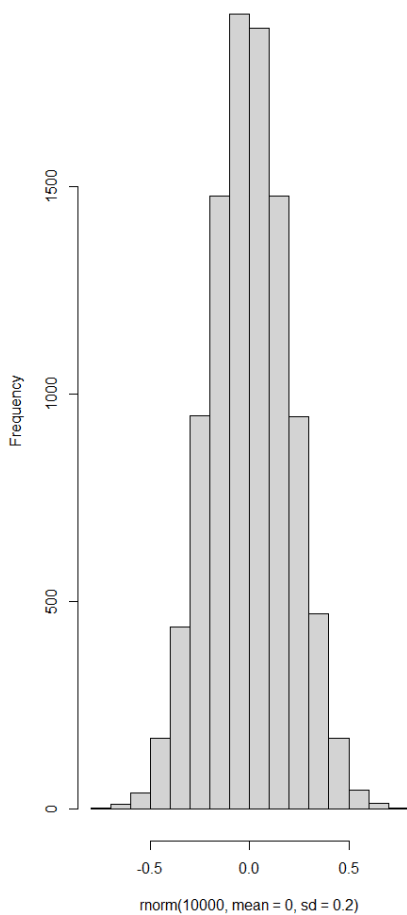


Q1:

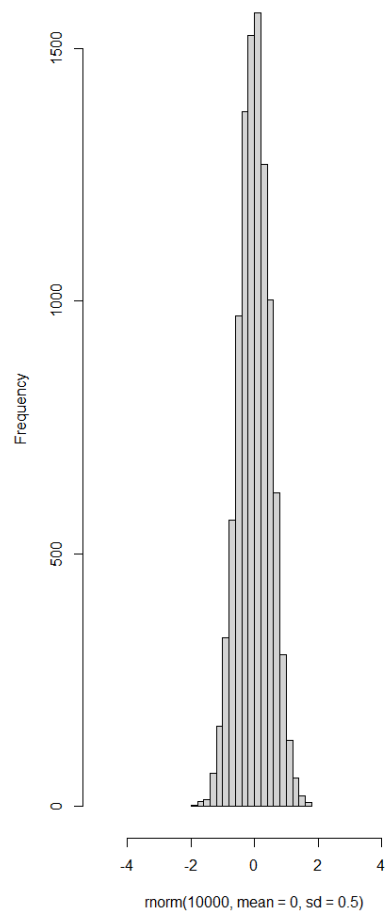
```
> su <- read.delim("su_raw_matrix.txt")
> mean(su$Liver_2.CEL)
[1] 241.8246
> sd(su$Liver_2.CEL)
[1] 1133.352
> colMeans(su)
      Brain_1.CEL      Brain_2.CEL Fetal_brain_1.CEL
      204.9763      315.0924      198.3439
Fetal_brain_2.CEL Fetal_liver_1.CEL Fetal_liver_2.CEL
      267.6551      209.8722      399.1482
      Liver_1.CEL      Liver_2.CEL
      160.8558      241.8246
> colSums(su)
      Brain_1.CEL      Brain_2.CEL Fetal_brain_1.CEL
      2588031      3978357      2504290
Fetal_brain_2.CEL Fetal_liver_1.CEL Fetal_liver_2.CEL
      3379413      2649846      5039645
      Liver_1.CEL      Liver_2.CEL
      2030966      3053278
> view(su)
> |
```

Q2:

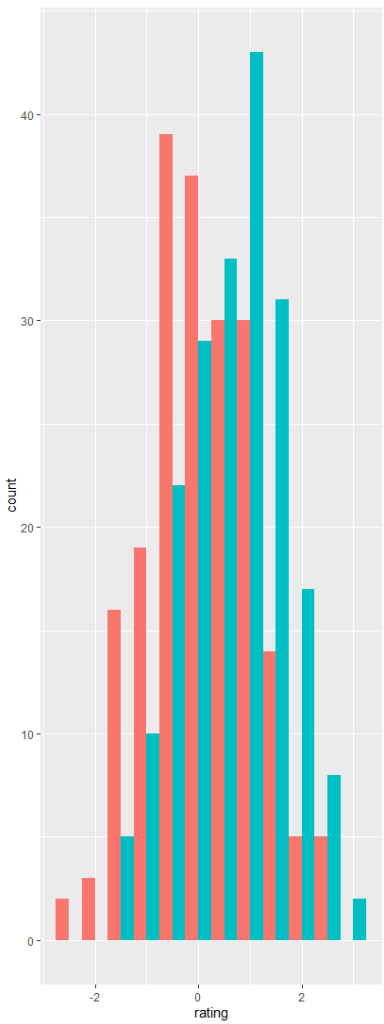
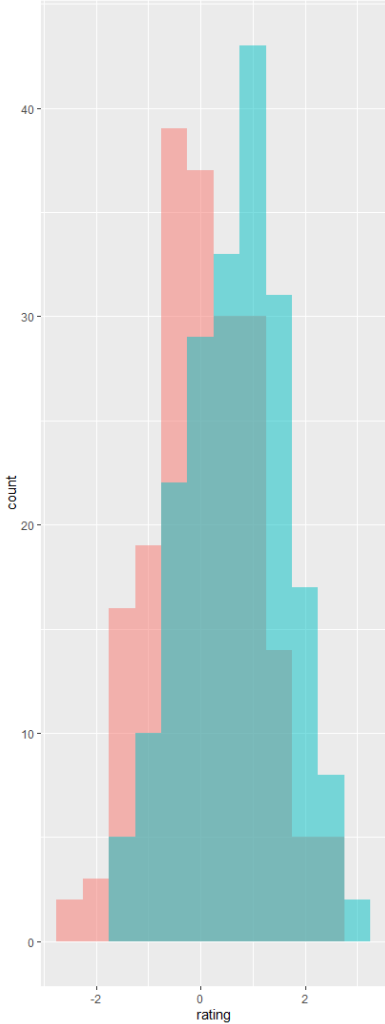
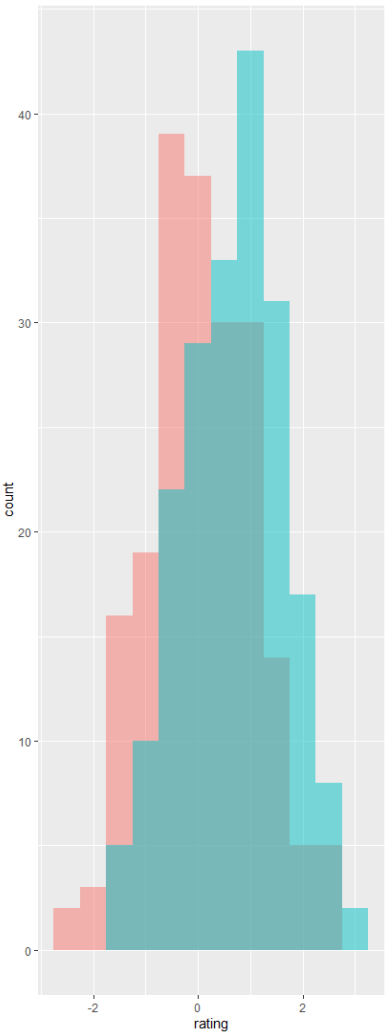
Histogram of $\text{rnorm}(10000, \text{mean} = 0, \text{sd} = 0.2)$



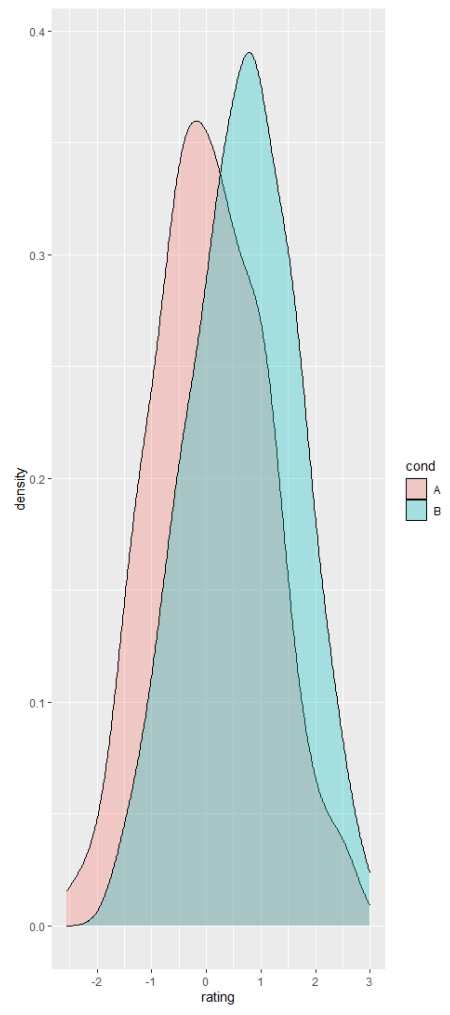
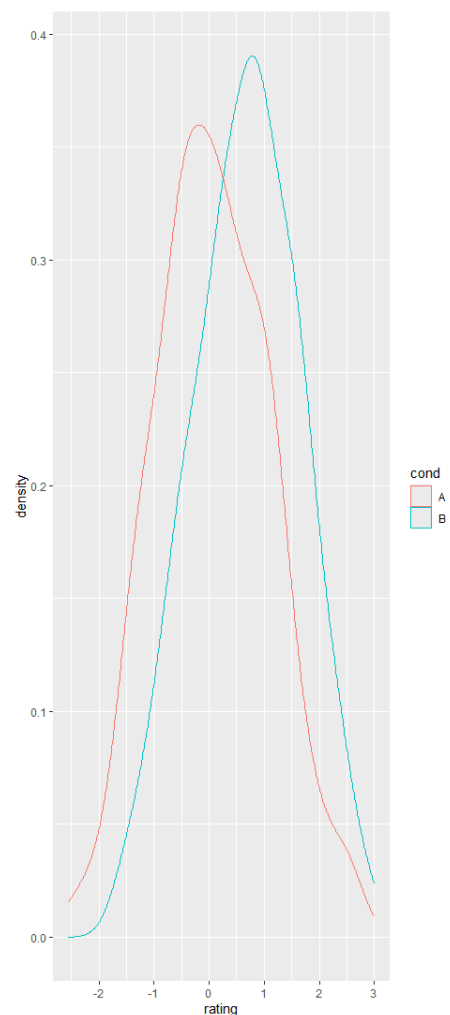
Histogram of $\text{rnorm}(10000, \text{mean} = 0, \text{sd} = 0.5)$



Q3: a, b, c



Q3: d, e



Q3: f -> b through e

