Package ‘Resourcerer’

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Title Reads annotation data from TIGR Resourcerer or convert the annotation data into Bioconductor data pacakge.

Version 1.32.0

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Description This package allows user either to read an annotation data file from TIGR Resourcerer as a matrix or convert the file into a Bioconductor annotation data package using the AnnBuilder package.

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Depends R (>= 1.9.0), Biobase, AnnotationDbi (>= 1.4.0)

Suggests human.db0, mouse.db0, rat.db0

biocViews Annotation, Microarray

LazyLoad yes

License LGPL

R topics documented:

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getResourcerer — *A function that downloads an annotation file from TIGR Resourcerer and then read the downloaded file in as a matrix*

Description

TIGR Resourcerer maintains various annotation files for Affymetrix or cDNA chips. This function allows users to read an annotation file into R as a matrix.

Usage

```
getResourcerer(which, organism, destDir =
file.path(.path.package("Resourcerer"), "temp"), baseUrl = "ftp://occams.dfci.harvard.edu/pub/bio/tgi/data/
```

Arguments

which	which a character string indicating which annotation file to be read in. The annotation files are stored in subdirectories for various organisms under baseUrl (see below)
organism	organism a character string for the name of the organism of interests
destDir	destDir a character string for the path of a directory where the downloaded file will be stored. If missing, the temp directory will be the default
baseUrl	baseUrl a character string for the url of Resourcerer ftp site where directories containing annotation files for human, rat, mouse ... are stored
clean	clean a boolean indicating whether the file downloaded from Resourcerer will be removed after the data contained have been read in
exten	exten a character string for the extension (e. g., zip) of the source data file to be processed

Details

baseUrl is the root directory of TIGR ftp site for Resourcerer that contains subdirectories holding data for different organism.

Value

Function getResourcerer returns a matrix derived from the source data. Column names of the returned matrix are taken directly from the source file provided by Resourcerer. Users are advised to visit the Resourcerer web site for more information about the source data files.

Author(s)

Jianhua Zhang

References

http://pga.tigr.org/tigr-scripts/magic/r1.pl

See Also

"resourcerer2BioC"

Examples

```
resourcerer <- getResourcerer("Agilent_Human1_cDNA.zip", organism = "human",
     destDir = file.path(.path.package("Resourcerer"), "temp"),
     baseUrl = "ftp://occams.dfci.harvard.edu/pub/bio/tgi/data/Resourcerer",
     clean = TRUE, exten = "zip")
resourcerer[1:3, ]
```

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loadFromUrl *Functions to load files from a web site*

Description

Given an url, these functions download a file from a given web site and unzip the file if it is compressed.

Usage

```
loadFromUrl(srcUrl, destDir = "", verbose=FALSE)
validateUrl(srcUrl)
unzipFile(fileName, where = file.path(.path.package("Resourcerer"),
"temp"), isgz = FALSE)
```

Arguments

srcUrl	srcUrl a character string for the url of the file to be downloaded
destDir	destDir a character string for a loacal directory where the file to be downloaded will be saved
where	where same as destDir
isgz	isga a boolean indicating whether the downloaded file is a gz file
fileName	fileName a character string for the name of a file
verbose	A booline indicating whether to print extra information.

Details

These functions used to be part of the AnnBuilder package which was replaced by AnnotationDbi.If the file is compressed, decompressing will be applied and the path for the decompressed file will be returned.

validateUrl will terminate the process if an invalid url is passed.

unzipFile decompress the file passed as fileName.

Value

loadFromUrl returns a character string for the name of the file saved locally.

Author(s)

Jianhua Zhang

Examples

```
## Not run:
# Get a dummy data file from Bioconductor web site
data <-
loadFromUrl("http://www.bioconductor.org/datafiles/wwwsources/Tll_tmpl.gz",
destDir = "")
unlink(data)

## End(Not run)
```

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resourcerer2BioC *A function that downloads an annotation file from TIGR Resourcerer and then creates a bioC annotation data package*

Description

TIGR Resourcerer maintains various annotation files for Affymetrix or cDNA chips. This function allows users to create a bioC annotation data package for the probes contained in the Resourcerer annotation file.

Usage

```
resourcerer2BioC(
which, organism = c("human", "mouse", "rat"),
   destDir = file.path(.path.package("Resourcerer"), "temp"),
   pkgName, pkgPath, baseMapType = c("gbNRef", "gb", "ug", "ll"),
   version = "1.1.0", baseUrl =
   "ftp://occams.dfci.harvard.edu/pub/bio/tgi/data/Resourcerer", check =
   FALSE, author = list(authors = "Anonymous", maintainer
    = "Anonymous <anonymous@email.com>"), exten = "zip")
```

Arguments

which	which a character string indicating which Resourcerer annotation file to be read in
destDir	destDir a character string for the path of a directory where the downloaded file will be stored. If missing, the temp directory will be the default
baseUrl	baseUrl a character string for the url of Resourcerer ftp site where directories containing annotation files for human, rat, mouse ... are stored
baseMapType	baseMapType a character string that is either "gb","ug", or "ll" to indicate whether the probe ids in baseName are mapped to GenBack accession numbers, UniGene ids, or LocusLink ids
pkgName	pkgName a character string for the name of the data package to be built (e. g. hgu95a, rgu34a)
pkgPath	pkgPath a character string for the full path of an existing directory where the built backage will be stored
organism	organism a character string for the name of the organism of concern (now can only be "human", "mouse", or "rat")
version	version a character string for the version number
author	author a list of character strings with an author element for the name of the author and maintainer element for the email address of the author
check	check a boolean incicating whether to check the mappings between probe ids and LocusLink ids obtained from Resourcer and bioC AnnotationDbi when baseMapType is 'll'
exten	exten a character string for the extension (e. g. zip) of the source data file to be processed

Details

baseUrl is the root directory of TIGR ftp site for Resourcerer that contains subdirectories holding data for different organism.

Value

Function resourcerer2BioC returns invisible() if successfully executed.

Author(s)

Jianhua Zhang

References

http://pga.tigr.org/tigr-scripts/magic/r1.pl

See Also

getResourcerer

Examples

```
######################################################################
 ## The example takes a loooong time (about an hour) to run ##
######################################################################
 if(interactive()){
   resourcerer2BioC("Agilent_Human1_cDNA.zip",  baseMapType = "gbNRef")
   unlink(file.path(.path.package("Resourcerer"), "temp",
          "Agilent_Human1_cDNA.db"), TRUE)
 }
```

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