

# Functional Annotation of Gene Lists

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# Functional Annotation

- After a bioinformatics analysis identifies a list of relevant probes, the follow-up questions are
  - What genes do the probes correspond to?
    - Look at probe map data
  - What are the functions of the specific genes?
    - Look at, e.g., <http://www.genecards.org>
  - What biological processes or pathways are associated with these genes?
    - Use, e.g., DAVID (<https://david.ncifcrf.gov>) to perform a gene set enrichment analysis

# Gene set enrichment analysis

In a list of interest, 50% of genes are related to a functional process, such as *cell cycle* (Gene Ontology, KEGG databases)

Out of all possible genes (background), 20% are related to the same functional process

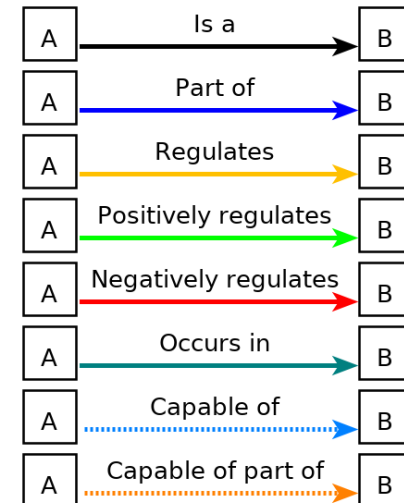
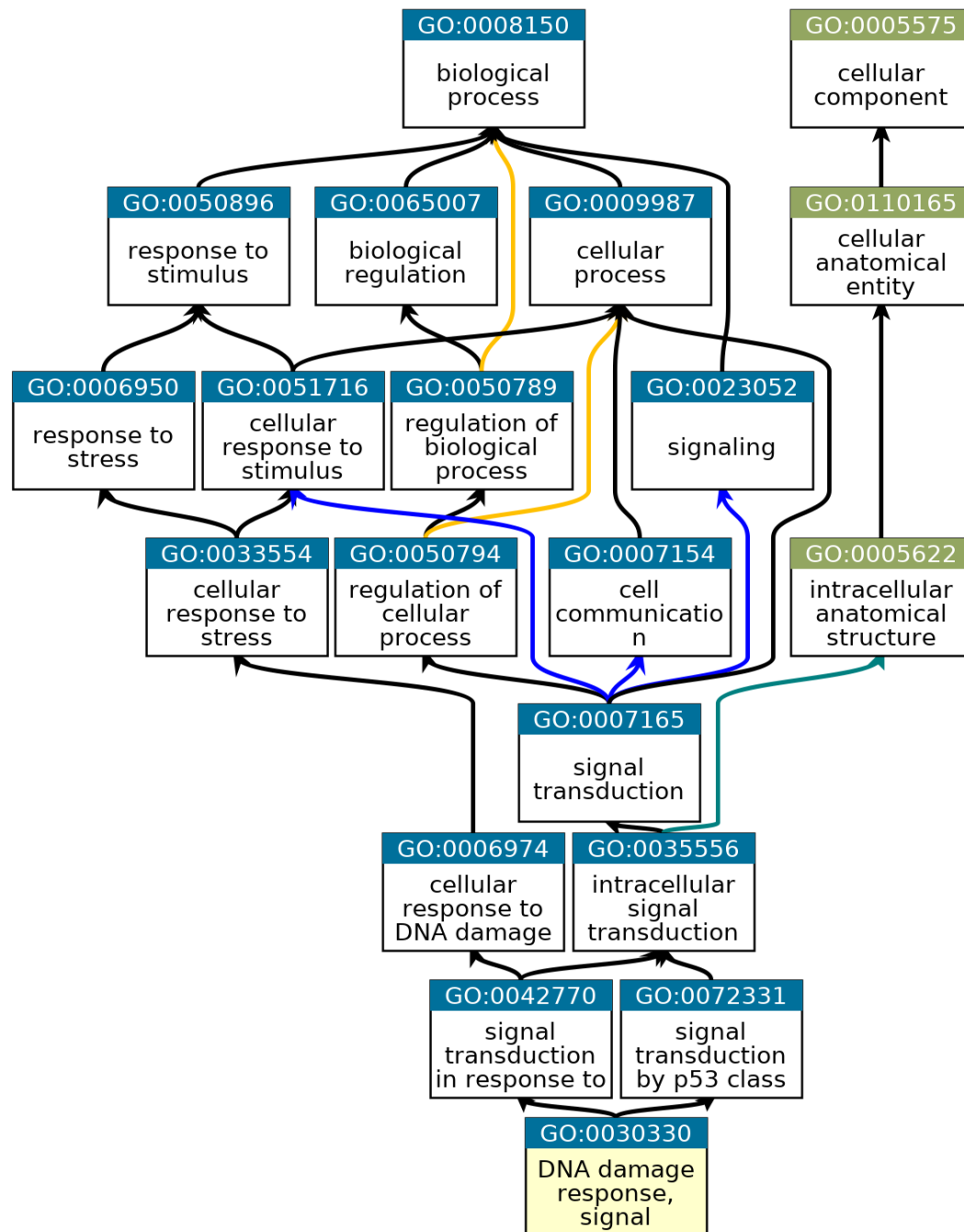
Gene list	
Gene1	Gene11
Gene2	Gene12
Gene3	Gene13
Gene4	Gene14
Gene5	Gene15
Gene6	...
Gene7	Gene19996
Gene8	Gene19997
Gene9	Gene19998
Gene10	Gene19999
	Gene20000
All genes (background)	

The gene list is 2.5 times as likely to contain a cell cycle related gene as is the background set

P-values (and adjusted p-values) determine whether the gene list is significantly enriched in cell cycle related genes

# Gene Ontology (GO)

- A controlled vocabulary for
  - Biological Processes (BP)
  - Molecular Functions (MF)
  - Cellular Components (CC)
- Relationships between terms leads to a "tree" structure
- <http://geneontology.org>
- Let's search TP53, look at Ontology, click on Term (*DNA damage response...*), and look at Graph Views, and view the term in QuickGO.



## Gene Ontology for TP53

# KEGG Pathways

- Molecular interactions and reactions related to metabolism, cellular processes, diseases, and others
- <http://www.genome.jp/kegg/pathway.html>
- Let's look at "pathways in cancer"

## “Pathways in Cancer” from KEGG Pathway Database

