NCBI News, January 2016

Genome Workbench 2.10 now available

Friday, January 29, 2016

Genome Workbench 2.10 includes a reworked BLAST tool and new functionalities in Tree View. For the full list of features, improvements and fixes, see the release notes.

Sequence Viewer 3.11 now available

Wednesday, January 27, 2016

Sequence Viewer 3.11, now available, contains a number of new features, improvements and bug fixes, including the ability to overlay multiple graphs in one track (for more information, please see the demo pages and API documentation), improved track descriptions for better integration with track management, updated SNP tracks, and tooltips for dbVar. A full list of features, improvements and bug fixes is included in the release notes.

Sequence Viewer is a graphical view of sequences and color-coded annotations on regions of sequences stored in the Nucleotide and Protein databases.

February 3rd webinar: "How to Upload and Analyze dbGaP Data in the Cloud"

Thursday, January 21, 2016

In two weeks, NCBI will show you how to upload and analyze dbGaP data through the SRA Toolkit and Amazon Web Services.

Date and time: Feb 3, 2016 1:00-2:00 PM EST

Registration link: https://attendee.gotowebinar.com/register/8258777454794963713

After the live presentation, the webinar will be uploaded to the NCBI YouTube channel. Any related materials will be accessible on the Webinars and Courses page; you can also find information about future webinars on this page.

RefSeq Release 74 now available on FTP

Wednesday, January 20, 2016

RefSeq Release 74 is now accessible online, on the FTP site, and through NCBI's programming utilities. This full release incorporates genomic, transcript and protein data available as of January 11, 2016 and includes 89,458,499 records, 56,496,614 proteins, 13,719,136 RNAs, and sequences from 57,993 organisms.

More information can be found in the release notes. For more information about the RefSeq project, please see the RefSeq homepage.

January 28th webinar: "Genomic Data Sharing with dbGaP: Registration and Submission" for IRP investigators

Wednesday, January 13, 2016

In two weeks, NCBI will present a webinar for Intramural Research Program (IRP) investigators engaged in Genome-Wide Association Studies (GWAS) and other genomic research efforts at NIH. Topics covered will include working with your Genomics Program Administrator to register your study in dbGaP and preparing your project metadata files, phenotypes and molecular data for submission to dbGaP.

Date and time: Jan 28, 2016 12:30-1:30 PM EST

Registration link: https://attendee.gotowebinar.com/register/6247720109478660865

After the live presentation, the webinar will be uploaded to the NCBI YouTube channel. Any related materials will be accessible on the Webinars and Courses page; you can also find information about future webinars on this page.