International Society for Biocuration

Biocuration 2012: Submit your abstract or paper by Nov. 30

The 5th Biocuration conference will be held in Cambridge from 7-10th April 2013. We would love to see you there!

Note that the deadline for abstract and paper submission is **November 30, 2012**.

For more information, visit the Biocuration 2013 website at: http://www.ebi.ac.uk/biocuration2013/

The Biocuration 2012 Meeting report has been published !

Recent advances in biocuration: Meeting Report from the fifth International Biocuration Conference

http://bitly.com/V7XLKg

Executive committee 2012-2013

For the upcoming year, and as on November 1, 2012, the ISB Executive committee is composed of Pascale Gaudet (Chair), Monica Munoz-Torres (Secretary), Marc Robinson-Rechavi (Treasurer), as well as Teresa Attwood, Alex Bateman, J.Mike Cherry, Renate Kania, Claire O'Donovan and Chisato Yamasaki.

We'd like to thank Lorna Richardson for serving on the ISB Executive committee since 2009!

News from the ISB community

DisGeNET: A database integrating gene-disease associations

Contributed by Laura Inés Furlong, Hospital del Mar Medical Research Institute (IMIM), Barcelona, Spain

DisGeNET integrates integrating gene-disease associations from several expert curated public data sources and the literature (Bauer-Mehren et al., 2011, PMID: 21695124). We are happy to announce that the 2.0 update of DisGeNET has just been released. Using DisGeNET, you can answer the questions like:

- *Which are the genes underlying schizophrenia?*
- *What are the diseases associated to glucose-6-phosphate dehydrogenase gene?*
- *Which diseases are caused by changes in protein phosphorylation?*
- *Can I find a genetic basis for the comorbidity of myochardial infarction and diabetes?*

DisGeNET has also been recently used as part of a workflow that allows the automatic filtering and substantiation of drug safety signals (Bauer-Mehren et al., 2012, PMID: 22496632). In this update, we include information coming from UniProt, the Comparative Toxicogenomics DatabaseTM, the Genetic Association Database and Mouse Genomics Database. This version contains information on approximately 100 000 associations between more than 9000 genes and 6000 diseases. DisGeNET uses controlled vocabularies for genes and proteins (NCBI Gene, HUGO, UniProt), diseases (Unified Medical Language System® Concept Unique Identifiers) and the associations between genes and diseases (The gene-disease association ontology is available at http://ibi.imim.es/DisGeNET-Dev/ontologies/GeneDiseaseAssociation.owl). Additionally, diseases are classified according to the MeSH hierarchy for diseases. To explore the data contained in the database, you can go to the DisGeNET web interface (http://ibi.imim.es/DisGeNET/web/v02/search), work with a network representation of the data using the DisGeNET plugin develope for Cytoscape (Bauer-Mehren et al., 2010, PMID: 20861032), or download a local copy of the database in SQLite format.

CAMEO Ligand Annotation - or closing the loop from accurate ligand annotations in proteins to making biologically relevant ligand binding site predictions from protein sequences

Contributed by Juergen Haas , Swiss Institute of Bioinformatics, Biozentrum, University of Basel, Switzerland

Predicting ligand binding sites from protein sequences has the potential of yielding high impact on life science research - but only if the predictions are specific and accurate enough to help addressing relevant biological questions. Thus, in Continuous Automated Model EvaluatiOn (CAMEO) we assess ligand binding site predictions on a weekly basis to evaluate the current state of the art of prediction methods, identify possible bottlenecks, and further stimulate the development of new methods for predicting ligand binding sites. Hence, accurate knowledge about ligands is crucial to ensure only biologically relevant ligands are included in the assessment. This will in turn result in improved prediction methods and thus on the longer term in more accurate predictions.

CAMEO Ligand Annotation allows to conveniently annotate ligands via a web interface featuring an interactive 3D molecular browser to visualize ligands and surrounding residues. The homepage furtherfeatures a complete list of entries which are currently open for assessment. We apply a sliding window of 3 weeks to the assessment during which annotations can be made by registered annotators and ambiguous annotations will be reviewed by our curators.

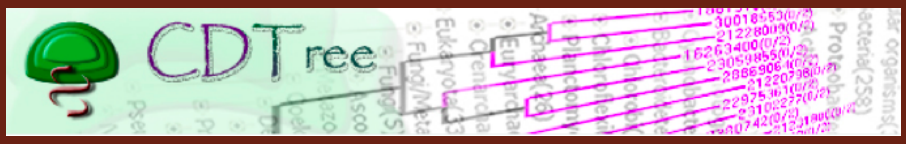
So please share your in-depth knowledge on specific ligands at http://www.cameo3d.org/annotation!

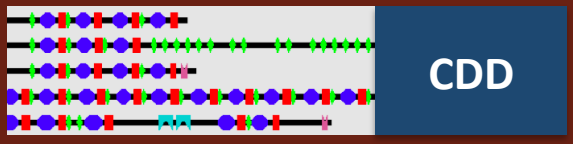
News from the ISB community

NCBI's CDTree/Cn3 tools

Contributed by Myra Derbyshire, Renata Geer, and Aron Marchler-Bauer

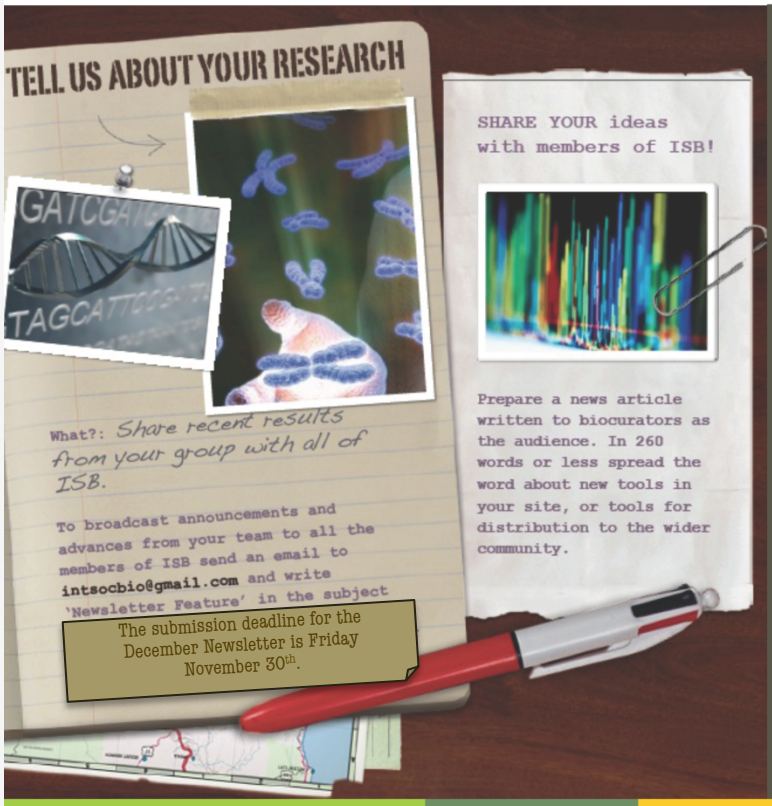
CDTree/Cn3D are interactive tools for the visualization of biomolecular 3D structure, 3D structure superpositions, and corresponding multiple sequence alignments (MSA), as well as protein domain family classifications as provided by NCBI's Conserved Domain Database (CDD). In addition to serving as helper applications for the web browser to download and examine content provided by CDD, CDTree/Cn3D can also serve as standalone applications to import or construct and maintain MSA representations of proteins and protein domain families, as well as hierarchically organized multiple-model representations of evolutionarily and/or functionally diverse protein and domain families. CDTree/Cn3D offer: interactive and automated construction MSAs; visualization of multiple aligned 3D structures together with sequence alignment; convenient ways to examine the structural implications of sequence conservation and variation; and phylogenetic analysis capabilities, including integrated views of taxonomic diversity and protein domain architectures. They also serve as an interface to NCBI's BLAST services, enabling users to mine the NCBI nonredundant protein database for novel sequences that belong in a family, or to extend the scope of a conserved family representation by running iterative searches. CDTree/Cn3D can be used as productivity tools to maintain a notebook that accompanies protein family classification efforts, allowing for the annotation of sites and other conserved or interesting features, as well as bibliography accompanying a family classification. They are the main curation tools of NCBI's CDD (http://bitly.com/VT3Rde). CDTree is accessible from http://1.usa.gov/svhY0g and comes bundled with Cn3D. Cn3D can also be downloaded separately from http://bitly.com/dIVjdk, and a tutorial (http://bitly.com/dhk6B1) illustrates how the program can be used.





Job opportunities

- Scientific Data Wrangler, National Capitol Contracting, Bethesda, Maryland
  http://nccsite.com/careers/open-positions
- Software developer, BioModels.net team at EBI, Hinxton, UK
  http://bit.ly/U1RR7R
- Bioinformatics analyst, the Harvard School of Public Health Bioinformatics Core, MA, USA http://biocurator.org/jobs/20121024_CRM_Position.pdf
- Bioinformatics Programmer/Analyst, Dupont, Welmington, DE, US
  http://bitly.com/VpRtWz
- Computational Biologist,Bioinformatician/Statistician and Post-doc for the Galaxy project, Penn State (USA), Emory (USA), Versailles (France), Heidelberg (Germany)
  http://bit.ly/VLkTtV
- Research position at the Integrative Biomedical Informatics research group, Hospital del Mar Medical Research Institute (IMIM), Barcelona, Spain
  http://biocurator.org/jobs/Position_IBI_2012.pdf
- Postdoctoral Research Associate; Microbial ontology. Department of Microbiology and Molecular Genetics, Michigan State University East Lansing, MI, USA
  http://www.linkedin.com/jobs?viewJob=&jobId=3826453
- Scientific Curator - Cancer Cell Type Ontology (OncoCL) Project, Jackson Laboratory, Bar Harbor Maine, USA
  http://biocurator.org/jobs/MGI-Sci_Curator-OncoCL.pdf
- Postdoctoral position in the Genome Technology Branch (GTB) of the National Human Genome Research Institute (NHGRI)
  http://biocurator.org/jobs/Postdoc-NHGRI.pdf
- Database and Semantic Web Developer, University of Colorado, Boulder, USA
  http://t.co/C7dvQX9g



Executive Committee Meetings

The ISB Executive Committee meets monthly. Minutes from the meetings are posted on the ISB website http://www.biocurator.org/executive_committee_minutes.html

ISB Newsletter Archive

Previous issues of this Newsletter can be found on the ISB website at http://biocurator.org/newsletter.shtml

Kind regards, The ISB Executive Committee.

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