

StarTrek:Application Examples

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2016-10-05

Introduction

In this vignette, we demonstrate the application of **StarTrek** as tool for pathways analysis integrating different data types . For basic use of the **StarTrek** package, please refer to the vignette Working with StarTrek package.

In many cases, **StarTrek** is used as tool to measure pathway activity and pathway cross-talk. However, **StarTrek** can also be combined with other tools (within or out of the scope of R and Bioconductor [Gentleman et al ., 2004, Carey et al., 2005]), to build exible analysis pipelines. In this vignette we demonstrate the cooperation between **StarTrek** and other tools with several examples. # Installation

To install use the code below.

```
source("https://bioconductor.org/biocLite.R")
biocLite("SpidermiR")
```

SpidermiRquery: Searching network

You can easily search GeneMania data using the **SpidermiRquery** function.

SpidermiRquery_species: Searching by species

The user can query the species supported by GeneMania, using the function **SpidermiRquery_species**:

References