Package: proteinProfiles (via r-universe)

October 10, 2026

Type Package

Title Protein Profiling

Version 1.53.0

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Imports graphics, stats

Depends R (>= 2.15.2)

Suggests testthat

Description Significance assessment for distance measures of time-course protein profiles

License GPL-3

LazyLoad yes

BiocViews Annotation, Proteomics, TimeCourse, Clustering

Repository https://bioc.r-universe.dev

Date/Publication 2026-04-28 12:37:23 UTC

RemoteUrl https://github.com/bioc/proteinProfiles

RemoteRef HEAD

RemoteSha fbc96f82f7191600f53cde672f5a56ce8eb485c7

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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.

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See Also

filterFeatures, grepAnnotation, profileDistance, plotProfileDistance

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annotation *grepAnnotation*

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(annotation, pattern="^28S",
column="Protein.Name")

index_ribosome <- grepAnnotation(annotation, "Ribosome", "KEGG")
```

`filterFeatures` *filterFeatures*

Description

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

Usage

```
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 indicationg 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

```
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)
```

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

```
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.

d1 Vector of numerics with mean distances

$$d_1$$

of randomly selected groups of proteins.

p Numeric with p-value

$$p$$

.

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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