Package ‘proteinProfiles’
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proteinProfiles-package

proteinProfiles package

Description

Significance assessment for distance measures of time-course protein profiles

Details

The package is published under the GPL-3 license.
Author(s)

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See Also

filterFeatures, grepAnnotation, profileDistance, plotProfileDistance

Description

Find protein group of interest based on pattern matching against the annotation data.

Usage

grepAnnotation(anno, pattern, column, ...)

Arguments

anno Data frame with annotation to analyze. The row names have to match rownames in the matrix containing the protein abundance data. Different columns correspond to different annotation columns, e.g. from different sources.

pattern Character string representing a (sub)string or regular expression matched against the annotation. For details, see ‘grep’.

column Column of the annotation data ‘pattern’ is matched against.

... Optional arguments, passed to the ‘grep’ function.

Value

Protein identifiers (rownames of ‘anno’) specifying the protein group of interest in the data set.

See Also

grep, filterRatios, proteinProfiles

Examples

data(ips_sample)

index_28S <- grepAnnotation(anno, pattern="^28S",
column="Protein.Name")

index_ribosome <- grepAnnotation(anno, "Ribosome", "KEGG")
filterFeatures

Description
Filter out proteins exceeding a certain fraction of missing data points.

Usage

```r
filterFeatures(values, maxNAfraction, verbose=FALSE, plot=FALSE, ...)
```

Arguments
- `values`: Numeric matrix containing the data to analyze.
- `maxNAfraction`: Numeric threshold specifying the maximum fraction of data points that can be missing ("NA") to still keep the protein.
- `verbose`: Logical indicating whether to print the number of proteins before and after filtering (default: FALSE).
- `plot`: Logical indicating whether to plot a diagnostic plot showing the distribution of the fraction of missing data points associated with the proteins (default: FALSE).
- `...`: Arguments passed to the "plot" method.

Value
Numeric matrix with the same structure as ‘values’, with elements not matching the filter criteria removed.

Examples

```r
data(ips_sample)
ratios_filtered <- filterFeatures(ratios, 0.2, verbose=TRUE)
```

ips_sample-data

IPS sample data

Description
IPS sample data, separated in protein ratios and annotation.

Usage

data(ips_sample)
profileDistance

Format

**ratios** Matrix with protein profiles. Rows correspond to proteins, columns to samples.

**annotation** Data frame with annotation columns, with row names matching those of ‘ratios.’

Examples

data(ips_sample)
str(ratios)
str(annotation)

profileDistance  profileDistance

Description

Compute distance between a protein group of interest and assess its significance by comparing it to the distances of randomly selected groups of proteins.

Usage

```r
profileDistance(values, index, nSample=1000, seed)
plotProfileDistance(z, ...)
```

Arguments

- `values` Numeric matrix containing the protein data to analyze.
- `index` Protein identifiers for the protein group of interest in the data set ‘values’, as returned from `grepAnnotation` or an equivalent function.
- `nSample` Integer specifying the number of randomly selected groups of proteins with the same number of elements as specified by ‘index’, serving as a reference for the significance assessment (default: 1000).
- `seed` Random seed, relevant for the permutation step. For details, see the ‘seed’ function.
- `z` Return object from ‘profileDistance.’
- `...` Optional arguments passed to the ‘plot’ function.

Value

List with elements:

- `d0` Numeric with mean distance $d_0$ of profiles for the proteins of interest.
profileDistance

\[ \mathbf{d}_1 \] Vector of numerics with mean distances of randomly selected groups of proteins.

\[ \mathbf{p} \] Numeric with p-value.

Examples

data(ips_sample)

index_28S <- grepAnnotation(annotation, pattern="^28S",
column="Protein.Name")

z <- profileDistance(ratios, index_28S)

z$p.value

plotProfileDistance(z)
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