Package ‘protag’

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Title Search Tagged Peptides & Draw Highlighted Mass Spectra

Version 1.0.0

Description In a typical protein labelling procedure, proteins are chemically tagged with a functional group, usually at specific sites, then digested into peptides, which are then analyzed using matrix-assisted laser desorption ionization - time of flight mass spectrometry (MALDI-TOF MS) to generate peptide fingerprint. Relative to the control, peptides that are heavier by the mass of the labelling group are informative for sequence determination. Searching for peptides with such mass shifts, however, can be difficult. This package, designed to tackle this inconvenience, takes as input the mass list of two or multiple MALDI-TOF MS mass lists, and makes pairwise comparisons between the labeled groups vs. control, and restores centroid mass spectra with highlighted peaks of interest for easier visual examination. Particularly, peaks differentiated by the mass of the labelling group are defined as a “pair”, those with equal masses as a “match”, and all the other peaks as a “mismatch”. For more bioanalytical background information, refer to following publications: Jingjing Deng (2015) <doi:10.1007/978-1-4939-2550-6_19>; Elizabeth Chang (2016) <doi:10.7171/jbt.16-2702-002>.

Depends R (>= 2.10)

Imports ggplot2, dplyr, RColorBrewer, grDevices

License GPL-2

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Suggests testthat

NeedsCompilation no

Author Bo Yuan [aut, cre]

Maintainer Bo Yuan <yuanbo.faith@gmail.com>

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Description

This example data is loosely based on the predicted MALDI-TOF mass list of tryptic peptides of equine myoglobin, created using entry P68082 (MYG_HORSE) in UniProtKB (https://www.uniprot.org/uniprot/P68082) with further modification. Labeled peptides, either singly or doubly dimethylated, present 28 or 36 Da shift relative to the control.

Usage

myoglobin

Format

a tibble dataset of 193 rows and 7 variables.

Author(s)

Bo Yuan <yuanbo.faith@gmail.com>

mass the mass of singly protonated peptides, in Dalton. Cysteins were alkylated with iodoacetate.

position the positions of the N- and C-termini of peptides, counting from signal amino acid methionine. The position number of N-terminus of mature protein starts at number 2.

no.MC number of mis-cleavages, which are cites of C-termini of lysines and arginines (without following proline) where trypsin fail to digest apart.

peptide.sequence the sequence of the tryptic peptides of myoglobin, composed of amino acids’ single-letter abbreviations.

group four experimental groups, consisting "label1", "label2", "label3", and "control"

erp error of the mass, in Dalton.

erp.ppm error of the mass, in parts per million (ppm).

intensity peak intensity, in "counts".

References

https://www.uniprot.org/uniprot/P68082
Description

In a typical protein labelling procedure, proteins are chemically tagged with a functional group, usually at a specific site, digested into peptides, which are then analyzed using matrix-assisted laser desorption ionization - time of flight mass spectrometry (MALDI-TOF MS) to generate peptide fingerprint. Relative to the control, peptides that are heavier by the mass of the labelling group are informative for sequence determination. Searching for peptides with such mass shifts, however, can be difficult. This package, designed to tackle this inconvenience, takes as input the mass list of two or multiple MALDI-TOF MS mass lists, and makes pairwise comparisons between the labeled groups vs. control, and restores centroid mass spectra with highlighted peaks of interest for easier visual examination. Particularly, peaks differentiated by the mass of the labelling group are defined as a “pair”, those with equal masses as a “match”, and all the other peaks as a “mismatch”. For more bioanalytical background information, refer to following publications: Jingjing Deng (2015) <doi:10.1007/978-1-4939-2550-6_19>; Elizabeth Chang (2016) <doi:10.7171/jbt.16-2702-002>.

Author(s)

Bo Yuan | yuanbo.faith@gmail.com

tag.search

description

This function takes a mass list dataset containing columns of "mass", "intensity" and "group" (contains the "control" observations), and searches within specified error tolerance for "paired" peaks, "matched" peaks, and "mismatched" peaks. Mass spectra peaks with m/z difference being the designated variable "delta" (within error tolerance) are defined as a "pair", and peaks of the same m/z (within error tolerance) as "match"; otherwise defined as "mismatch".

Usage

tag.search(dataset, delta = NA, error.Da.pair = 0.5, error.Da.match = 0.5, error.ppm.pair = Inf, error.ppm.match = Inf, intens.log.transform = FALSE)

Arguments

dataset a tidy dataset containing the mass list. At least three numeric columns are required: "mass", "intensity" and "group". The "mass" refers to m/z values; "intensity" refers to peak height/area; "group" must contain the "control" observations.
delta
a single numeric value, or a numeric vector when multiple m/z difference is of interest. The variable "delta" reflects the mass difference between the labelled proteins/peptides vs. the non-labelled (the control), caused by the chemically-labelling group.

error.Da.pair
error tolerance for the paired peaks, in Dalton; default at 0.5.

error.Da.match
error tolerance for the matched peaks, in Dalton; default at 0.5.

error.ppm.pair
error tolerance threshold for the paired peaks, in ppm. For paired peaks p and q, the tolerance threshold is defined as 0.5 * (p+q) * error.ppm.pair / 10^6. When the absolute difference between the measured vs. theoretical delta is lower than the error tolerance, then the associated two peaks are considered a pair. The default value of error.ppm.pair is Inf (positive infinite); that is, the error tolerance by default is controled by error.Da.pair. When error.ppm.pair is otherwise set, say at 100 (ppm), then the practical error tolerance value is the smallest of either the Dalton control or ppm control. When the ppm control is more desirable than Dalton control, consider setting error.Da.pair = Inf.

error.ppm.match
error tolerance for the matched peaks, in ppm. Error tolerance control for matched peaks is similar to the case of paired peaks.

intens.log.transfrom
default to FALSE. If set to TRUE, peak intensities will be logarithmically transformed. This is useful for displaying low-intensity peaks that would otherwise be overshadowed and less visible in the mass spectra.

Value

a tidy dataset, with the original input dataset augmented with additional columns. The content in the input dataset remain unchanged (though the display sequence may change).

Examples

search.result <- tag.search(myoglobin, delta = c(14, 28), error.Da.pair = .3)
search.result
tag.spectra.listplot(search.result)

tag.spectra.butterflyplot

tag.spectra.butterflyplot

description

This function takes the output dataset from tag.search, and draw using ggplot2 the centroid mass spectra displayed in a mirrored or "butterfly" manner. Peaks from the same "pair" (with designated m/z difference) are highlighted in differentiating colors, distinguished away from peaks of the "match" (with the same m/z) and the "mismatch" (neither of the prior two cases).
tag.spectra.butterflyplot

Usage

tag.spectra.butterflyplot(search.output.list, show.peak.pair = TRUE,
show.peak.match = TRUE, show.peak.mismatch = TRUE,
show.annotation.pair = TRUE, show.annotation.match = TRUE,
show.annotation.mismatch = TRUE, size.peak.pair = 2,
size.peak.match = 1, size.peak.mismatch = 0.5, size.divider = 0.3,
size.annotation.pair = NA, size.annotation.match = NA,
size.annotation.mismatch = NA, size.groupname = NA,
alpha.peak.pair = 0.8, alpha.peak.match = 0.5,
alpha.peak.mismatch = 0.2, alpha.annotation.pair = 0.8,
alpha.annotation.match = 0.5, alpha.annotation.mismatch = 0.2,
color.pair = 1, color.match = "black", color.mismatch = "black",
color.groupname = "black", color.divider = "black",
angle.annotation = 90, angle.groupname = 90, gap.groupname = 0.1,
gap.annotation = 0.05)

Arguments

search.output.list
the output list from function tag.search

show.peak.pair if TRUE, show the paired peaks
show.peak.match if TRUE, show the matched peaks
show.peak.mismatch if TRUE, show the mismatched peaks
show.annotation.pair if TRUE, show the m/z annotations for the paired peaks
show.annotation.match if TRUE, show the m/z annotations for the matched peaks
show.annotation.mismatch if TRUE, show the m/z annotations for the mismatched peaks
size.peak.pair adjust the peak width of the paired peaks. All size.xxx arguments take a numeric
value, same functionality as line width or text size control in ggplot2
size.peak.match adjust the peak width of the matched peaks
size.peak.mismatch adjust the peak width of the mismatched peaks
size.divider adjust divider width
size.annotation.pair adjust the m/z annotation text size for the paired peaks
size.annotation.match adjust the m/z annotation text size for the matched peaks
size.annotation.mismatch adjust the m/z annotation text size for the mismatched peaks
size.groupname adjust the text size for groupnames (e.g., "control", "experiment1", "experiment2", etc.).
alpha.peak.pair
    adjust the transparency of the paired peaks. All alpha.xxx arguments take a
    numeric value [0,1]

alpha.peak.match
    adjust the transparency of the matched peaks

alpha.peak.mismatch
    adjust the transparency of the mismatched peaks

alpha.annotation.pair
    adjust the transparency of the m/z annotations for the paired peaks

alpha.annotation.match
    adjust the transparency of the m/z annotations for the matched peaks

alpha.annotation.mismatch
    adjust the transparency of the m/z annotations for the mismatched peaks

color.pair
    control the color for the paired peaks and the associated m/z annotations. Each
    pair will be of the same color, and different pairs of differentiating colors. In
    case of multiple mass shifts being of interest within a pair, e.g., delta = c(14, 28,
    56), then peaks with m/z difference of either 14, 28 or 56, all belonging to the
    same pair, will be of the same color. Apart from the default color set, users could
    otherwise choose color from RColorBrewer palettes, e.g., color.pair = "Set1", or
    color.pair = "Blues". Colors for peaks (paired, matched, and mismatched) and the respectively associated annotations are designed to be of the same set of color for maximum clarity.

color.match
    control the color for the matched peaks with the associated m/z annotations,
    with default in "black". Users may otherwise reset to different colors, e.g.,
    color.match = "firebrick". As the matched peaks and mismatched peaks are
    usually of less research interest than paired peaks, the matched and mismatched
    peaks are respectively designed to be of monocolor.

color.mismatch
    control the color for the mismatched peaks with the associated m/z annotations,
    with default in "black".

color.groupname
    control the color for the groupnames, with default in "black".

color.divider
    control the color of the central divider

angle.annotation
    adjust the angle for the m/z annotations, taking a numeric value. This argument
    is useful to avoid annotation overlap, and is particularly handy when the plot is
    reoriented with coord_flip().

angle.groupname
    adjust the angle of the groupnames.

gap.groupname
    adjust the horizontal position of groupnames. A positive numeric value adjusts
    the distance between groupnames and the left bound of the mass spectra; negative
    values shifts the groupnames to the right side.

gap.annotation
    adjust the distance between m/z annotations and the top of the peak.
Details

Though similar to tag.spectra.listplot, tag.spectra.butterflyplot is specifically designed for comparison of TWO mass spectra with the highest annotation clarity. That is, the “group” variable of the associated feeding dataset should contain only two unique levels, “control” and another named level. In case of existence of more than two levels in the “group” variable, all levels except “control” will be plotted overlapped with tag.spectra.butterflyplot; and it is recommended to use tag.spectra.listplot instead for multiple spectra drawing.

Value

a ggplot2 plot.

Examples

```r
subset <- myoglobin[myoglobin$group %in% c("control", "label1"), ]
search.result <- tag.search(subset, delta = c(14, 28), error.Da.pair = .3)
tag.spectra.butterflyplot(search.result)
```

Description

This function takes the output dataset from tag.search, and draw using ggplot2 the centroid mass spectra displayed in a listed manner. Peaks from the same "pair" (with designated m/z difference) are highlighted in differentiating colors, distinguished away from peaks of the “match” (with the same m/z) and the “mismatch” (neither of the prior two cases).

Usage

```r
tag.spectra.listplot(search.output.list, show.peak.pair = TRUE, show.peak.match = TRUE, show.peak.mismatch = TRUE, show.annotation.pair = TRUE, show.annotation.match = TRUE, show.annotation.mismatch = FALSE, size.peak.pair = 2, size.peak.match = 1, size.peak.mismatch = 0.5, size.divider = 0.3, size.annotation.pair = NA, size.annotation.match = NA, size.annotation.mismatch = NA, size.groupname = NA, alpha.peak.pair = 0.8, alpha.peak.match = 0.5, alpha.peak.mismatch = 0.2, alpha.annotation.pair = 0.8, alpha.annotation.match = 0.5, alpha.annotation.mismatch = 0.2, color.pair = 1, color.match = "black", color.mismatch = "black", color.groupname = "black", color.divider = "black", angle.annotation = 90, angle.groupname = 90, gap.groupname = 0.02, gap.annotation = 0.15, peak.height.shrink = 0.7)
```
Arguments

- **search.output.list**
  the output list from function `tag.search`

- **show.peak.pair**
  if TRUE, show the paired peaks

- **show.peak.match**
  if TRUE, show the matched peaks

- **show.peak.mismatch**
  if TRUE, show the mismatched peaks

- **show.annotation.pair**
  if TRUE, show the m/z annotations for the paired peaks

- **show.annotation.match**
  if TRUE, show the m/z annotations for the matched peaks

- **show.annotation.mismatch**
  if TRUE, show the m/z annotations for the mismatched peaks

- **size.peak.pair**
  adjust the peak width of the paired peaks. All size.xxx arguments take a numeric value, same functionality as line width or text size control in ggplot2

- **size.peak.match**
  adjust the peak width of the matched peaks

- **size.peak.mismatch**
  adjust the peak width of the mismatched peaks

- **size.divider**
  adjust divider width

- **size.annotation.pair**
  adjust the m/z annotation text size for the paired peaks

- **size.annotation.match**
  adjust the m/z annotation text size for the matched peaks

- **size.annotation.mismatch**
  adjust the m/z annotation text size for the mismatched peaks

- **size.groupname**
  adjust the text size for groupnames (e.g., "control", "experiment1", "experiment2", etc.).

- **alpha.peak.pair**
  adjust the transparency of the paired peaks. All alpha.xxx arguments take a numeric value [0,1]

- **alpha.peak.match**
  adjust the transparency of the matched peaks

- **alpha.peak.mismatch**
  adjust the transparency of the mismatched peaks

- **alpha.annotation.pair**
  adjust the transparency of the m/z annotations for the paired peaks

- **alpha.annotation.match**
  adjust the transparency of the m/z annotations for the matched peaks

- **alpha.annotation.mismatch**
  adjust the transparency of the m/z annotations for the mismatched peaks
tag.spectra.listplot 9

color.pair control the color for the paired peaks and the associated m/z annotations. Each pair will be of the same color, and different pairs of differentiating colors. In case of multiple mass shifts being of interest within a pair, e.g., delta = c(14, 28, 56), then peaks with m/z difference of either 14, 28 or 56, all belonging to the same pair, will be of the same color. Apart from the default color set, users could otherwise choose color from RColorBrewer palettes, e.g., color.pair = "Set1", or color.pair = "Blues". Colors for peaks (paired, matched, and mismatched) and the respectively associated annotations are designed to be of the same set of color for maximum clarity.

color.match control the color for the matched peaks with the associated m/z annotations, with default in "black". Users may otherwise reset to different colors, e.g., color.match = "firebrick". As the matched peaks and mismatched peaks are usually of less research interest than paired peaks, the matched and mismatched peaks are respectively designed to be of monocolor.

color.mismatch control the color for the mismatched peaks with the associated m/z annotations, with default in "black".

color.groupname control the color for the groupnames, with default in "black".

color.divider control the color of the central divider

angle.annotation adjust the angle for the m/z annotations, taking a numeric value. This argument is useful to avoid annotation overlap, and is particularly handy when the plot is reoriented with coord_flip().

angle.groupname adjust the angle of the groupnames.

gap.groupname adjust the horizontal position of groupnames. A positive numeric value adjusts the distance between groupnames and the left bound of the mass spectra; negative values shifts the groupnames to the right side.

gap.annotation adjust the distance between m/z annotations and the top of the peak.

peak.height.shrink Taking a numeric value [0, 1], a small shrinking factor renders smaller peak height, and generates more space between peak and the central divider, leaving more space for annotations. This argument resolves overlap among annotations with upper-floor-residing peaks, a problem unique to listplot. Therefore, this argument is not used in the butterflyplot.

Details

This function is designed for comparison of multiple mass spectra. In case of comparison of two mass spectra, it is recommended to use tag.spectra.butterflyplot for the highest annotation clarity.

Value

a ggplot2 plot.
Examples

```r
search.result <- tag.search(myoglobin, delta = c(14, 28), error.Da.pair = .3)
search.result
tag.spectra.listplot(search.result)
```
Index

*Topic datasets
  myoglobin, 2

myoglobin, 2

protag, 3
protag-package (protag), 3

tag.search, 3
tag.spectra.butterflyplot, 4
tag.spectra.listplot, 7