

GeneWeaver is an online system for the integration of functional genomics experiments. The GeneWeaver web-based software system contains a database of experimental results and set of interactive tools for analysis and visualization. The database provides storage of functional genomics experiments in the form of gene sets, gene set descriptions and gene set association scores from multiple species. Currently 10 species are available, *Mus musculus*, *Homo sapiens*, *Rattus norvegicus*, *Danio rerio*, *Drosophila melanogaster*, *Macaca mulatta*, *Caenorhabditis elegans*, *Saccharomyces cerevisiae*, *Gallus gallus*, *Canis familiaris*.

GeneWeaver allows users to integrate diverse gene sets across species, tissue and experimental platform. Sets can be stored, shared and compared privately, among user defined groups of investigators, and across all users. Gene sets can come from many different sources, including but not limited to: Microarray expression studies, Gene Ontology annotations, Text Mining tools, conserved modules, candidate genes, or even just a list of genes that you find interesting. The gene sets are connected at a gene level, using homology to relate gene sets from different species into an integrated database. This database stores all the gene sets uploaded, and allows users to share the data with others, or restrict data to collaborative groups only. The database also provides a single integrated data source for comparative genomics tools.

- The "**Quick Start**" **guide** is designed to help get new users up and running quickly with a basic two page GeneWeaver Guide.
- The GeneWeaver **GeneWeaver Tutorial** provides a guided tutorial exercise to get you familiar with using and interpreting basic GeneWeaver analyses and tools through applied examples. The exercise is suitable for use in demonstrations and courses.
- **Function Reference** is a table of the inputs and outputs of GeneWeaver functions.
- The "**How Do I...?**" pages provide an interactive GeneWeaver walkthrough with a work-flow based outline.
- To learn more about how to work with other researchers and their data within GeneWeaver check out **Users and Groups**.
- **GeneWeaver Movie** provides video clips featuring examples of the use of GeneWeaver tools.
- **FAQ**

While GeneWeaver contains over 30,000 sets of publicly available sets of genes, it is often the case that individual gene sets of interest are not among these. Registered users can upload **Single**

Gene Sets and make use of the **Batch Gene Set Upload** process.

Controlling the quality and validity of the large-scale analysis of secondary data requires the enforcement of interpretable standards for gene set construction and description. GeneWeaver's use of discrete analysis eliminates many barriers to the integration of heterogeneous data sets across species and experiments. However, it is important for users to be able to rapidly interpret the nature of gene sets retrieved from the site, requiring a minimal standard for metadata associated with secondary data. For this purpose, both unstructured textual descriptions of the data and structured ontology annotations to the terms in these descriptions are used to define gene sets. Our **Curation Standards** page provides detailed guidance to GeneWeaver curation policies and sample curation types. We have also included a brief explanation of the **Curation Process**, which includes a guide to our *new* curation interface.

Our database includes data obtained from numerous **external data resources**. GeneWeaver allows users to conduct text searches on metadata and raw data stored in our database. These include searches by permission level, species, curation tier, gene set information or genes of interest. Please see our **Search Help** page for more details on text search options. Occasionally it is useful to search for gene sets anchored on genes or gene sets of interest based on their overlap with neighboring gene sets. **Anchored Biclique of Biomolecular Associations (ABBA)** is a tool that allows you to accomplish this task.

GeneWeaver uses a set of analysis tools to operate on genes and gene sets. These tools evaluate a range of data inputs for the purposes of elucidating hierarchical relationships among a set of gene sets of interest. They can be used to visualize bipartite clusters (**Hierarchical Similarity [HiSim] Graph**), or visualize genes with the more common intersections, **GeneSet Graph**. Generation and visualization of a maximal triclique using the intersection of gene sets with the **Triclique Viewer Tool** can allow users to discover novel relationships between gene ontology terms. The overlap/similarity of gene sets, themselves can be visualized with **Jaccard Similarity** and **Hypergeometric Tests** plots. These set overlaps are also available for **Clustering**, while component gene intersections can be found on our **Gene Intersection Lists**. The **Boolean Algebra** tool uses advanced set logic to integrate multiple genesets. For each tool, GeneWeaver allows users to expand their search beyond a single species using **Homology Mapping**.

GeneSet Details Pages allow users to view vital information about gene sets of interest, including associated genes, homologs, and references to external links. **Gene Intersection Lists** are useful for determining which information is shared between gene sets of interest. In addition, GeneWeaver tools allow users to **Combine** gene sets of interest or perform more complex set operations based on **Boolean Algebra**. Gene sets may also be annotated with information about **Emphasis Genes**, allowing users to augment GeneWeaver tools with gene-specific information.

- Public access to the GeneWeaver **analysis codebase** along with appropriate **schema build scripts** is available.
- Please **contact** the GeneWeaver Team for information on how a new **module** may be incorporated into the GeneWeaver environment.
- All of the Publications referenced by GeneWeaver GeneSets have been collected into a EndNote formatted library that can be found here.
- You can find a detailed description of GeneWeaver's usage, data sharing and privacy policies **here**.
- These pages also include information on GeneWeaver related **Publications** and **How To Cite** GeneWeaver. In addition, our **QR Code** allows you to rapidly connect viewers of your printed work to GeneWeaver.
- Please feel free to **Contact the GeneWeaver Team** with any questions you might have about the data or tools.
- The GeneWeaver Team would also like to **Acknowledge** the many folks who contribute to and support our efforts. Importantly, the GeneWeaver / The Ontological Discovery Environment was *initiated as a project of the NIAAA Integrative Neuroscience Initiative on Alcoholism (U01AA13499, U24AA13513), and is supported by R01 02-AA18776 NIAAA/NIDA.*

These pages are maintained by the GeneWeaver team and the **Chesler Lab** at **The Jackson Laboratory in Bar Harbor, Maine**.

Visit the **Help page** for information on how to add new content and edit existing WikiHelp pages. If you have further questions please contact Jason **Bubier**, GeneWeaver Data Curator or Elissa Chesler.