Package 'sicegar'

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Type Package

Title Analysis of Single-Cell Viral Growth Curves

Version 0.3.0

Description Aims to quantify time intensity data by using sigmoidal and double sigmoidal curves. It fits straight lines, sigmoidal, and double sigmoidal curves on to time vs intensity data. Then all the fits are used to make decision on which model best describes the data. This method was first developed in the context of single-cell viral growth analysis (for details, see Caglar et al. (2018) <doi:10.7717/peerj.4251>), and the package name stands for ``SIngle CEll Growth Analysis in R".

URL https://github.com/wilkelab/sicegar/, https://hardin47.github.io/sicegar/

Imports minpack.lm, fBasics, ggplot2, stats, dplyr

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Suggests covr, cowplot, testthat, knitr, rmarkdown

VignetteBuilder knitr

BugReports https://github.com/hardin47/sicegar/issues

Collate 'globals.R' 'categorize.R' 'categorize_h0.R' 'mainFunctions.R' 'multipleFitFunction.R' 'multipleFitFunction_h0.R' 'sigmoidalFitFunctions.R' 'sigmoidalFitFunctions_h0.R' 'doublesigmoidalFitFunctions.R' 'doublesigmoidalFitFunctions_h0.R' 'normalizationFunction.R' 'sicegar.R' 'dataInputCheck.R' 'parameterCalculation.R' 'parameterCalculation_h0.R' 'figureGeneration.R'

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Contents

`categorize` *Categorize input data by comparing the AIC values of the three fitted models.*

Description

Categorizes the input data using the results of two model fits and chosen thresholds.

Usage

```
categorize(
  parameterVectorSigmoidal,
  parameterVectorDoubleSigmoidal,
  threshold_intensity_range = 0.1,
  threshold_minimum_for_intensity_maximum = 0.3,
  threshold_bonus_sigmoidal_AIC = 0,
  threshold_sm_tmax_IntensityRatio = 0.85,
  threshold_dsm_tmax_IntensityRatio = 0.75,
  threshold_AIC = -10,
  threshold_t0_max_int = 1e+10,
  showDetails = FALSE
)
```

Arguments

`parameterVectorSigmoidal`
: Output of the sigmoidalFitFunction.

`parameterVectorDoubleSigmoidal`
: Output of the doublesigmoidalFitFunction.

`threshold_intensity_range`
: Minimum for intensity range, i.e. it is the lower limit for the allowed difference between the maximum and minimum of the intensities (Default is 0.1, and the values are based on actual, not the rescaled data.).

`threshold_minimum_for_intensity_maximum`
: Minimum allowed value for intensity maximum. (Default is 0.3, and the values are based on actual, not the normalized data.).

`threshold_bonus_sigmoidal_AIC`
: Bonus AIC points for sigmoidal fit. Negative values help the sigmoidal model to win. Only helps in competition between sigmoidal and double sigmoidal fit at decision step "9", i.e. if none of the models fail in any of the tests and stay as a candidate until the last step (Default is 0).

`threshold_sm_tmax_IntensityRatio`
: The threshold for the minimum intensity ratio between the intensity at the last observed time points and the theoretical maximum intensity of the sigmoidal curve. If the value is below the threshold, then the data can not be represented with the sigmoidal model. (Default is 0.85)

`threshold_dsm_tmax_IntensityRatio`
: The threshold for the minimum intensity ratio between the intensity at the last observed time points and the maximum intensity of the double sigmoidal curve. If the value is above the threshold, then the data can not be represented with the double sigmoidal model. (Default is 0.75)

`threshold_AIC` Maximum AIC values in order to have a meaningful fit (Default is -10).

`threshold_t0_max_int`
: Maximum allowed intensity of the fitted curve at time is equal to zero (t=0). (Default is 1E10, and the values are based on actual, not the normalized data.).

`showDetails` Logical to choose if we want to see details or not. Default is "FALSE"

Value

The returned object contains extensive information about the decision process, but the key component is the decision variable. The decision variable can be one of the following four; "no_signal", "sigmoidal","double sigmoidal" or "ambiguous".

Examples

```
# runif() is used here for consistency with previous versions of the sicegar package. However,
# rnorm() will generate symmetric errors, producing less biased numerical parameter estimates.
# We recommend errors generated with rnorm() for any simulation studies on sicegar.
# Example 1 with double sigmoidal data
time=seq(3, 24, 0.1)

#simulate intensity data and add noise
noise_parameter <- 0.2
intensity_noise <- runif(n = length(time), min = 0, max = 1) * noise_parameter
intensity <- sicegar::doublesigmoidalFitFormula(time,
                                                finalAsymptoteIntensityRatio = .3,
                                                maximum = 4,
                                                slope1Param = 1,
                                                midPoint1Param = 7,
                                                slope2Param = 1,
                                                midPointDistanceParam = 8)
intensity <- intensity + intensity_noise

dataInput <- data.frame(intensity = intensity, time = time)
normalizedInput <- sicegar::normalizeData(dataInput,
                                          dataInputName = "sample001")


# Fit sigmoidal model
sigmoidalModel <- sicegar::multipleFitFunction(dataInput = normalizedInput,
                                               model = "sigmoidal",
                                               n_runs_min = 20,
                                               n_runs_max = 500,
                                               showDetails = FALSE)

# Fit double sigmoidal model
doubleSigmoidalModel <- sicegar::multipleFitFunction(dataInput = normalizedInput,
                                                     model = "doublesigmoidal",
                                                     n_runs_min = 20,
                                                     n_runs_max = 500,
                                                     showDetails = FALSE)


# Calculate additional parameters
sigmoidalModel <- sicegar::parameterCalculation(sigmoidalModel)
doubleSigmoidalModel <- sicegar::parameterCalculation(doubleSigmoidalModel)

outputCluster <- sicegar::categorize(parameterVectorSigmoidal = sigmoidalModel,
                                     parameterVectorDoubleSigmoidal = doubleSigmoidalModel)
```

```
utils::str(outputCluster)
```

`categorize_h0` *Categorize input data by comparing the AIC values of the three fitted models.*

Description

Categorizes the input data using the results of two model fits and chosen thresholds.

Usage

```
categorize_h0(
  parameterVectorSigmoidal,
  parameterVectorDoubleSigmoidal,
  threshold_intensity_range = 0.1,
  threshold_minimum_for_intensity_maximum = 0.3,
  threshold_bonus_sigmoidal_AIC = 0,
  threshold_sm_tmax_IntensityRatio = 0.85,
  threshold_dsm_tmax_IntensityRatio = 0.75,
  threshold_AIC = -10,
  threshold_t0_max_int = 1e+10,
  showDetails = FALSE
)
```

Arguments

`parameterVectorSigmoidal`
: Output of the sigmoidalFitFunction.

`parameterVectorDoubleSigmoidal`
: Output of the doublesigmoidalFitFunction.

`threshold_intensity_range`
: Minimum for intensity range, i.e. it is the lower limit for the allowed difference between the maximum and minimum of the intensities (Default is 0.1, and the values are based on actual, not the rescaled data.).

`threshold_minimum_for_intensity_maximum`
: Minimum allowed value for intensity maximum. (Default is 0.3, and the values are based on actual, not the normalized data.).

`threshold_bonus_sigmoidal_AIC`
: Bonus AIC points for sigmoidal fit. Negative values help the sigmoidal model to win. Only helps in competition between sigmoidal and double sigmoidal fit at decision step "9", i.e. if none of the models fail in any of the tests and stay as a candidate until the last step (Default is 0).

threshold_sm_tmax_IntensityRatio
: The threshold for the minimum intensity ratio between the intensity at the last observed time points and the theoretical maximum intensity of the sigmoidal curve. If the value is below the threshold, then the data can not be represented with the sigmoidal model. (Default is 0.85)

threshold_dsm_tmax_IntensityRatio
: The threshold for the minimum intensity ratio between the intensity at the last observed time points and the maximum intensity of the double sigmoidal curve. If the value is above the threshold, then the data can not be represented with the double sigmoidal model. (Default is 0.75)

threshold_AIC
: Maximum AIC values in order to have a meaningful fit (Default is -10).

threshold_t0_max_int
: Maximum allowed intensity of the fitted curve at time is equal to zero (t=0). (Default is 1E10, and the values are based on actual, not the normalized data.).

showDetails
: Logical to choose if we want to see details or not. Default is "FALSE"

Value

The returned object contains extensive information about the decision process, but the key component is the decision variable. The decision variable can be one of the following four; "no_signal", "sigmoidal","double sigmoidal" or "ambiguous".

Examples

```
# runif() is used here for consistency with previous versions of the sicegar package. However,
# rnorm() will generate symmetric errors, producing less biased numerical parameter estimates.
# We recommend errors generated with rnorm() for any simulation studies on sicegar.
# Example 1 with double sigmoidal data
time=seq(3, 24, 0.1)

#simulate intensity data and add noise
noise_parameter <- 0.2
intensity_noise <- runif(n = length(time), min = 0, max = 1) * noise_parameter
intensity <- sicegar::doublesigmoidalFitFormula_h0(time,
                                                   finalAsymptoteIntensityRatio = .3,
                                                   maximum = 4,
                                                   slope1Param = 1,
                                                   midPoint1Param = 7,
                                                   slope2Param = 1,
                                                   midPointDistanceParam = 8,
                                                   h0 = 1)
intensity <- intensity + intensity_noise

dataInput <- data.frame(intensity = intensity, time = time)
normalizedInput <- sicegar::normalizeData(dataInput,
                                          dataInputName = "sample001")


# Fit sigmoidal model
sigmoidalModel <- sicegar::multipleFitFunction_h0(dataInput = normalizedInput,
```

```
                                                model = "sigmoidal",
                                                n_runs_min = 20,
                                                n_runs_max = 500,
                                                showDetails = FALSE)

# Fit double sigmoidal model
doubleSigmoidalModel <- sicegar::multipleFitFunction_h0(dataInput = normalizedInput,
                                                        model = "doublesigmoidal",
                                                        n_runs_min = 20,
                                                        n_runs_max = 500,
                                                        showDetails = FALSE)


# Calculate additional parameters
sigmoidalModel <- sicegar::parameterCalculation_h0(sigmoidalModel)
doubleSigmoidalModel <- sicegar::parameterCalculation_h0(doubleSigmoidalModel)

outputCluster <- sicegar::categorize_h0(parameterVectorSigmoidal = sigmoidalModel,
                                    parameterVectorDoubleSigmoidal = doubleSigmoidalModel)

utils::str(outputCluster)
```

`dataCheck` *Checks if data is in correct format.*

Description

Checks if the input data is appropriate and if it is not, the function converts it into a suitable form. The input data frame should contain two columns named time and intensity related to time variable and intensity variable respectively. If the data frame is in a list its name in the list should be $timeIntensityData.

Usage

```
dataCheck(data, showDetails = TRUE)
```

Arguments

`data`	the input data. It can be either a list that contains a data frame in .$timeIntensityData or can be a data frame by itself.
`showDetails`	logical, if TRUE the function will provide an output "check done" if everything is OK. Default is FALSE

Examples

```
# runif() is used here for consistency with previous versions of the sicegar package. However,
# rnorm() will generate symmetric errors, producing less biased numerical parameter estimates.
# We recommend errors generated with rnorm() for any simulation studies on sicegar.
```

```
# Example 1

# generate data frame
time <- seq(3, 48, 0.5)
intensity <- runif(length(time), 3.0, 7.5)
dataInput <- data.frame(time, intensity)

# Apply dataCheck function
dataOutputVariable <- dataCheck(dataInput)

# Example 2

# generate data frame
time <- seq(3, 48, 0.5)
intensity <- runif(length(time), 3.0, 7.5)
dataInput <- data.frame(time, intensity)

# Normalize Data
dataOutput <- normalizeData(dataInput)
dataInput2 <- dataOutput

# Apply dataCheck function
dataOutputVariable2 <- dataCheck(dataInput2)
```

`doublesigmoidalFitFormula` *Double Sigmoidal Formula*

Description

Calculates intensities using the double sigmoidal model fit and the parameters (maximum, final asymptote intensity, slope1Param, midpoint1Param, slope2Param, and midpoint distance).

Usage

```
doublesigmoidalFitFormula(
  x,
  finalAsymptoteIntensityRatio,
  maximum,
  slope1Param,
  midPoint1Param,
  slope2Param,
  midPointDistanceParam
)
```

Arguments

`x`	the "time" column of the dataframe

`finalAsymptoteIntensityRatio`
: this is the ratio between the final asymptote intensity and maximum intensity of the fitted curve.

`maximum`
: the maximum intensity that the double sigmoidal function reaches.

`slope1Param`
: the slope parameter of the sigmoidal function at the steepest point in the exponential phase of the viral production.

`midPoint1Param`
: the x axis value of the steepest point in the function.

`slope2Param`
: the slope parameter of the sigmoidal function at the steepest point in the lysis phase. i.e when the intensity is decreasing.

`midPointDistanceParam`
: the distance between the time of steepest increase and steepest decrease in the intensity data. In other words the distance between the x axis values of arguments of slope1Param and slope2Param.

Value

Returns the predicted intensities for the given time points with the double sigmoidal fitted parameters for the double sigmoidal fit.

Examples

```
# runif() is used here for consistency with previous versions of the sicegar package. However,
# rnorm() will generate symmetric errors, producing less biased numerical parameter estimates.
# We recommend errors generated with rnorm() for any simulation studies on sicegar.
time <- seq(3, 24, 0.1)

#simulate intensity data and add noise
noise_parameter <- 0.2
intensity_noise <- stats::runif(n = length(time), min = 0, max = 1) * noise_parameter
intensity <- doublesigmoidalFitFormula(time,
                                       finalAsymptoteIntensityRatio = .3,
                                       maximum = 4,
                                       slope1Param = 1,
                                       midPoint1Param = 7,
                                       slope2Param = 1,
                                       midPointDistanceParam = 8)
intensity <- intensity + intensity_noise

dataInput <- data.frame(intensity = intensity, time = time)
normalizedInput <- normalizeData(dataInput)
parameterVector <- doublesigmoidalFitFunction(normalizedInput, tryCounter = 2)


#Check the results
if(parameterVector$isThisaFit){
 intensityTheoretical <-
       doublesigmoidalFitFormula(
               time,
          finalAsymptoteIntensityRatio = parameterVector$finalAsymptoteIntensityRatio_Estimate,
               maximum = parameterVector$maximum_Estimate,
```

```
                slope1Param = parameterVector$slope1Param_Estimate,
                midPoint1Param = parameterVector$midPoint1Param_Estimate,
                slope2Param = parameterVector$slope2Param_Estimate,
                midPointDistanceParam = parameterVector$midPointDistanceParam_Estimate)

 comparisonData <- cbind(dataInput, intensityTheoretical)

 require(ggplot2)
 ggplot(comparisonData) +
   geom_point(aes(x = time, y = intensity)) +
   geom_line(aes(x = time, y = intensityTheoretical)) +
   expand_limits(x = 0, y = 0)
   }

if(!parameterVector$isThisaFit){
  print(parameterVector)
  }
```

---

doublesigmoidalFitFormula_h0 *Double Sigmoidal Formula with h0*

Description

Calculates intensities using the double sigmoidal model fit and the parameters (maximum, final asymptote intensity, slope1Param, midpoint1Param, slope2Param, and midpoint distance).

Usage

```
doublesigmoidalFitFormula_h0(
  x,
  finalAsymptoteIntensityRatio,
  maximum,
  slope1Param,
  midPoint1Param,
  slope2Param,
  midPointDistanceParam,
  h0
)
```

Arguments

x	the "time" column of the dataframe
finalAsymptoteIntensityRatio	this is the ratio between the final asymptote intensity and maximum intensity of the fitted curve.

maximum	the maximum intensity that the double sigmoidal function reaches.
slope1Param	the slope parameter of the sigmoidal function at the steepest point in the exponential phase of the viral production.
midPoint1Param	the x axis value of the steepest point in the function.
slope2Param	the slope parameter of the sigmoidal function at the steepest point in the lysis phase. i.e when the intensity is decreasing.
midPointDistanceParam	the distance between the time of steepest increase and steepest decrease in the intensity data. In other words the distance between the x axis values of arguments of slope1Param and slope2Param.
h0	the lower asymptote (baseline) intensity

Value

Returns the predicted intensities for the given time points with the double sigmoidal fitted parameters for the double sigmoidal fit.

Examples

```
# runif() is used here for consistency with previous versions of the sicegar package. However,
# rnorm() will generate symmetric errors, producing less biased numerical parameter estimates.
# We recommend errors generated with rnorm() for any simulation studies on sicegar.
time <- seq(3, 24, 0.1)

#simulate intensity data and add noise
noise_parameter <- 0.2
intensity_noise <- stats::runif(n = length(time), min = 0, max = 1) * noise_parameter
intensity <- doublesigmoidalFitFormula_h0(time,
                                    finalAsymptoteIntensityRatio = .3,
                                    maximum = 4,
                                    slope1Param = 1,
                                    midPoint1Param = 7,
                                    slope2Param = 1,
                                    midPointDistanceParam = 8,
                                    h0 = 1)
intensity <- intensity + intensity_noise

dataInput <- data.frame(intensity = intensity, time = time)
normalizedInput <- normalizeData(dataInput)
parameterVector <- doublesigmoidalFitFunction_h0(normalizedInput, tryCounter = 1)


#Check the results
# doublesigmoidalFitFunction_h0() is run on the startList param values (because 'tryCounter = 1')
# use multipleFitFunction() for multiple random starts in order to optimize
if(parameterVector$isThisaFit){
 intensityTheoretical <-
       doublesigmoidalFitFormula_h0(
               time,
          finalAsymptoteIntensityRatio = parameterVector$finalAsymptoteIntensityRatio_Estimate,
```

```
                maximum = parameterVector$maximum_Estimate,
                slope1Param = parameterVector$slope1Param_Estimate,
                midPoint1Param = parameterVector$midPoint1Param_Estimate,
                slope2Param = parameterVector$slope2Param_Estimate,
                midPointDistanceParam = parameterVector$midPointDistanceParam_Estimate,
                h0 = parameterVector$h0_Estimate)

 comparisonData <- cbind(dataInput, intensityTheoretical)

 require(ggplot2)
 ggplot(comparisonData) +
   geom_point(aes(x = time, y = intensity)) +
   geom_line(aes(x = time, y = intensityTheoretical)) +
   expand_limits(x = 0, y = 0)
   }

if(!parameterVector$isThisaFit){
  print(parameterVector)
  }
```

---

doublesigmoidalFitFunction

Double sigmoidal fit function with h0.

Description

The function fits a double sigmoidal curve to given data by using likelihood maximization (LM) algorithm and provides the parameters (maximum, final asymptote intensity, slope1Param, midpoint1Param, slope2Param, and midpoint distance) describing the double sigmoidal fit as output. It also contains information about the goodness of fits such as AIC, BIC, residual sum of squares, and log likelihood.

Usage

```
doublesigmoidalFitFunction(
  dataInput,
  tryCounter,
  startList = list(finalAsymptoteIntensityRatio = 0, maximum = 1, slope1Param = 1,
    midPoint1Param = 0.33, slope2Param = 1, midPointDistanceParam = 0.29),
  lowerBounds = c(finalAsymptoteIntensityRatio = 0, maximum = 0.3, slope1Param = 0.01,
    midPoint1Param = -0.52, slope2Param = 0.01, midPointDistanceParam = 0.04),
  upperBounds = c(finalAsymptoteIntensityRatio = 1, maximum = 1.5, slope1Param = 180,
    midPoint1Param = 1.15, slope2Param = 180, midPointDistanceParam = 0.63),
  min_Factor = 1/2^20,
  n_iterations = 1000
)
```

Arguments

dataInput	A dataframe or a list containing the dataframe. The dataframe should be composed of at least two columns. One represents time, and the other represents intensity. The data should be normalized with the normalize data function sicegar::normalizeData() before being imported into this function.
tryCounter	A counter that shows the number of times the data was fit via maximum likelihood function.
startList	The vector containing the initial set of parameters that algorithm tries for the first fit attempt for the relevant parameters. The vector composes of seven elements; 'finalAsymptoteIntensityRatio', 'maximum', 'slope1Param', 'midPoint1Param' , 'slope2Param', 'midPointDistanceParam', and 'h0'. Detailed explanations of those parameters can be found in vignettes. Defaults are finalAsymptoteIntensityRatio = 0, maximum = 1, slope1Param = 1, midPoint1Param = 0.33, slope2Param = 1, midPointDistanceParam=0.29, and h0 = 0. The numbers are in normalized time intensity scale.
lowerBounds	The lower bounds for the randomly generated start parameters. The vector is composed of seven elements; 'finalAsymptoteIntensityRatio', 'maximum', 'slope1Param', 'midPoint1Param' , 'slope2Param', 'midPointDistanceParam', and 'h0'. Detailed explanations of those parameters can be found in vignettes. Defaults are finalAsymptoteIntensityRatio = 0, maximum = 0.3, slope1Param = .01, midPoint1Param = -0.52, slope2Param = .01, midPointDistanceParam = 0.04, and h0 = -0.1. The numbers are in normalized time intensity scale.
upperBounds	The upper bounds for the randomly generated start parameters. The vector is composed of seven elements; 'finalAsymptoteIntensityRatio', 'maximum', 'slope1Param', 'midPoint1Param' , 'slope2Param', 'midPointDistanceParam', and 'h0'. Detailed explanations of those parameters can be found in vignettes. Defaults are finalAsymptoteIntensityRatio = 1, maximum = 1.5, slope1Param = 180, midPoint1Param = 1.15, slope2Param = 180, midPointDistanceParam = 0.63, and h0 = 0.3. The numbers are in normalized time intensity scale.
min_Factor	Defines the minimum step size used by the fitting algorithm. Default is 1/2^20.
n_iterations	Defines maximum number of iterations used by the fitting algorithm. Default is 1000.

Value

Returns the fitted parameters and goodness of fit metrics.

Examples

```
# runif() is used here for consistency with previous versions of the sicegar package. However,
# rnorm() will generate symmetric errors, producing less biased numerical parameter estimates.
# We recommend errors generated with rnorm() for any simulation studies on sicegar.
time=seq(3, 24, 0.1)

#simulate intensity data and add noise
noise_parameter <- 0.2
intensity_noise <- stats::runif(n = length(time), min = 0, max = 1) * noise_parameter
```

```
intensity <- doublesigmoidalFitFormula(time,
                                       finalAsymptoteIntensityRatio = .3,
                                       maximum = 4,
                                       slope1Param = 1,
                                       midPoint1Param = 7,
                                       slope2Param = 1,
                                       midPointDistanceParam = 8)
intensity <- intensity + intensity_noise

dataInput <- data.frame(intensity = intensity, time = time)
normalizedInput <- normalizeData(dataInput)
parameterVector <- doublesigmoidalFitFunction(normalizedInput, tryCounter = 2)


#Check the results
if(parameterVector$isThisaFit){
    intensityTheoretical <-
         doublesigmoidalFitFormula(
             time,
         finalAsymptoteIntensityRatio = parameterVector$finalAsymptoteIntensityRatio_Estimate,
             maximum = parameterVector$maximum_Estimate,
             slope1Param = parameterVector$slope1Param_Estimate,
             midPoint1Param = parameterVector$midPoint1Param_Estimate,
             slope2Param = parameterVector$slope2Param_Estimate,
             midPointDistanceParam = parameterVector$midPointDistanceParam_Estimate)

 comparisonData <- cbind(dataInput, intensityTheoretical)

 require(ggplot2)
 ggplot(comparisonData) +
   geom_point(aes(x = time, y = intensity)) +
   geom_line(aes(x = time, y = intensityTheoretical)) +
   expand_limits(x = 0, y = 0)}

if(!parameterVector$isThisaFit) {print(parameterVector)}
```

`doublesigmoidalFitFunction_h0` *Double sigmoidal fit function with h0.*

Description

The function fits a double sigmoidal curve to given data by using likelihood maximization (LM) algorithm and provides the parameters (maximum, final asymptote intensity, slope1Param, midpoint1Param, slope2Param, and midpoint distance) describing the double sigmoidal fit as output. It also contains information about the goodness of fits such as AIC, BIC, residual sum of squares, and log likelihood.

Usage

```
doublesigmoidalFitFunction_h0(
  dataInput,
  tryCounter,
  startList = list(finalAsymptoteIntensityRatio = 0, maximum = 1, slope1Param = 1,
   midPoint1Param = 0.33, slope2Param = 1, midPointDistanceParam = 0.29, h0 = 0.1),
  lowerBounds = c(finalAsymptoteIntensityRatio = 0, maximum = 0.3, slope1Param = 0.01,
   midPoint1Param = -0.52, slope2Param = 0.01, midPointDistanceParam = 0.04, h0 = 0),
  upperBounds = c(finalAsymptoteIntensityRatio = 1, maximum = 1.5, slope1Param = 180,
   midPoint1Param = 1.15, slope2Param = 180, midPointDistanceParam = 0.63, h0 = 0.3),
  min_Factor = 1/2^20,
  n_iterations = 1000
)
```

Arguments

dataInput	A dataframe or a list containing the dataframe. The dataframe should be composed of at least two columns. One represents time, and the other represents intensity. The data should be normalized with the normalize data function sicegar::normalizeData() before being imported into this function.
tryCounter	A counter that shows the number of times the data was fit via maximum likelihood function.
startList	The vector containing the initial set of parameters that algorithm tries for the first fit attempt for the relevant parameters. The vector composes of seven elements; 'finalAsymptoteIntensityRatio', 'maximum', 'slope1Param', 'midPoint1Param' , 'slope2Param', 'midPointDistanceParam', and 'h0'. Detailed explanations of those parameters can be found in vignettes. Defaults are finalAsymptoteIntensityRatio = 0, maximum = 1, slope1Param = 1, midPoint1Param = 0.33, slope2Param = 1, midPointDistanceParam=0.29, and h0 = 0. The numbers are in normalized time intensity scale.
lowerBounds	The lower bounds for the randomly generated start parameters. The vector is composed of seven elements; 'finalAsymptoteIntensityRatio', 'maximum', 'slope1Param', 'midPoint1Param' , 'slope2Param', 'midPointDistanceParam', and 'h0'. Detailed explanations of those parameters can be found in vignettes. Defaults are finalAsymptoteIntensityRatio = 0, maximum = 0.3, slope1Param = .01, midPoint1Param = -0.52, slope2Param = .01, midPointDistanceParam = 0.04, and h0 = -0.1. The numbers are in normalized time intensity scale.
upperBounds	The upper bounds for the randomly generated start parameters. The vector is composed of seven elements; 'finalAsymptoteIntensityRatio', 'maximum', 'slope1Param', 'midPoint1Param' , 'slope2Param', 'midPointDistanceParam', and 'h0'. Detailed explanations of those parameters can be found in vignettes. Defaults are finalAsymptoteIntensityRatio = 1, maximum = 1.5, slope1Param = 180, midPoint1Param = 1.15, slope2Param = 180, midPointDistanceParam = 0.63, and h0 = 0.3. The numbers are in normalized time intensity scale.
min_Factor	Defines the minimum step size used by the fitting algorithm. Default is 1/2^20.
n_iterations	Defines maximum number of iterations used by the fitting algorithm. Default is 1000.

Value

Returns the fitted parameters and goodness of fit metrics.

Examples

```
# runif() is used here for consistency with previous versions of the sicegar package. However,
# rnorm() will generate symmetric errors, producing less biased numerical parameter estimates.
# We recommend errors generated with rnorm() for any simulation studies on sicegar.
time=seq(3, 24, 0.1)

#simulate intensity data and add noise
noise_parameter <- 0.2
intensity_noise <- stats::runif(n = length(time), min = 0, max = 1) * noise_parameter
intensity <- doublesigmoidalFitFormula_h0(time,
                                    finalAsymptoteIntensityRatio = .3,
                                    maximum = 4,
                                    slope1Param = 1,
                                    midPoint1Param = 7,
                                    slope2Param = 1,
                                    midPointDistanceParam = 8,
                                    h0 = 1)
intensity <- intensity + intensity_noise

dataInput <- data.frame(intensity = intensity, time = time)
normalizedInput <- normalizeData(dataInput)
parameterVector <- doublesigmoidalFitFunction_h0(normalizedInput, tryCounter = 1)


#Check the results
# doublesigmoidalFitFunction_h0() is run on the startList param values (because 'tryCounter = 1')
# use multipleFitFunction() for multiple random starts in order to optimize
if(parameterVector$isThisaFit){
    intensityTheoretical <-
         doublesigmoidalFitFormula_h0(
             time,
         finalAsymptoteIntensityRatio = parameterVector$finalAsymptoteIntensityRatio_Estimate,
             maximum = parameterVector$maximum_Estimate,
             slope1Param = parameterVector$slope1Param_Estimate,
             midPoint1Param = parameterVector$midPoint1Param_Estimate,
             slope2Param = parameterVector$slope2Param_Estimate,
             midPointDistanceParam = parameterVector$midPointDistanceParam_Estimate,
             h0 = parameterVector$h0_Estimate)

 comparisonData <- cbind(dataInput, intensityTheoretical)

 require(ggplot2)
 ggplot(comparisonData) +
   geom_point(aes(x = time, y = intensity)) +
   geom_line(aes(x = time, y = intensityTheoretical)) +
   expand_limits(x = 0, y = 0)}

if(!parameterVector$isThisaFit) {print(parameterVector)}
```

figureModelCurves *Generate model associated figures.*

Description

Generates figures using ggplot that shows the input data and the fitted curves.

Usage

```
figureModelCurves(
  dataInput,
  sigmoidalFitVector = NULL,
  doubleSigmoidalFitVector = NULL,
  showParameterRelatedLines = FALSE,
  xlabelText = "time",
  ylabelText = "intensity",
  fittedXmin = 0,
  fittedXmax = NA,
  use_h0 = FALSE
)
```

Arguments

dataInput	A dataframe or a list containing the dataframe. The data frame should be composed of at least two columns. One represents time, and the other represents intensity. The data should be normalized with the normalize data function sicegar::normalizeData() before imported into this function.
sigmoidalFitVector	the output of the sicegar::sigmoidalFitFunction(), or the augmented version of the output generated by sicegar::parameterCalculation(), which contains parameters from the sigmoidal model. Default is NULL.
doubleSigmoidalFitVector	the output of the sicegar::doubleSigmoidalFitFunction(), or the augmented version of the output generated by sicegar::parameterCalculation(), which contains parameters from the double sigmoidal model. Default is NULL.
showParameterRelatedLines	if equal to TRUE, figure will show parameter related lines on the curves. Default is FALSE.
xlabelText	the x-axis name; with default "time"
ylabelText	the y-axis name; with default "intensity"
fittedXmin	the minimum of the fitted data that will be plotted (Default 0)
fittedXmax	the maximum of the fitted data that will be plotted (Default timeRange)
use_h0	Boolean which decides whether to fix the lower asymptote of h0 at 0 (FALSE, default) or to freely estimate h0 (TRUE)

Value

Returns inflection curve figures.

Examples

```
# runif() is used here for consistency with previous versions of the sicegar package. However,
# rnorm() will generate symmetric errors, producing less biased numerical parameter estimates.
# We recommend errors generated with rnorm() for any simulation studies on sicegar.
time <- seq(3, 24, 0.1)

#simulate intensity data and add noise
noise_parameter <- 0.2
intensity_noise <- runif(n = length(time), min = 0, max = 1) * noise_parameter
intensity <- sicegar::doublesigmoidalFitFormula(time,
                                                finalAsymptoteIntensityRatio = .3,
                                                maximum = 4,
                                                slope1Param = 1,
                                                midPoint1Param = 7,
                                                slope2Param = 1,
                                                midPointDistanceParam = 8)
intensity <- intensity + intensity_noise

dataInput <- data.frame(intensity = intensity, time = time)
normalizedInput <- sicegar::normalizeData(dataInput, dataInputName = "sample001")


# Do the double sigmoidal fit
doubleSigmoidalModel <- sicegar::multipleFitFunction(dataInput = normalizedInput,
                                                     model = "doublesigmoidal",
                                                     n_runs_min = 20,
                                                     n_runs_max = 500,
                                                     showDetails = FALSE)

doubleSigmoidalModel <- sicegar::parameterCalculation(doubleSigmoidalModel)

fig01 <- sicegar::figureModelCurves(dataInput = normalizedInput,
                                    doubleSigmoidalFitVector = doubleSigmoidalModel,
                                    showParameterRelatedLines = TRUE)
print(fig01)
```

`fitAndCategorize` *Fit and categorize.*

Description

Fits the sigmoidal and double-sigmoidal models to the data and then categorizes the data according to which model fits best.

Usage

```
fitAndCategorize(
  dataInput,
  dataInputName = NA,
  n_runs_min_sm = 20,
  n_runs_max_sm = 500,
  n_runs_min_dsm = 20,
  n_runs_max_dsm = 500,
  showDetails = FALSE,
  startList_sm = list(maximum = 1, slopeParam = 1, midPoint = 0.33),
  lowerBounds_sm = c(maximum = 0.3, slopeParam = 0.01, midPoint = -0.52),
  upperBounds_sm = c(maximum = 1.5, slopeParam = 180, midPoint = 1.15),
  min_Factor_sm = 1/2^20,
  n_iterations_sm = 1000,
 startList_dsm = list(finalAsymptoteIntensityRatio = 0, maximum = 1, slope1Param = 1,
    midPoint1Param = 0.33, slope2Param = 1, midPointDistanceParam = 0.29),
 lowerBounds_dsm = c(finalAsymptoteIntensityRatio = 0, maximum = 0.3, slope1Param =
  0.01, midPoint1Param = -0.52, slope2Param = 0.01, midPointDistanceParam = 0.04),
 upperBounds_dsm = c(finalAsymptoteIntensityRatio = 1, maximum = 1.5, slope1Param = 180,
    midPoint1Param = 1.15, slope2Param = 180, midPointDistanceParam = 0.63),
 min_Factor_dsm = 1/2^20,
 n_iterations_dsm = 1000,
 threshold_intensity_range = 0.1,
 threshold_minimum_for_intensity_maximum = 0.3,
 threshold_bonus_sigmoidal_AIC = 0,
 threshold_sm_tmax_IntensityRatio = 0.85,
 threshold_dsm_tmax_IntensityRatio = 0.75,
 threshold_AIC = -10,
 threshold_t0_max_int = 1e+10,
 stepSize = 1e-05,
 startList_sm_h0 = list(maximum = 1, slopeParam = 1, midPoint = 0.33, h0 = 0),
 lowerBounds_sm_h0 = c(maximum = 0.3, slopeParam = 0.01, midPoint = -0.52, h0 = -0.1),
 upperBounds_sm_h0 = c(maximum = 1.5, slopeParam = 180, midPoint = 1.15, h0 = 0.3),
 startList_dsm_h0 = list(finalAsymptoteIntensityRatio = 0, maximum = 1, slope1Param = 1,
   midPoint1Param = 0.33, slope2Param = 1, midPointDistanceParam = 0.29, h0 = 0),
 lowerBounds_dsm_h0 = c(finalAsymptoteIntensityRatio = 0, maximum = 0.3, slope1Param =
  0.01, midPoint1Param = -0.52, slope2Param = 0.01, midPointDistanceParam = 0.04, h0 =
    -0.1),
 upperBounds_dsm_h0 = c(finalAsymptoteIntensityRatio = 1, maximum = 1.5, slope1Param =
  180, midPoint1Param = 1.15, slope2Param = 180, midPointDistanceParam = 0.63, h0 =
    0.3),
 use_h0 = FALSE,
 ...
)
```

Arguments

dataInput	Unnormalized input data that will be fitted then transferred into relevant functions
dataInputName	Name of data set (Default is 'NA').
n_runs_min_sm	This number indicates the lower limit of the successful fitting attempts for sigmoidal model. It should be smaller than the upper limit of the fitting attempts (n_runs_max_sm). Default is 20
n_runs_max_sm	This number indicates the upper limit of the fitting attempts for sigmoidal model. Default is 500
n_runs_min_dsm	This number indicates the lower limit of the successful fitting attempts for double sigmoidal model. It should be smaller than the upper limit of the fitting attempts (n_runs_max_dsm). Default is 20
n_runs_max_dsm	This number indicates the upper limit of the fitting attempts for sigmoidal model for double sigmoidal model. Default is 500
showDetails	Logical if TRUE prints details of intermediate steps of individual fits (Default is FALSE).
startList_sm	The vector containing the initial set of parameters that sigmoidal fit algorithm tries for the first fit attempt. The vector is composed of three elements; 'maximum', 'slopeParam' and, 'midPoint'. Detailed explanations of those parameters can be found in vignettes. Defaults are maximum = 1, slopeParam = 1 and, midPoint = 0.33. The numbers are in normalized time intensity scale.
lowerBounds_sm	The lower bounds for the randomly generated start parameters for the sigmoidal fit. The vector is composed of three elements; 'maximum', 'slopeParam' and, 'midPoint'. Detailed explanations of those parameters can be found in vignettes. Defaults are maximum = 0.3, slopeParam = 0.01, and midPoint = -0.52. The numbers are in normalized time intensity scale.
upperBounds_sm	The upper bounds for the randomly generated start parameters for the sigmoidal fit. The vector is composed of three elements; 'maximum', 'slopeParam' and, 'midPoint'. Detailed explanations of those parameters can be found in vignettes. Defaults are maximum = 1.5, slopeParam = 180, midPoint = 1.15. The numbers are in normalized time intensity scale.
min_Factor_sm	Defines the minimum step size used by the sigmoidal fit algorithm. Default is 1/2^20.
n_iterations_sm	Defines maximum number of iterations used by the sigmoidal fit algorithm. Default is 1000
startList_dsm	The vector containing the initial set of parameters that double sigmoidal fit algorithm tries for the first fit attempt. The vector is composed of six elements; 'finalAsymptoteIntensityRatio', 'maximum', 'slope1Param', 'midPoint1Param' , 'slope2Param', and 'midPointDistanceParam'. Detailed explanations of those parameters can be found in vignettes. Defaults are finalAsymptoteIntensityRatio = 0, maximum = 1, slope1Param = 1, midPoint1Param = 0.33, slope2Param = 1, and midPointDistanceParam=0.29. The numbers are in normalized time intensity scale.

`lowerBounds_dsm`
: The lower bounds for the randomly generated start parameters for double sigmoidal fit. The vector is composed of six elements; 'finalAsymptoteIntensityRatio', 'maximum', 'slope1Param', 'midPoint1Param' , 'slope2Param', and 'midPointDistanceParam'. Detailed explanations of those parameters can be found in vignettes. Defaults are finalAsymptoteIntensityRatio = 0, maximum = 0.3, slope1Param = .01, midPoint1Param = -0.52, slope2Param = .01, and midPointDistanceParam = 0.04. The numbers are in normalized time intensity scale.

`upperBounds_dsm`
: The upper bounds for the randomly generated start parameters for double sigmoidal fit. The vector is composed of six elements; 'finalAsymptoteIntensityRatio', 'maximum', 'slope1Param', 'midPoint1Param' , 'slope2Param', and 'midPointDistanceParam'. Detailed explanations of those parameters can be found in vignettes. Defaults are finalAsymptoteIntensityRatio = 1, maximum = 1.5, slope1Param = 180, midPoint1Param = 1.15, slope2Param = 180, and midPointDistanceParam = 0.63. The numbers are in normalized time intensity scale.

`min_Factor_dsm`
: Defines the minimum step size used by the double sigmoidal fit algorithm. Default is 1/2^20.

`n_iterations_dsm`
: Define maximum number of iterations used by the double sigmoidal fit algorithm. Default is 1000

`threshold_intensity_range`
: Minimum for intensity range, i.e. it is the lower limit for the allowed difference between the maximum and minimum of the intensities (Default is 0.1, and the values are based on actual, not the normalized data.).

`threshold_minimum_for_intensity_maximum`
: Minimum allowed value for intensity maximum. (Default is 0.3, and the values are based on actual, not the normalized data.).

`threshold_bonus_sigmoidal_AIC`
: Bonus AIC points for sigmoidal fit. Negative values help the sigmoidal model to win. Only helps in competition between sigmoidal and double sigmoidal fit at decision step "9", i.e. if none of the models fail in any of the tests and stay as a candidate until the last step (Default is 0).

`threshold_sm_tmax_IntensityRatio`
: The threshold for the minimum intensity ratio between the intensity of the last observed time points and theoretical maximum intensity of the sigmoidal curve. If the value is below the threshold, then the data can not be represented with the sigmoidal model. (Default is 0.85)

`threshold_dsm_tmax_IntensityRatio`
: The threshold for the minimum intensity ratio between the intenstiy of the last observed time points and maximum intensity of the double sigmoidal curve. If the value is above the threshold, then the data can not be represented with the double sigmoidal model. (Default is 0.75)

`threshold_AIC`
: Maximum AIC value in order to have a meaningful fit (Default is -10).

`threshold_t0_max_int`
: Maximum allowed intensity of the fitted curve at time equal to zero (t=0). (Default is 1E10, and the values are based on actual, not the normalized data.).

`stepSize`
: Step size used by the fitting algorithm. Smaller numbers give more accurate results than larger numbers, and larger numbers give the results faster than small numbers. The default value is 0.00001.

`startList_sm_h0`
: The vector containing the initial set of parameters that sigmoidal fit algorithm tries for the first fit attempt. The vector is composed of four elements; 'maximum', 'slopeParam', 'midPoint', and 'h0'. Detailed explanations of those parameters can be found in vignettes. Defaults are maximum = 1, slopeParam = 1 and, midPoint = 0.33, h0 = 0. The numbers are in normalized time intensity scale.

`lowerBounds_sm_h0`
: The lower bounds for the randomly generated start parameters for the sigmoidal fit. The vector is composed of four elements; 'maximum', 'slopeParam', 'midPoint', and 'h0'. Detailed explanations of those parameters can be found in vignettes. Defaults are maximum = 0.3, slopeParam = 0.01, midPoint = -0.52, and h0 = -0.1. The numbers are in normalized time intensity scale.

`upperBounds_sm_h0`
: The upper bounds for the randomly generated start parameters for the sigmoidal fit. The vector is composed of four elements; 'maximum', 'slopeParam', 'midPoint', and 'h0'. Detailed explanations of those parameters can be found in vignettes. Defaults are maximum = 1.5, slopeParam = 180, midPoint = 1.15, and h0 = 0.3. The numbers are in normalized time intensity scale.

`startList_dsm_h0`
: The vector containing the initial set of parameters that double sigmoidal fit algorithm tries for the first fit attempt. The vector is composed of seven elements; 'finalAsymptoteIntensityRatio', 'maximum', 'slope1Param', 'midPoint1Param' , 'slope2Param', 'midPointDistanceParam', and 'h0'. Detailed explanations of those parameters can be found in vignettes. Defaults are finalAsymptoteIntensityRatio = 0, maximum = 1, slope1Param = 1, midPoint1Param = 0.33, slope2Param = 1, midPointDistanceParam=0.29, h0 = 0. The numbers are in normalized time intensity scale.

`lowerBounds_dsm_h0`
: The lower bounds for the randomly generated start parameters for double sigmoidal fit. The vector is composed of seven elements; 'finalAsymptoteIntensityRatio', 'maximum', 'slope1Param', 'midPoint1Param' , 'slope2Param', 'midPointDistanceParam', and 'h0'. Detailed explanations of those parameters can be found in vignettes. Defaults are finalAsymptoteIntensityRatio = 0, maximum = 0.3, slope1Param = .01, midPoint1Param = -0.52, slope2Param = .01, midPointDistanceParam = 0.04, and h0 = -0.1. The numbers are in normalized time intensity scale.

`upperBounds_dsm_h0`
: The upper bounds for the randomly generated start parameters for double sigmoidal fit. The vector is composed of seven elements; 'finalAsymptoteIntensityRatio', 'maximum', 'slope1Param', 'midPoint1Param' , 'slope2Param', 'midPointDistanceParam', and 'h0'. Detailed explanations of those parameters can

	be found in vignettes. Defaults are finalAsymptoteIntensityRatio = 1, maximum = 1.5, slope1Param = 180, midPoint1Param = 1.15, slope2Param = 180, midPointDistanceParam = 0.63, and h0 = 0.3. The numbers are in normalized time intensity scale.
use_h0	Boolean which decides whether to fix the lower asymptote of h0 at 0 (FALSE, default) or to freely estimate h0 (TRUE)
...	All other arguments that model functions ("sigmoidalFitFunction" and, "doublesigmoidalFitFunction") may need.

Value

Returns the parameters related with the curve fitted to the input data.

Examples

```
# runif() is used here for consistency with previous versions of the sicegar package. However,
# rnorm() will generate symmetric errors, producing less biased numerical parameter estimates.
# We recommend errors generated with rnorm() for any simulation studies on sicegar.
# Example 1
time <- seq(3, 24, 0.5)

#simulate intensity data and add noise
noise_parameter <- 0.2
intensity_noise <- stats::runif(n = length(time), min = 0, max = 1) * noise_parameter
intensity <- sicegar::doublesigmoidalFitFormula(time,
                                                finalAsymptoteIntensityRatio = .3,
                                                maximum = 4,
                                                slope1Param = 1,
                                                midPoint1Param = 7,
                                                slope2Param = 1,
                                                midPointDistanceParam = 8)
intensity <- intensity + intensity_noise

dataInput <- data.frame(intensity = intensity, time = time)

fitObj <- sicegar::fitAndCategorize(dataInput = dataInput)
```

---

multipleFitFunction *multiple fit function.*

Description

Calls the fitting algorithms to fit the data multiple times with starting from different randomly generated initial parameters in each run. Multiple attempts at fitting the data are necessary to avoid local minima.

Usage

```
multipleFitFunction(
  dataInput,
  dataInputName = NA,
  model,
  n_runs_min = 20,
  n_runs_max = 500,
  showDetails = FALSE,
  ...
)
```

Arguments

dataInput	A dataframe or a list containing the dataframe. The dataframe should be composed of at least two columns. One represents time, and the other represents intensity. The data should be normalized with the normalize data function sicegar::normalizeData() before being imported into this function.
dataInputName	Name of data set (Default is 'NA').
model	Type of fit model that will be used. Can be "sigmoidal", or "double_sigmoidal".
n_runs_min	This number indicates the lower limit of the successful fitting attempts. It should be smaller than the upper limit of the fitting attempts (n_runs_max). Default is 20.
n_runs_max	This number indicates the upper limit of the fitting attempts. Default is 500.
showDetails	Logical if TRUE prints details of intermediate steps of individual fits (Default is FALSE).
...	All other arguments that model functions ("sigmoidalFitFunction" and, "doubleSigmoidalFitFunction") may need.

Value

Returns the parameters related with the model fitted for the input data.

Examples

```
# runif() is used here for consistency with previous versions of the sicegar package. However,
# rnorm() will generate symmetric errors, producing less biased numerical parameter estimates.
# We recommend errors generated with rnorm() for any simulation studies on sicegar.
# Example 1 (sigmoidal function with normalization)
time <- seq(3, 24, 0.5)

#simulate intensity data and add noise
noise_parameter <- 2.5
intensity_noise <- stats::runif(n = length(time), min = 0, max = 1) * noise_parameter
intensity <- sigmoidalFitFormula(time, maximum = 4, slopeParam = 1, midPoint = 8)
intensity <- intensity + intensity_noise

dataInput <- data.frame(intensity = intensity, time = time)
normalizedInput <- normalizeData(dataInput, dataInputName = "sample001")
```

```
parameterVector <- multipleFitFunction(dataInput = normalizedInput,
                                       model = "sigmoidal",
                                       n_runs_min = 20,
                                       n_runs_max = 500)

#Check the results
if(parameterVector$isThisaFit){
  intensityTheoretical <- sigmoidalFitFormula(time,
                            maximum = parameterVector$maximum_Estimate,
                            slopeParam = parameterVector$slopeParam_Estimate,
                            midPoint = parameterVector$midPoint_Estimate)

 comparisonData <- cbind(dataInput, intensityTheoretical)

 print(parameterVector$residual_Sum_of_Squares)

 require(ggplot2)
 ggplot(comparisonData)+
   geom_point(aes(x = time, y = intensity)) +
   geom_line(aes(x = time, y = intensityTheoretical), color = "orange") +
   expand_limits(x = 0, y = 0)
}



if(!parameterVector$isThisaFit){
  print(parameterVector)
}

# Example 2 (doublesigmoidal function with normalization)
time <- seq(3, 24, 0.1)

#simulate intensity data with noise
noise_parameter <- 0.2
intensity_noise <- stats::runif(n = length(time), min = 0, max = 1) * noise_parameter
intensity <- doublesigmoidalFitFormula(time,
                                       finalAsymptoteIntensityRatio = .3,
                                       maximum = 4,
                                       slope1Param = 1,
                                       midPoint1Param = 7,
                                       slope2Param = 1,
                                       midPointDistanceParam = 8)
intensity <- intensity + intensity_noise

dataInput <- data.frame(intensity = intensity, time = time)
normalizedInput <- normalizeData(dataInput)
parameterVector <- multipleFitFunction(dataInput = normalizedInput,
                           dataInputName="sample001",
                           model = "doublesigmoidal",
                           n_runs_min = 20,
                           n_runs_max = 500,
                           showDetails = FALSE)
```

```
#Check the results
if(parameterVector$isThisaFit){
 intensityTheoretical <-
       doublesigmoidalFitFormula(
              time,
          finalAsymptoteIntensityRatio = parameterVector$finalAsymptoteIntensityRatio_Estimate,
              maximum = parameterVector$maximum_Estimate,
              slope1Param = parameterVector$slope1Param_Estimate,
              midPoint1Param = parameterVector$midPoint1Param_Estimate,
              slope2Param = parameterVector$slope2Param_Estimate,
              midPointDistanceParam = parameterVector$midPointDistanceParam_Estimate)

 comparisonData <- cbind(dataInput, intensityTheoretical)

 require(ggplot2)
 ggplot(comparisonData) +
   geom_point(aes(x = time, y = intensity)) +
   geom_line(aes(x = time, y = intensityTheoretical), color = "orange") +
   expand_limits(x = 0, y = 0)
 }

if(!parameterVector$isThisaFit){
  print(parameterVector)
  }
```

`multipleFitFunction_h0` *multiple fit function h0.*

Description

Calls the fitting algorithms to fit the data multiple times with starting from different randomly generated initial parameters in each run. Multiple attempts at fitting the data are necessary to avoid local minima.

Usage

```
multipleFitFunction_h0(
  dataInput,
  dataInputName = NA,
  model,
  n_runs_min = 20,
  n_runs_max = 500,
  showDetails = FALSE,
  ...
)
```

Arguments

dataInput	A dataframe or a list containing the dataframe. The dataframe should be composed of at least two columns. One represents time, and the other represents intensity. The data should be normalized with the normalize data function sicegar::normalizeData() before being imported into this function.
dataInputName	Name of data set (Default is 'NA').
model	Type of fit model that will be used. Can be "sigmoidal", or "double_sigmoidal".
n_runs_min	This number indicates the lower limit of the successful fitting attempts. It should be smaller than the upper limit of the fitting attempts (n_runs_max). Default is 20.
n_runs_max	This number indicates the upper limit of the fitting attempts. Default is 500.
showDetails	Logical if TRUE prints details of intermediate steps of individual fits (Default is FALSE).
...	All other arguments that model functions ("sigmoidalFitFunction" and, "doubleSigmoidalFitFunction") may need.

Value

Returns the parameters related with the model fitted for the input data.

Examples

```
# runif() is used here for consistency with previous versions of the sicegar package. However,
# rnorm() will generate symmetric errors, producing less biased numerical parameter estimates.
# We recommend errors generated with rnorm() for any simulation studies on sicegar.
# Example 1 (sigmoidal function with normalization)
time <- seq(3, 24, 0.5)

#simulate intensity data and add noise
noise_parameter <- 2.5
intensity_noise <- stats::runif(n = length(time), min = 0, max = 1) * noise_parameter
intensity <- sigmoidalFitFormula_h0(time, maximum = 4, slopeParam = 1, midPoint = 8, h0 = 1)
intensity <- intensity + intensity_noise

dataInput <- data.frame(intensity = intensity, time = time)
normalizedInput <- normalizeData(dataInput, dataInputName = "sample001")
parameterVector <- multipleFitFunction_h0(dataInput = normalizedInput,
                                    model = "sigmoidal",
                                    n_runs_min = 20,
                                    n_runs_max = 500)

#Check the results
if(parameterVector$isThisaFit){
  intensityTheoretical <- sigmoidalFitFormula_h0(time,
                           maximum = parameterVector$maximum_Estimate,
                           slopeParam = parameterVector$slopeParam_Estimate,
                           midPoint = parameterVector$midPoint_Estimate,
                           h0 = parameterVector$h0_Estimate)
```

```
 comparisonData <- cbind(dataInput, intensityTheoretical)

 print(parameterVector$residual_Sum_of_Squares)

 require(ggplot2)
 ggplot(comparisonData)+
   geom_point(aes(x = time, y = intensity)) +
   geom_line(aes(x = time, y = intensityTheoretical), color = "orange") +
   expand_limits(x = 0, y = 0)
}



if(!parameterVector$isThisaFit){
  print(parameterVector)
}

# Example 2 (doublesigmoidal function with normalization)
time <- seq(3, 24, 0.1)

#simulate intensity data with noise
noise_parameter <- 0.2
intensity_noise <- stats::runif(n = length(time), min = 0, max = 1) * noise_parameter
intensity <- doublesigmoidalFitFormula_h0(time,
                                    finalAsymptoteIntensityRatio = .3,
                                    maximum = 4,
                                    slope1Param = 1,
                                    midPoint1Param = 7,
                                    slope2Param = 1,
                                    midPointDistanceParam = 8,
                                    h0 = 1)
intensity <- intensity + intensity_noise

dataInput <- data.frame(intensity = intensity, time = time)
normalizedInput <- normalizeData(dataInput)
parameterVector <- multipleFitFunction_h0(dataInput = normalizedInput,
                           dataInputName="sample001",
                           model = "doublesigmoidal",
                           n_runs_min = 20,
                           n_runs_max = 500,
                           showDetails = FALSE)


#Check the results
if(parameterVector$isThisaFit){
 intensityTheoretical <-
       doublesigmoidalFitFormula_h0(
              time,
          finalAsymptoteIntensityRatio = parameterVector$finalAsymptoteIntensityRatio_Estimate,
              maximum = parameterVector$maximum_Estimate,
              slope1Param = parameterVector$slope1Param_Estimate,
              midPoint1Param = parameterVector$midPoint1Param_Estimate,
              slope2Param = parameterVector$slope2Param_Estimate,
```

```
                midPointDistanceParam = parameterVector$midPointDistanceParam_Estimate,
                h0 = parameterVector$h0_Estimate)

 comparisonData <- cbind(dataInput, intensityTheoretical)

 require(ggplot2)
 ggplot(comparisonData) +
   geom_point(aes(x = time, y = intensity)) +
   geom_line(aes(x = time, y = intensityTheoretical), color = "orange") +
   expand_limits(x = 0, y = 0)
 }

if(!parameterVector$isThisaFit){
  print(parameterVector)
  }
```

---

normalizeData *Normalization of given data*

Description

Maps the given time-intensity data into a rescaled dataframe where time is scaled to between 0 and 1, and intensity is scaled to be between 0 and 1.

Usage

```
normalizeData(dataInput, dataInputName = NA)
```

Arguments

dataInput	A dataframe or a list containing the dataframe. The data frame should be composed of at least two columns. One represents time, and the other represents intensity.
dataInputName	experiment name (Default is 'NA').

Value

Function returns a new dataframe, scaling factors and scaling constants that connects the initial data frame to the new one. The new data frame includes 2 columns: normalized time and normalized intensity. The time and intensity constants and scaling factors are the parameters to transform data from the unnormalized dataframe to normalized data frame.

Examples

```
# runif() is used here for consistency with previous versions of the sicegar package. However,
# rnorm() will generate symmetric errors, producing less biased numerical parameter estimates.
# We recommend errors generated with rnorm() for any simulation studies on sicegar.
# generateRandomData
time <- seq(3, 48, 0.5)
intensity <- runif(length(time), 3.0, 7.5)
dataInput <- data.frame(time, intensity)

# Normalize Data
dataOutput <- normalizeData(dataInput, dataInputName="sample001")
```

---

parameterCalculation *additional parameter calculation with help of fits*

Description

Generates useful values for external use, using parameters existing in the parameterVector.

Usage

```
parameterCalculation(parameterVector, stepSize = 1e-05)
```

Arguments

parameterVector	Output of multiple fit function sicegar::multipleFitFunction() that gives the variables generated by the sigmoidal or double sigmoidal fit.
stepSize	Step size used by the fitting algorithm. Smaller numbers gave more accurate results than larger numbers, and larger numbers gave the results faster than small numbers. The default value is 0.00001.

Value

Returns the expanded parameter vector. This vector includes useful derived values such as time and intensity of the start point, in addition to the standard values that the fit algorithms produce that are necessary to define the curves.

Examples

```
# runif() is used here for consistency with previous versions of the sicegar package. However,
# rnorm() will generate symmetric errors, producing less biased numerical parameter estimates.
# We recommend errors generated with rnorm() for any simulation studies on sicegar.
time <- seq(3, 24, 0.1)

#simulate intensity data with noise
noise_parameter <- 0.2
```

```
intensity_noise <- stats::runif(n = length(time), min = 0, max = 1) * noise_parameter
intensity <- sicegar::doublesigmoidalFitFormula(time,
                                          finalAsymptoteIntensityRatio = .3,
                                          maximum = 4,
                                          slope1Param = 1,
                                          midPoint1Param = 7,
                                          slope2Param = 1,
                                          midPointDistanceParam = 8)
intensity <- intensity+intensity_noise

dataInput <- data.frame(intensity = intensity, time = time)
normalizedInput <- sicegar::normalizeData(dataInput)
parameterVector <- sicegar::multipleFitFunction(dataInput = normalizedInput,
                                          dataInputName = "sample01",
                                          model = "doublesigmoidal",
                                          n_runs_min = 20,
                                          n_runs_max = 500,
                                          showDetails = FALSE)

if(parameterVector$isThisaFit){
       parameterVector <- sicegar::parameterCalculation(parameterVector)
}

print(t(parameterVector))
```

`parameterCalculation_h0` *additional parameter calculation with help of fits*

Description

Generates useful values for external use, using parameters existing in the parameterVector.

Usage

```
parameterCalculation_h0(parameterVector, stepSize = 1e-05)
```

Arguments

`parameterVector`	Output of multiple fit function sicegar::multipleFitFunction() that gives the variables generated by the sigmoidal or double sigmoidal fit.
`stepSize`	Step size used by the fitting algorithm. Smaller numbers gave more accurate results than larger numbers, and larger numbers gave the results faster than small numbers. The default value is 0.00001.

Value

Returns the expanded parameter vector. This vector includes useful derived values such as time and intensity of the start point, in addition to the standard values that the fit algorithms produce that are necessary to define the curves.

Examples

```
# runif() is used here for consistency with previous versions of the sicegar package. However,
# rnorm() will generate symmetric errors, producing less biased numerical parameter estimates.
# We recommend errors generated with rnorm() for any simulation studies on sicegar.
time <- seq(3, 24, 0.1)

#simulate intensity data with noise
noise_parameter <- 0.2
intensity_noise <- stats::runif(n = length(time), min = 0, max = 1) * noise_parameter
intensity <- sicegar::doublesigmoidalFitFormula_h0(time,
                                          finalAsymptoteIntensityRatio = .3,
                                          maximum = 4,
                                          slope1Param = 1,
                                          midPoint1Param = 7,
                                          slope2Param = 1,
                                          midPointDistanceParam = 8,
                                          h0 = 1)
intensity <- intensity+intensity_noise

dataInput <- data.frame(intensity = intensity, time = time)
normalizedInput <- sicegar::normalizeData(dataInput)
parameterVector <- sicegar::multipleFitFunction_h0(dataInput = normalizedInput,
                                          dataInputName = "sample01",
                                          model = "doublesigmoidal",
                                          n_runs_min = 20,
                                          n_runs_max = 500,
                                          showDetails = FALSE)

if(parameterVector$isThisaFit){
       parameterVector <- sicegar::parameterCalculation_h0(parameterVector)
}

print(t(parameterVector))
```

---

preCategorize *Checks for signal in the data.*

Description

Checks if the signal is present in the data. Often a high percentage of high through-put data does not contain a signal. Checking if data does not contain signal before doing a sigmoidal or double sigmoidal fit can make the analysis of data from high-throughput experiments much faster.

Usage

```
preCategorize(
  normalizedInput,
  threshold_intensity_range = 0.1,
  threshold_minimum_for_intensity_maximum = 0.3
)
```

Arguments

`normalizedInput`
: is the output of the sicegar::normalizeData() function.

`threshold_intensity_range`
: minimum for intensity range, i.e. it is the lower limit for the allowed difference between the maximum and minimum of the intensities (Default is 0.1, and the values are based on actual, not the rescaled data.).

`threshold_minimum_for_intensity_maximum`
: minimum allowed value for intensity maximum. (Default is 0.3, and the values are based on actual, not the rescaled data.).

Value

Function returns a brief decision list that includes information about the decision process. Post important part of this information is decisionList$decisionwhich might be either "no_signal" or "not_no_signal".

Examples

```
# runif() is used here for consistency with previous versions of the sicegar package. However,
# rnorm() will generate symmetric errors, producing less biased numerical parameter estimates.
# We recommend errors generated with rnorm() for any simulation studies on sicegar.
# Example 1 with double sigmoidal data

time=seq(3, 24, 0.1)

#simulate intensity data and add noise
noise_parameter = 0.2
intensity_noise = runif(n = length(time), min = 0, max = 1) * noise_parameter
intensity = sicegar::doublesigmoidalFitFormula(time,
                                               finalAsymptoteIntensityRatio = .3,
                                               maximum = 4,
                                               slope1Param = 1,
                                               midPoint1Param = 7,
                                               slope2Param = 1,
                                               midPointDistanceParam = 8)
intensity <- intensity + intensity_noise

dataInput <- data.frame(intensity = intensity, time = time)
normalizedInput <- sicegar::normalizeData(dataInput, dataInputName = "sample001")
isThis_nosignal <- sicegar::preCategorize(normalizedInput = normalizedInput)
```

```
# Example 2 with no_signal data

time <- seq(3, 24, 0.1)

#simulate intensity data and add noise
noise_parameter <- 0.05
intensity_noise <- runif(n = length(time), min = 0, max = 1) * noise_parameter * 2e-04
intensity <- sicegar::doublesigmoidalFitFormula(time,
                                                finalAsymptoteIntensityRatio = .3,
                                                maximum = 2e-04,
                                                slope1Param = 1,
                                                midPoint1Param = 7,
                                                slope2Param = 1,
                                                midPointDistanceParam = 8)
intensity <- intensity + intensity_noise

dataInput <- data.frame(intensity=intensity, time=time)
normalizedInput <- sicegar::normalizeData(dataInput,dataInputName = "sample001")
isThis_nosignal <- sicegar::preCategorize(normalizedInput = normalizedInput)
```

`sameSourceDataCheck` *Check that data came from the same source.*

Description

Checks if the provided data and models came from same source by looking to ".dataInputName" columns of the inputs.

Usage

```
sameSourceDataCheck(dataInput, sigmoidalFitVector, doubleSigmoidalFitVector)
```

Arguments

`dataInput`	a dataframe composed of two columns. One is for time and the other is for intensity. Should be normalized data generated by sicegar::normalizeData().
`sigmoidalFitVector`	is the output of sigmoidalFitFunction. Default is NULL.
`doubleSigmoidalFitVector`	is the output of double sigmoidal fit function. Default is NULL.

Value

Returns TRUE if models came from same source, FALSE otherwise.

sigmoidalFitFormula *sigmoidalFitFormula*

Description

Calculates intensities for given time points (x) by using sigmoidal fit model and parameters (maximum, slopeParam, and midpoint).

Usage

```
sigmoidalFitFormula(x, maximum, slopeParam, midPoint)
```

Arguments

x	the "time" column of the dataframe.
maximum	the maximum intensity that the sigmoidal function can reach as time approaches infinity.
slopeParam	the slope parameter of the sigmoidal function at the steepest point.
midPoint	the x axis value of the steepest point in the function.

Value

Returns the predicted intensities for given time points with the given sigmoidal fit parameters.

Examples

```
# runif() is used here for consistency with previous versions of the sicegar package. However,
# rnorm() will generate symmetric errors, producing less biased numerical parameter estimates.
# We recommend errors generated with rnorm() for any simulation studies on sicegar.
time <- seq(3, 24, 0.5)

#simulate intensity data and add noise
noise_parameter <- 0.1
intensity_noise <- stats::runif(n = length(time), min = 0, max = 1) * noise_parameter
intensity <- sigmoidalFitFormula(time, maximum = 4, slopeParam = 1, midPoint = 8)
intensity <- intensity + intensity_noise

dataInput <- data.frame(intensity = intensity, time = time)
normalizedInput <- normalizeData(dataInput)
parameterVector <- sigmoidalFitFunction(normalizedInput, tryCounter = 2)

#Check the results
if(parameterVector$isThisaFit){
 intensityTheoretical <- sigmoidalFitFormula(time,
                                             maximum = parameterVector$maximum_Estimate,
                                          slopeParam = parameterVector$slopeParam_Estimate,
                                              midPoint = parameterVector$midPoint_Estimate)
```

```
 comparisonData <- cbind(dataInput, intensityTheoretical)

 require(ggplot2)
 ggplot(comparisonData) +
   geom_point(aes(x = time, y = intensity)) +
   geom_line(aes(x = time, y = intensityTheoretical)) +
   expand_limits(x = 0, y = 0)
}

if(!parameterVector$isThisaFit){
  print(parameterVector)
}
```

`sigmoidalFitFormula_h0` *sigmoidalFitFormula_h0*

Description

Calculates intensities for given time points (x) by using sigmoidal fit model and parameters (maximum, slopeParam, midpoint, and h0).

Usage

```
sigmoidalFitFormula_h0(x, maximum, slopeParam, midPoint, h0)
```

Arguments

`x`	the "time" column of the dataframe.
`maximum`	the maximum intensity that the sigmoidal function can reach while time approaches infinity.
`slopeParam`	the slope parameter of the sigmoidal function at the steepest point.
`midPoint`	the x axis value of the steepest point in the function.
`h0`	the lower asymptote (baseline) intensity

Value

Returns the predicted intensities for given time points with the given sigmoidal fit parameters.

Examples

```
# runif() is used here for consistency with previous versions of the sicegar package. However,
# rnorm() will generate symmetric errors, producing less biased numerical parameter estimates.
# We recommend errors generated with rnorm() for any simulation studies on sicegar.
time <- seq(3, 24, 0.5)

#simulate intensity data and add noise
noise_parameter <- 0.1
intensity_noise <- stats::runif(n = length(time), min = 0, max = 1) * noise_parameter
intensity <- sigmoidalFitFormula_h0(time, maximum = 4, slopeParam = 1, midPoint = 8, h0 = 1)
intensity <- intensity + intensity_noise

dataInput <- data.frame(intensity = intensity, time = time)
normalizedInput <- normalizeData(dataInput)
parameterVector <- sigmoidalFitFunction_h0(normalizedInput, tryCounter = 1)

#Check the results
# sigmoidalFitFunction_h0() is run on the startList param values (because 'tryCounter = 1')
# use multipleFitFunction() for multiple random starts in order to optimize
if(parameterVector$isThisaFit){
 intensityTheoretical <- sigmoidalFitFormula_h0(time,
                                                maximum = parameterVector$maximum_Estimate,
                                            slopeParam = parameterVector$slopeParam_Estimate,
                                                midPoint = parameterVector$midPoint_Estimate,
                                                  h0 = parameterVector$h0_Estimate)

 comparisonData <- cbind(dataInput, intensityTheoretical)

 require(ggplot2)
 ggplot(comparisonData) +
   geom_point(aes(x = time, y = intensity)) +
   geom_line(aes(x = time, y = intensityTheoretical)) +
   expand_limits(x = 0, y = 0)
}

if(!parameterVector$isThisaFit){
  print(parameterVector)
}
```

`sigmoidalFitFunction` *Sigmoidal fit function*

Description

The function fits a sigmoidal curve to given data by using likelihood maximization (LM) algorithm and provides the parameters (maximum, slopeParam, midPoint, and h0) describing the sigmoidal fit as output. It also contains information about the goodness of fits such as AIC, BIC, residual sum of squares, and log likelihood.

Usage

```
sigmoidalFitFunction(
  dataInput,
  tryCounter,
  startList = list(maximum = 1, slopeParam = 1, midPoint = 0.33),
  lowerBounds = c(maximum = 0.3, slopeParam = 0.01, midPoint = -0.52),
  upperBounds = c(maximum = 1.5, slopeParam = 180, midPoint = 1.15),
  min_Factor = 1/2^20,
  n_iterations = 1000
)
```

Arguments

dataInput	A dataframe or a list containing the dataframe. The dataframe should be composed of at least two columns. One represents time, and the other represents intensity. The data should be normalized with the normalize data function sicegar::normalizeData() before being imported into this function.
tryCounter	A counter that shows the number of times the data was fit via maximum likelihood function.
startList	A vector containing the initial set of parameters that the algorithm tries for the first fit attempt for the relevant parameters. The vector is composed of four elements; 'maximum', 'slopeParam', 'midPoint', and 'h0'. Detailed explanations of those parameters can be found in vignettes. Defaults are maximum = 1, slopeParam = 1, midPoint = 0.33, and h0 = 0. The numbers are in normalized time intensity scale.
lowerBounds	The lower bounds for the randomly generated start parameters. The vector is composed of four elements; 'maximum', 'slopeParam', 'midPoint', and 'h0'. Detailed explanations of those parameters can be found in vignettes. Defaults are maximum = 0.3, slopeParam = 0.01, midPoint = -0.52, and h0 = -0.1. The numbers are in normalized time intensity scale.
upperBounds	The upper bounds for the randomly generated start parameters. The vector is composed of four elements; 'maximum', 'slopeParam','midPoint', and 'h0'. Detailed explanations of those parameters can be found in vignettes. Defaults are maximum = 1.5, slopeParam = 180, midPoint = 1.15, and h0 = 0.3. The numbers are in normalized time intensity scale.
min_Factor	Defines the minimum step size used by the fitting algorithm. Default is 1/2^20.
n_iterations	Defines maximum number of iterations used by the fitting algorithm. Default is 1000

Value

Returns fitted parameters for the sigmoidal model.

Examples

```
# runif() is used here for consistency with previous versions of the sicegar package. However,
# rnorm() will generate symmetric errors, producing less biased numerical parameter estimates.
```

```
# We recommend errors generated with rnorm() for any simulation studies on sicegar.
time <- seq(3, 24, 0.5)

#simulate intensity data and add noise
noise_parameter <- 0.1
intensity_noise <- stats::runif(n = length(time), min = 0, max = 1) * noise_parameter
intensity <- sigmoidalFitFormula(time, maximum = 4, slopeParam = 1, midPoint = 8)
intensity <- intensity + intensity_noise

dataInput <- data.frame(intensity = intensity, time = time)
normalizedInput <- normalizeData(dataInput)
parameterVector <- sigmoidalFitFunction(normalizedInput, tryCounter = 2)

#Check the results
if(parameterVector$isThisaFit){
intensityTheoretical <- sigmoidalFitFormula(time,
                                            maximum = parameterVector$maximum_Estimate,
                                          slopeParam = parameterVector$slopeParam_Estimate,
                                            midPoint = parameterVector$midPoint_Estimate)

comparisonData <- cbind(dataInput, intensityTheoretical)

require(ggplot2)
ggplot(comparisonData) +
 geom_point(aes(x = time, y = intensity)) +
 geom_line(aes(x = time, y = intensityTheoretical)) +
 expand_limits(x = 0, y = 0)
}

if(!parameterVector$isThisaFit){
  print(parameterVector)
}
```

`sigmoidalFitFunction_h0` *Sigmoidal fit function with h0 estimation*

Description

The function fits a sigmoidal curve to given data by using likelihood maximization (LM) algorithm and provides the parameters (maximum, slopeParam, midPoint, and h0) describing the sigmoidal fit as output. It also contains information about the goodness of fits such as AIC, BIC, residual sum of squares, and log likelihood.

Usage

```
sigmoidalFitFunction_h0(
  dataInput,
  tryCounter,
```

```
  startList = list(maximum = 1, slopeParam = 1, midPoint = 0.33, h0 = 0),
  lowerBounds = c(maximum = 0.3, slopeParam = 0.01, midPoint = -0.52, h0 = -0.1),
  upperBounds = c(maximum = 1.5, slopeParam = 180, midPoint = 1.15, h0 = 0.3),
  min_Factor = 1/2^20,
  n_iterations = 1000
)
```

Arguments

dataInput	A dataframe or a list containing the dataframe. The dataframe should be composed of at least two columns. One represents time, and the other represents intensity. The data should be normalized with the normalize data function sicegar::normalizeData() before being imported into this function.
tryCounter	A counter that shows the number of times the data was fit via maximum likelihood function.
startList	A vector containing the initial set of parameters that the algorithm tries for the first fit attempt for the relevant parameters. The vector is composed of four elements; 'maximum', 'slopeParam', 'midPoint', and 'h0'. Detailed explanations of those parameters can be found in vignettes. Defaults are maximum = 1, slopeParam = 1, midPoint = 0.33, and h0 = 0. The numbers are in normalized time intensity scale.
lowerBounds	The lower bounds for the randomly generated start parameters. The vector is composed of four elements; 'maximum', 'slopeParam', 'midPoint', and 'h0'. Detailed explanations of those parameters can be found in vignettes. Defaults are maximum = 0.3, slopeParam = 0.01, midPoint = -0.52, and h0 = -0.1. The numbers are in normalized time intensity scale.
upperBounds	The upper bounds for the randomly generated start parameters. The vector is composed of four elements; 'maximum', 'slopeParam','midPoint', and 'h0'. Detailed explanations of those parameters can be found in vignettes. Defaults are maximum = 1.5, slopeParam = 180, midPoint = 1.15, and h0 = 0.3. The numbers are in normalized time intensity scale.
min_Factor	Defines the minimum step size used by the fitting algorithm. Default is 1/2^20.
n_iterations	Defines maximum number of iterations used by the fitting algorithm. Default is 1000

Value

Returns fitted parameters for the sigmoidal model.

Examples

```
# runif() is used here for consistency with previous versions of the sicegar package. However,
# rnorm() will generate symmetric errors, producing less biased numerical parameter estimates.
# We recommend errors generated with rnorm() for any simulation studies on sicegar.
time <- seq(3, 24, 0.5)

#simulate intensity data and add noise
noise_parameter <- 0.1
```

```
intensity_noise <- stats::runif(n = length(time), min = 0, max = 1) * noise_parameter
intensity <- sigmoidalFitFormula_h0(time, maximum = 4, slopeParam = 1, midPoint = 8, h0 = 1)
intensity <- intensity + intensity_noise

dataInput <- data.frame(intensity = intensity, time = time)
normalizedInput <- normalizeData(dataInput)
parameterVector <- sigmoidalFitFunction_h0(normalizedInput, tryCounter = 1)

#Check the results
# sigmoidalFitFunction_h0() is run on the startList param values (because 'tryCounter = 1')
# use multipleFitFunction() for multiple random starts in order to optimize
if(parameterVector$isThisaFit){
intensityTheoretical <- sigmoidalFitFormula_h0(time,
                                          maximum = parameterVector$maximum_Estimate,
                                      slopeParam = parameterVector$slopeParam_Estimate,
                                          midPoint = parameterVector$midPoint_Estimate,
                                          h0 = parameterVector$h0_Estimate)

comparisonData <- cbind(dataInput, intensityTheoretical)

require(ggplot2)
ggplot(comparisonData) +
 geom_point(aes(x = time, y = intensity)) +
 geom_line(aes(x = time, y = intensityTheoretical)) +
 expand_limits(x = 0, y = 0)
}

if(!parameterVector$isThisaFit){
  print(parameterVector)
}
```

---

unnormalizeData *Unnormalization of given data*

Description

Maps the given time-intensity data into a rescaled frame where time is between zero and one intensity is also between zero and one.

Usage

```
unnormalizeData(dataInput)
```

Arguments

dataInput	a list file composed of two parts First part is the data that will be unnormalized, which is a dataframe composed of two columns. One is for time and the other is for intensity Second part is the scaling parameters of the data which is a vector that has three components. The first is related with time and second two are

related with intensity. The second value represents the min value of the intensity set. First and third values represent the difference between max and min value in the relevant column.

Value

Returns a dataframe, scaling factors, and scaling constants for time and intensity. The other data frame includes 2 columns: normalized time and normalized intensity. The time and intensity constants and scaling factors are the parameters to transform data from given set to scaled set.

Examples

```
# runif() is used here for consistency with previous versions of the sicegar package. However,
# rnorm() will generate symmetric errors, producing less biased numerical parameter estimates.
# We recommend errors generated with rnorm() for any simulation studies on sicegar.
# generateRandomData
time <- seq(3, 48, 0.5)
intensity <- runif(length(time), 3.0, 7.5)
dataInput <- data.frame(time, intensity)
# Normalize Data
dataOutput <- normalizeData(dataInput)
dataInput2 <- dataOutput
# Un Normalize it
dataOutput2 <- unnormalizeData(dataInput2)
```

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