

Z-score heat map, yeast bp-bp

HBG

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R Markdown

This is an R Markdown document. Markdown is a simple formatting syntax for authoring HTML, PDF, and MS Word documents. For more details on using R Markdown see <http://rmarkdown.rstudio.com>.

When you click the **Knit** button a document will be generated that includes both content as well as the output of any embedded R code chunks within the document. You can embed an R code chunk like this:

```
library("microbenchmark")
library("matrixStats")

GOcategory.file <- read.csv("../Data/yeast.bp.term.csv", header=TRUE, stringsAsFactors=F)
go.cat <- GOcategory.file$GO.term

# dimension of the z-score
dim <- length(go.cat)

biogrid <- matrix(as.numeric(unlist(read.table("yeast.bp.matrix.csv", header=F, sep=","))), ncol=dim)
obs <- c(biogrid) #observed values

perm <- c()

for (i in 1:50) {
  name <- paste("ms02.yeast", "/", "bp-bp", "/", "ms02.", i, ".bp.matrix.csv", sep="")
  mat <- matrix(as.numeric(unlist(read.table(name, header=F, sep=","))), ncol=dim)
  perm <- rbind(perm, c(mat))
}

mean <- colMeans(perm)
std <- colSds(perm)

zscore <- round((obs-mean)/std, 3)
z <- t(matrix(zscore, ncol=dim))

write.table(z, file="yeast.bp.zscore.csv", sep=",", row.names=F, col.names=F)
```

Including Plots

You can also embed plots, for example:

```
library('gplots')

##
## Attaching package: 'gplots'

## The following object is masked from 'package:stats':
##
## lowess
```

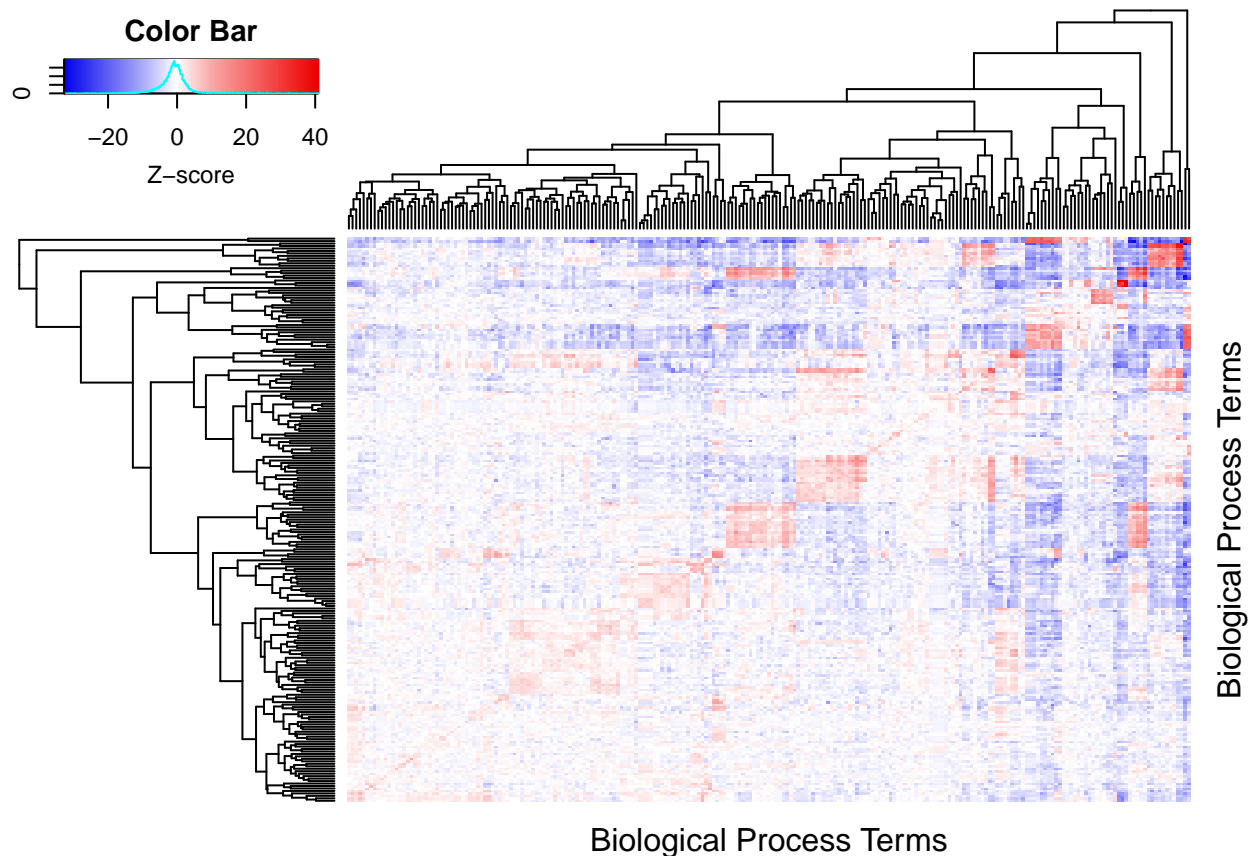
```

colnames(z) <- go.cat
rownames(z) <- go.cat

colors = c(seq(min(z),-10.1,length=100),seq(-9.9,9.9,length=100),seq(10.1,max(z),length=100))
my_palette <- colorRampPalette(c("blue2", "white", "red2"))(n = 299)

#png(filename = "yeast.bp.z.heatmap.png",width=6, height=6, res=1200, unit="in")
hm <- heatmap.2(z, col=my_palette, breaks=colors,
  trace='none', offsetRow = 0, offsetCol = 0,
  ylab="Biological Process Terms", xlab="Biological Process Terms",
  margins = c(2,2), key.title = "Color Bar", key.xlab="Z-score", key.ylab=NA,
  labCol = NA, labRow = NA,
  scale="none", dendrogram = "both", symbreaks=T, symm=F, symkey = F)

```



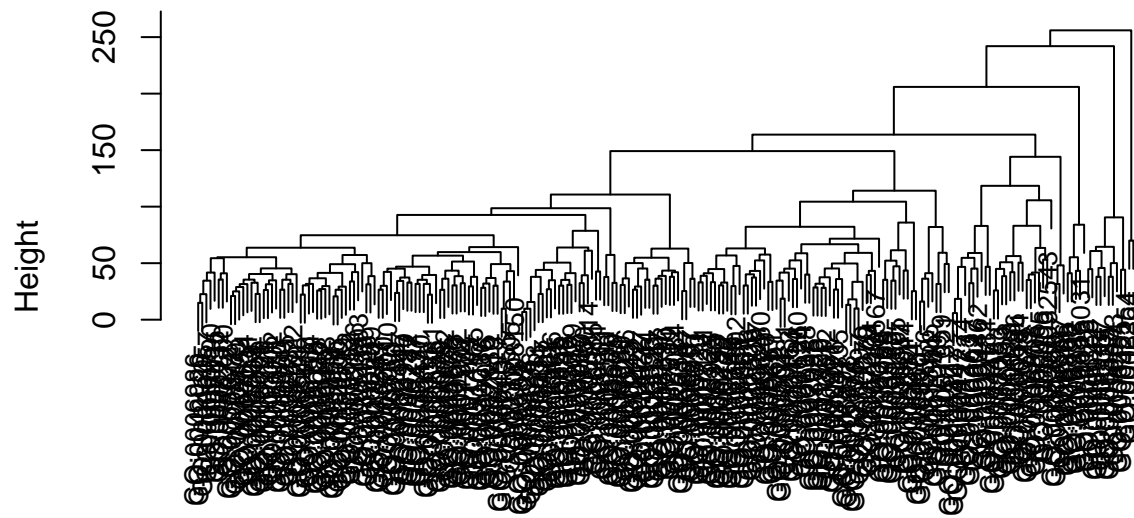
```

#dev.off()

hc <- as.hclust(hm$colDendrogram)
#pdf("bg163.bp.le20.z1k.hc.tree.pdf", width=40, height=5,paper='special')
plot(hc, xlab="GO Terms", main="Zscore of Biological Process, Hierarchical Clustering", cex=.8)

```

Zscore of Biological Process, Hierarchical Clustering



GO Terms
as.hclust.dendrogram (*, "NA")

#dev.off()