

Introduction to web-based analysis with GeneWeaver.

This is a guided tour of geneweaver.org designed to highlight the use of major tools. Steps and explanations are given to generate the results shown. Additional tools, features, usage hints and approaches are marked “Tip”.

GeneWeaver is a web-based gene-centered database with integrated tools. It can combine diverse data sets from multiple species and experiment types, and allows simple and powerful data sharing publicly or across collaborative groups.

Point your browser to www.geneweaver.org.

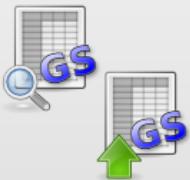


GeneWeaver.org

A system for the integration of functional genomics experiments.

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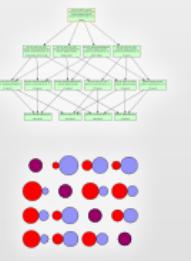
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Search for or Upload sets of genes



Collect GeneSets into Projects



Analyze and discover GeneSet relationships

Quick Search
Search Gene Weaver for any gene symbols, microarray probesets, terms in phenotype description, publication abstracts or authors, etc.
We've updated our search tools. Please be sure to clear your browser (shift+Reload) to enable these features.

Search in: GeneSets Genes Abstracts Ontologies [+>](#) 

Submit for Curation
Know of a study you'd like to see in GeneWeaver? Want to fast-track your own data?
[Submit experimental results for curation here.](#)

News and Notes

2013: GeneWeaver user publication
Potential translational targets revealed by linking mouse grooming behavioral phenotypes to gene expression using public databases Andrew Roth, Evan J. Kyzar, Jonathan Cachat, Adam Michael Stewart, Jeremy Green, Siddharth Gaikwad, Timothy P. O'Leary, Boris Tabakoff, Richard E. Brown, Allan V. Kalueff. *Progress in Neuro-Psychopharmacology & Biological Psychiatry* 40:313-325.

2013: GeneWeaver user publication (Includes Deposited Data)
Mechanistic basis of infertility of mouse intersubspecific hybrids Bhattacharyya T, Gregorova S, Mihola O, Anger M, Sebestova J, Denny P, Simecek P, Forejt J. *PNAS* 2013 110 (6) E468-E477.

2012: GeneWeaver Publication
Cross species integration of functional genomics experiments Jay, JJ. *Int Rev Neurobiol* 104:1-24.

Oct 2012: GeneWeaver user publication
The Mammalian Phenotype Ontology as a unifying standard for experimental and high-throughput phenotyping data. Smith CL, Eppig JT. *Mamm Genome*. 23(9-10):653-68

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Gene Weaver / The Ontological Discovery Environment was initiated as a project of the NIAAA Integrative Neuroscience Initiative on Alcoholism (U01AA13499, U24AA13513), and is supported by RO1 AA18776. This page is maintained by Erich Baker and Elissa Chesler. For applicable policies see our [privacy](#), [data sharing](#), and [usage](#) documents.

Data in GeneWeaver is organized into sets of genes, or GeneSets. These sets contain some simple metadata, such as a name, description, and publication info, along with the set of genes. All of this information can be searched to find a set of interest.

Searching GeneWeaver for data sets is possible through the Quick Search (found on the front page) or via the "Search" page found in the menu.

Quick Search

Search Gene Weaver for any gene symbols, microarray probesets, terms in phenotype description, publication abstracts or authors, etc.

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Search in: GeneSets Genes Abstracts Ontologies - +

 Search

Search for "Nicotine hippocampus" now to find all the public GeneSets relating to Nicotine studies in the Hippocampus that have already been upload to GeneWeaver.

Tip: From the search results page you can click on the plus sign to show a little more detail about the set, such as species and publication info. You can also click on the GeneSet name to see the full details and the list of genes included in the set on a separate page.

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Search for GeneSets

General Tiers Species Attributions

Global Filters

Include **provisional** (15)
 Include **deprecated** (0)
Group: Any (25)
Geneset Size: 1 to 263

Tiers

I: Resources (15)
 II: Pro-Curated (0)
 III: Curated (10)
 IV: Provisional (0)
 V: Private (2)

Species

Mus musculus (11)
 Homo sapiens (15)
 Rattus norvegicus (1)

Attribution

No Attribution (12)
 DRG (15)

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Nicotine Hippocampus

Search in: GeneSets Genes Abstracts Ontologies [+](#)  [Search](#)

Add Selected to Project ▾ [Analyze](#) ▾

Select GeneSets using the check boxes below. Then, add them to a project or analyze them using the buttons above.

Sort: Relevance Page: 1

	Tier	Species	Genes	Description
<input type="checkbox"/>	+ Tier III	Mouse	263 Genes	GS14888: Differentially expressed genes modulated by nicotine in five combined brain regions (Amyg, HP, NA, PFC and VTA) for C3H/HeJ mice
<input type="checkbox"/>	+ Tier III	Mouse	174 Genes	GS14889: Differentially expressed genes modulated by nicotine in five combined brain regions (Amyg, HP, NA, PFC and VTA) for C57BL/6J mice
<input type="checkbox"/>	+ Tier III	Rat	74 Genes	GS14885: Co-expression cluster of Nicotine Dependence genes significantly expressed in the adolescent PFC, VS and Hippocampus.
<input type="checkbox"/>	+ Tier III	Mouse	20 Genes	GS14890: Downregulated genes in five combined brain regions, Amyg, HP, NA, PFC and VTA, in C57BL/6J mice
<input type="checkbox"/>	+ Tier III	Mouse	51 Genes	GS14891: Upregulated genes in five combined brain regions, Amyg, HP, NA, PFC and VTA, in C57BL/6J mice
<input type="checkbox"/>	+ Tier III	Mouse	16 Genes	GS14892: Downregulated genes in five brain regions, NA, PFC, and VTA, in C3H/HeJ mice
<input type="checkbox"/>	+ Tier III	Mouse	70 Genes	GS14893: Upregulated genes in three brain regions, NA, PFC, and VTA, in C3H/HeJ mice
<input type="checkbox"/>	+ Tier III	Mouse	29 Genes	GS14887: Coregulated genes in both C3H/HeJ and C57BL/6J strains within five combined brain regions (Amyg, HP, NA, PFC and VTA)
<input type="checkbox"/>	+ Tier I	Human	DRG 1 Genes provisional	GS86761: Table 6: QRT-PCR confirmation of microarray gene expression changes Main effect of smoking: Immune response [DRG]
<input type="checkbox"/>	+ Tier I	Human	DRG 1 Genes provisional	GS86791: Table 6: QRT-PCR confirmation of microarray gene expression changes Smoking x schizophrenia interaction: NMDA postsynaptic density [DRG]

Tip: You can restrict your search to specific species, collaboration groups, or curation level (i.e. user-submitted or expert curated data). You can also narrow the search scope by searching only the GeneSets, the Genes, the Abstracts or the Ontologies.

Tip: Creating powerful queries with boolean search is also possible using "AND", "OR", "NOT" and parentheses to craft a precise query.



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Search for GeneSets

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Global Filters

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Attribution

No Attribution (12)
 DRG (15)

[Toggle All](#)

Nicotine Hippocampus

Search in: GeneSets Genes Abstracts Ontologies + [Search](#)

[Add Selected to Project ▾](#) [Analyze ▾](#)

Select GeneSets using the check boxes below. Then, add them to a project or analyze them using the buttons above.

[Select All Results](#) Sort: Relevance ▾ Page: 1

1 - 27 of 27 genesets

- + Tier III Mouse 263 Genes GS14888: Differentially expressed genes modulated by nicotine in five combined brain regions (Amyg, HP, NA, PFC and VTA) for C3H/HeJ mice
- + Tier III Mouse 174 Genes GS14889: Differentially expressed genes modulated by nicotine in five combined brain regions (Amyg, HP, NA, PFC and VTA) for C57BL/6J mice
- + Tier III Rat 74 Genes GS14885: Co-expression cluster of Nicotine Dependence genes significantly expressed in the adolescent PFC, VS and Hippocampus.
- + Tier III Mouse 20 Genes GS14890: Downregulated genes in five combined brain regions, Amyg, HP, NA, PFC and VTA, in C57BL/6J mice
- + Tier III Mouse 51 Genes GS14891: Upregulated genes in five combined brain regions, Amyg, HP, NA, PFC and VTA, in C57BL/6J mice
- + Tier III Mouse 16 Genes GS14892: Downregulated genes in five brain regions, NA, PFC, and VTA, in C3H/HeJ mice
- + Tier III Mouse 70 Genes GS14893: Upregulated genes in three brain regions, NA, PFC, and VTA, in C3H/HeJ mice
- + Tier III Mouse 29 Genes GS14887: Coregulated genes in both C3H/HeJ and C57BL/6J strains within five combined brain regions (Amyg, HP, NA, PFC and VTA)
- + Tier I Human DRG 1 Genes provisional GS86761: Table 6: QRT-PCR confirmation of microarray gene expression changes Main effect of smoking: Immune response [DRG]
- + Tier I Human DRG 1 Genes provisional GS86791: Table 6: QRT-PCR confirmation of microarray gene expression changes Smoking x schizophrenia interaction: NMDA postsynaptic density [DRG]

From the GeneSet details page, you can read more about the set, including a link to the provided publication in PubMed, if available. On the second half of the page, you will find a list of the genes in the GeneSet, along with a set of linkouts to other sites, and the score associated with the gene (type of score value depends on the source)

Tip: Using the “Display using” drop-down box, you can change the type of identifier used in the list. You can also export the displayed genes to a tab-separated file for use in other software.

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GeneSet Details
Gene Set #14885 - Co-expression cluster of Nicotine Dependence genes significantly expressed in the adolescent PFC, VS and Hippocampus. [[edit](#)] [[delete](#)]

Description: Studies analyzing brain samples from female rats that had been injected with nicotine at four different ages show that nicotine exerts the greatest influence during adolescence. Using DNA microarrays, gene expression correlates were obtained from the prefrontal cortex (PFC), ventral striatum (VS), and hippocampus. Principal cluster analysis was then used to identify 76 genes that changed significantly in at least one of these three brain regions during the experiment.

Uploaded: 20 Jan 2009
Owner: erdog@gmail.com
Species: Rattus norvegicus
Authors: Polotskaya OO, Fryxell KJ, Merchant AD, Locklear LL, Ker KF, McDonald CG, Eppolito AK, Smith LN, Wheeler TL, Smith RF

Title: Nicotine causes age-dependent changes in gene expression in the adolescent female rat brain.
Journal: *Neurotoxicology and Teratology* Jan-Feb 2007, Vol 29, pp. 126-40
Abstract: Humans often start smoking during adolescence. Recent results suggest that rodents may also be particularly vulnerable to nicotine dependence during adolescence. We examined the effect of chronic nicotine exposure on gene expression profiles during adolescence in female rats, who were dosed with nicotine (and control animals were dosed with saline) via subcutaneously implanted osmotic minipumps. Brain samples were collected at four ages before puberty (postnatal day 25), at about the time of puberty in females (postnatal day 35), and after puberty (postnatal days 45 and 55). The expression of 7931 genes in three brain areas was measured using DNA microarrays. Quantitative RT-PCR was also employed to confirm the expression patterns of selected genes. We used a novel clustering technique (principal cluster analysis) to classify 162 nicotine-regulated genes into five clusters, of which only one (cluster A) showed similar patterns of gene expression across all three brain areas (ventral striatum, prefrontal cortex, and hippocampus). Three clusters of genes (A, B, and C) showed dramatic peaks in their nicotine responses at the same age (p35). The other two clusters (D1 and D2) showed smaller peaks and/or valleys in their nicotine responses at p35 and p45. Thus, the age of maximal gene expression response to nicotine in female rats corresponds approximately to the age of maximal behavioral response and the age of puberty. PUBLMED: 17234382
[Find other GeneSets from this publication.](#)

Ontological Associations:
[Update associations](#)

- D020133: Reverse Transcriptase Polymerase Chain Reaction (PubMed MeSH Annotations; Publication, NCBO Annotator)
- D018722: Nicotinic Agonists (PubMed MeSH Annotations)
- D000367: Age Factors (PubMed MeSH Annotations)
- D001921: Brain (PubMed MeSH Annotations; Description, NCBO Annotator; Publication, NCBO Annotator)
- MA:0000891: striatum (Description, NCBO Annotator; Publication, NCBO Annotator)
- D012807: Smoking (Description, NCBO Annotator; Publication, NCBO Annotator)
- D023701: Sminigrinmorphia (Description, NCBO Annotator)
- DR14029: Tobacco Use Disorder (Description, NCBO Annotator; Publication, NCBO Annotator)

go back to the search results now.

Gene List

74 data points, using thresholds: avg value > 0.5

Display using: **Gene Symbol***

[Export Data](#)

Gene Symbol	LinkOuts	Data Value
Acadl	<img alt="LinkOut icons: Ensembl, Entrez, Google Scholar, PubChem, UniProt, ChEMBL, BioGRID, Reactome, KEGG, PPI, OMIM, HGNC, MGI, RGD, TAIR, FlyBase, SGD, WormBase, MIP, Bgee, GAGE, GAGE2, GAGE3, GAGE4, GAGE5, GAGE6, GAGE7, GAGE8, GAGE9, GAGE10, GAGE11, GAGE12, GAGE13, GAGE14, GAGE15, GAGE16, GAGE17, GAGE18, GAGE19, GAGE20, GAGE21, GAGE22, GAGE23, GAGE24, GAGE25, GAGE26, GAGE27, GAGE28, GAGE29, GAGE30, GAGE31, GAGE32, GAGE33, GAGE34, GAGE35, GAGE36, GAGE37, GAGE38, GAGE39, GAGE40, GAGE41, GAGE42, GAGE43, GAGE44, GAGE45, GAGE46, GAGE47, GAGE48, GAGE49, GAGE50, GAGE51, GAGE52, GAGE53, GAGE54, GAGE55, GAGE56, GAGE57, GAGE58, GAGE59, GAGE60, GAGE61, GAGE62, GAGE63, GAGE64, GAGE65, GAGE66, GAGE67, GAGE68, GAGE69, GAGE70, GAGE71, GAGE72, GAGE73, GAGE74, GAGE75, GAGE76, GAGE77, GAGE78, GAGE79, GAGE80, GAGE81, GAGE82, GAGE83, GAGE84, GAGE85, GAGE86, GAGE87, GAGE88, GAGE89, GAGE90, GAGE91, GAGE92, GAGE93, GAGE94, GAGE95, GAGE96, GAGE97, GAGE98, GAGE99, GAGE100, GAGE101, GAGE102, GAGE103, 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On the search results page, you can use the checkboxes and drop-down menu to add GeneSets to a new project. Projects allow you to run tools and analyze sets of GeneSets.

Click "Select All" to highlight all the Nicotine GeneSets and then use the drop-down box to select "Create new Project..." to add the GeneSets to a new project. When prompted, supply an informative name for the new project and click OK.

The screenshot shows the GeneWeaver.org search interface. The top navigation bar includes links for Home, Search, Manage GeneSets, Analyze GeneSets, About, Curation, Help, and user authentication (Logged in as jbubier, Edit Groups, Logout, Issue Tracker). The main search query is "Nicotine Hippocampus". The search filters are set to "Search in: GeneSets, Genes, Abstracts, Ontologies". A modal dialog box is open, prompting the user to "Select GeneSets using the check boxes below. Then, add them to a project". It contains a checkbox for "Select All Results" and a text input field where "Nicotine Studies" has been typed. Below this are "OK" and "Cancel" buttons. To the right of the modal, there is a sidebar titled "Add Selected to Project" with a dropdown menu showing options like "Create New Project..." (selected), "Edit Existing Project", and "Analyze". A list of projects is displayed, including "Nicotine Studies" and several others such as "AgingSeminar", "Alcohol", and "AxisAging".

When a new Project is created, you will be taken to the “Analyze GeneSets” page, where you can see the Project, its GeneSets, and the analysis tools available. Projects can be wholly or piecewise selected for analysis. The Analysis tools, listed on the left, provide a graphical depiction of the tools’ results to aid with selection.

Tip: GeneSets can be easily removed from a project by clicking the “remove” icon on the right side. If you no longer wish to keep a project, you can completely clear it out by clicking the “delete” icon, which will delete the project but not the GeneSets it contains.

Tip: Most of the analysis tools have options to tweak their output. These options are available by clicking the plus sign next to the tool.

The screenshot shows the GeneWeaver.org interface. At the top, there's a navigation bar with links for Home, Search, Manage GeneSets, Analyze GeneSets, About, and Help. It also shows that the user is logged in as DemoUser with options to Edit Groups or Logout. Below the navigation is a section titled "Analyze GeneSets". On the left, there's a sidebar titled "Analysis Tools" listing various tools with small icons: HiSim Graph, GeneSet Graph, Jaccard Overlap, GeneSet Clustering, ABBA Gene-Centered Search, Boolean Algebra, and Combine GeneSets. To the right of the sidebar is a list of projects, each with a checkbox, a plus sign, the project name, the number of gene sets, and a "Rename" link. Some projects have a red box indicating they are deprecated. To the far right of each project entry is a "Delete" icon. The projects listed are: Alcohol - 9 GeneSets (Shared With Addiction12), Demo Nicotine - 9 GeneSets, ExperimentalDrd2 - 10 GeneSets, Mechanical Pain - 43 GeneSets (6 deprecated), Nicotine Studies - 8 GeneSets (selected), PainandOpioid - 62 GeneSets (21 deprecated), Pain Overlap - 3 GeneSets (Shared With Addiction12), Phenome - 6 GeneSets, testing2 - 75 GeneSets (18 deprecated), Thermal Pain - 47 GeneSets (3 deprecated), Tutorial Example - 4 GeneSets (Shared With Addiction12), Tutorial Plus Upload your own - 5 GeneSets, Visceral Pain - 6 GeneSets, and Visceral Union - 6 GeneSets.

Project	GeneSets	Status	Action
Alcohol - 9 GeneSets	9	Shared With Addiction12	Delete
Demo Nicotine - 9 GeneSets	9		Delete
ExperimentalDrd2 - 10 GeneSets	10		Delete
Mechanical Pain - 43 GeneSets	43	6 deprecated	Delete
Nicotine Studies - 8 GeneSets	8		Delete
PainandOpioid - 62 GeneSets	62	21 deprecated	Delete
Pain Overlap - 3 GeneSets	3		Delete
Phenome - 6 GeneSets	6		Delete
testing2 - 75 GeneSets	75	18 deprecated	Delete
Thermal Pain - 47 GeneSets	47	3 deprecated	Delete
Tutorial Example - 4 GeneSets	4	Shared With Addiction12	Delete
Tutorial Plus Upload your own - 5 GeneSets	5		Delete
Visceral Pain - 6 GeneSets	6		Delete
Visceral Union - 6 GeneSets	6		Delete

To run an analysis tool, simply select Projects and/or GeneSets and then click the button on the left representing the tool you wish to run.

Tip: Projects are very useful for organizing similar studies. For example, by keeping experimental nicotine data in one project, and morphine data in another project, you can simply select both projects at once to run a comparative analysis, while keeping the collections distinct.

Select your nicotine project and then run the "HiSim Graph" tool. You will be shown a status page while the tool is running (or waiting to run) which keeps you informed of the progress of the analysis.

Analyze GeneSets

Analysis Tools

- HiSim Graph**
Biclique-based analysis is used to generate hierarchical maps of gene set interactions.
- GeneSet Graph**
Visualize the Gene-GeneSet graph.
- Jaccard Overlap**
This tool computes the Jaccard Coefficient (a measure of similarity) for multiple genesets.
- GeneSet Clustering**
Jaccard Distance (a measure of dissimilarity) is used to cluster GeneSets

- + Alcohol - 9 GeneSets**
 - + Demo Nicotine - 9 Gen**
 - + ExperimentalDrd2 - 10**
 - + Mechanical Pain - 43 G**
 - Nicotine Studies - 8 Ge**
- Add notes
- + Tier III** **Rat** **74 Genes**
Dependence genes significantly modulated in the Hippocampus.
- + Tier III** **Mouse** **263 G**
modulated by nicotine in the hippocampus.

Status:

```
0:00 - Running Biclique algorithm...
0:00 - Determining Subset Relationships...
0:00 - 10.0% Determining Subset Relationships...
0:00 - 20.0% Determining Subset Relationships...
0:00 - 30.0% Determining Subset Relationships...
0:00 - 40.0% Determining Subset Relationships...
0:00 - 50.0% Determining Subset Relationships...
0:00 - 60.0% Determining Subset Relationships...
0:00 - 70.0% Determining Subset Relationships...
0:00 - 80.0% Determining Subset Relationships...
0:00 - 90.0% Determining Subset Relationships...
0:00 - 100.0% Determining Subset Relationships...
0:00 - Building Trees...
0:00 - Drawing Trees...
DONE
```

View result (1)

Tip: If you close the window, all is not lost! Simply go to Analyze->Results to find your analysis history. Tools will not stop running if you close the page, so you can always come back to them.

Alternatively you could just have Selected All than clicked Analyze and then the tool you wish to use (HiSim Graph in this case) without creating a project.

GeneWeaver.org
A system for the integration of functional genomics experiments.

Logged in as DemoUser
[Edit Groups](#) | [Logout](#)

Home Search ▾ Manage GeneSets ▾ Analyze GeneSets ▾ About Help

Help | Feedback

Search for GeneSets

General Tiers Species Attributions

Global Filters

Include **provisional** (15)
 Include **deprecated** (0)
Group: Any (25)
Geneset Size: 1 to 263

Tiers

I: Resources (15)
 II: Pro-Curated (0)
 III: Curated (10)
 IV: Provisional (0)
 V: Private (0)

Species

Mus musculus (9)
 Homo sapiens (15)
 Rattus norvegicus (1)

Attribution

No Attribution (10)
 DRG (15)

Nicotine Hippocampus

Search in: GeneSets Genes Abstracts Ontologies - +  **Search**

Add Selected to Project ▾ **Analyze** ▾

Select GeneSets using the check boxes below. Then, add them to a project or analyze them.

Select All Results 1 - 25 of 25 genesets

 **Tier III** **Mouse** 263 Genes GS14888: Differentially expressed genes modulated by nicotine in hippocampus, Amygdala, PFC and VTA for C3H/HeJ mice

 **Tier III** **Mouse** 174 Genes GS14889: Differentially expressed genes modulated by nicotine in hippocampus, Amygdala, PFC and VTA for C57BL/6J mice

 **Tier III** **Rat** 74 Genes GS14885: Co-expression cluster of Nicotine Dependence genes in PFC, VS and Hippocampus.

 **Tier III** **Mouse** 20 Genes GS14890: Downregulated genes in five combined brain regions in C57BL/6J mice

 **Tier III** **Mouse** 51 Genes GS14891: Upregulated genes in five combined brain regions in C57BL/6J mice

 **Tier III** **Mouse** 16 Genes GS14892: Downregulated genes in five brain regions, NA, PFC, and VTA, in C3H/HeJ mice

 **Tier III** **Mouse** 70 Genes GS14893: Upregulated genes in three brain regions, NA, PFC, and VTA, in C3H/HeJ mice

 **Tier III** **Mouse** 29 Genes GS14887: Coregulated genes in both C3H/HeJ and C57BL/6J strains within five combined brain regions (Amygdala, Hippocampus, PFC and VTA)

 **Tier I** **Human** **DRG** 1 Genes **provisional** GS86761: Table 6: QRT-PCR confirmation of microarray gene expression changes Main effect of smoking: Immune response [DRG]

 **Tier I** **Human** **DRG** 1 Genes **provisional** GS86791: Table 6: QRT-PCR confirmation of microarray gene expression changes Smoking x schizophrenia interaction: NMDA postsynaptic density [DRG]

 **Tier I** **Human** **DRG** 2 Genes **provisional** GS86827: Table 6: QRT-PCR confirmation of microarray gene expression changes

Analysis Tools

 BidiQue-based analysis is used to generate hierarchical maps of gene set interactions

 Visualize the Gene-GeneSet graph.

 This tool computes the Jaccard Coefficient (a measure of similarity) for multiple genesets.

 Jaccard Distance (a measure of dissimilarity) is used to cluster Genesets

The HiSim Graph tool organizes multi-set intersections into a hierarchical directed acyclic graph (DAG). This organization infers an ontological relationship directly from the empirical data present in the original input sets. Genes in nodes at the top of the graph play a role in multiple phenotypes.

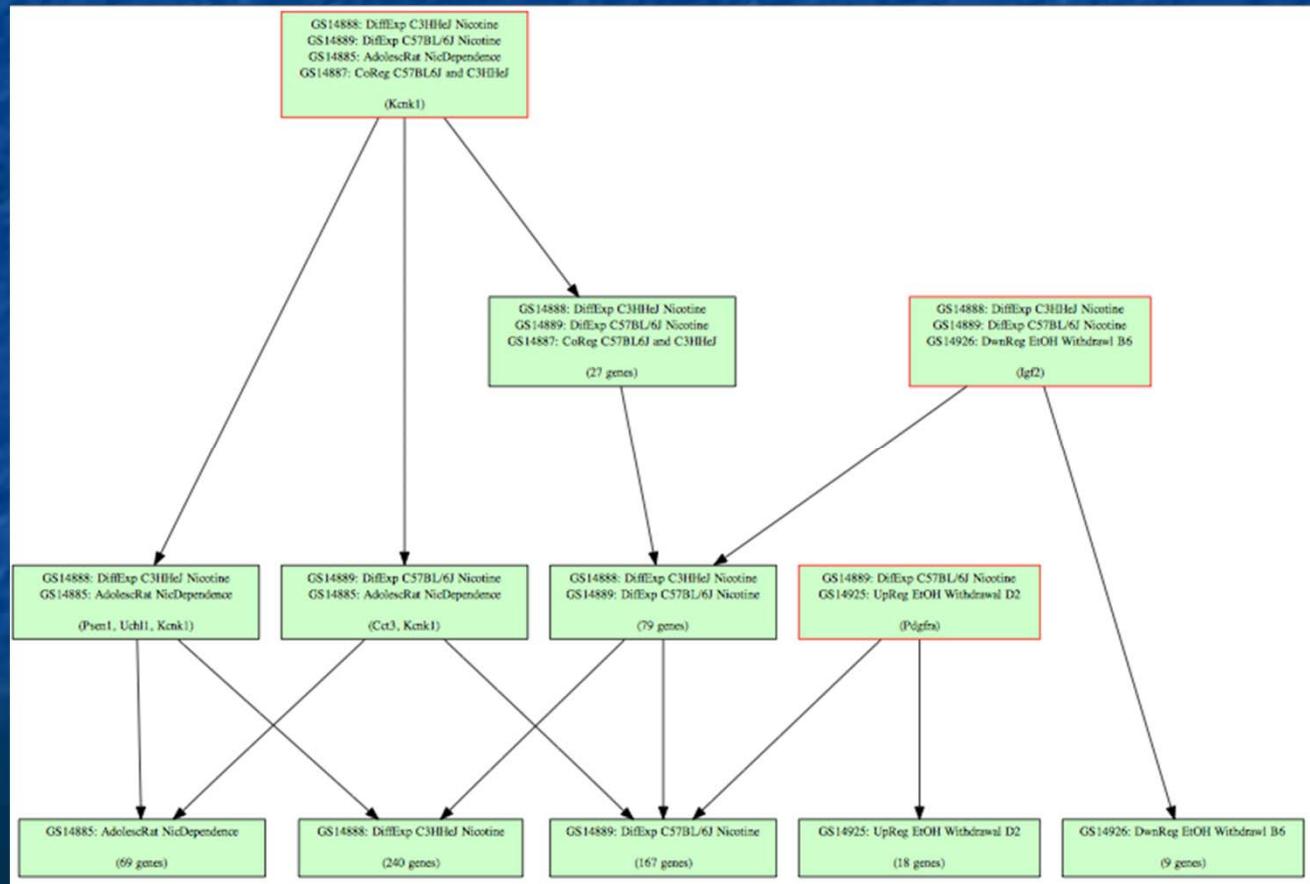
Click on the topmost node in the map to examine the genes it contains more closely.

4-way

3-way

2-way

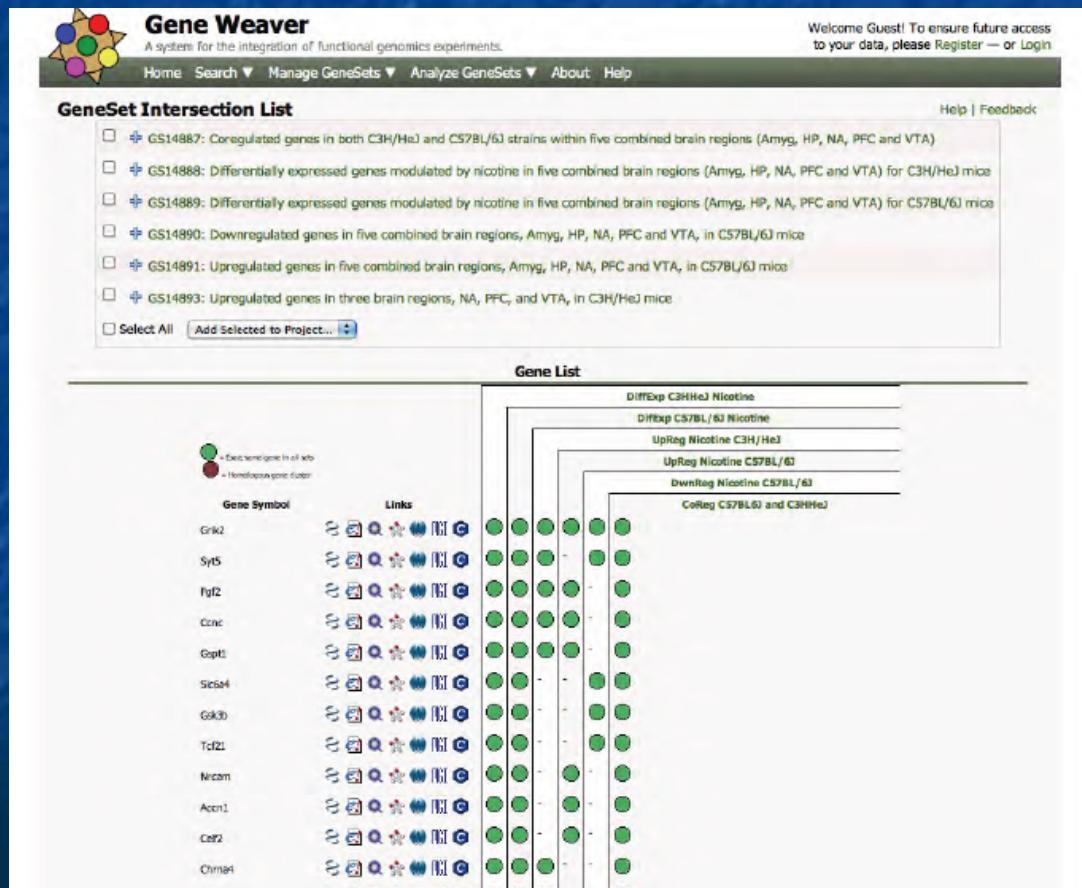
original
input



The GeneSet Intersection List shows all the sets in consideration, and a matrix of the genes associated with them. When a single species-specific gene is shown, a green circle is visible, but when multi-species data are compared, homology clusters are indicated with brown circles. In the example below, you could read it as "genes with homology to Kcnk1 are found in all 4 mouse and rat GeneSets."

Tip: Linkouts for more information are also available (as with the geneset details page).

Tip: This page can also be exported to a CSV-file (readable by Excel) for other uses by clicking the link at the bottom of the page.



Let's say we want to share our Nicotine project with a group of collaborators. First, we need to create or join a group. You can do this from your profile page, which is accessed by clicking your name in the top right corner.

The screenshot shows the Gene Weaver web application interface. At the top, there is a navigation bar with links for Home, Search, Manage GeneSets, Analyze GeneSets, About, and Help. On the far right of the top bar, it says "Logged in as Jeremy" with links for Edit Groups and Logout, and a teal arrow points to the "Logged in as Jeremy" text. Below the navigation bar, the main content area has a title "Account and Groups". Under "Manage Groups", there is a table with columns "Group Name" and "Actions". A yellow callout box is overlaid on this table, containing text about groups and instructions to enter a group name in the input field below. The input field contains "tutorial", and there are "Join" and "Create" buttons. To the right of the table, there is an "Update Account" section with fields for Name (Jeremy Jay) and Email (Jeremy.Jay@jax.org), and a "save changes" button. Below that is a "Change Password" section with fields for Current Password, New Password, and Confirm New Password, along with a "Change Password" button.

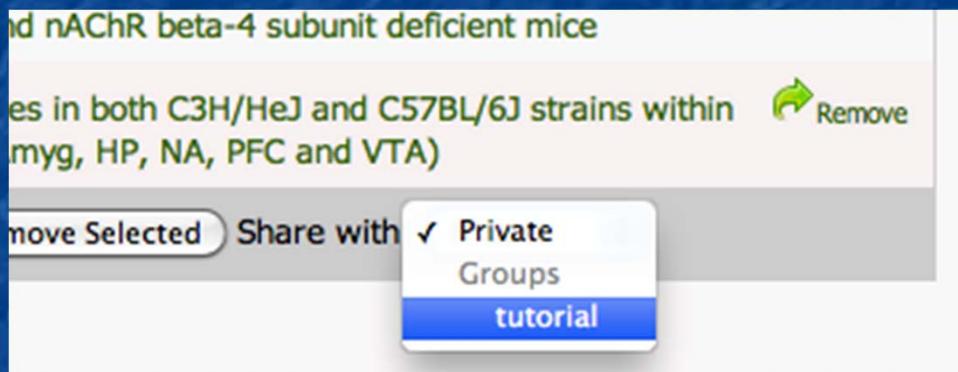
Type a group name in the Group box. To create a new group, click Create, or to join an existing group, click Join. For now, join the group “tutorial”.

Tip: To see other members of your groups, click on “[list]” to view their email addresses.

Tip: You can also update your email address and/or password from this page.

Let's go back to the "Analyze GeneSets" page.

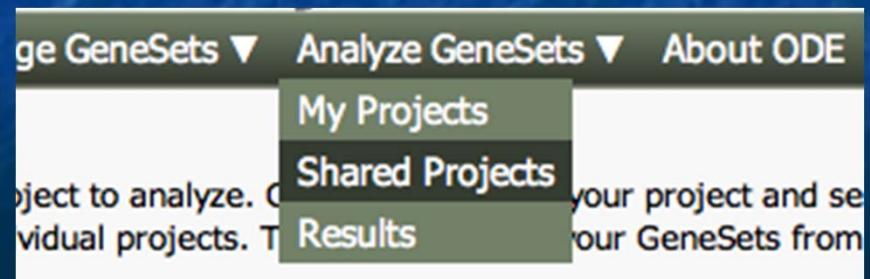
Shared Projects provide a useful way to share analyses with collaboration groups. Any project you have can be shared by clicking the plus sign to expand it, then using the "Share with" drop-down menu to select a group to share it with.



Share your project with the "tutorial" group now.

Tip: Shared Projects can only be shared with one group at a time. To share the same project with multiple groups, you can simply make a copy of the project and share it separately.

To view your Shared Projects, go to Analyze GeneSets -> Shared Projects in the menu.



Shared Projects are read-only for everyone but the owner, so you will notice that there are fewer manipulations available on this page. If you want to modify a Project, you have to copy it to your own Projects. You can do this by selecting GeneSets and using the drop-down menu provided.

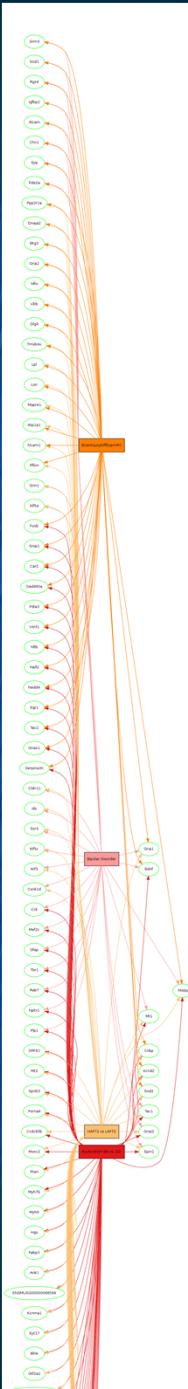
You should see anyone else's nicotine projects, along with a small example project called "Tutorial Example." Select this project and copy it to a new Project of your own.

Tip: You can run tools directly from this page, as long as you don't need your own projects.

The screenshot shows a list of projects and their associated gene sets. The first project, 'Nicotine Studies - 10 GeneSets', is collapsed. The second project, 'Tutorial Example - 4 GeneSets', is expanded, revealing four specific gene sets: GS3649, GS1250, GS1778, and GS1139. Each gene set entry includes a checkbox and a brief description. At the bottom of the expanded list is a button labeled 'Add Selected to Project...' with a dropdown arrow.

- + Nicotine Studies - 10 GeneSets (Shared By jeremy.jay@jax.org)
- Tutorial Example - 4 GeneSets (Shared By jeremy.jay@jax.org)
 - + GS3649: Candidate genes for bipolar (manic-depressive) and related disorders in mouse brain in response to Methamphetamine or Valproate
 - + GS1250: High-density microarray analysis of hippocampal gene expression profiles
 - + GS1778: Tabakoff et al 2003: Differential Gene Expression of acute functional effect of ethanol (HAFT2 vs LAFT2)
 - + GS1139: Differential expression response 4 hr after 2g/kg EtOH in C57BL/6J mice

Add Selected to Project... ▾



Let's browse the genes in this new project. Select it and run the "View GeneSets" tool. This tool simply draws a node for every gene, and one for every GeneSet, and connects them with a line if they are associated. To aid comprehension, genes are arranged by connectedness (degree) from left to right (lower-higher).

You'll notice that the resulting image is very tall and hard to read (and this was only 4 genesets!). This is an example of when it is good to change tool options. Options can be changed from the "Analyze GeneSets" page, or from the results page by clicking "Show Tool Options." (shown below)

The image at left has a MinDegree of 2, let's increase that to 3 and then re-run the tool.

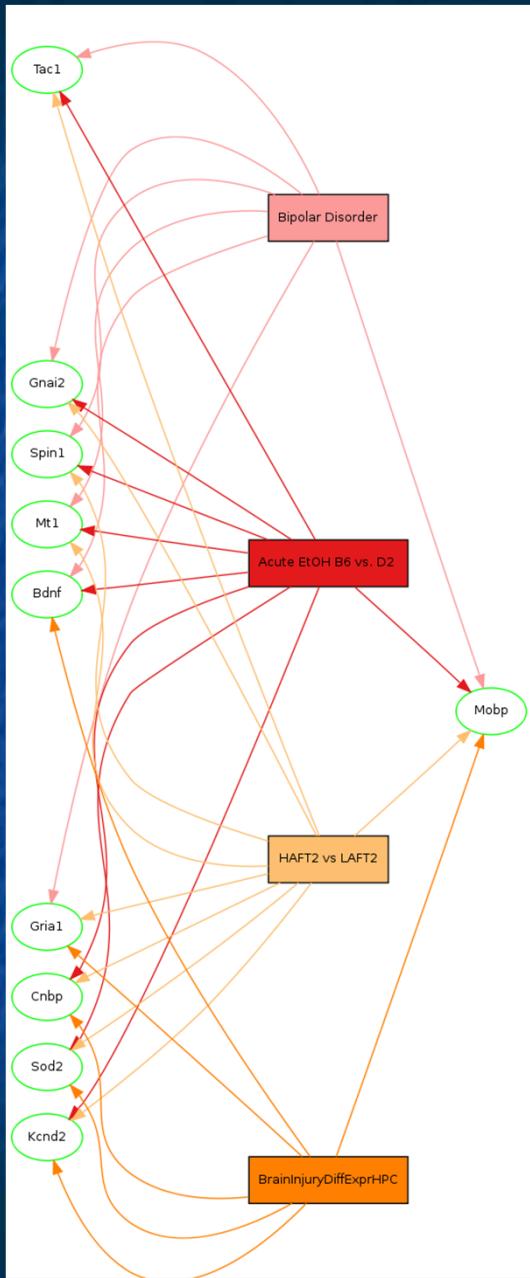
GeneSet Graph

Tool Options [hide]

Homology: Included Excluded Collapse homologous genes across species

MinDegree: Minimum Degree (connectedness) of displayed genes

SupressDisconnected: Off On If enabled, disconnected genes and GeneSets will not be displayed.



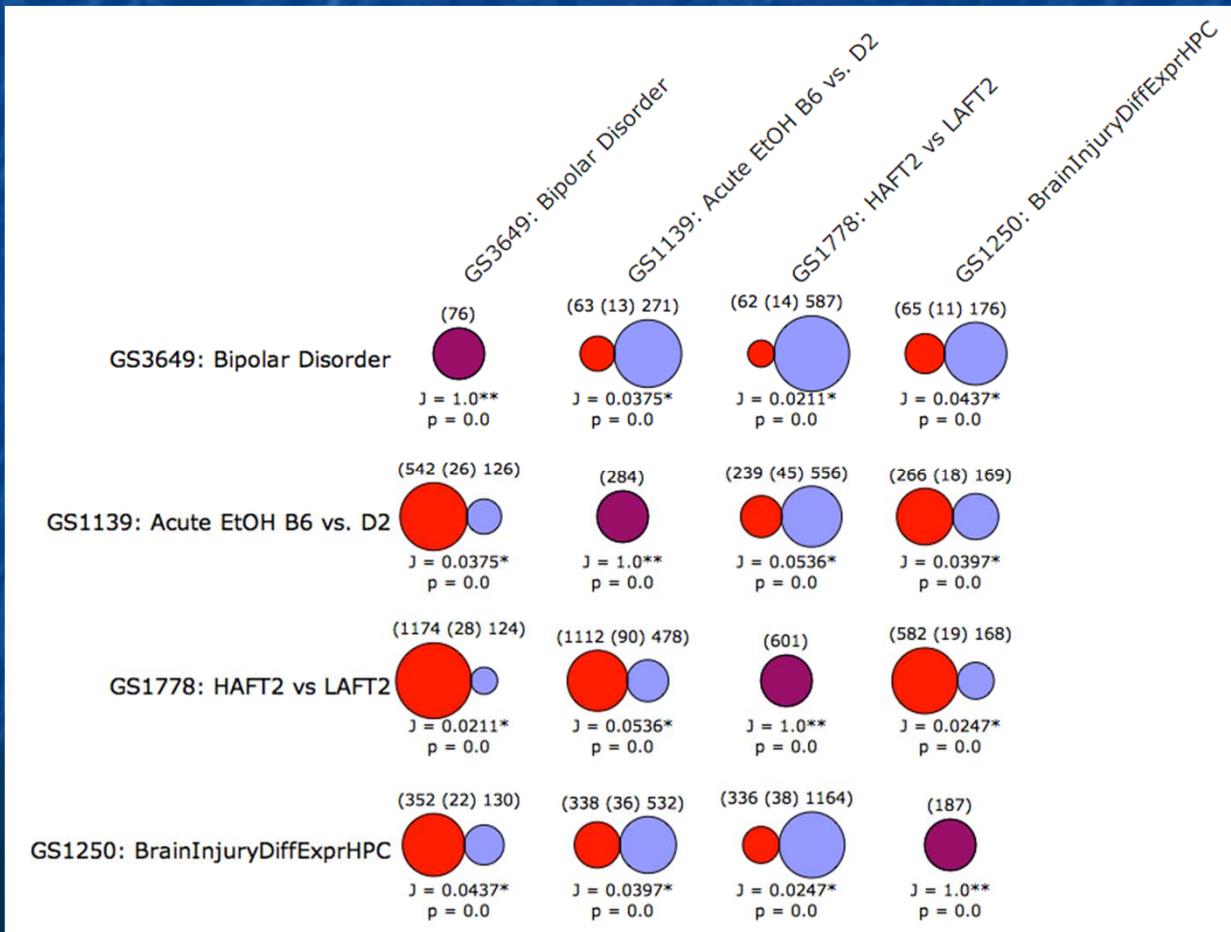
That's better. From this result, we can see that Mobb is connected to all 4 GeneSets and might warrant further study. Some of the 3-way genes might be interesting as well.

Tip: You can click on any gene in this image to search GeneWeaver for other genesets that contain that gene.

Let's try out one more tool before we move on. Using the same Project, run the "Jaccard Similarity" tool.

The Jaccard Similarity results give a large-scale, pairwise view of GeneSet overlaps. The Jaccard similarity coefficient is a positive match score for the similarity of set-set composition. Using this tool, you can quickly see when sets are highly overlapping or completely disjoint, and refine projects with more informative GeneSets.

Tip: Click on any intersection to bring up the GeneSet Intersection page discussed earlier in this tutorial.



Working with other people's data is fun and all, but.... What's in it for me?

Uploading your own data to GeneWeaver is fast and easy! Let's get started by going to "Manage GeneSets" -> "Upload GeneSet". This brings us to the upload page, where we need to provide a little bit of information:

Upload GeneSet
A * indicates required fields.

GeneSet Metadata

Please enter some descriptive info about this GeneSet.

GeneSet Name*:

GeneSet Figure Label*:

GeneSet Description*:

Access Restrictions*:

Reference Info

If this experiment has been published and listed in PubMed, just enter the Pubmed ID below to automatically fill in the publication info, otherwise you may manually enter publication information. Providing this will allow others to discover and use your data more quickly, provide a means to link here directly from PubMed, and streamline our curation efforts.

PubMed ID:

Manual Entry

Gene List

Provide a list of genes to associate with the descriptive info from above.

Species:

Gene Identifiers:

Input Gene List*:

Name – Shown in GeneSet Lists and Projects. Short but descriptive is best.

Label – Used to label nodes in results. Less than 24 characters recommended.

Description – Used to describe the experiment and selection criteria for the set. Should probably be similar to the Table caption for published results.

Availability – Describes who can access this set, Everyone (Public), just you (Private), or groups of collaborators (Group). GeneSets can be shared with multiple groups.

Species - Select the species that the genes map to (to map the correct genes).

Input File – You can either upload a plain text file, or copy and past a list by using the "copy/paste genes" button.

We'll go through these steps using an existing publication, but feel free to use your own.

Kuntz-Melcavage et al. Gene expression changes following extinction testing in a heroin behavioral incubation model. BMC Neurosci. 2009 Aug 7;10:95.

(PMID [19664213](#))

Data from Additional file 1:

Changed genes on array. The data provided are the complete list of 66 genes that were identified to have changed expression at the $p < 0.02$ level of significance.

<http://www.biomedcentral.com/1471-2202/10/95/additional/>

	A	B	C	D	E	F
1	Additional File 1: Changed genes on array					
2	Gene	Alias	Accession #	Fold Change	Probe ID	
3	brain derived neurotrophic factor	bdnf	NM_012513	1.868	A_44_P437896	
4	nuclear receptor subfamily 4, group A, member 3, transcript variant 1	Nr4a3	NM_031628	1.754	A_43_P12619	
5	monocyte to macrophage differentiation-associated	Mmd	NM_001007673	1.736	A_44_P391982	
6	FUN14 domain containing 1	Fundc1	NM_001025027	1.714	A_44_P181464	
7	imprinted and ancient	Impact	NM_001012235	1.68	A_43_P16775	
8	Cbp/p300-interacting transactivator, with Glu/Asp-rich carboxy-terminal domain, 2	Cited2	NM_053698	1.664	A_44_P307980	
9	electron-transfer-flavoprotein, beta polypeptide	Etfb	NM_001004220	1.652	A_43_P11315	
10	XK-related protein 4 (XRG4)	XRG4	NM_001011971	1.641	A_44_P398608	
11	neuron-derived orphan receptor 1 mRNA, complete cds		DQ268830	1.586	A_44_P654444	
12	cAMP responsive element binding protein-like 2	Crebl2	NM_001015027	1.577	A_44_P519174	
13	early growth response 1 (Egr1)	EGR1	NM_012551	1.574	A_44_P233080	
14	ATPase, H transporting lysosomal V1 subunit B2	Atotfv1b2	NM_057213	1.571	A_44_P149114	

	A	B	C	D	E	F
1	Additional File 1: Changed genes on array					
2	Gene					
3	brain derived neurotrophin					
4	nuclear receptor subfa					
5	monocyte to macrophag					
6	FUN14 domain containing					
7	imprinted and ancient					
8	Cbp/p300-interacting transact					
9	electron-transfer-flavoprote					
10	XK-related protein 4 (Xrp4)					
11	neuron-derived orphan n					
12	cAMP responsive element-					
13	early growth response 1 (Egr1)					
14	ATPase H transporting lysosomal V1 subunit B2					

We need to do a little data cleanup before uploading.

GeneWeaver uploads should be simple, 2-column input with gene or probe identifiers on the left and scores on the right. So, for this file we need to delete a bunch of columns. We also should remove the blanks for good measure.

Once it is cleaned up, we can save it as a Tab Delimited Text file, which can be directly uploaded to GeneWeaver.

For this tutorial though, we can save a step. Highlight all the data and copy it (Edit->Copy). Then go back to your browser and the GeneWeaver upload page.

Tip: If you're lazy but still want to follow along, the result of this data wrangling can be downloaded here:

<http://geneweaver.org/docs/tutorial example data.txt>

	A	B
1	Alias	Fold Change
2	bdnf	1.868
3	Nr4a3	1.754
4	Mmd	1.736
5	Fundc1	1.714
6	Impact	1.68
7	Cited2	1.664
8	Etfb	1.652
9	XRG4	1.641
10	Crebl2	1.586
11	EGR1	1.577
12	Atp6v1b2	1.574
13	Dmtf1	1.561
14	Cdkn1b	1.546
15	Dusp6	1.542
16	Hmgcs1	1.529
17	LOC36058	1.52
18	Nos3	1.519
19	Crk	1.505

Paste the data into the gene list text box at the bottom. Don't forget to pick the species (so the genes match correctly). Then, make sure all the other fields on the page are filled in. Providing a PubMed ID enables GeneWeaver to store the abstract and other info for searches. When you're finished click "Upload GeneSets".

GeneSet Metadata

Please enter some descriptive info about this GeneSet.

GeneSet Name*: Heroin drug-seeking in rats following 14 day enforced abstinence

GeneSet Figure Label*: rat heroin-seeking

GeneSet Description*: Changed genes on array. The data provided are the 66 genes that were identified to have changed exp 0.02 level of significance.

Access Restrictions*: Private
Public
Groups
INIA
cerebellum

Reference Info

If this experiment has been published and listed in PubMed, just enter the PubMed ID and we will automatically fill in the publication info, otherwise you may manually enter publication details. Providing this will allow others to discover and use your data more quickly, prevent duplication of work, cite your work here directly from PubMed, and streamline our curation efforts.

PubMed ID: 19664213
Manual Entry

Gene List

Provide a list of genes to associate with the descriptive info from above.

Species: Rattus norvegicus

Gene Identifiers: Gene Symbol

Input Gene List*: Have a text file already handy? Switch to file upload

Alias Fold Change	
bdnf	1.868
Nr4a3	1.754
Mmd	1.736
Fundc1	1.714
Impact	1.68
Cited2	1.664
Etfb	1.652
XRG4	1.641
Crebl2	1.577
EGR1	1.574
Atp6v1b2	1.571
Dmrt1	1.561
Cdkn1b	1.546
Dusp6	1.542
Hmgcs1	1.529
LOC360586	1.52
Nos3	1.519
Crk	1.505
Tmem49	1.505

When upload completes, you will be taken to your new GeneSet details page. From here, you can add it to Projects and do further analysis.

GeneSet Details

Uploaded GeneSet data points in 30 seconds.

You can now view it below:

Gene Set #83616 - Heroin drug-seeking in rats following 14 day enforced abstinence

Description: Changed genes on array. The data provided are the complete list of 66 genes whose expression at the p < 0.02 level of significance.

Owner: jjay@utk.edu

Species: Rattus norvegicus

Authors: Kuntz-Melcavage KL, Brucklacher RM, Grigson PS, Freeman WM, Vrana K

Title: Gene expression changes following extinction testing in a heroin behavior

Journal: BMC neuroscience Aug 2009 , Vol 10 , pp. 95

Abstract: BACKGROUND: A number of gene expression studies have investigated changes in gene expression that persist following relapse. In this study, genome-wide gene expression analysis was performed in rats following an extinction session (90 min) in rats that expressed behavioral changes following extinction testing in a heroin behavior. As an important modulator of goal-directed behavior, the media genomic analysis. Rats were trained to self-administer heroin during 3 h of administration period, rats were reintroduced to the self-administration condition they could seek heroin, but received none. Extinction sessions were conducted under enforced abstinence to demonstrate behavioral incubation. RESULTS: Below expression) of heroin-seeking and goal-directed behavior after the 14 d of enforced abstinence, animals displayed heightened drug-seeking behavior when re-exposed to heroin. This increased drug-seeking took place despite the extinction session. Whole genome gene expression analysis was performed by time PCR (RT-qPCR). Microarrays identified 66 genes whose expression was < 0.02 following 14 d of abstinence and the 90-minute extinction session confirmed by RT-qPCR demonstrated significant alterations in bdnf, calbindin, and Cntn4. Ontological analysis indicates that several of the genes confirmed to be changed through that role may impact learning and behavior. The importance of drug-taking sessions suggest that such genes may be important for relapse. The knowledge of heroin-induced changes and further highlights similarities between the two models.

19664213

Gene List

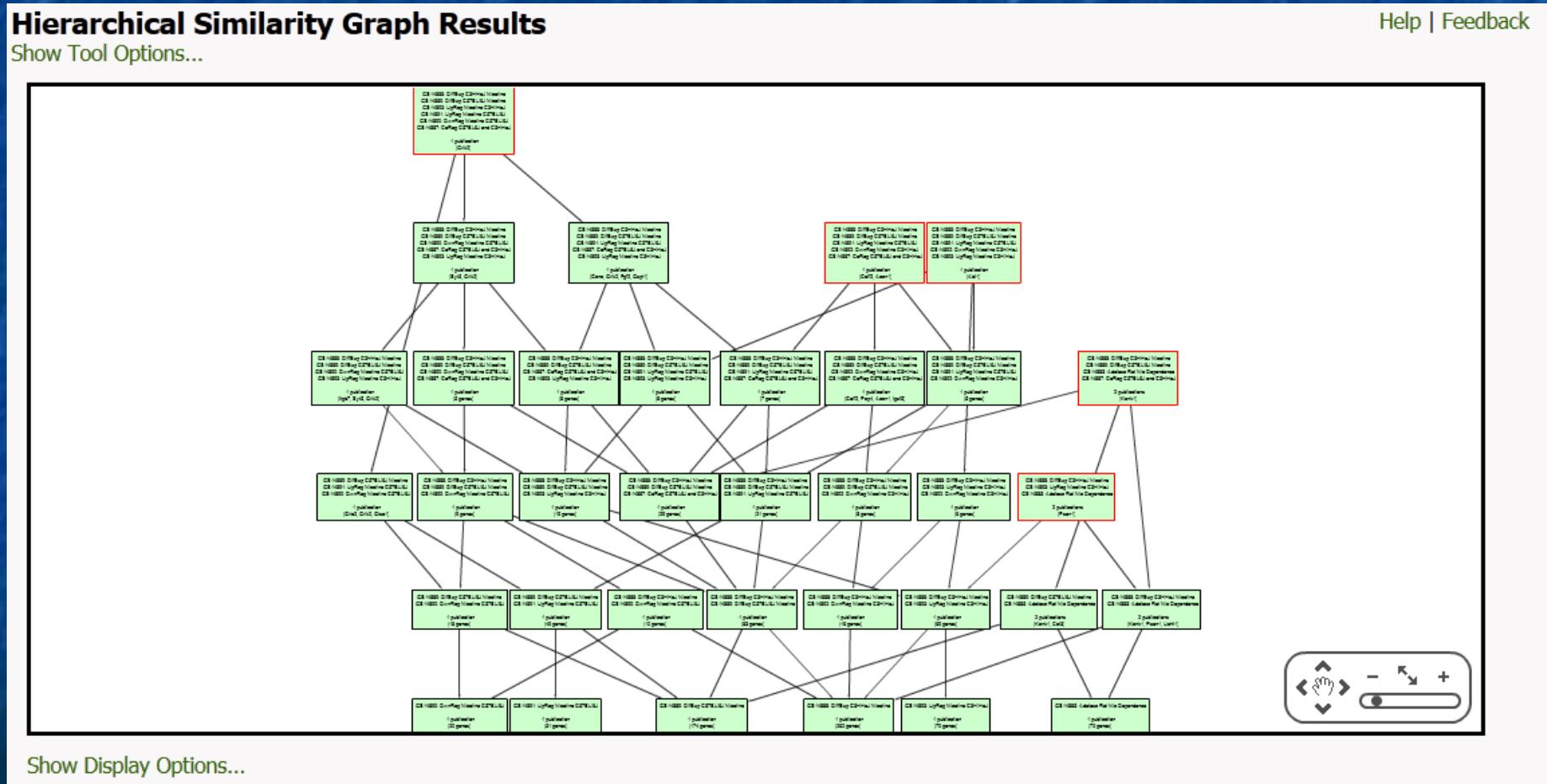
63 data points, using thresholds: 1.868 > |effect size| > 0.556

Display using: Gene Symbol*

Export Data

Gene Symbol	LinkOuts	Data Value
Accn1		1.41100
Acsl4		1.43300
Atp2c1		1.40200
Atp6v1b2		1.57100
Bdnf		1.86800
Calb1		1.42200
Cdkn1b		1.54600
Chka		1.44800
Cited2		1.66400
Cntn4		1.48900
Crebl2		1.57700
Crk		1.50500
Crybb1		0.67600
Ctnnb1		1.42300

An example of the HiSim Graph results for the Tutorial Example project and the newly uploaded set. Notice that both Mouse and Rat data are integrated and overlapping in the results due to GeneWeaver's usage of homology.



Many features of the HiSim Graph can be modified by clicking on 'Show tool options' or 'Display Options'

Hierarchical Similarity Graph Results

Show Tool Options...

Phenome Map Results

Tool Options [hide]

Help | Feedback

DisableBootstrap: False Disable Bootstrap filtering of large graphs

HideUnEmphasized: False Hide Nodes that do not contain any emphasis genes

Homology: Included Collapse homologous genes across species

Excluded

MaxInNode: 4 Number of gene symbols to display in nodes.

MaxLevel: 40 Maximum number of nodes to show in a level of the graph. (0 for no limit)

MinGenes: 1 The Minimum number of genes required to produce a node.

Permutations: 0 Number of Monte Carlo permutations to run.

PermutationTimeLimit: 5 Maximum number of minutes to let the permutation testing run for.

p-Value: 1.0 Set p-value threshold for trimming edges.

UseFDR: False Apply False Discovery Rate correction when trimming edges.

Re-Run Tool

Display Options [hide]

Highlight Genes: Enter Gene ID... Add Remove

Show Labels:

My Projects

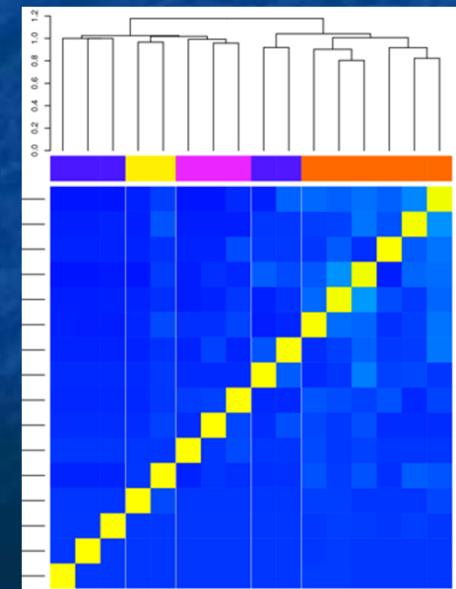
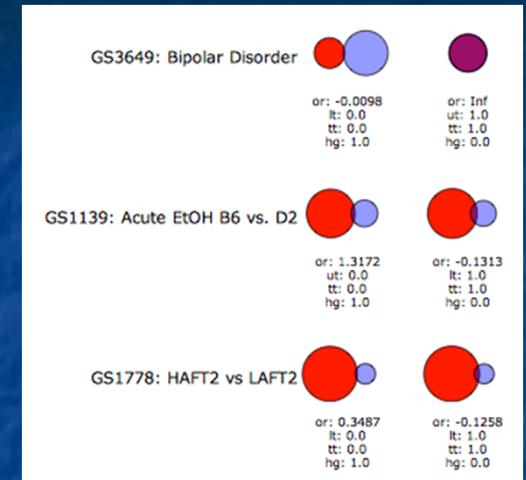
Highlight Projects: Ctrl-Click to select multiple

Highlight GeneSets: Ctrl-Click to select multiple

Download Graph File: PDF Export...

Other tools are also available for use which were not covered in this tutorial:

- Hypergeometric tests look very similar to the Jaccard Similarity tool, but show the results of Fisher's exact test on all pairwise GeneSet intersections.
- Jaccard Clustering uses hierarchical clustering to organize GeneSets by their similarity to each other. (Beta)
- Project Utilities allow you to manipulate your projects at a high level, creating new projects from the intersection of multiple projects, collapsing GeneSets in a project into a single new GeneSet to use later, filtering out GeneSets by similarity, and more.
- Our new ABBA tool, found in the menu under "Search" -> "for Genes", allows you to query the entire GeneWeaver database for genes with similar relationships to genes from a list of interest.



- This tutorial was intended to provide an introduction to practical approaches to the tools in GeneWeaver.
- There are many tools and approaches that can be combined to create particular workflows to address a variety of genetics questions. Additional tutorials and documentation can be found on the website.
- If you have any suggestions, comments, or questions please use the "Feedback" link located on every page.

