

Session 12 – Non- Linear Models

Assignment - 1



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**Introduction**



This assignment will help you to understand the key concepts learnt in this session.

**Objective**



This assignment will test your skills on the Basics of Regression Analysis and Modeling using Non-linear Models.

**Prerequisites**



Not Applicable

**Associated Data Files**



Not Applicable

**Problem Statement**



**#1. Use the given link Data Set.**

yeast <- read.table("C:/Users/Mymaster/Desktop/Data Analytics/Assignments\_Questions/yeast.txt", quote="\"", comment.char="")

View(yeast)

yeastdata <- yeast

dim(yeastdata)

install.packages("reshape")

View(yeastdata)

library(reshape)

yeastdata <- rename (yeastdata, c(V1 = "Sequence Name",

V2 = "mcg",

V3 = "gvh",

V4 = "alm",

V5 = "mit",

V6 = "erl",

V7 = "pox",

V8 = "vac",

V9 = "nuc",

V10 = "Class Distribution"))

View(yeastdata)

**#Answer the below questions:**

**# a. Perform ANOVA test on the discriminant analysis scores of nuclear localization signals of both nuclear**

**#and non-nuclear proteins by class variables (Target).**

results <- aov (yeastdata$nuc ~ yeastdata$`Class Distribution`)

summary(results)

Since p value is significantly lesser than 0.05 we have strong evidence to reject null hypothesis and coclude that there is atleast one class significantly different than others.

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

plot(yeastdata$nuc ~ yeastdata$`Class Distribution`, col = heat.colors(10), xlab = "Class Distribution", ylab = "Score of discriminant analysis" , main = "Boxplot across classes")

**Expected Output**

Not Applicable

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