filtering exercise

Download `data2filter.txt` from the Schedule and import into R. It contains numeric values for 100 genes in 10 samples: 5 cases (case1 ... case5), and 5 controls. Type `library("tidyverse")` to load.

Q1: With `dplyr` functions `filter` or `select`, create a tibble containing only the data for genes with above-average values in `case1`. Which genes did it choose? Do the same thing for genes with above-average values in `ctrl1`. Did it find the same genes? (Send answers in Piazza.)

[Hint: to print more rows of a tibble, use **print(tib,n=20)** to print 20 rows.]

Q2: Create a new tibble with just the genes and the data from the control columns. Do this using a *range* of values, i.e., do not write out the names of all the controls.

Next, create a tibble with all data from all samples *except* case2, case3, and case4. You should only need to type two sample names to do this.

Send the commands you used (Q2), and the answer to Q1 above, in Piazza.