The Rat Genome Database: Resources for Genomics Research

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http://rgd.mcw.edu

Abstract:

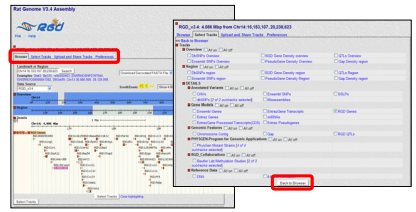
It probably isn't surprising that the "Rat Genome Database" has a wealth of resources for researchers interested in genomics. But if you haven't visited the RGD website recently (http://rgd.mcw.edu), you might not be aware of the broad utility of the tools available there. RGD's rat Genome Browser (GBrowse) allows users to visualize and explore details of the rat genome. Whether you want to compare gene models from different sources, view the SNPs and other variants for a particular chromosomal region, or explore the syntenic regions and orthologous genes between rat, mouse and human, GBrowse is the place to do it. In addition, as individual rat strains are sequenced, specific variant tracks for each species will be incorporated into the browser to facilitate comparisons between strains.

If you want a wider view of genomic regions associated with a particular function, process, pathway, disease or phenotype, the RGD GView tool gives a full-genome view of genes and QTLs annotated to such terms. Zoom in for a more detailed view, or add additional terms to the search to visualize where, for instance, regions associated with two different diseases overlap.

For researchers interested in really digging into rat data from a variety of sources, RGD's new RatMine tool gives powerful and flexible options for searching, extracting and utilizing data from RGD, Ensembl, UniProtKB, KEGG and more. Built on the "InterMine" technology, RatMine gives researcher the option of utilizing a suite of standard template queries to explore the data, or constructing their own queries to answer specific questions. In addition to queries, RatMine makes use of lists of objects such as genes, proteins and SNPs. Whether the list was derived from a query, uploaded by a researcher or is one of a number of lists provided in the tool, RatMine supplies a variety of functions and "widgets" that allow researchers to view analyses such as ontology term enrichment, manipulate lists to compare or contrast results from different experiments or queries, or feed the members of one list back into other queries to extract additional data from the database. Currently, RGD is in the process of establishing links between RGD gene and QTL report pages and queries in RatMine to give researchers one-click access to data such as the list of genes that fall within a QTL, or whether any non-synonymous SNPs can be found within a gene.

Finally, for researchers interested in inter-strain variations, the RGD SNPlotyper tool allows users to select a region of the genome and a variety of rat strains to ascertain which SNPs in that region are polymorphic between the strains. Built on the solid foundation of RGD's core data, tools such as GBrowse, GView, RatMine and SNPlotyper are valuable assets for researchers doing genomics research.

Genome Browser (GBrowse)



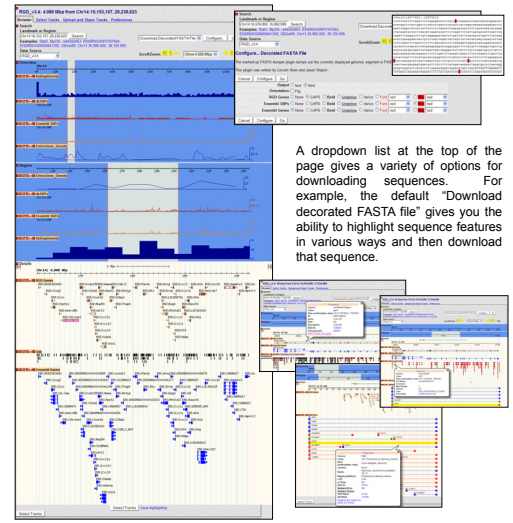
RGD's Genome Browser (GBrowse) has recently been updated. Although many of the functions are the same, the look and feel have changed. Also, the tool has been upgraded with additional functionality and with increased speed and performance.

Undoubtedly the most obvious difference is the change to tabbed sections. Rather than scrolling down the page to find the "Change tracks" menu, this functionality only requires a single click on the tab at the top of the display, or on either of two buttons beneath it, to access a page with choices of tracks to display.

As before, the "Overview" section gives a chromosome-level view. However, now that section includes its own tracks, such as gene and SNP density tracks.

A new "Region" section displays the region selected in the Overview at higher magnification and also contains tracks such as SNP density to give users a better view of that segment and its immediate environs.

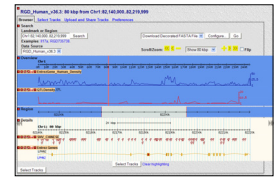
The "Details" section lets you zero in on your region of interest. Drag-and-drop tracks give you the ability to "place" your tracks in whatever order you need. This facilitates comparisons between tracks, such as comparing gene models from different databases, locating SNPs within a gene, or checking for sequence gaps in your region of interest.



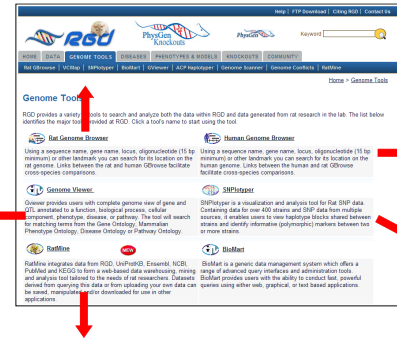
A dropdown list at the top of the page gives a variety of options for downloading sequences. For example, the default "Download decorated FASTA file" gives you the ability to highlight sequence features in various ways and then download that sequence.

Mousing over or clicking on an object exposes balloon pop-ups which supply object-specific information and links. For instance, for genes these include links to RGD and Entrez Gene report pages as well as a new option to get a downloadable list of SNPs in that gene.

In the QTL popup balloon you'll still find information such as QTL symbol and statistical values, but now additional data is given about the strains used and related QTLs if any are available. A link to the SNPlotyper tool facilitates searching for polymorphic SNPs between the strains used to generate the QTL.

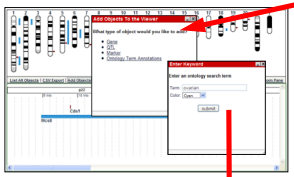


For comparative purposes RGD also has a Human Genome Browser. Access it from the RGD tools page, or use the "Data Source" dropdown list in the rat GBrowse and select "RGD_Human_v36.3". The functionality of the two browsers is essentially the same.

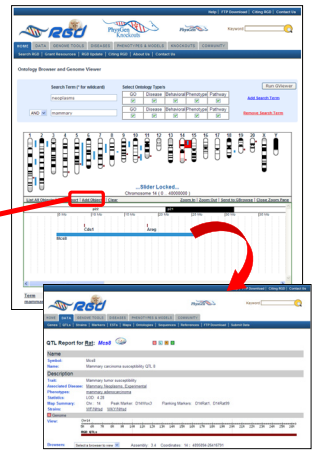


Genome Viewer (GViewer)

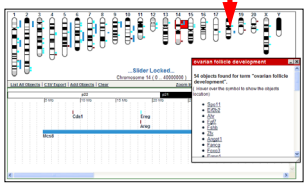
The GViewer tool provides a genome-wide view of genes and QTLs which are annotated to one or more ontology terms of interest. Once you have completed your search, you can click on a chromosome to open a zoom pane which gives you a closer look at the objects which map to your selected area.



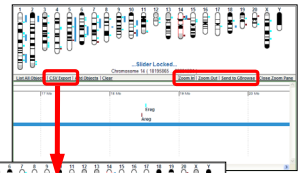
Use the "Add Objects" button to search for genes, QTLs or markers by name, or to find genes and/or QTLs annotated to another ontology term. The option to specify the color makes it easy to distinguish objects added via different searches.

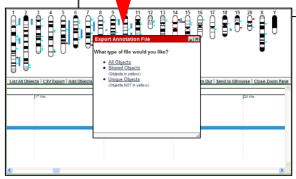


Clicking on a gene or QTL in the zoom pane will take you to the RGD report page for that object .



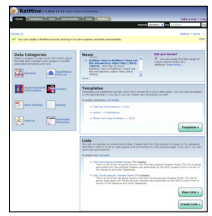
Use the "Zoom in/Zoom out" buttons to reduce or increase the size of the section in the zoom pane. To view your results in their full genomic context, click "Send to GBrowse".



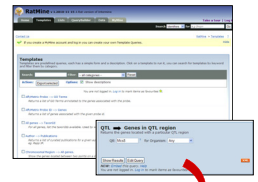


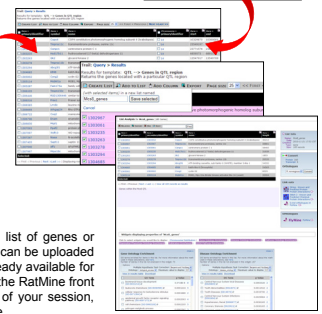
Use the "CSV Export" button to download a list of the objects being displayed in the GViewer window. If you have made multiple searches you can choose to download information on all of the objects, just those that are shared between your searches, or only those which are not shared between your searches. The output is a comma-separated list which can then be opened in a spreadsheet such as Excel, or used in other applications.

RatMine



RatMine is a data warehousing, mining and analysis tool based on the InterMine technology. RatMine incorporates data from multiple sources such as RGD, Entrez Gene, UniProtKB and KEGG and makes it available via a wide variety of predefined queries or "Templates"

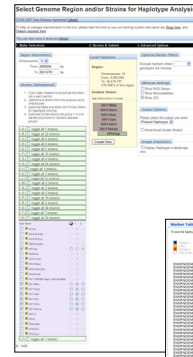




Data analysis in RatMine begins with a list—for example, a list of genes or proteins. These lists can come from template queries or they can be uploaded by the user. In addition, there are a number of useful lists already available for use. To upload or view a list, click the "Lists" button or tab on the RatMine front page. Rather than losing your lists and queries at the end of your session, register for a free account and login to save them for future use.

The list analysis page shows information about the items in your list, in this case a list of genes. It also gives you options to convert the genes in your list to proteins which would give you somewhat different analysis options, and to send the items in your list to a number of external sites for further analysis. However, the core of the list analysis page is the ontology term and other enrichment widgets. These leverage the power of RGD's gene, disease, phenotype and pathway ontology annotations to show you what functions, pathways and processes are more highly represented in your dataset compared to the control set of all rat genes

SNPlotyper



RGD's SNPlotyper tool is designed to allow the user to easily view and download information about what SNPs are polymorphic between individual strains or groups of strains within a user-specified region of the genome.

Results can be viewed as a "visual haplotype" where differences in genotype are denoted by different colors. Overlapping QTLs are also shown.

Results can also be viewed in and downloaded from a table showing SNP IDs, bp location and the surrounding nucleotide sequence.