

GO terms and genes selection

Input:

Results of random forest algorithm and permutations implemented in GOexpress package – pVal object

Adjacency matrix and it's heatmap representation

Adjacency matrix was builded using mapping attribute from output object after random forest algorithm implementation

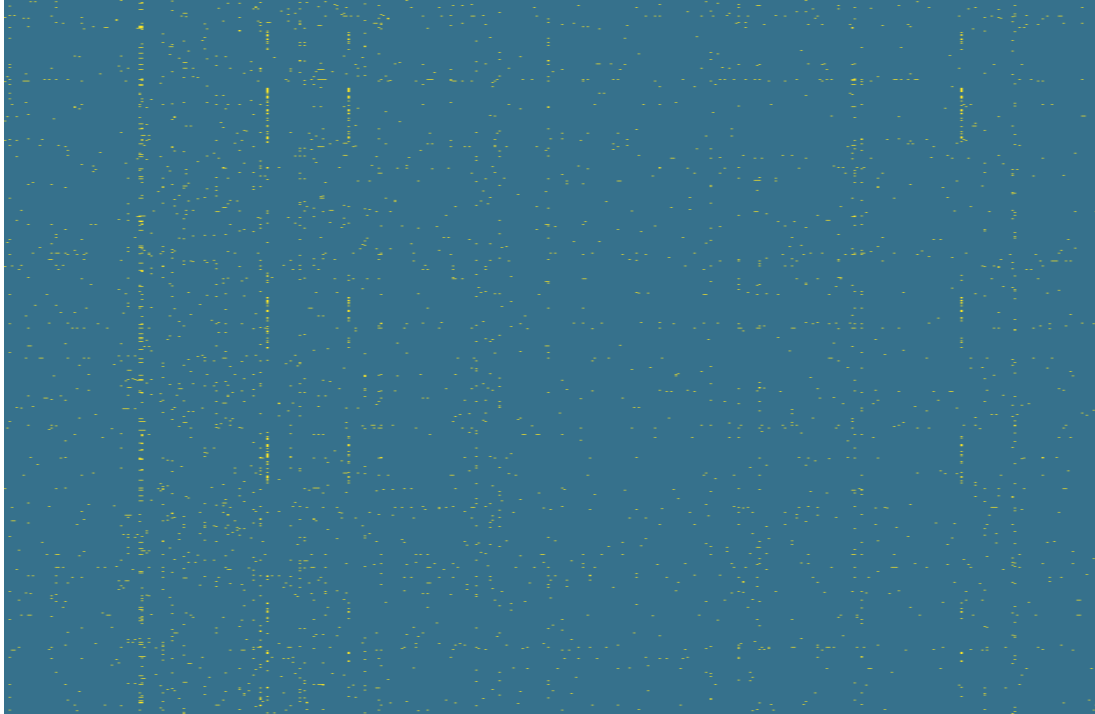
```
bp <- subset_scores(result = pVal,
                    namespace = "biological_process",
                    total = 10,
                    p.val=0.01)
m <- table(bp$mapping$gene_id, bp$mapping$go_id)
attributes(m)$class <- 'matrix'
```

Filtering 1000 most ranked genes linked mapped to 'Biological processes' namespace

```
m <- m[rownames(bp$genes)[1:1000], ]
```

Heatmap representation of matrix

```
m <- m[rownames(bp$genes)[1:1000], ]
superheat(m, legend = F)
```



Binary clustering of rows and columns

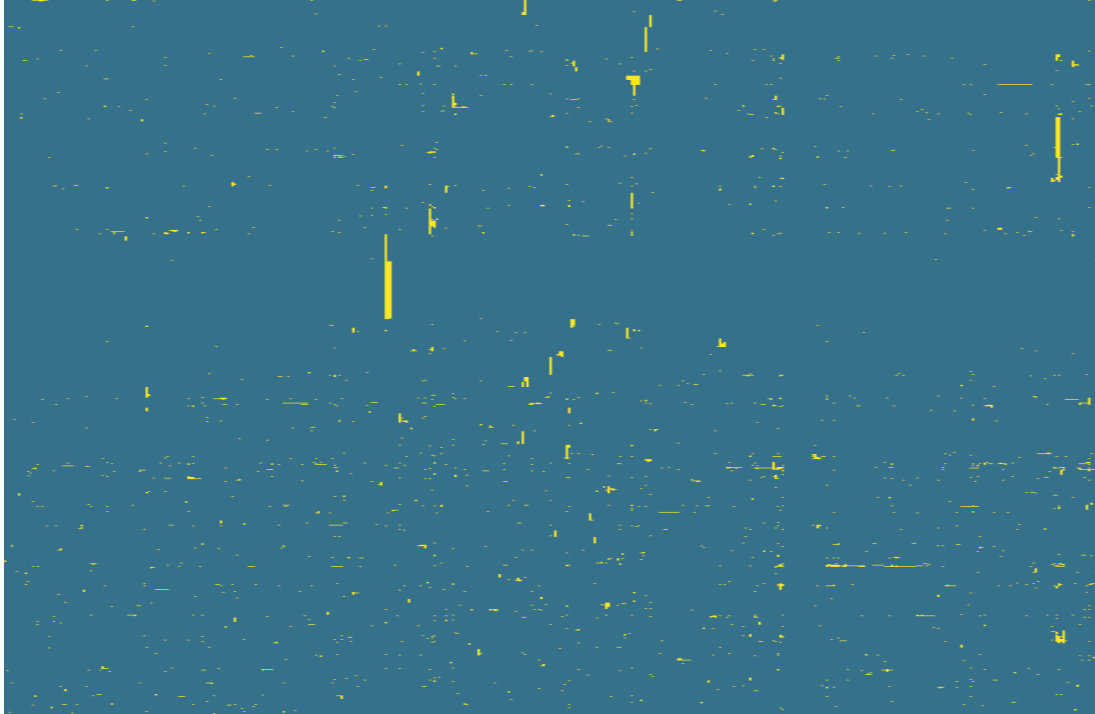
```
a <- hclust(dist(t(m), method = 'binary'))  
b <- hclust(dist(m, method = 'binary'))
```

Reordering of rows and columns of matrix

```
m <- m[b$order, a$order]
```

Heatmap representation of matrix after binary clustering and reordering

```
superheat(m, legend = F)
```



In the heatmap “hot spots” of enrichment shown in yellow. In the study we have chosen the „hot spot“ with maximal count of genes and maximal count of corresponding GO terms (bivariate maximum).

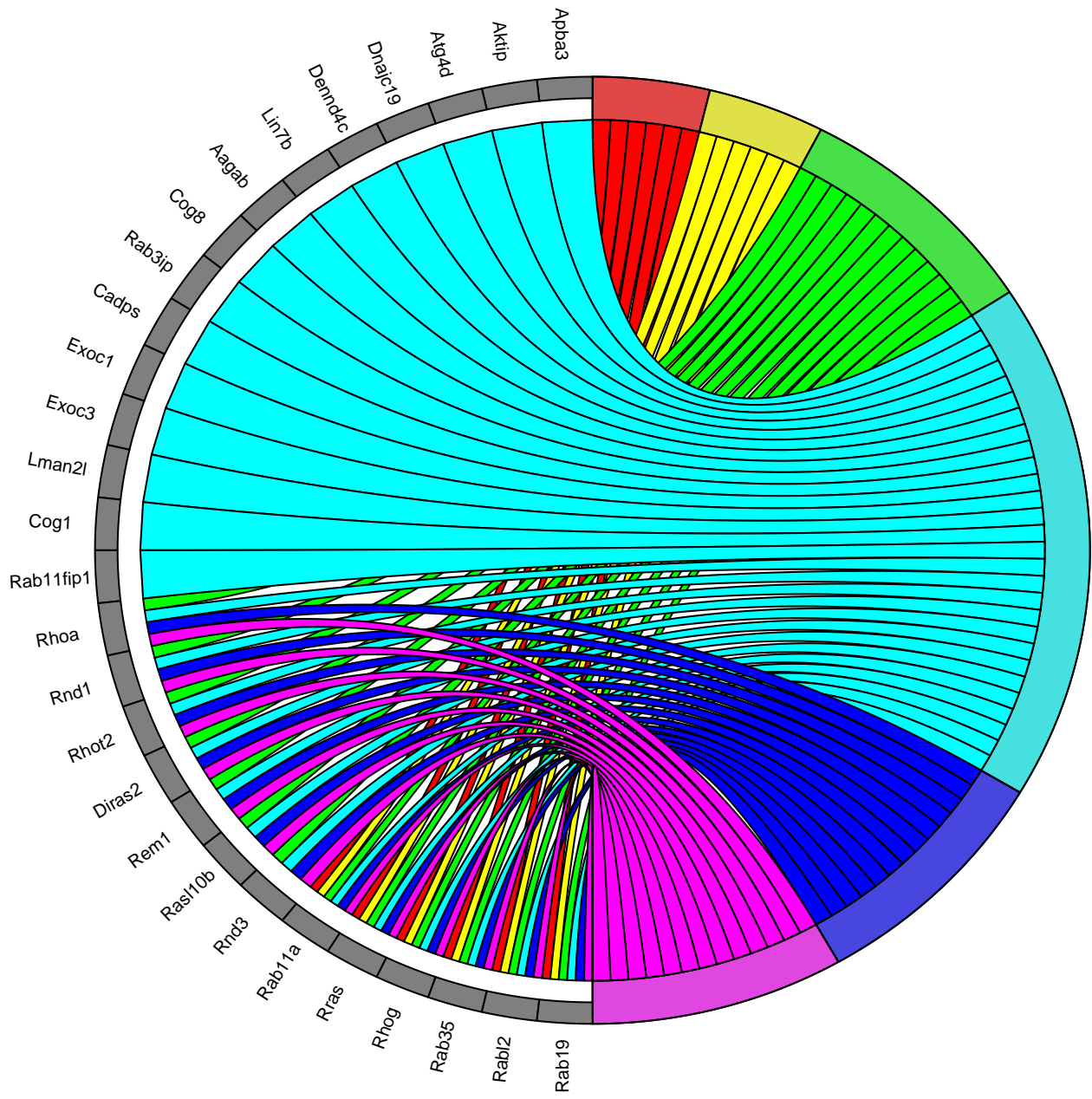
```
t <- m[867:894, 269:274]
```

```
superheat(t, legend = F,  
          bottom.label.text.size = 3,  
          bottom.label.text.angle = 90,  
          left.label.text.size = 3,  
          left.label.text.angle = 0,  
          bottom.label.size = 0.2,  
          left.label.size = 0.6,  
          padding = 0.2)
```

ENSMUSG00000029923						
ENSMUSG00000022621						
ENSMUSG00000029518						
ENSMUSG00000073982						
ENSMUSG00000038387						
ENSMUSG00000004771						
ENSMUSG00000017144						
ENSMUSG00000020684						
ENSMUSG00000000359						
ENSMUSG00000047842						
ENSMUSG00000025733						
ENSMUSG00000054855						
ENSMUSG00000007815						
ENSMUSG00000031488						
ENSMUSG00000018661						
ENSMUSG00000001143						
ENSMUSG000000034152						
ENSMUSG000000036435						
ENSMUSG000000054423						
ENSMUSG000000064181						
ENSMUSG000000031916						
ENSMUSG000000037257						
ENSMUSG000000003872						
ENSMUSG000000038024						
ENSMUSG000000027679						
ENSMUSG000000002820						
ENSMUSG000000031667						
ENSMUSG000000004931						
	GO:0006886	GO:0006913	GO:0007165	GO:0015031	GO:0006184	GO:0007264

Circular visualization of results

```
rownames(t) <- mapIds(org.Mm.eg.db, keys = rownames(t), column = "SYMBOL",
                     keytype = "ENSEMBL", multiVals = 'first')
GOChord(t, gene.size = 4, nlfc = 0)+
  theme(legend.text = element_text(size = 13),
        legend.title = element_text(size = 15, face = 'bold'))
```



GO Terms

■ GO:0006886	■ GO:0006913	■ GO:0007165	■ GO:0015031
■ GO:0006184	■ GO:0007264		