Computing for Statistical Genetics
Session 6. Writing big loops

`http://faculty.washington.edu/kenrice/niehs.csv` contains data modified from a microarray experiment performed at the Jackson Labs. There are 6 pairs of mice, each containing a treatment and control mouse. The expression of 1907 genes is recorded for each mouse (actually log-expression is used); treatment mice are denoted T1, T2, … T6 and control mice are C1, C2, … C6.

After taking a *careful* look at the data, write code to compute the 1907 differences in log-expression (i.e. T1-C1, T2-C2 etc), and the p-values obtained from 1907 t-tests, each comparing to zero the mean difference in expression for a gene. Summarize what you find.

(For keen people: try writing the code twice, using `for()` loops and then using `apply()`. Compare the time R takes to complete the analysis under these approaches; the `system.time()` command will be helpful)