

Resourcerer

April 19, 2009

<code>getResourcerer</code>	<i>A function that downloads an annotation file from TIGR Resourcerer and then read the downloaded file in as a matrix</i>
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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/Resourcerer", clean = TRUE, exten
```

Arguments

<code>which</code>	<code>which</code> a character string indicating which annotation file to be read in. The annotation files are stored in subdirectories for various organisms under <code>baseUrl</code> (see below)
<code>organism</code>	<code>organism</code> a character string for the name of the organism of interests
<code>destDir</code>	<code>destDir</code> 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
<code>baseUrl</code>	<code>baseUrl</code> a character string for the url of Resourcerer ftp site where directories containing annotation files for human, rat, mouse ... are stored
<code>clean</code>	<code>clean</code> a boolean indicating whether the file downloaded from Resourcerer will be removed after the data contained have been read in
<code>exten</code>	<code>exten</code> 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,]
```

<code>resourcerer2BioC</code>	<i>A function that downloads an annotation file from TIGR Resourcerer and then creates a bioC annotation data package</i>
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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 GenBank 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 package 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 indicating whether to check the mappings between probe ids and LocusLink ids obtained from Resourcer and bioC AnnBuilder 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",  
    "AgilentHuman1cDNA"), TRUE)  
}
```

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