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DESeq:
DESeq <- function(exprsFile,classFile,output){
 exprs <- as.matrix(read.csv(exprsFile, header=TRUE, sep = ",",row.names = 1,as.is=TRUE))
 storage.mode(exprs) = "integer"
 classcond <- as.data.frame(read.csv(classFile, header=TRUE, sep = ",",
                     \#row.names = 1,
                     as.is=TRUE))
 DESeq.cds = newCountDataSet(countData = exprs, conditions = classcond$Condition)
 DESeg.cds = estimateSizeFactors(DESeg.cds)
 DESeq.cds = estimateDispersions(DESeq.cds, sharingMode = "maximum", method = "pooled",
fitType = "local")
 DESeq.test = nbinomTest(DESeq.cds, "Tumor", "Normal")
 DESeg.pvalues = DESeg.test$pval
 DESeq.adjpvalues = p.adjust(DESeq.pvalues, method = "BH")
 tstout = cbind(rownames(exprs), DESeq.adjpvalues)
 write.table(tstout,output, sep = ",", col.names = F, row.names = F)
edaeR:
edgeR <- function(exprsFile,classFile,output){
 exprs <- as.matrix(read.csv(exprsFile, header=TRUE, sep = ",",row.names = 1,as.is=TRUE))
 classcond <- as.data.frame(read.csv(classFile, header=TRUE, sep = ",",
                  \#row.names = 1,
                  as.is=TRUE))
 edgeR.dgelist = DGEList(counts=exprs, group = classcond$Condition)
 edgeR.dgelist = calcNormFactors(edgeR.dgelist, method = "TMM")
 edgeR.dgelist = estimateCommonDisp(edgeR.dgelist)
 edgeR.dgelist = estimateTagwiseDisp(edgeR.dgelist, trend = "movingave")
 edgeR.test = exactTest(edgeR.dgelist)
 edgeR.pvalues = edgeR.test$table$PValue
 edgeR.adjpvalues = p.adjust(edgeR.pvalues, method = "BH")
 edgeR.logFC = edgeR.test$table$logFC
 tstout = cbind(rownames(exprs),edgeR.adjpvalues,edgeR.logFC)
 write.table(tstout, output, sep = ",", col.names = F, row.names = F)
voom:
voom <- function(exprsFile,classFile,output){</pre>
 library(edgeR)
 library(limma)
 exprs <- as.matrix(read.csv(exprsFile, header=TRUE, sep = ",",
                 row.names = 1,
                  as.is=TRUE))
 classcond <- as.data.frame(read.csv(classFile, header=TRUE, sep = ",",
                      \#row.names = 1,
                      as.is=TRUE))
 nf = calcNormFactors(exprs, method = "TMM")#TMM normalization method
 voom.data = voom(exprs, design = model.matrix(~classcond$Condition), lib.size =
colSums(exprs) * nf)
 voom.data$genes = rownames(exprs)
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voom.fitlimma = ImFit(voom.data, design = model.matrix(~classcond$Condition))
 voom.fitbayes = eBayes(voom.fitlimma)
 voom.pvalues = voom.fitbayes$p.value[, 2]
 voom.adjpvalues = p.adjust(voom.pvalues, method = "BH")
 tstout = cbind(rownames(exprs),voom.adjpvalues)
 write.table(tstout,paste(output,"voom.csv",sep=""), sep = ",", col.names = F, row.names = F)
VST:
vst <-function(exprs,classFile,output){
 exprs <- as.matrix(read.csv(exprs, header=TRUE, sep = ",",row.names = 1,as.is=TRUE))
 storage.mode(exprs) = "integer"
 classcond <- as.data.frame(read.csv(classFile, header=TRUE, sep = ",",
                     \#row.names = 1,
                     as.is=TRUE))
 DESeq.cds = newCountDataSet(countData = exprs, conditions = classcond$Condition)
 DESeg.cds = estimateSizeFactors(DESeg.cds)
 DESeq.cds = estimateDispersions(DESeq.cds, method = "blind", fitType = "local")
 DESeq.vst = getVarianceStabilizedData(DESeq.cds)
 DESeq.vst.fitlimma = ImFit(DESeq.vst, design = model.matrix(~classcond$Condition))
 DESeq.vst.fitbayes = eBayes(DESeq.vst.fitlimma)
 DESeq.vst.pvalues = DESeq.vst.fitbayes$p.value[, 2]
 DESeg.vst.adipvalues = p.adiust(DESeg.vst.pvalues, method = "BH")
 tstout = cbind(rownames(exprs), DESeq.vst.adjpvalues)
 write.table(tstout, output, sep = ",", col.names = F, row.names = F)
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