

Working with Gene Lists and Over-representation Analysis

MBV-INF4410

Thursday, September 16th, 2010

Ian Donaldson

<http://donaldson.uio.no>

This talk is a remix of two talks presented in 2009 at the Canadian Bioinformatics Workshops by Gary Bader and Quaid Morris. Many thanks to Gary, Quaid and the CBW for making this material available.

Ian Donaldson, September 14th

<http://baderlab.org>

<http://morrislab.med.utoronto.ca/>

<http://www.bioinformatics.ca/workshops/2009/course-content>

(see Interpreting Gene Lists from -omics Studies.

Module 1: Introduction to gene lists (Chair: Gary Bader) and

Module 2: Finding over-represented gene functions in gene lists (Chair: Quaid Morris)

This page is available in the following languages:

Afrikaans বাংলাৰাখী Català Dansk Deutsch Ελληνικά English English (CA) English (GB) English (US) Esperanto
Castellano Castellano (AR) Español (CL) Castellano (CO) Español (Ecuador) Castellano (MX) Castellano (PE)
Euskara Suomi français français (CA) Galego עברית hrvatski Magyar Italiano 日本語 한국어 Macedonian Melayu
Nederlands Norsk Sesotho sa Leboa polski Português română slovenski jezik српски srpski (latinica) Sotho svenska
中文 華語 (台灣) isiZulu



Attribution-Share Alike 2.5 Canada

You are free:



to Share — to copy, distribute and transmit the work



to Remix — to adapt the work



Under the following conditions:



Attribution. You must attribute the work in the manner specified by the author or licensor (but not in any way that suggests that they endorse you or your use of the work).



Share Alike. If you alter, transform, or build upon this work, you may distribute the resulting work only under the same or similar licence to this one.

- For any reuse or distribution, you must make clear to others the licence terms of this work.
- Any of the above conditions can be waived if you get permission from the copyright holder.
- The author's moral rights are retained in this licence.

[Disclaimer](#)

Your fair dealing and other rights are in no way affected by the above.

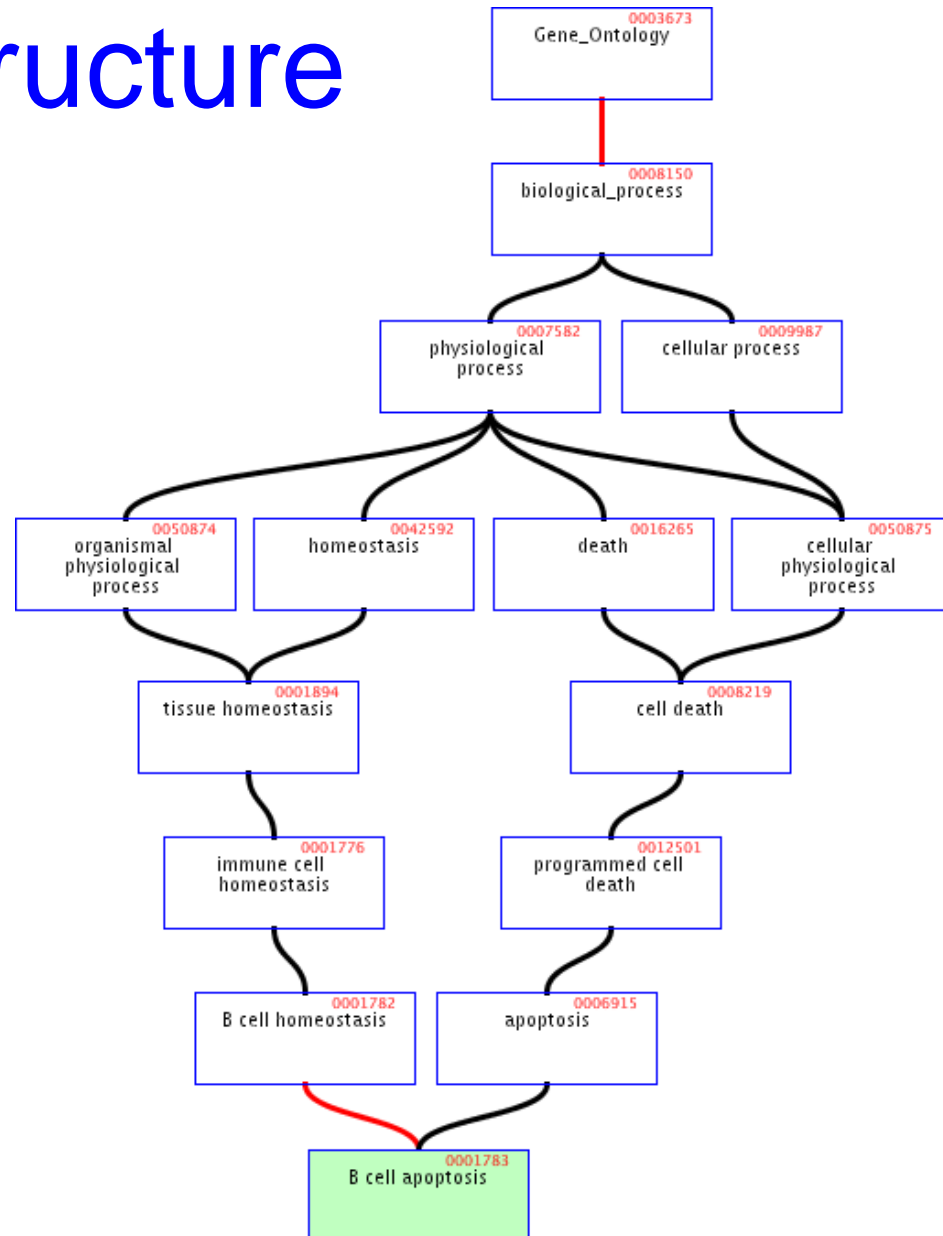
This is a human-readable summary of the Legal Code (the full licence) available in the following languages:
[English](#) [French](#)

What is the Gene Ontology (GO)?

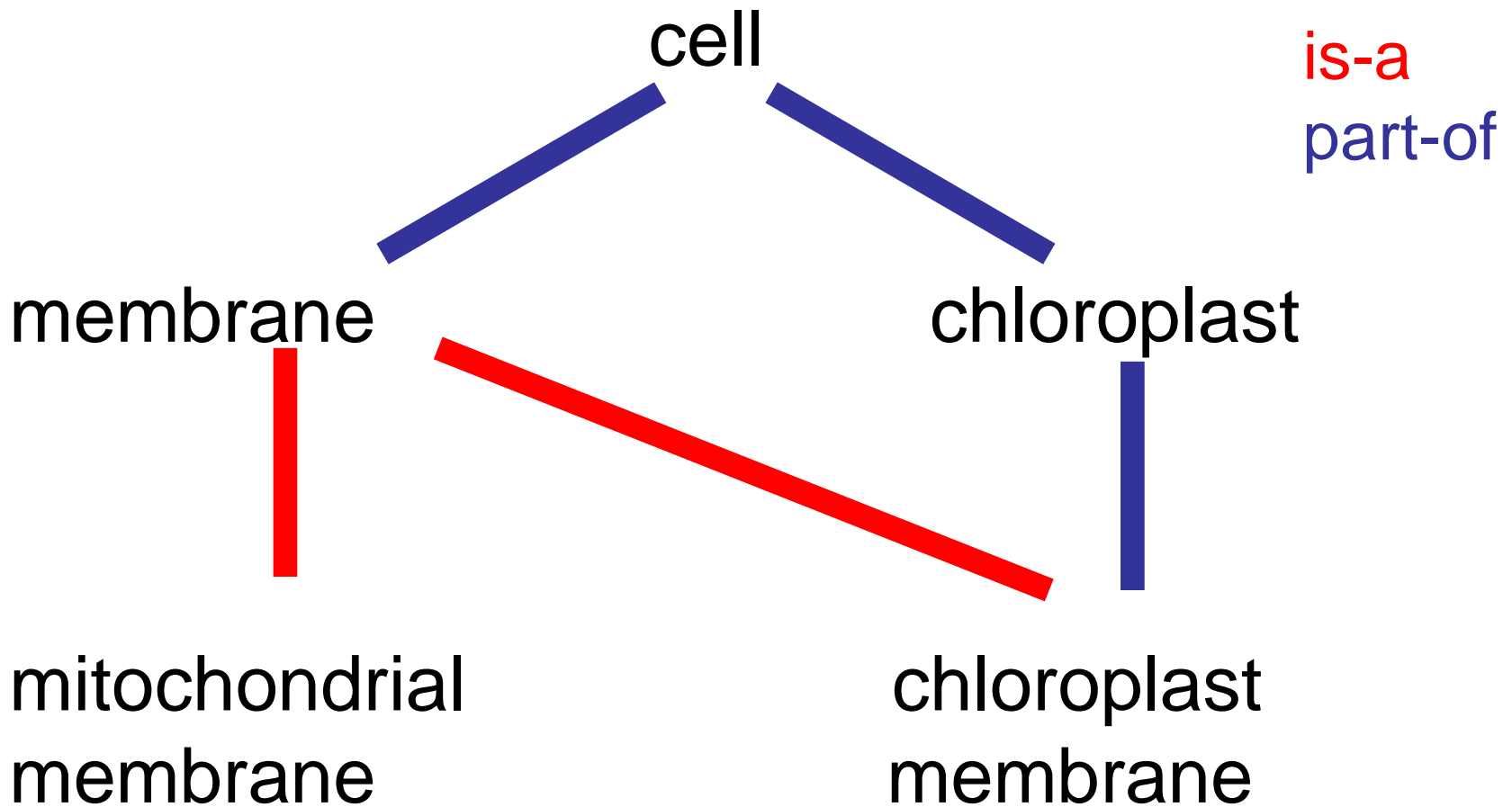
- Set of biological phrases (terms) which are applied to genes:
 - protein kinase
 - apoptosis
 - membrane
- Ontology: A formal system for describing knowledge

GO Structure

- Terms are related within a hierarchy
 - is-a
 - part-of
- Describes multiple levels of detail of gene function
- Terms can have more than one parent or child



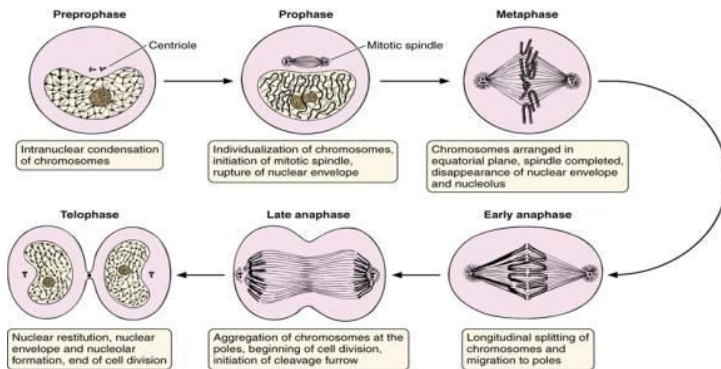
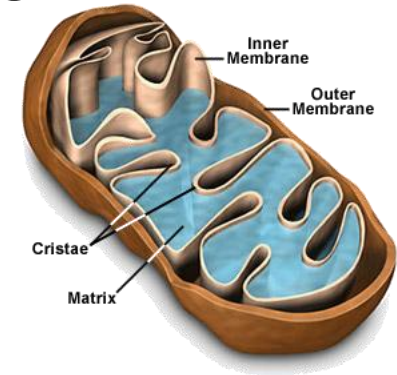
GO Structure



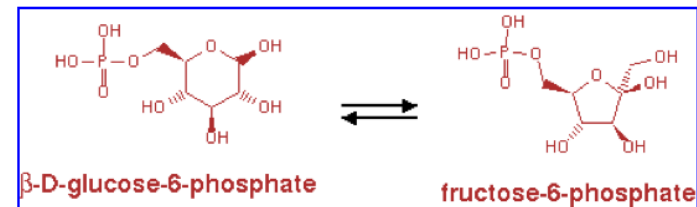
Species independent. Some lower-level terms are specific to a group, but higher level terms are not

What GO Covers?

- GO terms divided into three aspects:
 - cellular component
 - molecular function
 - biological process



Cell division



glucose-6-phosphate
isomerase activity

Terms

- Where do GO terms come from?
 - GO terms are added by editors at EBI and gene annotation database groups
 - Terms added by request
 - Experts help with major development
 - 27734 terms, 98.9% with definitions.
 - 16731 biological_process
 - 2385 cellular_component
 - 8618 molecular_function
 - As of July 6, 2009

Annotations

- Genes are linked, or associated, with GO terms by trained curators at genome databases
 - Known as ‘gene associations’ or GO annotations
 - Multiple annotations per gene
- Some GO annotations created automatically

Annotation Sources

- Manual annotation
 - Created by scientific curators
 - High quality
 - Small number (time-consuming to create)
- Electronic annotation
 - Annotation derived without human validation
 - Computational predictions (accuracy varies)
 - Lower 'quality' than manual codes
- Key point: be aware of annotation origin

For your information

Evidence Types

- **ISS:** Inferred from Sequence/Structural Similarity
- **IDA:** Inferred from Direct Assay
- **IPI:** Inferred from Physical Interaction
- **IMP:** Inferred from Mutant Phenotype
- **IGI:** Inferred from Genetic Interaction
- **IEP:** Inferred from Expression Pattern
- **TAS:** Traceable Author Statement
- **NAS:** Non-traceable Author Statement
- **IC:** Inferred by Curator
- **ND:** No Data available



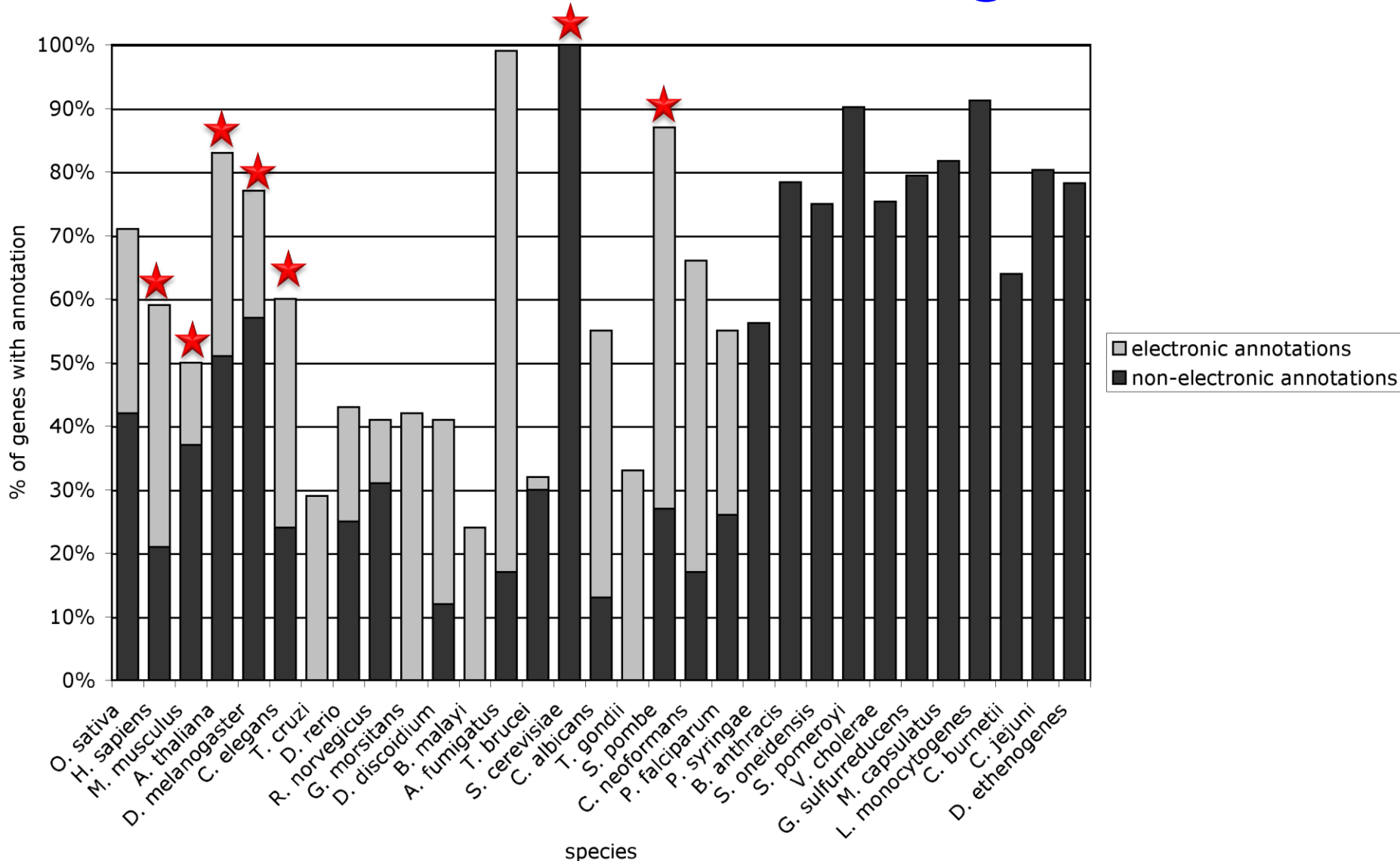
- **IEA:** Inferred from electronic annotation



Species Coverage

- All major eukaryotic model organism species
- Human via GOA group at UniProt
- Several bacterial and parasite species through TIGR and GeneDB at Sanger
- New species annotations in development

Variable Coverage



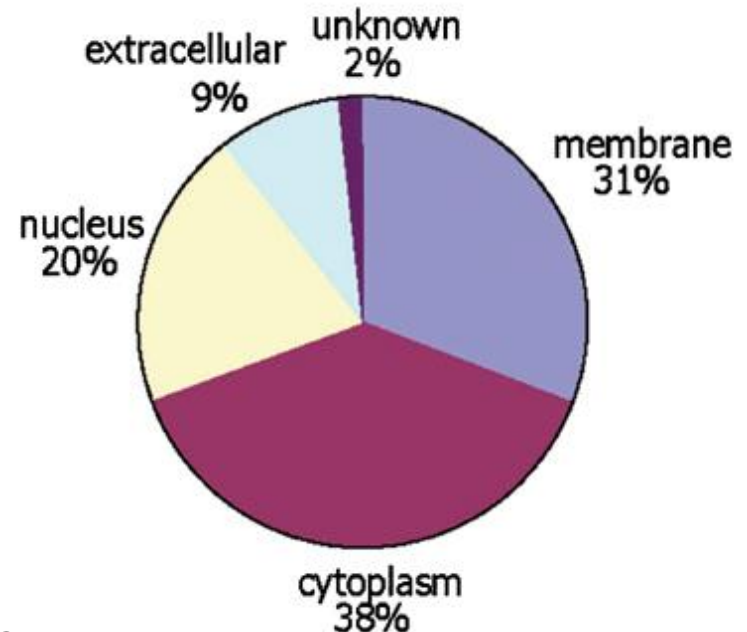
For your information

Contributing Databases

- [Berkeley *Drosophila* Genome Project \(BDGP\)](#)
- [dictyBase](#) (*Dictyostelium discoideum*)
- [FlyBase](#) (*Drosophila melanogaster*)
- [GeneDB](#) (*Schizosaccharomyces pombe*, *Plasmodium falciparum*, *Leishmania major* and *Trypanosoma brucei*)
- [UniProt Knowledgebase](#) (Swiss-Prot/TrEMBL/PIR-PSD) and [InterPro](#) databases
- [Gramene](#) (grains, including rice, *Oryza*)
- [Mouse Genome Database \(MGD\) and Gene Expression Database \(GXD\)](#) (*Mus musculus*)
- [Rat Genome Database \(RGD\)](#) (*Rattus norvegicus*)
- [Reactome](#)
- [Saccharomyces Genome Database \(SGD\)](#) (*Saccharomyces cerevisiae*)
- [The Arabidopsis Information Resource \(TAIR\)](#) (*Arabidopsis thaliana*)
- [The Institute for Genomic Research \(TIGR\)](#): databases on several bacterial species
- [WormBase](#) (*Caenorhabditis elegans*)
- [Zebrafish Information Network \(ZFIN\)](#): (*Danio rerio*)

GO Slim Sets

- GO has too many terms for some uses
 - Summaries (e.g. Pie charts)
- GO Slim is an official reduced set of GO terms
 - Generic, plant, yeast

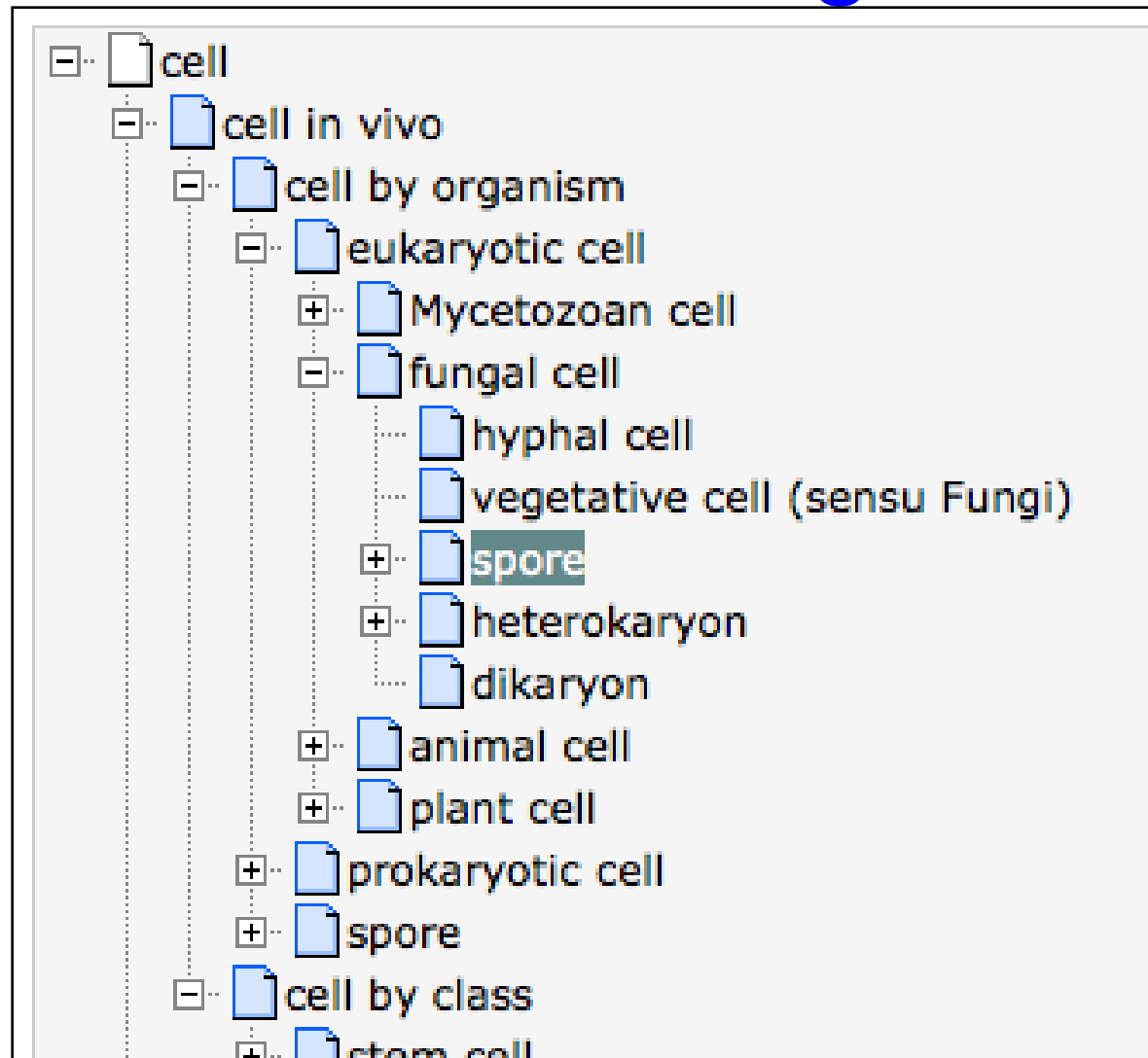


Crockett DK et al. Lab Invest. 2005
Nov;85(11):1405-15

GO Software Tools

- GO resources are freely available to anyone without restriction
 - Includes the ontologies, gene associations and tools developed by GO
- Other groups have used GO to create tools for many purposes
 - <http://www.geneontology.org/GO.tools>

Other Ontologies



Overview of over representation analysis

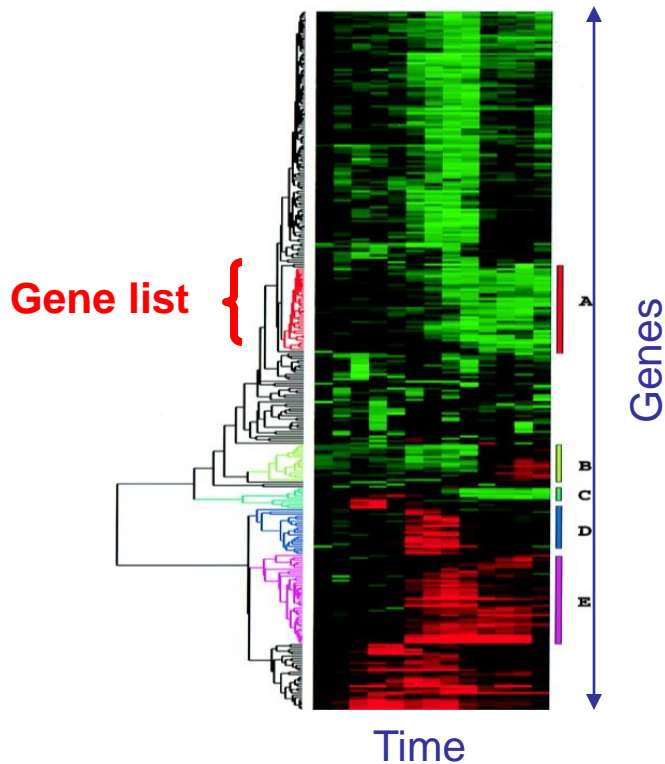
- Theory:
 - Review: What is a P-value? The good ole' T-test.
 - Fisher's Exact Test, the bread and butter of ORA
 - Correcting for multiple testing
 - Enrichment analysis with gene rankings

Over-representation analysis (ORA) in a nutshell

- Given:
 1. Gene list: e.g. RRP6, MRD1, RRP7, RRP43, RRP42 (yeast), or Gene Scores: RRP6 (4.0), MRD1 (3.0) etc
 2. Gene annotations: e.g. Gene ontology, transcription factor binding sites in promoter
- ORA Question: *Are any of the gene annotations surprisingly enriched in the gene list?*
- Details:
 - How to assess “surprisingly” (statistics)
 - How to correct for repeating the tests

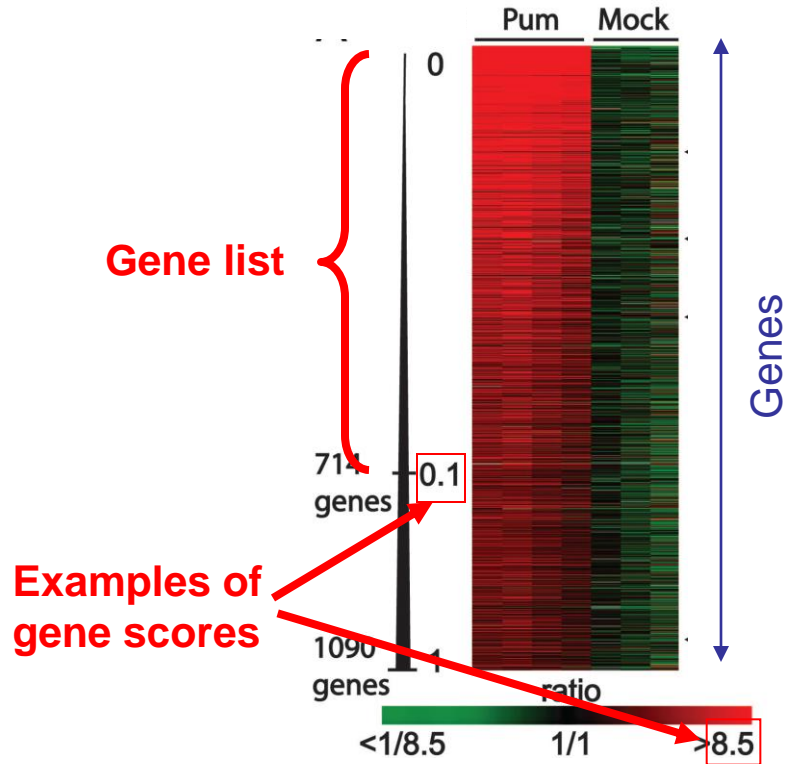
Examples of sources of gene lists

Clustering



Source Eisen et al. (1998) PNAS 95

Thresholding a gene "score"



Source: Gerber et al. (2006) PNAS103

Overview

- Theory:
 - Review: What is a P-value?
 - Fisher's Exact Test, the bread and butter of ORA
 - Correcting for multiple testing
 - Enrichment analysis with gene rankings

What is a P-value?

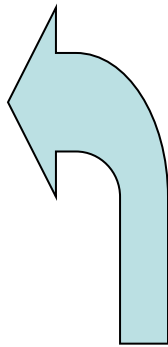
- The P-value is (a bound) on the probability that the “null hypothesis” is true,
- Calculated by calculating **statistics** using the data and testing the probability of observing those statistics, or ones more extreme, given a sample of the same size distributed according to the null hypothesis,
- Intuitively: *P-value is the probability of a false positive result* (aka “Type I error”)

Fisher's exact test: the bread and butter of ORA

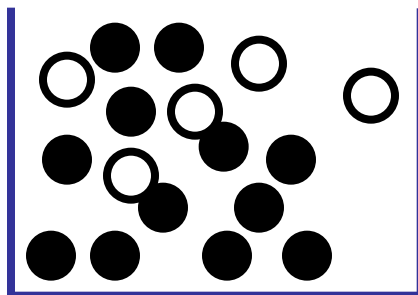
a.k.a., the hypergeometric test

Gene list

- RRP6
- MRD1
- RRP7
- RRP43
- RRP42



Formal question: *What is the probability of finding 4 or more “white” genes in a random sample of 5 genes?*

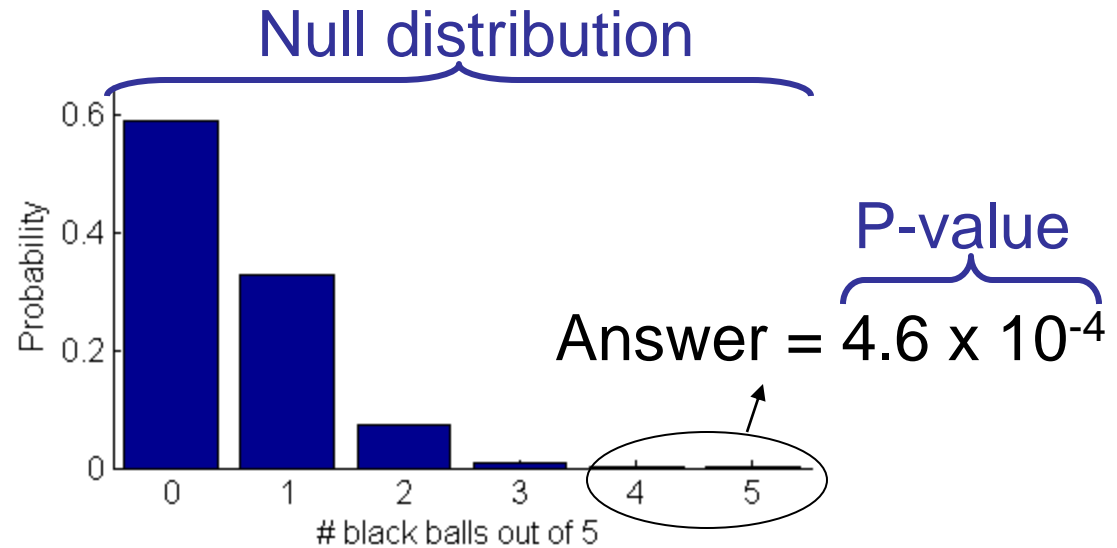
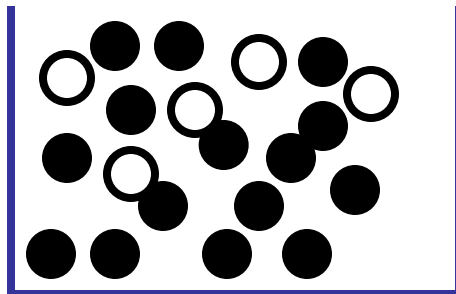
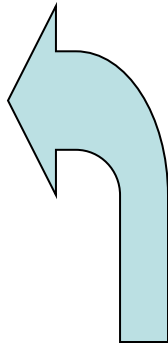


Background population:
500 white genes,
5000 black genes

Fisher's exact test cont.

Gene list

- RRP6
- MRD1
- RRP7
- RRP43
- RRP42



Background population:
500 white genes,
5000 black genes

Fisher's exact test: a.k.a., the hypergeometric test

In R, use the `dhyper` function to calculate the probability of seeing x white balls drawn from an urn of white balls (m) and black balls (n) when you randomly draw k balls.

```
dhyper(x, m, n, k)
```

You can calculate the probability of seeing x (or more – up to k) white balls using:

```
sum(dhyper(x:k, m, n, k))
```

Important details

- To test for *under-enrichment* of “white”, test for *over-enrichment* of “black”.
- Need to choose “background population” appropriately, e.g., if only portion of the total gene complement is queried (or available for annotation), only use that population as background.
- To test for enrichment of more than one independent types of annotation, apply Fisher’s exact test separately for each type. ***More on this later***

What have we learned?

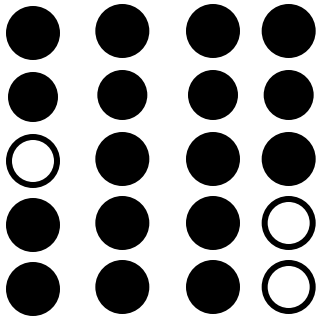
- Fisher's exact test is used for ORA of gene lists for a single type of annotation,
- P-value for Fisher's exact test
 - is “the probability that a random draw of the same size as the gene list from the background population would produce the observed number of annotations in the gene list or more.”,
 - and depends on size of both gene list and background population as well and # of “white” genes in gene list and background.

Correcting for multiple testing: overview

- Why do we need to correct? Winning the P-value lottery.
- Controlling the Family-wise Error Rate (FWER) with the Bonferroni-correction
- Controlling the false-discovery rate (FDR): Benjamini-Hochberg, Storey-Tibshirani, Q-values and all that

How to win the P-value lottery, part 1

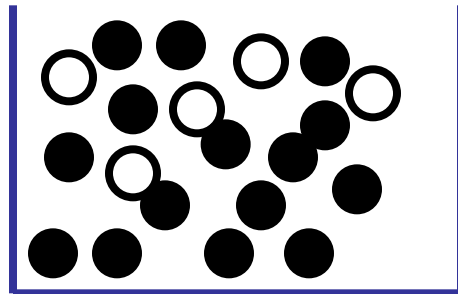
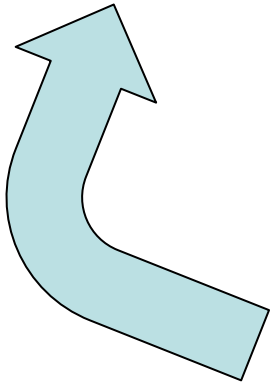
Random draws



... 7,834 draws later ...



*Expect a random draw
with observed
enrichment once every
 $1 / P\text{-value}$ draws*

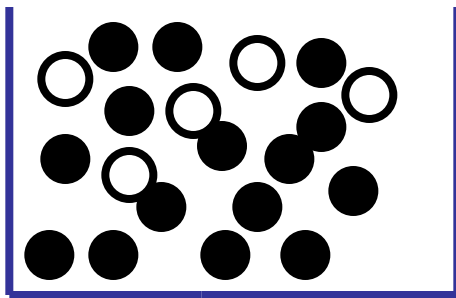
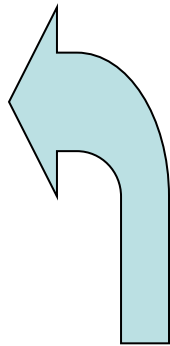


Background population:
500 white genes,
5000 black genes

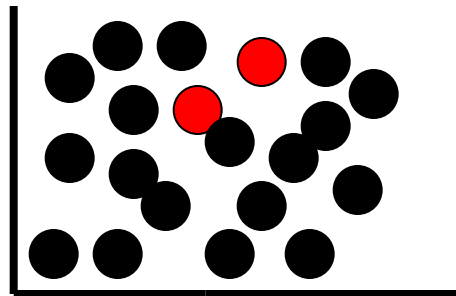
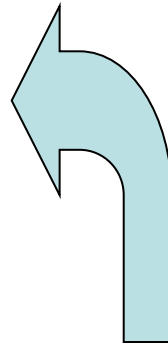
How to win the P-value lottery, part 2

Keep the gene list the same, evaluate different annotations

- RRP6
- MRD1
- RRP7
- RRP43
- RRP42

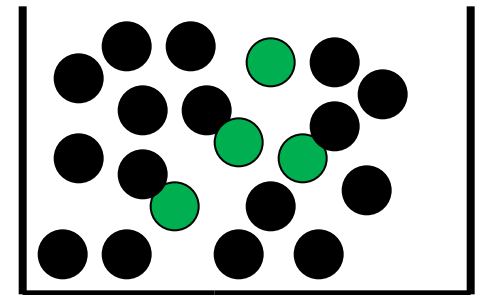
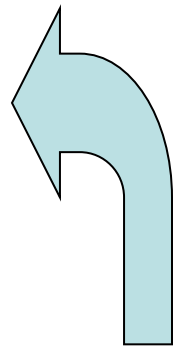


- RRP6
- MRD1
- RRP7
- RRP43
- RRP42



...

- RRP6
- MRD1
- RRP7
- RRP43
- RRP42



Bingo!...you win.

ORA tests need correction

From the Gene Ontology website:

Current ontology statistics: **25206** terms

- **14825** biological process
- **2101** cellular component
- **8280** molecular function

Two types of multiple test corrections

- Controlling the **Family-Wise Error Rate (FWER)** controls the probability that any test is a false positive
- Controlling the **False Discovery Rate (FDR)** controls the proportion of positive tests (i.e. rejections of the null hypothesis) that are false positives

Controlling Family-Wise Error Rate using the Bonferroni correction

If $M = \#$ of annotations tested:

Corrected P-value = $M \times$ original P-value

Corrected P-value is greater than or equal to the probability that any single one of the observed enrichments could be due to random draws. The jargon for this correction is “**controlling for the *Family-Wise Error Rate (FWER)***”

Bonferroni correction caveats

- Bonferroni correction is very stringent and can “wash away” real enrichments.
- Often users are willing to accept a less stringent condition, the “false discovery rate” (FDR), which leads to a gentler correction when there are real enrichments.

False discovery rate (FDR)

- FDR is *the expected **proportion** of the observed enrichments that are due to random chance.*
- Compare to Bonferroni correction which is *the probability that **any one** of the observed enrichments is due to random chance.*

Reducing multiple test correction stringency

- The correction to the P-value threshold α depends on the # of tests that you do, so, no matter what, the more tests you do, the more sensitive the test needs to be
- Can control the stringency by reducing the number of tests: e.g. use GO slim or restrict testing to the appropriate GO annotations.

What have we learned

- When testing multiple annotations, need to correct the P-values (or, equivalently, α) to avoid winning the P-value lottery.
- There are two types of corrections:
 - **Bonferroni** controls the probability any one test is due to random chance (aka FWER) and is very stringent
 - **B-H** controls the FDR, i.e., expected proportion of “hits” that are due to random chance
- Can control stringency by carefully choosing which annotation categories to test.