**GDCRNA tools DEG ALL**

if (!requireNamespace("BiocManager", quietly=TRUE))

install.packages("BiocManager")

BiocManager::install("GDCRNATools")

if (!requireNamespace("BiocManager", quietly=TRUE))

install.packages("BiocManager")

BiocManager::install("GDCRNATools", version = "devel")

library(GDCRNATools)

library(DT)

### load RNA counts data

data(rnaCounts)

####### Normalization of RNAseq data #######

rnaExpr <- gdcVoomNormalization(counts = rnaCounts, filter = FALSE)

####### Parse and filter RNAseq metadata #######

metaMatrix.RNA <- gdcParseMetadata(project.id = 'TCGA-CESC',

data.type = 'RNAseq',

write.meta = FALSE)

metaMatrix.RNA <- gdcFilterDuplicate(metaMatrix.RNA)

metaMatrix.RNA <- gdcFilterSampleType(metaMatrix.RNA)

datatable(as.data.frame(metaMatrix.RNA[1:5,]), extensions = 'Scroller',

options = list(scrollX = TRUE, deferRender = TRUE, scroller = TRUE))

DEGAll <- gdcDEAnalysis(counts = rnaCounts,

group = metaMatrix.RNA$sample\_type,

comparison = 'Early-late', # early – stage I vs late stage II-IV.

method = 'edgeR')

datatable(as.data.frame(DEGAll),

options = list(scrollX = TRUE, pageLength = 5))

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SURVIVAL ANALYSIS

library("survminer")

require("survival")

mrnacut\_point<-read.csv("survival mrna.csv")

row.names(mrnacut\_point)=mrnacut\_point$X

mrnacut\_point$X<-NULL

fit<- survfit(Surv(Time, vital\_status) ~ Age, data = Rcut\_point) # example of mrna cut poin and survival analysis.

res.cut <- surv\_cutpoint(mrnacut\_point, time = "OS", event = "vital\_status",

variables = c("KCNQ4", "TNFAIP6", "OSM", "PDE3A", "SEMA5A",

"ADAMTS12", "ACHE","SIK1", "NR5A2", "CDHR1", "SDK2",

"PRLR", "PLCL1", "TMEM255A", "IRF4", "PI15", "MME",

"TNC", "SEMA3A", "HGF", "IL11", "C5AR2","ALDH1A2",

"PDK4", "HLA.DOA", "PRUNE2", "MMP11", "AZGP1", "CSF3",

"FAM3D", "CDA", "ULBP1", "L1CAM", "HSPB6", "ACKR2",

"DKK1", "CD36"))

summary(res.cut)

class(res.cut)

dfres.cut<- as.data.frame(res.cut)

write.csv(res.cut, file="mrnacutpoint.csv")

palette = "npg"

plot(res.cut, "CD36", palette = "npg")

res.cat <- surv\_categorize(res.cut)

head(res.cat)

fit <- survfit(Surv(OS, vital\_status) ~CD36, data = res.cat)

ggsurvplot(fit, risk.table = TRUE, conf.int = TRUE)

ggsurvplot(fit, linetype = "strata",

conf.int = TRUE, pval = TRUE,

palette = "Dark2")