Package ‘pepStat’

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Contents

<table>
<thead>
<tr>
<th>Function</th>
<th>Page</th>
</tr>
</thead>
<tbody>
<tr>
<td>baselineCorrect.pSet</td>
<td>2</td>
</tr>
<tr>
<td>baseline_correct</td>
<td>3</td>
</tr>
<tr>
<td>create_db</td>
<td>3</td>
</tr>
<tr>
<td>makeCalls</td>
<td>4</td>
</tr>
<tr>
<td>makePeptideSet</td>
<td>6</td>
</tr>
<tr>
<td>normalizeArray</td>
<td>8</td>
</tr>
</tbody>
</table>
baselineCorrect.pSet

Baseline intensities

Description

Correct intensities by subtracting PRE visit sample intensities.

Usage

baselineCorrect.pSet(pSet, verbose = FALSE)

Arguments

pSet A peptideSet with sample PRE and POST visits.
verbose A logical. If TRUE, information regarding the pairedness of the data will be displayed.

Details

If samples are not PAIRED (One PRE and POST for each ptid), then the average expression of all PRE visit samples is substracted from each sample.

Value

A matrix of the baseline corrected intensities, with as many columns as there are samples POST visit

Author(s)

Raphael Gottardo, Gregory Imholte
**baseline_correct**

**Description**
Correct intensities by subtracting PRE visit sample intensities.

**Usage**
```r
baseline_correct(pSet, verbose = FALSE)
```

**Arguments**
- `pSet`: A peptideSet with sample PRE and POST visits.
- `verbose`: A logical. If TRUE, information regarding the pairedness of the data will be displayed.

**Details**
The function will try to pair as many sample as possible. The remaining subjects with a POST and no PRE will use the average expression of all baseline samples. Subjects with baseline only will not be represented in the resulting matrix.

**Value**
A matrix of the baseline corrected intensities, with as many columns as there are samples POST visit

**Author(s)**
Renan Sauteraud

---

**create_db**

**Create a peptide collection**

**Description**
Constructor to create peptide collection to be used in `summarizePeptides`.

**Usage**
```r
create_db(position)
```
makeCalls

Make antibody binding positivity calls

Arguments

position A data.frame or GRanges object. If a data.frame is provided, it should contain 'start' and 'end' or 'width' columns as well as a peptide column. If position is a GRanges object, then it must either have peptide as names or contain a peptide metadata column.

Details

position can have additional columns. These columns will be kept in the resulting peptide collection. This is especially useful to include clades and grouping parameters for the makeCalls function.

If the input contains all the z-scores (z1 to z5), then they will not be re-calculated. If some (but not all) z-scores are missing, a warning message will be sent and the z-scores are re-calculated.

Author(s)

Renan Sauteraud

See Also

GRanges

Examples

```r
#construct data.frame object
starts <- seq(1, 30, 3)
ends <- starts + 14
peptides <- sapply(1:10, function(x) {paste0(AA[floor(runif(15, 1, 20))], collapse = "")})
data <- data.frame(start = starts, end = ends, peptide = peptides)
#from data.frame
new_pep <- create_db(data)
#from GRanges
new_pep <- create_db(new_pep)
```
Usage

makeCalls(peptideSet, cutoff = 1.2, method = "absolute", freq = TRUE, 
group = NULL, verbose = FALSE)

Arguments

peptideSet  A peptideSet object. The peptides, after normalization and possibly data 
smoothing.
cutoff  A numeric. If FDR, the FDR threshold. Otherwise, a cutoff for the background 
corrected intensities.
method  A character. The method used to make positivity calls. "absolute" and "FDR" 
are available. See details below.
freq  A logical. If set to TRUE, return the percentage of slides calling a peptide 
positive. Otherwise, return a logical indicating binding events.
group  A character. Only used when freq is set to TRUE. A character indicating a 
variable by which to group slides. If non-null the percentage is calculated by 
group.
verbose  A logical. If set to TRUE, progress information will be displayed.

Details

This function requires specific variables ptid and visit in pData(peptideSet). The variable ptid 
should indicate subjects, and the variable visit should be a factor with levels pre and post.

If slides are paired for subjects, intensities corresponding to post-visit are subtracted from pre. 
If slides are not paired, slides with pre have intensities averaged by peptides, and averaged peptide 
intensities are subtracted from slides that have entry post. Calls are made on these baseline corrected 
intensities.

When method = FDR, a left-tail method is used to generate a threshold controlling the False Discov-
ery Rate at level cutoff. When method = absolute, Intensities exceeding the threshold are labelled 
as positive.

When freq = TRUE a group variable may be specified. The argument group indicates the name of 
a variable in pData(peptideSet) by which positive calls should be grouped. The call frequency for 
each peptide is calculated within groups.

Value

If freq = TRUE, a numeric matrix with peptides as rows and groups as columns where the values 
are the frequency of response in the group. If freq = FALSE, a logical matrix indicating binding 
events for each peptide in each subject.

Author(s)

Greg Imholte
Examples

```r
## This example curated from the vignette -- please see vignette("pepStat")
## for more information
if (require("pepDat")) {

## Get example GPR files + associated mapping file
dirToParse <- system.file("extdata/gpr_samples", package = "pepDat")
mapFile <- system.file("extdata/mapping.csv", package = "pepDat")

## Make a peptide set
pSet <- makePeptideSet(files = NULL, path = dirToParse,
                         mapping.file = mapFile, log=TRUE)

## Plot array images -- useful for quality control
plotArrayImage(pSet, array.index = 1)
plotArrayResiduals(pSet, array.index = 1, smooth = TRUE)

## Summarize peptides, using pep_hxb2 as the position database
data(pep_hxb2)
psSet <- summarizePeptides(pSet, summary = "mean", position = pep_hxb2)

## Normalize the peptide set
pnSet <- normalizeArray(psSet)

## Smooth
psmSet <- slidingMean(pnSet, width = 9)

## Make calls
calls <- makeCalls(psmSet, freq = TRUE, group = "treatment",
                   cutoff = .1, method = "FDR", verbose = TRUE)

## Produce a summary of the results
summary <- restab(psmSet, calls)
}
```

---

**makePeptideSet**

**peptideSet constructor**

### Description

This function reads GenePix results (.gpr) files and creates a peptideSet object gathering experiment information.

### Usage

```r
makePeptideSet(files = NULL, path = NULL, mapping.file = NULL,
                use.flags = FALSE, rm.control.list = NULL, empty.control.list = NULL,
                bgCorrect.method = "normexp", log = TRUE, check.row.order = FALSE,
                verbose = FALSE)
```
Arguments

files  A character vector. If NULL, all files with a .gpr extension in the specified path will be read.
path  A character string. The directory where the .gpr files to read are located.
mapping.file  A character string or data.frame. A mapping file that gives information for each sample. See details section below for a list of required fields.
use.flags  A logical. Should spots with flag value -99 or lower be excluded?
rm.control.list  A character vector. The name of the controls to be excluded from the peptideSet.
empty.control.list  A character vector. The name of the empty controls. If non NULL, the intensity of these empty spots will be substraction from remaining intensities.
bgCorrect.method  A character string. The name of the method used for background correction. This is passed to limma's backgroundCorrect method. See details section below and ?backgroundCorrect for more information.
log  A logical. If TRUE, intensities will be log2 transformed after BG correction.
check.row.order  A logical. Should slides be reduced to a common set of peptides?
verbose  A logical. Displays progress and additional information.

Details

GenePix results files (.gpr) are read when found in either the files or path arguments. By default, the foreground and background median intensities of the "red" channels, "F635 Median" and "B635 Median", are read. The background correction specified in bgCorrect.method is passed to the backgroundCorrect method in the limma package.

The mapping.file can be either a filename or a data.frame. In any case, it should contain at least three columns labeled "filename", "ptid" and "visit". The filenames given here should match those read from the path or files argument, or be a subset of it. For each ptid (patient ID), the visit column should have at least one "pre" and one "post" sample. Any additional column will be kept into the resulting peptideSet and can be used later on for grouping.

If check.row.order = TRUE, the final set of probes is taken to be those with IDs found in all arrays that were read.

Row, Column and Block spatial array position for each probe are stored in the featureRanges slot of the returned object.

Value

A peptideSet object that contain the intensities, peptide sequences and annotations available in the mapping file.

Author(s)

Raphael Gottardo, Gregory Imholte
normalizeArray

Normalize tiling array data using sequence information

Description

This function is used to normalize the peptide microarray data using sequence information.

Usage

normalizeArray(peptideSet, method = "ZpepQuad", robust = TRUE,
                centered = TRUE)

Arguments

- **peptideSet**: A peptideSet. The expression data for the peptides as well as annotations and ranges.
- **method**: A character. The normalization method to be used. Can be "Zpep" or "ZpepQuad".
- **robust**: A logical. If TRUE, reweighted least-squares estimates are computed.
- **centered**: A logical. If TRUE, recenter the data.

Details

The available methods are "Zpep" and "ZpepQuad". These methods fit a linear model using either linear or linear and quadratic terms (respectively), regressing intensity on the peptides' five Z-scale scores. A peptide Z-scale score is obtained by summing over the Z-scale values in Sandburg et al (1998) of the amino acids the peptide comprises.

Peptide Z-scale scores may be provided in the featureRange slot of peptideSet. This slot is a GRanges object x, and the function will seek five columns labelled z1 through z5 in values(x).
normalizeArray

If these are not found, the function attempts to calculate Z-scales from sequence information found in peptide(peptideSet).

If robust = TRUE the linear model is fit with $t_4$ distributed errors. The method returns the residuals of each peptide intensity in the fitted linear model. If centered = TRUE the fitted intercept term is added back to the residuals of the fit.

Value

A peptideSet object with updated normalized intensity values.

Author(s)

Raphael Gottardo, Gregory Imholte

References


See Also

summarizePeptides, makeCalls

Examples

## This example curated from the vignette -- please see vignette("pepStat")
## for more information
if (require("pepDat")) {

## Get example GPR files + associated mapping file
dirToParse <- system.file("extdata/gpr_samples", package = "pepDat")
mapFile <- system.file("extdata/mapping.csv", package = "pepDat")

## Make a peptide set
pSet <- makePeptideSet(files = NULL, path = dirToParse,
mapping.file = mapFile, log=TRUE)

## Plot array images -- useful for quality control
plotArrayImage(pSet, array.index = 1)
plotArrayResiduals(pSet, array.index = 1, smooth = TRUE)

## Summarize peptides, using pep_hxb2 as the position database
data(pep_hxb2)
psSet <- summarizePeptides(pSet, summary = "mean", position = pep_hxb2)

## Normalize the peptide set
pnSet <- normalizeArray(psSet)

## Smooth
psmSet <- slidingMean(pnSet, width = 9)
## Make calls

calls <- makeCalls(psmSet, freq = TRUE, group = "treatment",
cutoff = .1, method = "FDR", verbose = TRUE)

## Produce a summary of the results
summary <- restab(psmSet, calls)

---

**peptideSet**

**peptideSet class**

### Description

This class gathers all information from gpr files, annotation data and sequence data.

### Details

See '?peptideSet-methods' for a list of accessors and method associated with the class.

### Slots

- **featureRange**: A GRanges object. The ranges and sequences of the peptides and their associated annotation.
- **phenoData**: An AnnotatedDataFrame. Annotation for the samples.
- **assayData**
- **featureData**
- **annotation**
- **protocolData**: Slots inherited from ExpressionSet.

### Author(s)

Greg Imholte

### See Also

ExpressionSet, peptideSet-methods
Description

Methods for handling peptideSet objects

Accessors

nrow(x): The number of peptides in x.
ncol(x): The number of samples in x.
start(x): Get the starts of the peptides.
end(x): Get the ends of the peptides.
width(x): Get the widths of the peptides.
position(x): Get the coordinates of the central amino-acid of each peptide, given by: \( \text{round}((\text{start}(x) + \text{end}(x))/2) \).
ranges(x): Returns a GRanges object that contains the annotations for the peptides.
ranges(x)<- value Set annotations for the peptides.
values(x): Returns a SplitDataFrameList. Accessor for the values of the featureRange slot.
clade(x): If available, returns the clade information for each peptide as a matrix.
peptide(x): Get the sequence of the peptides.
peptide(x) <- value Set the sequence of the peptides.
featureID(x): Get the ID of the peptides.
pepZscore(x): If available, returns a matrix of the zScores for each peptide.
pepZscore(x) <- value Set the zScores for each peptide

Display

show(object): Display a peptideSet object.
summary(object): Summarize a peptideSet object.

Subset

x[i, j]: Subset x by peptides (i), or samples (j).
subset(x, subset, drop=FALSE): Subset x given an expression 'subset'. 
plotArrayImage

Plot microarray images

Description
Plot a color image of the intensities on a slide. These plots are helpful to diagnose spatial abnormalities.

Usage
plotArrayImage(peptideSet, array.index = NULL, low = "white", high = "steelblue", ask = dev.interactive(orNone = TRUE) & 1 < length(array.index))

plotArrayResiduals(peptideSet, array.index = NULL, smooth = FALSE, low = "blue", high = "red", ask = dev.interactive(orNone = TRUE) & 1 < length(array.index))

Arguments
peptideSet A peptideSet object. The object must contain all the original probes. See details below.
array.index A vector subsetting exprs(peptideSet), indicating which slides to plot
smooth A logical, a 2D spatial smoother is applied to residuals, the fitted residuals are plotted.
low A character string. The color of the lowest slide intensity. passed to scale_fill_gradient2.
the fitted residuals are plotted.
high A character string. The color of the highest slide intensity. passed to scale_fill_gradient2.
ask A logical. If TRUE, the user is asked before each plot. See par(ask=.)

Details
The most coherent results are achieved when the peptideSet object is read with makePeptideSet with empty.control.list = NULL and rm.control.list = NULL

Author(s)
Gregory Imholte

Examples
## This example curated from the vignette -- please see vignette("pepStat")
## for more information
if (require("pepDat")) {

## Get example GPR files + associated mapping file
restab <- system.file("extdata/gpr_samples", package = "pepDat")
mapFile <- system.file("extdata/mapping.csv", package = "pepDat")

## Make a peptide set
pSet <- makePeptideSet(files = NULL, path = dirToParse,
                        mapping.file = mapFile, log=TRUE)

## Plot array images -- useful for quality control
plotArrayImage(pSet, array.index = 1)
plotArrayResiduals(pSet, array.index = 1, smooth = TRUE)

## Summarize peptides, using pep_hxb2 as the position database
data(pep_hxb2)
psSet <- summarizePeptides(pSet, summary = "mean", position = pep_hxb2)

## Normalize the peptide set
pnSet <- normalizeArray(psSet)

## Smooth
psmSet <- slidingMean(pnSet, width = 9)

## Make calls
calls <- makeCalls(psmSet, freq = TRUE, group = "treatment",
                   cutoff = .1, method = "FDR", verbose = TRUE)

## Produce a summary of the results
summary <- restab(psmSet, calls)

---

restab

**Result table**

**Description**
Tabulate the results of a peptide microarray analysis.

**Usage**

restab(peptideSet, calls)

**Arguments**

- **peptideSet** A peptideSet object.
- **calls** A matrix, as returned by the makeCalls function.

**Details**

The peptideSet should be the one used in the function call to makeCalls that generated the calls used. They should have identical peptides.
Value

A data.frame with the peptides and some information from the peptideSet as well as the frequency of binding for each group of the calls.

Examples

```r
## This example curated from the vignette -- please see vignette("pepStat")
## for more information
if (require("pepDat")) {
  ## Get example GPR files + associated mapping file
  dirToParse <- system.file("extdata/gpr_samples", package = "pepDat")
  mapFile <- system.file("extdata/mapping.csv", package = "pepDat")

  ## Make a peptide set
  pSet <- makePeptideSet(files = NULL, path = dirToParse,
                         mapping.file = mapFile, log=TRUE)

  ## Plot array images -- useful for quality control
  plotArrayImage(pSet, array.index = 1)
  plotArrayResiduals(pSet, array.index = 1, smooth = TRUE)

  ## Summarize peptides, using pep_hxb2 as the position database
  data(pep_hxb2)
  psSet <- summarizePeptides(pSet, summary = "mean", position = pep_hxb2)

  ## Normalize the peptide set
  pnSet <- normalizeArray(psSet)

  ## Smooth
  psmSet <- slidingMean(pnSet, width = 9)

  ## Make calls
  calls <- makeCalls(psmSet, freq = TRUE, group = "treatment",
                     cutoff = .1, method = "FDR", verbose = TRUE)

  ## Produce a summary of the results
  summary <- restab(psmSet, calls)
}
```

shinyPepStat

Launch the pepStat Shiny Application

Description

Launches the pepStat Shiny application, providing an interactive interface for constructing peptide sets, normalizing intensities, generating calls. Quality control is also facilitated through interactive plotting features.
Usage

shinyPepStat()

Examples

if (interactive()) {
  shinyPepStat()
}

Usage

slidingMean(peptideSet, width = 9, verbose = FALSE, split.by.clade = TRUE)

Arguments

- **peptideSet**: A peptideSet. The expression data for the peptides as well as annotations and ranges. The range information is required to run this function.
- **width**: A numeric. The width of the sliding window.
- **verbose**: A logical. If set to TRUE, progress information will be displayed.
- **split.by.clade**: A logical. If TRUE, the peptides will be smoothed by clade (See details section below for more information).

Details

Peptide membership in the sliding mean window is determined by its position and the width argument. Two peptides are in the same window if the difference in their positions is less than or equal to width/2. A peptide’s position is taken to be position(peptideSet).

A peptide’s intensity is replaced by the mean of all peptide intensities within the peptide’s sliding mean window.

When split.by.clade = TRUE, peptides are smoothed within clades defined by the clade column of the GRanges object occupying the featureRange slot of peptideSet. If set to FALSE, a peptide at a given position will borrow information from the neighboring peptides as well as the ones from other clades around this position.

Value

A peptideSet object with smoothed intensities.
summarizePeptides

Author(s)

   Gregory Imholte

See Also

   summarizePeptides, normalizeArray

Examples

   ## This example curated from the vignette -- please see vignette("pepStat")
   ## for more information
   if (require("pepDat")) {

   ## Get example GPR files + associated mapping file
dirToParse <- system.file("extdata/gpr_samples", package = "pepDat")
mapFile <- system.file("extdata/mapping.csv", package = "pepDat")

   ## Make a peptide set
pSet <- makePeptideSet(files = NULL, path = dirToParse,
                        mapping.file = mapFile, log=TRUE)

   ## Plot array images -- useful for quality control
plotArrayImage(pSet, array.index = 1)
plotArrayResiduals(pSet, array.index = 1, smooth = TRUE)

   ## Summarize peptides, using pep_hxb2 as the position database
data(pep_hxb2)
psSet <- summarizePeptides(pSet, summary = "mean", position = pep_hxb2)

   ## Normalize the peptide set
pnSet <- normalizeArray(psSet)

   ## Smooth
psmSet <- slidingMean(pnSet, width = 9)

   ## Make calls
calls <- makeCalls(psmSet, freq = TRUE, group = "treatment",
cutoff = .1, method = "FDR", verbose = TRUE)

   ## Produce a summary of the results
summary <- restab(psmSet, calls)
   }

summarizePeptides  Add information to a peptideSet and summarize peptides
summarizePeptides

Description

This function merges the replicates and adds information from a peptide collection to a peptideSet. This collection can include coordinates, alignment information, Z-scales, and other peptide information.

Usage

summarizePeptides(peptideSet, summary = "median", position = NULL)

Arguments

peptideSet A peptideSet, as created by makePeptideSet
summary A character string. The method used for merging replicates. Available are: "mean" and "median".
position A data.frame or GRanges object. A peptide collection such as the ones available in pepDat. See details below and vignettes for more information.

Details

The object in the position argument will be passed to create_db, it can either be a GRanges object with a peptide as a metadata column, or a data.frame that can be used to create such GRanges. Some peptide collections can be found in the pepDat package.

Value

An object of class peptideSet with added columns and updated ranges.

Author(s)

Raphael Gottardo, Greory Imholte

See Also

makePeptideSet, create_db, create_db

Examples

## This example curated from the vignette -- please see vignette("pepStat")
## for more information
if (require("pepDat")) {

  ## Get example GPR files + associated mapping file
dirToParse <- system.file("extdata/gpr_samples", package = "pepDat")
mapFile <- system.file("extdata/mapping.csv", package = "pepDat")

  ## Make a peptide set
pSet <- makePeptideSet(files = NULL, path = dirToParse,
                       mapping.file = mapFile, log=TRUE)

  ## Plot array images -- useful for quality control
plotArrayImage(pSet, array.index = 1)
plotArrayResiduals(pSet, array.index = 1, smooth = TRUE)

## Summarize peptides, using pep_hxb2 as the position database
data(pep_hxb2)
psSet <- summarizePeptides(pSet, summary = "mean", position = pep_hxb2)

## Normalize the peptide set
pnSet <- normalizeArray(psSet)

## Smooth
psmSet <- slidingMean(pnSet, width = 9)

## Make calls
calls <- makeCalls(psmSet, freq = TRUE, group = "treatment",
cutoff = .1, method = "FDR", verbose = TRUE)

## Produce a summary of the results
summary <- restab(psmSet, calls)
Index

[, peptideSet, ANY, ANY, ANY-method
  (peptideSet-methods), 11
backgroundCorrect, 8
baseline_correct, 3
baselineCorrect.pSet, 2
clade (peptideSet-methods), 11
clade, GRanges-method
  (peptideSet-methods), 11
clade, peptideSet-method
  (peptideSet-methods), 11
clade-methods (peptideSet-methods), 11
create_db, 3, 17
dend, peptideSet-method
  (peptideSet-methods), 11
ExpressionSet, 10
featureID (peptideSet-methods), 11
featureID, peptideSet-method
  (peptideSet-methods), 11
featureID-method (peptideSet-methods), 11
GRanges, 4
makeCalls, 4, 9
makePeptideSet, 6, 17
NormalizeArray (normalizeArray), 8
normalizeArray, 8, 16
peptide (peptideSet-methods), 11
peptide, peptideSet-method
  (peptideSet-methods), 11
peptide-method (peptideSet-methods), 11
peptide<- (peptideSet-methods), 11
peptide<-, peptideSet, character-method
  (peptideSet-methods), 11
peptideSet, 8, 10
peptideSet-class (peptideSet), 10
peptideSet-methods, 11
pepZscore (peptideSet-methods), 11
pepZscore, GRanges-method
  (peptideSet-methods), 11
pepZscore, peptideSet-method
  (peptideSet-methods), 11
pepZscore-method (peptideSet-methods), 11
pepZscore<- (peptideSet-methods), 11
pepZscore<-, GRanges, data.frame-method
  (peptideSet-methods), 11
pepZscore<-, peptideSet, data.frame-method
  (peptideSet-methods), 11
plotArrayImage, 12
plotArrayResiduals (plotArrayImage), 12
position (peptideSet-methods), 11
position, peptideSet-method
  (peptideSet-methods), 11
position-method (peptideSet-methods), 11
ranges, peptideSet-method
  (peptideSet-methods), 11
ranges<-, peptideSet-method
  (peptideSet-methods), 11
read.maimages, 8
restab, 13
shinyPepStat, 14
show, peptideSet-method
  (peptideSet-methods), 11
slidingMean, 15
start, peptideSet-method
  (peptideSet-methods), 11
subset, peptideSet-method
  (peptideSet-methods), 11
summarizePeptides, 9, 16, 16
summary, peptideSet-method
  (peptideSet-methods), 11

19
values, peptideSet-method
  (peptideSet-methods), 11

width, peptideSet-method
  (peptideSet-methods), 11