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New Databases and Tools

dbVar

The newly released Database of Genomic Structural Variation (dbVar) contains data and analyses from studies on large-scale genomic variation and provides associations of defined variants with phenotype information. The dbVar homepage provides additional documentation including an overview of structural variation, a Frequently Asked Questions list, and information on submitting data. A dbVar RSS feed has also been established to provide announcements and updates.

NLM Press Release

NCBI scientists have assisted in the design of a computational model to accurately detect signals of regulatory elements responsible for development of the human heart and it's maintenance of function. An NIH Press Release provides more information on this project.

Bookshelf

New books added to the Bookshelf include: *Patient Safety and Quality: An Evidence-Based Handbook for Nurses, Familial Cancer Syndromes,* and *UMLS Reference Manual*. To view these and other books see: www.ncbi.nlm.nih.gov/sites/entrez?db=Books.

E-Utilities Documentation

The Entrez Programming Utilities (E-Utilities) Help documentation has been added to the NCBI Bookshelf. This help document has been split into chapters for better organization and is now fully integrated with the Entrez search and retrieval system as a part of the Bookshelf database.

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Microbial Genomes

Twenty-two finished microbial genomes were added to the NCBI databases during February. The original sequence data files submitted to GenBank/EMBL/DDBJ are on the FTP site: ftp.ncbi.nih.gov/genbank/genomes/Bacteria/. The RefSeq provisional versions of these genomes are also available: ftp.ncbi.nih.gov/genomes/Bacteria/.

GenBank News

GenBank release 176.0 is available on the NCBI Web Service and FTP site. The current release incorporates sequence data as of February 19, 2010. Release notes containing detailed information are available on the FTP site: ftp.ncbi.nlm.nih.gov/genbank/gbrel.txt.

Updates and Enhancements

BLAST

The NCBI BLAST development team reports on improvements in the updated C++ BLAST software in the December issue of *BMC Bioinformatics*:

Camacho C, Coulouris G, Avagyan V, Ma N, Papadopoulos J, Bealer K, Madden TL. BLAST+: architecture and applications. *BMC Bioinformatics*. 2009. Dec 15;10:421. PMID: 20003500; PMCID: PMC2803857.

The article illustrates the new BLAST+ suites' improved user interface, enhanced performance for long sequences, and better integration with the NCBI Web BLAST service.

Exhibits

NCBI will have an exhibit booth at the American Association for Cancer Research annual meeting held April 17-21 in Washington, D.C.

Announce Lists and RSS Feeds

Eighteen topic-specific mailing lists are available which provide email announcements about changes and updates to NCBI resources including dbGaP, BLAST, GenBank, and Sequin. The various lists are described on the Announcement List summary page: www.ncbi.nlm.nih.gov/Sitemap/Summary/email_lists.html. To receive updates on the *NCBI News*, please see: www.ncbi.nlm.nih.gov/About/news/announce_submit.html

Twelve RSS feeds are now available from NCBI including news on PubMed, PubMed Central, NCBI Bookshelf, LinkOut, HomoloGene, UniGene, and NCBI Announce. Please see: www.ncbi.nlm.nih.gov/feed/

Send comments and questions about NCBI resources to: info@ncbi.nlm.nih.gov, or by calling 301-496-2475 between the hours of 8:30 a.m. and 5:30 p.m. EST, Monday through Friday.