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 0.1.5. 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

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

Germination count data

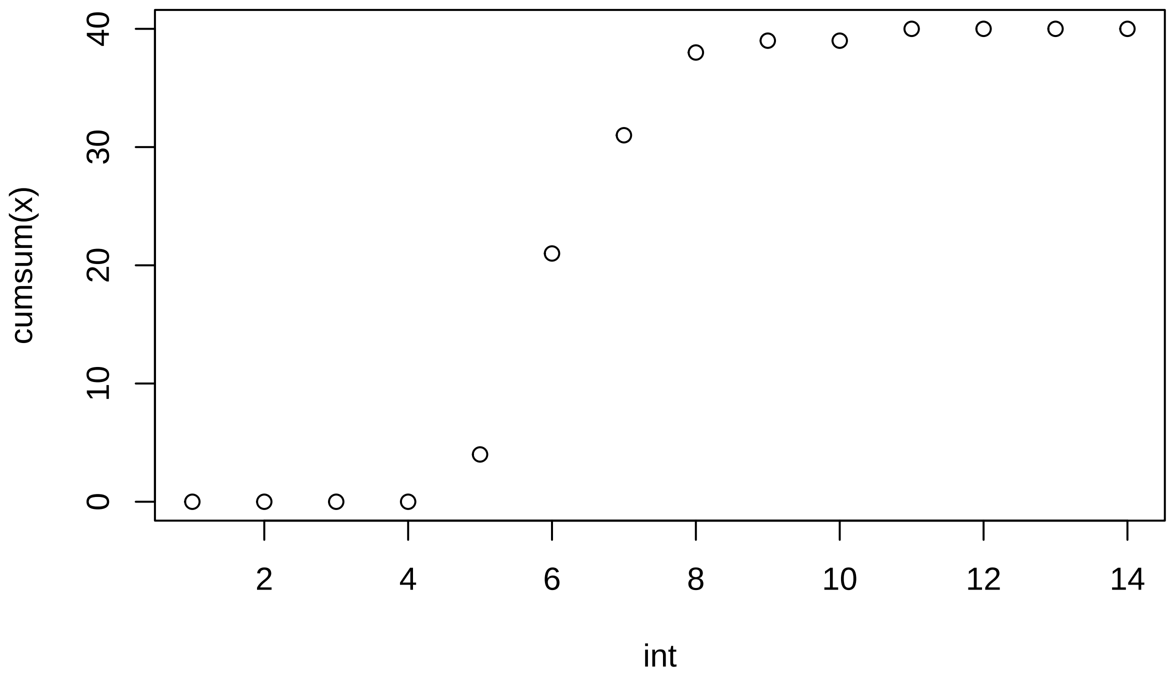
Typically in a germination test, the germination count data of a fixed number of seeds is recorded at regular intervals for a definite period of time or until all the seeds have germinated. These germination count data can be either partial or cumulative (Table 2).

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`.

```
[1] "Package 'pander' and pandoc are required to generate this table"
```

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)

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

`GermPercent()`

```
[1] 80
```

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

```
[1] 80
```

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

```
[1] 80
```

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

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

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

```
[1] 5
```

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

```
[1] 11
```

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

```
[1] 6
```

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

```
[1] 6
```

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

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

```
[1] 5 6
```

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

```
[1] 5
```

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

```
[1] 11
```

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

```
[1] 6
```

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

```
[1] 6
```

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

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

```
[1] 5 6
```

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

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

t50()

```
[1] 5.970588
```

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

```
[1] 5.941176
```

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

```
[1] 5.970588
```

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

```
[1] 5.941176
```

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

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

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

```
[1] 6.7
```

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

```
[1] 1.446154
```

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

```
[1] 0.1901416
```

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

```
[1] 0.1794868
```

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

```
[1] 6.7
```

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

```
[1] 19.04012
```

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

```
[1] 0.2394781
```

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

```
[1] 0.6512685
```

```

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

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

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

```
[1] 0.1492537
```

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

```
[1] 14.92537
```

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

```
[1] 0.0007176543
```

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

```
[1] 0.004235724
```

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

```
[1] 0.1674877
```

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

```
[1] 0.1683168
```

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

```
[1] 0.1492537
```

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

```
[1] 14.92537
```

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

```
[1] 0.009448666
```

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

```
[1] 0.005334776
```

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

```
[1] 0.1674877
```

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

```
[1] 0.1683168
```

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

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

GermSpeed(), GermSpeedAccumulated(), GermSpeedCorrected()

```
[1] 6.138925
```

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

```
[1] 34.61567
```

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

```
[1] 0.07673656
```

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

```
[1] 0.4326958
```

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

```
[1] 12.27785
```

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

```
[1] 69.23134
```

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

```
[1] 6.138925
```

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

```
[1] 34.61567
```

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

```
[1] 0.07673656
```

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

```
[1] 0.4326958
```

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

```
[1] 12.27785
```

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

```
[1] 69.23134
```

```

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

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

GermSpeed(), GermSpeedAccumulated(), GermSpeedCorrected()

```
[1] 6.138925
```

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

```
[1] 34.61567
```

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

```
[1] 0.07673656
```

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

```
[1] 0.4326958
```

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

```
[1] 12.27785
```

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

```
[1] 69.23134
```

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

```
[1] 6.138925
```

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

```
[1] 34.61567
```

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

```
[1] 0.07673656
```

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

```
[1] 0.4326958
```

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

```
[1] 12.27785
```

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

```
[1] 69.23134
```

```

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

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

`WeightGermPercent()`

```
[1] 47.42857
```

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

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

```
[1] 47.42857
```

```

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

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

MeanGermPercent(), MeanGermNumber()

```
[1] 5.714286
```

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

```
[1] 2.857143
```

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

```
[1] 5.714286
```

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

```
[1] 2.857143
```

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

```
[1] 5.714286
```

```

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

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

TimsonsIndex(), GermRateGeorge()

```
[1] 664
```

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

```
[1] 664
```

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

```
[1] 8.3
```

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

```
[1] 47.42857
```

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

```
[1] 332
```

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

```
[1] 344
```

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

```
[1] 344
```

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

```
[1] 4.410256
```

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

```
[1] 24.57143
```

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

```
[1] 172
```

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

```
[1] 332
```

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

```
[1] 664
```

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

```
[1] 664
```

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

```
[1] 8.3
```

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

```
[1] 47.42857
```

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

```
[1] 332
```

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

```
[1] 344
```

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

```
[1] 344
```

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

```
[1] 4.410256
```

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

```
[1] 24.57143
```

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

```
[1] 172
```

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

```
[1] 332
```

```

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

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

GermIndex()

```
[1] 5.84
```

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

```
[1] 5.84
```

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

```
[1] 7.3
```

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

```
[1] 5.84
```

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

```
[1] 5.84
```

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

```
[1] 7.3
```

```

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

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

EmergenceRateIndex()

```
[1] 292
```

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

```
[1] 292
```

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

```
[1] 7.3
```

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

```
[1] 5.970149
```

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

```
[1] 8.375
```

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

```
[1] 292
```

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

```
[1] 292
```

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

```
[1] 7.3
```

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

```
[1] 5.970149
```

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

```
[1] 8.375
```

```

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

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

PeakValue(), GermValue()

```
[1] 9.5
```

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

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

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

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

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

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

$testend
[1] 16
```

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

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

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

```
17            0         17                     160                    80.0 4.705882
18            2         18                     162                    81.0 4.500000
19            0         19                     162                    81.0 4.263158
20            2         20                     164                    82.0 4.100000
```

```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
```

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

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

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

$testend
[1] 16
```

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

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

[[2]]
   germ.counts intervals Cumulative.germ.counts Cumulative.germ.percent       DGS
1            0         1                      0                     0.0 0.000000
2            0         2                      0                     0.0 0.000000
```

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

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

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

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

$testend
[1] 16
```

```

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

```r
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] 0.05267935
```

```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."

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.

```
[1] "Package 'pander' and pandoc are required to generate this table"
```

Examples

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

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

```
FourPHFfit()

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

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

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

$a
[1] 80

$b
```

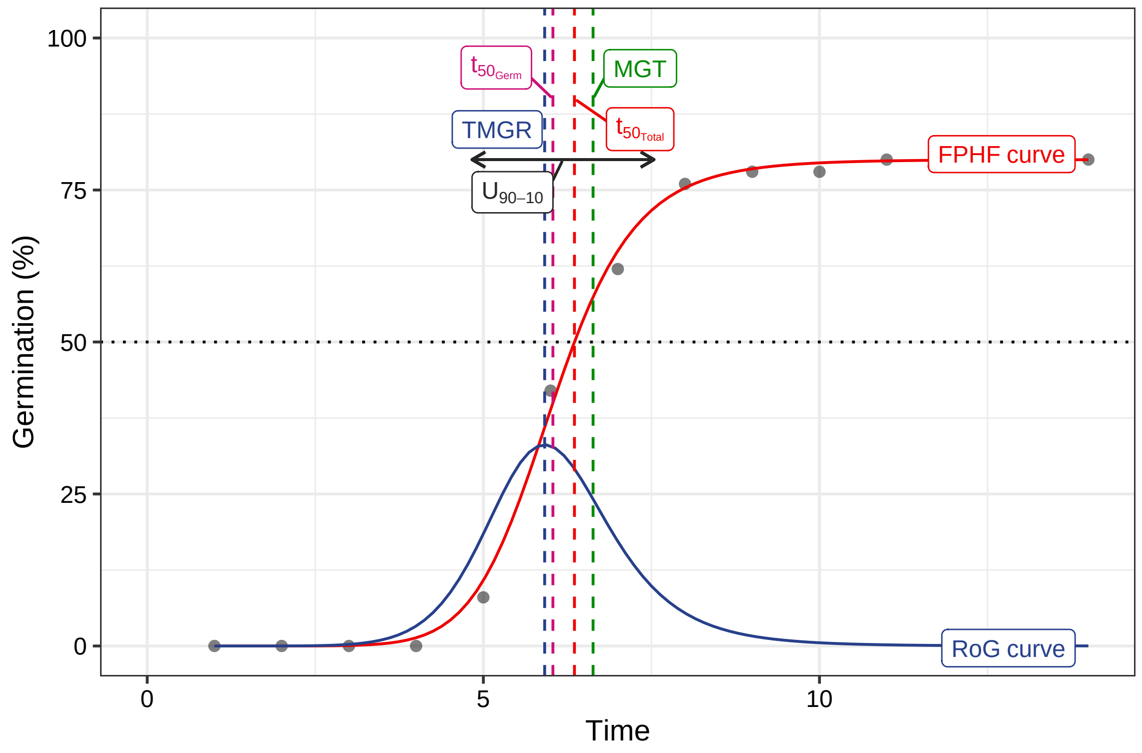
```
[1] 9.881947

$c
[1] 6.034954

$y0
[1] 0

$lag
[1] 0

$Dlag50
[1] 6.034954

$t50.total
[1] 6.355122

$txp.total
      10       60
4.956266 6.744598

$t50.Germinated
[1] 6.034954

$txp.Germinated
      10       60
4.831809 6.287724

$Uniformity
        90         10 uniformity
  7.537688   4.831809   2.705880

$TMGR
[1] 5.912195

$AUC
[1] 1108.975

$MGT
[1] 6.632252

$Skewness
[1] 1.098973

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

$isConv
[1] TRUE

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

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

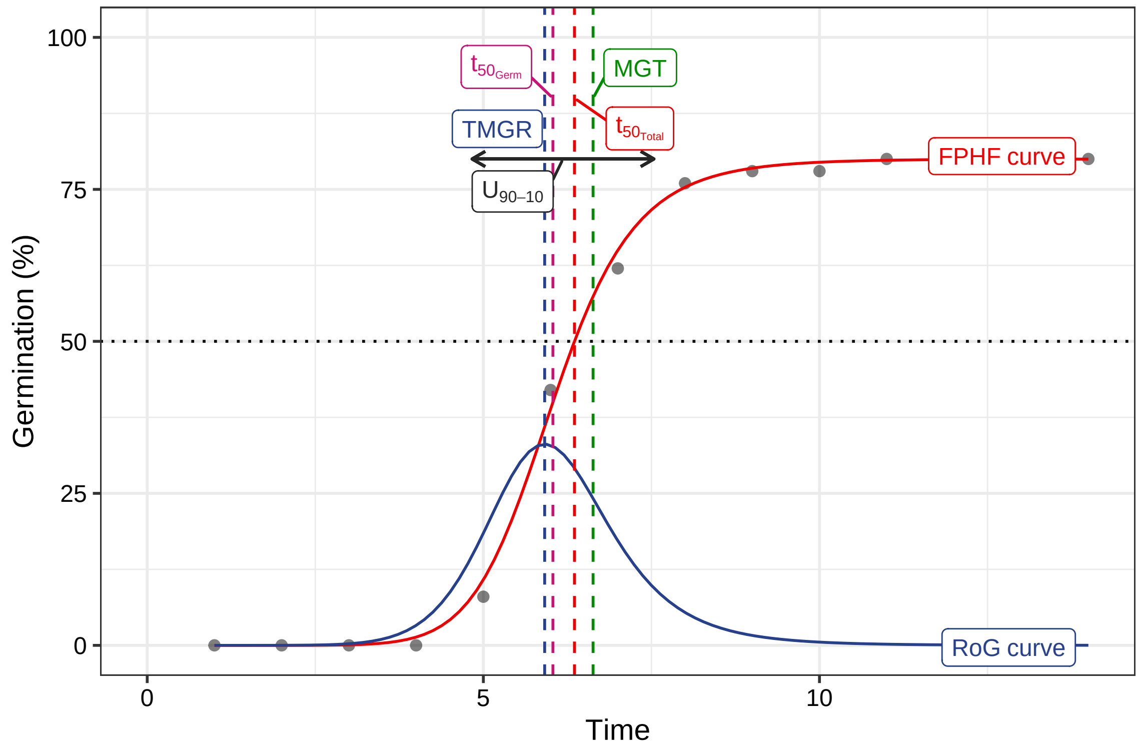
```
$data
   gp csgp intervals
1   0    0         1
2   0    0         2
3   0    0         3
4   0    0         4
5   8    8         5
6  34   42         6
7  20   62         7
8  14   76         8
9   2   78         9
10  0   78        10
11  2   80        11
12  0   80        12
13  0   80       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

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

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

$a
[1] 80

$b
[1] 9.881927

$c
[1] 6.034953

$y0
[1] 0

$lag
[1] 0

$Dlag50
[1] 6.034953

$t50.total
[1] 6.355121
```

```
$txp.total
      10       60 
4.956263 6.744599 

$t50.Germinated
[1] 6.034953

$txp.Germinated
      10       60 
4.831806 6.287723 

$Uniformity
        90         10 uniformity 
  7.537691   4.831806   2.705885 

$TMGR
[1] 5.912194

$AUC
[1] 1108.976

$MGT
[1] 6.632252

$Skewness
[1] 1.098973

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

$isConv
[1] TRUE

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

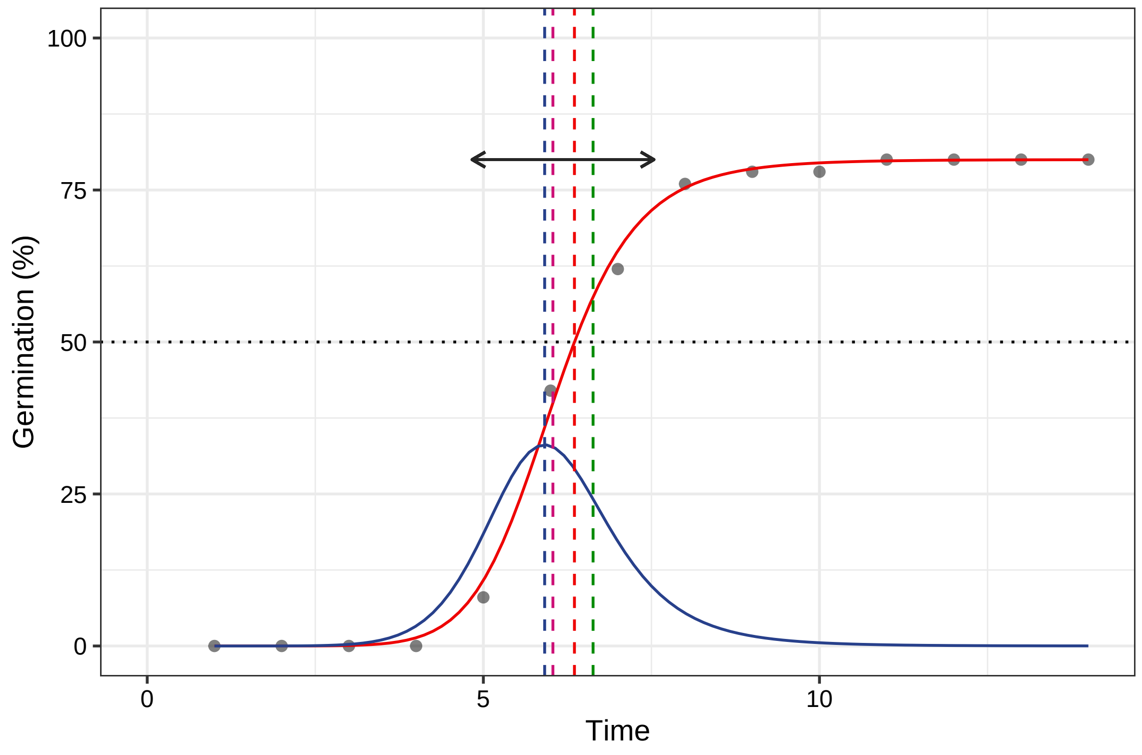
```
x <- c(0, 0, 0, 0, 4, 17, 10, 7, 1, 0, 1, 0, 0, 0)
y <- c(0, 0, 0, 0, 4, 21, 31, 38, 39, 39, 40, 40, 40, 40)
int <- 1:length(x)
total.seeds = 50

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

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

# Default plots
plot(fit1)
```



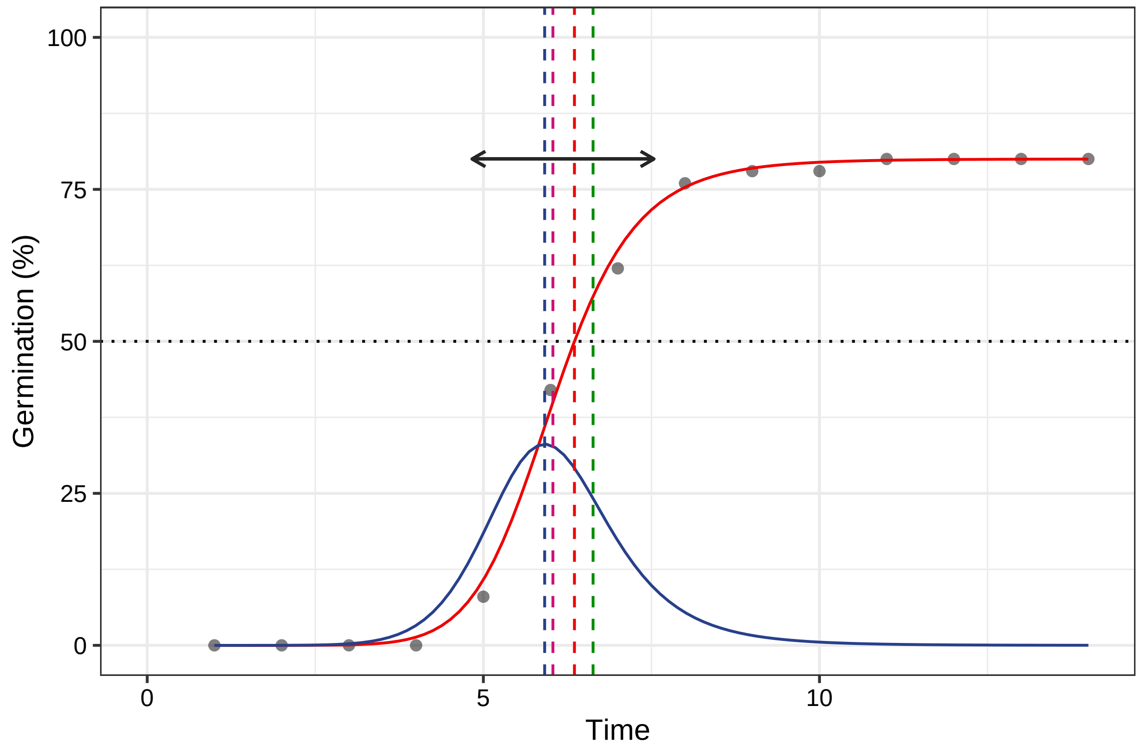
```
plot(fit2)
```



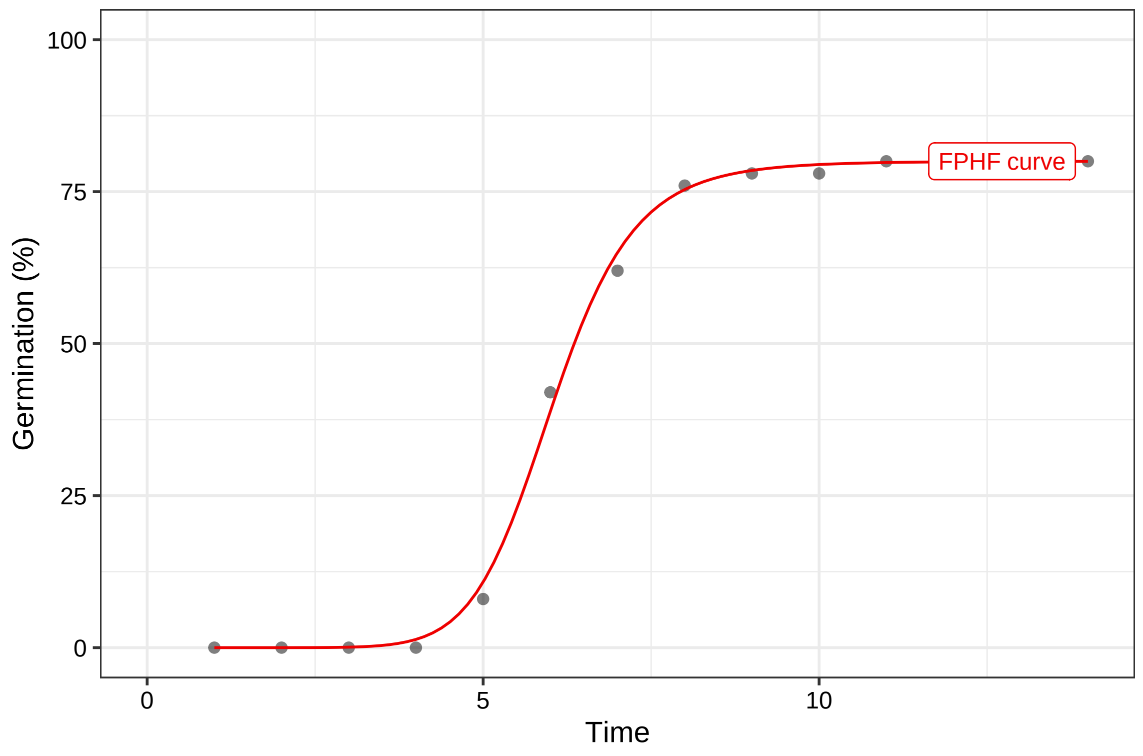
```
# No labels
plot(fit1, plotlabels = FALSE)
```



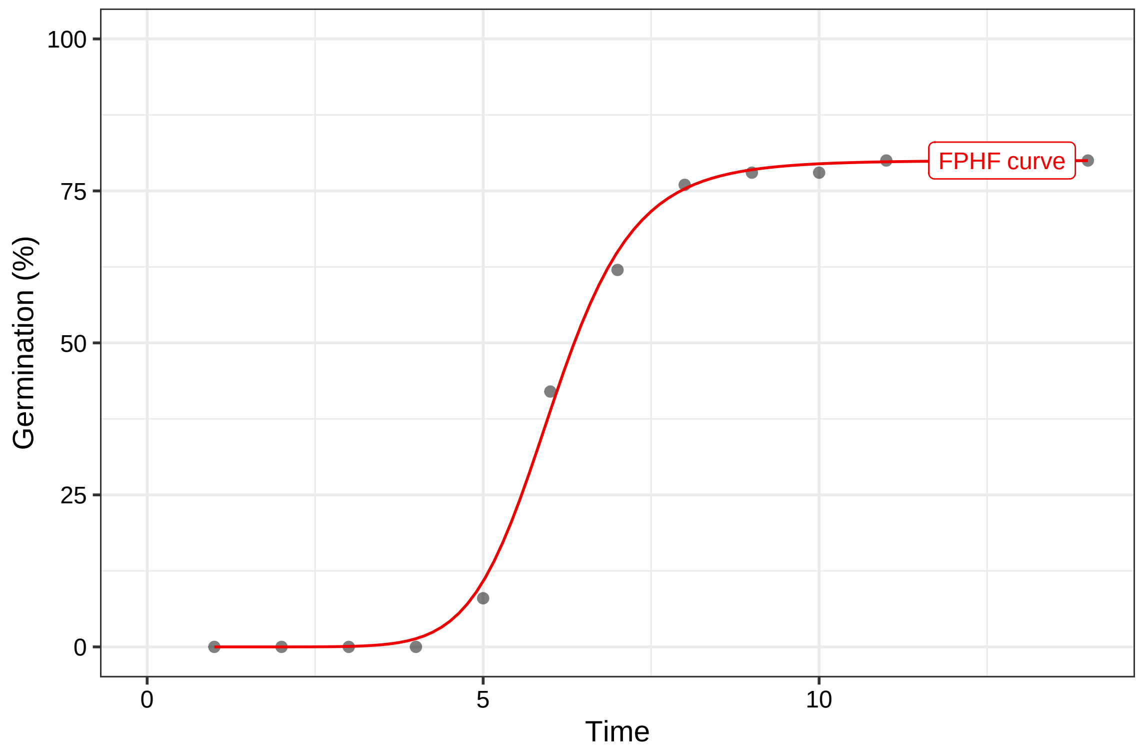
```r
plot(fit2, plotlabels = FALSE)
```



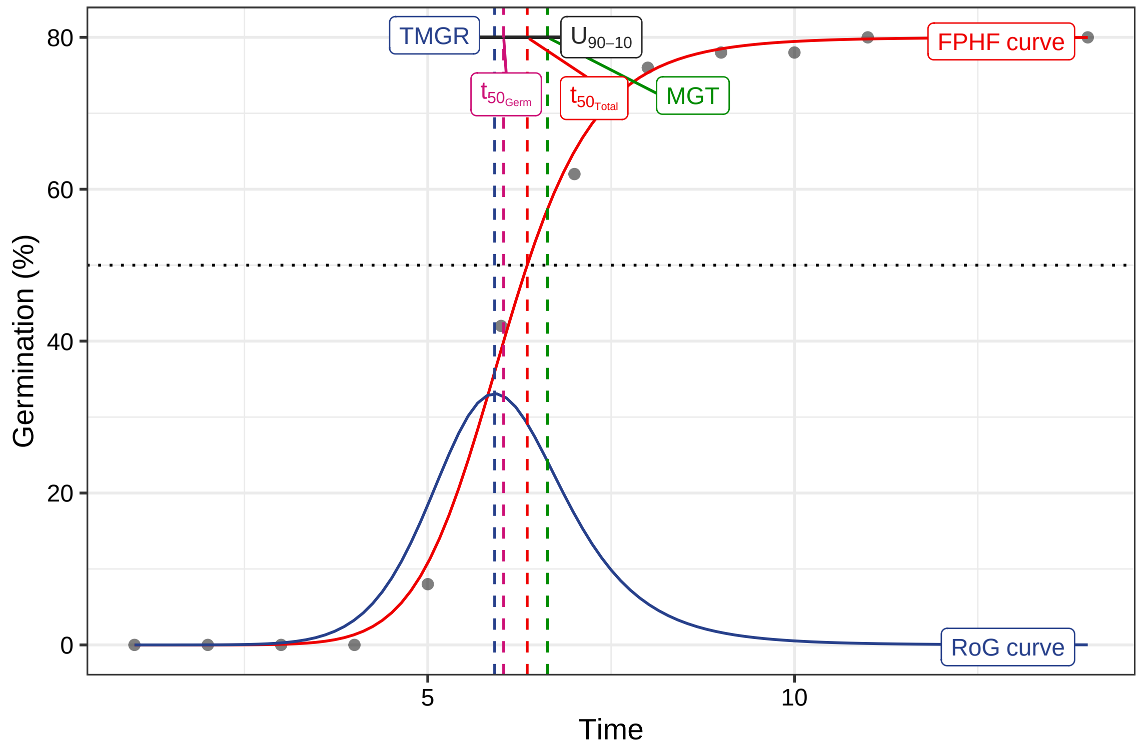
```r
# Only the FPHF curve
plot(fit1, rog = FALSE, t50.total = FALSE, t50.germ = FALSE,
     tmgr = FALSE, mgt = FALSE, uniformity = FALSE)
```



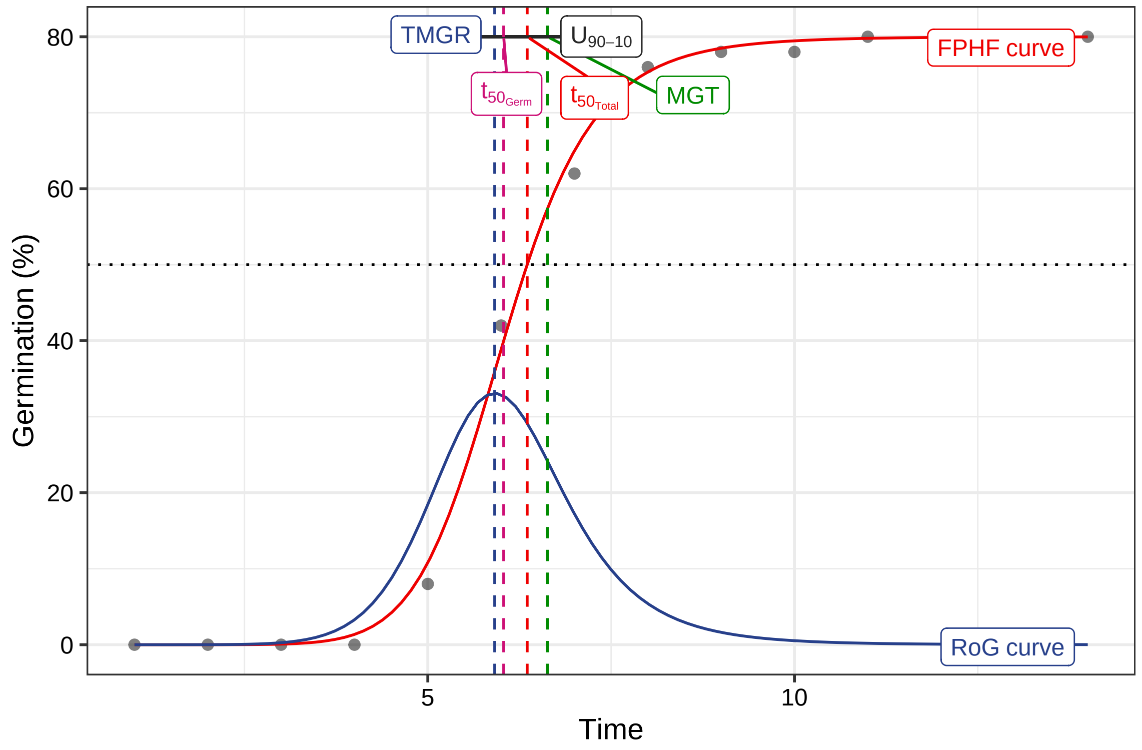
```
plot(fit2, rog = FALSE, t50.total = FALSE, t50.germ = FALSE,
     tmgr = FALSE, mgt = FALSE, uniformity = FALSE)
```



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



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



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 Tota
1        G1   1     0     0     0     0     4    17    10     7     1     0     1     0     0     0
2        G2   1     0     0     0     1     3    15    13     6     2     1     0     1     0     0
3        G3   1     0     0     0     2     3    18     9     8     2     1     1     1     0     0
4        G4   1     0     0     0     0     4    19    12     6     2     1     1     1     0     0
5        G5   1     0     0     0     0     5    20    12     8     1     0     0     1     1     0
6        G1   2     0     0     0     0     3    21    11     7     1     1     1     1     0     0
7        G2   2     0     0     0     0     4    18    11     7     1     0     1     0     0     0
8        G3   2     0     0     0     1     3    14    12     6     2     1     0     1     0     0
9        G4   2     0     0     0     1     3    19    10     8     1     1     1     1     0     0
10       G5   2     0     0     0     0     4    18    13     6     2     1     0     1     0     0
11       G1   3     0     0     0     0     5    21    11     8     1     0     0     1     1     0
12       G2   3     0     0     0     0     3    20    10     7     1     1     1     1     0     0
13       G3   3     0     0     0     0     4    19    12     8     1     1     0     1     1     0
14       G4   3     0     0     0     0     3    21    11     6     1     0     1     1     0     0
15       G5   3     0     0     0     0     4    17    10     8     1     1     1     0     0     0
   GermPercent FirstGermTime LastGermTime PeakGermTime TimeSpreadGerm t50_Coolbear t50_Farooq MeanGermTi
1     80.00000             5           11            6              6     5.970588   5.941176     6.7000
2     82.35294             4           12            6              8     6.192308   6.153846     6.8571
3     93.75000             4           12            6              8     6.000000   5.972222     6.8660
4     90.19608             5           12            6              7     6.041667   6.000000     6.8913
5     96.00000             5           13            6              8     5.975000   5.950000     6.8125
6     93.87755             5           12            6              7     5.976190   5.952381     6.8695
7     87.50000             5           11            6              6     5.972222   5.944444     6.6904
8     85.10638             4           12            6              8     6.208333   6.166667     6.8750
9     86.53846             4           12            6              8     6.000000   5.973684     6.8660
10    90.00000             5           12            6              7     6.076923   6.038462     6.8222
11    94.11765             5           13            6              8     5.928571   5.904762     6.7916
12    86.27451             5           12            6              7     5.975000   5.950000     6.8863
13    95.91837             5           13            6              8     6.083333   6.041667     6.9361
14    91.66667             5           12            6              7     5.928571   5.904762     6.7727
15    87.50000             5           11            6              6     6.050000   6.000000     6.8095
   SEGermTime CVGermTime MeanGermRate   VarGermRate   SEGermRate      CVG GermRateRecip_Coolbear GermRateR
1   0.1901416  0.1794868    0.1492537 0.0007176543 0.004235724 14.92537              0.1674877
2   0.2197333  0.2076717    0.1458333 0.0009172090 0.004673148 14.58333              0.1614907
3   0.2391061  0.2335882    0.1456311 0.0011572039 0.005071059 14.56311              0.1666667
4   0.2180907  0.2146419    0.1451104 0.0009701218 0.004592342 14.51104              0.1655172
```

```
5   0.2221275  0.2259002    0.1467890 0.0010995627 0.004786184 14.67890            0.1673640
6   0.2122088  0.2095140    0.1455696 0.0009301809 0.004496813 14.55696            0.1673307
7   0.1818989  0.1761967    0.1494662 0.0006935558 0.004063648 14.94662            0.1674419
8   0.2297923  0.2113940    0.1454545 0.0009454531 0.004861721 14.54545            0.1610738
9   0.2260777  0.2208604    0.1456311 0.0010345321 0.004794747 14.56311            0.1666667
10  0.2017321  0.1983606    0.1465798 0.0008453940 0.004334343 14.65798            0.1645570
11  0.2227295  0.2272072    0.1472393 0.0011191581 0.004828643 14.72393            0.1686747
12  0.2210295  0.2129053    0.1452145 0.0009558577 0.004660905 14.52145            0.1673640
13  0.2324392  0.2297410    0.1441718 0.0010970785 0.004831366 14.41718            0.1643836
14  0.2078370  0.2035568    0.1476510 0.0009033254 0.004531018 14.76510            0.1686747
15  0.1994129  0.1897847    0.1468531 0.0007767634 0.004300508 14.68531            0.1652893
   GermSpeed_Count GermSpeed_Percent GermSpeedAccumulated_Count GermSpeedAccumulated_Percent GermSpeedCo
1         6.138925          12.27785                   34.61567                     69.23134
2         6.362698          12.47588                   35.54058                     69.68741
3         6.882179          14.33787                   38.29725                     79.78594
4         6.927417          13.58317                   38.68453                     75.85202
5         7.318987          14.63797                   41.00786                     82.01571
6         6.931782          14.14649                   38.77620                     79.13509
7         6.448449          13.43427                   36.38546                     75.80304
8         6.053175          12.87909                   33.77079                     71.85275
9         6.830592          13.13575                   38.11511                     73.29829
10        6.812698          13.62540                   38.19527                     76.39054
11        7.342796          14.39764                   41.17452                     80.73436
12        6.622258          12.98482                   37.00640                     72.56158
13        7.052320          14.39249                   39.29399                     80.19182
14        6.706782          13.97246                   37.69490                     78.53103
15        6.363925          13.25818                   35.69697                     74.36868
   GermSpeedCorrected_Accumulated WeightGermPercent MeanGermPercent MeanGermNumber TimsonsIndex TimsonsI
1                       0.4326958          47.42857        5.714286       2.857143     8.000000
2                       0.4315642          47.89916        5.882353       3.000000     9.803922
3                       0.4085040          54.46429        6.696429       3.214286    14.583333
4                       0.4288937          52.24090        6.442577       3.285714     7.843137
5                       0.4271652          56.14286        6.857143       3.428571    10.000000
6                       0.4130508          54.51895        6.705539       3.285714     6.122449
7                       0.4158338          51.93452        6.250000       3.000000     8.333333
8                       0.3968068          49.39210        6.079027       2.857143    10.638298
9                       0.4404413          50.27473        6.181319       3.214286     9.615385
10                      0.4243919          52.57143        6.428571       3.214286     8.000000
11                      0.4374793          55.18207        6.722689       3.428571     9.803922
12                      0.4289379          50.00000        6.162465       3.142857     5.882353
13                      0.4096608          55.24781        6.851312       3.357143     8.163265
14                      0.4112171          53.86905        6.547619       3.142857     6.250000
15                      0.4079653          51.19048        6.250000       3.000000     8.333333
   TimsonsIndex_KhanUngar GermRateGeorge GermIndex GermIndex_mod EmergenceRateIndex_Melville
1               0.5714286              4  5.840000      7.300000                         292
2               0.7002801              5  5.882353      7.142857                         300
3               1.0416667              7  6.687500      7.133333                         321
4               0.5602241              4  6.411765      7.108696                         327
5               0.7142857              5  6.900000      7.187500                         345
6               0.4373178              3  6.693878      7.130435                         328
7               0.5952381              4  6.395833      7.309524                         307
8               0.7598784              5  6.063830      7.125000                         285
9               0.6868132              5  6.173077      7.133333                         321
10              0.5714286              4  6.460000      7.177778                         323
```

```
11            0.7002801            5  6.784314    7.208333                    346
12            0.4201681            3  6.137255    7.113636                    313
13            0.5830904            4  6.775510    7.063830                    332
14            0.4464286            3  6.625000    7.227273                    318
15            0.5952381            4  6.291667    7.190476                    302
   EmergenceRateIndex_Melville_mod EmergenceRateIndex_BilbroWanjura EmergenceRateIndex_Fakorede PeakValu
1                         7.300000                         5.970149                    8.375000  9.50000
2                         7.142857                         6.125000                    8.326531  9.31372
3                         7.133333                         6.553398                    7.324444 10.41666
4                         7.108696                         6.675079                    7.640359 10.04901
5                         7.187500                         7.045872                    7.096354 11.25000
6                         7.130435                         6.696203                    7.317580 10.71428
7                         7.309524                         6.277580                    7.646259 10.41666
8                         7.125000                         5.818182                    8.078125  9.57446
9                         7.133333                         6.553398                    7.934815  9.85576
10                        7.177778                         6.596091                    7.580247 10.25000
11                        7.208333                         7.067485                    7.216146 11.02941
12                        7.113636                         6.389439                    7.981921  9.80392
13                        7.063830                         6.776074                    7.231326 10.96938
14                        7.227273                         6.496644                    7.388430 10.67708
15                        7.190476                         6.167832                    7.782313 10.15625
   GermValue_Czabator GermValue_DP GermValue_Czabator_mod GermValue_DP_mod    CUGerm GermSynchrony GermU
1            54.28571     57.93890               54.28571         39.56076 0.7092199     0.2666667
2            54.78662     52.58713               54.78662         40.99260 0.5051546     0.2346109
3            69.75446     68.62289               69.75446         53.42809 0.3975265     0.2242424
4            64.74158     70.43331               64.74158         48.86825 0.4672113     0.2502415
5            77.14286     80.16914               77.14286         56.23935 0.4312184     0.2606383
6            71.84506     76.51983               71.84506         53.06435 0.4934701     0.2792271
7            65.10417     69.41325               65.10417         47.37690 0.7371500     0.2729384
8            58.20345     56.00669               58.20345         43.67948 0.4855842     0.2256410
9            60.92165     58.13477               60.92165         45.30801 0.4446640     0.2494949
10           65.89286     70.91875               65.89286         49.10820 0.5584666     0.2555556
11           74.14731     77.39782               74.14731         54.27520 0.4288905     0.2686170
12           60.41632     64.44988               60.41632         44.71582 0.4760266     0.2737844
13           75.15470     78.16335               75.15470         54.94192 0.4023679     0.2506938
14           69.90947     74.40140               69.90947         51.41913 0.5383760     0.2991543
15           63.47656     67.62031               63.47656         46.48043 0.6133519     0.2497096
```

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)
```

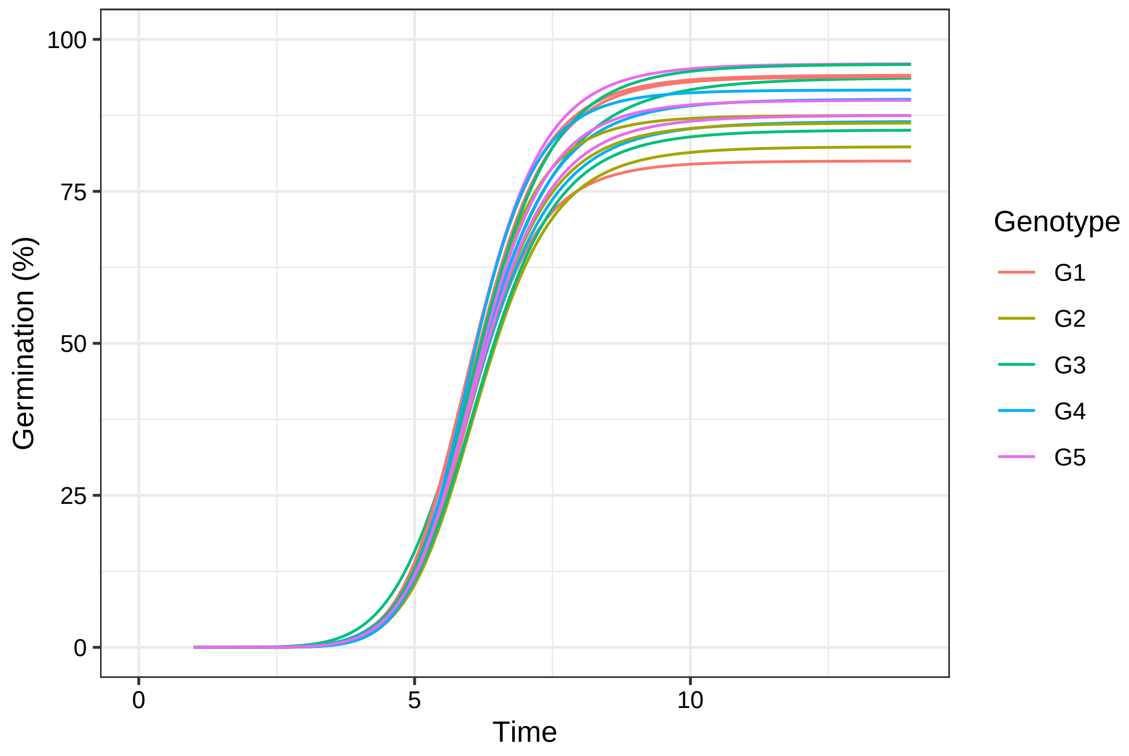
```
   Genotype Rep Day01 Day02 Day03 Day04 Day05 Day06 Day07 Day08 Day09 Day10 Day11 Day12 Day13 Day14 Tota
1        G1   1     0     0     0     0     4    17    10     7     1     0     1     0     0     0
```

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

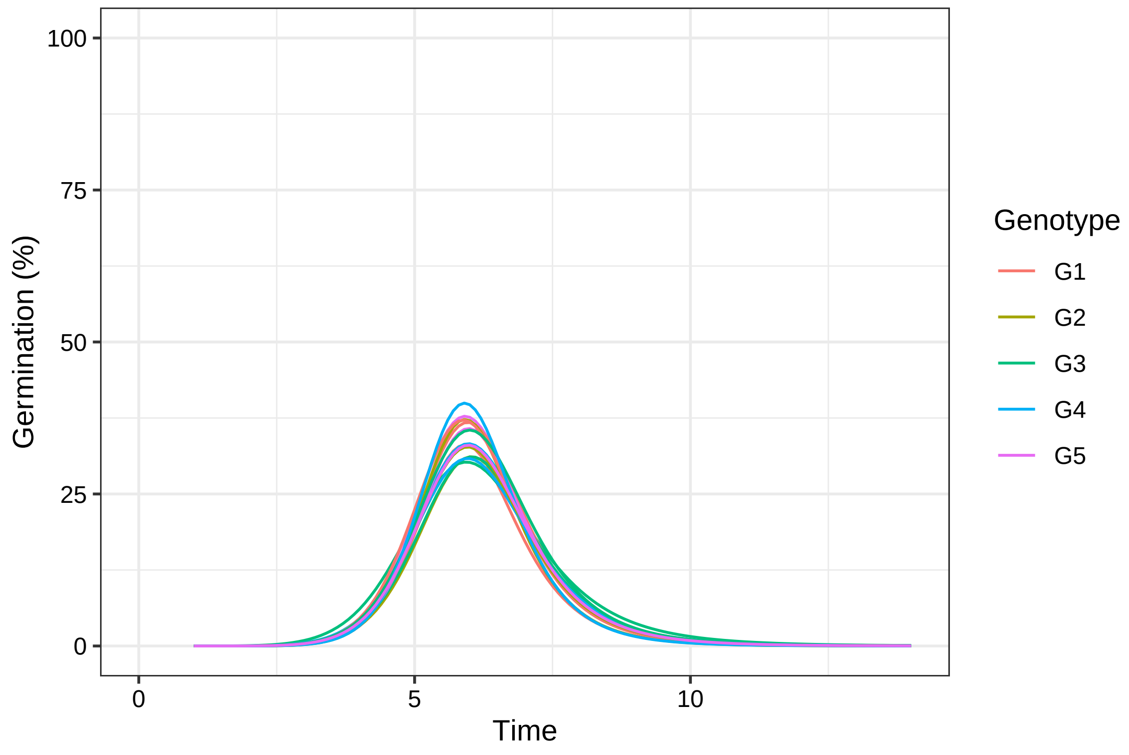
```
8       4.841106   3.073056
9       4.746574   3.157466
10      4.860681   2.818494
11      4.764249   2.839354
12      4.806015   2.957830
13      4.816395   3.033943
14      4.869401   2.562960
15      4.813086   2.972718
```

Multiple fitted curves generated in batch can also be plotted.

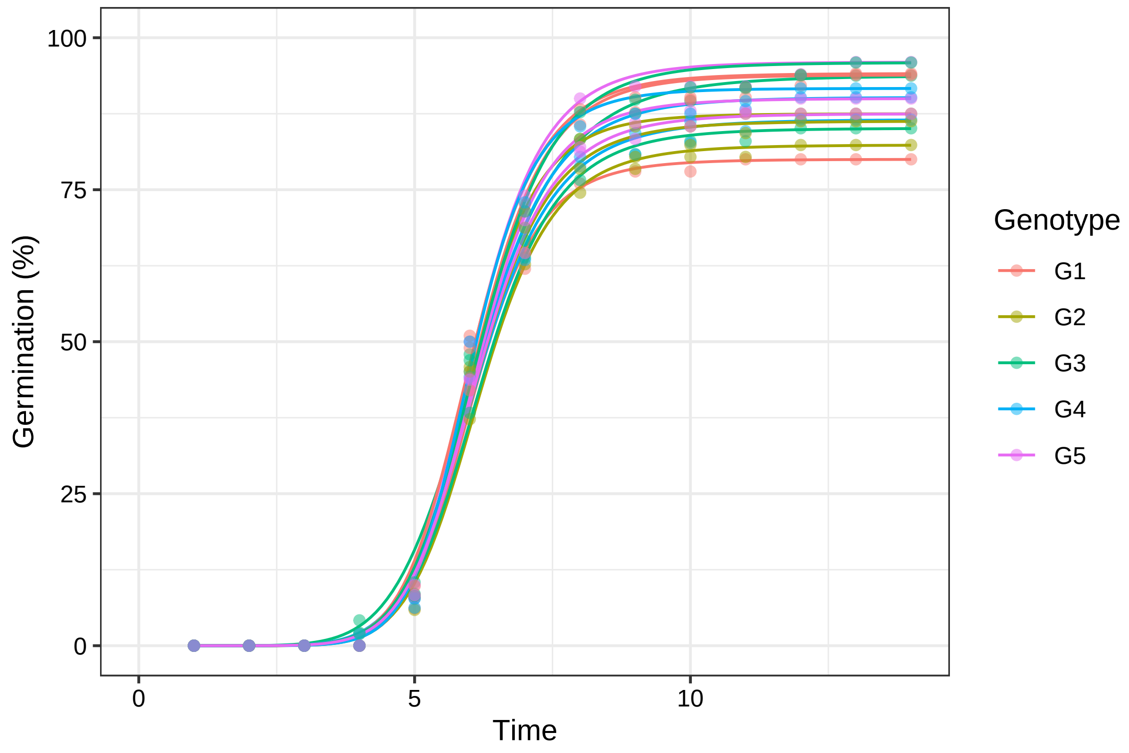
```r
data(gcdata)

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")
```



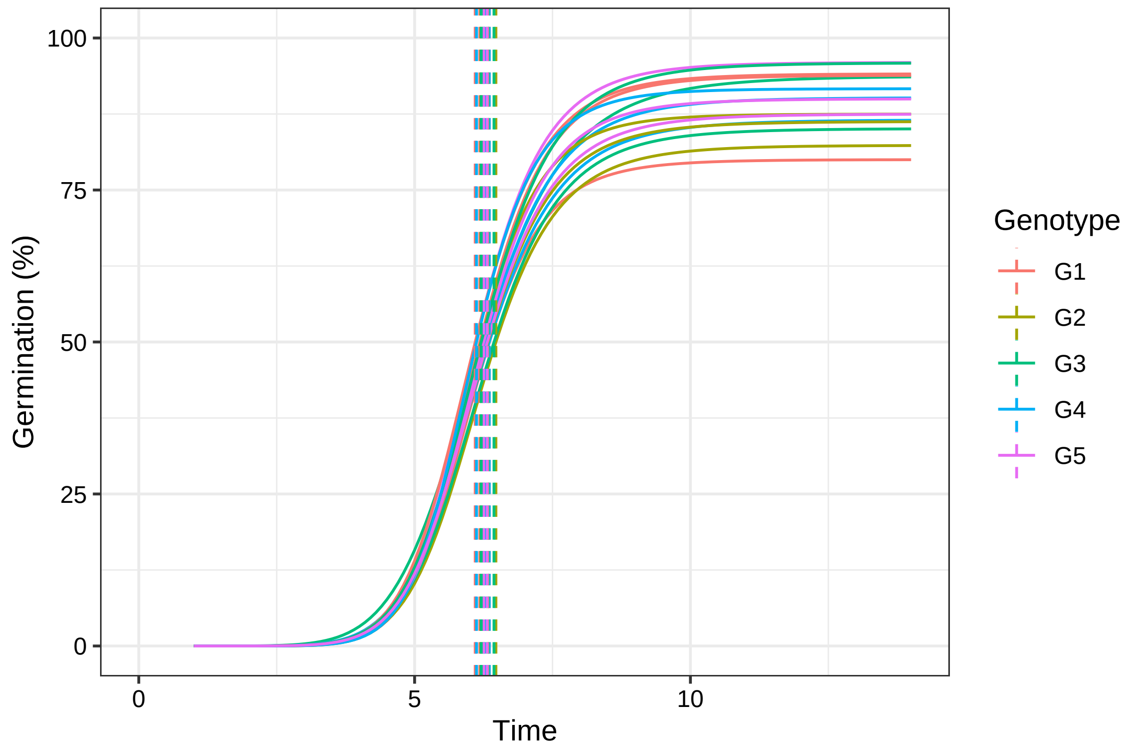
```r
# Plot ROG curves
plot(fits, rog = TRUE, group.col = "Genotype")
```



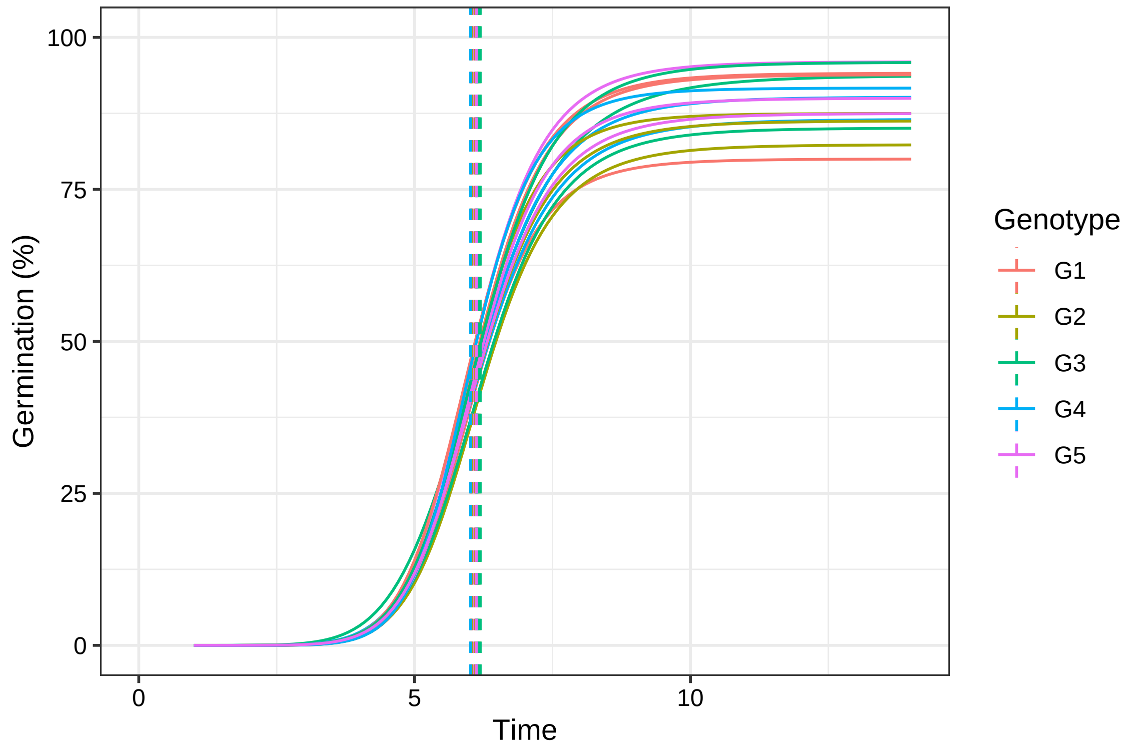
```
# Plot FPHF curves with points
plot(fits, group.col = "Genotype", show.points = TRUE)
```



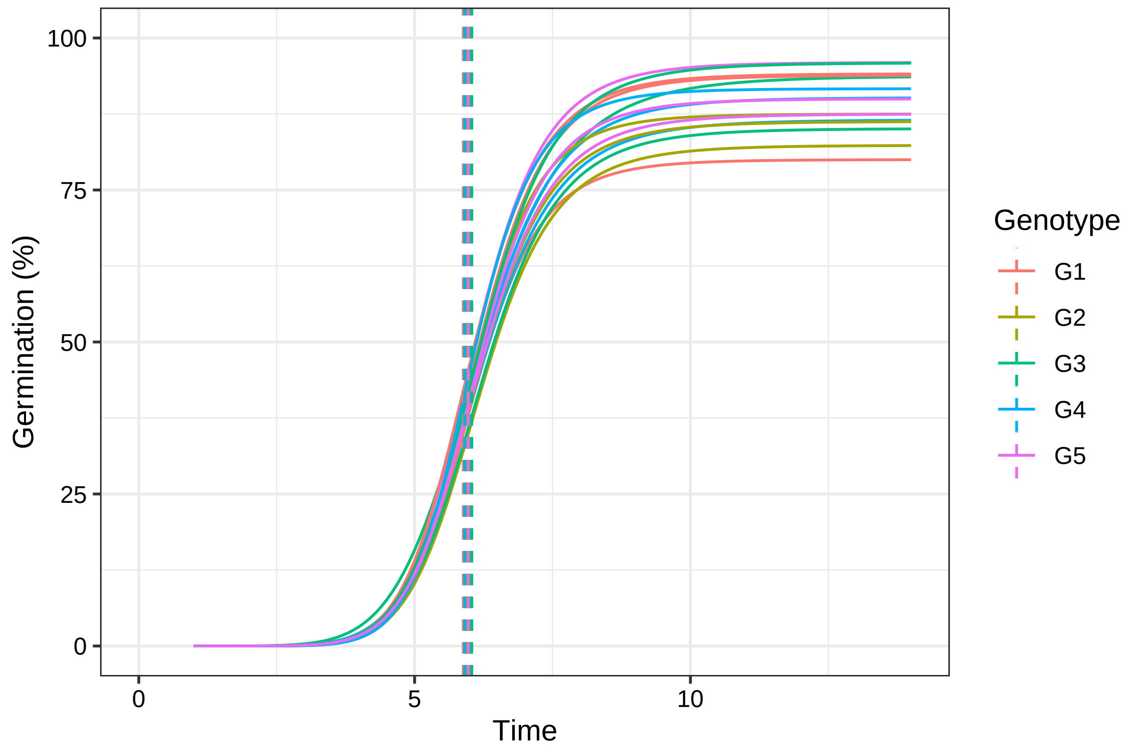
```
# Plot FPHF curves with annotations
plot(fits, group.col = "Genotype", annotate = "t50.total")
```



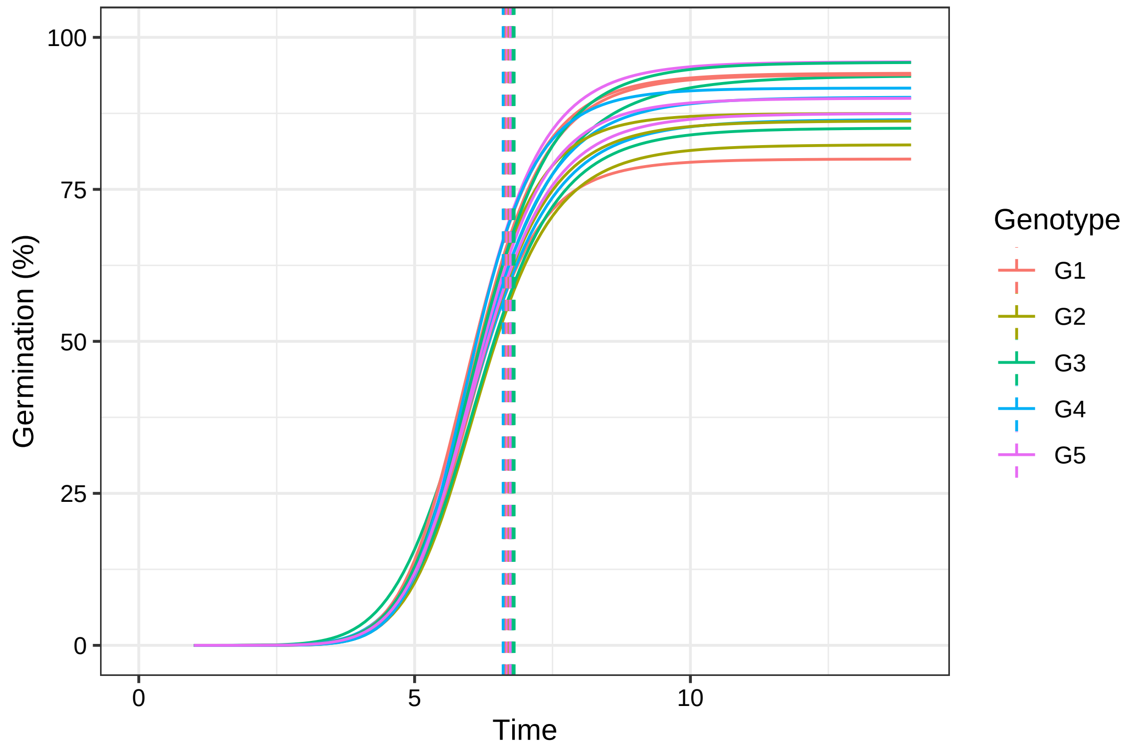
```r
plot(fits, group.col = "Genotype", annotate = "t50.germ")
```



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



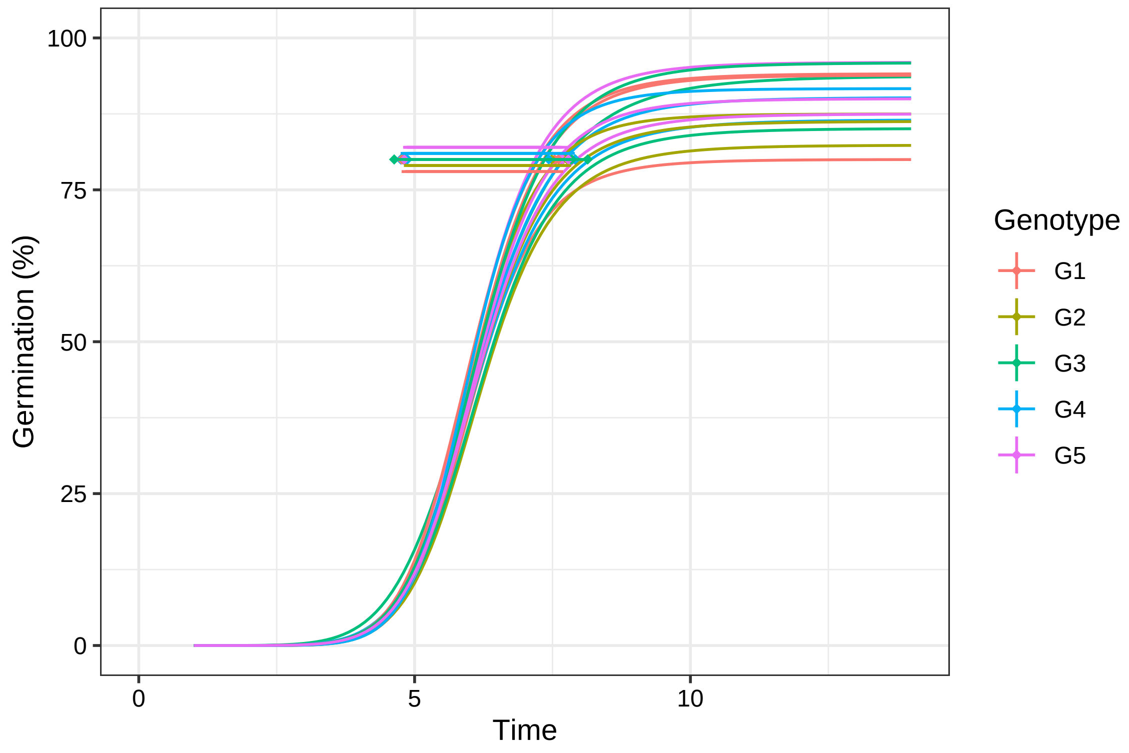
```
plot(fits, group.col = "Genotype", annotate = "mgt")
```



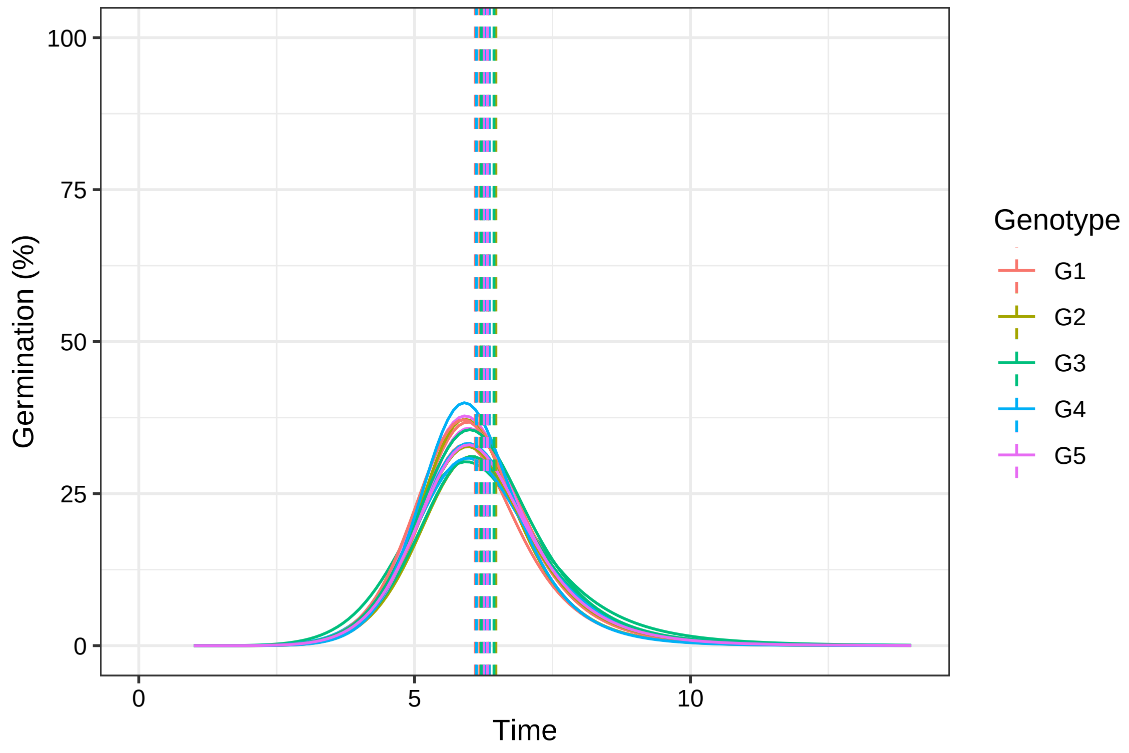
```
plot(fits, group.col = "Genotype", annotate = "uniformity")
```

```
Warning: position_dodge requires non-overlapping x intervals
```

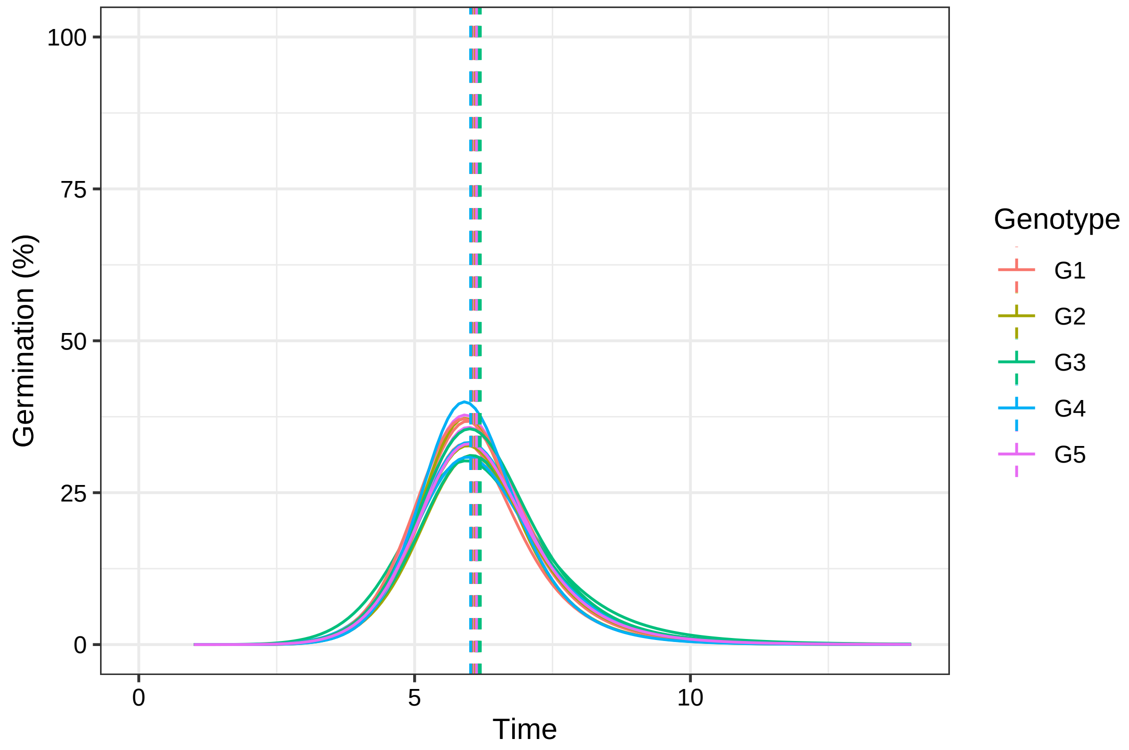
```
Warning: position_dodge requires non-overlapping x intervals
```



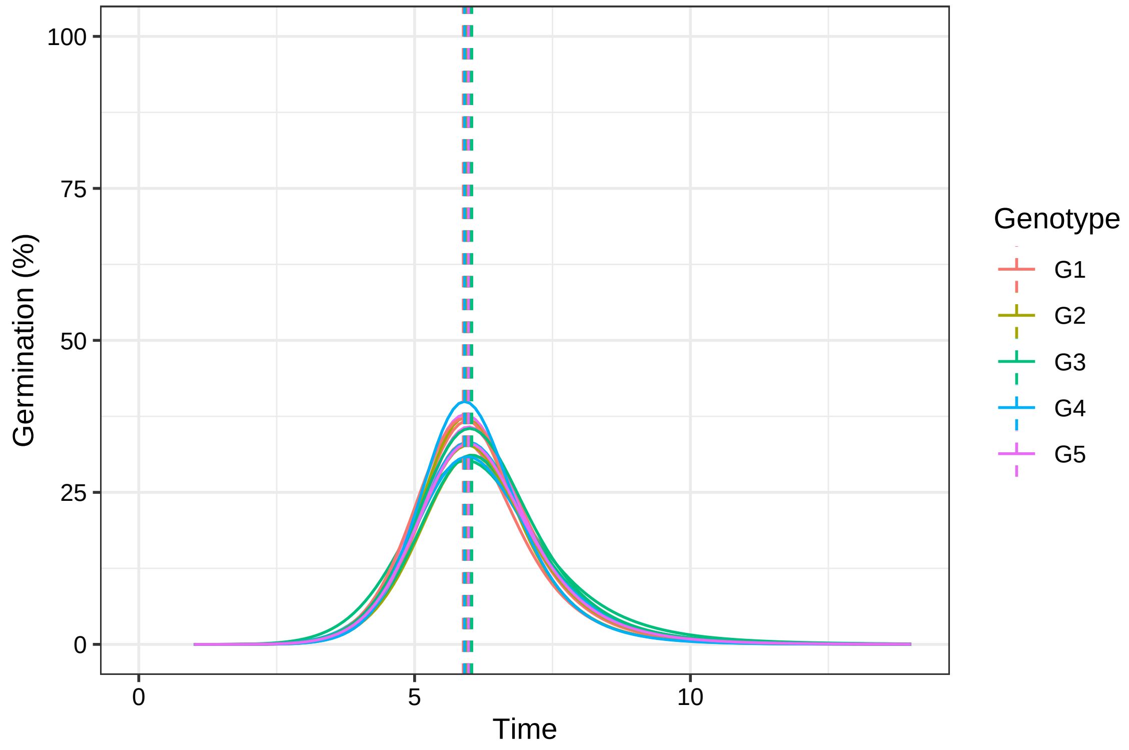
```
# Plot ROG curves with annotations
plot(fits, rog = TRUE, group.col = "Genotype", annotate = "t50.total")
```



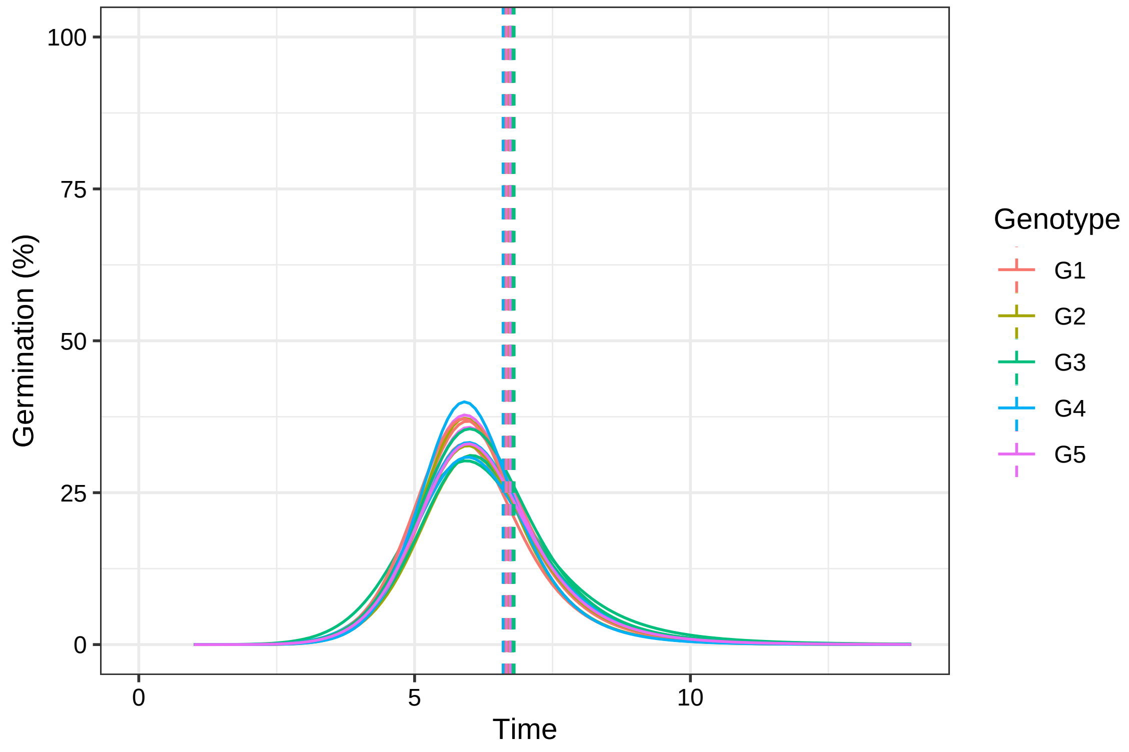
```
plot(fits, rog = TRUE, group.col = "Genotype", annotate = "t50.germ")
```



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

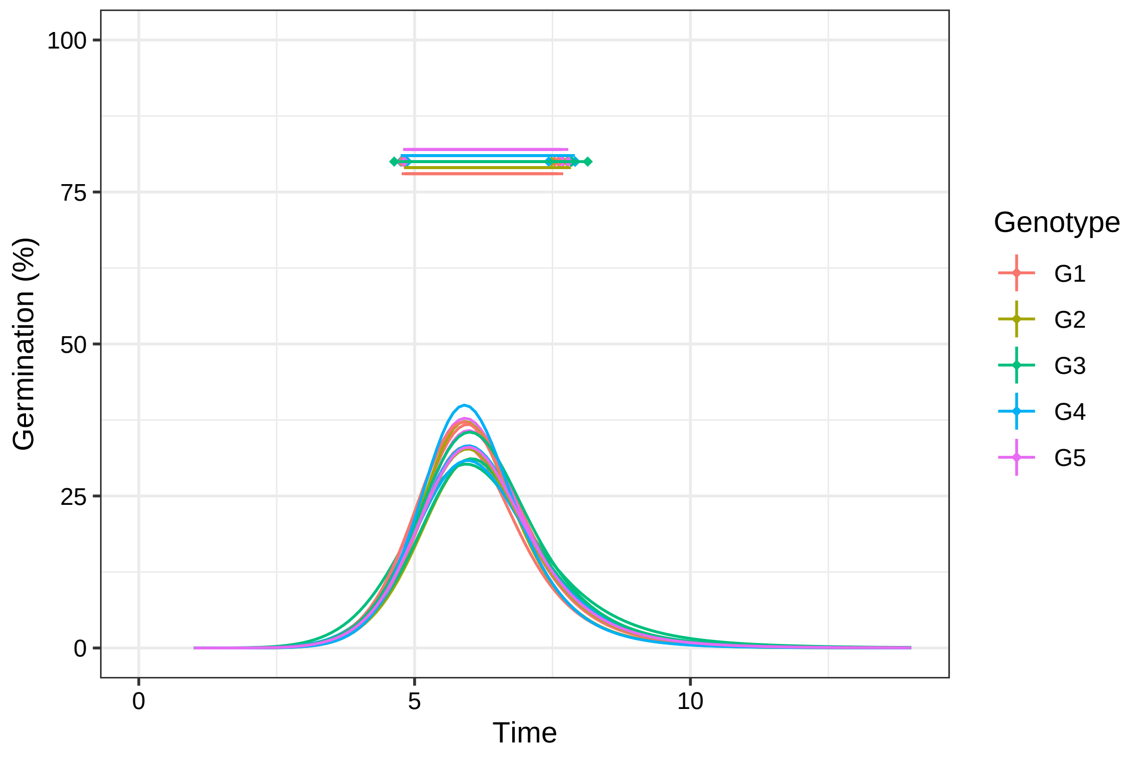


```
plot(fits, rog = TRUE, group.col = "Genotype", annotate = "mgt")
```

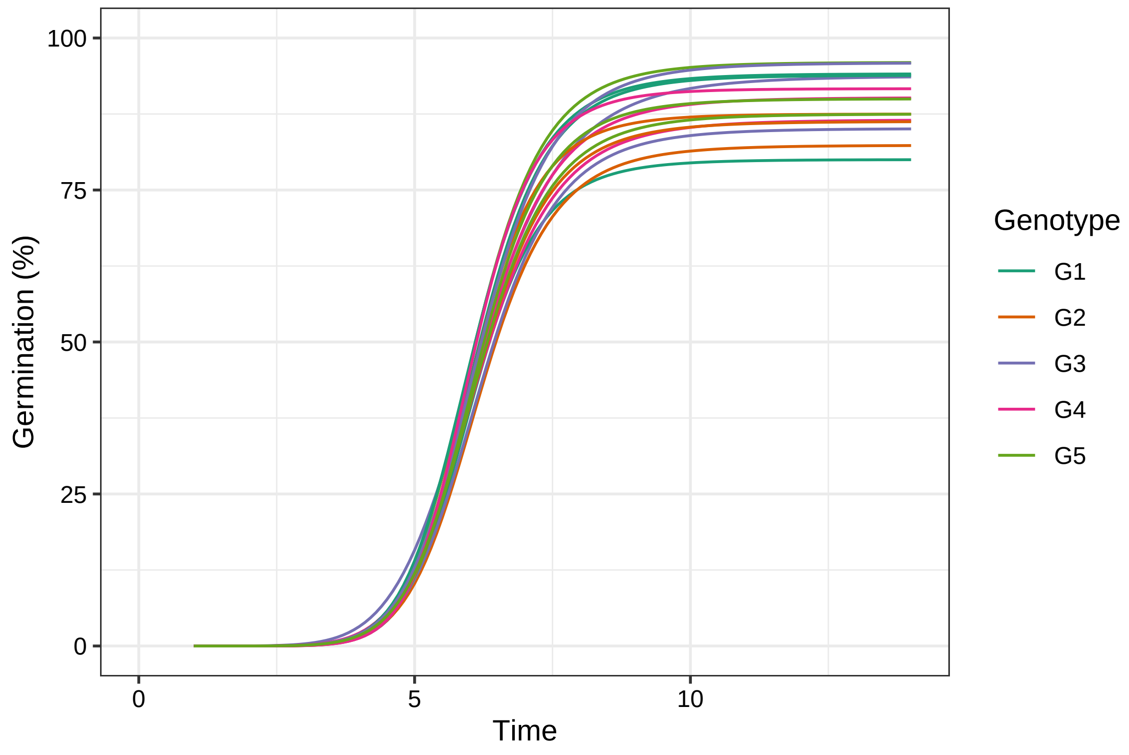


```
plot(fits, rog = TRUE, group.col = "Genotype", annotate = "uniformity")
```

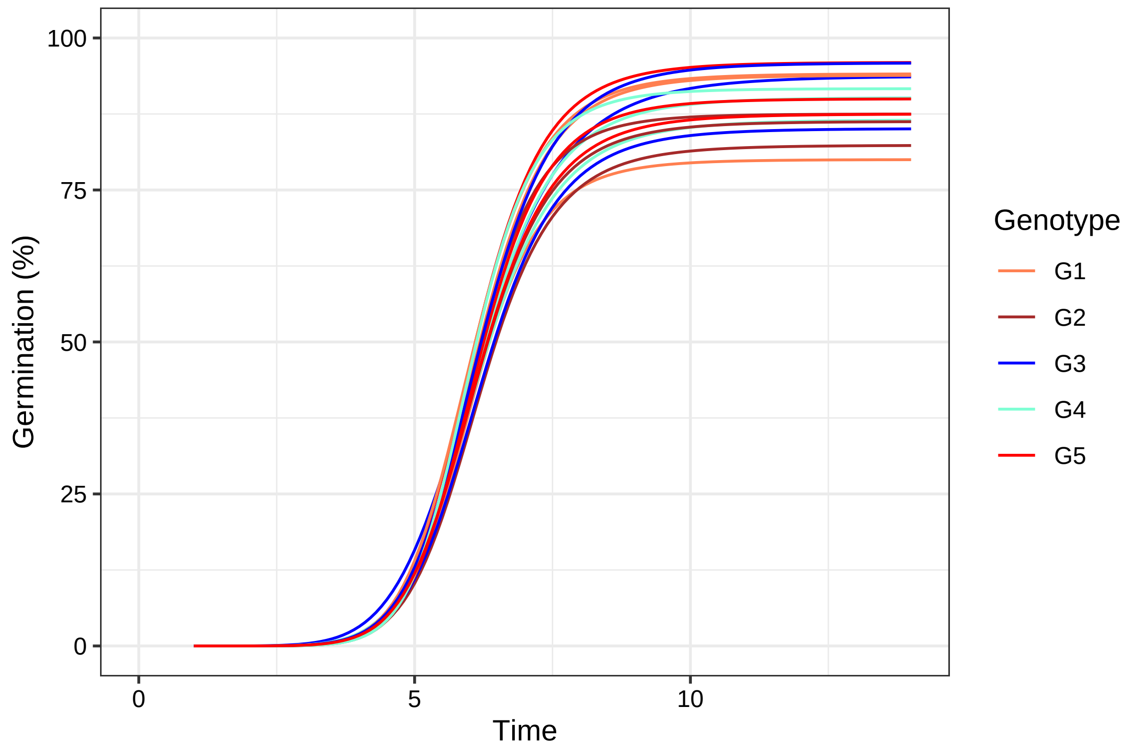
```
Warning: position_dodge requires non-overlapping x intervals

Warning: position_dodge requires non-overlapping x intervals
```



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

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



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



Citing germinationmetrics

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

  Aravind, J., Vimala Devi, S., Radhamani, J., Jacob, S. R., and Kalyani Srinivasan (2021).
  germinationmetrics: Seed Germination Indices and Curve Fitting. R package version 0.1.5,
  https://github.com/aravind-j/germinationmetricshttps://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
    year = {2021},
    note = {R package version 0.1.5},
    note = {https://github.com/aravind-j/germinationmetrics},
    note = {https://cran.r-project.org/package=germinationmetrics},
  }

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

Session Info

```
sessionInfo()
```

```
R Under development (unstable) (2021-02-02 r79929)
Platform: x86_64-w64-mingw32/x64 (64-bit)
Running under: Windows 10 x64 (build 19041)

Matrix products: default

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

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

other attached packages:
[1] germinationmetrics_0.1.5 ggplot2_3.3.3

loaded via a namespace (and not attached):
 [1] whoami_1.3.0           bitops_1.0-6           fs_1.5.0               xopen_1.0.0
 [5] usethis_2.0.0          devtools_2.3.2         RColorBrewer_1.1-2     covr_3.5.1
 [9] httr_1.4.2             rprojroot_2.0.2        hunspell_3.0.1         tools_4.1.0
[13] backports_1.2.1        R6_2.5.0               DBI_1.1.1              lazyeval_0.2.2
[17] colorspace_2.0-0       withr_2.4.1            tidyselect_1.1.0       prettyunits_1.1.1
[21] processx_3.4.5         curl_4.3               compiler_4.1.0         cli_2.3.0
[25] xml2_1.3.2             desc_1.2.0             labeling_0.4.2         scales_1.1.1
[29] callr_3.5.1            goodpractice_1.0.2.9000 pkgdown_1.6.1         stringr_1.4.0
[33] digest_0.6.27          rmarkdown_2.6          lintr_2.0.1            pkgconfig_2.0.3
[37] htmltools_0.5.1.1      sessioninfo_1.1.1      fastmap_1.1.0          highr_0.8
[41] rlang_0.4.10           rstudioapi_0.13        farver_2.0.3           generics_0.1.0
```

```
[45] jsonlite_1.7.2      dplyr_1.0.4        RCurl_1.98-1.2       magrittr_2.0.1
[49] Rcpp_1.0.6          munsell_0.5.0      lifecycle_0.2.0      stringi_1.5.3
[53] yaml_2.2.1          mathjaxr_1.2-0     gbRd_0.4-11          pkgbuild_1.2.0
[57] plyr_1.8.6          grid_4.1.0         ggrepel_0.9.1        crayon_1.4.0
[61] pander_0.6.3        knitr_1.31         ps_1.5.0             pillar_1.4.7
[65] reshape2_1.4.4      clisymbols_1.2.0   pkgload_1.1.0        XML_3.99-0.5
[69] glue_1.4.2          praise_1.0.0       evaluate_0.14        rex_1.2.0
[73] data.table_1.13.6   remotes_2.2.0      vctrs_0.3.6          Rdpack_2.1
[77] testthat_3.0.1      gtable_0.3.0       purrr_0.3.4          rcmdcheck_1.3.3
[81] tidyr_1.1.2         rematch2_2.1.2     assertthat_0.2.1     cachem_1.0.2
[85] xfun_0.20           rbibutils_2.0      broom_0.7.4          roxygen2_7.1.1
[89] cyclocomp_1.1.0     minpack.lm_1.2-1   tibble_3.0.6         tinytex_0.29
[93] memoise_2.0.0       ellipsis_0.3.1     xmlparsedata_1.0.4
```

References

El-Kassaby, Y. A., Moss, I., Kolotelo, D., and Stoehr, M. (2008). Seed germination: Mathematical representation and parameters extraction. *Forest Science* 54, 220–227. doi:10.1093/forestscience/54.2.220.