Reactome Pathway Analysis

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Contents

1 Introduction

This package is designed for reactome pathway-based analysis. Reactome is an open-source, open access, manually curated and peer-reviewed pathway database.

2 Pathway Enrichment Analysis

Enrichment analysis is a widely used approach to identify biological themes. Here, we implement hypergeometric model to assess whether the number of selected genes associated with reactome pathway is larger than expected. The p values were calculated based the hypergeometric model [1],

```
require(DOSE)
data(geneList)
de <- names(geneList)[abs(geneList) > 1]
head(de)
```

```
## [1] "4312"  "8318"  "10874" "55143" "55388" "991"
```

```
require(ReactomePA)
x <- enrichPathway(gene = de, pvalueCutoff = 0.05,
    readable = T)
```

```
## Loading required package:  org.Hs.eg.db
```

```
head(summary(x))
```

```
##              ID                                   Description GeneRatio  BgRatio
## 1474244 1474244          Extracellular matrix organization    59/584 266/6960
## 69205     69205                G1/S-Specific Transcription    12/584  15/6960
## 69278     69278                        Cell Cycle, Mitotic    83/584 489/6960
## 1640170 1640170                                 Cell Cycle    90/584 554/6960
## 1442490 1442490                       Collagen degradation    22/584  60/6960
## 113510   113510 E2F mediated regulation of DNA replication    16/584  34/6960
##            pvalue p.adjust   qvalue
## 1474244 1.32e-12 3.46e-10 2.77e-10
## 69205   3.94e-11 5.18e-09 4.15e-09
## 69278   1.25e-10 1.10e-08 8.80e-09
## 1640170 2.08e-10 1.37e-08 1.09e-08
## 1442490 9.66e-10 5.08e-08 4.07e-08
## 113510  2.61e-09 1.14e-07 9.15e-08
##
## 1474244
## 69205
## 69278                                                CDC45/CDCA8/MCM10/CDC20/FOXM1/KIF
## 1640170 CDC45/CDCA8/MCM10/CDC20/FOXM1/KIF23/CENPE/MYBL2/CCNB2/NDC80/NCAPH/RRM2/U
## 1442490
## 113510
##         Count
## 1474244    59
## 69205      12
## 69278      83
## 1640170    90
## 1442490    22
## 113510     16
```

2.1 Visualize enrichment result

We also implement a bar plot and category-gene-network for visualization. It is very common to visualize the enrichment result in bar or pie chart. We believe the pie chart is misleading and only provide bar chart.

```
barplot(x, showCategory = 8)
```

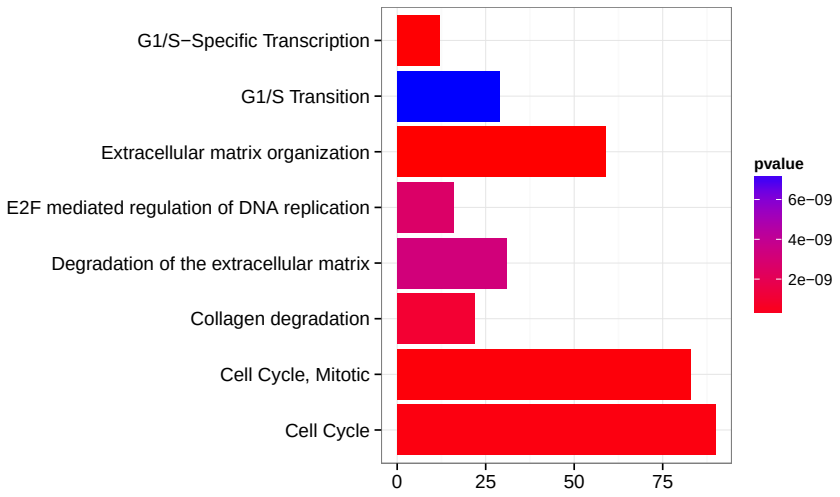

Figure 1: barplot of Reactome Pathway enrichment result.

In order to consider the potentially biological complexities in which a gene may belong to multiple annotation categories, we developed `cnetplot` function to extract the complex association between genes and diseases.

```
cnetplot(x, categorySize = "pvalue", foldChange = geneList)
```

2.2 Comparing enriched reactome pathways among gene clusters with clusterProfiler

We have developed an R package *clusterProfiler* [2] for comparing biological themes among gene clusters. *ReactomePA* works fine with *clusterProfiler* and can compare biological themes at reactome pathway perspective.

```
require(clusterProfiler)
data(gcSample)
res <- compareCluster(gcSample, fun = "enrichPathway")
plot(res)
```

3 Gene Set Enrichment Analysis

A common approach in analyzing gene expression profiles was identifying differential expressed genes that are deemed interesting. The `enrichPathway` function

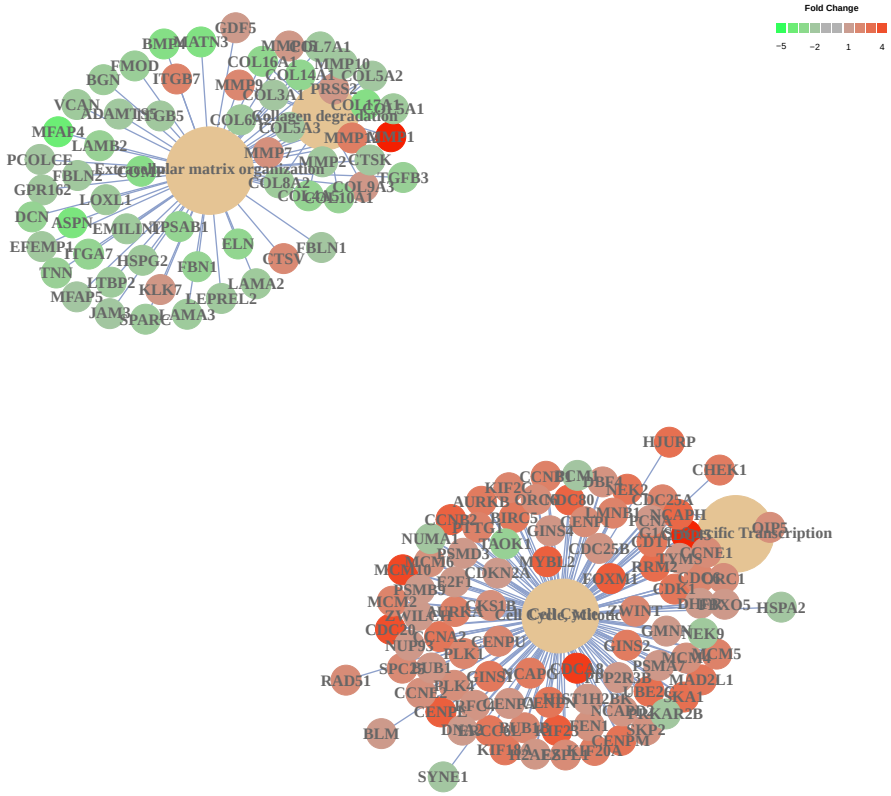

Figure 2: cnetplot of Reactome Pathway enrichment result.

we demonstrated previously were based on these differential expressed genes. This approach will find genes where the difference is large, but it will not detect a situation where the difference is small, but evidenced in coordinated way in a set of related genes. Gene Set Enrichment Analysis (GSEA) directly addressed this limitation. All genes can be used in GSEA; GSEA aggregates the per gene statistics across genes within a gene set, therefore making it possible to detect situations where all genes in a predefined set change in a small but coordinated way.

```
y <- gseAnalyzer(geneList, nPerm = 100, minGSSize = 120,
    pvalueCutoff = 0.05, pAdjustMethod = "BH", verbose = FALSE)
res <- summary(y)
head(res)
```

```
##              ID                                 Description setSize
## 556833   556833     Metabolism of lipids and lipoproteins     424
## 162906   162906                             HIV Infection     191
## 1280218 1280218                  Adaptive Immune System     520
```

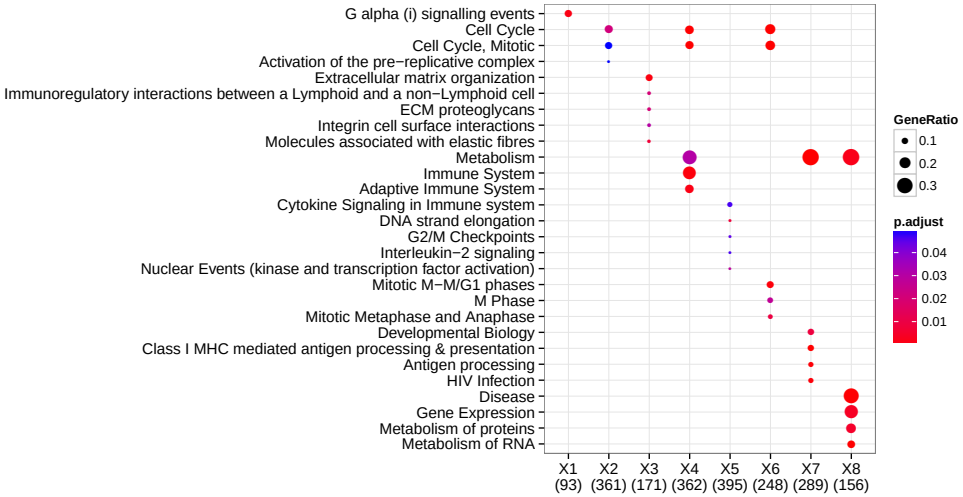

Figure 3: ReactomePA with clusterProfiler.

```
## 168256   168256                                Immune System     951
## 1280215 1280215       Cytokine Signaling in Immune system     254
## 71291     71291 Metabolism of amino acids and derivatives     168
##         enrichmentScore pvalues p.adjust qvalues
## 556833           -0.290       0        0       0
## 162906            0.466       0        0       0
## 1280218           0.356       0        0       0
## 168256            0.316       0        0       0
## 1280215           0.347       0        0       0
## 71291             0.329       0        0       0
```

3.1 Visualize GSEA result

```
topID <- res[1, 1]
topID
```

```
## [1] "556833"
```

```
plot(y, geneSetID = topID)
```

4 Pathway Visualization

In *ReactomePA*, we also implemented `viewPathway` to visualized the pathway.

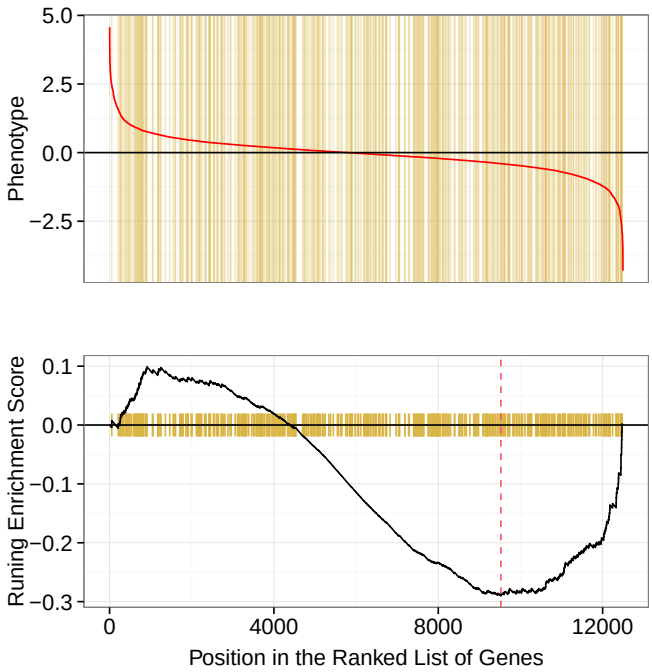

Figure 4: plotting gsea result

```
viewPathway("E2F mediated regulation of DNA replication",
    readable = TRUE, foldChange = geneList)

## Loading required package:  graphite
```

5 Session Information

The version number of R and packages loaded for generating the vignette were:

- R version 3.1.0 (2014-04-10), `x86_64-apple-darwin13.1.0`
- Locale: `C`
- Base packages: base, datasets, grDevices, graphics, methods, parallel, stats, utils
- Other packages: AnnotationDbi 1.26.0, Biobase 2.24.0, BiocGenerics 0.10.0, DBI 0.2-7, DOSE 2.2.0, GenomeInfoDb 1.0.2, RSQLite 0.11.4, ReactomePA 1.8.0, clusterProfiler 1.13.0, ggplot2 0.9.3.1, graph 1.42.0, graphite 1.10.0, knitr 1.5, org.Hs.eg.db 2.14.0
- Loaded via a namespace (and not attached): DO.db 2.8.0, GO.db 2.14.0, GOSemSim 1.22.0, IRanges 1.22.4, KEGG.db 2.14.0, MASS 7.3-32, Rcpp 0.11.1, codetools 0.2-8, colorspace 1.2-4, digest 0.6.4, evaluate 0.5.3, formatR 0.10, grid 3.1.0, gtable 0.1.2, highr 0.3,

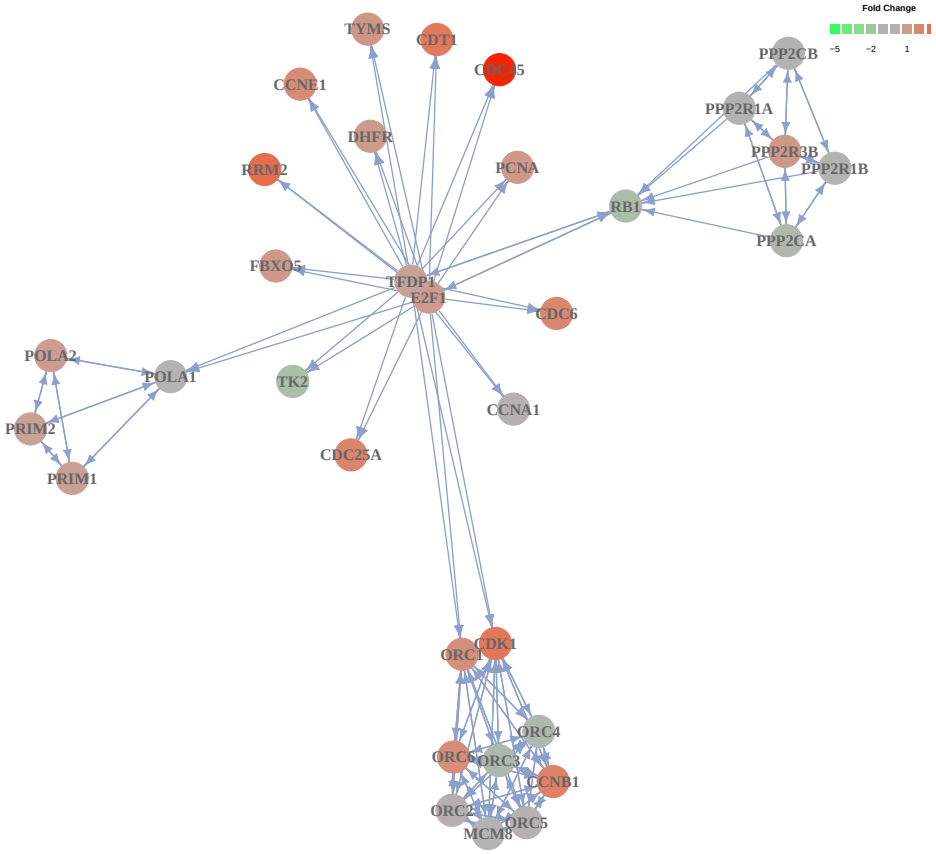

Figure 5: Reactome Pathway visualization.

igraph 0.7.1, labeling 0.2, munsell 0.4.2, plyr 1.8.1, proto 0.3-10, qvalue 1.38.0, reactome.db 1.48.0, reshape2 1.4, scales 0.2.4, stats4 3.1.0, stringr 0.6.2, tcltk 3.1.0, tools 3.1.0

References

[1] Elizabeth I Boyle, Shuai Weng, Jeremy Gollub, Heng Jin, David Botstein, J Michael Cherry, and Gavin Sherlock. GO::TermFinder–open source software for accessing gene ontology information and finding significantly enriched gene ontology terms associated with a list of genes. *Bioinformatics (Oxford, England)*, 20(18):3710–3715, December 2004. PMID: 15297299.

[2] Guangchuang Yu, Li-Gen Wang, Yanyan Han, and Qing-Yu He. clusterProfiler: an r package for comparing biological themes among gene clusters. *OMICS: A Journal of Integrative Biology*, 16(5):284–287, May 2012.