**Cancer Biomarker Discovery with DESeq2**

Analysis on airway dataset (simulates cancer vs control)

1. Load **libraries**

library(DESeq2)

library(airway)

library(pheatmap)

library(EnhancedVolcano)

library(ggplot2)

1. **Load data**

data(airway)

airway$dex <- as.factor(airway$dex) # ensure 'dex' is a factor

1. **Create DESeq2 object**

dds <- DESeqDataSet(airway, design = ~ cell + dex)

dds <- DESeq(dds)

res <- results(dds)

1. Filter significant DEGs

sig <- res[which(res$padj < 0.05 & abs(res$log2FoldChange) > 1), ]

1. Save results

dir.create("results", showWarnings = FALSE)

write.csv(as.data.frame(sig), "results/significant\_DEGs.csv")

1. Volcano Plot

png("results/volcano\_plot.png", width = 800, height = 600)

EnhancedVolcano(res,

lab = rownames(res),

x = "log2FoldChange",

y = "pvalue",

title = "Volcano Plot of DE Genes")

dev.off()

1. PCA Plot

vsd <- vst(dds, blind = FALSE)

png("results/pca\_plot.png", width = 800, height = 600)

plotPCA(vsd, intgroup = "dex")

dev.off()

1. MA Plot

png("results/ma\_plot.png", width = 800, height = 600)

plotMA(res, ylim = c(-5, 5))

dev.off()

1. Heatmap of top 50 DEGs

topGenes <- head(order(res$padj), 50)

png("results/heatmap\_top50.png", width = 1000, height = 800)

pheatmap(assay(vsd)[topGenes, ], scale = "row")

dev.off()