1) What would this code be doing? Golub is a gene-patient dataset. The dataset contains x patients and 3051 genes. Explain the code line per line. Explain why you need to perform the different steps. Explain what you expect in the output.

row\_mean = apply(golub, 1, mean, na.rm=TRUE)

golub\_meancentered = golub - row\_mean

dim(golub\_meancentered)

SD = apply(golub\_meancentered, 1, sd, na.rm=TRUE)

golub\_rescaled = golub\_meancentered/SD

dim(golub\_rescaled)

d.euclidian <- dist(golub\_rescaled, method="euclidian")

m <- as.matrix(dist(golub))

dim(m)

#(3051,3051)

kmeangolub100= kmeans(d.euclidian,100)

b) what will happen if you change the following parameter setting

kmeangolub10= kmeans(d.euclidian\_r,10)