# Stat 261, lab 5

## David Stenning

The data for this lab are in the file `MLLT3_small.vcf`. These are data on genomic variants in a gene called MLLT3. The file includes many meta-data lines that start with `##`, and then a header for the data columns that starts with `#`. The separator for the data columns is the tab character.

1. Use the appropriate `read_*` function to read these data into R, skipping the meta-data lines.

2. Use the `spec()` function to print a list of the column specifications. Copy this and make changes so that the `REF` and `ALT` variables are read in as factors.

3. Rename the first column `CHROM`. Hint: Beware the #-sign in the column name. This is what the text calls a "nonsyntactic" name. How do you refer to such a name?