GO analysis

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Contents

1. summary

See GO enrichment analysis in Section `3.1` and `3.2`.

2. Materials and Methods

Genes: Two lists of genes, up-regulated (n=345), down-regulated (n=898).

Organism: C. elegans

Annotation: Using a Bioconductor package, `org.Ce.eg.db` (version: `3.8.2`)

Tools: clusterProfiler (R package, `v3.12.0`)

GO analysis

GO enrichment analysis was performed with the R package clusterProfiler, with a Bonferroni correction and an adjusted p value of 0.01 and qvalue of 0.05 (Yu et al., 2012).

Reference

1. Yu G, Wang L-G, Han Y, He Q-Y. clusterProfiler: an R package for comparing biological themes among gene clusters. OMICS. 2012;16:284–7. https://doi.org/10.1089/omi.2011.0118.

3. Results

```
## 'select()' returned 1:many mapping between keys and columns


## Warning in bitr(df_up$`Wormbase Identifier`, "WORMBASE", "ENTREZID",
## org.Ce.eg.db, : 2.9% of input gene IDs are fail to map...


## 'select()' returned 1:many mapping between keys and columns


## Warning in bitr(df_down$`Wormbase Identifier`, "WORMBASE", "ENTREZID",
## org.Ce.eg.db, : 1% of input gene IDs are fail to map...
```

3.1 Down-regulated genes (n=898)

- GO classification

Gene classification based on GO distribution at `level=3`.

```
## Loading required package: DOSE
```
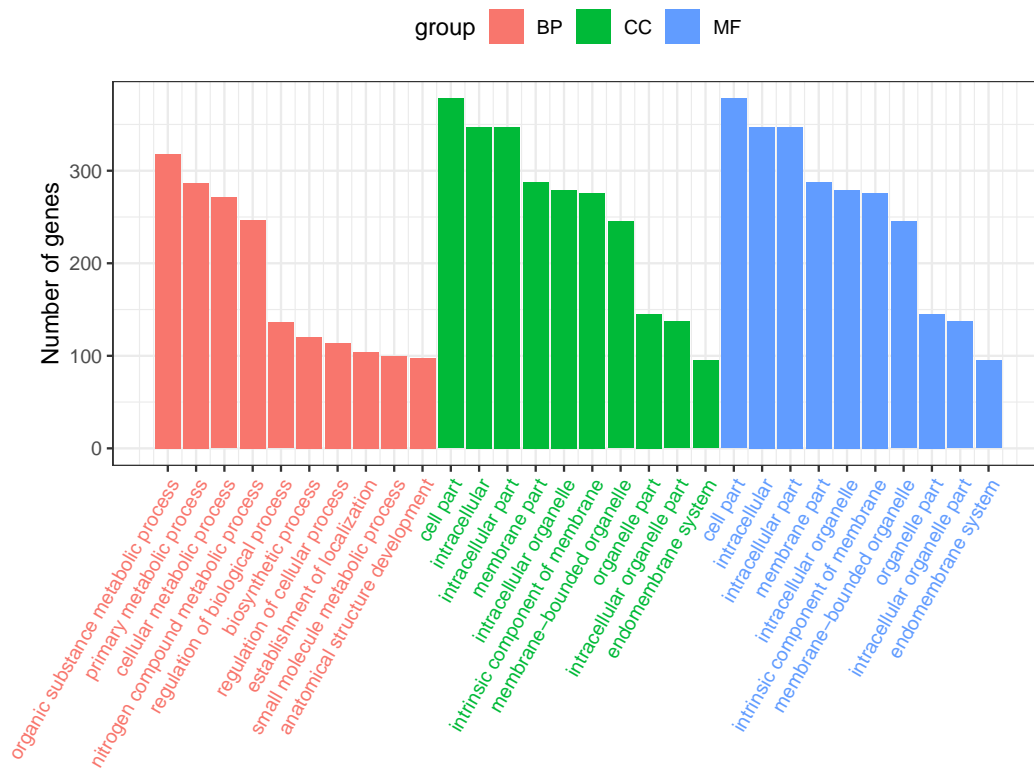
```
## DOSE v3.10.2  For help: https://guangchuangyu.github.io/DOSE
##
## If you use DOSE in published research, please cite:
## Guangchuang Yu, Li-Gen Wang, Guang-Rong Yan, Qing-Yu He. DOSE: an R/Bioconductor package for Disease
```
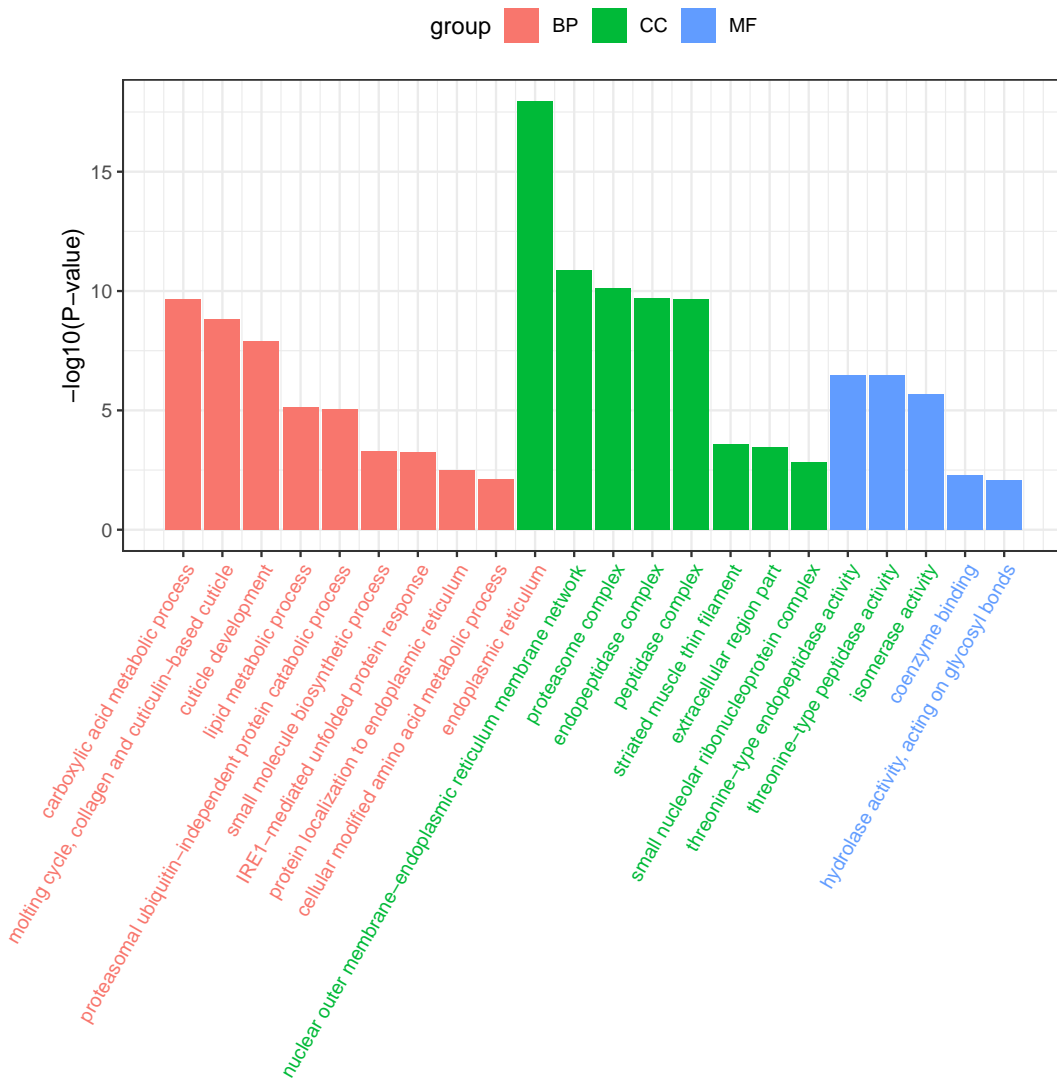

- GO enrichment analysis

Create the barplot like Figure 5D of Merkwirth et al., 2016 Cell.

GO Enrichment

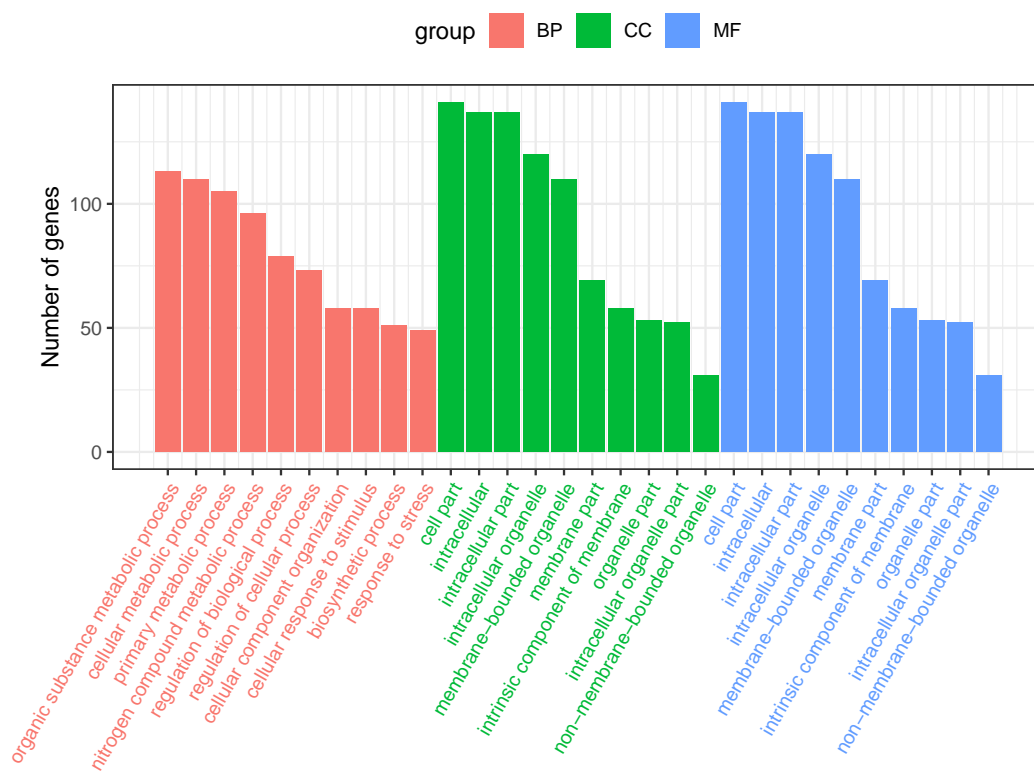Saving above plots to to file: `results/go_enrich.down.pdf`

```
## pdf
##   2
```

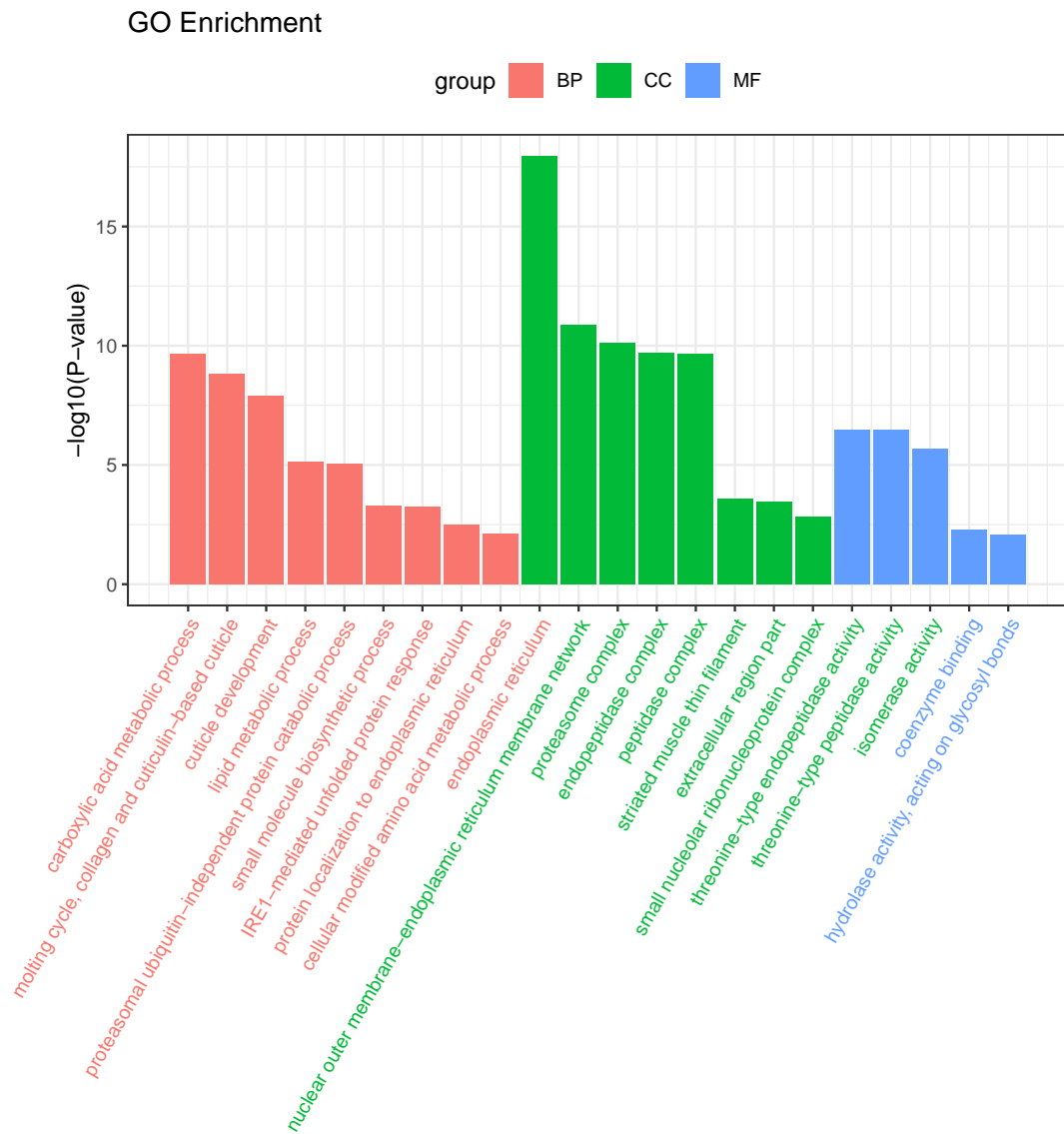Save the original enrichment results to file: `results/go_enrich.down.xlsx`

3.2 Up-regulated genes (n=345)
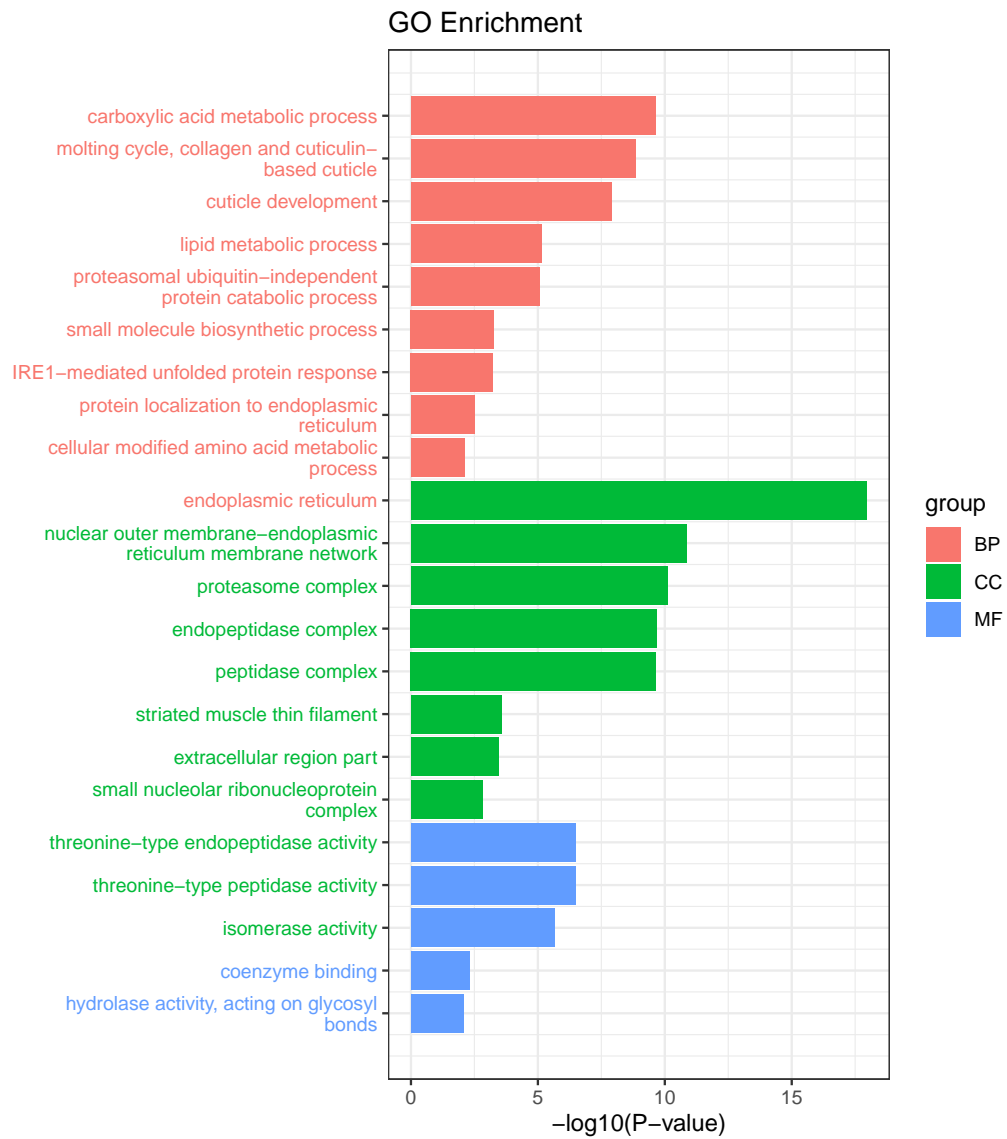
- GO classification

GO classification

- GO enrichment analysis

GO Enrichment

Create the barplot like Figure 5D of Merkwirth et al., 2016 Cell.

GO Enrichment

Saving above plots to to file: `results/go_enrich.up.pdf`

```
## pdf
##   2
```

Save the original enrichment results to file: `results/go_enrich.up.xlsx`