NCBI News, March 2013

New CDD Release v3.10 Includes an Updated PSSM Calculation

Tuesday, March 26, 2013

Conserved Domain Database (CDD) version 3.10 is now available with 1104 new or updated NCBI-curated and 48,034 total domain models. For more information, see the CDD News page.

In this new release, position-specific score matrices (PSSMs) are now provided in an extended format. They contain 28 rows instead of 26, and also come with intermediate data in addition to the final scoring matrix. The latter will make it possible to directly generate search databases for the current version of RPS-BLAST, DELTA-BLAST, as well as an upcoming new version of RPS-BLAST that supports composition-corrected scoring.

Please note: PSSMs been re-computed for a large fraction of the models in CDD, which has slightly affected the resulting sequence annotations.

To use pre-computed PSSMs for formatting RPS-BLAST search databases, the "makeprofiledb" application must be installed. Details on how to run "makeprofiledb" can be found in the CDD FTP README file.

NCBI Presents Genetic Variation and Medical Resources at the ACMG 2013 Meeting

Thursday, March 21, 2013

NCBI staff members are presenting the NIH Genetic Testing Registry (GTR) and other NCBI clinical genetics resources, including MedGen and ClinVar, at the American College of Medical Genetics and Genomics 2013 Annual Clinical Genetics Meeting in Phoenix, Arizona.

ACMG 2013 Presentations:

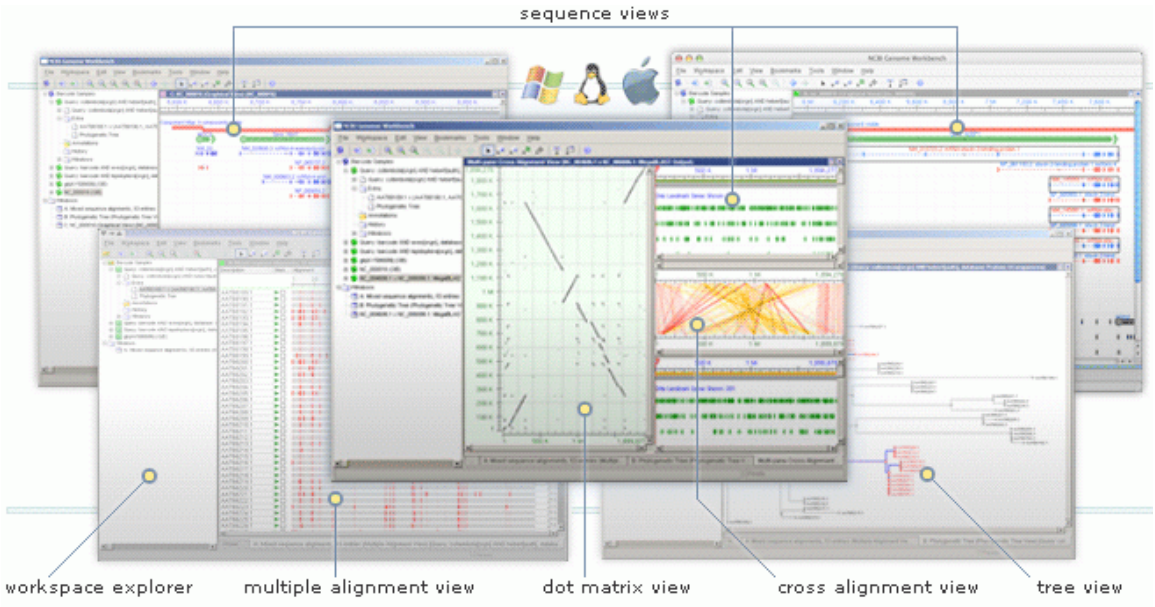
- Wednesday, March 20, 2013: The NIH Genetic Testing Registry (GTR): Public Meeting on Transition Plan with GeneTests
- Friday, March 22, 2013: Medical Variation and Phenotypes at NCBI: GTR, MedGen, and ClinVar

NLM Citation: NCBI News [Internet]. Bethesda (MD): National Center for Biotechnology Information (US); 1991-2012. NCBI News, March 2013.

Genome Workbench 2.7.0 Now Available

Wednesday, March 20, 2013

Version 2.7.0 of Genome Workbench is now available with many new features, improvements and some bug fixes.



From the Genome Workbench Release Notes:

New Features

- New, reimplemented SNP Table View (SNP Table View Tutorial)
- Graphical Sequence View: implemented new persistent markers on sequences (Sequence View Markers Tutorial)
- Implemented reader of 5-column feature table format
- Text View: Implemented search
- Genome Workbench project can now be opened as Table (Project Tree View, project context menu / Open Table View). New feature allows user to sort and search project content.

Bug Fixes and Improvements

- Multiple Alignment View: added new column “Organism name” (taxonomic name)
- Multiple Alignment View: fixed issues with BLAST results with multiple queries
- BLAST Search: improved Blast DB selection from the most recently used list
- BLAST: improved parameters selection interface not to allow mutually exclusive options

- Graphical Sequence View: fixed crash with protein alignments
- Graphical Sequence View: fixed crash with visualization of pile-up graph for alignments
- Graphical Sequence View: improved 'Project features for aligned sequences' mode for alignment tracks
- Graphical Sequence View: fixed display of alignments with local ids
- Graphical Sequence View: restored defline as part of sequence track label, sequence track tooltip improved to be pinnable
- Graphical Sequence View: implement 5' end visual tagging (sequence track)
- Splign tool: fixed crash
- Table Import: improved recognition of DOS/Unix line breaks, various small issues fixed
- OpenGL support: resolved issues with some limited functionality graphics drivers, improved work with Remote Desktop
- Tree View: improvements and fixes for PDF printing
- Generic Table View: implemented support for Copy from cell function
- Generic Table View: added support for disabled rows
- Table Views (all): added pop-up tooltip to show full content of extra long cells
- VCF support: improved label generation for VCF imported variants
- Alignment Summary View: fixed number of bugs and issues
- Text View: implemented molecule separation in Flat File mode
- Create Gene Model Tool: added option to propagate ncRNA features
- Status Bar: added explicit warning, when relaxed molecule id comparison is used in broadcasting
- BAM support: fixed crash working with network paths and some incorrect path locations
- Open Dialog: number of small GUI cleanups and improvements, improvements of MacOS copy and paste
- Broadcast Options dialog: save settings for program restart

RefSeq Release 58 is Available for FTP

Friday, March 15, 2013

The complete RefSeq release 58 contains 36,938,203 sequence records from 34,169,407 records including 3,345,543 RNAs, and 30,489,893 proteins from 22,460 different organisms.

Check out RefSeq's new homepage to learn more about The Project and see the Release statistics file or Release notes for more information about this particular release.

NCBI now provides interim GFF-formatted updates for human and mouse refseq annotations

Tuesday, March 12, 2013

The interim updates contain features projected from current RefSeq transcripts and curated genomic sequences and placed on the latest assembly version. The current RefSeqs include transcript variants that are new or have been updated since the last full annotation. The latest assembly version may include additional or updated genome patches compared to the assembly version used for the full annotation.

The General Feature Format (GFF)-formatted updates are available on the FTP site. For example, see the first interim update for the human assembly GRCh37.p11: ftp://ftp.ncbi.nlm.nih.gov/genomes/H_sapiens/GFF_interim.

Genome Workbench is the Featured Resource in OpenHelix's "Tip of the Week"

Thursday, March 07, 2013

Thanks to OpenHelix's Blog site for featuring our Genome Workbench as their "Top of the Week"! They describe it as "a useful program ... (with) a great set of videos to introduce you to the workbench's functions and features."

For more information about Genome Workbench, check out it's homepage and ample documentation at: http://www.ncbi.nlm.nih.gov/tools/gbench/

New Quick Tip on NCBI Insights Blog - How To Format Sequence Data For GenBank Submissions

Thursday, March 07, 2013

A new Quick Tip on the NCBI Insights blog shows how to properly format FASTA files for submission to GenBank. The post gives step-by-step instructions for submitting single- and multiple-nucleotide sequences.