

lumiRatIDMapping

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lumiRatIDMapping_dbconn
Collect information about the package annotation DB

Description

Some convenience functions for getting a connection object to (or collecting information about) the package annotation DB.

Usage

```
lumiRatIDMapping_dbconn()  
lumiRatIDMapping_dbfile()  
lumiRatIDMapping_dbInfo()
```

Details

lumiRatIDMapping_dbconn returns a connection object to the package annotation DB. **IMPORTANT: Don't call `dbDisconnect` on the connection object returned by lumiRatIDMapping_dbconn or you will break all the `AnnDbObj` objects defined in this package!**

lumiRatIDMapping_dbfile returns the path (character string) to the package annotation DB (this is an SQLite file).

lumiRatIDMapping_dbInfo prints other information about the package annotation DB.

Value

lumiRatIDMapping_dbconn: a DBIConnection object representing an open connection to the package annotation DB.

lumiRatIDMapping_dbfile: a character string with the path to the package annotation DB.

lumiRatIDMapping_dbInfo: none (invisible NULL).

See Also[dbConnect](#)**Examples**

```
## Show the database information (meta data)
lumiRatIDMapping_dbInfo()

## List the tables included in the database
conn <- lumiRatIDMapping_dbconn()
dbListTables(conn)
```

```
lumiRatIDMapping_nuID
```

Mapping nuIDs of Illumina Rat chips to the most recent Rattus norvegicus RefSeq release

Description

We mapped nuIDs of Illumina Rat chips by BLASTing each probe sequence (converted from nuID) against the the most recent Rattus norvegicus RefSeq release. The mapping also includes the mapping quality information, like mapping strength, uniqueness, number of hits.

Usage

```
lumiRatIDMapping_nuID()
```

Details

The nuID mapping information is kept in the nuID_MappingInfo table in the ID Mapping library. The nuID mapping table includes following fields (columns):

1. nuID: nuID for the probe sequence
2. Refseq: The refseq IDs with perfect matching with probe sequence. If there are more than one refseq IDs, they are separated by ",".
3. EntrezID: The Entrez gene IDs correspond to the refseq IDs. If there are more than one Entrez gene IDs, they are separated by ",".
4. Total_hits_of_EntrezID: The number of unique Entrez gene IDs matched with the probe sequence.
5. Refseq_old: the refseq ID provided by Illumina company

Procedures of nuID mappings:

Briefly, we first mapped each probe sequence (converted from nuID) against the corresponding RefSeq sequence. Only perfect mapping will be considered. When one probe maps to multiple Refseq sequences, we will further check whether these Refseq sequences correspond to the same Entrez gene. To make sure the probes have unique mapping, we only consider the probe sequences mapped to a single Entrez Gene when we build the lumi annotation packages (lumiHumanAll.db, lumiMouseAll.db and lumiRatAll.db).

Value

lumiRatIDMapping_nuID returns a nuID mapping summary of Illumina Rat chips.

References

1. Du, P., Kibbe, W.A. and Lin, S.M., "nuID: A universal naming schema of oligonucleotides for Illumina, Affymetrix, and other microarrays", *Biology Direct* 2007, 2:16 (31May2007).

Examples

```
## List the fields in the nuID_MappingInfo table
conn <- lumiRatIDMapping_dbconn()
dbListFields(conn, 'nuID_MappingInfo')

## Summary of nuID mapping
lumiRatIDMapping_nuID()
```

lumiRatIDMapping *Illumina ID Mapping information of all Rat expression chips*

Description

Welcome to the lumiRatIDMapping ID mapping Package. The purpose of this package is to provide ID mappings between different types of Illumina identifiers of Rat Expression chips and nuIDs, and also mappings from nuIDs to the the most recent *Rattus norvegicus* RefSeq release. The library includes the data tables corresponding to all released Illumian Rat Expression chips before the package releasing date. Each table includes columns "Search_key" ("Search_Key"), "Target" ("ILMN_Gene"), "Accession", "Symbol", "ProbeId" ("Probe_Id") and "nuID". It also includes a nuID_MappingInfo table, which keeps the mapping information of nuID to RefSeq ID and its related mapping quality information. Another table, metadata, keeps other information, like RefSeq version, species. The package is supposed to be used together with the Bioconductor lumi package.

You can learn what objects this package supports with the following command:

```
ls("package:lumiRatIDMapping")
```

Each of these objects has their own manual page detailing where relevant data was obtained along with some examples of how to use it.

Examples

```
ls("package:lumiRatIDMapping")
```

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