



Data Analysis Tools, Pharmacogenomics Among 'Moving Targets' for Informatics Discussed at ISMB 2010

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By [Uduak Grace Thomas](#)

More than 2,000 scientists working in computer science and biology attended the annual Intelligent Systems for Molecular Biology conference in Boston last week.

Between watching the World Cup final, scanning the job opportunities board, and meeting with like-minded colleagues over coffee, participants were immersed in current research in bioinformatics spanning a broad range of disciplines — eight parallel tracks covered a spectrum of topics, including RNA folding, analyzing large genomic datasets, the use of computational biology in drug design, and the rapidly growing personalized medicine field.

“Last year we had a slight focus on imaging and neurobiology. This year we have much more of a focus on epigenetics and pharmacogenomics,” said Burkhard Rost, a professor in the department of biochemistry and molecular biophysics at Columbia University and president of the International Society for Computational Biology, told *BioInform*.

In addition to the parallel sessions, six keynote addresses focused on biological challenges that will require new computational tools in areas such as gene regulation, protein folding, analyzing Pleistocene-era genomes, cancer research, and genomic variation.

“I think a challenge for both the society and the meeting is that computational biology is a very broad discipline, the scientific interests have a very broad range,” said conference co-chair Jill Mesirov, associate director and chief informatics officer at the Broad Institute. “That is a good thing because it is the richness of the community, but it’s also a challenge because people come here with many different interests. We try to support that through the multiple tracks.”

Conference co-chair Michal Linal, a professor at the Hebrew University of Jerusalem and chair of the European Conference in Computational Biology, called the bioinformatics field “a moving target,” which she said the organizers took into account as they planned

the conference and that they tried to “predict the future” when deciding what tracks to include.

“Whatever was true two years ago is not relevant,” she said. “We are trying to keep ourselves relevant for what will happen, not what was happening. We developed some of those tracks to respond to this.”

In addition to the main session, two days of satellite and special interest group meetings covered open source software for bioinformatics, high throughput sequencing, and regulatory genomics, as well as other areas.

In a first for ISMB, there was a tutorial session focused on teaching bioinformatics in high school — a sign that the discipline is quickly becoming a requirement for biology education. The tutorial is part of the ISCB Educational Outreach Program, which promotes life sciences education for high school teachers

Another first was a lecture on cancer stem cells that was open to the general public delivered by Robert Weinberg, a researcher at the Whitehead Institute for Biomedical Research.

“There are parts of computational biology which are very much genomics, there are parts of computational biology which are closer to biochemistry and to drug discovery,” Mesirov said. “All those areas have different aspects and often use the computational underpinnings different ways. But I think there are a lot of recurrent themes across all those areas which bind us together.”

Olga Troyanskaya, conference chair and associate professor in the department of computer science at Princeton University, added, “One thing we have really tried to emphasize in the conference is the biomedical underpinnings”.

She noted that while much of the work in bioinformatics is focused on “specific technical problems,” there is “really a huge motivation that is coming from biological and clinical problems.”

In one keynote, Steven Brenner, a professor at the University of California, Berkeley, and this year’s ISCB Overton prize winner, spoke about using evolutionary principles as well as statistical and computational methods to understand biology.

Chris Sander, chair of the Computational Biology Center at Memorial Sloan-Kettering Cancer Center and the recipient of this year’s Senior Scientist prize, spoke on the systems biology of cancer cells. Sander’s research focuses on techniques and applications that are relevant in cancer medicine.

Other keynote speakers were Susan Lindquist from the Whitehead Institute, Svante Paabo from the Max Planck Institute for Evolutionary Anthropology, and David Altshuler and

George Church, both from Harvard Medical School and the Broad Institute of MIT and Harvard.

Dealing with Data

Computational methods to handle sequence data analysis and alignment is a recurring issue at ISMB and this year was no exception. A team from the Computational Biology Research Center in Japan led by Paul Horton presented several methods for analyzing and aligning RNA sequence data. The team presented the alignment tool LAST as a faster alternative to the well known BLAST and one that handles repetitive regions in genomic data better.

The CBRC team also presented RECOUNT, an error-correction tool based on the expectation maximization model which Horton's team optimized for next generation sequence data.

Researchers from the Institut Pasteur in France presented a web based tool called Mobyle which they described as an open source integrated bioinformatics platform for performing web-based analysis of sequence data.

According to Mobyle's creators, the tool lets users publish command line tools through a graphical interface and then connect these tools in order to manipulate, analyze, and visualize their data. The team is developing a workflow interface for Mobyle that will be available in the fall.

Emerging Fields

While a number of talks at the conference focused on data analysis tools, emerging topics such as epigenetics and pharmacogenomics were also recurring themes in the keynote addresses and in some of the special sessions.

In addition to his keynote speech, Brenner gave a presentation during a session focused on computational approaches in pharmacogenomics on his team's efforts to create a "genome commons" database that integrates existing data on genetic variation and human disease as well as data analysis tools.

Brenner's team is also developing the Genome Commons Navigator, which "prioritizes and predicts phenotypes of genetic variants within an individual genome. The team plans to make the resources available for "making pharmacogenomic recommendations to clinicians," Brenner said.

ISMB 2011 will be held in Vienna, Austria.

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