

Package ‘prozor’

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Type Package

Title Minimal Protein Set Explaining Peptide Spectrum Matches

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Description Determine minimal protein set explaining peptide spectrum matches.

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LazyData TRUE

Imports Matrix, doParallel, foreach, seqinr

URL <https://github.com/wolski/prozor>

BugReports <https://github.com/wolski/prozor/issues>

Repository CRAN

NeedsCompilation no

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annotatePeptides *annotate peptides with protein ids*

Description

annotate peptides with protein ids

Usage

```
annotatePeptides(pepinfo, fasta, digestPattern = "([RK])|(^)|(M)",
  mcCores = NULL)
```

Arguments

pepinfo - list of peptides - sequence, optional modified sequence, charge state.
 fasta - object as created by read.fasta in package seqinr
 digestPattern - default "([RK])|(^)|(M)"
 mcCores number of cores to use

Examples

```
library(prozor)
library(doParallel)
library(foreach)
library(seqinr)
data(pepdata)
head(pepdata)

file = file.path(path.package("prozor"), "extdata/shortfasta.fasta" )
fasta = read.fasta(file = file, as.string = TRUE, seqtype="AA")
# we use a subset of the data to speedup the computation
#res = annotatePeptides(pepdata, fasta)
res = annotatePeptides(pepdata[1:20,], fasta, mcCores=1)
head(res)
```

greedy *given matrix (columns protein rows peptides), compute minimal protein set using greedy algorithm*

Description

given matrix (columns protein rows peptides), compute minimal protein set using greedy algorithm

Usage

```
greedy(pepprot)
```

Arguments

pepprot matrix as returned by prepareMatrix

Value

list of protein peptide assignments (where winner takes all)

Examples

```
library(prozor)

data(protpepmetashort)
xx = prepareMatrix(protpepmetashort, weight= "count")
dim(xx)
es = greedy(as.matrix(xx))
```

pepdata	<i>Table containing peptide information</i>
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Description

Table containing peptide information

prepareMatrix	<i>given table of peptide protein assignments generate matrix</i>
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Description

given table of peptide protein assignments generate matrix

Usage

```
prepareMatrix(data, weight = "count")
```

Arguments

data generated by annotatePeptides
weight weight type to use options are "count", "AA" "coverage"

Value

sparse matrix

Examples

```

data(protpepmetashort)
library(Matrix)
colnames(protpepmetashort)
dim(protpepmetashort)
xx = prepareMatrix(protpepmetashort, weight= "count")
#xx = prepareMatrix(protpepmetashort, weight = "AA")
#xx = prepareMatrix(protpepmetashort, weight = "coverage")
image(as.matrix(xx))
corProt = cor(as.matrix(xx))
par(mfrow =c(2,1))
image(corProt)
rownames(corProt)

# penalise peptides matching many proteins
xxn = t(apply(xx, 1, function(x){x/sum(x)}))
dim(xxn)
corProtn = cor(as.matrix(xxn))
image(corProtn)
rownames(corProtn)

```

 protpepmeta

Generated from pepdata using method annotatePeptides

Description

Generated from pepdata using method annotatePeptides

 protpepmetashort

Small version of prot meta dataset to speed up computation

Description

Small version of prot meta dataset to speed up computation

 prozor

Minimal Protein set Explaining Peptides

Description

Minimal Protein set Explaining Peptides

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