


```

study2_sd = round(apply(study2$result[,-1]/100 ,2, sd), 2)
study2_sd

study1_mean2 = round(apply(study1$result2[,-1] ,2, mean), 2)
study1_mean2
study2_mean2 = round(apply(study2$result2[,-1] ,2, mean), 2)
study2_mean2

study1_sd2 = round(apply(study1$result2[,-1] ,2, sd), 2)
study1_sd2
study2_sd2 = round(apply(study2$result2[,-1] ,2, sd), 2)
study2_sd2

##### Box Plots: Test Errors #####
par(mfrow=c(1,2))
res1 <- cbind(study1$result[,2], study1$result[,4], study1$result[,6],
study1$result[,8], study1$result[,10])
boxplot(res1, main="Colon cancer dataset: Boxplots of overall test error
rates", ylab="Test error rate", xlab="Classification technique",
col = c("red", "sienna", "palevioletred1", "royalblue2", "orange"), names =
c("penalizedLDA_L1", "penalizedLDA_FL", "SPLSDA", "SDA", "RF"))

res2 <- cbind(study2$result[,2], study2$result[,4], study2$result[,6],
study2$result[,8], study2$result[,10])
boxplot(res2, main="Leukemia cancer dataset: Boxplots of overall test error
rates", ylab="Test error rate", xlab="Classification technique",
col = c("red", "sienna", "palevioletred1", "royalblue2", "orange"), names =
c("penalizedLDA_L1", "penalizedLDA_FL", "SPLSDA", "SDA", "RF"))

```