

# Package ‘cellGrowth’

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**Maintainer** Julien Gagneur <gagneur@genzentrum.lmu.de>

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**Title** Fitting cell population growth models

**Author** Julien Gagneur <gagneur@genzentrum.lmu.de>, Andreas Neudecker  
<a.neudecker@arcor.de>

**Description** This package provides functionalities for the fitting of  
cell population growth models on experimental OD curves.

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Visualization, TimeCourse

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**Imports** lattice

**Collate** 'bandwidthCV.R' 'baranyi.R' 'fitCellGrowth.R'  
'fitCellGrowths.R' 'getRowColumn.R' 'getWellIdsTecan.R'  
'gompertz.R' 'guessCellGrowthParams.R' 'logistic.R'  
'plot.cellGrowthFit.R' 'plot.well.R' 'plotPlate.R'  
'readGenios.R' 'readYeastGrower.R' 'rosso.R' 'standardWellId.R'  
'wellDataFrame.R'

**NeedsCompilation** no

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bandwidthCV	<i>Bandwidth cross-validation</i>
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## Description

Perform cross-validation to detect optimal bandwidth

## Usage

```
bandwidthCV(well, fileParser = readYeastGrower,
  getWellIds = getWellIdsTecan,
  bandwidths = seq(0.5 * 3600, 10 * 3600, length.out = 30),
  nFold = 10, nWell = 100, cutoff = 0.95,
  calibration = identity, scaleY = log2)
```

## Arguments

well	well dataframe. See <a href="#">wellDataFrame</a> .
fileParser	Converts the file generated by the machine to proper R format. See <a href="#">readYeastGrower</a> for details.
getWellIds	function or vector. If function its parameter is the return value of fileParser. It should return a vector containing the well ids (e.g. A01, A02, ...). You can set the well ids vector directly. See <a href="#">getWellIdsTecan</a> .
bandwidths	vector of bandwidths to test on
nFold	integer. In how many parts is the sample divided for cross-validation?
nWell	integer. How many wells out of the well dataframe will be used for cross validation?
cutoff	scalar between 0 and 1. See details.
calibration	function or list of functions. If function, calibration is applied to all raw data. If list, the well dataframe must contain a column machine. Depending on that column the according function in the list is applied to the raw data. See details
scaleY	function applied to the calibrated data.

## Details

This function needs a few minutes time. The "optimal" bandwidth is the largest bandwidth which is in 95% (cutoff parameter) of all cases within one standard deviation of the best bandwidth. This should make the derivative of the fitted curve more robust. The raw values from the machine might not be directly optical densities (OD), which is needed to infer doubling time. Calibration functions for each machine can be provided to map raw values into OD using the calibration parameter.

**Value**

list with entries

bandwidth	"optimal" bandwidth
well	well dataframe
bandwidths	tested bandwidths
err2	squared error
err2std	Standard deviation of squared error
muStd	Standard deviation of max growth rate
oneStdOfMini	bandwidths within one std of best

**Author(s)**

Julien Gagneur and Andreas Neudecker

**Examples**

```
folder <- system.file("extdata", package="cellGrowth")
well <- wellDataFrame(file.path(folder, "plateLayout.txt"), file.path(folder, "machineRun.txt"))

## for a fast example, we use nWell = 1 here. Use a large number (default 100) for real life applications
bw <- bandwidthCV(well, nWell=1)
```

---

baranyi

*Baranyi growth model*

---

**Description**

Baranyi growth model as defined in Kelly et al.

**Usage**

```
baranyi(x, mu, l, z0, zmax)
```

**Arguments**

x	numeric vector: time points for which log(OD) must be computed
mu	numeric scalar: maximal growth rate parameter
l	numeric scalar: time lag parameter
z0	numeric scalar: minimal log(OD) parameter
zmax	numeric scalar: maximal log(OD) parameter

**Value**

numeric vector: log(OD) for the time points given in x

**Author(s)**

Julien Gagneur

## References

Kelly et al., The use of dummy data points when fitting bacterial growth curves, IMA Journal of Mathematics Applied in Medicine and Biology (1999) 16, 155-170

## Examples

```
x = 1:1000
y = baranyi(x, mu=0.01, l=200, z0=1, zmax=5)
plot(x,y)
```

---

fitCellGrowth	<i>Fit growth curves</i>
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## Description

Fit a cell growth curve

## Usage

```
fitCellGrowth(x, z, model = "locfit",
  locfit.h = 3 * 60 * 60, locfit.deg = 2,
  relative.height.at.lag = 0.1)
```

## Arguments

x	numeric vector: time points
z	numeric vector: log(OD)
model	which model to fit.
locfit.h	numeric: h parameter (window size) in call to <a href="#">locfit</a> . The default value is set to three hours assuming x given in seconds. You can detect a better bandwidth by calling <a href="#">bandwidthCV</a>
locfit.deg	numeric: deg parameter (polynomials degree) in call to <a href="#">locfit</a>
relative.height.at.lag	Parameter used by <a href="#">guessCellGrowthParams</a>

## Details

For the non-parametric "locfit" model, local regression is done by a call to [locfit](#). The returned maximum growth rate values the maximum value of the fitted derivative over the data points. For the parametric models "logistic", "gompertz", "rosso" and "baranyi", the function does a non-least square fit by calling [nls](#). Initial parameters values are generated by [guessCellGrowthParams](#). The returned maximum growth rate values the mu parameter of these models.

## Value

Fit as returned by [locfit](#) for the "locfit" model and as returned by [nls](#) for the "logistic", "gompertz", "rosso" and "baranyi" models. The returned value also has an attribute `maxGrowthRate` valuing the inferred maximum growth rate as well as an attribute `pointOfMaxGrowthRate` valuing the datapoint at which the growth rate is maximal. Also, it has an attribute `max` valuing the inferred maximum among the time points as well as `pointOfMax` valuing the datapoint of max fitted value. It gets the additional class `cellCurveFit` assigned.

**Author(s)**

Julien Gagneur and Moritz Matthey

**See Also**

[nls](#), [locfit](#), [baranyi](#), [gompertz](#), [logistic](#), [rosso](#), [guessCellGrowthParams](#), [fitCellGrowths](#)

**Examples**

```
x = 1:1000
z = gompertz(x, mu=0.01, l=200, z0=1, zmax=5) + rnorm(length(x),sd=0.1)
f = fitCellGrowth(x, z, model = "gompertz")
floc = fitCellGrowth(x, z, model = "locfit", locfit.h=500)
plot(x,z, main="simulated data\nGompertz model")
lines(x, predict(f,x), lwd=2, col="red")
lines(x, predict(floc,x), lwd=2, col="blue")
legend( "right", legend=c("gompertz fit", "locfit"), lwd=1, col=c("red","blue") )
```

---

fitCellGrowths

*Fit multiple growth curves*


---

**Description**

Fit growth curves for multiple wells

**Usage**

```
fitCellGrowths(well, plot.folder = NULL,
  model = "locfit", xlab = "time",
  ylab = expression(log2(Absorption)), scaleX = 1,
  scaleY = log2, calibration = identity,
  fileParser = readYeastGrower,
  getWellIds = getWellIdsTecan, locfit.h = 3 * 60 * 60,
  bandwidths = seq(0.5 * 3600, 10 * 3600, length.out = 30),
  nFold = 10, nWell = 100, cutoff = 0.95, ...)
```

**Arguments**

well	data.frame with mandatory columns directory, filename, well. See <a href="#">wellDataFrame</a>
plot.folder	see details
model	model to choose for fitting growth curve
fileParser	Converts the file generated by the machine to proper R format. See <a href="#">readYeastGrower</a> for details.
xlab	plot parameter
ylab	plot parameter
scaleX	useful if you want to get the doubling in another unit, e.g. days instead of seconds.
scaleY	function applied to the calibrated data.

calibration	function or list of functions. If function, calibration is applied to all raw data. If list, the well dataframe must contain a column machine. Depending on that column the according function in the list is applied to the raw data. See details
getWellIds	function or vector. If function its parameter is the return value of fileParser. It should return a vector containing the well ids (e.g. A01, A02, ...). You can set the well ids vector directly. See <a href="#">getWellIdsTecan</a> .
locfit.h	bandwidth parameter for local polynomial fitting. If set to "bandwidthCV" bandwidth is automatically selected through <a href="#">bandwidthCV</a>
bandwidths	passed to <a href="#">bandwidthCV</a> if locfit.h="bandwidthCV"
nFold	passed to <a href="#">bandwidthCV</a> if locfit.h="bandwidthCV"
nWell	passed to <a href="#">bandwidthCV</a> if locfit.h="bandwidthCV"
cutoff	passed to <a href="#">bandwidthCV</a> if locfit.h="bandwidthCV"
...	Parameter is passed to <a href="#">fitCellGrowth</a>

### Details

Essentially a wrapper for [fitCellGrowth](#). The function gets a well object and fits a growth curve on all wells. It computes the doubling frequency observed in a well and extracts the maximal growth rate ( 1/minimal doubling time). The raw values from the machine might not be directly optical densities (OD), which is needed to infer doubling time. Calibration functions for each machine can be provided to map raw values into OD using the calibration parameter. If the parameter plot.folder is set, the function creates a folder within plot.folder for each file in the well object. For each well a plot is written into that folder, named well\_id.png.

### Value

dataframe with entries	
maxGrowthRate	maximal growth rate
pointOfMaxGrowthRate	datapoint where growth rate is maximal
max	inferred maximum among the time points
pointOfMax	datapoint of the max fitted value

### Author(s)

Julien Gagneur and Andreas Neudecker

### See Also

[fitCellGrowth](#)

### Examples

```
plateLayout <- system.file("extdata", "plateLayout.txt", package="cellGrowth")
machineRun <- system.file("extdata", "machineRun.txt", package="cellGrowth")
well <- wellDataFrame(plateLayout,machineRun)
cal <- function(x){x+1}
fit <- fitCellGrowths(well,plot.folder="data",calibration=cal)
```

---

getRowColumn	<i>Convert well ids to row and column</i>
--------------	---

---

**Description**

Converts well ids to row and column

**Usage**

```
getRowColumn(wellId)
```

**Arguments**

wellId            vector of well ids

**Value**

vector of lists containing row and column

**Author(s)**

Andreas Neudecker

**Examples**

```
getRowColumn(c("A01", "B05"))
```

---

getWellIdsTecan	<i>Get aliases for wells</i>
-----------------	------------------------------

---

**Description**

The aliases are generated by extracting the information from parsed data of the file generated by the tecan machine. See [readYeastGrower](#) and [readGenios](#).

**Usage**

```
getWellIdsTecan(data)
```

**Arguments**

data            parsed data of the file. See [readYeastGrower](#) and [readGenios](#)

**Value**

vector containing the aliases

**Author(s)**

Julien Gagneur, Andreas Neudecker

**Examples**

```
data <- readYeastGrower( system.file("extdata", "Plate1_YPFruc.txt", package="cellGrowth"))
ids <- getWellIdsTecan(data)
```

---

gompertz

*Gompertz growth model*

---

**Description**

Gompertz growth model as defined in Zwietering et al.

**Usage**

```
gompertz(x, mu, l, z0, zmax)
```

**Arguments**

x	numeric vector: time points for which log(OD) must be computed
mu	numeric scalar: maximal growth rate parameter
l	numeric scalar: time lag parameter
z0	numeric scalar: minimal log(OD) parameter
zmax	numeric scalar: maximal log(OD) parameter

**Value**

numeric vector: log(OD) for the time points given in x

**Author(s)**

Julien Gagneur

**References**

Zwietering, et al. Modeling of the Bacterial Growth Curve, APPLIED AND ENVIRONMENTAL MICROBIOLOGY, 1990.

**Examples**

```
x = 1:1000
y = gompertz(x, mu=0.01, l=200, z0=1, zmax=5)
plot(x,y)
```



---

guessCellGrowthParams *Guess growth models parameters*

---

### Description

Guess initial parameters values for growth models

### Usage

```
guessCellGrowthParams(x, z, relative.height.at.lag = 0.1)
```

### Arguments

x	numeric vector: time points
z	codenumeric vector: log(OD)
relative.height.at.lag	numeric scalar (see Details)

### Details

The `relative.height.at.lag` parameter should be close to the relative height of the point, where the curve reaches its maximal slope. If the fitting fails, try to set this parameter to a different value.

### Value

A list with entries:

mu	numeric scalar: maximal growth rate parameter
l	numeric scalar: time lag parameter
z0	numeric scalar: minimal log(OD) parameter
zmax	numeric scalar: maximal log(OD) parameter

### Author(s)

Julien Gagneur

### Examples

```
x <- 1:1000
z <- gompertz(x, mu=0.01, l=200, z0=1, zmax=5)+rnorm(length(x),mean=0,sd=0.25)
guess <- guessCellGrowthParams(x,z,relative.height.at.lag=0.5)
fit <- nls(z~gompertz(x,mu,l,z0,zmax),start=guess)
plot(x,z)
lines(x,predict(fit,x),lwd=2,col="red")
```

---

logistic	<i>Logistic growth model</i>
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---

**Description**

Logistic growth model as defined in Zwietering et al.

**Usage**

```
logistic(x, mu, l, z0, zmax)
```

**Arguments**

x	numeric vector: time points for which log(OD) must be computed
mu	numeric scalar: maximal growth rate parameter
l	numeric scalar: time lag parameter
z0	numeric scalar: minimal log(OD) parameter
zmax	numeric scalar: maximal log(OD) parameter

**Value**

numeric vector: log(OD) for the time points given in x

**Author(s)**

Julien Gagneur

**References**

Zwietering, et al. Modeling of the Bacterial Growth Curve, APPLIED AND ENVIRONMENTAL MICROBIOLOGY, 1990.

**Examples**

```
x = 1:1000  
y = logistic(x, mu=0.01, l=200, z0=1, zmax=5)  
plot(x,y)
```

---

plot.cellGrowthFit      *Generic plot function for datatype cellGrowthFit*

---

### Description

Plot of a growth curve showing raw data and fitted curve

### Usage

```
plot.cellGrowthFit(x, scaleX = 1, xlab = "time",
  ylab = "log2(OD)", lwd = 0.5, ...)
```

### Arguments

x	growth curve object. See <a href="#">fitCellGrowth</a>
scaleX	scalar affecting the scaling of the x-axis.
xlab	plot parameter
ylab	plot parameter
lwd	plot parameter
...	optional plot parameters passed to the plot function

### Author(s)

Andreas Neudecker

### Examples

```
# Parse file
dat = readYeastGrower( system.file("extdata", "Plate1_YPFruc.txt", package="cellGrowth") )

# fit
n <- names( dat$OD)[36]
fit <- fitCellGrowth(x=dat$time,z=log2(dat$OD[[n]]), model = "locfit")
plot(fit)
```

---

plot.well      *Generic plot function for datatype well*

---

### Description

Plots well plate as lattice xyplot.

### Usage

```
plot.well(x, file = NULL, labelColumn = NULL,
  calibration = identity, ...)
```

**Arguments**

x	the well object
file	which plate file to plot? If NULL (default) the first file is taken.
labelColumn	column in the well object to take label for the wells from
calibration	function or list of functions. If calibration is a function it is applied to all raw data. If it is a list, the well dataframe must contain a column named machine. Depending on that column the according function in the list is applied to the raw data.
...	optional plot parameters, see details

**Details**

This function calls `plotPlate` for the plate plate. The ... parameter is passed to the `plotPlate` function.

**Author(s)**

Andreas Neudecker

---

plotPlate	<i>Plot of a well plate</i>
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---

**Description**

Plot of a well plate directly from a file using a lattice xyplot

**Usage**

```
plotPlate(file, labels = NULL,
          fileParser = readYeastGrower,
          getWellIds = getWellIdsTecan, calibration = identity,
          extractRowColumn = getRowColumn, cex = 0.05,
          scaleX = 1, scaleY = log2, strip.lines = 1.05,
          strip.cex = 0.8, xlab = "time", ylab = "log2(OD)",
          main = basename(file),
          scales = list(x = list(rot = 45)), ...)
```

**Arguments**

file	file name
labels	vector of characters indicating the label of the wells
fileParser	the file parser which reads the file generated by the machine
getWellIds	function or vector. If getWellIds is a function its parameter is the parsed data of the file parsed by fileParser. It should return a vector containing the well identifiers, e.g. A01, A02, .. You can as well set the well identifiers as a vector directly
calibration	calibration function applied to the raw data (before scaleY is applied)
extractRowColumn	function which converts well identifiers into row and column names

cex	plot parameter
scaleX	factor which scales the x-axis
scaleY	function how to convert the y-axis ( e.g. log2 )
strip.lines	height in lines of the labels
strip.cex	text-size of the labels
xlab	plot parameter
ylab	plot parameter
main	plot parameter
scales	plot parameter
...	optional plot parameter. See details

### Details

All plot parameters are passed to the [xyplot](#) function

### Author(s)

Andreas Neudecker

### Examples

```
plotPlate( system.file("extdata", "tecan_genios.txt", package="cellGrowth"), fileParser=readGenios)
```

---

readGenios	<i>Read Tecan Genios data files</i>
------------	-------------------------------------

---

### Description

Read raw data file form Tecan Genios instrument

### Usage

```
readGenios(file)
```

### Arguments

file	filename
------	----------

### Value

a list with entries:

time	a numeric vector of time points
OD	a data.frame vector of measured OD. The colnames are the well names.
read	a numeric vector of read numbers
temperature	a numeric vector of temperatures
header	a character vector: the header of the file

**Author(s)**

Julien Gagneur

**See Also**[readYeastGrower](#)**Examples**

```
# Get file names
# Parse file
dat = readGenios( system.file("extdata", "tecan_genios.txt", package="cellGrowth") )

# fit
n <- names( dat$OD)[36]
fit <- fitCellGrowth(x=dat$time,z=log2(dat$OD[[n]]), model = "locfit",locfit.h=6*60*60)
plot(fit)
```

---

readYeastGrower	<i>Read Yeast Grower data files</i>
-----------------	-------------------------------------

---

**Description**

Read raw data file from Yeast Grower software

**Usage**

```
readYeastGrower(file)
```

**Arguments**

file	filename
------	----------

**Value**

a list with entries:

time	a numeric vector of time points
OD	a data.frame vector of measured OD. The colnames are the well names.
read	a numeric vector of read numbers
temperature	a numeric vector of temperatures
header	a character vector: the header of the file

**Author(s)**

Julien Gagneur

**See Also**[readGenios](#)

**Examples**

```
# Get file names
# Parse file
dat = readYeastGrower( system.file("extdata", "Plate1_YPFruc.txt", package="cellGrowth") )

# fit
n <- names( dat$OD)[36]
fit <- fitCellGrowth(x=dat$time,z=log2(dat$OD[[n]]), model = "locfit")
plot(fit)
```

---

rosso	<i>Rosso growth model</i>
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---

**Description**

Rosso growth model

**Usage**

```
rosso(x, mu, l, z0, zmax)
```

**Arguments**

x	vector: time points for which log(OD) must be computed
mu	scalar: maximal growth rate parameter
l	scalar: time lag parameter
z0	scalar: minimal log(OD) parameter
zmax	scalar: maximal log(OD) parameter

**Details**

Rosso model is  $z_0$  if  $x \leq l$   $z_{\max} - \log( 1 + (\exp(z_{\max} - z_0) - 1) * \exp(-\mu * (x - l)) )$  otherwise

**Value**

vector: log(OD) for the time points given in x

**Author(s)**

Julien Gagneur

**Examples**

```
x = 1:1000
y = rosso(x, mu=0.01, l=200, z0=1, zmax=5)
plot(x,y)
```

---

standardWellId	<i>Make standard names for well ids</i>
----------------	---

---

**Description**

Make standard names for well in 96 well plates

**Usage**

```
standardWellId(wellId)
```

**Arguments**

wellId            vector of well ids

**Details**

A1 -> A01 A01 -> A01

**Value**

standard well name

**Author(s)**

Julien Gagneur

**Examples**

```
standardWellId( c("A1", "B01", "H2"))
```

---

wellDataFrame	<i>Create a well data frame</i>
---------------	---------------------------------

---

**Description**

Load a plate layout file and a file specifying the machine runs

**Usage**

```
wellDataFrame(plateLayoutFile, machineRunFile)
```

**Arguments**

plateLayoutFile

a file containing the plate layout. The file must contain a column named plate and a column named well

machineRunFile a file containing the machine runs The file must contain columns named directory, filename and plate specifying the directory and filename of the data for the corresponding run. The column use is optional. If present, only rows with use == TRUE are put into the dataframe.



**Details**

See the provided example files for the layout and machine run file formats.

**Value**

an object of class `well` and `data.frame`

**Author(s)**

Andreas Neudecker

**Examples**

```
plateLayout <- system.file("extdata", "plateLayout.txt", package="cellGrowth")
machineRun <- system.file("extdata", "machineRun.txt", package="cellGrowth")
well <- wellDataFrame(plateLayout,machineRun)
plot(well,plate=1)
```

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