```
##Logvalues
logchl5<-log10(ChlValues)
logtp5<- log10(TP)


##normality test Anderson-Darling & Lillie Test
library(nortest)
ad.test(ChlValues)
ad.test(logchl5)


lillie.test(logchl5)
lillie.test(ChlValues)


## Log Correlations:
cor.test(Pro1, logchl5, method = "spearman")
cor.test(Pro2, logchl5, method = "spearman")
cor.test(Pro3, logchl5, method = "spearman")
cor.test(Pro4, logchl5, method = "spearman")
cor.test(Pro5, logchl5, method = "spearman")
cor.test(Pro6, logchl5, method = "spearman")
cor.test(Pro7, logchl5, method = "spearman")
cor.test(Pro8, logchl5, method = "spearman")
cor.test(Pro9, logchl5, method = "spearman")
cor.test(Pro10, logchl5, method = "spearman")
cor.test(Pro11, logchl5, method = "spearman")
cor.test(Pro12, logchl5, method = "spearman")
cor.test(Pro13, logchl5, method = "spearman")
cor.test(Pro14, logchl5, method = "spearman")
cor.test(Pro15, logchl5, method = "spearman")
cor.test(Pro16, logchl5, method = "spearman")
cor.test(Pro17, logchl5, method = "spearman")
cor.test(Population, logchl5, method = "spearman")


##PCA
library(factoextra)
finaldata4 <- (Global_with_Land_Use_Population_V1.3.3)
PCA <- prcomp(finaldata4[,c(9, 22:39)], scale = TRUE)
fviz_pca_var(GLuke,repel = TRUE, addEllipse=FALSE) + theme_classic()


##PCA w/ names Same data previous PCA data has different titles
finaldata5 <- (Global_with_Names)
PCAnames <- prcomp(finaldata5[,c(9, 22:39)], scale = TRUE)
fviz_pca_var(PCAnamesLog,repel = TRUE, addEllipse=FALSE) + theme_classic()


## Random Forest
library(randomForest)
rfmodel<-randomForest(ChlValues ~ Pro1+Pro2+Pro3+Pro4+Pro5+Pro6+Pro7+Pro8+Pro9+Pro10+Pro11+Pro12+Pro13+Pro14+Pro15+Pro16+Pro17+Population, data =
Global_with_Land_Use_Population_V1.3.3, proximity=TRUE, ntree=500, mtry= 5)
rfmodel$importance


##BrokenStick Analysis
bstick <- get_eigenvalue(PCAnames)
head(bstick)
bstick
summary(bstick)
bstick$eigenvalue
bstick$variance.percent
bstick$cumulative.variance.percent
(bstick)
fviz_screeplot(PCAnames)
screeplot(PCAnames)
summary(screeplot(PCAnames))
```