Package ‘IdMappingRetrieval’

April 14, 2017

Type Package

Title ID Mapping Data Retrieval

Version 1.22.0

Date 2016-01-18

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Description Data retrieval for identifier mapping performance analysis

License GPL-2

Depends R.oo, XML, RCurl, rChoiceDialogs

Imports biomaRt, ENVISIONQuery, AffyCompatible, R.methodsS3, utils

LazyLoad yes

  ‘IdMappingRetrieval-package.R’ ‘serviceManager.R’

biocViews Annotation, MultipleComparison

NeedsCompilation no

R topics documented:

IdMappingRetrieval-package .................................................. 2
Annotation ................................................................. 3
AnnotationAffx ............................................................ 4
AnnotationEnsembl ......................................................... 5
AnnotationEnsemblCsv ....................................................... 7
AnnotationEnvision ........................................................ 9
AnnotationNetAffx .......................................................... 11
ServiceManager ............................................................ 12

Index 14
Id Mapping Retrieval

Description
**Annotation**

Package: IdMappingRetrieval  
Type: Package  
Version: 0.99.0  
Date: 2011-06-26  
License: GPL-2  
LazyLoad: yes

**Author(s)**

Alex Lisovich, Roger Day

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**Description**

Package:  
Class Annotation

```
Object  
~~|  
~~+-Annotation
```

**Directly known subclasses:**

AnnotationAffx, AnnotationEnsembl, AnnotationEnsemblCsv, AnnotationEnvision, AnnotationNetAffx

public abstract static class Annotation  
extends Object

This is the base annotation class from which the concrete classes like AnnotationAffx, AnnotationEnvision etc. are derived

**Usage**

```
Annotation(cacheFolderName="", primaryColumn="From", secondaryColumn="To", swap=FALSE, species="Homo sapiens")
```

**Arguments**

- `cacheFolderName`
  - The path to a service cashing directory for a given Annotation object. The path is relative to the caching subsystem root directory. Default is 'Affymetrix'.

- `primaryColumn`
  - Primary column to be retrieved from a data frame obtained for a given service when getIdMap() on a given annotation object is called. Default is 'From'.

- `secondaryColumn`
  - Secondary column(s) to be retrieved from a data frame obtained for a given service when getIdMap on a given annotation object is called. Default is 'To'.
swap A logical indicating if primary and secondary column(s) need to be swapped at the end of the IdMap retrieval during the getIdMap() call. Default is FALSE.

species A character vector or NA indicating if filtering of the results on a particular set of species should be performed if a given service provides the species information. If NA, no filtering is performed. Default is "Homo sapiens".

verbose if TRUE enables diagnostic messages. Default is FALSE.

Additional parameters

Fields and Methods

Methods:

- getDataFrame: Get the entire data set available from a particular service in a form of a data frame.
- getFolderName: Get caching folder name for a given Annotation object.
- getIdMap: Get an IdMap object using the data retrieved by a particular service represented by annotation object.
- getServiceRoot: Get a root directory for a particular annotation object.
- setOptions: Set the parameters for an annotation object.

Methods inherited from Object:

$. $<-$ [ [ [<- as.character attach attachLocally clearCache clone detach equals extend finalize gc getEnvironment getFields getInstantiationTime getStaticInstance hasField hashCode ll load objectSize print registerFinalizer save

Author(s)

Alex Lisovich, Roger Day

The AnnotationAffx class

Description

Package: AnnotationAffx

Object

~~|--
|---Annotation
|-----|
|------ AnnotationAffx

Directly known subclasses:

AnnotationNetAffx

public static class AnnotationAffx
extends Annotation
The AnnotationAffx class encapsulates the functionality allowing to retrieve data from the Affymetrix annotation data online repository through the getIdMap() and getDataFrame() calls.

Usage

```
AnnotationAffx(cacheFolderName="Affymetrix", primaryColumn="Probe.Set.ID", secondaryColumn="SwissProt", swap=TRUE, ...)
```

Arguments

- `cacheFolderName`: The path to a service cashing directory for a given AnnotationAffx object. The path is relative to the caching subsystem root directory. Default is 'Affymetrix'.
- `primaryColumn`: Primary column to be retrieved from a data frame obtained from the Affymetrix annotation repository when getIdMap() is called. Default is 'Probe.Set.ID'.
- `secondaryColumn`: Secondary column to be retrieved from a data frame obtained from the Affymetrix annotation repository when getIdMap() is called. Default is 'SwissProt'.
- `swap`: Logical indicating if primary and secondary column(s) need to be swapped at the end of the IdMap retrieval during the getIdMap() call. Default is `TRUE`. Additional parameters, see `Annotation`.

Fields and Methods

Methods:

- Methods inherited from `Annotation`:
  - `getArrayType`, `getArrayTypes`, `getColumns`, `getCredentials`, `getDataFrame`, `getFolderName`, `getIdMap`, `getRoot`, `getServiceRoot`, `init`, `readDF`, `setCredentials`, `setOptions`

- Methods inherited from `Object`:
  - `$`, `$<-`, `[[`, `[[<-`, `as.character`, `attach`, `attachLocally`, `clearCache`, `clone`, `detach`, `equals`, `extend`, `finalize`, `gc`, `getEnvironment`, `getFields`, `getInstatinationTime`, `getStaticInstance`, `hasField`, `hashCode`, `Il`, `load`, `objectSize`, `print`, `registerFinalizer`, `save`

Author(s)

Alex Lisovich, Roger Day
```java
public static class AnnotationEnsembl
extends Annotation

The AnnotationEnsembl class encapsulates the functionality allowing to retrieve data from the Ensembl BioMart online query system using biomaRt R package through the Annotation.getIdMap() and Annotation.getDataFrame() calls on this object.

Usage

AnnotationEnsembl(cacheFolderName="Ensembl", primaryColumn=c("uniprot_swissprot_accession", "uniprot_sptrembl"), secondaryColumn=NA, swap=FALSE, species="hsapiens_gene_ensembl", full.merge=TRUE, ...)

Arguments

- cacheFolderName: The symbolic name of a service represented by a given AnnotationEnsembl object.
- primaryColumn: Primary column(s) to be retrieved from a data frame obtained from the Ensembl csv file when getIdMap() is called. As the Ensembl returns the match results for SwissProt and Trembl accessions in separate columns, it is possible to retrieve either or them or merge them together by explicitly specifying the set of columns to be merged. Default is c('uniprot_swissprot_accession', 'uniprot_sptrembl').
- secondaryColumn: Secondary column (containing probeset IDs) to be retrieved from a data frame obtained from the Ensembl csv file when getIdMap() is called. If NA (default), the column name(s) derived automatically from the array type parameter during the getDataFrame() call. It should be noted that the probeset ID column name in Ensembl data format is array specific ("Affy.HG.U133.PLUS.2" for example) and therefore needs to be selected on per array basis if specified explicitly.
- swap: A logical indicating if primary and secondary column(s) need to be swapped at the end of the IdMap retrieval during the getIdMap() call. Default is TRUE.
- species: Character vector or NA indicating if filtering of the results on a particular set of species should be performed if a given service provides the species information. If NA, no filtering is performed. Default is 'hsapiens_gene_ensembl'.
- full.merge: A logical indicating which version of primary columns merging algorithm to use. If TRUE (default), all unique pairs <probeset ID, SwissProt> and <probeset ID, Trembl> are generated, and if FALSE, only those pairs from <probeset ID, Trembl> for which Uniprot ID is not present in <probeset ID, SwissProt> pairs are included.

Fields and Methods

Methods:
No public methods defined.


**Methods inherited from Annotation:**
getArrayType, getArrayTypes, getColumns, getCredentials, getDataFrame, getFolderName, getIdMap, 
getRoot, getServiceRoot, init, readDF, setCredentials, setOptions

**Methods inherited from Object:**
$, $<-, [, [<-., as.character, attach, attachLocally, clearCache, clone, detach, equals, extend, finalize, gc, 
getEnvironment, getFields, getInstantiationTime, getStaticInstance, hasField, hashCode, ll, 
load, objectSize, print, registerFinalizer, save

**Author(s)**
Alex Lisovich, Roger Day

**Examples**

```r
## Not run:
Annotation$init(); #create Ensembl annotation object
annObj<-AnnotationEnsembl(species="hsapiens_gene_ensembl");
## End(Not run)
```

---

**Description**

Package:  
Class **AnnotationEnsemblCsv**

```
Object
~~|
~~~---Annotation
~~~~~~~|
~~~~~~~~~---AnnotationEnsembl
~~~~~~~~~~~~~~|
~~~~~~~~~~~~~---AnnotationEnsemblCsv
```

**Directly known subclasses:**

public static class **AnnotationEnsemblCsv**
extends **AnnotationEnsembl**

The **AnnotationEnsemblCsv** class encapsulates the functionality allowing to retrieve data from the Ensembl interactive online query system. The ID matching information filtered on species and the microarray chip type is retrieved as comma delimited csv file. The **AnnotationEnsemblCsv** object encapsulates the functionality allowing to interactively choose the Ensembl query results csv file and convert it into a data frame during the getIdMap() and getDataFrame() calls on the **AnnotationEnsemblCsv** object.
AnnotationEnsemblCsv

Usage

AnnotationEnsemblCsv(cacheFolderName="EnsemblCsv", primaryColumn=c("UniProt.SwissProt.Accession", "UniProt.TrEMBL.Accession"), secondaryColumn=NA, swap=FALSE, full.merge=TRUE, df_filename=NULL, ...)

Arguments

cacheFolderName
The symbolic name of a service represented by a given AnnotationEnsembl object.

primaryColumn
Primary column(s) to be retrieved from a data frame obtained from the Ensembl csv file when getIdMap() is called. As the Ensembl returns the match results for SwissProt and Trembl accessions in separate columns, it is possible to retrieve either or them or merge them together by explicetely specifying the set of columns to be merged. Default is c('uniprot_swissprot_accession','uniprot_sptrembl').

secondaryColumn
secondaryColumn Secondary column (containing probeset IDs) to be retrieved from a data frame obtained from the Ensembl csv file when getIdMap() is called. If NA (default), the column name(s) derived automatically from the array type parameter during the getDataFrame() call. It should be noted that the probeset ID column name in Ensembl data format is array specific ('Affy.HG.U133.PLUS.2' for example) and therefore needs to be selected on per array basis if specified explicitely.

swap
A logical indicating if primary and secondary column(s) need to be swapped at the end of the IdMap retrieval during the getIdMap() call. Default is TRUE.

full.merge
A logical indicating which version of primary columns merging algorithm to use. If TRUE (default), all unique pairs <probeset ID, SwissProt> and <probeset ID, Trembl> are generated, and if FALSE, only those pairs from <probeset ID, Trembl> for which Uniprot ID is not present in <probeset ID, SwissProt> pairs are included.

df_filename
Character string or NULL. In the first case the character string contains the name of conversion results file and in the second case the file name is determined interactively through the Open File dialog during the call to Annotation.getIdMap() or Annotation.getDataFrame() on the AnnotationEnsemblCsv object.

... Additional parameters, see Annotation.

Fields and Methods

Methods:
No public methods defined.

Methods inherited from AnnotationEnsembl:
getColumns, getColumns1, getColumns2, readDF

Methods inherited from Annotation:
getArrayType, getArrayTypes, getColumns, getCredentials, getDataFrame, getFolderName, getIdMap, getRoot, getServiceRoot, init, readDF, setCredentials, setOptions

Methods inherited from Object:
$, $<-, [], [<-, as.character, attach, attachLocally, clearCache, clone, detach, equals, extend, finalize, gc, getEnvironment, getFields, getInstantiationTime, getStaticInstance, hasField, hashCode, ll, load, objectSize, print, registerFinalizer, save

Author(s)

Alex Lisovich, Roger Day
**AnnotationEnvision**

### Examples

```r
## Not run:
Annotation$init();
# create Ensembl annotation object
annObj<-AnnotationEnsemblCsv(cacheFolderName="EnsemblCsv");

## End(Not run)
```

### Description

Package: AnnotationEnvision

Class **AnnotationEnvision**

```r

Object
---
```- Annotation

```r

~~~~~~~~
```- AnnotationEnvision

**Directly known subclasses:**

public static class **AnnotationEnvision**

extends **Annotation**

The AnnotationEnvision class encapsulates the functionality allowing to retrieve data from the Envision online query system. The Envision online query system allows to retrieve the ID matching information accompanied by multiple attributes like species and the microarray chip type in the form of the xml file. The AnnotationEnvision class encapsulates the functionality allowing to filter the Envision query results on species and microarray type attributes and convert it into a data frame during the getIdMap() and getDataFrame() calls on the AnnotationEnvision object.

**Usage**

```r
AnnotationEnvision(cacheFolderName="EnVision", primaryColumn=c("UniProt.SwissProt.Accession", "UniProt.TrEMBL.Accession"), secondaryColumn=NA, swap=TRUE, species="Homo sapiens", full.merge=TRUE, ...)
```

**Arguments**

- **cacheFolderName**
  The symbolic name of a service represented by a given AnnotationEnsembl object.

- **primaryColumn**
  Primary column(s) to be retrieved from a data frame obtained from the Ensembl csv file when getIdMap() is called. As the Ensembl returns the match results for SwissProt and Trembl accessions in separate columns, it is possible to retrieve either or them or merge them together by explicetely specifying the set of columns to be merged. Default is c(‘uniprot_swissprot_accession’,’uniprot_sptrembl’).
AnnotationEnvision

secondaryColumn

Secondary column (containing probeset IDs) to be retrieved from a data frame obtained from the Ensembl csv file when getIdMap() is called. If NA (default), the column name(s) derived automatically from the array type parameter during the getDataFrame() call. It should be noted that the probeset ID column name in Ensembl data format is array specific ("Affy.HG.U133.PLUS.2" for example) and therefore needs to be selected on per array basis if specified explicitly.

swap

A logical indicating if primary and secondary column(s) need to be swapped at the end of the IdMap retrieval during the getIdMap() call. Default is TRUE.

species

Character vector or NA indicating if filtering of the results on a particular set of species should be performed if a given service provides the species information. If NA, no filtering is performed. Default is 'Homo sapiens'.

full.merge

A logical indicating which version of primary columns merging algorithm to use. If TRUE (default), all unique pairs <probeset ID, SwissProt> and <probeset ID, Trembl> are generated, and if FALSE, only those pairs from <probeset ID, Trembl> for which Uniprot ID is not present in <probeset ID, SwissProt> pairs are included.

... Additional parameters, see Annotation.

Fields and Methods

Methods:
No public methods defined.

Methods inherited from Annotation:
getArrayType, getArrayType, getColumns, getCredentials, getDataFrame, getFolderName, getIdMap, getRoot, getServiceRoot, init, readDF, setCredentials, setOptions

Methods inherited from Object:
$, $<-, [<-, [=<, as.character, attach, attachLocally, clearCache, clone, detach, equals, extend, finalize, gc, getEnvironment, getFields, getInstantiationTime, getStaticInstance, hasField, hashCode, ll, load, objectSize, print, registerFinalizer, save

Author(s)

Alex Lisovich, Roger Day

Examples

## Not run:
Annotation$init();
#create Envision annotation object
annObj<AnnotationEnvision(species="Homo sapiens");

## End(Not run)
Description

Package:
Class AnnotationNetAffx

Object
~~|  
~~+--Annotation
~~~~|  
~~~~~~~~+--AnnotationAffx
~~~~~~~~|  
~~~~~~~~~~~~+--AnnotationNetAffx

Directly known subclasses:

public static class AnnotationNetAffx extends AnnotationAffx

The AnnotationNetAffx class encapsulates the functionality allowing to retrieve data from the NetAffx batch query system through the Annotation.getIdMap() and Annotation.getDataFrame() calls on this object. The NetAffx batch query system requires to submit the probeset IDs by providing text files in a special format, maximum 10000 IDs per file. The results are returned in a form of a tab delimited text file, one file per submission, so the query results for a whole array are presented by a set of such files. The AnnotationNetAffx object encapsulates the functionality allowing to interactively choose the set of result files and merge them into a single data frame during the Annotation.getIdMap() and Annotation.getDataFrame() calls on the AnnotationNetAffx object.

Usage

AnnotationNetAffx(cacheFolderName="NetAffxCsv", primaryColumn="Probe.Set.ID", secondaryColumn="SwissProt", swap=TRUE, ...)  

Arguments

cacheFolderName
The symbolic name of a service represented by a given AnnotationNetAffx object.

primaryColumn
Primary column to be retrieved from a data frame obtained from the Affymetrix annotation repository when getIdMap() is called. Default is 'Probe.Set.ID'.

secondaryColumn
Secondary column to be retrieved from a data frame obtained from the Affymetrix annotation repository when getIdMap() is called. Default is 'SwissProt'.

swap
A logical indicating if primary and secondary column(s) need to be swapped at the end of the IdMap retrieval during the getIdMap() call. Default is TRUE.
df_filename  Character vector, character string or NULL. In the first case the character vector contains the names of a resulting file set, in the second, the character string contains the name of directory in which the files are stored, and in the third the file set is determined interactively through the Open File dialog during the call to getIdMap() or getDataFrame() on the AnnotationAffxCsv object.

...  Additional parameters, see Annotation.

Fields and Methods

Methods:

Methods inherited from AnnotationAffx:
getColumns, getProbesetList, readDF, setCredentials

Methods inherited from Annotation:
getArrayType, getArrayTypes, getColumns, getCredentials, getDataFrame, getFolderName, getIdMap, getRoot, getServiceRoot, init, readDF, setCredentials, setOptions

Methods inherited from Object:
S. $<-, [], [[<-, as.character, attach, attachLocally, clearCache, clone, detach, equals, finalize, gc, getEnvironment, getFields, getInstantiationTime, getStaticInstance, hasField, hashCode, Il, load, objectSize, print, registerFinalizer, save

Author(s)

Alex Lisovich, Roger Day

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ServiceManager  The ServiceManager class

Description

Package:
Class ServiceManager

Object
~~|
~~+-ServiceManager

Directly known subclasses:

public static class ServiceManager
extends Object

ServiceManager class serves as a container for a set of specialized service objects and provides the means for (optionally interactive) handling of such a set simplifying the process of data retrieval from a variety of resources in a batch mode.
ServiceManager

Usage
ServiceManager(services=list(), ...)

Arguments
services   Annotation services to be contained within the ServiceManager object. Default is NULL.
...        Not used.

Fields and Methods

Methods:

addServices   Add services to the ServiceManager object.
getDataFrameList Collect raw data data from various online query systems utilizing Annotation service functionality.
getIdMapList   Collect ID mapping data from various online query systems utilizing Annotation service functionali-
getServices    Get list of annotation services encapsulated within the particular ServiceManager object.
setServices    Set the list of services for a ServiceManager object.

Methods inherited from Object:
$, $<-, [I, [I]<-, as.character, attach, attachLocally, clearCache, clone, detach, equals, extend, final-
ize, gc, getEnvironment, getFields, getInstantiationTime, getStaticInstance, hasField, hashCode, ll,
load, objectSize, print, registerFinalizer, save

Author(s)
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Index

∗Topic **classes**
- Annotation, 3
- AnnotationAffx, 4
- AnnotationEnsembl, 5
- AnnotationEnsemblCsv, 7
- AnnotationEnvision, 9
- AnnotationNetAffx, 11
- ServiceManager, 12

∗Topic **package**
- IdMappingRetrieval-package, 2

addServices, 13
- Annotation, 3, 4–12
- AnnotationAffx, 3, 4, 11
- AnnotationEnsembl, 3, 5, 7
- AnnotationEnsemblCsv, 3, 6, 7
- AnnotationEnvision, 3, 9
- AnnotationNetAffx, 3, 4, 11

character, 4
- FALSE, 4, 6, 8, 10

getDataFrame, 4
- getDataFrameList, 13
- getFolderName, 4
- getIdMap, 4
- getIdMapList, 13
- getServiceRoot, 4
- getServices, 13

IdMappingRetrieval
- (IdMappingRetrieval-package), 2
- IdMappingRetrieval-package, 2

logical, 4, 6, 8, 10, 11
- NA, 4, 6, 8, 10
- NULL, 12, 13

Object, 3–5, 7, 9, 11, 12
- ServiceManager, 12
- setOptions, 4
- setServices, 13
- TRUE, 4–6, 8, 10, 11