



Pacific Biosciences Uses ISMB Conference to Generate Interest in its Bioinformatics Tools

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During this year's Intelligent Systems for Molecular Biology conference in Boston, it was clear that even though Pacific Biosciences's SMRT sequencer will not be launched until later this year, the company is working hard to pique the informatics community's interest in the technology and provide the tools to use it.

Last week the company presented to ISMB delegates, DevNet, its recently launched ([BI 07/09/2010](#)) online network intended to support third-party development of informatics tools and standards for the company's single-molecule real-time sequencing technology platform.

At ISMB, Edwin Hauw, PacBio's senior project manager, software and informatics, told *BioInform* that DevNet is a "place for algorithm developers, third-party independent software vendors and our end customers to check out the company's offerings in terms of documentation and other resources."

The site provides access to data sets, source code, application programming interfaces, conversion tools, and documentation related to SMRT technology sequencing.

Also included on the site is a discussion board where Hauw says users can post or respond to questions as well as suggest improvements to the network. Users will also be able to vote for or against any improvements giving PacBio a sense of the kinds of tools that researchers need the most.

"It is [a] web 2.0 type of framework where we want to listen to what people have [to say]," he said. "We want to hear what developers would like us to deliver. It would make it easier to prioritize." The company plans to provide additional datasets and algorithms, according to Hauw. For example, PacBio will provide an *E. coli* dataset generated on its sequencing platform.

But DevNet wasn't the only finger PacBio had in the ISMB pie. The company was also involved in organizing the high-throughput sequencing special interest group meeting held July 9–10.

Furthermore, several research papers presented during the SIG meetings focused on algorithms to analyze and assemble genomic data produced by the company's single-molecule real-time technology.

For example, PacBio's Aaron Klammer and his team presented a paper describing a hybrid assembly of a bacterial genome using reads produced by the company's sequencer. The team's approach uses several algorithms tailored for PacBio's long reads during different stages of the assembly.

One of the algorithms used in the overlap phase of the assembly is the Branching Local Alignment with Successive Refinement algorithm, or BLASR, which aligns SMRT sequences to a reference genome. Mark Chaisson, an algorithm developer at PacBio, discussed BLASR in a separate presentation to ISMB delegates.

According to the research abstract, BLASR performs a branching search on a suffix array or Burrows-Wheeler transform to generate a set of possible positions for a read. The positions are "scored using global chaining methods and refined by sparse dynamic programming before producing detailed alignments."

Anna Ritz, a researcher in the computer science department at Brown, along with PacBio's Ali Bashir, developed an algorithm to analyze structural variations in DNA using strobe reads. The strobe sequencing protocol was developed by PacBio last year (*InSequence* 05/12/2009). A fourth paper focusing on analysis methods for detecting DNA methylation using SMRT technology was presented by Dale Webster, a bioinformatics analyst at PacBio.

Genomeweb system

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