Computing for Statistical Genetics
Session 8

For this session, try the questions in any order - try out the Bioconductor tools most relevant to your field.

Splots

1) (Getting started with Bioconductor)

Ensure you have Bioconductor installed.

Install the `splots` package from Bioconductor, and load it into your current session, with `library("splots")`

2) The dataset `ribogreen.rda` [an R binary file; use `load("ribogreen.rda")` to load it into R] contains a list of twelve 96-well plates with ribogreen measurements of RNA concentration. Your experimental protocol needs the concentration to be at least 150ng/μl. Use the `splots` package to visualize the data and identify potential problems with the plates.

Hexbin

1) (Getting started with vignettes)

Open the hexbin vignette with `openVignette("hexbin").` (openVignette() is in the Biobase library, part of the default Bioconductor installation)

Run the example from page 2 of the vignette (it uses simulated data)

2) Using the `niehs` data from session 6, use `hexbin` to plot the mean log-expression levels for the treatment against mean log-expression for controls, at all 1907 genes. Compare this to a 'plain' plot of the same thing.

Annotation

1. Try out the `annotate()` and `biomaRt()` functions on your favorite genes. Some suggestions are

- ADH4 one of the alcohol dehydrogenase genes
- TP53 the famous p53 tumor suppressor gene
- PENK codes for an endogenous opoid peptide

2. Find GO categories for the blood clotting protein Factor V (F5). Use the GO terms to find other blood coagulation genes.

3. Find the Affymetrix gene transcripts for the mouse version of Factor V

4. Make GenomeGraphs plots for AGT (angiotensinogen). Look at the vignettes for more details that can be added to the plot.