UCSD And SDSC To Host National Computational Molecular Biology Meetings

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Faculty and researchers affiliated with the University of California, San Diego's Jacobs School of Engineering and San Diego Supercomputer Center (SDSC) will host what has become one of the most influential conferences in the world dealing with bioinformatics. This year's Research in Computational Molecular Biology - RECOMB 2004 for short - will take place March 27-31 in San Diego (http://recomb04.sdsc.edu/), and will feature the best research in bioinformatics, combined with invited talks from experimental biologists. "This is a scientific forum for theoretical advances in computational biology and their applications in molecular biology and medicine," says UCSD pharmacology professor Philip Bourne, who is Director of Integrative Biosciences at SDSC and also Conference General Chair of RECOMB 2004. "The origins of the conference came from the mathematical and computational side of the field, but the effective use of computational techniques for biological innovation is also an important aspect of the conference." SDSC took the lead in sponsoring the 2004 conference.

"Roughly 700 people have registered for the conference, compared to only 250 at the first RECOMB in 1997," says Pavel Pevzner, the Ronald A. Taylor Chair Professor in computer science and engineering at the Jacobs School, who co-founded the conference and chairs RECOMB 2004's steering committee. "Now only 15 percent of submitted papers are accepted, which is comparable to the acceptance rate at top biology journals. And it is truly an international conference: last year's RECOMB was in Berlin, the next will be in Boston, then Venice."

Some of the big themes to be showcased at this year's conference include comparative genomics (as influenced by the complete sequencing of the human, mouse and other genomes), regulatory genomics, and gene networks. One of the highlights of each RECOMB conference is a collection of nine keynotes by internationally-recognized researchers about landmark advances in computational and experimental research and new directions in the field of computational molecular biology. Other topics include molecular sequence analysis, molecular evolution, protein structure, gene expression, drug design, combinatorial libraries, computational proteomics, as well as structural and functional genomics. Participating organizations will also use the meeting to unveil new resources for the community: SDSC's Bourne, who co-directs the Protein Data Bank (PDB) (http://www.rcsb.org/pdb/), says the supercomputer center will be demonstrating a new version of the the single worldwide repository for the processing and distribution of 3-D biological macromolecular structure data, now totaling nearly 25,000 structures.

Two UCSD biology professors will deliver keynotes this year: Russell Doolittle will deliver the Stanislaw Ulam Memorial Computational Biology Lecture, on lessons from 50 years of sequence analysis; and William McGinnis will talk about evolutionary change in developmental genetic networks. Another San Diego-based researcher delivering a keynote speech is Elizabeth Winzeler of the Scripps Research Institute, who will discuss systems biology and malaria. (For the full list, go to the conference website, click on Program Information, then Invited Keynotes.)

The conference will showcase over 350 research posters, and has also spawned satellite workshops to attract top researchers in specific fields such as comparative genomics and proteomics. This year, the First Annual RECOMB Regulatory Genomics satellite workshop will take place on the UCSD campus March 26-27. (http://www.cse.ucsd.edu/%7Eeeskin/recombreg04/) It is being organized by Jacobs School computer science and engineering professor Eleazar Eskin. Both Eskin and Pevzner are affiliated with the California Institute for Telecommunications and Information Technology [Cal-(IT)²]. "We now know that the vast majority of genes are almost identical between human and mouse, yet men and mice are so different," explains Eskin. "The differences most likely stem from variations in the networks that regulate genes, and one of the main challenges facing researchers today is deciphering these regulatory mechanisms. This workshop focuses on how genes interact and how the transcriptional mechanisms of the genes work."

The recent sequencing of the human and mouse genomes - and the upcoming release of the complete rat and chimpanzee genomes - are enabling research methods in bioinformatics to enhance understanding of gene regulation. Those methods include motif-finding algorithms that can help identify regulatory elements. Among the research challenges to be discussed at the satellite workshop: scaling to very large samples; incorporating multiple genomes; detection of weak signals; and incorporating different types of genomic data such as protein localization data and gene expression.

The Regulatory Genomics workshop will feature 14 invited talks and 10 refereed papers, with more than 125 specialists expected to attend. "We also have an industry roundtable on how basic science in the academic environment is transformed into mechanisms that bring drug discovery closer," says Eskin. "Scientists from Astrazeneca, Compugen, ZymoGenetics, Agilent, Novartis and Incyte will talk about how they are using new computational techniques for drug discovery." Other aspects of gene regulation to be covered during the workshop include: modeling and recognition of regulatory elements; identification and modeling of cis-regulatory regions; modeling the structure and function of the regulatory region; and comparative genomics.

One of the new computational tools that will be highlighted at the meeting is PathBLAST, designed by UCSD bioengineering professor Trey Ideker. It allows biologists to compare protein interaction networks - the cell's system through which genes and proteins communicate. As scientists begin to identify protein interaction networks, PathBLAST and tools like it can be used to quickly compare interaction networks among different organisms. "These kinds of studies could have a huge payoff in comparing such things as viral networks to human networks, possibly allowing drug companies to develop products that target cellular pathways unique to viruses," says Ideker. So far, scientists can use www.pathblast.org to compare networks of interest to those of certain yeast, bacteria, fruitfly and worm organisms.

According to RECOMB co-founder Pevzner, it is no coincidence that RECOMB 2004 and the satellite workshop on regulatory genomics are taking place in San Diego. "San Diego has become a bioinformatics superpower in the past five years," he says. "UCSD has hired informatics leaders in Bioengineering, in Computer Science and Engineering, at SDSC, Scripps Institution of Oceanography, School of Medicine and other departments. All of a sudden, UCSD has become one of the top universities in terms of accepted papers at major conferences, and the combination of traditional bioinformatics and systems biology has created major synergy for UCSD."

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