Elements of R for Genetics & Bioinformatics
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 functions in the annotate and biomart packages 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 opioid 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.