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title: "Class 8 PCA" author: "Noah Sasse" date: "2/15/2022" output: pdf_document

url <- "https://tinyurl.com/UK-foods" x <- read.csv(url) dim(x) rownames(x) <- x[,1] x <- x[,-1] head(x)
dim(x)

barplot(as.matrix(x), beside=T, col=rainbow(nrow(x))) pairs(x, col=rainbow(10), pch=16)

pca <- prcomp( t(x) ) summary(pca) plot(pca[, 1], pca[, 2], xlab="PC1", ylab="PC2", xlim=c(-270,500))
text(pca[, 1], pca[, 2], colnames(x))

v <- round( pcasdev^2/sum(pcasdev^2) * 100 ) v

z <- summary(pca) z$importance

barplot(v, xlab="Principal Component", ylab="Percent Variation") par(mar=c(10, 3, 0.35, 0)) barplot(
pcarotation[, 1], las = 2)par(mar = c(10, 3, 0.35, 0))barplot(pcarotation[, 2], las=2 )

biplot(pca) url2 <- "https://tinyurl.com/expression-CSV" rna.data <- read.csv(url2, row.names=1)
head(rna.data) dim(rna.data) pca <- prcomp(t(rna.data), scale=TRUE) plot(pca[, 1], pca[, 2],
xlab="PC1", ylab="PC2") summary(pca) plot(pca, main="Quick scree plot") pca.var <- pca$sdev^2
pca.var.per <- round(pca.var/sum(pca.var)*100, 1) pca.var.per barplot(pca.var.per, main="Scree Plot",
names.arg = paste0("PC", 1:10), xlab="Principal Component", ylab="Percent Variation") colvec <-
colnames(rna.data) colvec[grepl("wt", colvec)] <- "red" colvec[grepl("ko", colvec)] <- "blue"

plot(pca[, 1], pca[, 2], col=colvec, pch=16, xlab=paste0("PC1 (", pca.var.per[1], "%)"), ylab=paste0("PC2
(", pca.var.per[2], "%)"))

text(pca[, 1], pca[, 2], labels = colnames(rna.data), pos=c(rep(4,5), rep(2,5)))

library(ggplot2)

df <- as.data.frame(pca$x)

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## Our first basic plot

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ggplot(df) + aes(PC1, PC2) + geom_point() dfsamples <- colnames(rna.data)dfcondition <- sub-
str(colnames(rna.data),1,2)

p <- ggplot(df) + aes(PC1, PC2, label=samples, col=condition) + geom_label(show.legend = FALSE) p
p + labs(title="PCA of RNASeq Data", subtitle = "PC1 clearly separates wild-type from knock-out samples",
x=paste0("PC1 (", pca.var.per[1], "%)"), y=paste0("PC2 (", pca.var.per[2], "%)"), caption="BIMM143
example data") + theme_bw()

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