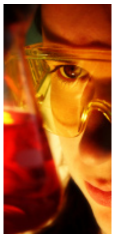

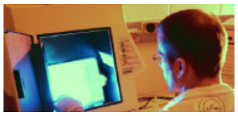

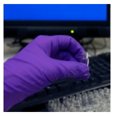

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Bioinformatics Organization

Bioinformatics to Systems Biology 2008

By Prashanth Suravajhala

The “Bioinformatics to Systems Biology 2008 (BSB ‘08)” virtual conference was held on July 14, and it was the second in a series of virtual conferences organized at by the Bioinformatics Organization. The four invited keynote speakers, viz., Drs. Gary Bader, Henning Schmidt, P.K. Suresh and Kasper Lage, addressed key issues in their respective expertise and presented the hallmark of research on broader subjects—Bioinformatics and Systems Biology.

Over the last ten years, the way in which bioinformatics has been delivering goods has changed considerably with the advent of new technologies, tools, cell biology and other wet lab methods and disease gene findings. This was well received by the attendees through the keynote presentations.

One of the primary goals in having such a conference was that it would be a great occasion for wet-lab researchers to meet bioinformaticists. While the first such conference, BSB ‘07 held last year, focused on introductory topics and a need of systems biology, with this conference we also had an opportunity for those involved to have a virtual meeting through “virtual posters” (a couple selected authors were invited to present their study).

The conference details were announced in May, and submissions were invited from research community in the form of two-page (extended) abstracts. In total, we received 11 submissions, of which 9 were selected based on the three-tier reviewing process. Topics from broadened horizons and the connection between bioinformatics and systems biology, but not limited to these two subjects alone, were preferred. The two selected works of authors (Drs. Kurt Vanhoutte and Pritish Varadwaj) presented their talks while the rest of the seven submissions were welcomed as virtual posters.

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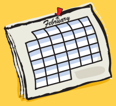

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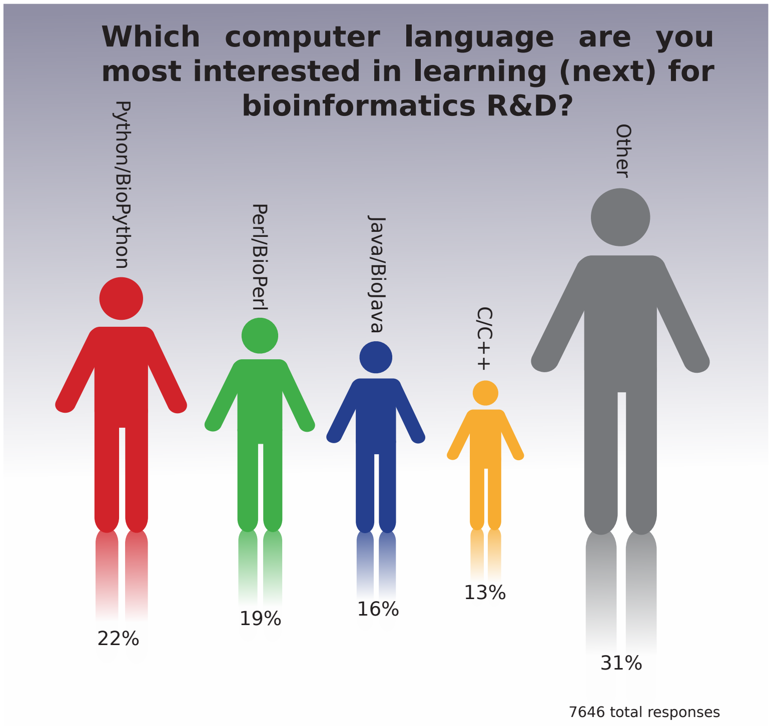
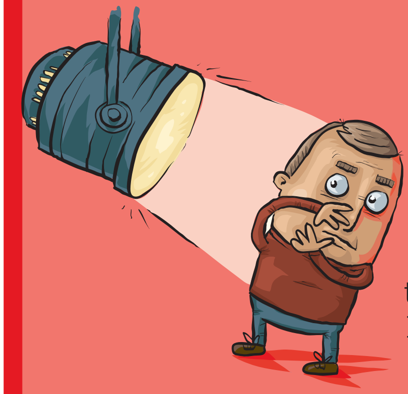
The BSB ‘08 was well received by over 140 people, who attended directly or indirectly. Organization president J.W. Bizzaro and co-director Prashanth Suravajhala chaired the sessions. The Bioinformatics Organization would like to thank all of the speakers and reviewers whose appraisal and input made it possible for the submitters to improve their full-length submissions.

Publication opportunity: Papers presented at the conference were considered for publication in the online, open-access Bioinformation Journal. We express thanks to the journal for having accepted the submissions while the full-length papers are under evaluation. The abstracts, reviewers’ list and full conference program along with presentations, video recordings can be found online at Bioinformatics.Org.

Future conferences: The directors of Bioinformatics.Org are putting together more tracks, highlights, short tutorials and workshops during a planned two-day event for BSB ‘09 and an “African Bioinformatics” virtual conference. Stay tuned!



Project spotlight



CD-HIT Representative Sequences.

CD-HIT stands for Cluster Database at High Identity with Tolerance. The program (cd-hit) takes a fasta format sequence database as input and produces a set of ‘non-redundant’ (nr) representative sequences as output. In addition cd-hit outputs a cluster file, documenting the sequence ‘groupies’ for each nr sequence representative. The idea is to reduce the overall size of the database without removing any sequence information by only removing ‘redundant’ (or highly similar) sequences. This is why the resulting database is called non-redundant (nr). Essentially, cd-hit produces a set of closely related protein families from a given fasta sequence database.

CD-HIT uses a ‘longest sequence first’ list removal algorithm to remove sequences above a certain identity threshold. Additionally the algorithm implements a very fast heuristic to find high identity segments between sequences, and so can avoid many costly full alignments.

With recent developments, cd-hit package offers new programs for DNA sequence clustering and comparing two databases. It also has lots of new options for clustering control.

CD-HIT was originally written by Weizhong Li and is now an open source project!

http://bifx.org/cd-hit/

Career Center

Job search

Looking for a job in the bioinformatics field?

Opportunity: Senior Research Investigator (#26054) BIOINFORMATICS @ Bristol-Myers Squibb

The successful applicant will collaboratively work with Therapeutic Area biology metabolic and cardiovascular diseases, oncology and immunology diseases, Toxicology, and Clinical Discovery groups within the BMS Research and Development. He or she will use their advanced knowledge of Biology, Computer Science and Statistics to validate drug targets and drug candidates in the BMS discovery and development pipeline using cutting edge bioinformatics and genomics technologies. Responsibilities also include establishing and maintaining close collaborative relationships with other groups in PRI and educating biologists across the PRI in the use of Genomic methods and tools.

For the full article:
http://bifx.org/forums/forum.php?forum_id=6745

Opportunity: Associate Research Scientist (#25926) Compound Managment @ Bristol-Myers Squibb

The Compound Management Process Scientist will be responsible for the execution of the day to day procedures necessary to accomplish the business critical function of Compound Management. Responsibilities include the execution of work orders, tracking of metrics, Quality Control of instrumentation and communication with scientific community. Individuals who seek challenges in improving workflows and integrating automation equipment are preferred.

For the full article:
http://bifx.org/forums/forum.php?forum_id=6739

Opportunity: BIOINFORMATICS/ COMPUTATIONAL BIOLOGY @ Buck Institute--Novato, CA (US)

The Buck Institute, 20 miles north of San Francisco, seeks to recruit a Faculty member working in the area of Computational Biology and/or Bioinformatics. Outstanding junior or senior scientists are encouraged to apply. The appointment can be made at the Assistant/Associate or Full Professor level. Candidates with an interest in developing computational tools and applications for complex biological data analysis in systems biology, or cellular processes are particularly encouraged to apply. The successful candidate will play a leadership role in developing collaborative interdisciplinary programs with other Institute Faculty in areas including, but not limited to, the biology of aging, stem cell biology, and cancer and neurodegenerative disease.

For the full article:
http://bifx.org/forums/forum.php?forum_id=6736

Upcoming events

CS101A Introduction to Bioinformatics Programming; Monday, 8 September » Friday, 12 September

Taught in the context of biological research, this course helps biologists learn how to use the scripting language Perl to automate certain tasks and how to use the database management system MySQL to store, manage and query biological information.

http://wiki.bioinformatics.org/CS101A_Introduction_to_Bioinformatics_Programming

CS101B Introduction to Statistics Programming; Monday, 22 September » Friday, 26 September

This course is geared towards biologists who routinely work with data and need to analyze and visualize it in a statistics package, and Excel is not providing them with that capability. This course teaches biologists how to do basic statistics and plotting of data with a statistical programming package such as R, and implement hypothesis tests and statistical techniques such as regression, PCA, etc. Automated biological data analysis, development of algorithms and workflows will also be covered.

http://wiki.bioinformatics.org/CS101B_Introduction_to_Statistics_Programming

BI201A Gene Expression Analysis; Monday, 29 September » Friday, 3 October

This course helps to demystify Affymetrix analysis so that any researcher can take the basic steps to go from a chip image to a list of genes that are up- or down-regulated in an experiment. Various tools will be covered, e.g. GCOS, Excel, MATLAB, and free tools like R and Dchip. It is geared towards researchers who conduct microarray experiments to study genome-wide expression changes and understand the underlying mechanisms of gene regulation in samples of interest.

http://wiki.bioinformatics.org/BI201A_Gene_Expression_Analysis

Workshop Metabonomics: A new tool for exploring biocomplexity; Wednesday, October 22 » Friday, October 24, 2008

In this workshop located in Valenica, Spain, an ensemble of international experts will discuss recent developments in the field, describe start of the art applications of metabonomics and examine detailed aspects such as experimental design and appropriate statistical methods for metabonomics. The topics of this event include Fluid Metabonomics, Tissue and Cell Metabolomics, Drug Discovery and Toxicity, Alternative Metabonomics Applications, Methods and Design.

http://www.cipf.es/Agenda/?lang=en&op=4-9

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