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1 yeast_data<-read.table(url="https://archive.ics.uci.edu/ml/machine-learning-databases/yeast/yeast.data",col.names = col-
2 names, as.is = TRUE, sep=";", as.factor=FALSE, as.numeric=TRUE, as.logical=TRUE, as.character=TRUE, as.data.frame=TRUE,
3 stringsAsFactors=FALSE)
4 summary(yeast_data)
5
6 ## Perform ANOVA test on the discriminant analysis scores of nuclear localization signals of both nuclear
7 and non-nuclear proteins by class variables (Target).
8 library(lattice)
9
10 yeast_test<-aov(yeast_data$nucc ~ yeast_data$class, yeast_data)
11 summary(yeast_test)
12 ##= There is no relationship between the discriminant analysis scores of nuclear localization signals of both nuclear
13 and non-nuclear proteins
14 #H0 = There is a relationship between the discriminant analysis scores of nuclear localization signals of both nuclear
15 and non-nuclear proteins
16 #H1 = There is a relationship between the discriminant analysis scores of nuclear localization signals of both nuclear
17 and non-nuclear proteins
18 #p<0.05
19 #Based on the pvalue we fail to reject the null hypothesis and conclude that there is no relationship between the disc-
20 riminal analysis scores of nuclear localization signals of both nuclear and non-nuclear proteins
21 #b. which class is significantly different from other?
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