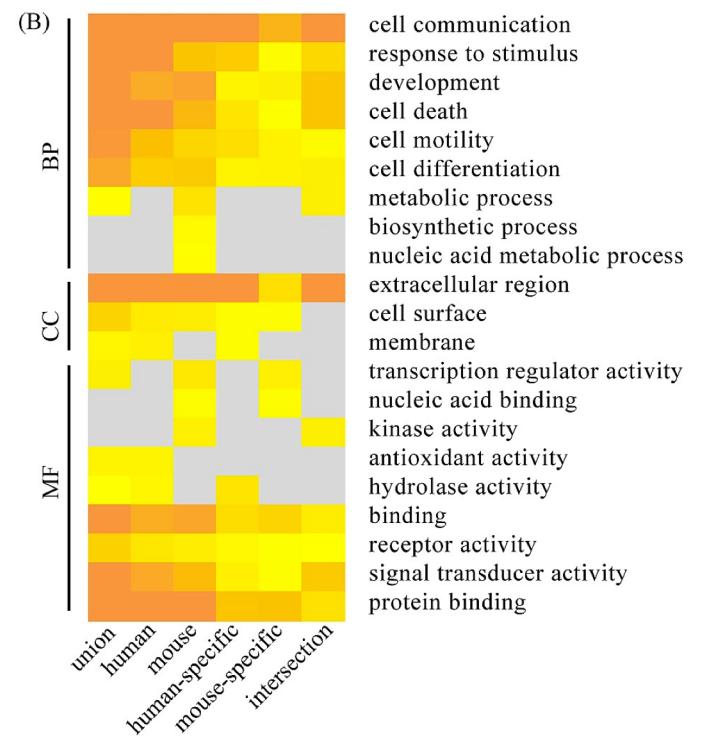
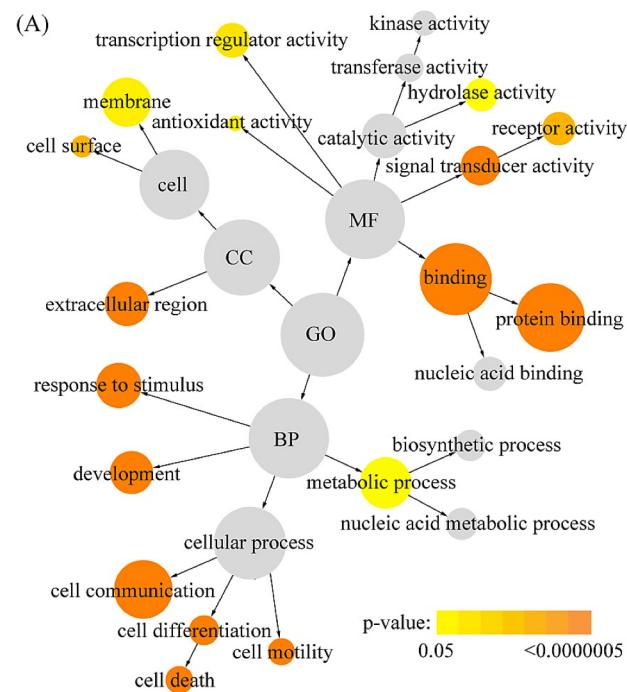
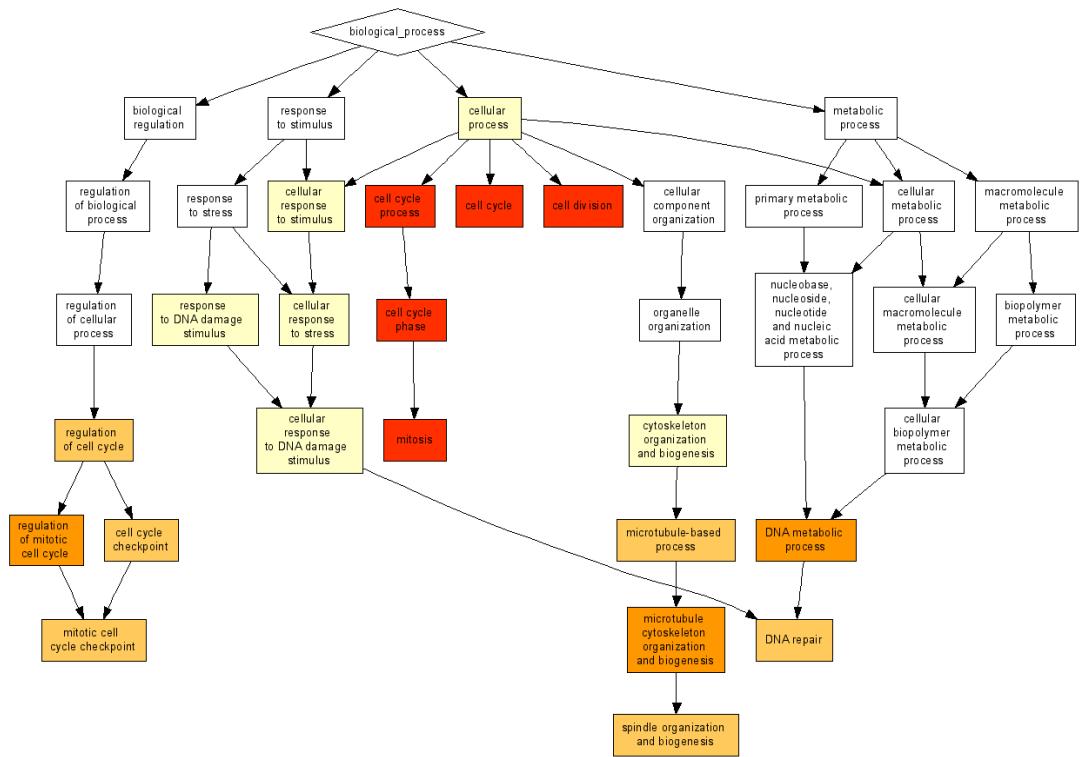
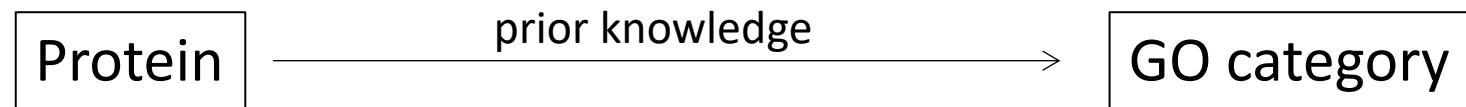


# GO enrichment analysis

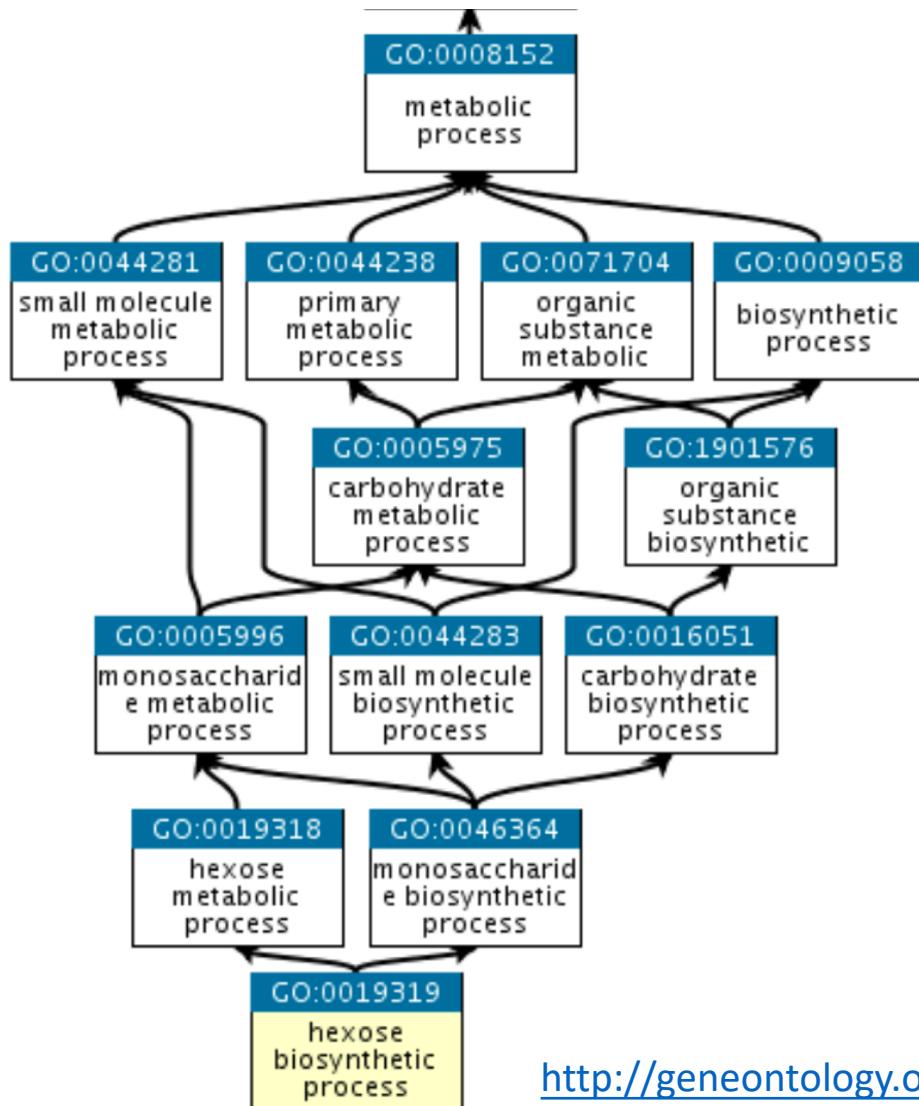


# What is GO?

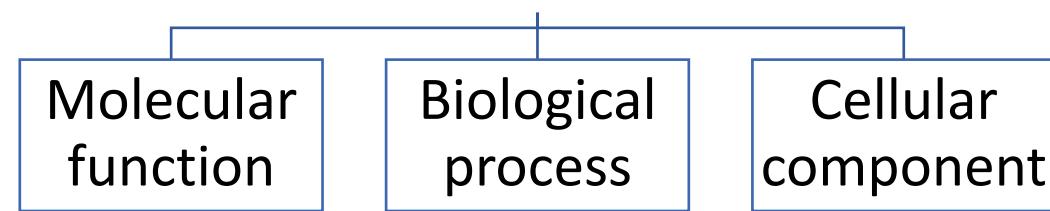
- The Gene Ontology (GO) describes our knowledge of the biological domain.



# Gene ontology structure



Three independent root ontology term



GO is loosely hierarchical, with 'child' terms being more specialized than their 'parent' terms

# GO term

- Cytochrome c
  - Molecular function - oxidoreductase activity
  - Biological process - oxidative phosphorylation
  - Cellular component - mitochondrial matrix
- Example

locusName	GO term
Prupe.1G001400	GO:0016747,GO:0008610,GO:0016020,GO:0006633
Prupe.1G006600	GO:0046983
Prupe.1G012200	
Prupe.1G012900	
Prupe.1G031300	GO:0003676
Prupe.1G031800	GO:0006468,GO:0005524,GO:0004672
Prupe.1G033800	GO:0006468,GO:0005524,GO:0004672
Prupe.1G034000	GO:0006468,GO:0005524,GO:0004672
Prupe.1G035500	GO:0055114,GO:0016491

# GO enrichment

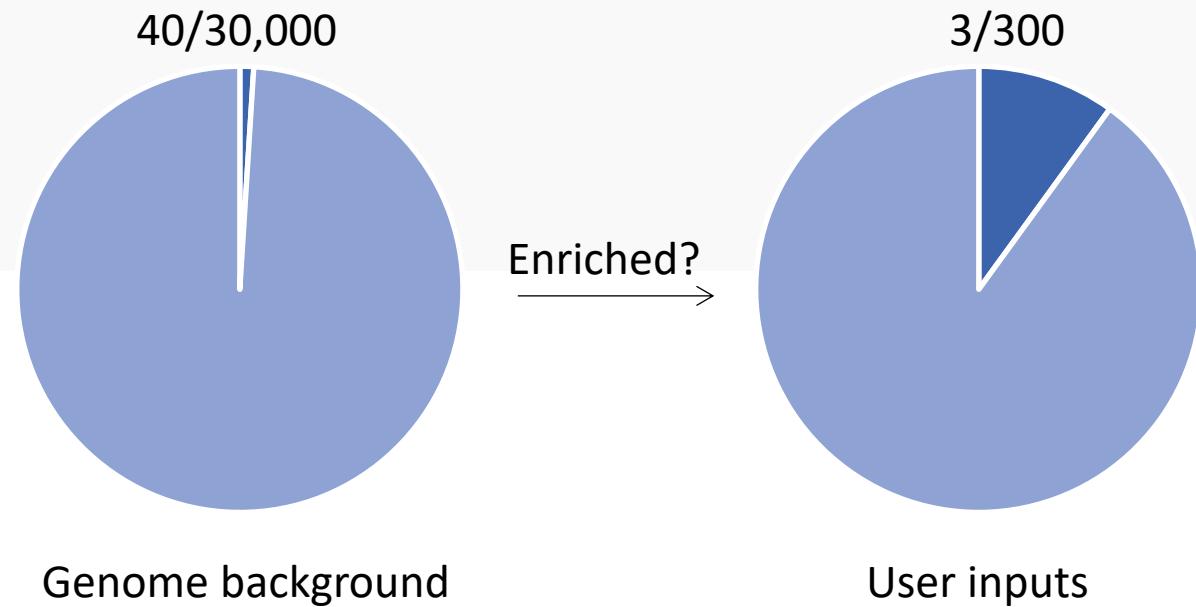


## A Hypothetical Example:

In human genome background (30,000 gene total), 40 genes are involved in p53 signaling pathway. A given gene list has found that 3 out of 300 belong to p53 signaling pathway. Then we ask the question if 3/300 is more than random chance comparing to the human background of 40/30000.

A 2x2 contingency table is built on above numbers:

	User Genes	Genome
In Pathway	3-1	40
Not In Pathway	297	29960



[https://david.ncifcrf.gov/content.jsp?file=functional\\_annotation.html](https://david.ncifcrf.gov/content.jsp?file=functional_annotation.html)

# GO enrichment tools

- [AgriGO](#) – plant genomes
- [BiNGO](#) – model organisms, Cytoscape plugin
- [Gorilla](#) – model organisms
- [DAVID](#) – human and animal genomes

# AgriGO enrichment output

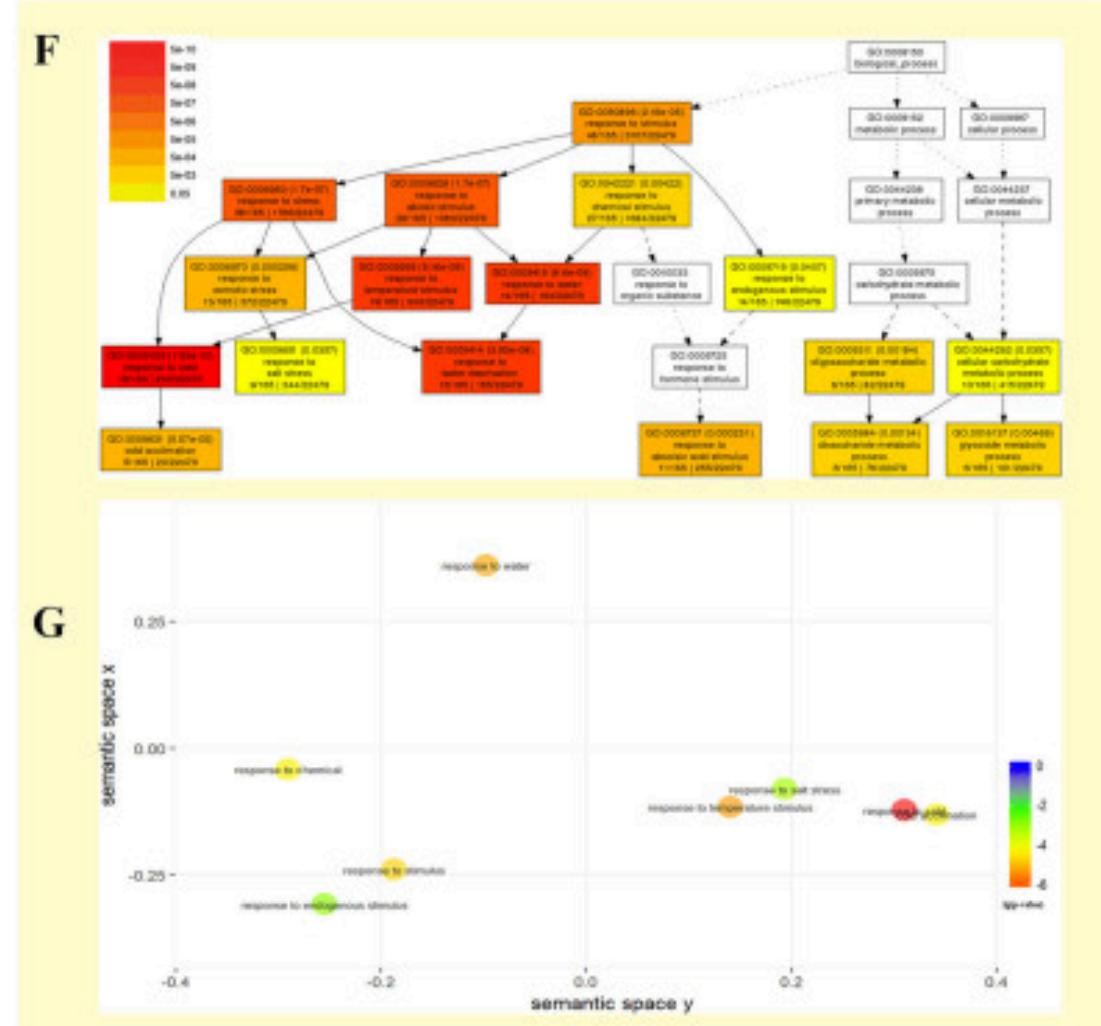
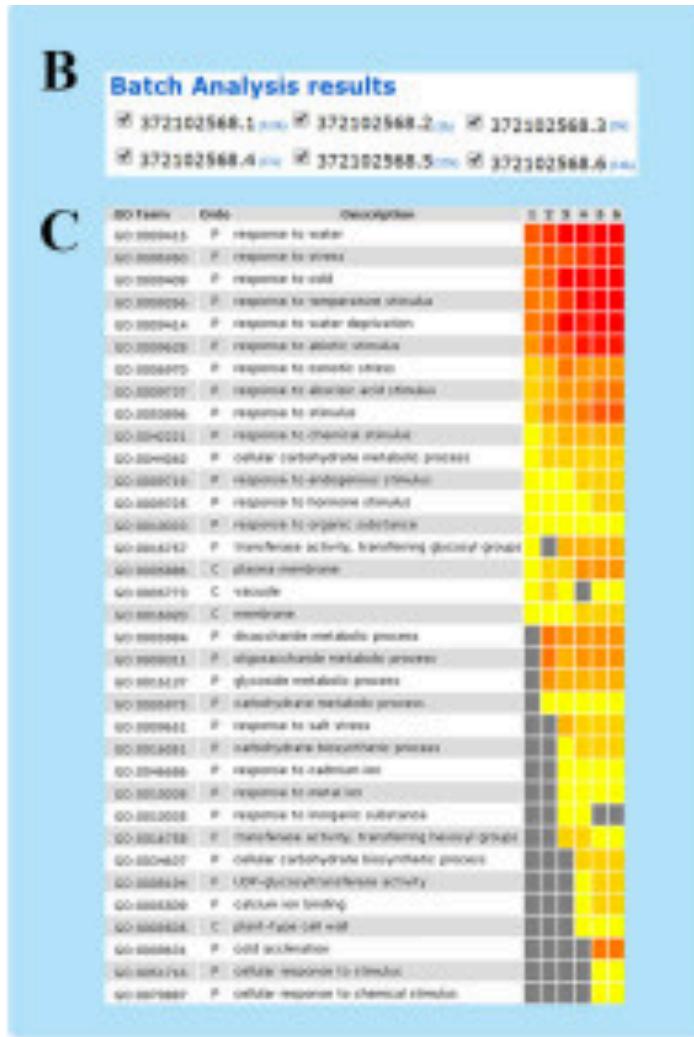
## Detail information

You can [  Browse in tree traversing mode ] [  Browse all GO terms ] [  Download ]

Or select from following significant terms to [ Draw graphical results ] [ Create bar chart ] [ Scatter Plots analysis ]

<input type="checkbox"/> GO term	Ontology	Description	Number in input list	Number in BG/Ref	p-value	FDR
<input type="checkbox"/> GO:0005985	P	sucrose metabolic process	9	44	4.1e-08	4.9e-05
<input type="checkbox"/> GO:0043038	P	amino acid activation	13	140	7.8e-07	0.00023
<input type="checkbox"/> GO:0043039	P	tRNA aminoacylation	13	140	7.8e-07	0.00023
<input type="checkbox"/> GO:0006418	P	tRNA aminoacylation for protein translation	13	138	6.6e-07	0.00023
<input type="checkbox"/> GO:0055067	P	monovalent inorganic cation homeostasis	7	35	1.6e-06	0.00031
<input type="checkbox"/> GO:0005984	P	disaccharide metabolic process	10	84	1.5e-06	0.00031
<input type="checkbox"/> GO:0045490	P	pectin catabolic process	6	26	3.7e-06	0.00062
<input type="checkbox"/> GO:0000272	P	polysaccharide catabolic process	8	69	2e-05	0.003
<input type="checkbox"/> GO:0009311	P	oligosaccharide metabolic process	10	117	2.9e-05	0.0038
<input type="checkbox"/> GO:0006771	P	riboflavin metabolic process	5	24	4.1e-05	0.0041

# GO enrichment visualization



# AgriGO demo

- <http://systemsbiology.cau.edu.cn/agriGOv2/>

# Reference

- <http://geneontology.org/>
- <https://david.ncifcrf.gov/>
- Tian T, Liu Y, Yan H, et al. agriGO v2.0: a GO analysis toolkit for the agricultural community, 2017 update. *Nucleic Acids Res.* 2017;45(W1):W122–W129. doi:10.1093/nar/gkx382