# Import Data Set

yeast <- read.table("E:/Acadgild/Class 6/Assignments/yeast.txt", quote="\"", comment.char="")

View(yeast)

names(yeast) <- c("seq","mcg", "gvh", "alm", "mit", "erl", "pox", "vac", "nuc", "class")

head(yeast)

dim(yeast)

sapply(yeast, function(x) sum(is.na(yeast)))

**# a. Perform ANOVA test on the discriminant analysis scores of nuclear localization signals of both nuclear and non-nuclear proteins by class variables (Target).**

Sol=

# HO : scores across the class variables is same

x <- aov(nuc~class, data = yeast)

summary(x)

# since p value is less than 0.05, scores across the class variables is

# not same at 95% confidence level

**# b. Which class is significantly different from others?**

Sol=

TukeyHSD(x)

# ERL is significantly different from others