

Package ‘rTANDEM’

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Type Package

Title Interfaces the tandem protein identification algorithm in R

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SystemRequirements rTANDEM uses expat and pthread libraries. See the README file for details.

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Description This package interfaces the tandem protein identification algorithm in R. Identification can be launched in the X!Tandem style, by using as sole parameter the path to a parameter file. But rTANDEM also provides extended syntax and functions to streamline launching analyses, as well as function to convert results, parameters and taxonomy to/from R. A related package, shinyTANDEM, provides visualization interface for result objects.

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Imports methods

Depends XML, Rcpp, data.table (>= 1.8.8)

Suggests biomaRt

LinkingTo Rcpp

NeedsCompilation yes

R topics documented:

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rTANDEM-package	<i>An R encapsulation of X!TANDEM ('Jackhammer' release, 2013.06.15)</i>
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Description

X!Tandem is an open source software for protein identification by tandem mass spectrometry, and rTANDEM encapsulates this software in R. rTANDEM provides a basic encapsulation of X!Tandem: it has a function that takes as an argument the path to an X!Tandem style parameter file and return the path to an X!tandem style output file. The package also presents functions to transform parameters or results files into R objects and vice versa. Some functions are also available to examine the results within R. An associated package, shinyTANDEM, provides a graphical interface to visualize results objects.

Details

Package: rTANDEM
 Type: Package
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References

Robertson Craig and Ronald C. Beavis, TANDEM: matching proteins with mass spectra, Bioinformatics, 2004, 20 1466-7. <http://www.thegpm.org/tandem/>

Examples

```
# X!Tandem call style: we call tandem(input) on a single
# rTParam object.

# We create rTParam and from X!Tandem xml files
# located in the installation folder:
param <- GetParamFromXML(system.file("extdata/input.xml", package="rTANDEM"))

# We create a rTTaxo object and identify a database for yeast
```

```

taxonomy <- rTTaxo(
  taxon="yeast",
  format="peptide",
  URL= system.file("extdata/fasta/scd.fasta.pro", package="rTANDEM")
)

# We will adjust those two objects to use one another and to use,
# the path of some data and configuration files located
# in the installation folder:
param <- setParamValue(param, 'list path', 'taxonomy information', taxonomy)
param <- setParamValue(param, 'list path', 'default parameters',
  value=system.file("extdata/default_input.xml", package="rTANDEM"))
param <- setParamValue(param, 'spectrum', 'path',
  value=system.file("extdata/test_spectra.mgf", package="rTANDEM"))
param <- setParamValue(param, 'output', 'xsl path',
  value=system.file("extdata/tandem-input-style.xsl", package="rTANDEM"))
param <- setParamValue(param, 'output', 'path',
  value=paste(getwd(), "output.xml", sep="/"))

# This is the main command to run rTANDEM. The output will be
# written to a file in the working directory and the function
# returns the path to this file.
output.file <- tandem(param)
output.file

```

accessors

Extract information from rTANDEM result object

Description

The GetProteins, GetPeptides and GetDegeneracy functions are used to extract information from the rTANDEM result object.

Usage

```

GetProteins(results, log.expect=0, min.peptides=1L)
GetPeptides(protein.uid, results, expect=1, score=0)
GetDegeneracy(peptide.id, results)

```

Arguments

results	An object of the class rTResult that contains the result of an rTANDEM or X!Tandem analysis.
log.expect	X!Tandem provides a score of protein identification that is presented in terms of the log of the expect value of the identification. This score can be used as a threshold to discard low confidence identifications from the protein list.
expect	The expect value of peptide identification. This statistic can be used as a threshold to discard low confidence identifications from the peptide list.
min.peptides	The number of peptides involved in the identification of a given protein is computed. This number can be used as a threshold to discard identifications based on too few peptides from the protein list.
protein.uid	The tandem identifier of the protein (a numeric).

peptide.id	The tandem identifier of the peptide (a character).
score	The tandem score of the peptide identification. This score can be used as a threshold to discard low confidence identifications from the peptide list.

Value

GetProteins and GetDegeneracy return a data.table of proteins. GetPeptides returns a data.table of peptides with their ptm (post-translational modifications). Note that this table is generated through a merge of the peptide table and the ptm table: hence, if peptides has two ptm, it will occupy to rows in the resulting data.table.

Examples

```
# To show how to use the accessor functions, we need an rTANDEM result.
# We can produce one by running the example from the rTANDEM function,
# and reading it to R with GetResultsFromXML:
# output.file.path <- example(rTANDEM)

results <- GetResultsFromXML(output.file.path[[1]])

# To get a data.table of the proteins identified by at least 2 peptides
# and with an expect value of 0.05 or better:
proteins <- GetProteins(results, log.expect=-1.3, min.peptides=2)
proteins[, -c(4,5), with=FALSE] # Columns are removed for better display

# To get a list of the peptides used to identify the first protein
# (YCR012W, uid=576):
peptides <- GetPeptides(protein.uid="576", results)
peptides

# To get the list of proteins to which proteins a peptide belongs:
# (If a peptide belongs to more than one protein, it should not be
# used for quantification, as a biomarker or a MRM target.)
proteins.of.the.peptide <- GetDegeneracy(peptide.id="169.1.1",
results)
proteins.of.the.peptide[,label]
```

converters

Converts X!Tandem xml files to R objects and vice versa

Description

Functions like GetTaxoFromXML("pathToXML"), GetParamFromXML("pathToXML"), GetResultsFromXML(pathToXML) creates R object from X!Tandem-style xml files. The functions WriteParamToXML(paramObject) and WriteTaxoToXML(paramObject) will create an X!Tandem-style xml file from an R object.

Usage

```
GetTaxoFromXML(xml.file)
GetParamFromXML(xml.file)
GetResultsFromXML(xml.file)
WriteParamToXML(param, file, embeddedParam=c("write", "skip", "merge"),
embeddedTaxo=c("write", "skip") )
WriteTaxoToXML(taxo, file)
```

Arguments

xml.file	The path to the xml file that is to be read.
file	The name of the xml file that is to be created.
param	An object of class rTPParam that will be used to create the corresponding xml file.
taxo	A rTTaxo object whose content will be written to an xml file.
embeddedParam	The behaviour to adopt if a rTPParam object contains an embedded rTPParam object in the "list path, default parameters" slot. The option "merge" will merge the two object together. The option "write" will call WriteParamToXML on the embedded rTPParam object and write it to the the given file name plus suffixe "_default_param". It will then replace the embedded object by its path in the original object. The option "skip" will just ignore this slot.
embeddedTaxo	The behaviour to adopt if the rTPParam object contains an embedded rTTaxo object in the "list path, taxonomy information" slot. The option "write" will call WriteTaxoToXML on the object and write it to the input file name plus suffixe "_taxonomy". It will then replace the rTTaxo object by its path in the container rTPParam object. The option "skip" will just ignore this slot.

Value

'WriteParamToXML' and 'WriteTaxoToXML' have no return value: they are used for their side-effect of creating an xml file. 'GetTaxoFromXML' returns an object of the S3 class rTTaxo, 'GetParamFromXML' return an object of the S3 class rTPParam, and 'GetResultsFromXML' returns and object of the S4 class rTResult.

Examples

```
## Not run:
# To write a parameter or taxonomy object to a single xml file:
WriteParamToXML(parameter_object, file="parameter_file")
# Produces the file 'parameter_file'.

# To write a parameter object which has an embedded default
# parameter set to two xml files:
WriteParamToXML(parameter_object, file="param_file",
embeddedParam="write")
# Produces the files 'param_file' and 'param_file_default_param'.

# To write a parameter object that contains an embedded taxonomy to
# two different xml files:
WriteParamToXML(parameter_object, file="parameter_file",
embeddedTaxo="write")
# Produces the files 'parameter_file' and 'parameter_file_taxonomy'.

# To write a taxonomy object to a n xml file:
WriteTaxoToXML(taxonomy_object, file="taxonomy")
# Produces the file 'taxonomy'.

# To read a taxonomy file in R:
taxonomy <- GetTaxoFromXML("taxonomy.xml")
# Read the xml file and create a taxonomy object of class rTTaxo.

# To read a parameter file in R:
```

```

param <- GetParamFromXML("parameters.xml")
# Read the xml file and create a parameter object of class rTParam.

# To read a result file in R:
results <- GetResultsFromXML("output.xml")
# Read the output from X!Tandem and creates a R object of class
# rTResult.

## End(Not run)

```

parameters

Creates and manipulates parameter objects for rTANDEM

Description

Those functions instantiate parameter objects for rTANDEM and manipulate their values. Many of those functions give default values, either for general settings (e.g. `setParamDefault`), for instrument specific settings (e.g. `setParamOrbitrap`), or for function specific settings (e.g. `setParamPTMTreeSearch`).

Usage

```

rTParam()
setParamValue(param, category, parameter=NULL, value)
setParamDefault(param=NULL)
setParamPTMTreeSearch(param=NULL)
setParamOrbitrap(param=NULL)
setParamIonTrap(param=NULL)
setParamQuadToF05da(param=NULL)
setParamQuadToF100ppm(param=NULL)
rTTaxo(taxon=NA, format=NA, URL=NA)
addTaxon(taxonomy=NULL, taxon, format="peptide", URL)
## S3 method for class 'rTParam'
print(x, ...)

```

Arguments

param	A parameter object of class rTParam.
x	A parameter object of class rTParam.
...	Further arguments passed to or from other methods.
category	A string representing a category of parameters (e.g. "output", "protein").
parameter	A string representing the name of a parameter.
value	The value to give to the parameter.
taxon	A string representing the name of a taxon (e.g. "homo sapiens").
taxonomy	A taxonomy object of class rTTaxo.
format	A string representing the type of the database. The four types are: "peptide", "saps", "mods" and "spectrum".
URL	A string representing the full path to the database file.

Value

The functions `rTParam`, and all functions `setParam...`, return an object of S3 class `rTParam`. The functions `rTTaxo` and `addTaxon` return an object of S3 class `rTTaxo`. `print.rTParam` is used for its side effect of displaying a parameter object.

References

thegpm.org/TANDEM/api/

See Also

[GetParamFromXML](#), [GetTaxoFromXML](#), [WriteTaxoToXML](#), [WriteParamToXML](#).

Examples

```
# Initialize an empty parameter object:
param <- rTParam()
print.rTParam(param)

# Set general values.
param <- setParamDefault(param)

# Add instrument specific values for a LTQ mass spectrometer.
param <- setParamIonTrap(param)
print.rTParam(param)
```

rTResult-class

Class "rTResult" and "rTResult_s"

Description

A `rTResult` object is designed to contain the information of a X!Tandem analysis and allow data mining of this information. `rTResult_s` is a sub-class that adds a `data.table` slot for holding spectra.

Objects from the Class

Objects can be created by calls to `new("rTResult", ...)` or `new("rTResult_s", ...)`.

Slots

```
result.file: Object of class "character" ~~
proteins: Object of class "data.table" ~~
peptides: Object of class "data.table" ~~
ptm: Object of class "data.table" ~~
spectra: Object of class "data.table" ~~
used.parameters: Object of class "data.frame" ~~
unused.parameters: Object of class "vector" ~~
sequence.source.paths: Object of class "vector" ~~
estimated.false.positive: Object of class "integer" ~~
```

```

total.peptides.used: Object of class "integer" ~~
total.proteins.used: Object of class "integer" ~~
total.spectra.assigned: Object of class "integer" ~~
total.spectra.used: Object of class "integer" ~~
total.unique.assigned: Object of class "integer" ~~
start.time: Object of class "character" ~~
xtandem.version: Object of class "character" ~~
quality.values: Object of class "vector" ~~
nb.input.models: Object of class "integer" ~~
nb.input.spectra: Object of class "integer" ~~
nb.partial.cleavages: Object of class "integer" ~~
nb.point.mutations: Object of class "integer" ~~
nb.potential.C.terminii: Object of class "integer" ~~
nb.potential.N.terminii: Object of class "integer" ~~
nb.unanticipated.cleavages: Object of class "integer" ~~
initial.modelling.time.total: Object of class "numeric" ~~
initial.modelling.time.per.spectrum: Object of class "numeric" ~~
load.sequence.models.time: Object of class "numeric" ~~
refinement.per.spectrum.time: Object of class "numeric" ~~

```

Methods

No methods defined with class "rTResult" in the signature.

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Examples

```
showClass("rTResult")
```

tandem	<i>Calls X!TANDEM ('Jackhammer' release, 2013.06.15) from R objects or xml files</i>
--------	--

Description

The function `tandem(input)` takes a `rTParam` object or the path of a parameter file as argument and calls `X!Tandem` on it. The function `rtandem(data.file, taxon, taxonomy, default.parameters)` is a wrapper that can be used to circumvent the need for a `rTParam` input object (or of an xml input file).

Usage

```
tandem(input)
rtandem(data.file, taxon, taxonomy, default.parameters, output.path=NA)
```

Arguments

input	A path to a X!Tandem style parameter file or a rTParam object.
data.file	The path to the file containing the raw data to be analysed (in 'DTA', 'PKL' or 'MGF' format).
taxon	A string containing the taxon to be used for the analysis (e.g. "yeast" or "Homo sapiens").
taxonomy	Either a rTTaxo object or the path to a X!Tandem style taxonomy xml file.
default.parameters	Either a rTParam object containing the default parameters to be used, or the path to a X!Tandem style default-parameters xml file.
output.path	The path and name of the output file. If this name ends by ".xml" and the option 'path hashing' is enabled, a timestamp will be inserted just before the ".xml".

Value

Both tandem(input) and rtandem(data.file, taxon, taxonomy, default.parameters) returns the path of the xml output file generated.

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References

Robertson Craig and Ronald C. Beavis, TANDEM: matching proteins with mass spectra, Bioinformatics, 2004, 20 1466-7. <http://www.thegpm.org/tandem/>

Examples

```
# X!Tandem call style: we call tandem(input) on a single
# rTParam object.

# We create rTParam from an X!Tandem xml file
# located in the installation folder:
param <- GetParamFromXML(system.file("extdata/input.xml", package="rTANDEM"))

# We create a rTTaxo object and identify a database for yeast
taxonomy <- rTTaxo(
  taxon="yeast",
  format="peptide",
  URL= system.file("extdata/fasta/scd.fasta.pro", package="rTANDEM")
)

# We will adjust those two objects to use one another and to use
# the path of some data and configuration files located
# in the installation folder:
```

```

param <- setParamValue(param, 'list path', 'taxonomy information', taxonomy)
param <- setParamValue(param, 'list path', 'default parameters',
  value=system.file("extdata/default_input.xml", package="rTANDEM"))
param <- setParamValue(param, 'spectrum', 'path',
  value=system.file("extdata/test_spectra.mgf", package="rTANDEM"))
param <- setParamValue(param, 'output', 'xsl path',
  value=system.file("extdata/tandem-input-style.xsl", package="rTANDEM"))
param <- setParamValue(param, 'output', 'path',
  value=paste(getwd(), "output.xml", sep="/"))

# This is the main command to run rTANDEM. The output will be
# written to a file in the working directory and the function
# returns the path to this file.
output.file <- tandem(param)
output.file

```

visualizers

Plot spectrum from a rTResult object

Description

Functions like `GetTaxoFromXML("pathToXML")`, `GetParamFromXML("pathToXML")`, `GetResultsFromXML(pathToXML)` creates R object from X!Tandem-style xml files. The functions `WriteParamToXML(paramObject)` and `WriteTaxoToXML(paramObject)` will create an X!Tandem-style xml file from an R object.

Usage

```
ms2.plot(spectrum.id, result)
```

Arguments

<code>spectrum.id</code>	The id of the spectrum to be plotted (from the field <code>result@spectra\$id</code>).
<code>result</code>	A result object of class <code>rTResult_s</code> .

Value

'plot.ms2' returns a plot of the spectrum.

Examples

```

require(rTANDEM)
result <- GetResultsFromXML(
  system.file("extdata/result.xml", package="rTANDEM")
)

## Get the first spectra of the dataset and plot it:
spectrum.id <- result@spectra$id[[1]]
ms2.plot(spectrum.id, result)

```

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