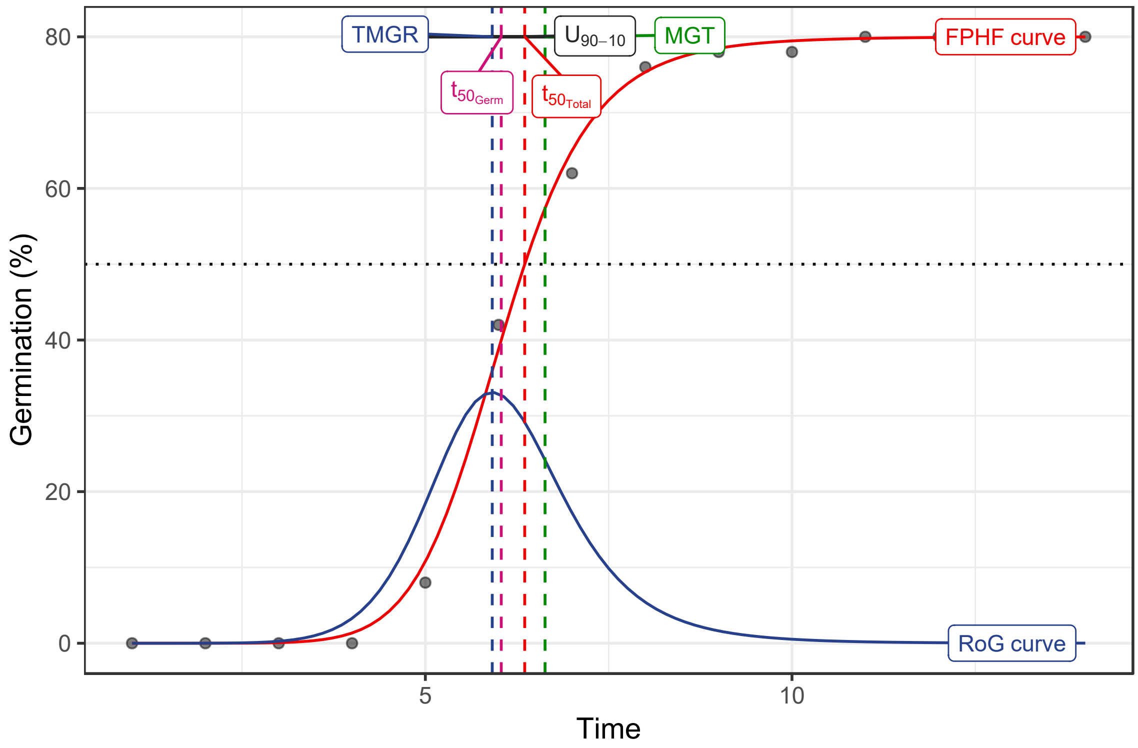

```
plot(fit2, rog = FALSE, t50.total = FALSE, t50.germ = FALSE,
     tmgr = FALSE, mgt = FALSE, uniformity = FALSE)
```




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




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



Citing germinationmetrics

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

  J. Aravind, S. Vimala Devi, J. Radhamani, Sherry Rachel Jacob
  and Kalyani Srinivasan (2018).  germinationmetrics: Seed
  Germination Indices and Curve Fitting. R package version
  0.1.0.9000,
  https://cran.r-project.org/package=germinationmetrics,
  https://doi.org/10.5281/zenodo.1219630.

A BibTeX entry for LaTeX users is

  @Manual{,
    title = {germinationmetrics: Seed Germination Indices and Curve Fitting},
    author = {{Aravind J} and {Vimala Devi S} and {Radhamani J} and {Sherry Rachel Jacob} and {Kalyani S
    year = {2018},
    note = {R package version 0.1.0.9000},
    note = {https://cran.r-project.org/package=germinationmetrics},
    note = {https://doi.org/10.5281/zenodo.1219630},
  }

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 version 3.5.1 (2018-07-02)
Platform: x86_64-w64-mingw32/x64 (64-bit)
Running under: Windows >= 8 x64 (build 9200)

Matrix products: default

locale:
[1] LC_COLLATE=English_India.1252  LC_CTYPE=English_India.1252
[3] LC_MONETARY=English_India.1252 LC_NUMERIC=C
[5] LC_TIME=English_India.1252

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

other attached packages:
[1] germinationmetrics_0.1.0.9000 readxl_1.1.0

loaded via a namespace (and not attached):
 [1] httr_1.3.1            tidyr_0.8.1           jsonlite_1.5
 [4] Rdpack_0.8-0          assertthat_0.2.0      xmlparsedata_1.0.1
 [7] highr_0.7             pander_0.6.2          cellranger_1.1.0
[10] yaml_2.2.0            remotes_1.1.1.9000    ggrepel_0.8.0
```

```
[13] pillar_1.3.0          backports_1.1.2      lattice_0.20-35
[16] glue_1.3.0            goodpractice_1.0.2   digest_0.6.15
[19] colorspace_1.3-2      htmltools_0.3.6      plyr_1.8.4
[22] clisymbols_1.2.0      pkgconfig_2.0.1      devtools_1.13.6
[25] bibtex_0.4.2          rcmdcheck_1.2.1      broom_0.5.0
[28] purrr_0.2.5           scales_0.5.0         processx_3.1.0
[31] tibble_1.4.2          ggplot2_3.0.0        withr_2.1.2
[34] lazyeval_0.2.1        magrittr_1.5         crayon_1.3.4
[37] memoise_1.1.0         evaluate_0.11        fs_1.2.4
[40] nlme_3.1-137          MASS_7.3-50          xml2_1.2.0
[43] praise_1.0.0          tools_3.5.1          hunspell_2.9
[46] cyclocomp_1.1.0       minpack.lm_1.2-1     gbRd_0.4-11
[49] stringr_1.3.1         munsell_0.5.0        bindrcpp_0.2.2
[52] callr_2.0.4           rex_1.1.2            compiler_3.5.1
[55] pkgdown_1.1.0.9000    covr_3.1.0           tinytex_0.6
[58] rlang_0.2.1           debugme_1.1.0        grid_3.5.1
[61] rstudioapi_0.7.0-9000 labeling_0.3         rmarkdown_1.10
[64] gtable_0.2.0          roxygen2_6.0.1       R6_2.2.2
[67] knitr_1.20            dplyr_0.7.6          bindr_0.1.1
[70] commonmark_1.5        rprojroot_1.3-2      lintr_1.0.2
[73] desc_1.2.0            stringi_1.2.4        whoami_1.1.2
[76] Rcpp_0.12.18          tidyselect_0.2.4     xfun_0.3
```

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