The idea is that log10 read counts are more or less normally distributed and logarithm could be the best way to describe dynamic range. Basically I calculate the mean of log 10 read counts of yeast\_01 and yeast\_1, which are y01 and y1, and then adjust log 10 read counts of human\_01 and human\_1 with (1-y01) and (2-y1) respectively.

So the final adjusted human counts are

10^(1-mean(log(Ycount))+log(Hcount)) for Human\_01

10^(2-mean(log(Ycount))+log(Hcount)) for Human\_1

The constants 2 and 1 can be changed but they must differ by 1.