

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

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2017-02-07

Abstract

Introduction

Workflow

get.info

All microarray raw data is stored in a CEL file, this file contains the GSM files, each one corresponding to each sample beyond the study, you can obtain each GSM file in an individual way, but, it is rather to 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 is identified with the letters GPL followed by a unique number. The information in the GPL file is related with the information of every probe set in the microarray chip, including the gene, function, type and another information to take advantage of the analysis of the results.

Take account: is necessary, in the case of the GSE file, that all information

get.affy

gene.symbol

exprs.mat

cof.var

dif.exprs

find.threshold

create.net