

Exercise 1

- Download the 12 Affymetrix arrays from the web site
- Load the arrays into R using `Read.Affy()` and construct the RMA expression indices
- For the sample affy data, fit the oneway ANOVA model to the RMA processed data. Adjust the p-values for FDR. Try googling some of the affy feature names for the significant genes.
- Use AmiGO to search the annotations for the top ten genes.

Exercise 2

- Download the Bottomly data and code
- Run the analysis using the `limma.analysis` file
- Run the additional analysis with the `exp.num` blocking variable
- Compare the results of the two analyses
- Use AmiGO to search the annotations for the top ten genes.