

# Package ‘growthcurver’

August 29, 2016

**Type** Package

**Title** Simple Metrics to Summarize Growth Curves

**Version** 0.2.1

**Date** 2016-03-24

**Description** This is a simple package that fits the logistic equation to microbial growth curve data (e.g., repeated absorbance measurements taken from a plate reader over time). From this fit, a variety of metrics are provided, including the maximum growth rate, the doubling time, the carrying capacity, the area under the logistic curve, and the time to the inflection point.

**LazyData** TRUE

**Depends** R (>= 2.10)

**Imports** caTools (>= 1.17.1), minpack.lm (>= 1.1), stats (>= 3.2.2), graphics (>= 3.2.2), grDevices (>= 3.2.2)

**URL** <https://github.com/sprouffske/growthcurver>

**BugReports** <https://github.com/sprouffske/growthcurver/issues>

**License** GPL (>= 2)

**Suggests** testthat, knitr, dplyr, ggplot2

**VignetteBuilder** knitr

**RoxygenNote** 5.0.0

**NeedsCompilation** no

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**Repository** CRAN

**Date/Publication** 2016-03-29 11:55:21

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gcfi	<i>Creates an object of class gcfi.</i>
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### Description

This is a constructor function for the "gcfi" class. This class is most often obtained as the return value when calling [SummarizeGrowth](#).

### Usage

```
gcfi(gc_vals, log_mod, data_t, data_n)
```

### Arguments

gc_vals	An object of class gcvals that contains the summarized metrics from fitting the growth model to a set of experimental observations. This is where the fitness proxy parameters can be found. See <a href="#">gcvals</a> for more information the information found in this object.
log_mod	An object of class nlsModel that contains the results of fitting the logistic growth model to the data
data_t	A numeric vector of times
data_n	A numeric vector of cell count or absorbance readings

### Value

An object of class gcfi, which is a list of three objects, that combines the parameters (vals = gc\_vals, model = log\_mod, data = list(data\_t, data\_n))

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gcvals	<i>Creates an object of type gcvals.</i>
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### Description

Constructor function for the "gcvals" class. This object is most often obtained when calling [SummarizeGrowth](#) (it is the first parameter in the [gcvals](#) object).

### Usage

```
gcvals(k, k_se, k_p, n0, n0_se, n0_p, r, r_se, r_p, sigma, df, t_mid, dt, auc_l,
      auc_e, note)
```

### Arguments

k	The carrying capacity parameter
k_se	The standard error of the carrying capacity parameter
k_p	The p value of the carrying capacity parameter
n0	The initial population size
n0_se	The standard error of the initial population size
n0_p	The p value of the initial population size
r	The growth rate
r_se	The standard error of the growth rate
r_p	The p value of the growthrate
sigma	Residual standard error from non-linear least squares fit of the model to the data
df	Degrees of freedom
t_mid	The time at the inflection point of the logistic curve (occurs at half of the carrying capacity)
dt	The maximum doubling time, obtained by evaluating the the unrestrained growth of the population with growth rate r
auc_l	The area under the curve of the fitted logistic equation from time 0 to time t
auc_e	The area under the curve of the measurements.
note	Feedback on common problems with fitting the logistic curve to the data

### Value

An object of class gcvals.

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growthdata

*Simulated growth curve data*

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### Description

A dataset containing absorbance measurements over time of microbes growing in a plate reader for 1 day. The growth curves for a whole plate are included.

### Usage

growthdata

### Format

A data frame with 145 observations and 97 variables:

**time** time, in hours

**A1** absorbance readings of well A1

**A2** absorbance readings of well A2

**A3** absorbance readings of well A3

**A4** absorbance readings of well A4

**A5** absorbance readings of well A5

**A6** absorbance readings of well A6

**A7** absorbance readings of well A7

**A8** absorbance readings of well A8

**A9** absorbance readings of well A9

**A10** absorbance readings of well A10

**A11** absorbance readings of well A11

**A12** absorbance readings of well A12

**B1** absorbance readings of well B1

**B2** absorbance readings of well B2

**B3** absorbance readings of well B3

**B4** absorbance readings of well B4

**B5** absorbance readings of well B5

**B6** absorbance readings of well B6

**B7** absorbance readings of well B7

**B8** absorbance readings of well B8

**B9** absorbance readings of well B9

**B10** absorbance readings of well B10

**B11** absorbance readings of well B11

- B12** absorbance readings of well B12
- C1** absorbance readings of well C1
- C2** absorbance readings of well C2
- C3** absorbance readings of well C3
- C4** absorbance readings of well C4
- C5** absorbance readings of well C5
- C6** absorbance readings of well C6
- C7** absorbance readings of well C7
- C8** absorbance readings of well C8
- C9** absorbance readings of well C9
- C10** absorbance readings of well C10
- C11** absorbance readings of well C11
- C12** absorbance readings of well C12
- D1** absorbance readings of well D1
- D2** absorbance readings of well D2
- D3** absorbance readings of well D3
- D4** absorbance readings of well D4
- D5** absorbance readings of well D5
- D6** absorbance readings of well D6
- D7** absorbance readings of well D7
- D8** absorbance readings of well D8
- D9** absorbance readings of well D9
- D10** absorbance readings of well D10
- D11** absorbance readings of well D11
- D12** absorbance readings of well D12
- E1** absorbance readings of well E1
- E2** absorbance readings of well E2
- E3** absorbance readings of well E3
- E4** absorbance readings of well E4
- E5** absorbance readings of well E5
- E6** absorbance readings of well E6
- E7** absorbance readings of well E7
- E8** absorbance readings of well E8
- E9** absorbance readings of well E9
- E10** absorbance readings of well E10
- E11** absorbance readings of well E11
- E12** absorbance readings of well E12

**F1** absorbance readings of well F1  
**F2** absorbance readings of well F2  
**F3** absorbance readings of well F3  
**F4** absorbance readings of well F4  
**F5** absorbance readings of well F5  
**F6** absorbance readings of well F6  
**F7** absorbance readings of well F7  
**F8** absorbance readings of well F8  
**F9** absorbance readings of well F9  
**F10** absorbance readings of well F10  
**F11** absorbance readings of well F11  
**F12** absorbance readings of well F12  
**G1** absorbance readings of well G1  
**G2** absorbance readings of well G2  
**G3** absorbance readings of well G3  
**G4** absorbance readings of well G4  
**G5** absorbance readings of well G5  
**G6** absorbance readings of well G6  
**G7** absorbance readings of well G7  
**G8** absorbance readings of well G8  
**G9** absorbance readings of well G9  
**G10** absorbance readings of well G10  
**G11** absorbance readings of well G11  
**G12** absorbance readings of well G12  
**H1** absorbance readings of well H1  
**H2** absorbance readings of well H2  
**H3** absorbance readings of well H3  
**H4** absorbance readings of well H4  
**H5** absorbance readings of well H5  
**H6** absorbance readings of well H6  
**H7** absorbance readings of well H7  
**H8** absorbance readings of well H8  
**H9** absorbance readings of well H9  
**H10** absorbance readings of well H10  
**H11** absorbance readings of well H11  
**H12** absorbance readings of well H12

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NAAtT                      *Number of Cells at Time t*

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### Description

This function gives the number of cells or absorbance (N) at time t when the parameters to the logistic equation are K, N0, and r.

### Usage

```
NAAtT(k, n0, r, t)
```

### Arguments

k	The carrying capacity
n0	The initial population size (absorbance or individuals)
r	The exponential "growth rate"
t	The time at which you want to know N

### Value

The number of cells, or N, at time t

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SummarizeGrowth                      *Summarize Growth Curves*

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### Description

This function finds the parameters that describe the input data's growth. It does so by fitting the logistic curve to your growth curve measurements.

### Usage

```
SummarizeGrowth(data_t, data_n, t_trim = 0, bg_correct = "min",
  blank = NA)
```

### Arguments

data_t	A vector of timepoints (data_n must also be provided and be the same length).
data_n	A vector of cell counts or absorbance readings.
t_trim	Measurements taken after this time should not be included in fitting the curve. If stationary phase is variable, this may give you a better fit. A value of 0 means no trimming. Defaults to no trimming (0).

bg_correct	The background correction method to use. No background correction is performed for the default "none". Specifying "min" subtracts the smallest value in a column from all the rows in that column, and specifying "blank" subtracts the values from the blank vector from the data_n vector.
blank	A vector of absorbance readings from a blank well (typically contains only media) used for background correction. The corresponding blank value is subtracted from the data_n vector for each timepoint. Defaults to NA.

### Details

The logistic curve equation is

$$N_t = \frac{N_0 K}{N_0 + (K - N_0)e^{-rt}}$$

where  $N_t$  is the number of cells (or the absorbance reading) at time  $t$ ,  $N_0$  is the initial cell count (or absorbance reading),  $K$  is the carrying capacity, and  $r$  is the growth rate.

The fitness proxies returned are the parameters of the logistic equation and the area under the curve (a measure that integrates the effects of  $N_0$ ,  $K$ , and  $r$ ). See [gcfits](#) for more documentation on these.

### Value

An object of type `gcfits` containing the "fitness" proxies, as well as the input data and the fitted model.

### See Also

See the accompanying Vignette for an example of how to use and interpret `SummarizeGrowth`. [bit.ly/1p7w6dJ](https://bit.ly/1p7w6dJ).

See also [gcfits](#).

### Examples

```
# We can check that the parameters that are found are the same
# as we use to generate fake experimental data. To do so, let's first
# generate the "experimental" data using the logistic equation,
# e.g., absorbance readings from a single well in a plate reader over time.

k_in <- 0.5 # the initial carrying capacity
n0_in <- 1e-5 # the initial absorbance reading
r_in <- 1.2 # the initial growth rate
N <- 50 # the number of "measurements" collected during the growth
# curve experiment

data_t <- 0:N * 24 / N # the times the measurements were made (in hours)
data_n <- NA~T(k = k_in, n0 = n0_in, r = r_in, t = data_t) # the measurements

# Now summarize the "experimental" growth data that we just generated
gc <- SummarizeGrowth(data_t, data_n)

# Get the possible metrics for fitness proxies
gc$vals$r # growth rate is a common choice for fitness
gc$vals$t_gen # doubling time, or generation time, is also common
```



```

gc$vals$k
gc$vals$n0
gc$vals$auc_l
gc$vals$auc_e
gc$vals$t_mid

# Compare the data with the fit visually by plotting it
plot(gc)

```

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SummarizeGrowthByPlate

*Summarize Growth Curves*


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### Description

This function finds the parameters that describe the input data's growth for a plate of growth curves. It does so by fitting the logistic curve to your growth curve measurements.

### Usage

```

SummarizeGrowthByPlate(plate, t_trim = 0, bg_correct = "min",
  plot_fit = FALSE, plot_file = "growthcurver.pdf")

```

### Arguments

plate	A data.table with at least two columns. One column contains timepoints that measurements were taken (e.g., hours) and must be named "time". An optional column can be included called "blank" that contains the blank readings for background correction (make sure to select the "blank" bg_correct option if you provide a blank column). Each remaining column contains the absorbance readings from a single well in a plate.
t_trim	Measurements taken after this time should not be included in fitting the curve. If stationary phase is variable, this may give you a better fit. A value of 0 means no trimming. Defaults to no trimming (0).
bg_correct	The background correction method to use. No background correction is performed for "none". Specifying "min" subtracts the smallest value in a column from all the rows in that column, and specifying "blank" subtracts the values from the blank vector from the data_n vector.
plot_fit	TRUE if you want to generate a pdf file that plots all columns provided in the plate along with the growthcurver's fit. The default value is FALSE, which generates no plots.
plot_file	The name of the file to save the plots to if you set plot_fit to TRUE. The default file is called "growthcurver.pdf".

## Details

The logistic curve equation is

$$N_t = \frac{N_0 K}{N_0 + (K - N_0)e^{-rt}}$$

where  $N_t$  is the number of cells (or the absorbance reading) at time  $t$ ,  $N_0$  is the initial cell count (or absorbance reading),  $K$  is the carrying capacity, and  $r$  is the growth rate.

The fitness proxies returned are the parameters of the logistic equation and the area under the curve (a measure that integrates the effects of  $N_0$ ,  $K$ , and  $r$ ). See [gcfits](#) for more documentation on these.

This method expects that your data adhere to a particular format.

- The data are provided in a `data.frame`
- One column in the `data.frame` is named "time" and contains the time measurements (e.g., hours).
- Each remaining column contains the readings from a single well in a plate reader. The name of the column will be used to identify the sample in the output data.
- There are no missing values or non-numeric data in the `data.frame`.

## Value

A `data.table` containing the summary metrics and residual error from the fit of the logistic curve to the data. The names of the input columns are used to identify each well (or sample).

## See Also

See the accompanying Vignette for an example of how to use and interpret `SummarizeGrowthByPlate`. [bit.ly/1p7w6dJ](https://bit.ly/1p7w6dJ)

## Examples

```
#Get the summary metrics for the entire plate of sample data provided
#with the Growthcurver package

#First, load the example data provided with Growthcurver. Note that there is
#a column named "time" -- this is necessary for Growthcurver to know which
#column contains the time measurements. In this dataset, the repeated
#measurements from a single well in a plate are given in a column of data.

myPlate <- growthdata
names(myPlate)

#Next, do the analysis for all the columns.
summary_plate <- SummarizeGrowthByPlate(plate = myPlate)

#The output is a data frame that contains the information on the best
#fit for each column of data.
head(summary_plate)      # Use head to display just the first few rows
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