

UNIVERSIDAD AUTÓNOMA DEL ESTADO DE MÉXICO FACULTAD DE CIENCIAS. LICENCIATURA EN BIOTECNOLOGÍA BIOINFORMÁTICA AVANZADA



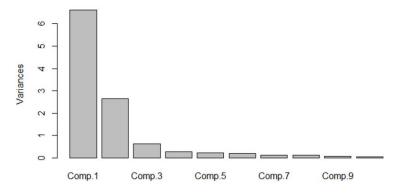
TAREA PCR

LÓPEZ CRUZ NANCY

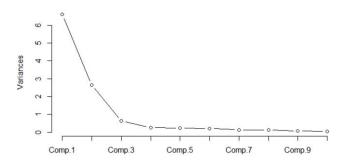
Comandos **Imágenes** > summary(mtcars) > pcaCars <- princomp(mtcars, cor = TRUE) > names(pcaCars) > summary(pcaCars) > plot(pcaCars) > plot(pcaCars, type = "l") carsHC <- hclust(dist(pcaCars\$scores),</pre> method ="ward.D2") > plot(carsHC) > carsClusters <- cutree(carsHC, k = 3) > plot(carsHC) > rect.hclust(carsHC, k=3, border="red") carsDf <- data.frame(pcaCars\$scores,</pre> "cluster" = factor(carsClusters)) > str(carsDf) > install.packages("ggplot2") > install.packages("ggrepel") > library(ggplot2) > library(ggrepel) > ggplot(carsDf,aes(x=Comp.1, y=Comp.2)) + geom text repel(aes(label = rownames(carsDf))) + theme_classic() + + geom_hline(yintercept = 0, color = "gray70") + +geom_vline(xintercept = 0, color = "gray70") + + $geom_point(aes(color = cluster), alpha = 0.55, size$ += 3) +xlab("PC1") + +ylab("PC2") ++xlim(-5, 6) ++ggtitle("PCA plot of Cars")

RESULTADOS

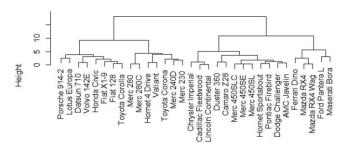
pcaCars



pcaCars

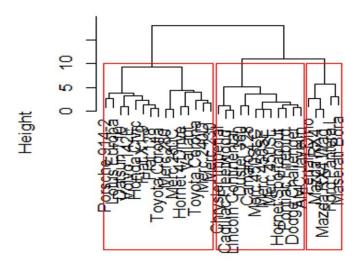


Cluster Dendrogram



dist(pcaCars\$scores) hclust (*, "ward.D2")

Cluster Dendrogram



dist(pcaCars\$scores) hclust (*, "ward.D2")

