



Gene Ontology Analysis

...of a selected list of
(differentially expressed) genes



Gene Ontology

Introduction

<http://www.geneontology.org>

- Searching for all of the available information about each gene of interest is very time consuming. This is hampered further by the wide variations in terminology.
- The Gene Ontology (GO) project is a collaborative effort to address the need for consistent descriptions of gene products in terms of their 'biology' and in a species-independent manner.
- About 12,000 defined concepts, in a DAG (Direct Acyclic Graphs) with two link types (part-of, is-a) under three roots:
 - Cellular component
 - Biological process
 - Molecular function.
- Used as annotations for genes (19,408 terms as of 22/1/06)



Gene Ontology

Introduction

<http://www.geneontology.org>

the Gene Ontology

Gene Ontology Home

The Gene Ontology project provides a controlled vocabulary to describe gene and gene product attributes in any organism. [Read more...](#)

Popular Links

Search the Gene Ontology Database

gene or protein name GO term or ID

This search uses the browser [AmiGO](#). [Browse](#) the Gene Ontology using AmiGO.

GO website

- GO downloads: including [ontology files](#), [annotations](#) and the [GO database](#).

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Gene Ontology

Introduction

- Gene Ontology (GO) is a collection of controlled vocabularies describing the biology of a gene product in any organism
- There are 3 independent sets of vocabularies, or ontologies:
 - **Molecular Function (MF)**
 - e.g. "DNA binding" and "catalytic activity"
 - **Cellular Component (CC)**
 - e.g. "organelle membrane" and "cytoskeleton"
 - **Biological Process (BP)**
 - e.g. "DNA replication" and "response to stimulus"

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Introduction

Molecular Function Gene Ontology Browser

GO term: **L-malate dehydrogenase activity**
Synonym: **NAD-L-malate dehydrogenase**
Synonym: **malic dehydrogenase**
GO id: **GO:0030060**
Definition: **Catalysis of the reaction: (S)-malate + NAD+ = oxaloacetate + NADH + H+. Also oxidizes some other 2-hydroxycarboxylic acids.**
Number of paths to Term: 2

denotes an 'is-a' relationship
denotes a 'part-of' relationship

Gene Ontology

- molecular_function
- enzyme activity
- oxidoreductase activity
- oxidoreductase activity, acting on CH-OH group of donors
- malate dehydrogenase activity
- D-malate dehydrogenase (decarboxylating) activity
- L-malate dehydrogenase activity [GO:0030060] (1 genes, 1 annotations)
- malate dehydrogenase (acceptor) activity
- malate dehydrogenase (NADP) activity
- malic enzyme activity +

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Introduction

Biological Process Gene Ontology Browser

GO term: **tricarboxylic acid cycle**
Synonym: **Krebs cycle**
Synonym: **citric acid cycle**
GO id: **GO:0006099**
Number of paths to Term: 2

denotes an 'is-a' relationship
denotes a 'part-of' relationship

Gene Ontology

- biological_process
- physiological processes
- metabolism
- carbohydrate metabolism
- main pathways of carbohydrate metabolism
- Entner-Doudoroff pathway
- gluconeogenesis +
- glycolysis +
- glyoxylate cycle
- pentose-phosphate shunt +
- TCA intermediate metabolism +
- tricarboxylic acid cycle [GO:0006099] (21 genes, 21 annotations)
- reductive citric acid pathway
- reductive tricarboxylic acid cycle

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Introduction

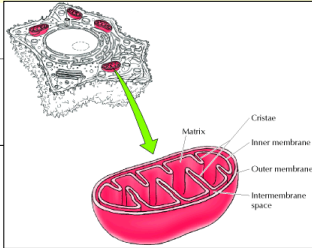
Cellular Component Gene Ontology Browser
Term Detail

GO term: **mitochondrion**
GO id: **GO:0005739**
Definition: **A semiautonomous, self replicating organelle that occurs in varying numbers, shapes, and sizes in the cytoplasm of virtually all eukaryotic cells. It is notably the site of tissue respiration.**
Number of paths to term: **1**

● denotes an 'is-a' relationship
 ● denotes a 'part-of' relationship

Gene Ontology

- cellular_component
- cell
- intracellular
- cytoplasm
- Golgi apparatus +
- hydrogenosome +
- lipid particle +
- melanosome
- membrane coat +
- microbody +
- microtubule organizing center +
- mitochondrion [GO:0005739] (504 genes, 675 annotations)



- kinetoplast
- mitochondrial degradosome
- mitochondrial derivative +
- mitochondrial intermembrane space
- mitochondrial matrix +
- mitochondrial membrane +
- mitochondrial permeability transition pore
- mRNA editing complex
- Nebenkern

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References

BIOINFORMATICS

REVIEW

Vol. 21 no. 18 2005, pages 3587–3595
doi:10.1093/bioinformatics/bti565

Databases and ontologies

Ontological analysis of gene expression data: current tools, limitations, and open problems

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Methodology article

Open Access

Iterative Group Analysis (iGA): A simple tool to enhance sensitivity and facilitate interpretation of microarray experiments

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Published: 29 March 2004

Received: 15 November 2003

BMC Bioinformatics 2004, 5:34

Accepted: 29 March 2004

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References

Khatri and Draghici, 2005

Table 2. In the GO visualization column, 'flat' indicates that the tool does not represent the hierarchical structure of the GO when displaying the results, 'tree' indicates that the tool displays the GO hierarchy as a tree, whereas 'DAG' indicates that the tool displays the GO as a directed acyclic graph. The other columns are self-explanatory

<http://vortex.cs.wayne.edu/projects.htm#Onto-Express>

Tool	Statistical model	Correction for multiple experiments	GO Visualization	Microarrays supported	Time to process 200 genes (s)
Onto-Express	χ^2 , binomial, hypergeometric, Fisher's exact test	Šidák, Holm, Bonferroni, FDR	Flat, Tree	172 commercial arrays (Affymetrix, SuperArray, Sigma-Genosys, ClonTech, PerkinElmer, Operon, Takara, NIA); can also upload a user-defined list	7, 8, 16, 28
GoMiner	Fisher's exact test	Relative enrichment	Tree, DAG	uploads from user	77, 123, 223, 340
DAVID	None	None	Not available	Not applicable	15, 17, 27, 54
EASEonline	Fisher's exact test	Bonferroni	Not available	27 arrays (Affymetrix only); can also upload a user-defined list	15, 19, 34, 74
GeneMerge	Hypergeometric	Bonferroni	Flat, no hierarchical structure	Uploads from user	6, 6, 6, 8
FuncAssociate	Fisher's exact test	None	Not available	Uploads from user	22, 27, 29, 50
GOTM	Hypergeometric	None	Tree	37 arrays (Affymetrix only); uploads from user	59, 60, 157,
FatiGO	Percentage	Step-down minP, FDR (Benjamini and Hochberg, 1995), FDR (Benjamini	Flat, Tree	Uploads from user	15, 49, 69, 105

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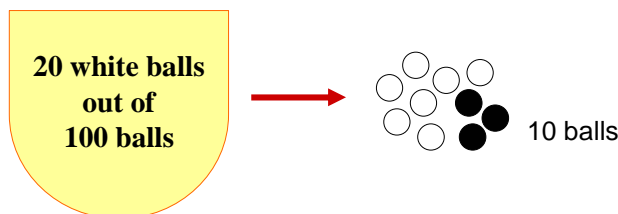


Analysis

The Hypergeometric Test

In a given list of genes of interest (eg. DE), is there a Gene Ontology term that is more represented than what it would be expected by chance only?

The hypergeometric distribution arises from sampling from a fixed population.



- We want to calculate the probability for drawing 7 or more white balls out of 10 balls given the distribution of balls in the urn

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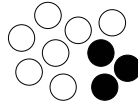


Analysis

Gene Ontology

The Hypergeometric Test

20 white balls
out of
100 balls



$$P(z, n, t, x) = \frac{\binom{t}{z} \binom{n-t}{x-z}}{\binom{n}{x}}$$

- t = N of balls draws from the ball → 10
- z = N of ball from the particular condition (ie. White) → 7
- n = N of ball in the urn → 100
- x = N of ball in the urn with the particular condition (ie. White) → 20

$P = 0.000368$

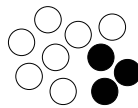


Analysis

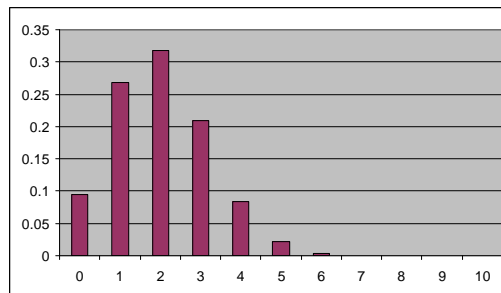
Gene Ontology

The Hypergeometric Test

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Gene Ontology

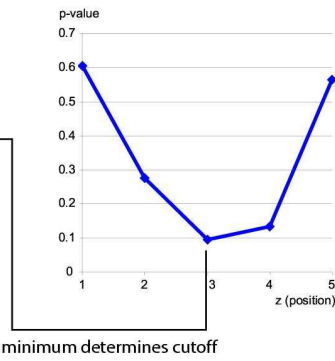
Analysis

The Hypergeometric Test

IGA: Iterative Group Analysis (Breitling et al. 2004)

- Gene 1
- Gene 2 = Group member 1 (t = 2; z = 1)
- Gene 3 = Group member 2 (t = 3; z = 2)
- Gene 4 = Group member 3 (t = 4; z = 3)
- Gene 5
- Gene 6
- Gene 7 = Groupmember 4 (t = 7; z = 4)
- Gene 8
- Gene 9
- Gene 10
- Gene 11
- Gene 12
- Gene 13 = Group member 5 (t = 13; z = 5)
- Gene 14

↑ Increasing fold-change



n = 14; x = 5

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Gene Ontology

Example

Reverter et al. (2004) J. Anim Sci 82:3430

Genes = 7,638

DE Genes



450

387

Table 3. Description gene ontology (GO) classes with a probability of change by chance alone less than 1.0×10^{-4} and for each experiment (Exp. 1, 2, and 3), number of elements (No.), and differentially expressed (DE) elements for each GO class

GO ^a	Description	No.	DE
Exp. 1: Downregulated in high-quality diet			
0006355	Regulation of transcription	50	14
0003714	Transcription co-repressor	19	12
0006937	Muscle contraction	17	7
0006412	Protein biosynthesis	82	21
0005509	Calcium ion binding	133	7
Exp. 1: Upregulated in high-quality diet			
0005584	Collagen type I	22	21
0003754	Chaperone activity	23	22
0001503	Ossification	19	6
0004129	Cytochrome-c oxidase	67	59
0005200	Structural cytoskeleton	110	33
Exp. 2: Downregulated in Holstein breed			
0016491	Oxidoreductase activity	149	21
0016740	Transferase activity	45	18
0003754	Chaperone activity	23	8
0016529	Sarcolemmal reticulum	24	20
0008151	Cell growth or maintenance	24	16
Exp. 2: Upregulated in Holstein breed			
0001501	Skeletal development	23	20
0003714	Transcription co-repressor	19	11
0017022	Myosin binding	7	4
0015992	Proton transport	35	10
0006412	Protein biosynthesis	82	26

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