

coexnet: An R package to build CO-EXpression NETworks from Microarray Data

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Abstract

Introduction

Workflow

1. `get.info`

All microarray raw data associated with the same study is stored in a CEL file, this file contains the GSM files, each one corresponding to each sample inside of the study, you can obtain each GSM file in an individual way, but, is rather obtain all the samples in the CEL file to avoid the work to join each GSM and additionally the way to analyse this kind of data is simultaneously (in future normalization process for example). Therefore, all the microarray chips are documented in the GEO Datasets database. Each one of them are identified with the letters GPL follows of a unique number. The information in the GPL file is related with the information of every probeset in the microarray chip, including the gene, function, type and another information to take advantage of the analysis of the results.

This function will create in your actual pathfile a folder with the GSE(unique number) name where are stored the GSM download files and otherwise the file GPL(unique number).soft file with the information of the microarray chip.

Take account: In some cases the information in the GSE and the GPL files are partial, take this in mind in the future analysis and is recommended not store the files in a temporal folder due to in many cases you will need the raw data to re-process the expression values using different methods.

2. `get.affy`

3. `gene.symbol`

4. `exprs.mat`

5. `cof.var`

6. `dif.exprs`

7. `find.threshold`

8. `create.net`