

GS01 0163

Analysis of Microarray Data

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Lecture 3: Linking Numbers to Biology

- So, why are we here?
- Why do we care?
- Affymetrix source for annotations
- List of Affymetrix annotations
- Updating the annotations in dChip
- What is GeneOntology?
- Using GeneOntology in dChip
- GoMiner

So, why are we here?

We want to learn about Gene Annotations.

Microarrays are *designed*, which means that someone first chooses a set of genes of interest, selects probe sequences to target those genes, and then places those sequences on a microarray. In order to interpret (and possibly to analyze) the data produced from a microarray experiment, you need to refer to the accompanying annotations, which describe both the probes and the targeted genes.

Things Change

One might naively think that gene annotations are static; meaning that they are produced when the microarray is designed and never change again. Let me disabuse you of that notion immediately. It is true that the biological sequences of the probes that were placed on the array do not change. However, our knowledge of the human genome continues to evolve, and thus our opinion about exactly what genes are targeted by those sequences must be continually updated.

For Affymetrix microarrays, the company maintains a web site that always contains their latest opinion on the nature and identity of the targeted genes.

Why Do We Care?

Recall from the last lecture that we compared microarray data from samples of acute lymphocytic leukemia (ALL) patients and mixed-lineage leukemia (MLL) patients. Using the criteria that the lower bound of fold change (LBFC) should be at least 1.2-fold and the mean difference in expression should be greater than 100, we found a list of 610 probe sets that were differentially expressed.

It is considered bad form to just hand the biologists a list of 610 genes and wish them good luck as they go on their way. They typically want to know: do these genes reflect particular biological functions that are different between the two groups of samples, or do they identify specific biological pathways or networks that are perturbed?

List of Differentially Expressed Genes

	A	B	AA	AB	AU	AV	AW	AX	AY
12	probe set	gene	baseline mean	baseline	experiment mean	experiment	fold change	lower bc	upper bo
13	37680_at	A kinase (PRKA) anchor protein (gravin) 12	2973.7	560.63	148.29	24.19	-20.05	-12.93	-30.28
14	1325_at	MAD, mothers against decapentaplegic homolog 1	7759.92	1390.4	595.18	64.06	-13.04	-8.89	-18.03
15	37280_at	MAD, mothers against decapentaplegic homolog 1	9124.17	1538.9	702.89	37.85	-12.98	-9.29	-16.88
16	37908_at	guanine nucleotide binding protein 11	2160.91	565.93	226.99	58.16	-9.52	-4.92	-18.23
17	34194_at	Homo sapiens mRNA; cDNA DKFZp564B076 (from	962.11	296.29	107.48	34.97	-8.95	-3.95	-21.14
18	753_at	nidogen 2 (osteonidogen)	2558.48	890.45	304.16	22.09	-8.41	-3.58	-13.49
19	1992_at	fragile histidine triad gene	1742.98	252.98	209.02	29.64	-8.34	-5.92	-11.72
20	1488_at	protein tyrosine phosphatase, receptor type, K	4128.67	1140	572.2	38.89	-7.22	-3.91	-10.70
21	1077_at	recombination activating gene 1	6927.92	1443.9	1021.43	204.85	-6.78	-4.09	-11.13
22	33910_at	Homo sapiens mRNA; cDNA DKFZp564P116 (from	460.85	209.6	72.66	7.64	-6.34	-1.59	-11.49
23	34800_at	leucine-rich repeats and immunoglobulin-like domain	5255.48	907	899.41	189.08	-5.84	-3.74	-9.53
24	35614_at	transcription factor-like 5 (basic helix-loop-helix)	7264.11	1378.1	1248.25	122.02	-5.82	-3.9	-8.05
25	41266_at	integrin, alpha 6	7923.59	1222.5	1445.79	200.87	-5.48	-3.84	-7.73
26	37343_at	inositol 1,4,5-triphosphate receptor, type 3	5231.99	747.28	966.99	97.72	-5.41	-3.98	-7.15
27	31892_at	protein tyrosine phosphatase, receptor type, M	801.09	336.26	150.51	9.57	-5.32	-1.64	-9.12
28	35669_at	KIAA0633 protein	1738.34	360.27	343.94	22.32	-5.05	-3.3	-6.93
29	38578_at	tumor necrosis factor receptor superfamily, member	4038.17	674.75	847.39	129.09	-4.77	-3.23	-6.94
30	37780_at	piccolo (presynaptic cytomatrix protein)	2856.4	830.13	601.56	40.43	-4.75	-2.46	-7.15
31	40570_at	forkhead box O1A (rhabdomyosarcoma)	10218.69	1178.1	2227.99	482.41	-4.59	-3.16	-7.34
32	39878_at	protocadherin 9	12518.61	2120.5	2816.54	552.51	-4.44	-2.89	-7.03
33	307_at	arachidonate 5-lipoxygenase	6743.7	992.9	1521.71	136.37	-4.43	-3.26	-5.80
34	38408_at	transmembrane 4 superfamily member 2	6543.7	1009.8	1489.02	230.77	-4.39	-3.04	-6.36

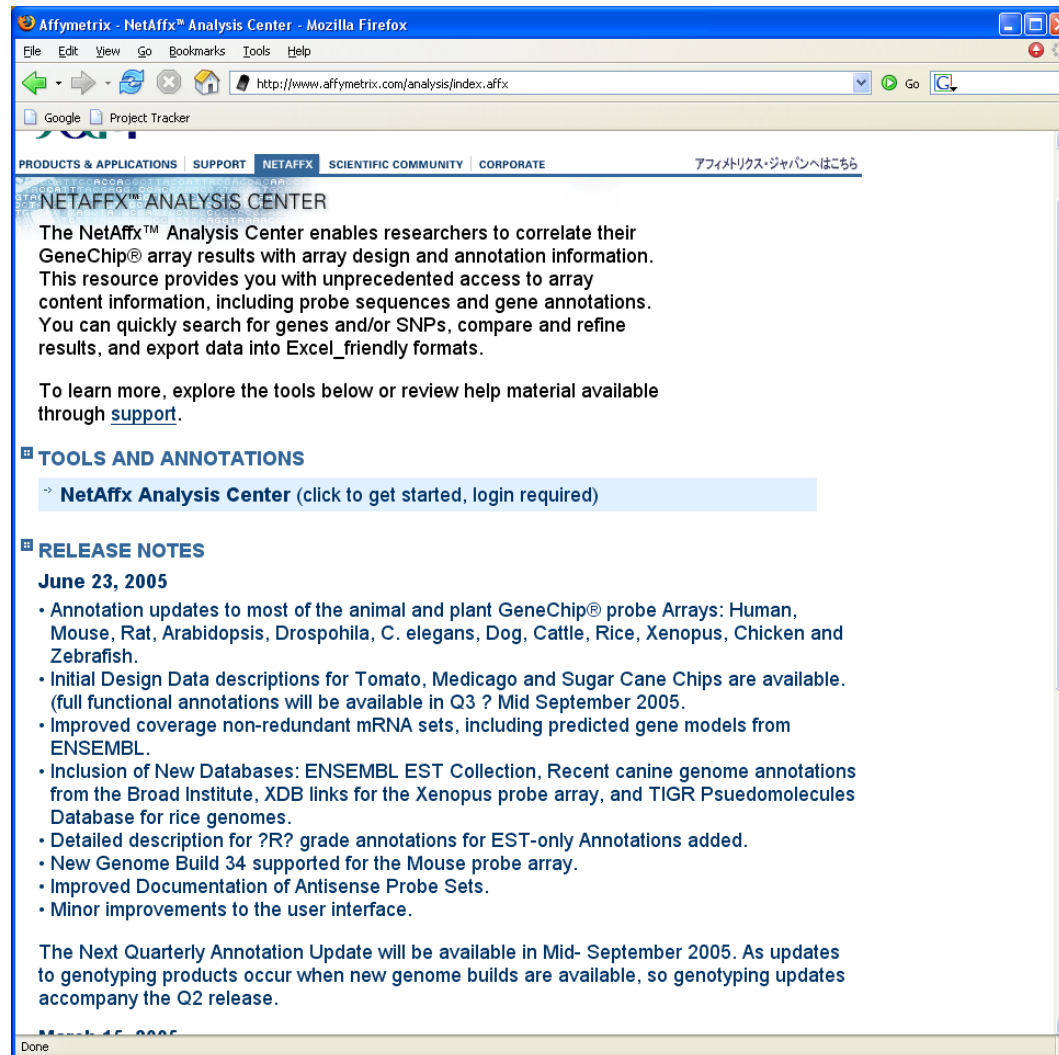
Affymetrix Web Site

http://www.affymetrix.com

The screenshot shows the Affymetrix website in a Mozilla Firefox browser window. The browser's address bar displays the URL `http://www.affymetrix.com/index.affx`. The website's header includes navigation links for `home`, `log out`, `register`, `your profile`, and `contact`, along with a `search site` input field. The Affymetrix logo is prominently displayed. Below the logo, there are navigation tabs for `PRODUCTS & APPLICATIONS`, `SUPPORT`, `NETAFFX`, `SCIENTIFIC COMMUNITY`, and `CORPORATE`. A secondary navigation bar in Japanese is also visible. The main content area features a large banner with the text `understand genome function` and a sub-headline `Succeeding with cardiac transplants`. To the right of the banner is a sidebar with three dropdown menus: `Research Areas` (set to `DNA`), `Fields of Study` (set to `Cancer`), and `Resources for` (set to `Academics`). The main content is organized into four columns: `Innovations`, `In the News`, `Research Highlights`, and `Product Updates`. The `Innovations` column lists `Small RNAs, big effects.`, `100,000 SNPs. One primer.`, and `Scientific Publications`. The `In the News` column features articles such as `HUGO Pacific Pan-Asian SNP Initiative to Explore Genetic Diversity for Nearly Half the World's Population` and `Researchers Identify Gene for a Primary Form of Sudden Infant Death Syndrome (SIDS)`. The `Research Highlights` column includes `Identical Twins, Different Cancers`, `Building Better Bones`, `A Simple Give and Take: Plant/Bacteria Symbiosis`, `Predicting Survival in Patients with Follicular Lymphoma`, and `Predicting Drug-Resistant Leukemia`. The `Product Updates` column lists `Special Offers for GeneChip Microarrays and Reagents`, `Introducing ArrayAssist® Lite Software for easy-to-use probe-level analysis`, `Introducing the GeneChip® Scanner 3000 MegAllele™ System for Custom and Application-Specific Genotyping`, and `Announcing the New GeneChip® Blood RNA Concentration Kit and Globin-Reduction Protocol`. A `Clinical Diagnostics` section is partially visible at the bottom right. The footer of the browser window shows `Transferring data from www.affymetrix.com...`

NETAFFX

Annotations are updated quarterly...



Affymetrix Support

Go to the Affymetrix support page to get the full annotations.



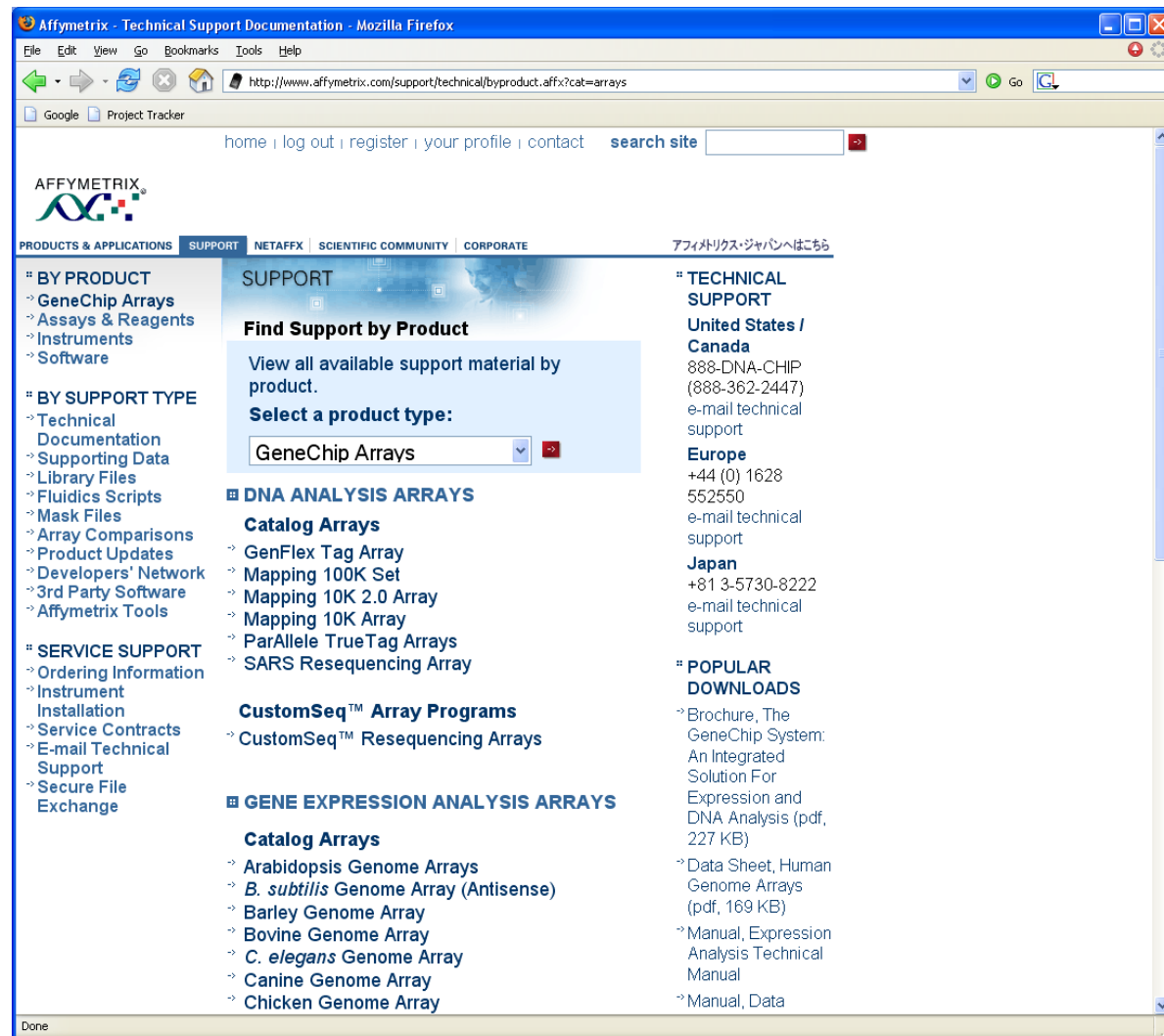
The screenshot shows the Affymetrix Support page in a Mozilla Firefox browser window. The address bar displays <http://www.affymetrix.com/support/index.affx>. The page features a navigation menu with links for home, log out, register, your profile, contact, and a search site. The main content area is titled "SUPPORT" and is organized into several sections:

- BY PRODUCT**: View all available support material by product. A dropdown menu is set to "GeneChip Arrays".
- BY SUPPORT TYPE**: View all available support material by type. A dropdown menu is set to "Technical Documentation".
- COMMON QUESTIONS**:
 - [How can I find out if my genes of interest are on GeneChip expression arrays?](#)
 - [Where can I get information on gene expression sample preparation?](#)
 - [Can I run Affymetrix software on Windows XP?](#)
- TECHNICAL SUPPORT**:
 - United States / Canada**: 888-DNA-CHIP (888-362-2447), e-mail technical support
 - Europe**: +44 (0) 1628 552550, e-mail technical support
 - Japan**: +81 3-5730-8222, e-mail technical support
- POPULAR DOWNLOADS**:
 - Brochure, The GeneChip System: An Integrated Solution For Expression and DNA Analysis (pdf, 227 KB)
 - Data Sheet, Human Genome Arrays (pdf, 169 KB)
 - Manual, Expression Analysis

The left sidebar contains a navigation menu with categories: PRODUCTS & APPLICATIONS, SUPPORT, NETAFFX, SCIENTIFIC COMMUNITY, and CORPORATE. Under SUPPORT, there are sub-sections for BY PRODUCT, BY SUPPORT TYPE, and SERVICE SUPPORT.

Support By Product

Follow the “support by product” link to “GeneChip Arrays”.



The screenshot shows the Affymetrix Technical Support Documentation website in a Mozilla Firefox browser window. The address bar displays the URL: <http://www.affymetrix.com/support/technical/byproduct.affx?cat=arrays>. The page features a navigation menu with categories like 'PRODUCTS & APPLICATIONS', 'SUPPORT', 'NETAFFX', 'SCIENTIFIC COMMUNITY', and 'CORPORATE'. The 'SUPPORT' section is active, and the 'BY PRODUCT' link is selected, leading to the 'GeneChip Arrays' page. The main content area is titled 'SUPPORT' and 'Find Support by Product'. It includes a dropdown menu for 'Select a product type:' with 'GeneChip Arrays' selected. Below this, there are three main sections: 'DNA ANALYSIS ARRAYS', 'CustomSeq™ Array Programs', and 'GENE EXPRESSION ANALYSIS ARRAYS'. Each section lists various array types and provides links to their respective support materials. The 'DNA ANALYSIS ARRAYS' section includes 'Catalog Arrays' such as 'GenFlex Tag Array', 'Mapping 100K Set', 'Mapping 10K 2.0 Array', 'Mapping 10K Array', 'ParAllele TrueTag Arrays', and 'SARS Resequencing Array'. The 'CustomSeq™ Array Programs' section includes 'CustomSeq™ Resequencing Arrays'. The 'GENE EXPRESSION ANALYSIS ARRAYS' section includes 'Catalog Arrays' such as 'Arabidopsis Genome Arrays', 'B. subtilis Genome Array (Antisense)', 'Barley Genome Array', 'Bovine Genome Array', 'C. elegans Genome Array', 'Canine Genome Array', and 'Chicken Genome Array'. On the right side of the page, there are sections for 'TECHNICAL SUPPORT' (United States / Canada, Europe, Japan) and 'POPULAR DOWNLOADS' (Brochure, The GeneChip System; Data Sheet, Human Genome Arrays; Manual, Expression Analysis Technical Manual; Manual, Data).

Affymetrix Annotations for HU133

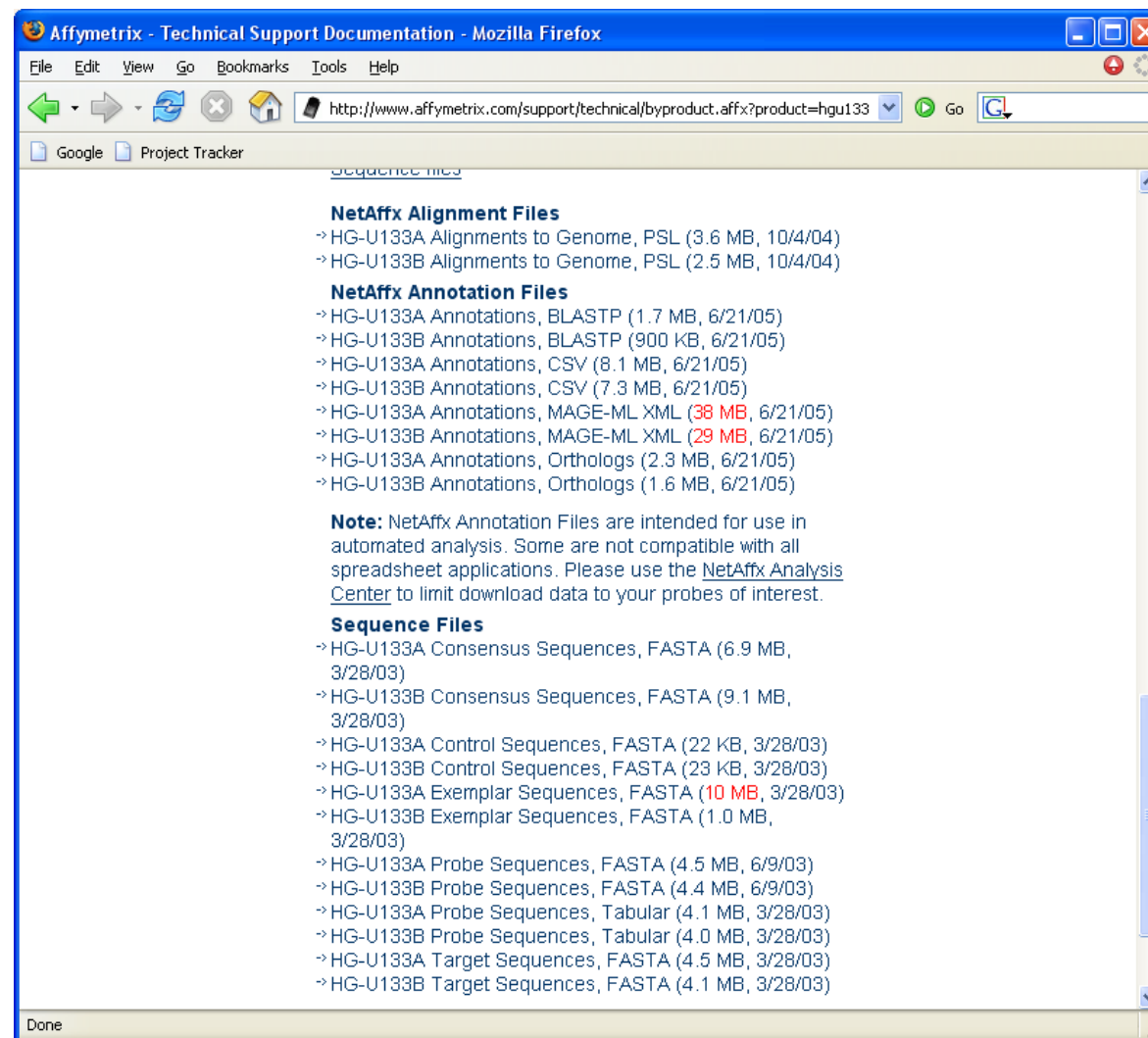
Scroll down to “Human Genome Arrays”; select “HG-U133 Set”

The screenshot shows a web browser window displaying the Affymetrix Technical Support Documentation page for the HU133 product. The page is organized into several sections:

- Navigation:** Includes links for home, log out, register, your profile, contact, and a search site.
- Menu:** Features tabs for PRODUCTS & APPLICATIONS, SUPPORT (selected), NETAFFX, SCIENTIFIC COMMUNITY, and CORPORATE.
- Left Sidebar:**
 - BY PRODUCT:** GeneChip Arrays, Assays & Reagents, Instruments, Software.
 - BY SUPPORT TYPE:** Technical Documentation, Supporting Data, Library Files, Fluidics Scripts, Mask Files, Array Comparisons, Product Updates, Developers' Network, 3rd Party Software, Affymetrix Tools.
 - SERVICE SUPPORT:** Ordering Information, Instrument Installation, Service Contracts, E-mail Technical Support, Secure File Exchange.
- Main Content Area:**
 - SUPPORT:** Human Genome U133 Set - Support Materials. For more information, please see the [product page](#).
 - PRODUCT UPDATES:** Product Update, Human Genome U133 Set Product Bulletin.
 - SUPPORT:** Application Notes: Probing Neurological Disorders Using GeneChip® Arrays: Latest Advances From Hereditary Disease Array Group (pdf, 74 KB).
 - Array Comparisons:**
 - User's Guide to Product Comparison Spreadsheets (pdf, 82 KB)
 - HG-U133 to HG-U133 Plus, Best Match (zip, 5 KB)
 - HG-U133 to HG-U133 Plus, Complex (zip, 24 MB)
 - HG-U133 to HG-U133 Plus, Good Match (zip, 5 KB)
 - HG-U133 to HG-U133 Plus, No Match (zip, 1 KB)
 - HG-U95 to HG-U133, Best Match (zip, 842 KB)
 - HG-U95 to HG-U133, Complex (zip, 23.3 MB)
 - HG-U95 to HG-U133, Good Match (zip, 900 KB)
 - HG-U95 to HG-U133, No Match (zip, 54 KB)
- Right Sidebar:**
 - TECHNICAL SUPPORT:** United States / Canada (888-DNA-CHIP), Europe (+44 (0) 1628 552550), Japan (+81 3-5730-8222).
 - POPULAR DOWNLOADS:** Brochure, The GeneChip System; Data Sheet, Human Genome Arrays; Manual, Expression Analysis Technical Manual; Manual, Data.

Affymetrix Annotations for HU133

Scroll to get a list of available files.



Affymetrix Main Annotation Files

There are three primary annotation files:

Probe Sequence File: Contains a complete listing of all the probes (25-mers) and probe sets on the microarray. (In tab-separated values format, the zipped file is 4.1MB; unzipped, it is 14.4MB.)

Alignment File: Contains mappings of targets and probes to the human genome. (In PSL format, the zipped file is 3.6MB; unzipped, it is 12.7MB.)

Annotation File: Contains the updated annotations of all the genes targeted by the microarray. (In comma-separated-value format, the zipped file is 6.1MB; unzipped, it is 47.9MB.)

Affymetrix Probe Sequences for HU133

The HG-U133A_probe_tab file lists the probe sequences.

	A	B	C	D	E	F
	Probe Set Name	Probe X	Probe Y	Probe Interrogation Position	Probe Sequence	Target Strandedness
1						
2	1007_s_at	467	181	3330	CACCCAGCTGGTCCTGTGGATGGGA	Antisense
3	1007_s_at	531	299	3443	GCCCCACTGGACAACACTGATTCCCT	Antisense
4	1007_s_at	86	557	3512	TGGACCCCACTGGCTGAGAATCTGG	Antisense
5	1007_s_at	365	115	3563	AAATGTTTTCTTGTGCCTGCTCCTG	Antisense
6	1007_s_at	207	605	3570	TCCTTGTGCCTGCTCCTGTACTTGT	Antisense
7	1007_s_at	593	599	3576	TGCCTGCTCCTGTACTTGTCTCTCAG	Antisense
8	1007_s_at	425	607	3583	TCCTGTACTTGTCTCAGCTTGGGC	Antisense
9	1007_s_at	552	101	3589	ACTTGTCTCAGCTTGGGCTTCTTC	Antisense
10	1007_s_at	680	607	3615	TCCTCCATCACCTGAAACACTGGAC	Antisense
11	1007_s_at	532	139	3713	AAGCCTATACGTTTCTGTGGAGTAA	Antisense
12	1007_s_at	143	709	3786	TTGGACATCTCTAGTGTAGCTGCCA	Antisense
13	1007_s_at	285	623	3793	TCTCTAGTGTAGCTGCCACATTGAT	Antisense
14	1007_s_at	383	479	3799	GTGTAGCTGCCACATTGATTTTTCT	Antisense
15	1007_s_at	129	279	3807	GCCACATTGATTTTTCTATAATCAC	Antisense
16	1007_s_at	62	651	3871	TACACTAATATATGGACCTAGCTTG	Antisense
17	1007_s_at	308	15	3878	ATATATGGACCTAGCTTGAGGCAAT	Antisense
18	1053_at	359	635	1090	TCACCAGAAGATATCATTGGCAACA	Antisense
19	1053_at	182	25	1102	ATCATTGGCAACATCTTTCGAGTGT	Antisense
20	1053_at	375	537	1108	GGCAACATCTTTCGAGTGTGTA AAA	Antisense
21	1053_at	284	569	1126	TGTA AAACTTTCCAAATGGCAGAAT	Antisense
22	1053_at	597	515	1180	GGATACACTCACATGAAAATAGCGG	Antisense

Affymetrix Alignment Information for HU133

The HG-U133A.link.psl file aligns the probes to the genome.

```

emacs@BSFC2-COOMBES
File Edit Options Buffers Tools Help
# Filename: HG-U133A.link.psl
# Array: HG-U133A
# Genome: Human_May_2004
# Date: Fri Sep  3 16:41:38 PDT 2004.
#
# This PSL file contains alignments of Affymetrix consensus and exemplar
# sequences to a genome, and the mapping of Affymetrix probe sets,
# poly-A sites, and poly-A stacks onto those sequences.
#
# Feature types are segregated in blocks, each preceded by a track line.
#
# For terms of use, see http://www.affymetrix.com/site/terms.affx
#
track name="HG-U133A netaffx consensus" description="Consensus Sequences"
0      16      192      1      2      5      2      174      -      HG
s-U133A:217524_X_AT      416      51      265      chr10      0      104279249
s      104279632      4      53,26,123,7,      151,206,232,358,      104279
s249,104279302,104279500,104279625,
0      17      244      10      4      27      4      33      +      HG
s-U133A:217625_X_AT      477      15      313      chr14      0      74280760
s      74281064      5      24,44,62,8,133,      15,43,90,171,180,      742807
s60,74280795,74280841,74280909,74280931,
0      18      388      0      3      14      8      501      -      HG
s-U133A:208120_X_AT      849      393      813      chr14      0      22175357
s      22176264      9      179,27,8,8,9,73,24,61,17,      36,215,245,261
s,272,281,354,378,439,      22175357,22175690,22175718,22175737,22175751,221
s75927,22176078,22176185,22176247,
0      21      256      1      2      25      2      7      -      HG
s-U133A:217650_X_AT      671      222      525      chr14      0      93075015
s      93075300      3      166,52,60,      146,324,389,      93075015,93075
s182,93075240,
0      22      294      0      4      302      5      937835      +      HG
s-U133A:217501_AT      811      34      652      chr16      0      20791663
s      21729814      6      114,30,55,45,7,65,      34,148,186,244,293,587
s,20791663,21055794,21433872,21433929,21549291,21729749,
--(Unix)-- HG-U133A.link.psl Tue Jul 19 2:42PM (Text File)--L??--Top-----
Mark set

```


What annotations does Affymetrix supply?

As noted earlier, HG-U133A_annot.csv contains 47.9MB worth of annotation information. What occupies all that space?

1	Probe Set ID	GeneChip Array	Species	Scienti	Annotation Date	Sequence Type	Sequence Source	Transcript ID(Array D	Target Desc Repr
2	1007_s_at	Human Genome U133A	Homo sapiens		20-Jun-05	Exemplar sequence	Affymetrix Propriet	U48705mRNA	U48705 /FEU487
3	1053_at	Human Genome U133A	Homo sapiens		20-Jun-05	Exemplar sequence	GenBank	M87338	M87338 /FIM873
4	117_at	Human Genome U133A	Homo sapiens		20-Jun-05	Exemplar sequence	Affymetrix Propriet	X51757cgs	X51757 /FEX517
5	121_at	Human Genome U133A	Homo sapiens		20-Jun-05	Exemplar sequence	GenBank	X69699	X69699 /FEX696
6	1255_g_at	Human Genome U133A	Homo sapiens		20-Jun-05	Exemplar sequence	Affymetrix Propriet	L36861expanded_cc	L36861 /FEL368
7	1294_at	Human Genome U133A	Homo sapiens		20-Jun-05	Exemplar sequence	GenBank	L13852	L13852 /FEL138
8	1316_at	Human Genome U133A	Homo sapiens		20-Jun-05	Exemplar sequence	Affymetrix Propriet	X55005mRNA	X55005 /FEX550
9	1320_at	Human Genome U133A	Homo sapiens		20-Jun-05	Exemplar sequence	Affymetrix Propriet	X79510cgs	X79510 /FEX795
10	1405_i_at	Human Genome U133A	Homo sapiens		20-Jun-05	Exemplar sequence	GenBank	M21121	M21121 /FIM21
22275	AFFX-r2-Hs28:	Human Genome U133A	Homo sapiens		20-Jun-05	Control sequence	Affymetrix Propriet	AFFX-r2-Hs28SrRNA	M11167.1 HAF
22276	AFFX-r2-Hs28:	Human Genome U133A	Homo sapiens		20-Jun-05	Control sequence	Affymetrix Propriet	AFFX-r2-Hs28SrRNA	M11167.1 HAF
22277	AFFX-r2-P1-cr:	Human Genome U133A	Homo sapiens		20-Jun-05	Control sequence	Affymetrix Propriet	AFFX-r2-P1-cre-3	Bacteriophaf
22278	AFFX-r2-P1-cr:	Human Genome U133A	Homo sapiens		20-Jun-05	Control sequence	Affymetrix Propriet	AFFX-r2-P1-cre-5	Bacteriophaf
22279	AFFX-ThrX-3_	Human Genome U133A	Homo sapiens		20-Jun-05	Control sequence	Affymetrix Propriet	AFFX-ThrX-3	B. subtilis /CAF
22280	AFFX-ThrX-5_	Human Genome U133A	Homo sapiens		20-Jun-05	Control sequence	Affymetrix Propriet	AFFX-ThrX-5	B. subtilis /CAF
22281	AFFX-ThrX-M_	Human Genome U133A	Homo sapiens		20-Jun-05	Control sequence	Affymetrix Propriet	AFFX-ThrX-M	B. subtilis /CAF
22282	AFFX-TrpnX-3	Human Genome U133A	Homo sapiens		20-Jun-05	Control sequence	Affymetrix Propriet	AFFX-TrpnX-3	B. subtilis /CAF
22283	AFFX-TrpnX-5	Human Genome U133A	Homo sapiens		20-Jun-05	Control sequence	Affymetrix Propriet	AFFX-TrpnX-5	B. subtilis /CAF
22284	AFFX-TrpnX-M	Human Genome U133A	Homo sapiens		20-Jun-05	Control sequence	Affymetrix Propriet	AFFX-TrpnX-M	B. subtilis /CAF

First, we note that the file seems to contain redundant copies of lots of information. Second, it has information on 22,283 probe sets, one per line, in 43 columns.

Description of annotation columns

Probe Set ID. The unique identifier that describes an Affymetrix probe set. Also used in CEL files and CDF files.

GeneChip Array. The chip type on which the probe set appears. The same entry is repeated for all probe sets.

Species Scientific Name. The scientific name of the species whose gene sequences are on the array. The same information is repeated for all probe sets.

Annotation Date. The date when the annotations were last updated. The same information is repeated for all probe sets.

Sequence Type. The kind of sequence used in the design of the array: can be “Consensus”, “Control”, or “Exemplar”.

Sequence Source. Where did the design sequence come from? Usually “GenBank”, but rarely (only 81 times on the HG-U133A) from “Affymetrix Proprietary Database”.

Transcript ID(Array Design). An identifier into one of several unspecified databases indicating the designed target sequence.

Target Description. Long text string describing the target, formed by combining several other fields.

Representative Public ID. For non-control sequences, a GenBank identifier.

Archival UniGene Cluster. The UniGene cluster identifier from the sequence at the time the array was designed (in this case, from UniGene build 133).

UniGene ID. UniGene cluster identifier from the build of UniGene current at the time the annotations were updated.

Genome Version. The build of the human genome used for sequence alignments. The same information is repeated for all probe sets.

Alignments. Location of the target sequence along the human genome, in base pairs along the chromosome.

Gene Title. Official gene title (either from UniGene or Entrez Gene).

Gene Symbol. Official gene symbol (either from UniGene or Entrez Gene).

Chromosomal Location. Location of the gene in terms of

cytogenetic bands; e.g., 16p12.

Unigene Cluster Type. Either absent if not present in this build of UniGene (indicated by “—”), “est”, “full length”, or “est /// full length”.

Ensembl. The unique identifier of the target sequence in the Ensembl database.

Entrez Gene. The unique identifier of the target sequence in Entrez Gene (formerly LocusLink). Sequences with these identifiers tend to be better understood and more reliable than genes without them. The identifiers refer to genetic loci that have been mapped explicitly because of their connection to specific diseases or biological processes.

SwissProt. The SwissProt identifier of the protein product

produced by the gene corresponding to the target sequence.

EC. Yet another database identifier.

OMIM. The unique identifier associated to the target sequence gene in the Online Mendelian Inheritance in Man (OMIM) database, describing the ways in which the gene is known to be associated with genetic diseases.

RefSeq Protein ID. The GenBank identifier of the consensus sequence for the protein produced by the target sequence.

RefSeq Transcript ID. The GenBank identifiers of the consensus sequences for the mRNA's produced by the target gene. (Alternative splicing accounts for multiples.) In many cases, this coincides with the "Representative Public ID".

FlyBase. Corresponding identifier in the drosophila database.

AGI. Unknown.

WormBase. Corresponding identifier in the *C. elegans* database.

MGI Name. Probably the identifier in the mouse database.

RGD Name. Probably the identifier in the rat database.

SGD accession number. The identifier in the saccharomyces database.

Gene Ontology Biological Process. List of identifiers for annotations of the target gene into the “biological process” section of GeneOntology. More about this later.

Gene Ontology Cellular Component. Similar.

Gene Ontology Molecular Function. Similar.

Pathway. List of pathways that the target sequence is involved in.

Protein Families. Families to which the protein belongs.

Protein Domains. Domains included in the protein.

InterPro. Another protein database.

Trans Membrane. Description of trans-membrane part of the protein, if known or if applicable.

QTL. Unknown.

Annotation Description. Text description of how the probe set was annotated.

Annotation Transcript Cluster. Unclear.

Transcript Assignments. Very long description of the annotations.

Annotation Notes. Additional comments.

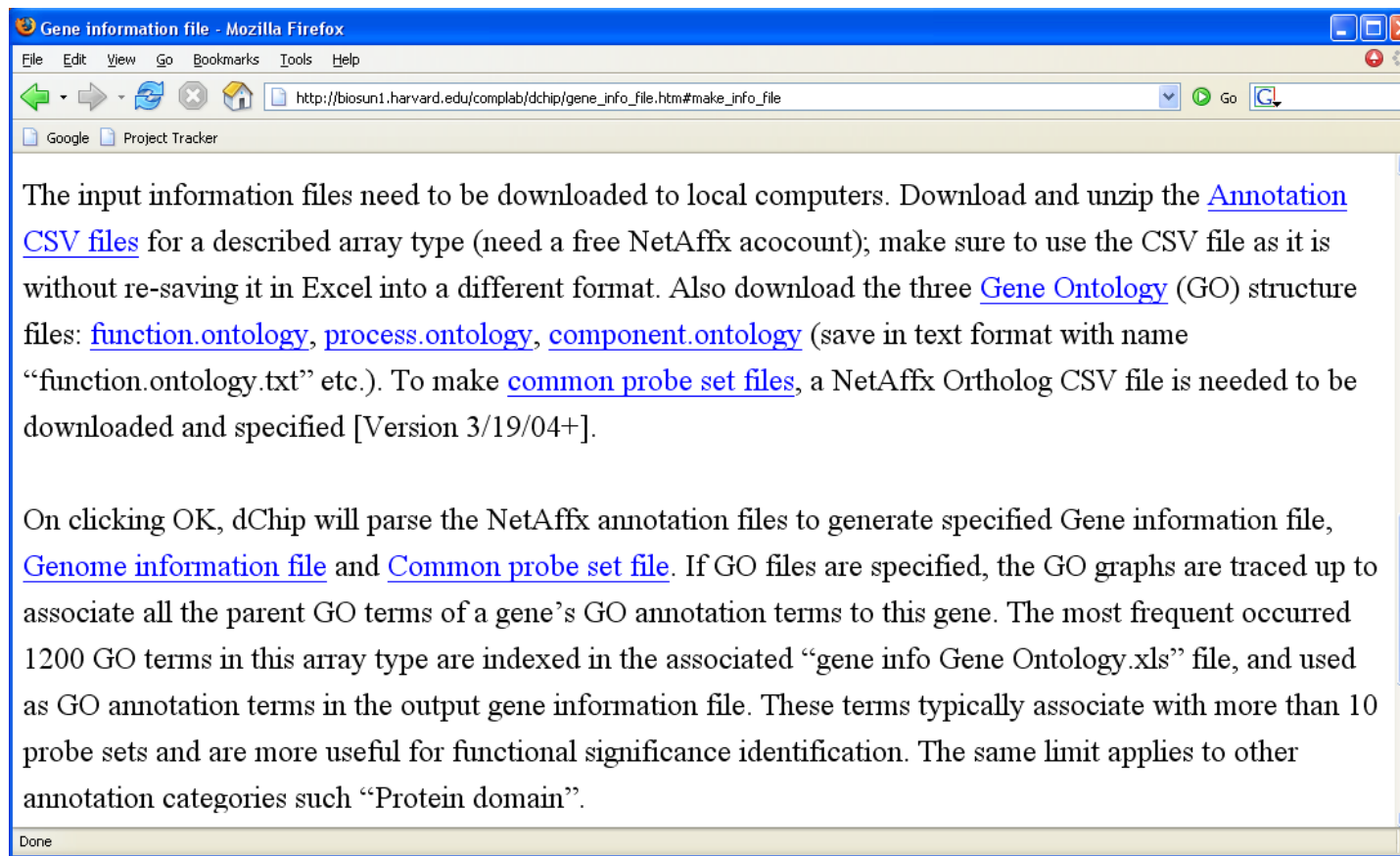
Updating annotations in dChip

In order for dChip (or any other Affymetrix microarray analysis package) to use the updated annotations, you have to tell the software package where to get the information.

In the case of dChip, their online manual page tells you how to build new gene information and genome information files.

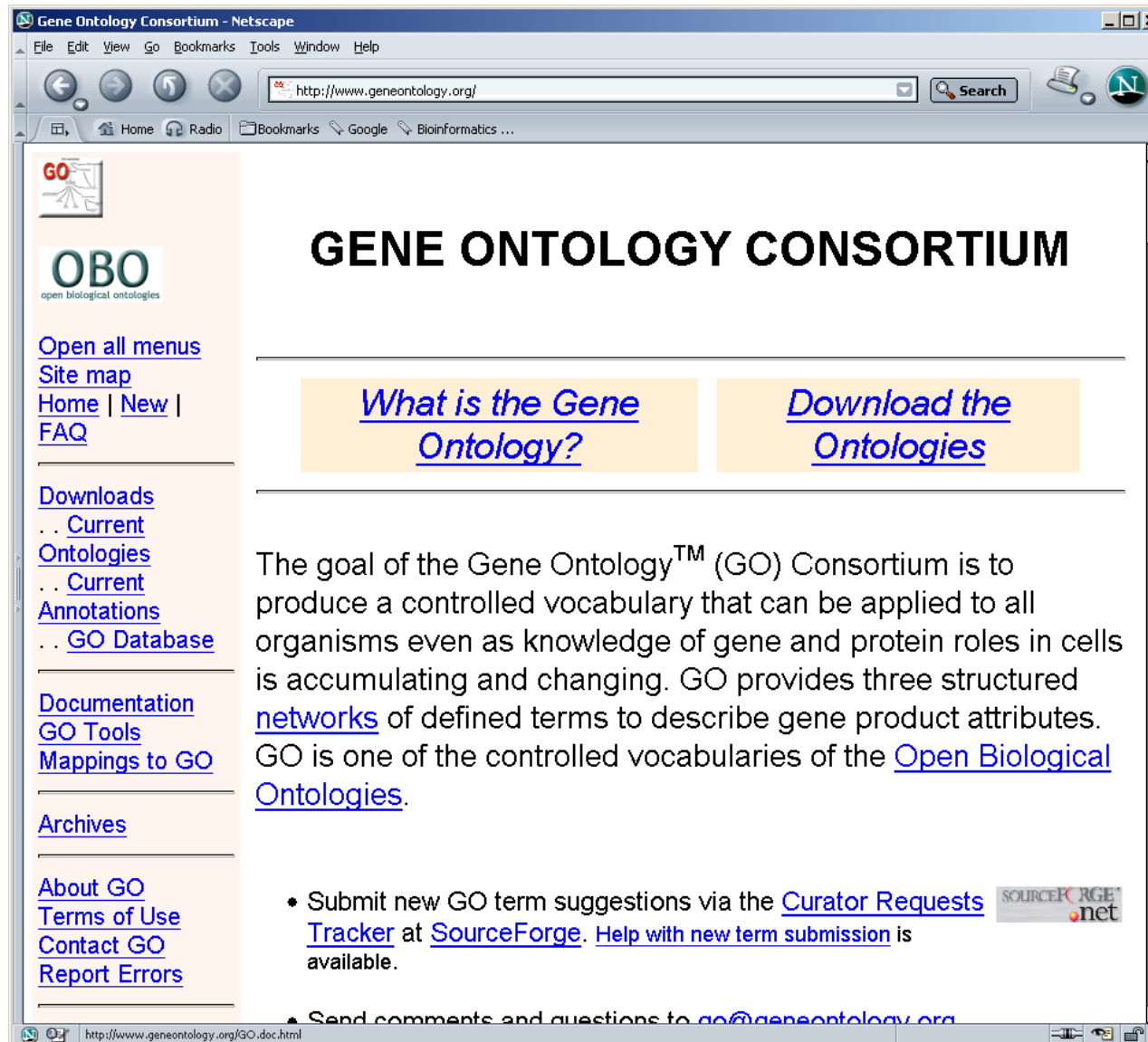
For many common chip types, the dChip web site contains up-to-date copies of these files. It's still useful to see where the data comes from how and how you can update your own versions.

dChip Manual on Gene Information



Requires the annotation CSV files from Affymetrix, along with three Gene Ontology files, which you can get from dChip or from the primary source.

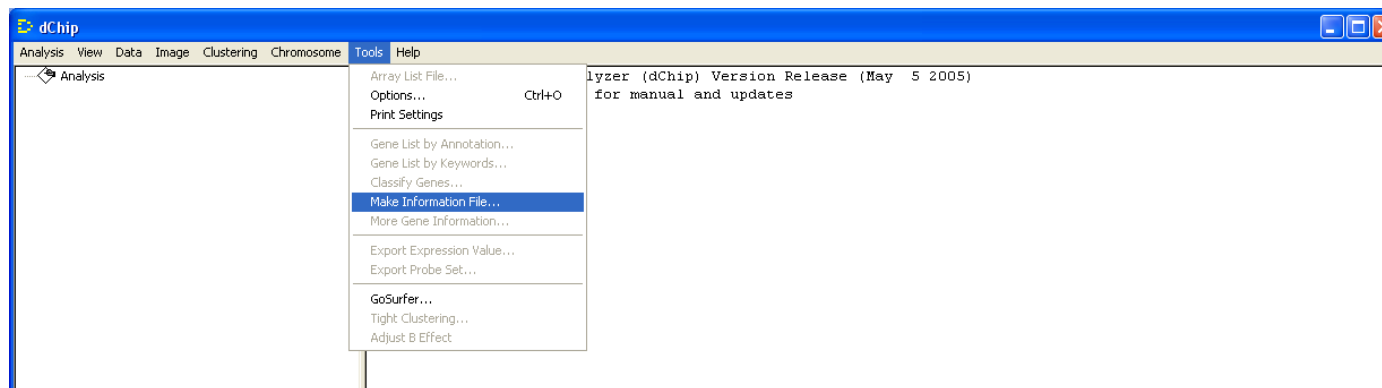
http://www.geneontology.org



The screenshot shows a Netscape browser window displaying the Gene Ontology Consortium website. The browser's address bar shows the URL <http://www.geneontology.org/>. The website features a navigation menu on the left with links such as "Open all menus", "Site map", "Home", "New", "FAQ", "Downloads", "Current Ontologies", "Current Annotations", "GO Database", "Documentation", "GO Tools", "Mappings to GO", "Archives", "About GO", "Terms of Use", "Contact GO", and "Report Errors". The main content area is titled "GENE ONTOLOGY CONSORTIUM" and includes two prominent buttons: "What is the Gene Ontology?" and "Download the Ontologies". Below these buttons, a paragraph explains the consortium's goal: "The goal of the Gene Ontology™ (GO) Consortium is to produce a controlled vocabulary that can be applied to all organisms even as knowledge of gene and protein roles in cells is accumulating and changing. GO provides three structured networks of defined terms to describe gene product attributes. GO is one of the controlled vocabularies of the Open Biological Ontologies." A bulleted list at the bottom provides instructions on how to submit new GO term suggestions via the Curator Requests Tracker at SourceForge and how to contact the consortium via email at go@geneontology.org. A SourceForge.net logo is also visible.

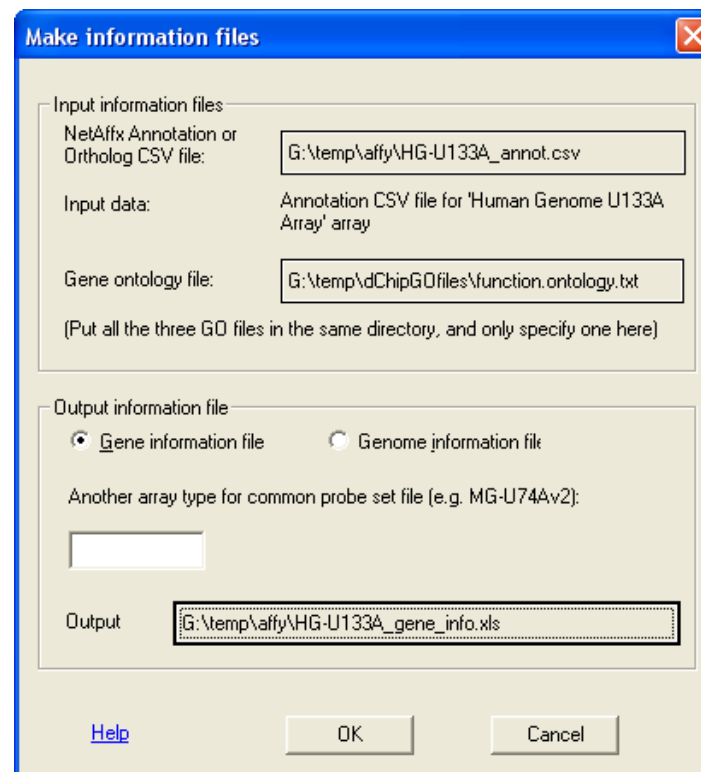
Making the Gene Information file

1. Get and unzip the file containing the updated annotation CSV file from Affymetrix.
2. Get the three updated text files from GeneOntology.
3. Rename the three GeneOntology files, adding the “.txt” extension.
4. Use “Tools” – > “Make information file” in dChip.

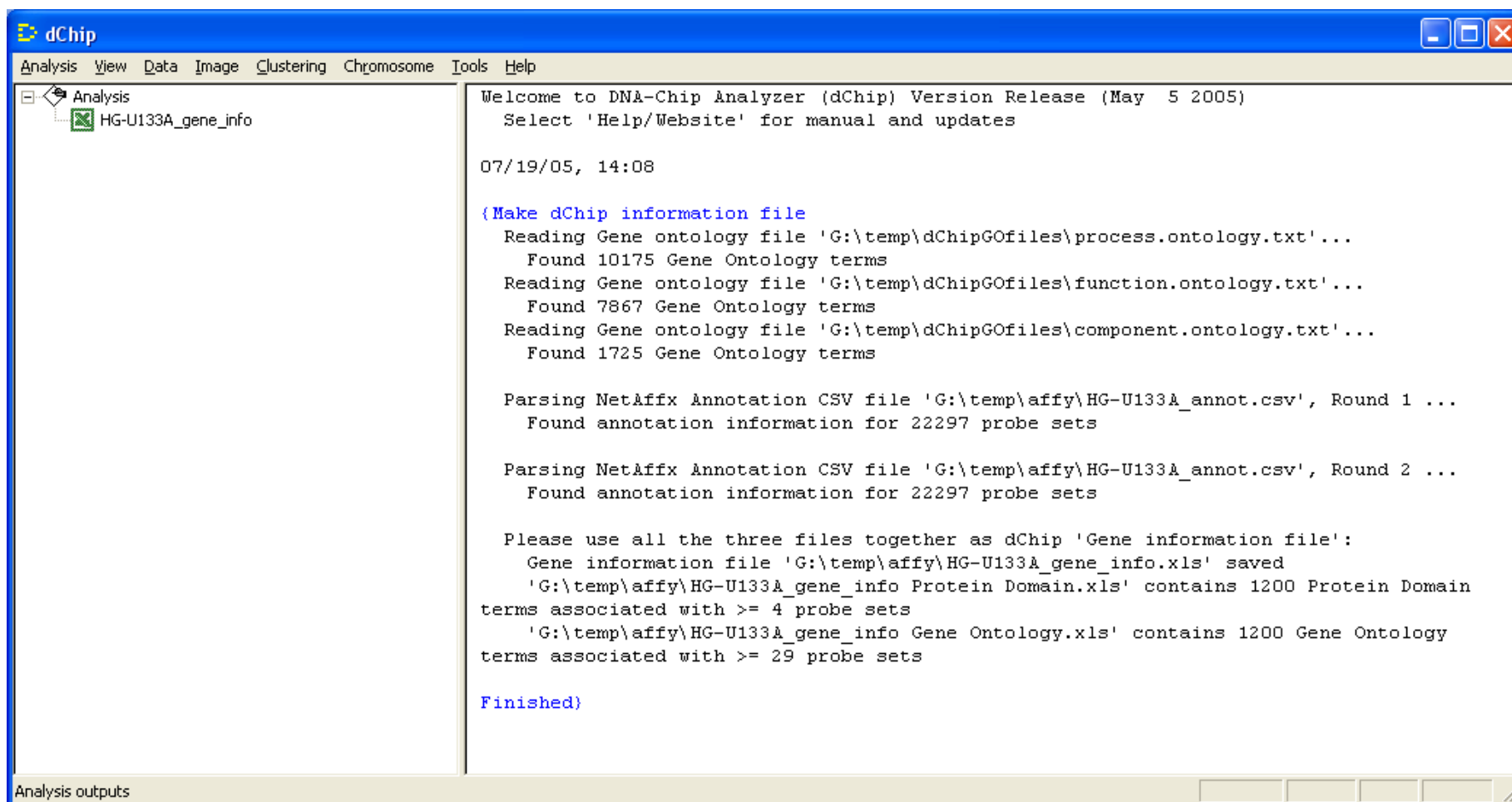


Making the Gene Information file

Specify the locations of the CSV file and the GeneOntology files. Also say where you want the output sent. Note that I edited the default output file name to (i) start with the standard chip name and (2) use the underscore character as a separator.



The Gene Information file



The screenshot shows the dChip software window with a menu bar (Analysis, View, Data, Image, Clustering, Chromosome, Tools, Help) and a tree view on the left containing 'Analysis' and 'HG-U133A_gene_info'. The main window displays the following text:

```
Welcome to DNA-Chip Analyzer (dChip) Version Release (May 5 2005)
Select 'Help/Website' for manual and updates

07/19/05, 14:08

{Make dChip information file
Reading Gene ontology file 'G:\temp\dChipGOfiles\process.ontology.txt'...
  Found 10175 Gene Ontology terms
Reading Gene ontology file 'G:\temp\dChipGOfiles\function.ontology.txt'...
  Found 7867 Gene Ontology terms
Reading Gene ontology file 'G:\temp\dChipGOfiles\component.ontology.txt'...
  Found 1725 Gene Ontology terms

Parsing NetAffx Annotation CSV file 'G:\temp\affy\HG-U133A_annot.csv', Round 1 ...
  Found annotation information for 22297 probe sets

Parsing NetAffx Annotation CSV file 'G:\temp\affy\HG-U133A_annot.csv', Round 2 ...
  Found annotation information for 22297 probe sets

Please use all the three files together as dChip 'Gene information file':
Gene information file 'G:\temp\affy\HG-U133A_gene_info.xls' saved
'G:\temp\affy\HG-U133A_gene_info Protein Domain.xls' contains 1200 Protein Domain
terms associated with >= 4 probe sets
'G:\temp\affy\HG-U133A_gene_info Gene Ontology.xls' contains 1200 Gene Ontology
terms associated with >= 29 probe sets

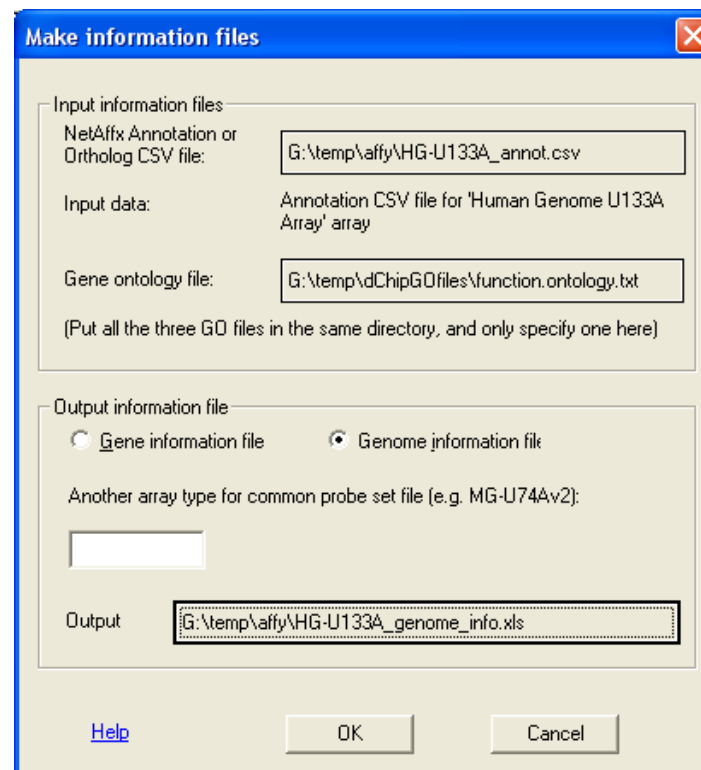
Finished}
```

Analysis outputs

This step produces the three dChip annotation files that were described in Lecture 2.

Making the Genome Information file

Using the same input files, you can also use dChip to create a “Genome information file”, which maps genes to specific positions along the genome.



The Genome Information file

Microsoft Excel - HG-U133A_genome_info.xls

File Edit View Insert Format Tools Data Window Help

D36 = 19816101

	A	B	C	D	E	F	G
	Probe Set	chromosome	Start	End	Strand	Cytoband	
1	1007_s_at	chr6	30964144	30975910	+		
2	1053_at	chr7	73090653	73113383	-		
3	117_at	chr1	158307503	158309435	+		
4	121_at	chr2	113691170	113752718	-		
5	1255_g_at	chr6	42248919	42255770	+		
6	1294_at	chr3	49817643	49826427	-		
7	1316_at	chr17	35472681	35499815	+		
8	1320_at	chr14	88004233	88086514	-		
9	1405_i_at	chr17	31222639	31231443	-		
10	1431_at	chr10	135229780	135241349	+		
11	1438_at	chr3	185771805	185782112	+		
12	1487_at	chr11	63829619	63840786	+		
13	1494_f_at	chr19	46286211	46293938	+		
14	1494_f_at	chr19	46041286	46048179	-		
15	1494_f_at	chr19	46073184	46079963	-		
16	1598_g_at	chr13	113546912	113590396	+		
17	160020_at	chr14	22375647	22386642	+		
18	1729_at	chr16	65745604	65751281	-		

Ready

What is GeneOntology?

GeneOntology uses controlled vocabularies to create a directed acyclic graph (DAG; a generalized tree) that describes the kinds of functions or properties that a gene might have. There are two parts to GeneOntology:

- Annotations, maintained in databases like Entrez Gene, that describe which genes actually have which functions.
- The DAG, maintained by the GeneOntology Consortium, that describes functions and relations between them:
 1. Biological process (what)
 2. Molecular function (how)
 3. Cellular component (where)

GeneOntology: The top level

Gene Ontology Consortium - Netscape

File Edit View Go Bookmarks Tools Window Help

http://www.geneontology.org/ Search

Home Radio Bookmarks Google Bioinformatics ...

The Ontologies

Molecular Function Ontology	the tasks performed by individual gene products; examples are <i>carbohydrate binding</i> and <i>ATPase activity</i>
Biological Process Ontology	broad biological goals, such as <i>mitosis</i> or <i>purine metabolism</i> , that are accomplished by ordered assemblies of molecular functions
Cellular Component Ontology	subcellular structures, locations, and macromolecular complexes; examples include <i>nucleus</i> , <i>telomere</i> , and <i>origin recognition complex</i>

Additional information

FAQ	Answers to questions that are very commonly asked about the Gene Ontology.
Introduction	A description of the aims of the Gene Ontology Consortium and an explanation of how the ontologies work.
Editorial Style Guide	Rules governing content and stylistic aspects of GO terms, such as phrasing, spelling, case, etc.

GeneOntology annotations in Entrez Gene

You can find the GeneOntology annotations for individual genes in Entrez Gene. For genes with known functions, the Entrez Gene page will contain a section titled “GeneOntology”, which contains a list of the known functions for that gene.

Every GO annotation asserts that a specific gene has a specific function. As part of the design of GO, each assertion is itself annotated to explain the kinds of evidence the assertion is based on, as well as the organization or individual that supplied the annotation.

GO annotations of the androgen receptor

Gene - Mozilla Firefox

File Edit View Go Bookmarks Tools Help

http://www.ncbi.nlm.nih.gov/entrez/query.fcgi?db=gene&cmd=Retrieve&dopt=Graphics&list_uids=367

Gene information file Gene

► General gene information ?

GeneOntology
Provided by [GOA](#)

Function	Evidence
androgen binding	NAS PubMed
androgen receptor activity	IEA PubMed
androgen receptor activity	NAS PubMed
metal ion binding	IEA
protein dimerization activity	NAS PubMed
receptor activity	IEA
steroid binding	IEA
transcription factor activity	IEA

Process	Evidence
cell proliferation	NAS PubMed
cell-cell signaling	TAS PubMed
prostate gland development	NAS PubMed
regulation of transcription, DNA-dependent	IEA
sex differentiation	NAS PubMed
signal transduction	TAS PubMed
transcription	IEA
transport	TAS PubMed

Component	Evidence
nucleus	NR
nucleus	IEA

Done

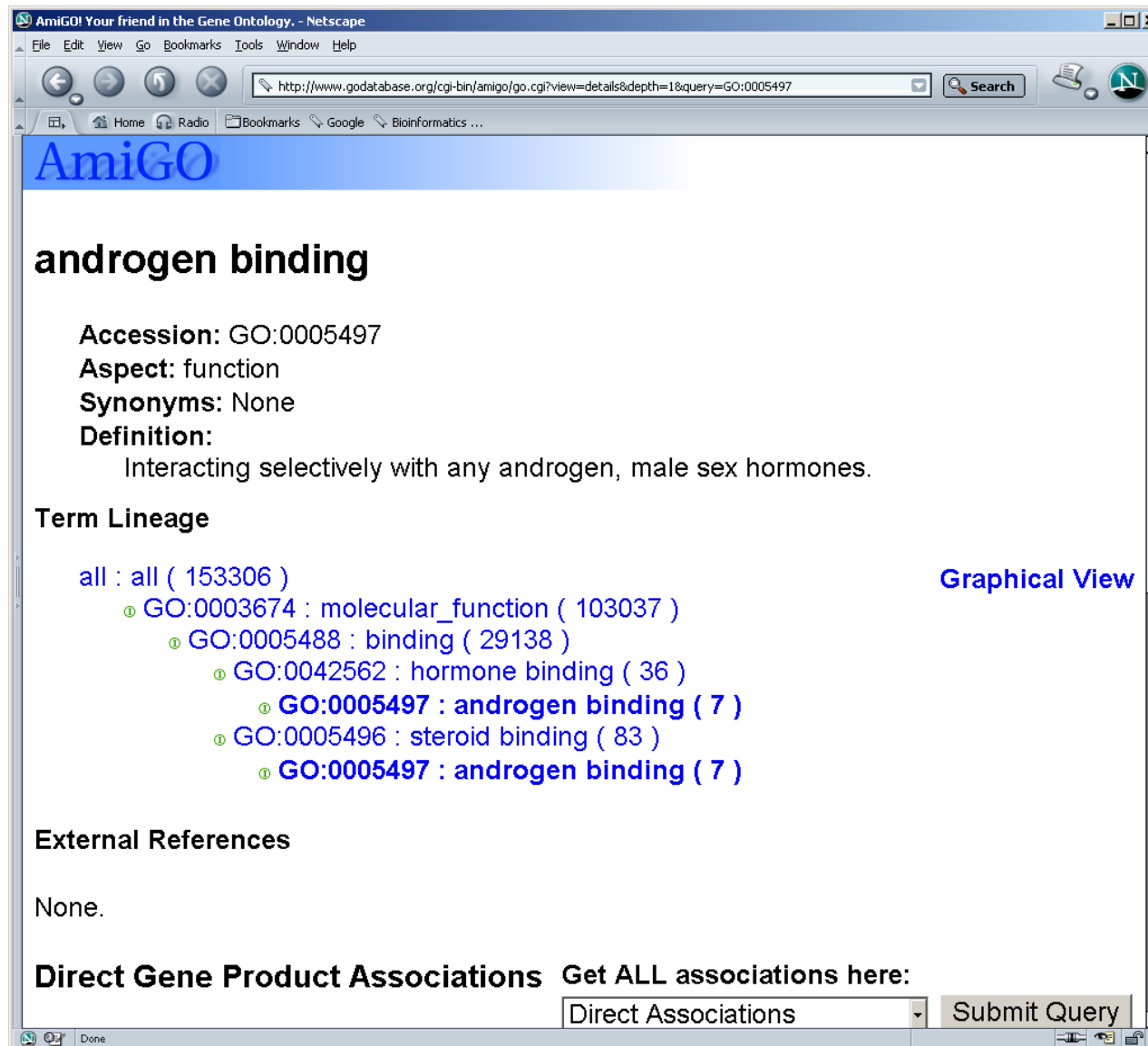
http://www.ebi.ac.uk/GOA/

The screenshot shows the Gene Ontology Annotation (GOA) website at EBI. The browser window title is "Gene Ontology Annotation @ EBI - Netscape". The address bar shows "http://www.ebi.ac.uk/GOA/". The page header includes the EMBL-EBI logo and navigation links: EBI Home, About EBI, Research, Services, Toolbox, Databases, Downloads, Submissions. A search bar is present with the text "Get Nucleotide sequences for" and a "Go" button. The main content area is titled "GOA DATABASE" and contains the following sections:

- GOA @EBI**: A section with a logo and text stating: "GOA is a project run by the European Bioinformatics Institute that aims to provide assignments of gene products to the Gene Ontology (GO) resource." It also includes a paragraph: "The goal of the Gene Ontology Consortium is to produce a dynamic controlled vocabulary that can be applied to all organisms, even while knowledge of gene and protein roles in cells is still accumulating and changing. In the GOA project, this vocabulary will be applied to a non-redundant set of proteins described in the UniProt Resource (Swiss-Prot/TrEMBL/PIR-PSD) and Ensembl databases that collectively provide complete proteomes for Homo sapiens and other organisms." and another paragraph: "In the first stage of this project, GO assignments have been applied to a data set representing the human proteome by a combination of electronic mappings and manual curation. Subsequently, GO assignments for all complete and incomplete proteomes that exist in UniProt have been".
- Access GOA**: A section with a search bar and a "Go" button, labeled "Search GOA via SRS".
- GO**: A section with a diagram of the Gene Ontology hierarchy and text: "The EBI's Gene Ontology Consortium pages. GO is an international consortium of scientists with the editorial office based at the EBI."
- UniProt/Swiss-Prot**: A section with a small image of a protein structure.

A sidebar on the left contains a "GOA Home" logo and a list of links: GOA Home, Introduction, Contents of Current Release, Data Searching and Retrieval, Forthcoming Changes, GOA News, and Feedback.

GO browsing



AmiGO! Your friend in the Gene Ontology. - Netscape

File Edit View Go Bookmarks Tools Window Help

http://www.godatabase.org/cgi-bin/amigo/go.cgi?view=details&depth=1&query=GO:0005497 Search

Home Radio Bookmarks Google Bioinformatics ...

AmiGO

androgen binding

Accession: GO:0005497
Aspect: function
Synonyms: None
Definition:
Interacting selectively with any androgen, male sex hormones.

Term Lineage

all : all (153306) [Graphical View](#)

- GO:0003674 : molecular_function (103037)
 - GO:0005488 : binding (29138)
 - GO:0042562 : hormone binding (36)
 - GO:0005497 : androgen binding (7)**
 - GO:0005496 : steroid binding (83)
 - GO:0005497 : androgen binding (7)

External References

None.

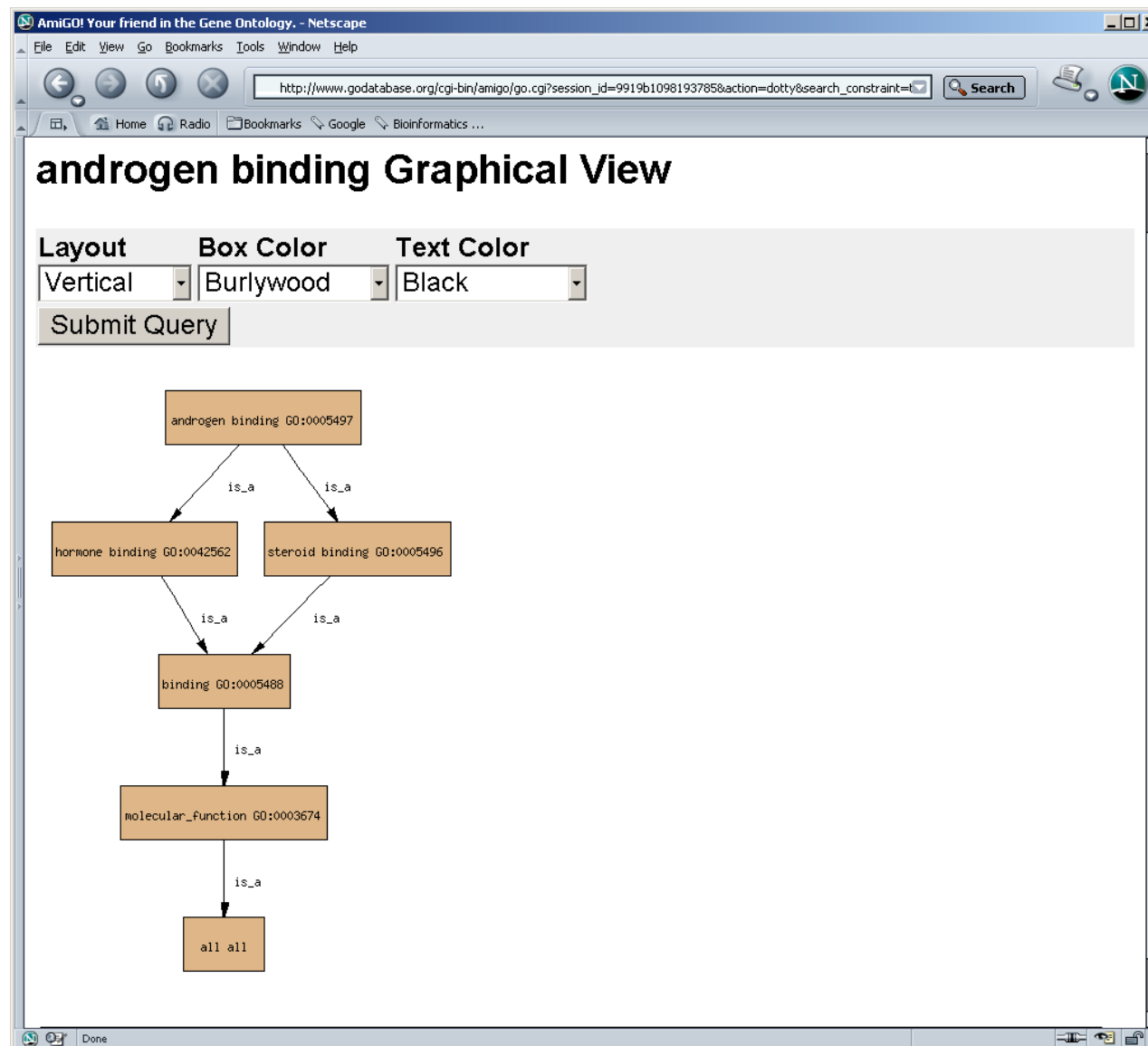
Direct Gene Product Associations

Get ALL associations here:

Direct Associations

Done

GO browsing



Edges are relationships

Edges in the DAG represent two kinds of relationships:

is_a : Used when the child node is a special case of the parent node. For example, `hormone binding` is_a kind of `binding`.

part_of : Used when the child node is a component of the parent node. For example, a `membrane` is part_of a `cell`

Genes may be annotated into different levels of the hierarchy, depending on how detailed the evidence is. In general, a gene not only has the function corresponding to the node with direct annotation, but also has every property at parent nodes up through the hierarchy.

GO annotations of the androgen receptor

Gene - Mozilla Firefox

File Edit View Go Bookmarks Tools Help

http://www.ncbi.nlm.nih.gov/entrez/query.fcgi?db=gene&cmd=Retrieve&dopt=Graphics&list_uids=367

Gene information file Gene

► General gene information ?

GeneOntology
Provided by [GOA](#)

Function	Evidence
androgen binding	NAS PubMed
androgen receptor activity	IEA PubMed
androgen receptor activity	NAS PubMed
metal ion binding	IEA
protein dimerization activity	NAS PubMed
receptor activity	IEA
steroid binding	IEA
transcription factor activity	IEA

Process	Evidence
cell proliferation	NAS PubMed
cell-cell signaling	TAS PubMed
prostate gland development	NAS PubMed
regulation of transcription, DNA-dependent	IEA
sex differentiation	NAS PubMed
signal transduction	TAS PubMed
transcription	IEA
transport	TAS PubMed

Component	Evidence
nucleus	NR
nucleus	IEA

Done

GeneOntology: Evidence Codes

IDA : inferred from direct assay; indicates that the annotation is based on a paper describing an experiment that directly tested this function for this gene

TAS : traceable author statement; based on a review article or textbook that includes references to the original experiments

IMP : inferred from mutant phenotype; based on experiments involving mutations, knockouts, antisense, etc.

IPI : inferred from physical interaction; based on assays (like co-immunoprecipitation) that demonstrate physical interactions between the gene in question and other gene products

IGI : inferred from genetic interaction; based on experiments (such as synthetic lethals, suppressors, functional complementation) that show a genetic interaction between the gene in question and another gene

ISS : inferred from sequence or structure similarity; based on BLAST results that have been reviewed for accuracy by a curator

IEP : inferred from expression pattern; based on Northern, Westerns, or microarray experiments that reveal information about the timing or location of expression

NAS : non-traceable author statement; statements in papers (abstract, introduction, discussion) that a curator cannot trace to another publication

IEA : inferred from electronic annotation; based on sequence similarity searches or database records that have not been reviewed by a curator

IC : inferred by curator; even though no direct evidence is available, the property can reasonably be inferred by the curator. For example, it is reasonable to infer from direct evidence of “transcription factor activity” that the gene product is found in the nucleus

ND : no biological data available; only used for annotations to “unknown”

NR : not recorded; used only for annotations created before curators started adding evidence codes

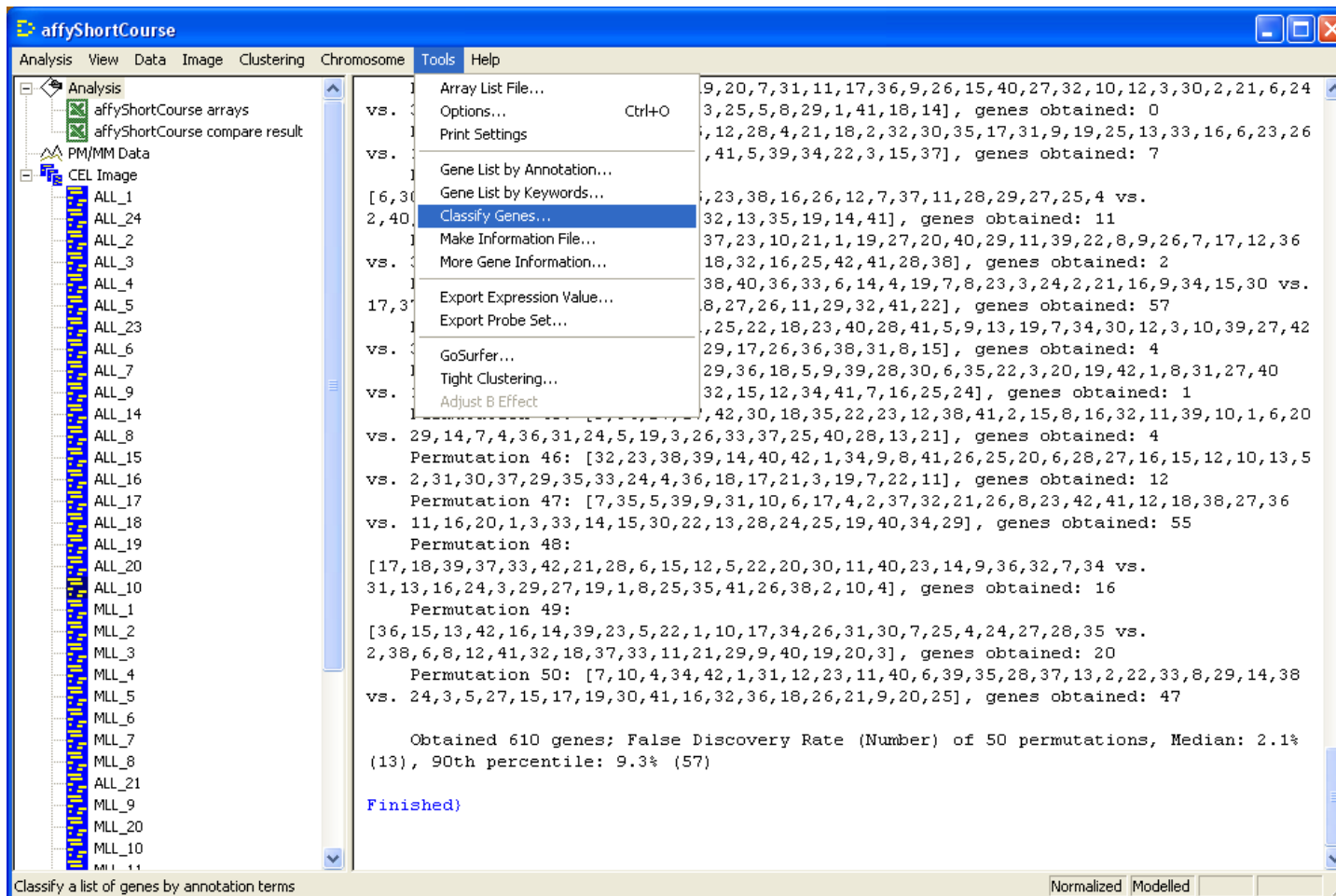
Quality of evidence

The evidence codes fall into a rough hierarchy indicating how strongly the annotation of function should be believed.

1. IDA, TAS
2. IMP, IPI, IGI
3. ISS, IEP
4. NAS
5. IEA
6. IC

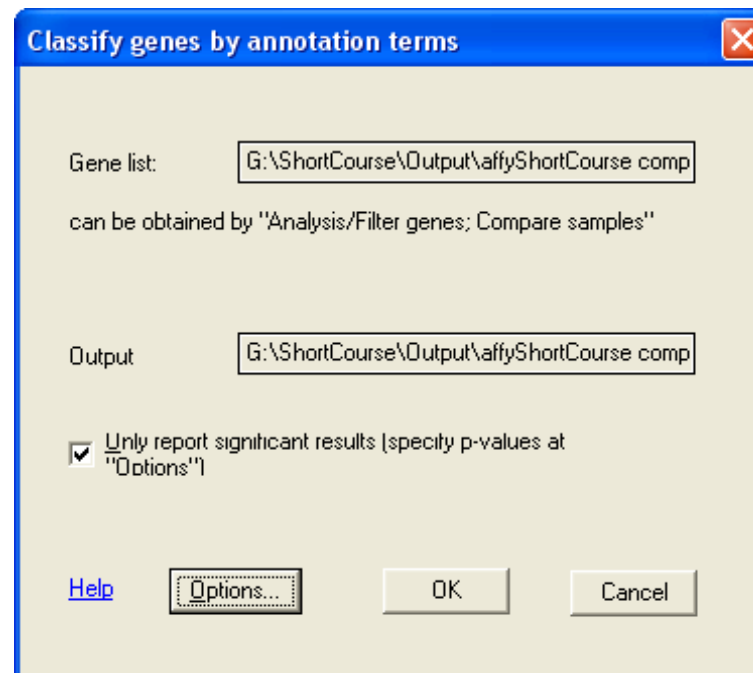
Using GeneOntology in dChip

After running a sample comparison to find interesting genes, use the menu item “Tools” – > “Classify genes”.



Using GeneOntology in dChip

For the gene list file, select the “compare result” file produced previously. It’s also a good idea to check the box telling dChip only to report the groups with significant p-values.



Using GeneOntology in dChip

The results are available in a few seconds.

affyShortCourse

Analysis View Data Image Clustering Chromosome Tools Help

Analysis

- affyShortCourse arrays
- affyShortCourse compare result
- affyShortCourse compare result classified
- PM/MM Data
 - CEL Image
 - ALL_1
 - ALL_24
 - ALL_2
 - ALL_3
 - ALL_4
 - ALL_5
 - ALL_23
 - ALL_6
 - ALL_7
 - ALL_9
 - ALL_14
 - ALL_8
 - ALL_15
 - ALL_16
 - ALL_17
 - ALL_18
 - ALL_19
 - ALL_20
 - ALL_10
 - MLL_1
 - MLL_2
 - MLL_3
 - MLL_4
 - MLL_5
 - MLL_6
 - MLL_7
 - MLL_8
 - ALL_21
 - MLL_9
 - MLL_20
 - MLL_10

Analysis outputs

Permutation 43:
[16,4,20,21,25,22,18,23,40,28,41,5,9,13,19,7,34,30,12,3,10,39,27,42 vs.
32,1,33,2,35,14,24,6,11,37,29,17,26,36,38,31,8,15], genes obtained: 4

Permutation 44: [26,2,13,4,29,36,18,5,9,39,28,30,6,35,22,3,20,19,42,1,8,31,27,40
vs. 14,38,37,10,17,33,21,11,23,32,15,12,34,41,7,16,25,24], genes obtained: 1

Permutation 45:
[9,34,27,17,42,30,18,35,22,23,12,38,41,2,15,8,16,32,11,39,10,1,6,20 vs.
29,14,7,4,36,31,24,5,19,3,26,33,37,25,40,28,13,21], genes obtained: 4

Permutation 46:
[32,23,38,39,14,40,42,1,34,9,8,41,26,25,20,6,28,27,16,15,12,10,13,5 vs.
2,31,30,37,29,35,33,24,4,36,18,17,21,3,19,7,22,11], genes obtained: 12

Permutation 47: [7,35,5,39,9,31,10,6,17,4,2,37,32,21,26,8,23,42,41,12,18,38,27,36
vs. 11,16,20,1,3,33,14,15,30,22,13,28,24,25,19,40,34,29], genes obtained: 55

Permutation 48:
[17,18,39,37,33,42,21,28,6,15,12,5,22,20,30,11,40,23,14,9,36,32,7,34 vs.
31,13,16,24,3,29,27,19,1,8,25,35,41,26,38,2,10,4], genes obtained: 16

Permutation 49:
[36,15,13,42,16,14,39,23,5,22,1,10,17,34,26,31,30,7,25,4,24,27,28,35 vs.
2,38,6,8,12,41,32,18,37,33,11,21,29,9,40,19,20,3], genes obtained: 20

Permutation 50: [7,10,4,34,42,1,31,12,23,11,40,6,39,35,28,37,13,2,22,33,8,29,14,38
vs. 24,3,5,27,15,17,19,30,41,16,32,36,18,26,21,9,20,25], genes obtained: 47

Obtained 610 genes; False Discovery Rate (Number) of 50 permutations, Median: 2.1%
(13), 90th percentile: 9.3% (57)

Finished)

{Classify genes using annotational terms
Read in genes listed in file G:\ShortCourse\Output\affyShortCourse compare
result.xls...
Found 610 genes

G:\ShortCourse\Output\affyShortCourse compare result classified.xls exported
Finished)

Normalized Modelled

What do the results look like?

1	probe set	gene	baseline mean	baseline	experiment mean	experiment	fold change	filtered
3	Found 21 Gene Ontology "protein tyrosine kinase" genes in a list with 391 annotated genes (all: 157/7685, PValue: 0.000042) ****							
4	40936_at	cysteine-rich motor neuron 1	7994	564	5144	612	-1.55	*
5	1485_at	EphA7	243	28	133	14	-1.83	*
6	2057_g_at	fibroblast growth factor receptor 1 (fms-re	5421	430	2717	100	-2	*
7	1964_g_at	fms-related tyrosine kinase 1 (vascular en	1555	167	982	51	-1.58	*
8	1545_g_at	fms-related tyrosine kinase 1 (vascular en	745	85	471	16	-1.58	*
9	34583_at	fms-related tyrosine kinase 3	9522	1513	16788	784	1.76	*
10	1065_at	fms-related tyrosine kinase 3	8414	1696	15615	933	1.86	*
11	40480_s_at	FYN oncogene related to SRC, FGR, YES	5038	514	3304	326	-1.52	*
12	34877_at	Janus kinase 1 (a protein tyrosine kinase)	15776	843	10823	834	-1.46	*
13	41594_at	Janus kinase 1 (a protein tyrosine kinase)	6687	345	4360	301	-1.53	*
14	1457_at	Janus kinase 1 (a protein tyrosine kinase)	3098	197	1886	177	-1.64	*
15	33238_at	lymphocyte-specific protein tyrosine kinas	3794	572	1936	258	-1.96	*
16	1988_at	platelet-derived growth factor receptor, alp	14547	602	10367	351	-1.4	*
17	36117_at	PTK2 protein tyrosine kinase 2	3730	242	2613	117	-1.43	*
18	37756_at	RYK receptor-like tyrosine kinase	1155	129	399	48	-2.89	*
19	539_at	RYK receptor-like tyrosine kinase	2294	107	1665	48	-1.38	*
20	572_at	TTK protein kinase	1309	128	792	76	-1.65	*
21	1674_at	v-yes-1 Yamaguchi sarcoma viral oncogen	1438	283	496	32	-2.9	*
22	32616_at	v-yes-1 Yamaguchi sarcoma viral related c	3247	219	4842	498	1.49	*
23	2024_s_at	v-yes-1 Yamaguchi sarcoma viral related c	1913	141	2960	322	1.55	*
24	1402_at	v-yes-1 Yamaguchi sarcoma viral related c	4141	289	6292	581	1.52	*
26	Found 12 Gene Ontology "protein tyrosine phosphatase" genes in a list with 391 annotated genes (all: 81/7685, PValue: 0.000740) *							
27	32916_at	protein tyrosine phosphatase, receptor typ	6814	927	3050	454	-2.23	*
28	31892_at	protein tyrosine phosphatase, receptor typ	801	336	151	10	-5.32	*

Interpreting the Results

Each group of entries in the results file is introduced by a line like:

```
Found 21 Gene Ontology "protein tyrosine kinase"  
genes in a list with 391 annotated genes (all:  
157/7685, PValue: 0.000042) *****
```

The part within quotation marks is the name of the GeneOntology category that was found to be significantly overrepresented among the differentially expressed genes.

The numbers tell us:

1. There were 7685 probe sets on the array with some kind of GeneOntology annotation.
2. There were 391 probe sets selected as differentially expressed that had some kind of GeneOntology annotation.
3. Of all the annotated probe sets, 157 had the “protein tyrosine kinase” function.
4. Of the selected annotated probe sets, 21 had the “protein tyrosine kinase” function.

The p-value comes from modeling the data using a hypergeometric distribution, which means it is the same value produced by Fisher’s Exact Test on a 2×2 contingency table.

What's wrong with the results?

First, the p-values have not been adjusted for multiple testing.

Second, we cannot tell if the software has accounted for the fact that the GeneOntology categories form a DAG. In particular, a gene with “protein tyrosine kinase” activity also inherits every annotation above it in the DAG.

AmiGO! Your friend in the Gene Ontology. - Mozilla Firefox

http://www.godatabase.org/cgi-bin/amigo/go.cgi?view=details&search_constraint=terms&depth=0&query=GO:C

AmiGO

Last updated: 2005-07-17

protein-tyrosine kinase activity

Accession: GO:0004713
Aspect: molecular_function
Synonyms: protein tyrosine kinase activity
Definition:
Catalysis of the reaction: ATP + a protein tyrosine = ADP + protein tyrosine phosphate.

Term Lineage

- all : all (217407) [Graphical View](#)
- GO:0003674 : molecular_function (150639)
- GO:0003824 : catalytic activity (49037)
- GO:0016740 : transferase activity (16314)
- GO:0016772 : transferase activity, transferring phosphorus-containing groups (9126)
- GO:0016301 : kinase activity (7308)
- GO:0004672 : protein kinase activity (4257)
- GO:0004713 : protein-tyrosine kinase activity (700)
- GO:0016773 : phosphotransferase activity, alcohol group as acceptor (5320)
- GO:0004672 : protein kinase activity (4257)
- GO:0004713 : protein-tyrosine kinase activity (700)

What's wrong with the results?

Third, by working with probe sets instead of genes, the counts are wrong.

probe set	gene	baseline mean	baseline	experiment mean	experiment	fold change	filtered
Found 21 Gene Ontology "protein tyrosine kinase" genes in a list with 391 annotated genes (all: 157/7685, PValue: 0.000042) *****							
40936_at	cysteine-rich motor neuron 1	7994	564	5144	612	-1.55	*
1485_at	EphA7	243	28	133	14	-1.83	*
2057_g_at	fibroblast growth factor receptor 1 (fms-re	5421	430	2717	100	-2	*
1964_g_at	fms-related tyrosine kinase 1 (vascular en	1555	167	982	51	-1.58	*
1545_g_at	fms-related tyrosine kinase 1 (vascular en	745	85	471	16	-1.58	*
34583_at	fms-related tyrosine kinase 3	9522	1513	16788	784	1.76	*
1065_at	fms-related tyrosine kinase 3	8414	1696	15615	933	1.86	*
40480_s_at	FYN oncogene related to SRC, FGR, YES	5038	514	3304	326	-1.52	*
34877_at	Janus kinase 1 (a protein tyrosine kinase)	15776	843	10823	834	-1.46	*
41594_at	Janus kinase 1 (a protein tyrosine kinase)	6687	345	4360	301	-1.53	*
1457_at	Janus kinase 1 (a protein tyrosine kinase)	3098	197	1886	177	-1.64	*
33238_at	lymphocyte-specific protein tyrosine kinas	3794	572	1936	258	-1.96	*
1988_at	platelet-derived growth factor receptor, alp	14547	602	10367	351	-1.4	*
36117_at	PTK2 protein tyrosine kinase 2	3730	242	2613	117	-1.43	*
37756_at	RYK receptor-like tyrosine kinase	1155	129	399	48	-2.89	*
539_at	RYK receptor-like tyrosine kinase	2294	107	1665	48	-1.38	*
572_at	TTK protein kinase	1309	128	792	76	-1.65	*
1674_at	v-yes-1 Yamaguchi sarcoma viral oncogen	1438	283	496	32	-2.9	*
32616_at	v-yes-1 Yamaguchi sarcoma viral related c	3247	219	4842	498	1.49	*
2024_s_at	v-yes-1 Yamaguchi sarcoma viral related c	1913	141	2960	322	1.55	*
1402_at	v-yes-1 Yamaguchi sarcoma viral related c	4141	289	6292	581	1.52	*
Found 12 Gene Ontology "protein tyrosine phosphatase" genes in a list with 391 annotated genes (all: 81/7685, PValue: 0.000740) *							
32916_at	protein tyrosine phosphatase, receptor typ	6814	927	3050	454	-2.23	*
31892_at	protein tyrosine phosphatase, receptor typ	801	336	151	10	-5.32	*

What alternatives are there?



The screenshot shows the GoMiner Home Page in a Netscape browser window. The browser title is "GoMiner Home Page - Netscape" and the address bar shows "http://discover.nci.nih.gov/gominer/". The page features a blue header with the "GoMINER" logo (Build:138) and the text "Genomics and Bioinformatics Group LMP, NCI, NIH" and "Medical Informatics & Bioimaging Lab, BME GA Tech/ Emory University". Below the header is a navigation menu with buttons for "Home", "Getting Started", "Requirements", "Installation", "Command Line", "Database", "FAQ", "Citing", "Mirrors", and "Credits". The main content area contains the following text:

GoMiner is a tool for biological interpretation of 'omic' data – including data from gene expression microarrays. Omic experiments often generate lists of dozens or hundreds of genes that differ in expression between samples, raising the question

What does it all mean biologically?

To answer this question, GoMiner leverages the [Gene Ontology \(GO\)](#) to identify the biological processes, functions and components represented in these lists. Instead of analyzing microarray results with a gene-by-gene approach, GoMiner classifies the genes into biologically coherent categories and assesses these categories. The insights gained through GoMiner can generate hypotheses to guide additional research.

To get started using GoMiner

- Read the [Instructions](#), and verify that your environment satisfies the system requirements
- Download the GoMiner program file, [gominer.jar](#)
- Read the [Quick Start](#) and try out the [sample files](#)

The browser status bar at the bottom shows "http://discover.nci.nih.gov/gominer/index.jsp".

http://discover.nci.nih.gov/gominer



The screenshot shows a Netscape browser window titled "GoMiner Installation - Netscape". The address bar contains the URL "http://discover.nci.nih.gov/gominer/installation.jsp". The page features a blue header with the "GoMINER" logo (Build:138) and contact information for the Genomics and Bioinformatics Group at LMP, NCI, NIH, and the Medical Informatics & Bioimaging Lab at BME GA Tech/Emory University. A navigation menu includes links for Home, Getting Started, Requirements, Installation (highlighted in red), Command Line, Database, FAQ, Citing, Mirrors, and Credits. The main content area is titled "Core Application" and lists several steps for installation, including verifying system requirements, downloading the gominer.jar file, and running it from the command line. Below this, the "Install Helper Applications" section is introduced, mentioning web browser components and the Adobe SVG Viewer.

GoMINER Build:138

Genomics and Bioinformatics Group
LMP, NCI, NIH

Medical Informatics & Bioimaging Lab,
BME GA Tech/
Emory University

Home Getting Started Requirements **Installation** Command Line Database FAQ Citing Mirrors Credits

Core Application

- Verify that your machine satisfies the [system requirements](#)
- Download the GoMiner program file, [gominer.jar](#)
- Install the optional components (if any) listed below you want to use.
- Either double-click the jar file, or run "java -jar gominer.jar" from the command line
- For large input files (>10,000 genes) run "java -Xms256M -Xmx256M -jar gominer.jar"
This will allocate more memory to run the application.
- For optimal performance, [install a local copy](#) of the server and database.

Install Helper Applications

The first two helper applications are web browser components, and provide additional visualization features.

Adobe SVG Viewer

GoMiner: Getting Started

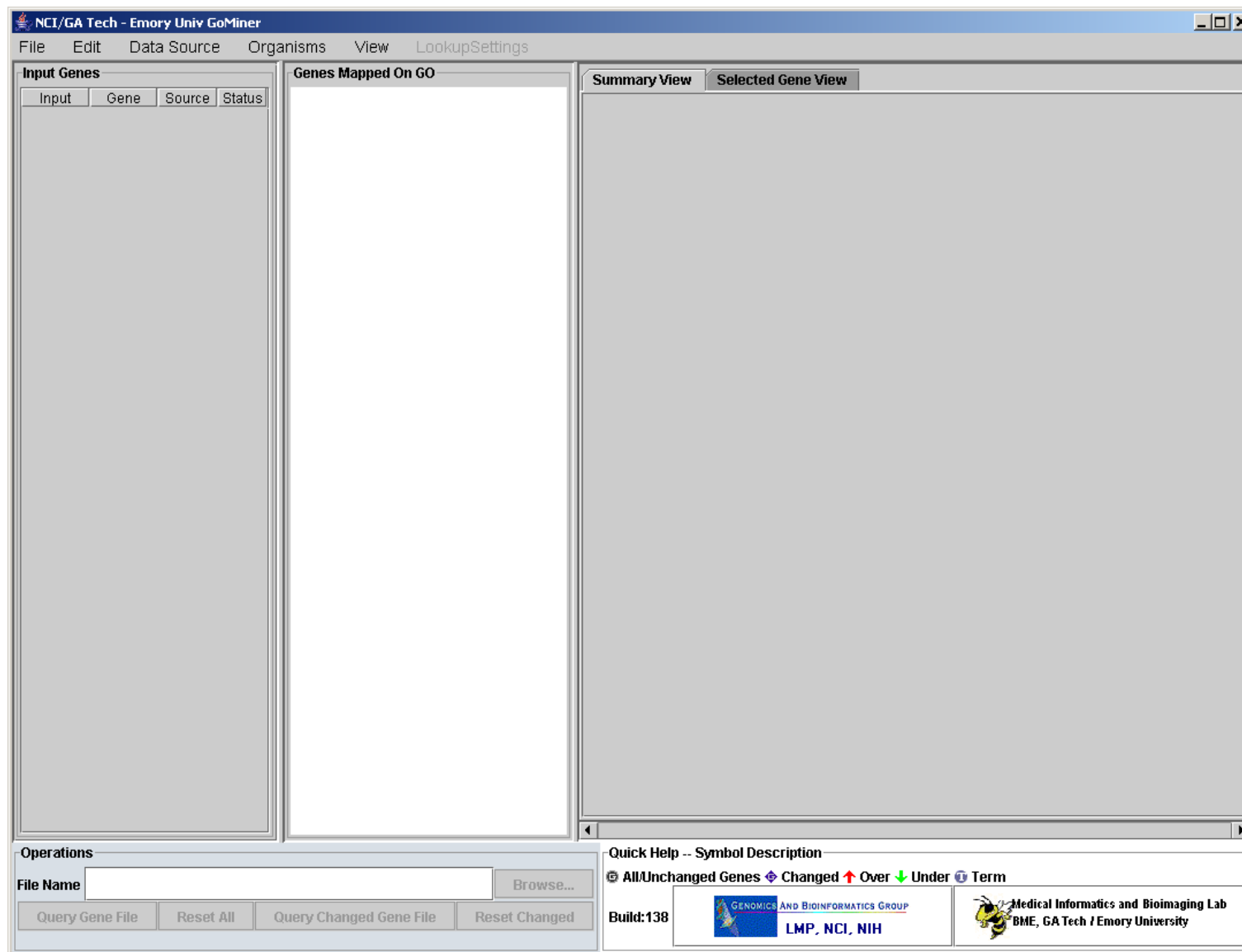
You need a machine with

- Java 1.3 or higher
- Windows 98 or higher, Mac OS X or higher, Solaris, Linux, or FreeBSD
- High-speed internet access

Download the GoMiner Java code, install it, and double-click on it to start the program.

Then go to “File” – > “Load GO Terms” and click “OK”. Wait a few minutes while the program loads the GeneOntology information from the NCI.

GoMiner Start



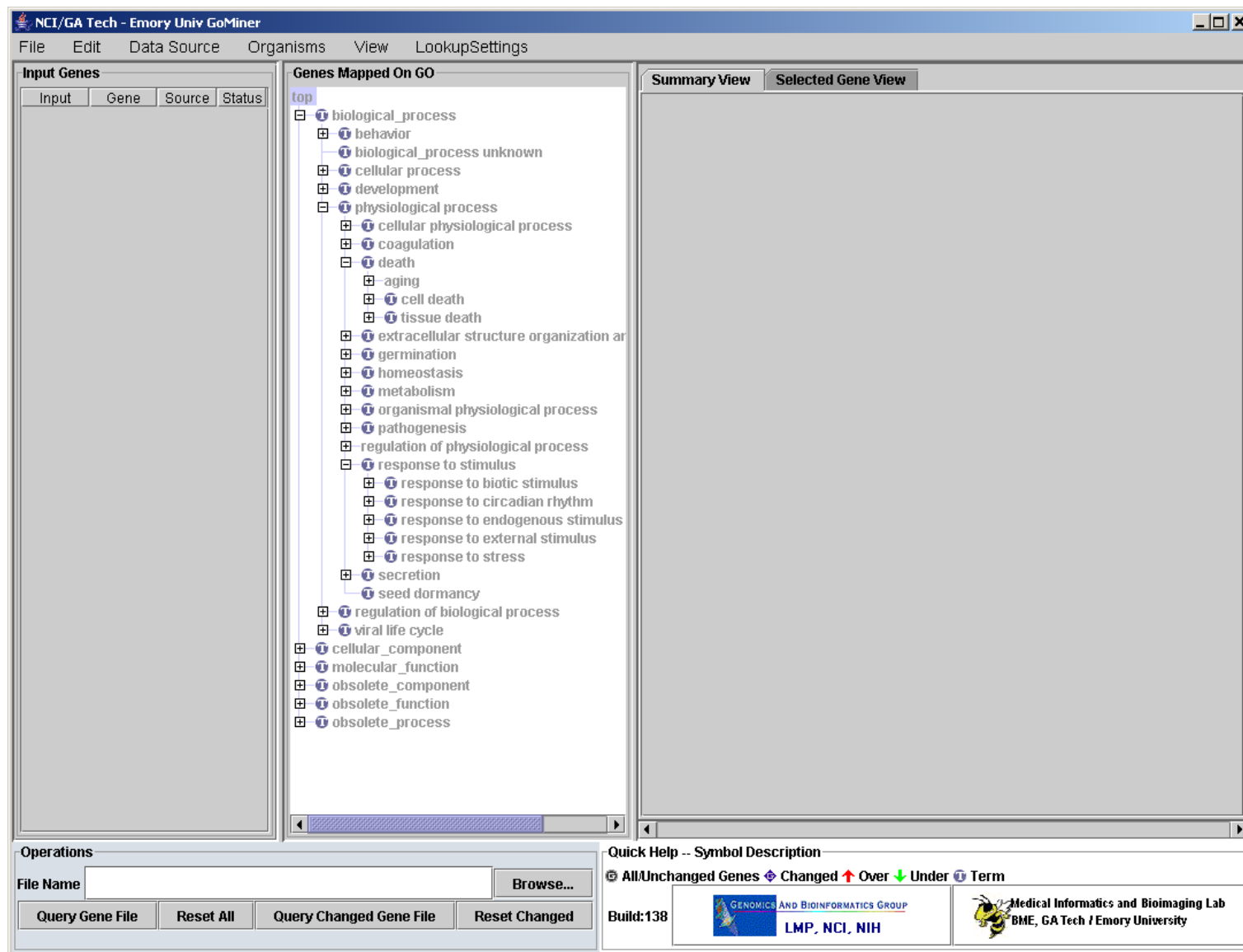
GoMiner: GO terms loaded

The screenshot displays the NCI/GA Tech - Emory Univ GoMiner web application. The interface is divided into several sections:

- Input Genes:** A table with columns for Input, Gene, Source, and Status.
- Genes Mapped On GO:** A list of GO terms, including biological_process, cellular_component, molecular_function, obsolete_component, obsolete_function, and obsolete_process.
- Summary View / Selected Gene View:** A large empty area for displaying gene details.
- Operations:** A section with a File Name input field and a Browse... button, along with buttons for Query Gene File, Reset All, Query Changed Gene File, and Reset Changed.
- Quick Help -- Symbol Description:** A section with radio buttons for All/Unchanged Genes, Changed, Over, Under, and Term, and a Build:138 label.

Logos for the GENOMICS AND BIOINFORMATICS GROUP (LMP, NCI, NIH) and the Medical Informatics and Bioimaging Lab (BME, GA Tech / Emory University) are visible in the bottom right corner.

GoMiner as GO browser



Getting array data into GoMiner

1. Go to “Data Source” and select “UniProt (Hs)” to restrict to human gene annotations
2. Need a file containing a list of all genes in the experiment, one HUGO symbol per line. Use the “Browse” button, and then click “Query Gene File” to load this information. This may take some time...
3. Need a file containing a list of genes that changed. Can be one HUGO symbol per line. Optionally, you can include a second column with 1 (overexpressed) or -1 (underexpressed). Use “Browse” and “Query Changed Gene File” to load this data.

Note: GeneLink or Source can convert from various gene ids to HUGO symbols.

GoMiner with array gene list loaded

Input Genes

Input	Gene	Source	Status
YWHAE	143E...	UniProt	⊗
SFN	143S...	UniProt	⊗
PPP2R...	2A5A...	UniProt	⊗
PPP2R...	2A5B...	UniProt	⊗
PPP2R...	2A5D...	UniProt	⊗
PPP2R...	2A5E...	UniProt	⊗
PPP2R...	2A5G...	UniProt	⊗
PPP2R...	2AAA...	UniProt	⊗
PPP2R...	2AAB...	UniProt	⊗
PPP2R...	2ABA...	UniProt	⊗
PPP2R...	2ABB...	UniProt	⊗
HLA-DMA	2DMA...	UniProt	⊗
HLA-D...	2DMB...	UniProt	⊗
HLA-DOA	2DOA...	UniProt	⊗
HLA-DRA	2DRA...	UniProt	⊗
BH3BP2	3BP2...	UniProt	⊗
SLC3A2	4F2_H...	UniProt	⊗
A2M	A2MG...	UniProt	⊗
ACTN1	AAC1...	UniProt	⊗
PRKAB1	AAKB...	UniProt	⊗
PRKAG1	AAKG...	UniProt	⊗
ATBF1	ABF1...	UniProt	⊗
ABL1	ABL1...	UniProt	⊗
ABL2	ABL2...	UniProt	⊗
ABR	ABR_H...	UniProt	⊗
ACY1	ACY1...	UniProt	⊗
ADAM17	AD17...	UniProt	⊗
ADA	ADA_H...	UniProt	⊗
ADD3	ADDG...	UniProt	⊗
ADH6	ADH6...	UniProt	⊗
ADK	ADK_H...	UniProt	⊗
AOX1	ADO_H...	UniProt	⊗
ADSS	ADSS	UniProt	⊗
SLC25A5	ADT2...	UniProt	⊗
MLLT2	AF4_H...	UniProt	⊗
GLA	AGAL...	UniProt	⊗
ANGPT1	AGP1...	UniProt	⊗
ANGPT2	AGP2...	UniProt	⊗
AHR	AHR_H...	UniProt	⊗

Genes Mapped On GO

- top (1299)
 - biological_process (1245)
 - behavior (8)
 - biological_process_unknown (27)
 - cellular_process (847)
 - development (220)
 - physiological process (1139)
 - IGF2_HUMAN (IGF2) - (UniProt)
 - IGFA_HUMAN (IGF1) - (UniProt)
 - O43200 (TSHR) - (UniProt)
 - PGH1_HUMAN (PTGS1) - (UniProt)
 - PGH2_HUMAN (PTGS2) - (UniProt)
 - REL1_HUMAN (RLN1) - (UniProt)
 - RLF_HUMAN (RLF) - (UniProt)
 - cellular physiological process (568)
 - coagulation (16)
 - death (123)
 - aging (2)
 - cell death (122)
 - cell aging (1)
 - cytolysis (3)
 - programmed cell death (120)
 - apoptosis (120)
 - regulation of programmed cell de...
 - extracellular structure organization and b...
 - homeostasis (13)
 - metabolism (823)
 - organismal physiological process (254)
 - pathogenesis (3)
 - regulation of physiological process (239)
 - response to stimulus (359)
 - secretion (2)
 - regulation of biological process (403)
 - viral life cycle (8)
 - cellular_component (1070)
 - molecular_function (1215)
 - obsolete_component
 - obsolete_function
 - obsolete_process

Summary View Selected Gene View

Category Name	P-Chng	P-Undr	P-Ovr	Tot	Chng	Undr	Ovr	Category ID
ATP-dependent hel...	1.0000	1.0000	1.0000	11	0	0	0	GO:00080...
transcription elong...	1.0000	1.0000	1.0000	1	0	0	0	GO:00080...
protein C-terminus ...	1.0000	1.0000	1.0000	2	0	0	0	GO:00080...
microtubule binding	1.0000	1.0000	1.0000	3	0	0	0	GO:00080...
regulation of heart r...	1.0000	1.0000	1.0000	1	0	0	0	GO:00080...
circulation	1.0000	1.0000	1.0000	9	0	0	0	GO:00080...
beta-catenin binding	1.0000	1.0000	1.0000	1	0	0	0	GO:00080...
chemokine activity	1.0000	1.0000	1.0000	18	0	0	0	GO:00080...
oligopeptide transp...	1.0000	1.0000	1.0000	1	0	0	0	GO:00151...
peptide transporter ...	1.0000	1.0000	1.0000	2	0	0	0	GO:00151...
L-amino acid trans...	1.0000	1.0000	1.0000	1	0	0	0	GO:00151...
acidic amino acid tr...	1.0000	1.0000	1.0000	1	0	0	0	GO:00151...
amino acid transpo...	1.0000	1.0000	1.0000	2	0	0	0	GO:00151...
hexose transporter ...	1.0000	1.0000	1.0000	2	0	0	0	GO:00151...
monosaccharide tr...	1.0000	1.0000	1.0000	2	0	0	0	GO:00151...
carbohydrate trans...	1.0000	1.0000	1.0000	3	0	0	0	GO:00151...
nitric oxide metabol...	1.0000	1.0000	1.0000	4	0	0	0	GO:00462...
sodium ion transpo...	1.0000	1.0000	1.0000	1	0	0	0	GO:00150...
hydrogen ion trans...	1.0000	1.0000	1.0000	3	0	0	0	GO:00150...
monovalent inorga...	1.0000	1.0000	1.0000	3	0	0	0	GO:00150...
ion transporter activ...	1.0000	1.0000	1.0000	4	0	0	0	GO:00150...
protein phosphatas...	1.0000	1.0000	1.0000	3	0	0	0	GO:00150...
thrombin receptor a...	1.0000	1.0000	1.0000	1	0	0	0	GO:00150...
glutathione disulfid...	1.0000	1.0000	1.0000	1	0	0	0	GO:00150...
peptide disulfide ox...	1.0000	1.0000	1.0000	1	0	0	0	GO:00150...
disulfide oxidoredu...	1.0000	1.0000	1.0000	4	0	0	0	GO:00150...
protein transport	1.0000	1.0000	1.0000	26	0	0	0	GO:00150...
Cajal body	1.0000	1.0000	1.0000	1	0	0	0	GO:00150...
coreceptor activity	1.0000	1.0000	1.0000	6	0	0	0	GO:00150...
glucuronosyltransf...	1.0000	1.0000	1.0000	2	0	0	0	GO:00150...
nuclear organizatio...	1.0000	1.0000	1.0000	25	0	0	0	GO:00069...
organelle organizat...	1.0000	1.0000	1.0000	32	0	0	0	GO:00069...
unfolded protein re...	1.0000	1.0000	1.0000	1	0	0	0	GO:00069...
alcohol catabolism	1.0000	1.0000	1.0000	4	0	0	0	GO:00461...
response to unfold...	1.0000	1.0000	1.0000	5	0	0	0	GO:00069...
ER-nuclear signali...	1.0000	1.0000	1.0000	1	0	0	0	GO:00069...
response to lipid hy...	1.0000	1.0000	1.0000	1	0	0	0	GO:00069...
phenol metabolism	1.0000	1.0000	1.0000	2	0	0	0	GO:00189...

Operations

File Name: C:\Source\GoMinerExample\total.gene Browse...

Quick Help -- Symbol Description

All/Unchanged Genes
 Changed
 Over
 Under
 Term

Build:138

GoMiner with changed gene list loaded

Input Genes

Input	Gene	Source	Status
YWHAE	143E_...	UniProt	⊖
SFN	143S_...	UniProt	⊖
PPP2R...	2A5A_...	UniProt	⊖
PPP2R...	2A5B_...	UniProt	⊖
PPP2R...	2A5D_...	UniProt	⊖
PPP2R...	2A5E_...	UniProt	⊖
PPP2R...	2A5G_...	UniProt	⊖
PPP2R...	2AAA_...	UniProt	⊖
PPP2R...	2AAB_...	UniProt	⊖
PPP2R...	2ABA_...	UniProt	⊖
PPP2R...	2ABB_...	UniProt	⊖
HLA-DMA	2DMA_...	UniProt	⊖
HLA-D...	2DMB_...	UniProt	⊖
HLA-DOA	2DOA_...	UniProt	⊖
HLA-DRA	2DRA_...	UniProt	⊖
BH3BP2	3BP2_...	UniProt	⊖
SLC3A2	4F2_H_...	UniProt	⊖
A2M	A2MG_...	UniProt	⊖
ACTN1	AAC1_...	UniProt	⊖
PRKAB1	AAKB_...	UniProt	⊖
PRKAG1	AAKG_...	UniProt	⊖
ATBF1	ABF1_...	UniProt	⊖
ABL1	ABL1_...	UniProt	⊖
ABL2	ABL2_...	UniProt	⊖
ABR	ABR_H_...	UniProt	⊖
ACY1	ACY1_...	UniProt	⊖
ADAM17	AD17_...	UniProt	⊖
ADA	ADA_H_...	UniProt	⊖
ADD3	ADDG_...	UniProt	⊖
ADH6	ADH6_...	UniProt	⊖
ADK	ADK_H_...	UniProt	⊖
AOX1	ADO_H_...	UniProt	⊖
ADSS	ADSS_...	UniProt	⊖
SLC25A5	ADT2_...	UniProt	⊖
MLLT2	AF4_H_...	UniProt	⊖
GLA	AGAL_...	UniProt	⊖
ANGPT1	AGP1_...	UniProt	⊖
ANGPT2	AGP2_...	UniProt	⊖
AHR	AHR_H_...	UniProt	⊖

Genes Mapped On GO

- biological_process (1299 1.00 p=1.00 1.00 p=1.00)
 - biological_process (1245 1.03 p=0.17 1.01 p=0.48 1.02 p=0.17)
 - cellular_process (847 0.99 p=0.58 0.97 p=0.69 0.98 p=0.67)
 - development (220 0.96 p=0.62 1.12 p=0.35 1.04 p=0.43)
 - physiological_process (1139 1.08 p=0.04 1.05 p=0.11 1.06 p=0.01)
 - cellular_physiological_process (568 1.02 p=0.48 0.99 p=0.57 1.00)
 - coagulation (16 1.10 p=0.61 0.90 p=0.69 0.99 p=0.62)
 - death (123 1.28 p=0.26 1.17 p=0.34 1.22 p=0.20)
 - cell_death (122 1.29 p=0.25 1.18 p=0.33 1.23 p=0.19)
 - cytolysis (3 0.00 p=1.00 4.81 p=0.19 2.64 p=0.33)
 - programmed_cell_death (120 1.32 p=0.24 1.08 p=0.45 1.14 p=0.45)
 - apoptosis (120 1.32 p=0.24 1.08 p=0.45 1.19 p=0.24)
 - regulation_of_programmed_cell_death (77 1.14 p=0.45 0.95 p=0.61 1.14 p=0.45)
 - homeostasis (13 0.00 p=1.00 5.55 p=0.00 3.05 p=0.02)
 - metabolism (823 0.90 p=0.91 1.14 p=0.04 1.03 p=0.33)
 - organismal_physiological_process (254 1.87 p=0.00 0.91 p=0.71)
 - regulation_of_physiological_process (239 1.10 p=0.38 1.39 p=0.05 1.10)
 - response_to_stimulus (359 1.47 p=0.01 1.09 p=0.34 1.26 p=0.02)
 - regulation_of_biological_process (403 1.18 p=0.18 1.25 p=0.06 1.22 p=0.06)
 - viral_life_cycle (8 2.19 p=0.38 1.80 p=0.44 1.98 p=0.27)
- cellular_component (1070 0.97 p=0.78 0.97 p=0.78 0.97 p=0.84)
- molecular_function (1215 0.95 p=0.96 0.91 p=1.00 0.93 p=1.00)
- obsolete_component
- obsolete_function
- obsolete_process

Summary View Selected Gene View

Category Name	P-Chng	P-Undr	P-Ovr	Tot	Chng	Undr	Ovr	Category ID
cytoplasmic seque...	0.0002	0.0178	0.0260	4	4	2	2	GO:00429...
negative regulatio...	0.0002	0.0178	0.0260	4	4	2	2	GO:00429...
transcription factor...	0.0002	0.0178	0.0260	4	4	2	2	GO:00429...
regulation of transc...	0.0002	0.0178	0.0260	4	4	2	2	GO:00429...
regulation of protei...	0.0002	0.0178	0.0260	4	4	2	2	GO:00423...
regulation of nucleo...	0.0002	0.0178	0.0260	4	4	2	2	GO:00468...
chemokine activity	0.0008	0.0782	0.0060	18	8	3	5	GO:00080...
G-protein-coupled r...	0.0008	0.0782	0.0060	18	8	3	5	GO:00016...
chemokine recepto...	0.0008	0.0782	0.0060	18	8	3	5	GO:00423...
chemotaxis	0.0012	0.0547	0.0112	37	12	5	7	GO:00069...
taxis	0.0012	0.0547	0.0112	37	12	5	7	GO:00423...
response to wound...	0.0015	0.0227	0.0296	75	19	9	10	GO:00096...
response to chemi...	0.0018	0.0814	0.0097	54	15	6	9	GO:00422...
response to pathog...	0.0030	0.2972	0.0055	6	4	1	3	GO:00096...
regulation of transp...	0.0030	0.0414	0.0593	6	4	2	2	GO:00510...
immune response	0.0033	0.0002	0.4695	207	39	24	15	GO:00069...
response to pest, p...	0.0036	0.0178	0.0743	123	26	13	13	GO:00096...
extracellular space	0.0038	0.0039	0.2217	47	13	8	5	GO:00056...
protein threonine/tyr...	0.0063	0.0558	0.0794	7	4	2	2	GO:00047...
MAP kinase kinase ...	0.0063	0.0558	0.0794	7	4	2	2	GO:00047...
response to pathog...	0.0063	0.3374	0.0092	7	4	1	3	GO:00428...
antigen processing	0.0070	0.0001	1.0000	15	6	6	0	GO:00303...
antigen presentation	0.0070	0.0001	1.0000	15	6	6	0	GO:00198...
MHC class II recept...	0.0074	0.0024	0.5475	11	5	4	1	GO:00450...
response to extern...	0.0075	0.0400	0.0743	123	25	12	13	GO:00096...
defense response	0.0088	0.0008	0.4993	225	40	24	16	GO:00069...
response to biotic s...	0.0089	0.0013	0.4397	246	43	25	18	GO:00096...
inflammatory respo...	0.0096	0.1695	0.0232	52	13	5	8	GO:00069...
innate immune res...	0.0096	0.1695	0.0232	52	13	5	8	GO:00450...
physiological proce...	0.0099	0.0372	0.1127	1139	153	70	83	GO:00075...
metal ion homeost...	0.0114	1.0000	0.0008	12	5	0	5	GO:00068...
cell ion homeostasis	0.0114	1.0000	0.0008	12	5	0	5	GO:00068...
di-, tri-valent inorga...	0.0114	1.0000	0.0008	12	5	0	5	GO:00300...
cation homeostasis	0.0114	1.0000	0.0008	12	5	0	5	GO:00300...
ion homeostasis	0.0114	1.0000	0.0008	12	5	0	5	GO:00508...
response to abiotic ...	0.0119	0.1597	0.0309	65	15	6	9	GO:00096...
transforming growt...	0.0159	1.0000	0.0048	2	2	0	2	GO:00306...
NF-kappaB-nucleu...	0.0159	0.1107	0.1338	2	2	1	1	GO:00423...

Operations

File Name: C:\Source\GoMinerExample\undr.over.2col

Query Gene File | Reset All | Query Changed Gene File | Reset Changed

Quick Help -- Symbol Description

⊖ All/Unchanged Genes ⊕ Changed ↑ Over ↓ Under ⊕ Term

Build:138

GENOMICS AND BIOINFORMATICS GROUP
LMP, NCI, NIH

Medical Informatics and Bioimaging Lab
BME, GA Tech / Emory University

GoMiner subgraphs

NCI/GA Tech - Emory Univ GoMiner

File Edit Data Source Organisms View LookupSettings

Input Genes

Input	Gene	Source	Status
YWHAE	143E_...	UniProt	⊕
SFN	143S_...	UniProt	⊕
PPP2R...	2A5A_...	UniProt	⊕
PPP2R...	2A5B_...	UniProt	⊕
PPP2R...	2A5D_...	UniProt	⊕
PPP2R...	2A5E_...	UniProt	⊕
PPP2R...	2A5G_...	UniProt	⊕
PPP2R...	2AAA_...	UniProt	⊕
PPP2R...	2AAB_...	UniProt	⊕
PPP2R...	2ABA_...	UniProt	⊕
PPP2R...	2ABB_...	UniProt	⊕
HLA-DMA	2DMA_...	UniProt	⊕
HLA-D...	2DMB_...	UniProt	⊕
HLA-DOA	2DOA_...	UniProt	⊕
HLA-DRA	2DRA_...	UniProt	⊕
BH3BP2	3BP2_...	UniProt	⊕
SLC3A2	4F2_H_...	UniProt	⊕
A2M	A2MG_...	UniProt	⊕
ACTN1	AAC1_...	UniProt	⊕
PRKAB1	AAKB_...	UniProt	⊕
PRKAG1	AAKG_...	UniProt	⊕
ATBF1	ABF1_...	UniProt	⊕
ABL1	ABL1_...	UniProt	⊕
ABL2	ABL2_...	UniProt	⊕
ABR	ABR_H_...	UniProt	⊕
ACY1	ACY1_...	UniProt	⊕
ADAM17	AD17_...	UniProt	⊕
ADA	ADA_H_...	UniProt	⊕
ADD3	ADDG_...	UniProt	⊕
ADH6	ADH6_...	UniProt	⊕
ADK	ADK_H_...	UniProt	⊕
AOX1	ADO_H_...	UniProt	⊕
ADSS	ADSS_...	UniProt	⊕
SLC25A5	ADT2_...	UniProt	⊕
MLLT2	AF4_H_...	UniProt	⊕
GLA	AGAL_...	UniProt	⊕
ANGPT1	AGP1_...	UniProt	⊕
ANGPT2	AGP2_...	UniProt	⊕
AHR	AHR_H_...	UniProt	⊕

Genes Mapped On GO

- 1299 1.00 p=1.00 1.00 p=1.00 1.00 p=1.00
- biological_process (1245 1.03 p=0.17 1.01 p=0.48 1.02 p=0.17)
- biological_process unknown (27 1.30 p=0.46 0.53 p=0.86 0.88 p=0.01)
- cellular process (847 0.99 p=0.58 0.97 p=0.69 0.98 p=0.67)
- development (220 0.96 p=0.62 1.12 p=0.35 1.04 p=0.43)
- physiological process (1139 1.08 p=0.04 1.05 p=0.11 1.06 p=0.01)
- cellular physiological process (568 1.02 p=0.48 0.99 p=0.57 1.00 p=0.51)
- coagulation (16 1.10 p=0.61 0.90 p=0.69 0.99 p=0.62)
- death (123 1.28 p=0.26 1.17 p=0.34 1.22 p=0.20)
- cell death (122 1.29 p=0.25 1.18 p=0.33 1.23 p=0.19)
- cytolysis (3 0.00 p=1.00 4.81 p=0.19 2.64 p=0.33)
- programmed cell death (120 1.32 p=0.24 1.08 p=0.45 1.19 p=0.24)
- apoptosis (120 1.32 p=0.24 1.08 p=0.45 1.19 p=0.24)
- AHR_HUMAN (AHR)
- ASP2_HUMAN (TP5)
- BAD_HUMAN (BAD)
- BCL2_HUMAN (BCL)
- BIRC2_HUMAN (BIRC2) - (UniProt)
- DAD1_HUMAN (DAD1) - (UniProt)
- DAP1_HUMAN (DAP) - (UniProt)
- DPF2 (REQ) - (UniProt)
- ICE6_HUMAN (CASP6) - (UniProt)
- IKBA_HUMAN (NFKBIA) - (UniProt)
- NIP2_HUMAN (BNIP2) - (UniProt)
- P300_HUMAN (EP300) - (UniProt)
- PAK1_HUMAN (PAK1) - (UniProt)
- Q8WX32 (BAG1) - (UniProt)
- T10C_HUMAN (TNFRSF10C) - (UniProt)
- T10D_HUMAN (TNFRSF10D) - (UniProt)
- TN13_HUMAN (TNFAIP3) - (UniProt)
- apoptotic program (16 1.10 p=0.61 0.00 p=1.00 0.50)
- regulation of apoptosis (77 1.14 p=0.45 0.94 p=0.63)
- regulation of programmed cell death (77 1.14 p=0.45 0.94 p=0.63)
- homeostasis (13 0.00 p=1.00 5.55 p=0.00 3.05 p=0.02)
- metabolism (823 0.90 p=0.91 1.14 p=0.04 1.03 p=0.33)
- organismal physiological process (254 1.87 p=0.00 0.91 p=0.71)
- regulation of physiological process (239 1.10 p=0.38 1.39 p=0.05 1.10 p=0.05)
- response to stimulus (359 1.47 p=0.01 1.09 p=0.34 1.26 p=0.02)
- regulation of biological process (403 1.18 p=0.18 1.25 p=0.06 1.22 p=0.06)
- viral life cycle (9 2.40 p=0.39 1.90 p=0.44 1.09 p=0.27)

Summary View Selected Gene View

Selected Single Gene View

top (1299 1.00 p=1.00 1.00 p=1.00 1.00 p=1.00)

- biological_process (1245 1.03 p=0.17 1.01 p=0.48 1.02 p=0.17)
- cellular process (847 0.99 p=0.58 0.97 p=0.69 0.98 p=0.67)
- cellular physiological process (568 1.02 p=0.48 0.99 p=0.57 1.00 p=0.51)
- cell death (122 1.29 p=0.25 1.18 p=0.33 1.23 p=0.19)
- programmed cell death (120 1.32 p=0.24 1.08 p=0.45 1.19 p=0.24)
- physiological process (1139 1.08 p=0.04 1.05 p=0.11 1.06 p=0.01)
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- cell death (122 1.29 p=0.25 1.18 p=0.33 1.23 p=0.19)
- programmed cell death (120 1.32 p=0.24 1.08 p=0.45 1.19 p=0.24)

Operations

File Name C:\Source\GoMinerExample\undr.over.2col Browse...

Query Gene File Reset All Query Changed Gene File Reset Changed

Quick Help -- Symbol Description

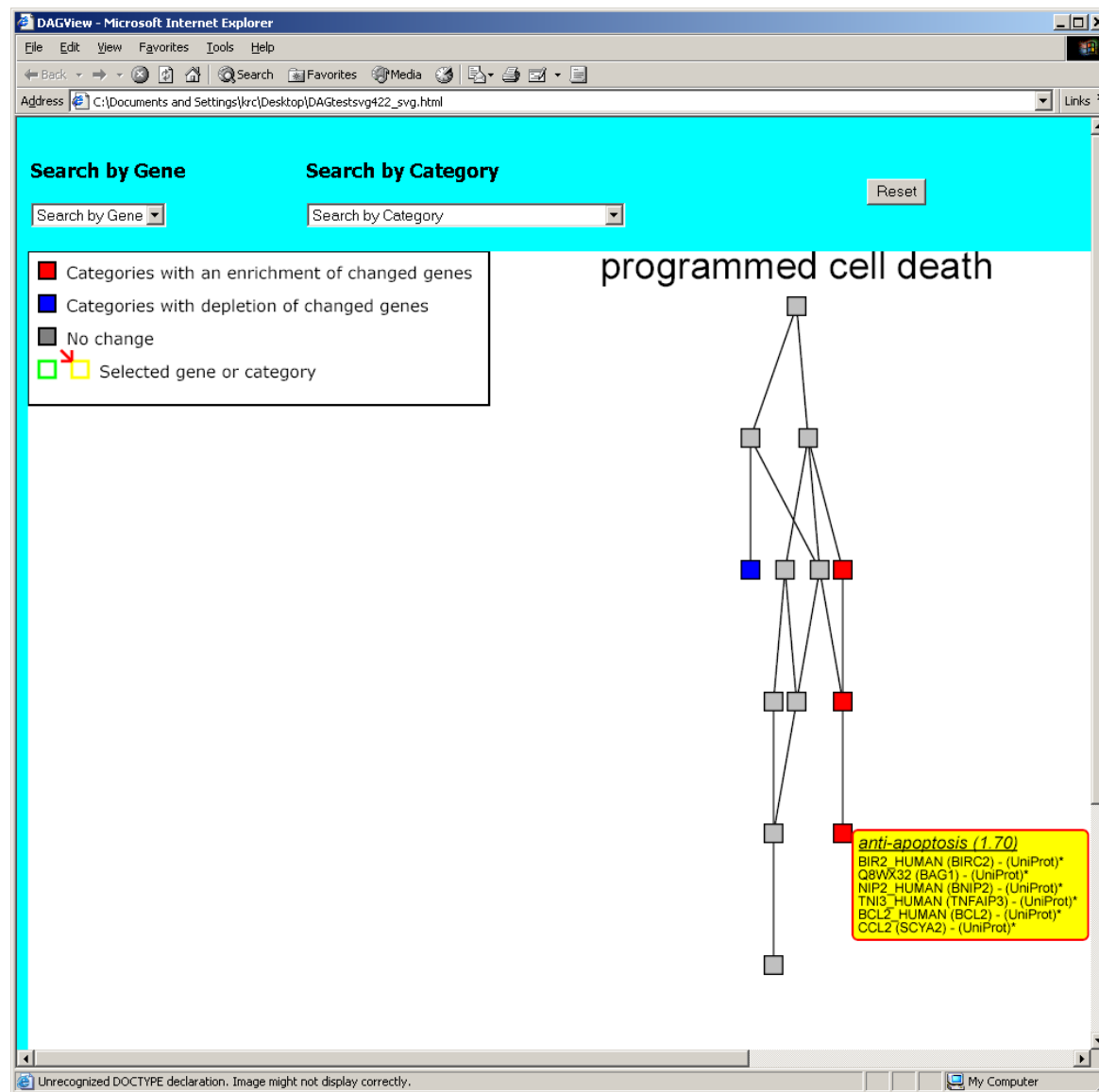
All/Unchanged Genes Changed Over Under Term

Build:138

GENOMICS AND BIOINFORMATICS GROUP LMP, NCI, NIH

Medical Informatics and Bioimaging Lab BME, GA Tech / Emory University

GoMiner subgraphs



Intepreting GoMiner results

Enrichment is computed as

$$\frac{\text{changed genes in category} / \text{total genes in category}}{\text{changed genes on array} / \text{all genes on array}}$$

Statistical evidence of enrichment is based on a Fisher exact test.

Intepreting GoMiner results

The p-values from the Fisher test are not corrected for multiple testing, but they should be since one is potentially looking at all GO categories. The categories are not independent, so it is not clear exactly how one should correct for multiple testing.

If one filters the gene list from the array before testing differential expression (for example, by removing low expressing or low variance genes), should those genes be included in the “query gene file” for the experiment?

The Fisher exact test is not completely appropriate, since genes can have multiple overlapping annotations into the GO DAG.

No existing test exploits the quality of evidence for the GO annotations.