Package 'BrainStars'

October 15, 2020

Type Package

Title query gene expression data and plots from BrainStars (B*)

Version 1.32.0

Date 2012-03-06

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Description This package can search and get gene expression data
and plots from BrainStars (B*). BrainStars is a quantitative
expression database of the adult mouse brain. The database has
genome-wide expression profile at 51 adult mouse CNS regions.

Depends RCurl, Biobase, methods

Imports RJSONIO, Biobase

License Artistic-2.0

LazyLoad yes

Collate 'BrainStars.r' 'annotation.r' 'expression.r' 'figure.r'

biocViews Microarray, OneChannel, DataImport

git_url https://git.bioconductor.org/packages/BrainStars

git_branch RELEASE_3_11

git_last_commit e4f20fe

git_last_commit_date 2020-04-27

Date/Publication 2020-10-15

R topics documented:

BrainStars   *BrainStars API client for R*

Description

This R package can search and get gene expression data and plots from BrainStars (or B*, http://brainstars.org/).

Details

BrainStars is a quantitative expression database of the adult mouse brain. The database has genome-wide expression profile at 51 adult mouse CNS regions.

For 51 CNS regions, slices (0.5-mm thick) of mouse brain were cut on a Mouse Brain Matrix, frozen, and the specific regions were punched out bilaterally with a microdissecting needle (gauge 0.5 mm) under a stereomicroscope. For each region, we took samples every 4 hours, starting at ZT0 (Zeitgaber time 0; the time of lights on), for 24 hours (6 time-point samples for each region), and we pooled the samples from the different time points. We independently sampled each region twice (n=2).

These samples were purified their RNA, and measured with Affymetrix GeneChip Mouse Genome 430 2.0 arrays. Expression values were then summarized with the RMA method. After several analysis with the expression data, the data and analysis results were stored in the BrainStars database.

BrainStars database has a REST API to query gene expression data and some kind of figures written by Dr. Takeya Kasukawa. This package is wrapper for BrainStars REST API in R. BrainStars data, images and texts (excluding ABA data and images) are licensed under a Creative Commons Attribution 2.1 Japan License.

References

Takeya Kasukawa*, Koh-hei Masumoto*, Itoshi Nikaido*, Mamoru Nagano, Kenichiro D. Uno, Kaori Tsujino, Carina Hanashima, Yasufumi Shigeyoshi, and Hiroki R. Ueda: Quantitative Expression Profile of Distinct Functional Regions in the Adult Mouse Brain, PLoS ONE 6(8), e23228, 2011. (doi:10.1371/journal.pone.0023228) *equally contributed

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getBrainStars   *Get various information in BrainStars*

Description

This function queries various information from BrainStars The function is a wrapper of All BrainStars API.

Usage

```
getBrainStars(query, type, base.url, json)
```

Arguments

`query`	keyword
`type`	BrainStars API name. (expression, search, probeset, marker, multistate, onestate, ntnh and genefamily)
`base.url`	URL of Brainstars database.
`json`	TRUE is json mode of response. (Defalut is FALSE)

Details

Brain API is for keyword search and is based on Tokyo Manifesto and TogoWS REST interface.

Type: expression (query) "query" is a vector of ProbeSet IDs.

Type: search, probeset and onestate Keyword for retrieving a list of hit entries: (query+string)[/(offset),(limit)].

Keyword for retrieving the count of hit entries: (query+string)/count.

Type: genefamily Keyword search format: (category)/(keyword)/(offset),(limit)

You can indicate gene category name in the following words:

- "tf": transcription factors
- "transmem": transmembrane genes
- "channel": channel genes
- "gpcr": GPCR genes
- "adhesion": cell adhesion genes
- "excellmat": extracellular matrix genes
- "structural": structural protein genes
- "neurogenesis": neurogenesis related genes
- "hox": homeobox genes
- "nucrcpt": nuclear receptor genes
- "ntnh": neurotransmitter/neurohormone genes
- "axon": axon guidance genes
- "fox": forkhead genes

Type: marker List API is for retrieving a list of gene marker candidates. Keyword search format: high,low/(region)/(offset),(limit).

Count of entriest search format: high,low/(region)/count.

"high" is highly expressed regions. "low" is low expressed regions. (region) means CNS region name.

Type: ntnh List API is for retrieving inferred connections among CNS regions by neurotransmitter/neurohormone (ntnh).

Keyword search format: high,low/(ligand-region)/(receptor-region)/(offset),(limit).

Count of entries search format: high,low/(ligand-region)/(receptor-region)/count.

"high": high state regions, "up": up state regions.

(ligand-region): Ligand CNS region. (receptor-region): Receptor CNS region.

Type: multistate List API is for retrieving a list of multi-state gene candidates. Keyword search format: high,up,low,down/(region)/(offset),(limit).

Count of entries search format: high,up,low,down/(region)/count.

"high": high state regions, "up": up state regions, "low": low state regions, "down": down state regions.

(region) means CNS region name.

output: If json is TRUE, you get response in JSON character. Dafault is matrix or list. If you chose "expression" type, you can get response in ExpressionSet. When you indicate "probeset" type, you can get annotations in list.

If the result has at least one hit entries, a matrix of entries is returned. If not, 404 Not found error code is returned. "offset,limit" can be used to retrieve a part of hit entries. If "offset,limit" is not given, all hits are returned.

If "count" was included in "query", the count of hit entries is returned in matrix, list, ExpressionSet or JSON format

Value

A matrix, ExpressionSet, list of annotation or character vector of Search API response in JSON.

Examples

```
my.search   <- getBrainStars(query = "receptor",   type = "search")
my.probeset <- getBrainStars(query = "1439627_at", type = "probeset")
my.tf       <- getBrainStars(query = "tf",         type = "genefamily")
my.eset     <- getBrainStars(query = "1439627_at", type = "expression")

my.probeset.json <- getBrainStars(
  query = "1439627_at",
  type = "probeset",
  json = TRUE
)
```

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getBrainStarsFigure   *Get plot of gene expression profile by one gene*

Description

This function get plot of gene expression profile from BrainStars

Usage

```
getBrainStarsFigure(query, fig.type, fig.format)
```

Arguments

query	id Affymetrix GeneChip ID (Mouse Genome 430 2.0 array)
fig.type	"exprmap", "exprgraph", "switchhist", "switchgraph", "switchmap", "multihist", "multigraph", "multimap"
fig.format	"png" or "pdf"

Value

A "raw" vector of figure image. The figure image file is saved current directory.

Examples

```
getBrainStarsFigure("1439627_at", "exprmap",    "png")
getBrainStarsFigure("1439627_at", "exprgraph",   "png")

getBrainStarsFigure("1439627_at", "switchhist",  "pdf")
getBrainStarsFigure("1439627_at", "switchgraph", "pdf")
getBrainStarsFigure("1439627_at", "switchmap",   "pdf")

getBrainStarsFigure("1439627_at", "multihist",  "png")
getBrainStarsFigure("1439627_at", "multigraph", "png")
getBrainStarsFigure("1439627_at", "multimap",    "png")
```

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