Package ‘NPARC’

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Type Package

Title Non-parametric analysis of response curves for thermal proteome profiling experiments

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Encoding UTF-8

LazyData true

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Depends R (>= 4.0.0)

Imports dplyr, tidyr, BiocParallel, broom, MASS, rlang, magrittr, stats, methods

Suggests testthat, devtools, knitr, rprojroot, rmarkdown, ggplot2, BiocStyle

VignetteBuilder knitr

biocViews Software, Proteomics

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### fitSingleSigmoid

**Description**

Fit sigmoid model

**Usage**

```r
grobfit(x, y, start = c(Pl = 0, a = 550, b = 10))
```

**Arguments**

- `x` numeric vector of the independent variables (typically temperature)
- `y` numeric vector of the dependent variables (typically relative abundance measurements)
- `start` numeric vector of start parameters for the melting curve equation

**Details**

Fits the following function to the data: $y = (1 - Pl)/(1 + exp((b - a/x))) + Pl$

**Value**

model summary of type "nls"

**Examples**

```r
data(stauro_TPP_data_tidy)
stk4 <- dplyr::filter(stauro_TPP_data_tidy, grepl("STK4", uniqueID))
fitSingleSigmoid(stk4$temperature, stk4$relAbundance)
```
getParams

Control parameters for model fitting

Description
Control parameters for model fitting

Usage
getParams(start = c(P1 = 0, a = 550, b = 10), maxAttempts = 100)

Arguments

- start: Numeric vector of start parameters for the melting curve equation
- maxAttempts: Number of resampling steps in case of unsuccessful model fits

Value
list of two elements: 1) "start" listing the starting parameters for melting curve fitting, 2) "maxAttempts" listing the maximal number of attempts the fit should be allowed

Examples

data(stauro_TPP_data_tidy)
df <- dplyr::filter(stauro_TPP_data_tidy, grepl("MAPK|ATP|CDK|GTP|CRK", uniqueID))
testResults <- runNPARC(x = df$temperature,
y = df$relAbundance,
id = df$uniqueID,
groupAlt = df$compoundConcentration,
dfType = "empirical",
control = getParams(maxAttempts = 50))

NPARC

NPARC package

Description
Non-parametric analysis of response curves

Details
See the preprint on Childs, Bach, Franken et al. (2019): Non-parametric analysis of thermal proteome profiles reveals novel drug-binding proteins
NPARCfit

Fit null and alternative models for Non-parametric analysis of response curves

Description

Fit melting curve and return model metrics as well as predictions for the null and alternative models.

Usage

NPARCfit(x, y, id, control = getParams(), groupsNull = NULL, groupsAlt, BPPARAM = BiocParallel::SerialParam(progressbar = TRUE), returnModels = FALSE)

Arguments

x numeric vector of the independent variables (typically temperature)
y numeric vector of the dependent variables (typically relative abundance measurements)
id character vector with the protein ID to which each data point belongs.
control list of parameters used to control specific parts of the analyse
groupsNull one or more vectors with grouping variables for the null models. See details.
groupsAlt one or more vectors with grouping variables for the alternative models. See details.
BPPARAM BiocParallel parameter object to invoke curve fitting in parallel. Default: BiocParallel::SerialParam()
returnModels boolean value. If true, the fitted models are returned together with the test results

Details

groupsNull or groupsAlt can either be a single vector each, or data.frames of the same length as x and y with one column per factor

Value

data frame with fitted model parameters and additional columns listing e.g. residuals sum of squares

Examples

data(stauro_TPP_data_tidy)
df <- dplyr::filter(stauro_TPP_data_tidy, grepl("CDK|GTP|CRK", uniqueID))
testResults <- NPARCfit(x = df$temperature,
y = df$relAbundance,
   id = df$uniqueID,
groupsAlt = df$compoundConcentration)
**NPARCtest**

*Perform F-test*

**Description**

Perform F-test

**Usage**

NPARCtest(modelMetrics, dfType = c("empirical", "theoretical"))

**Arguments**

- **modelMetrics**: data.frame with results of the model fit in long format.
- **dfType**: character value indicating the method for degrees of freedom computation for the F-test. Theoretical yields the textbook solution. Empirical yields estimates derived from the distribution moments of the RSS.

**Value**

data frame with fitted model parameters and additional columns listing e.g. residuals sum of squares of null and alternative model and raw and adjusted p values retrieved from testing

**Examples**

data(stauro_TPP_data_tidy)
df <- dplyr::filter(stauro_TPP_data_tidy, grepl("CDK|GTP|CRK", uniqueID))
fits <- NPARCfit(x = df$temperature,
y = df$relAbundance,
id = df$uniqueID,
groupsNull = NULL,
groupsAlt = df$compoundConcentration,
returnModels = FALSE)
modelMetrics <- fits$metrics
testRes <- NPARCtest(modelMetrics, dfType = "theoretical")

**runNPARC**

*Non-parametric analysis of response curves*

**Description**

Wrapper function for melting curve fitting and hypothesis testing.

**Usage**

runNPARC(x, y, id, groupsNull = NULL, groupsAlt,
BPPARAM = BiocParallel::SerialParam(progressbar = TRUE),
dfType = c("theoretical", "empirical"), control = getParams())
Arguments

- **x**: numeric vector of the independent variables (typically temperature)
- **y**: numeric vector of the dependent variables (typically relative abundance measurements)
- **id**: character vector with the protein ID to which each data point belongs.
- **groupsNull**: one or more vectors with grouping variables for the null models. See details.
- **groupsAlt**: one or more vectors with grouping variables for the alternative models. See details.
- **BPPARAM**: BiocParallel parameter object to invoke curve fitting in parallel. Default: BiocParallel::SerialParam()
- **dfType**: character value indicating the method for degrees of freedom computation for the F-test. Theoretical yields the text-book solution. Empirical yields estimates derived from the distribution moments of the RSS.
- **control**: list of parameters used to control specific parts of the analysis.

Details

- **groupsNull** or **groupsAlt** can either be a single vector each, or data.frames of the same length as x and y with one column per factor.

Value

data frame with fitted model parameters and additional columns listing e.g. residuals sum of squares of null and alternative model.

Examples

data(stauro_TPP_data_tidy)
df <- dplyr::filter(stauro_TPP_data_tidy, grepl("CDK|GTP|CRK", uniqueID))
testResults <- runNPARC(x = df$temperature,
                       y = df$relAbundance,
                       id = df$uniqueID,
                       groupsAlt = df$compoundConcentration,
                       dfType = "empirical")

stauro_TPP_data_tidy  **TPP dataset of staurosporine treated cells.**

Description

Data from a thermal proteome profiling (TPP) experiment investigating the ATP-competitive pan-kinase inhibitor staurosporine on K562 cells. The data has been downloaded the data from the supplement of the respective publication and converted into tidy format.
stauro_TPP_data_tidy

Usage

data(stauro_TPP_data_tidy)

Format

An object of class "data.frame"

References

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