
Instructions for use of CGGA: Co-expressed gene groups analysis (CGGA).

Instructions

If you want to test **CGGA** in the *DeRisi* data you need:

1. Download the windows Executable version of **CGGA** : CGGA.exe
2. Download the annotations file (-A): Derisi_annotations.txt
3. Download the *g-rank* file (-I): g_rank_over_expressed.txt (for over expressed genes).

Derisi Dataset Analysis

You may then want to try an analysis of the case: Derisi data, provided in the article:
So you have to put in the dos command line the following instruction:

```
C:\CGGA.exe -Ig_rank_over_expressed.txt -ADerisi_annotations.txt -Oexample.outfile.txt
```

Where

-A: Annotation file. (In our case obtained from SGOD database).

-I: Variability of genetic expression file (Here, using SAM output for over-expressed genes).

-O: Results file.

Microarray Analysis

Now you're ready to try with your microarray dataset. You'll need an annotation file, -A, obtained from any of the vast sources of annotation in bioinformatics, and a variability of expression file, -I ordered by decreasing expression variability (you can choose you're preferred variability measure: fold change, t-statistic, anova, f-score etc.).

In both cases you've to put your files preserving our format presented in the example files: -A: Derisi_annotations.txt and -I: g_rank_over_expressed.txt.