

Using the BrainStars package

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1 Overview of BrainStars

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 (Zeitgeber 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.

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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.

1.1 Gene Expression

A gene expression describes the expression level of gene on the array. This entry returns *ExpressionSet* object.

1.2 Figure

BrainStars can be export five type of figures following:

- `exprgraph` Barplot of gene expression level by brain regions
- `exprmap` Gene expression level on brain slice images by brain regions
- `switchgraph` ...
- `switchhist` ...

1.3 Marker

Marker genes were ones whose levels in a specific CNS region are higher (or lower) than in others. These marker genes were identified based on the multi-state gene analysis.

1.4 Search

You can search for entries with gene name, gene symbol, synonym, Entrez GeneID, and probe set ID. (2) Push "search" button for performing keyword search.

2 Getting Started using brainstars

Getting expression data from BrainStars is easy. `getBrainStarsExpression` interprets its input to determine how to get the data from BrainStars and then parse the data into *ExpressionSet* object. Usage is quite simple:

```
> library(brainstars)
```

This loads the brainstars library.

```
> my.eset <- getBrainStarsExpression("1439627_at")
```

Now, `my.eset` contains the R data structure (of class *ExpressionSet*) that represents the entry 1439627_at from BrainStars.

We can retrieve some kind of barplots from BrainStars.

```
> getBrainStarsFigure("1439627_at", "exprgraph")
```

Downloading...

Done.

```
> getBrainStarsFigure("1439627_at", "exprmap")
```

Downloading...

Done.

```
> getBrainStarsFigure("1439627_at", "switchgraph")
```

Downloading...

Done.

```
> getBrainStarsFigure("1439627_at", "switchhist")
```

Downloading...

Done.

You can find "id.type.png" files in current directory.

```
> recep.list <- getBrainStarsSearch("receptor/10,5")
```

Downloading...

Done.

```
> recep.count <- getBrainStarsSearch("receptor/count")
```

Downloading...

Done.

Markers,

```
> my.genes.json <- getBrainStarsMarker("high/LS/count")
```

Downloading...

<http://brainstars.org/marker/high/LS/count?content-type=application/json>

Done.

Keyword search,

```
> recep.list <- getBrainStarsSearch("receptor/10,5")
```

Downloading...

Done.

```
> recep.count <- getBrainStarsSearch("receptor/count")
```

Downloading...

Done.

3 Brainstars Data Structures

The brainstars data structures ...

4 Conclusion

The brainstars package provides a ...