

# Package ‘TPP2D’

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---

annotateDataList	<i>Annotate imported data list using a config table</i>
------------------	---

---

### Description

Annotate imported data list using a config table

### Usage

```
annotateDataList(dataList, geneNameVar, configLong, intensityStr, fcStr)
```

**Arguments**

dataList	list of datasets from different MS runs corresponding to a 2D-TPP dataset
geneNameVar	character string of the column name that describes the gene name of a given protein in the raw data files
configLong	long formatted data frame of a corresponding config table
intensityStr	character string indicating which columns contain raw intensities measurements
fcStr	character string indicating which columns contain the actual fold change values. Those column names containing the suffix fcStr will be regarded as containing fold change values.

**Value**

data frame containing all data annotated by information supplied in the config table

**Examples**

```
data("config_tab")
data("raw_dat_list")
dataList <- import2dMain(configTable = config_tab,
                        data = raw_dat_list,
                        idVar = "protein_id",
                        fcStr = "rel_fc_",
                        addCol = "gene_name",
                        naStrs = NA,
                        intensityStr = "signal_sum_",
                        nonZeroCols = "qusm",
                        qualColName = "qupm")
configLong <- configWide2Long(configWide = config_tab)
annotateDataList(dataList = dataList,
                 geneNameVar = "gene_name",
                 configLong = configLong,
                 intensityStr = "signal_sum_",
                 fcStr = "rel_fc_")
```

---

bootstrapNull

*Bootstrap null distribution of F statistics for FDR estimation*

---

**Description**

Bootstrap null distribution of F statistics for FDR estimation

**Usage**

```
bootstrapNull(
  df,
  maxit = 500,
  independentFiltering = FALSE,
```

```

fcThres = 1.5,
minObs = 20,
optim_fun_h0 = .min_RSS_h0,
optim_fun_h1 = .min_RSS_h1_slope_pEC50,
optim_fun_h1_2 = NULL,
gr_fun_h0 = NULL,
gr_fun_h1 = NULL,
gr_fun_h1_2 = NULL,
ncores = 1,
B = 20,
byMsExp = TRUE
)

```

### Arguments

df	tidy data_frame retrieved after import of a 2D-TPP dataset, potential filtering and addition of a column "nObs" containing the number of observations per protein
maxit	maximal number of iterations the optimization should be given, default is set to 500
independentFiltering	boolean flag indicating whether independent filtering should be performed based on minimal fold changes per protein profile
fcThres	numeric value of minimal fold change (or inverse fold change) a protein has to show to be kept upon independent filtering
minObs	numeric value of minimal number of observations that should be required per protein
optim_fun_h0	optimization function that should be used for fitting the H0 model
optim_fun_h1	optimization function that should be used for fitting the H1 model
optim_fun_h1_2	optional additional optimization function that will be run with parameters retrieved from optim_fun_h1 and should be used for fitting the H1 model with the trimmed sum model, default is NULL
gr_fun_h0	optional gradient function for optim_fun_h0, default is NULL
gr_fun_h1	optional gradient function for optim_fun_h1, default is NULL
gr_fun_h1_2	optional gradient function for optim_fun_h1_2, default is NULL
ncores	numeric value of numbers of cores that the function should use to parallelize
B	numeric value of rounds of bootstrap, default: 20
byMsExp	boolean flag indicating whether resampling of residuals should be performed separately for data generated by different MS experiments, default TRUE, recommended

### Value

data frame containing F statistics of proteins with permuted 2D thermal profiles that are informative on the Null distribution of F statistics

**Examples**

```

data("simulated_cell_extract_df")
temp_df <- simulated_cell_extract_df %>%
  filter(clustername %in% paste0("protein", 1:3)) %>%
  group_by(representative) %>%
  mutate(nObs = n()) %>%
  ungroup
boot_df <- bootstrapNull(temp_df, B = 2/10)

```

---

bootstrapNullAlternativeModel

*Bootstrap null distribution of F statistics for FDR estimation based on resampling alternative model residuals*

---

**Description**

Bootstrap null distribution of F statistics for FDR estimation based on resampling alternative model residuals

**Usage**

```

bootstrapNullAlternativeModel(
  df,
  params_df,
  maxit = 500,
  independentFiltering = FALSE,
  fcThres = 1.5,
  minObs = 20,
  optim_fun_h0 = TPP2D:::min_RSS_h0,
  optim_fun_h1 = TPP2D:::min_RSS_h1_slope_pEC50,
  optim_fun_h1_2 = NULL,
  gr_fun_h0 = NULL,
  gr_fun_h1 = NULL,
  gr_fun_h1_2 = NULL,
  BPPARAM = BiocParallel::SerialParam(progressbar = TRUE),
  B = 20,
  byMsExp = TRUE,
  verbose = FALSE
)

```

**Arguments**

df	tidy data frame retrieved after import of a 2D-TPP dataset, potential filtering and addition of a column "nObs" containing the number of observations per protein
params_df	data frame listing all null and alternative model parameters as obtained by 'getModelParamsDf'

<code>maxit</code>	maximal number of iterations the optimization should be given, default is set to 500
<code>independentFiltering</code>	boolean flag indicating whether independent filtering should be performed based on minimal fold changes per protein profile
<code>fcThres</code>	numeric value of minimal fold change (or inverse fold change) a protein has to show to be kept upon independent filtering
<code>minObs</code>	numeric value of minimal number of observations that should be required per protein
<code>optim_fun_h0</code>	optimization function that should be used for fitting the H0 model
<code>optim_fun_h1</code>	optimization function that should be used for fitting the H1 model
<code>optim_fun_h1_2</code>	optional additional optimization function that will be run with parameters retrieved from <code>optim_fun_h1</code> and should be used for fitting the H1 model with the trimmed sum model, default is NULL
<code>gr_fun_h0</code>	optional gradient function for <code>optim_fun_h0</code> , default is NULL
<code>gr_fun_h1</code>	optional gradient function for <code>optim_fun_h1</code> , default is NULL
<code>gr_fun_h1_2</code>	optional gradient function for <code>optim_fun_h1_2</code> , default is NULL
<code>BPPARAM</code>	BiocParallel parameter for optional parallelization of null distribution generation through bootstrapping, default: <code>BiocParallel::SerialParam()</code>
<code>B</code>	numeric value of rounds of bootstrap, default: 20
<code>byMsExp</code>	boolean flag indicating whether resampling of residuals should be performed separately for data generated by different MS experiments, default TRUE, recommended
<code>verbose</code>	logical indicating whether to print each protein while its profile is bootstrapped

**Value**

data frame containing F statistics of proteins with permuted 2D thermal profiles that are informative on the Null distribution of F statistics

**Examples**

```
data("simulated_cell_extract_df")
temp_df <- simulated_cell_extract_df %>%
  filter(clustername %in% paste0("protein", 1:3)) %>%
  group_by(representative) %>%
  mutate(nObs = n()) %>%
  ungroup
temp_params_df <- getModelParamsDf(temp_df)
boot_df <- bootstrapNullAlternativeModel(
  temp_df, params_df = temp_params_df, B = 2)
```

---

 competeModels

 Compete H0 and H1 models per protein and obtain F statistic
 

---

### Description

Compete H0 and H1 models per protein and obtain F statistic

### Usage

```
competeModels(
  df,
  fcThres = 1.5,
  independentFiltering = FALSE,
  minObs = 20,
  optim_fun_h0 = .min_RSS_h0,
  optim_fun_h1 = .min_RSS_h1_slope_pEC50,
  optim_fun_h1_2 = NULL,
  gr_fun_h0 = NULL,
  gr_fun_h1 = NULL,
  gr_fun_h1_2 = NULL,
  maxit = 750
)
```

### Arguments

df	tidy data frame retrieved after import of a 2D-TPP dataset, potential filtering and addition of a column "nObs" containing the number of observations per protein
fcThres	numeric value of minimal fold change (or inverse fold change) a protein has to show to be kept upon independent filtering
independentFiltering	boolean flag indicating whether independent filtering should be performed based on minimal fold changes per protein profile
minObs	numeric value of minimal number of observations that should be required per protein
optim_fun_h0	optimization function that should be used for fitting the H0 model
optim_fun_h1	optimization function that should be used for fitting the H1 model
optim_fun_h1_2	optional additional optimization function that will be run with parameters retrieved from optim_fun_h1 and should be used for fitting the H1 model with the trimmed sum model, default is NULL
gr_fun_h0	optional gradient function for optim_fun_h0, default is NULL
gr_fun_h1	optional gradient function for optim_fun_h1, default is NULL
gr_fun_h1_2	optional gradient function for optim_fun_h1_2, default is NULL
maxit	maximal number of iterations the optimization should be given, default is set to 500

**Value**

data frame summarising the fit characteristics of H0 and H1 models and thereof resulting computed F statistics per protein

**Examples**

```
data("simulated_cell_extract_df")
temp_df <- simulated_cell_extract_df %>%
  filter(clustername %in% paste0("protein", 1:10)) %>%
  group_by(representative) %>%
  mutate(nObs = n()) %>%
  ungroup
computeModels(temp_df)
```

---

computeFstat

*Compute F statistic from H1 and H0 model characteristics*

---

**Description**

Compute F statistic from H1 and H0 model characteristics

**Usage**

```
computeFstat(h0_df, h1_df)
```

**Arguments**

h0_df	data frame with H0 model characteristics for each protein
h1_df	data frame with H1 model characteristics for each protein

**Value**

data frame with H0 and H1 model characteristics for each protein and respectively computed F statistics

**Examples**

```
data("simulated_cell_extract_df")
temp_df <- simulated_cell_extract_df %>%
  filter(clustername %in% paste0("protein", 1:20)) %>%
  group_by(representative) %>%
  mutate(nObs = n()) %>%
  ungroup

h0_df <- fitH0Model(temp_df)
h1_df <- fitH1Model(temp_df)

computeFstat(h0_df, h1_df)
```



---

`computeFStatFromParams`*Compute F statistics from parameter data frame*

---

**Description**

Compute F statistics from parameter data frame

**Usage**

```
computeFStatFromParams(params_df)
```

**Arguments**

`params_df` data frame listing all null and alternative model parameters as obtained by 'getModelParamsDf'

**Value**

data frame of all proteins and computed F statistics and parameters that were used for the computation

**Examples**

```
data("simulated_cell_extract_df")
params_df <- getModelParamsDf(simulated_cell_extract_df)
computeFStatFromParams(params_df)
```

---

`configWide2Long`*Transform configuration table from wide to long*

---

**Description**

Transform configuration table from wide to long

**Usage**

```
configWide2Long(configWide)
```

**Arguments**

`configWide` data frame containing a config table

**Value**

data frame containing config table in long format

**Examples**

```
data("config_tab")
configWide2Long(configWide = config_tab)
```

---

config_tab	<i>Example config table for a import of a simulated 2D-TPP cell extract dataset</i>
------------	---

---

**Description**

Config table for import of simulated example dataset obtained by 2D-TPP experiments for analysis by the TPP2D-package. It's a data frame with the columns "Compound" describing the compound used for the assay, "Experiment" listing MS experiment ids of the separate runs (typically comprising two multiplexed adjacent temperature), "Temperature": the temperature used for a given sub-experiment, the respective TMT labels "126"- "131L", RefCol referring to the label used as a reference label for computing relative fold changes (usually the label used for the control treatment). Please note that when the data is not supplied as a list of already imported data frames the config table for the import function should be a path to a txt, csv or xlsx file containing an additional column "Path" listing for each row the respective path to a searched protein output file.

**Usage**

```
data("config_tab")
```

**Format**

"Compound" describing the compound used for the assay, "Experiment" listing MS experiment ids of the separate runs (typically comprising two multiplexed adjacent temperature), "Temperature": the temperature used for a given sub-experiment, the respective TMT labels "126"- "131L", RefCol referring to the label used as a reference label for computing relative fold changes (usually the label used for the control treatment).

---

filterOutContaminants	<i>Filter out contaminants</i>
-----------------------	--------------------------------

---

**Description**

Filter out contaminants

**Usage**

```
filterOutContaminants(dataLong)
```

**Arguments**

dataLong	long format data frame of imported dataset
----------	--

**Value**

data frame containing full dataset filtered to contain no contaminants

**Examples**

```
data("simulated_cell_extract_df")
filterOutContaminants(simulated_cell_extract_df)
```

---

findHits	<i>Find hits according to FDR threshold</i>
----------	---

---

**Description**

Find hits according to FDR threshold

**Usage**

```
findHits(fdr_df, alpha)
```

**Arguments**

fdr_df	data frame obtained from computeFdr
alpha	significance threshold, default is set to 0.1

**Value**

data frame of significant hits at  $FDR \leq \alpha$

**Examples**

```
data("simulated_cell_extract_df")
temp_df <- simulated_cell_extract_df %>%
  filter(clustername %in% paste0("protein", 1:5)) %>%
  group_by(representative) %>%
  mutate(nObs = n()) %>%
  ungroup
example_out <- fitAndEvalDataset(temp_df)
example_null <- bootstrapNull(temp_df, B = 1)
fdr_df <- getFDR(example_out, example_null)
findHits(fdr_df, 0.1)
```

---

fitAndEvalDataset	<i>Fit H0 and H1 model to 2D thermal profiles of proteins and compute F statistic</i>
-------------------	---

---

## Description

Fit H0 and H1 model to 2D thermal profiles of proteins and compute F statistic

## Usage

```
fitAndEvalDataset(
  df,
  maxit = 500,
  optim_fun_h0 = .min_RSS_h0,
  optim_fun_h1 = .min_RSS_h1_slope_pEC50,
  optim_fun_h1_2 = NULL,
  gr_fun_h0 = NULL,
  gr_fun_h1 = NULL,
  gr_fun_h1_2 = NULL,
  ec50_lower_limit = NULL,
  ec50_upper_limit = NULL,
  slopEC50 = TRUE
)
```

## Arguments

df	tidy data_frame retrieved after import of a 2D-TPP dataset, potential filtering and addition of a column "nObs" containing the number of observations per protein
maxit	maximal number of iterations the optimization should be given, default is set to 500
optim_fun_h0	optimization function that should be used for fitting the H0 model
optim_fun_h1	optimization function that should be used for fitting the H1 model
optim_fun_h1_2	optional additional optimization function that will be run with parameters retrieved from optim_fun_h1 and should be used for fitting the H1 model with the trimmed sum model, default is NULL
gr_fun_h0	optional gradient function for optim_fun_h0, default is NULL
gr_fun_h1	optional gradient function for optim_fun_h1, default is NULL
gr_fun_h1_2	optional gradient function for optim_fun_h1_2, default is NULL
ec50_lower_limit	lower limit of ec50 parameter
ec50_upper_limit	lower limit of ec50 parameter
slopEC50	logical flag indicating whether the h1 model is fitted with a linear model describing the shift of the pEC50 over temperatures

**Value**

data frame with H0 and H1 model characteristics for each protein and respectively computed F statistics

**Examples**

```
data("simulated_cell_extract_df")
temp_df <- simulated_cell_extract_df %>%
  group_by(representative) %>%
  mutate(nObs = n()) %>%
  ungroup
fitAndEvalDataset(temp_df)
```

---

fitH0Model

*Fit H0 model and evaluate fit statistics*


---

**Description**

Fit H0 model and evaluate fit statistics

**Usage**

```
fitH0Model(df, maxit = 500, optim_fun = .min_RSS_h0, gr_fun = NULL)
```

**Arguments**

df	tidy data_frame retrieved after import of a 2D-TPP dataset, potential filtering and addition of a column "nObs" containing the number of observations per protein
maxit	maximal number of iterations the optimization should be given, default is set to 500
optim_fun	optimization function that should be used for fitting the H0 model
gr_fun	optional gradient function for optim_fun, default is NULL

**Value**

data frame with H0 model characteristics for each protein

**Examples**

```
data("simulated_cell_extract_df")
temp_df <- simulated_cell_extract_df %>%
  filter(clustername %in% paste0("protein", 1:5)) %>%
  group_by(representative) %>%
  mutate(nObs = n()) %>%
  ungroup
```

```
fitH0Model(temp_df)
```

---

```
fitH1Model
```

```
Fit H1 model and evaluate fit statistics
```

---

### Description

Fit H1 model and evaluate fit statistics

### Usage

```
fitH1Model(
  df,
  maxit = 500,
  optim_fun = .min_RSS_h1_slope_pEC50,
  optim_fun_2 = NULL,
  gr_fun = NULL,
  gr_fun_2 = NULL,
  ec50_lower_limit = NULL,
  ec50_upper_limit = NULL,
  slopEC50 = TRUE
)
```

### Arguments

df	tidy data_frame retrieved after import of a 2D-TPP dataset, potential filtering and addition of a column "nObs" containing the number of observations per protein
maxit	maximal number of iterations the optimization should be given, default is set to 500
optim_fun	optimization function that should be used for fitting the H0 model
optim_fun_2	optional second optimization function for fitting the H1 model that should be used based on the fitted parameters of the optimization for based on optim_fun
gr_fun	optional gradient function for optim_fun, default is NULL
gr_fun_2	optional gradient function for optim_fun_2, default is NULL
ec50_lower_limit	lower limit of ec50 parameter
ec50_upper_limit	lower limit of ec50 parameter
slopEC50	logical flag indicating whether the h1 model is fitted with a linear model describing the shift of the pEC50 over temperatures

**Value**

data frame with H1 model characteristics for each protein

**Examples**

```
data("simulated_cell_extract_df")
temp_df <- simulated_cell_extract_df %>%
  filter(clustername %in% paste0("protein", 1:5)) %>%
  group_by(representative) %>%
  mutate(nObs = n()) %>%
  ungroup

fith1Model(temp_df)
```

---

getFDR

*Get FDR for given F statistics based on true and null dataset*


---

**Description**

Get FDR for given F statistics based on true and null dataset

**Usage**

```
getFDR(df_out, df_null, squeezeDenominator = TRUE)
```

**Arguments**

df\_out            data frame containing results from analysis by fitAndEvalDataset  
df\_null           data frame containing results from analysis by bootstrapNull  
squeezeDenominator            logical indicating whether F statistic denominator should be shrunked using limma::squeezeVar

**Value**

data frame annotating each protein with a FDR based on it's F statistic and number of observations

**Examples**

```
data("simulated_cell_extract_df")
temp_df <- simulated_cell_extract_df %>%
  filter(clustername %in% paste0("protein", 1:5)) %>%
  group_by(representative) %>%
  mutate(nObs = n()) %>%
  ungroup
example_out <- fitAndEvalDataset(temp_df)
example_null <- bootstrapNull(temp_df, B = 1)
getFDR(example_out, example_null)
```

---

<code>getModelParamsDf</code>	<i>Get H0 and H1 model parameters</i>
-------------------------------	---------------------------------------

---

**Description**

Get H0 and H1 model parameters

**Usage**

```
getModelParamsDf(
  df,
  minObs = 20,
  optim_fun_h0 = .min_RSS_h0,
  optim_fun_h1 = .min_RSS_h1_slope_pEC50,
  optim_fun_h1_2 = NULL,
  gr_fun_h0 = NULL,
  gr_fun_h1 = NULL,
  gr_fun_h1_2 = NULL,
  slopEC50 = TRUE,
  maxit = 500,
  qualColName = "qupm"
)
```

**Arguments**

<code>df</code>	tidy data_frame retrieved after import of a 2D-TPP dataset, potential filtering and addition of a column "nObs" containing the number of observations per protein
<code>minObs</code>	numeric value of minimal number of observations that should be required per protein
<code>optim_fun_h0</code>	optimization function that should be used for fitting the H0 model
<code>optim_fun_h1</code>	optimization function that should be used for fitting the H1 model
<code>optim_fun_h1_2</code>	optional additional optimization function that will be run with parameters retrieved from <code>optim_fun_h1</code> and should be used for fitting the H1 model with the trimmed sum model, default is NULL
<code>gr_fun_h0</code>	optional gradient function for <code>optim_fun_h0</code> , default is NULL
<code>gr_fun_h1</code>	optional gradient function for <code>optim_fun_h1</code> , default is NULL
<code>gr_fun_h1_2</code>	optional gradient function for <code>optim_fun_h1_2</code> , default is NULL
<code>slopEC50</code>	logical flag indicating whether the h1 model is fitted with a linear model describing the shift of the pEC50 over temperatures
<code>maxit</code>	maximal number of iterations the optimization should be given, default is set to 500
<code>qualColName</code>	name of column indicating quantification quality e.g. number of unique peptides used for quantification, default: "qupm"



**Value**

a data.frame with fitted null and alternative model parameters

**Examples**

```
data("simulated_cell_extract_df")
getModelParamsDf(simulated_cell_extract_df)
```

---

getPEC504Temperature    *Get pEC50 for a protein of interest at a specific temperatures (optimally the melting point of the protein)*

---

**Description**

Get pEC50 for a protein of interest at a specific temperatures (optimally the melting point of the protein)

**Usage**

```
getPEC504Temperature(fstat_df, protein, temperaturePEC50 = 60)
```

**Arguments**

fstat\_df            data frame as obtained after calling getModelParamsDf, containing fitted null and alternative model parameters for each protein

protein            character string referring to the protein of interest

temperaturePEC50    temperature (numeric) at which pEC50 should be inferred

**Value**

numeric value specifying the pEC50 for the indicated protein and temperature

**Examples**

```
data("simulated_cell_extract_df")

model_params_df <- getModelParamsDf(
  df = filter(simulated_cell_extract_df,
             clustertype == "tp1"))

getPEC504Temperature(
  fstat_df = model_params_df,
  protein = "tp1",
  temperaturePEC50 = 60)
```

---

getPvalues	<i>Compute p-values for given F statistics based on true and null dataset</i>
------------	---

---

### Description

Compute p-values for given F statistics based on true and null dataset

### Usage

```
getPvalues(df_out, df_null, pseudo_count = 1, squeezeDenominator = FALSE)
```

### Arguments

df_out	data frame containing results from analysis by fitAndEvalDataset
df_null	data frame containing results from analysis by bootstrapNull
pseudo_count	numeric larger or equal to 0 added to both counts of protein with an F-statistic higher than a threshold theta of the true and bootstrapped datasets
squeezeDenominator	logical indicating whether F statistic denominator should be shrunk using limma::squeezeVar

### Value

data frame annotating each protein with a FDR based on it's F statistic and number of observations

### Examples

```
data("simulated_cell_extract_df")
temp_df <- simulated_cell_extract_df %>%
  filter(clustertype %in% paste0("protein", 1:3)) %>%
  group_by(representative) %>%
  mutate(nObs = n()) %>%
  ungroup
example_out <- fitAndEvalDataset(temp_df)
example_null <- bootstrapNull(temp_df, B = 2)
getPvalues(
  example_out,
  example_null)
```

---

`gg_qq`*Plot qq-plot of true data and bootstrapped null with ggplot*

---

**Description**

Plot qq-plot of true data and bootstrapped null with ggplot

**Usage**

```
gg_qq(  
  x,  
  y,  
  xlab = "F-statistics from sampled Null distr.",  
  ylab = "observed F-statistics",  
  alpha = 0.25,  
  gg_theme = theme_classic(),  
  offset = 1,  
  plot_diagonal = TRUE  
)
```

**Arguments**

<code>x</code>	vector containing values of values of first distribution to compare
<code>y</code>	vector containing values of values of second distribution to compare
<code>xlab</code>	x-axis label
<code>ylab</code>	y-axis label
<code>alpha</code>	transparency parameter between 0 and 1
<code>gg_theme</code>	ggplot theme, default is <code>theme_classic()</code>
<code>offset</code>	offset for x and y axis on top of maximal values
<code>plot_diagonal</code>	logical parameter indicating whether an identity line should be plotted

**Value**

A ggplot displaying the qq-plot of a true and a bootstrapped null distribution

**Examples**

```
data("simulated_cell_extract_df")  
recomputeSignalFromRatios(simulated_cell_extract_df)
```

---

import2dDataset	<i>Import 2D-TPP dataset using a config table</i>
-----------------	---

---

### Description

Import 2D-TPP dataset using a config table

### Usage

```
import2dDataset(
  configTable,
  data,
  idVar = "representative",
  intensityStr = "sumionarea_protein_",
  fcStr = "rel_fc_protein_",
  nonZeroCols = "qssm",
  geneNameVar = "clustername",
  addCol = NULL,
  qualColName = "qupm",
  naStrs = c("NA", "n/d", "NaN"),
  concFactor = 1e+06,
  medianNormalizeFC = TRUE,
  filterContaminants = TRUE
)
```

### Arguments

configTable	character string of a file path to a config table
data	possible list of datasets from different MS runs corresponding to a 2D-TPP dataset, circumvents loading datasets referencend in config table, default is NULL
idVar	character string indicating which data column provides the unique identifiers for each protein.
intensityStr	character string indicating which columns contain raw intensities measurements
fcStr	character string indicating which columns contain the actual fold change values. Those column names containing the suffix fcStr will be regarded as containing fold change values.
nonZeroCols	column like default qssm that should be imported and requested to be non-zero in analyzed data
geneNameVar	character string of the column name that describes the gene name of a given protein in the raw data files
addCol	character string indicating additional column to import
qualColName	character string indicating which column can be used for additional quality criteria when deciding between different non-unique protein identifiers.

naStrs	character vector indicating missing values in the data table. When reading data from file, this value will be passed on to the argument <code>na.strings</code> in function <code>read.delim</code> .
concFactor	numeric value that indicates how concentrations need to be adjusted to yield total unit e.g. default <code>mmol - 1e6</code>
medianNormalizeFC	perform median normalization (default: <code>TRUE</code> ).
filterContaminants	boolean variable indicating whether data should be filtered to exclude contaminants (default: <code>TRUE</code> ).

### Value

tidy data frame representing a 2D-TPP dataset

### Examples

```
data("config_tab")
data("raw_dat_list")
import_df <- import2dDataset(configTable = config_tab,
                             data = raw_dat_list,
                             idVar = "protein_id",
                             intensityStr = "signal_sum_",
                             fcStr = "rel_fc_",
                             nonZeroCols = "qusm",
                             geneNameVar = "gene_name",
                             addCol = NULL,
                             qualColName = "qupm",
                             naStrs = c("NA", "n/d", "NaN"),
                             concFactor = 1e6,
                             medianNormalizeFC = TRUE,
                             filterContaminants = TRUE)
```

---

import2dMain

*Import 2D-TPP dataset main function*

---

### Description

Import 2D-TPP dataset main function

### Usage

```
import2dMain(
  configTable,
  data,
  idVar,
  fcStr,
```

```

    addCol,
    naStrs,
    intensityStr,
    qualColName,
    nonZeroCols
  )

```

### Arguments

configTable	character string of a file path to a config table
data	possible list of datasets from different MS runs corresponding to a 2D-TPP dataset, circumvents loading datasets referencend in config table, default is NULL
idVar	character string indicating which data column provides the unique identifiers for each protein.
fcStr	character string indicating which columns contain the actual fold change values. Those column names containing the suffix fcStr will be regarded as containing fold change values.
addCol	character string indicating additional column to import
naStrs	character vector indicating missing values in the data table. When reading data from file, this value will be passed on to the argument na.strings in function read.delim.
intensityStr	character string indicating which columns contain raw intensities measurements
qualColName	character string indicating which column can be used for additional quality criteria when deciding between different non-unique protein identifiers.
nonZeroCols	column like default qssm that should be imported and requested to be non-zero in analyzed data

### Value

list of data frames containing different datasets

### Examples

```

data("config_tab")
data("raw_dat_list")
dataList <- import2dMain(configTable = config_tab,
                        data = raw_dat_list,
                        idVar = "protein_id",
                        fcStr = "rel_fc_",
                        addCol = "gene_name",
                        naStrs = NA,
                        intensityStr = "signal_sum_",
                        nonZeroCols = "qusm",
                        qualColName = "qupm")

```

---

plot2dTppFcHeatmap      *Plot heatmap of 2D thermal profile fold changes of a protein of choice*

---

**Description**

Plot heatmap of 2D thermal profile fold changes of a protein of choice

**Usage**

```
plot2dTppFcHeatmap(df, name, drug_name = "", midpoint = 1)
```

**Arguments**

df	tidy data frame of a 2D-TPP dataset
name	gene name (clustername) of protein that should be visualized
drug_name	character string of profiled drug name
midpoint	midpoint of fold changes for color scaling, default: 1

**Value**

A ggplot displaying the thermal profile as a heatmap of fold changes of a protein of choice in a dataset of choice

**Examples**

```
data("simulated_cell_extract_df")
plot2dTppFcHeatmap(simulated_cell_extract_df,
  "tp2", drug_name = "drug1")
```

---

plot2dTppFit      *Plot H0 or H1 fit of 2D thermal profile intensities of a protein of choice*

---

**Description**

Plot H0 or H1 fit of 2D thermal profile intensities of a protein of choice

**Usage**

```
plot2dTppFit(
  df,
  name,
  model_type = "H0",
  optim_fun = .min_RSS_h0,
  optim_fun_2 = NULL,
  maxit = 500,
  xlab = "-log10(conc.)",
  ylab = "log2(summed intensities)",
  dot_size = 1,
  line_type = "solid",
  fit_color = "gray30"
)
```

**Arguments**

df	tidy data frame of a 2D-TPP dataset
name	gene name (clustername) of protein that should be visualized
model_type	character string indicating whether the "H0" or the "H1" model should be fitted
optim_fun	optimization function that should be used for fitting either the H0 or H1 model
optim_fun_2	optional additional optimization function that will be run with paramters retrieved from optim_fun and should be used for fitting the H1 model with the trimmed sum model, default is NULL
maxit	maximal number of iterations the optimization should be given, default is set to 500
xlab	character string of x-axis label of plot
ylab	character string of y-axis label of plot
dot_size	numeric indicating the size of the data points to plot
line_type	character string defining the line type of the fitted curve, default "dashed"
fit_color	character string defining the color of the fitted curve

**Value**

A ggplot displaying the thermal profile of a protein of choice in a dataset of choice

**Examples**

```
data("simulated_cell_extract_df")
plot2dTppProfile(simulated_cell_extract_df, "protein1")
```



---

plot2dTppProfile      *Plot 2D thermal profile intensities of a protein of choice*

---

**Description**

Plot 2D thermal profile intensities of a protein of choice

**Usage**

```
plot2dTppProfile(df, name)
```

**Arguments**

df                    tidy data frame of a 2D-TPP dataset  
name                  gene name (clustername) of protein that should be visualized

**Value**

A ggplot displaying the thermal profile of a protein of choice in a dataset of choice

**Examples**

```
data("simulated_cell_extract_df")  
plot2dTppProfile(simulated_cell_extract_df, "protein1")
```

---

plot2dTppRelProfile      *Plot 2D thermal profile ratios of a protein of choice*

---

**Description**

Plot 2D thermal profile ratios of a protein of choice

**Usage**

```
plot2dTppRelProfile(df, name)
```

**Arguments**

df                    tidy data frame of a 2D-TPP dataset  
name                  gene name (clustername) of protein that should be visualized

**Value**

A ggplot displaying the thermal profile ratios of a protein of choice in a dataset of choice

## Examples

```
data("simulated_cell_extract_df")
plot2dTppRelProfile(simulated_cell_extract_df, "protein1")
```

---

plot2dTppVolcano      *Plot Volcano plot of TPP2D results*

---

## Description

Plot Volcano plot of TPP2D results

## Usage

```
plot2dTppVolcano(
  fdr_df,
  hits_df,
  alpha = 0.5,
  title_string = "",
  x_lim = NULL,
  y_lim = NULL,
  facet_by_obs = FALSE
)
```

## Arguments

fdr_df	data frame obtained from ‘getFDR’
hits_df	hits_df data frame obtained from ‘findHits’
alpha	transparency level of plotted points
title_string	character argument handed over to ggtitle
x_lim	vector with two numerics indicating the x axis limits
y_lim	vector with two numerics indicating the y axis limits
facet_by_obs	logical indicating whether plot should be faceted by number of observations, default: FALSE

## Value

a ggplot displaying a volcano plot of the results obtained after a TPP2D analysis

**Examples**

```

data("simulated_cell_extract_df")
temp_df <- simulated_cell_extract_df %>%
  filter(clustername %in% paste0("protein", 1:5)) %>%
  group_by(representative) %>%
  mutate(nObs = n()) %>%
  ungroup
example_params <- getModelParamsDf(temp_df)
example_fstat <- computeFStatFromParams(example_params)
example_null <- bootstrapNullAlternativeModel(
  df = temp_df, params_df = example_params,
  B = 2)
fdr_df <- getFDR(example_fstat, example_null)
hits_df <- findHits(fdr_df, 0.1)
plot2dTppVolcano(fdr_df = fdr_df, hits_df = hits_df)

```

---

raw_dat_list	<i>Example raw data for a subset of a simulated 2D-TPP cell extract dataset</i>
--------------	---

---

**Description**

Simulated example dataset obtained by 2D-TPP experiments for analysis by the TPP2D-package. It contains a list of data frames resembling raw data files returned from a MS database search with 200 simulated protein profiles (protein1-200) and 3 spiked-in true positives (TP1-3).

**Usage**

```
data("raw_dat_list")
```

**Format**

list of data frames with columns representative (protein id), clustername (gene name), temperature, log\_conc, raw\_value, rel\_value, value and log2\_value

---

recomputeSignalFromRatios	<i>Recompute robust signal intensities based on bootstrapped TMT channel ratios</i>
---------------------------	---

---

**Description**

Recompute robust signal intensities based on bootstrapped TMT channel ratios

**Usage**

```
recomputeSignalFromRatios(df)
```

**Arguments**

df                    tidy data\_frame retrieved after import of a 2D-TPP dataset

**Value**

A data\_frame with recomputed signal intensities (columnname: value) and log2 transformed signal intensities (columnname: log2\_value) that more reliably reflect relative ratios between the TMT channels

**Examples**

```
data("simulated_cell_extract_df")
recomputeSignalFromRatios(simulated_cell_extract_df)
```

---

renameColumns	<i>Rename columns of imported data frame</i>
---------------	--

---

**Description**

Rename columns of imported data frame

**Usage**

```
renameColumns(dataLong, idVar, geneNameVar)
```

**Arguments**

dataLong            long format data frame of imported dataset

idVar                character string indicating which data column provides the unique identifiers for each protein.

geneNameVar        character string of the column name that describes the gene name of a given protein in the raw data files

**Value**

data frame containing imported data with renamed columns

**Examples**

```
data("config_tab")
data("raw_dat_list")

dataList <- import2dMain(configTable = config_tab,
                        data = raw_dat_list,
                        idVar = "protein_id",
                        fcStr = "rel_fc_",
                        addCol = "gene_name",
```

```
naStrs = NA,
intensityStr = "signal_sum_",
nonZeroCols = "qusm",
qualColName = "qupm")
configLong <- configWide2Long(configWide = config_tab)
annoDat <- annotateDataList(dataList = dataList,
                           geneNameVar = "gene_name",
                           configLong = configLong,
                           intensityStr = "signal_sum_",
                           fcStr = "rel_fc_")
renameColumns(annoDat,
              idVar = "protein_id",
              geneNameVar = "gene_name")
```

---

resolveAmbiguousProteinNames

*Resolve ambiguous protein names*

---

## Description

Resolve ambiguous protein names

## Usage

```
resolveAmbiguousProteinNames(df, includeIsoforms = FALSE)
```

## Arguments

**df** tidy data\_frame retrieved after import of a 2D-TPP dataset

**includeIsoforms** logical indicating whether protein isoform should be kept for analysis

## Value

data frame with resolved protein name ambiguity

## Examples

```
tst_df <- bind_rows(tibble(representative = rep(1:3, each = 3),
                          clustername = rep(letters[1:3], each = 3)),
                  tibble(representative = rep(c(4, 5), c(3, 2)),
                          clustername = rep(c("a", "b"), c(3, 2))))

resolveAmbiguousProteinNames(tst_df)
```

---

runTPP2D	<i>Run complete TPP2D analysis</i>
----------	------------------------------------

---

## Description

Run complete TPP2D analysis

## Usage

```
runTPP2D(  
  df = NULL,  
  configTable = NULL,  
  data = NULL,  
  idVar = "protein_id",  
  intensityStr = "signal_sum",  
  fcStr = "rel_fc",  
  nonZeroCols = "qusm",  
  geneNameVar = "gene_name",  
  addCol = NULL,  
  qualColName = "qupm",  
  naStrs = c("NA", "n/d", "NaN"),  
  concFactor = 1e+06,  
  medianNormalizeFC = TRUE,  
  filterContaminants = TRUE,  
  recomputeSignalRatios = FALSE,  
  minObs = 20,  
  independentFiltering = FALSE,  
  fcThres = 1.5,  
  optim_fun_h0 = .min_RSS_h0,  
  optim_fun_h1 = .min_RSS_h1_slope_pEC50,  
  optim_fun_h1_2 = NULL,  
  gr_fun_h0 = NULL,  
  gr_fun_h1 = NULL,  
  gr_fun_h1_2 = NULL,  
  slopEC50 = TRUE,  
  maxit = 750,  
  BPPARAM = BiocParallel::SerialParam(progressbar = TRUE),  
  B = 20,  
  byMsExp = TRUE,  
  alpha = 0.1  
)
```

## Arguments

df	tidy data_frame retrieved after import of a 2D-TPP dataset, potential filtering and addition of a column "nObs" containing the number of observations per protein
----	---

configTable	character string of a file path to a config table
data	possible list of datasets from different MS runs corresponding to a 2D-TPP dataset, circumvents loading datasets referencend in config table, default is NULL
idVar	character string indicating which data column provides the unique identifiers for each protein.
intensityStr	character string indicating which columns contain raw intensities measurements
fcStr	character string indicating which columns contain the actual fold change values. Those column names containing the suffix fcStr will be regarded as containing fold change values.
nonZeroCols	column like default qssm that should be imported and requested to be non-zero in analyzed data
geneNameVar	character string of the column name that describes the gene name of a given protein in the raw data files
addCol	character string indicating additional column to import
qualColName	character string indicating which column can be used for additional quality criteria when deciding between different non-unique protein identifiers.
naStrs	character vector indicating missing values in the data table. When reading data from file, this value will be passed on to the argument na.strings in function read.delim.
concFactor	numeric value that indicates how concentrations need to be adjusted to yield total unit e.g. default mmol - 1e6
medianNormalizeFC	perform median normalization (default: TRUE).
filterContaminants	logical variable indicating whether data should be filtered to exclude contaminants (default: TRUE).
recomputeSignalRatios	logical variable indicaitng whether signals should be recomputed from relative fold changes, recommended if Isobarquant was used for protein quantification
minObs	number of minimal observations per protein to include it in the analysis
independentFiltering	logical variable indicating whether independent filtering should be performed based on minimal fold changes per protein profile
fcThres	numeric value of minimal fold change (or inverse fold change) a protein has to show to be kept upon independent filtering
optim_fun_h0	optimization function that should be used for fitting the H0 model
optim_fun_h1	optimization function that should be used for fitting the H1 model
optim_fun_h1_2	optional additional optimization function that will be run with paramters retrieved from optim_fun_h1 and should be used for fitting the H1 model with the trimmed sum model, default is NULL
gr_fun_h0	optional gradient function for optim_fun_h0, default is NULL
gr_fun_h1	optional gradient function for optim_fun_h1, default is NULL

gr_fun_h1_2	optional gradient function for optim_fun_h1_2, default is NULL
slopEC50	logical flag indicating whether the h1 model is fitted with a linear model describing the shift of the pEC50 over temperatures
maxit	maximal number of iterations the optimization should be given, default is set to 500
BPPARAM	= BiocParallel::SerialParam(progressbar = TRUE),
B	numeric value indicating number of rounds of bootstraps that should be performed to estimate the null distribution
byMsExp	logical indicating whether bootstrapping should be performed within MS experiments
alpha	FDR level that should be controlled

**Value**

a tpp2dExperiment object

**Examples**

```
data("simulated_cell_extract_df")
runTPP2D(df = simulated_cell_extract_df %>%
  filter(representative %in% 1:3),
  B = 1)
```

---

simulated\_cell\_extract\_df

*Example subset of a simulated 2D-TPP cell extract dataset*

---

**Description**

Simulated example dataset obtained by 2D-TPP experiments for analysis by the TPP2D-package. It contains a tidy data frame after import and recomputing of robust signal intensities with 200 simulated protein profiles (protein1-200) and 3 spiked-in true positives (TP1-3)

**Usage**

```
data("simulated_cell_extract_df")
```

**Format**

data frame with columns representative (protein id), clusturname (gene name), temperature, log\_conc, raw\_value, rel\_value, value and log2\_value



---

tpp2dExperiment-class *S4 TPP2D Experiment Class*

---

**Description**

S4 TPP2D Experiment Class

**Value**

an object of class tpp2dExperiment

**Slots**

configTable data.frame.  
idVar character.  
intensityStr character.  
fcStr character.  
nonZeroCols character.  
geneNameVar character.  
qualColName character.  
naStrs character.  
concFactor numeric.  
medianNormalizeFC logical.  
filterContaminants logical.  
minObs numeric.  
independentFiltering logical.  
fcThres numeric.  
optim\_fun\_h0 function.  
optim\_fun\_h1 function.  
slopEC50 logical.  
maxit numeric.  
BPPARAM character.  
B numeric  
byMsExp logical.  
alpha numeric.  
tidyDataTable data.frame.  
modelParamsDf data.frame  
resultTable data.frame  
bootstrapNullDf data.frame  
hitTable data.frame

**Examples**

```
tpp2dObj <- new("tpp2dExperiment")
```

---

TPP\_importCheckConfigTable

*Import and check configuration table*

---

**Description**

Import and check configuration table

**Usage**

```
TPP_importCheckConfigTable(infoTable, type = "2D")
```

**Arguments**

infoTable      character string of a file path to a config table (excel,txt or csv file) or data frame containing a config table

type            character string indicating dataset type default is 2D

**Value**

data frame with config table

**Examples**

```
data("config_tab")
TPP_importCheckConfigTable(config_tab, type = "2D")
```

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