

WormBase Newsletter

April 2005

WormBase includes 'WormMart'

WormBase has now made available 'WormMart' (<http://dev.wormbase.org/BioMart/martview>), the newest addition to the WormBase data mining repertoire. WormMart is an implementation of 'BioMart', and provides a flexible user-friendly interface for retrieving select data from WormBase en masse. Users begin by selecting a reference release of the database followed by a point of focus (for example, a 'Gene'). Queries can then be restricted to a list of IDs, or chromosomal or genetic map position. Next, a series of filters can be enabled, further restricting the returned results. For our example, an user might choose to filter the results to include only those genes that have alleles. Finally, a broad range of data can be selected that should be included in those features that pass through the filters. It is anticipated that WormMart will eventually replace the 'Batch' scripts.



WormBase has a new mirror site in Asia

WormBase is pleased to announce our first mirror site in Asia, <http://wormbase.ccbb.re.kr/>, housed at the Center for Computational Biology and Bioinformatics (CCBB) in South Korea. The site is administered by Chang Hyuk Kwon. We have also stabilized existing mirrors and developed a robust mechanism for keeping these sites up-to-date. We encourage users to utilize mirror sites closest to their geographical location. The mirror sites are located at:

Pasadena, CA, USA (Caltech) <http://caltech.wormbase.org/>

Crete, Greece (IMBB) <http://worm.imbb.forth.gr/>

Daejeon, South Korea (CCBB) <http://wormbase.ccbb.re.kr/>

If you are interested in hosting a mirror, please contact Todd Harris (harris@cshl.edu).

New improvements to performance of the website

WormBase has taken several steps in order to address concerns about performance. First, we have added additional hardware to the primary site. Second, we have implemented an object level caching mechanism. This mechanism should increase the speed of the site as frequently accessed pieces of data will be cached in memory and on disk. We continue to cache entire pages, in particular for popular pages such as the gene page. We have established a third mirror site and stabilized the existing mirrors. Finally, we are reorganizing complex pages with large amounts of data, into several simpler pages. We hope these improvements will help to provide the fastest access possible to the website.

WormBase displays protein motifs on the genome browser

It is now possible to explore the relationship of translated features to gene structure through the display of protein motifs and domains on the genome browser. To see these features, enable the 'Protein Motifs' track. When a motif or domain spans an exon boundary, a dashed grey line is displayed. This feature may also be useful for creating constructs for purposes of rescue or to study expression patterns. For an example, see: <http://www.wormbase.org/db/seq/gbrowse/wormbase?name=unc-26;source=wormbase;width=960;version=100;label=LOC1%3Aoverview-CG-MOTIFS>

New 'Variation' class includes information about polymorphisms, alleles and loci

WormBase release WS140 introduced a new 'Variation' class, meant to consolidate all the data on polymorphisms (previously handled as both alleles and loci) and to more effectively capture information about alleles. In keeping with this new class, the 'Allele' class has now been retired. To support the Variation class, the displays have been modified. See: <http://www.wormbase.org/db/gene/locus?name=unc-26> and <http://www.wormbase.org/db/gene/variation?name=e345>.

New data from the genome-wide RNAi screen in WormBase

The results from the systematic RNAi screen reported in Soennichsen et al., Nature 434, p462-469, are now available on the development site, along with links to movies and other relevant information at the PhenoBank (<http://www.worm.mpi-cbg.de/phenobank2/cgi-bin/MenuPage.py>). See [WBRNAi00049552](#) for an example.

WormBase Literature search is updated

A number of improvements have been made to the WormBase Literature search engine in line with the new Textpresso (www.textpresso.org) build release. The full text of over 1,000 new journal articles pertaining to worm biology have been added to the database; four new categories are available from the drop-down menus; improvements have been made to the interface, including a new 'sort' function.

New data submission form for RNA interference data

An on-line RNAi Data Submission Form is now available. The form allows authors to submit all experimental information necessary for an automated RNAi experiment report generation. Data entered using this form will be incorporated into the following database build directly. This should significantly speed up curation of individual RNAi experiments. It also provides a way for authors to propose new phenotype terms as well as to submit more detailed information about the experimental design. The form is available at http://elbrus.caltech.edu/cgi-bin/igor/rnaitools/rnai_submission and from the data submission page of WormBase: <http://www.wormbase.org/db/curate/base>.

Remote annotations available in 'Publication Quality Image' from the Genome browser

An often overlooked but very useful feature of the Genome Browser is the ability to display personal annotations in the context of a chosen view of the genome. These annotations can be entered as plain text or by uploading a file as described in the documentation at the bottom of the Genome Browser page (<http://www.wormbase.org/db/seq/gbrowse/wormbase?help=annotation>). Uploaded annotations can be displayed as images available from the 'Publication Quality Image' link and are generated in Scalable Vector graphics (SVG) format. These images can be edited in vector-based graphics applications such as Adobe Illustrator. Coupled with the ability to display uploaded annotations, it is now possible to quickly create a custom, high quality image suitable for publication.