

# Package ‘NPARC’

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**Type** Package

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

**Version** 1.16.0

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**Description** Perform non-parametric analysis of response curves as described by Childs, Bach, Franken et al. (2019): Non-parametric analysis of thermal proteome profiles reveals novel drug-binding proteins.

**License** GPL-3

**Encoding** UTF-8

**LazyData** true

**RoxygenNote** 6.1.1

**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	<i>Fit sigmoid model</i>
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### Description

Fit sigmoid model

### Usage

```
fitSingleSigmoid(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

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

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`getParams`*Control parameters for model fitting*

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**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$uniqueID,
  groupsAlt = df$compoundConcentration,
  dfType = "empirical",
  control = getParams(maxAttempts = 50))
```

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`NPARC`*NPARC package*

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**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](#)



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NPARCtest	<i>Perform F-test</i>
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**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 text-book 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 alterantive 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")
```

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runNPARC	<i>Non-parametric analysis of response curves</i>
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**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 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 analyse

**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 alterantive 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")
```

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stauro\_TPP\_data\_tidy *TPP dataset of staurosporine treated cells.*

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**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.

**Usage**

```
data(stauro_TPP_data_tidy)
```

**Format**

An object of class "data.frame"

**References**

Savitski et al. (2014): Tracking cancer drugs in living cells by thermal profiling of the proteome. Science 346, 1255784.

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