NewsBytes

Unraveling the Complex Functions of Proteins

At the birth of a new field, a conference can act as a midwife, making sure the infant enters the world smoothly. Such was the case for the Automated Function Prediction (AFP) conference held at the University of California, San Diego, at the end of August 2006. The field, in which researchers try to computationally determine a protein's function, appears to have arrived in good health.

"I feel we went quite far in creating an identity for this field," says **Adam Godzik, PhD**, program director in bioinformatics and systems biology for the Burnham Institute for Medical Research in La Jolla, California. The conference drew independent researchers who worked together for the first time to establish a common language, Godzik says, as well as a compilation of available methods and a way to evaluate the success of various techniques.

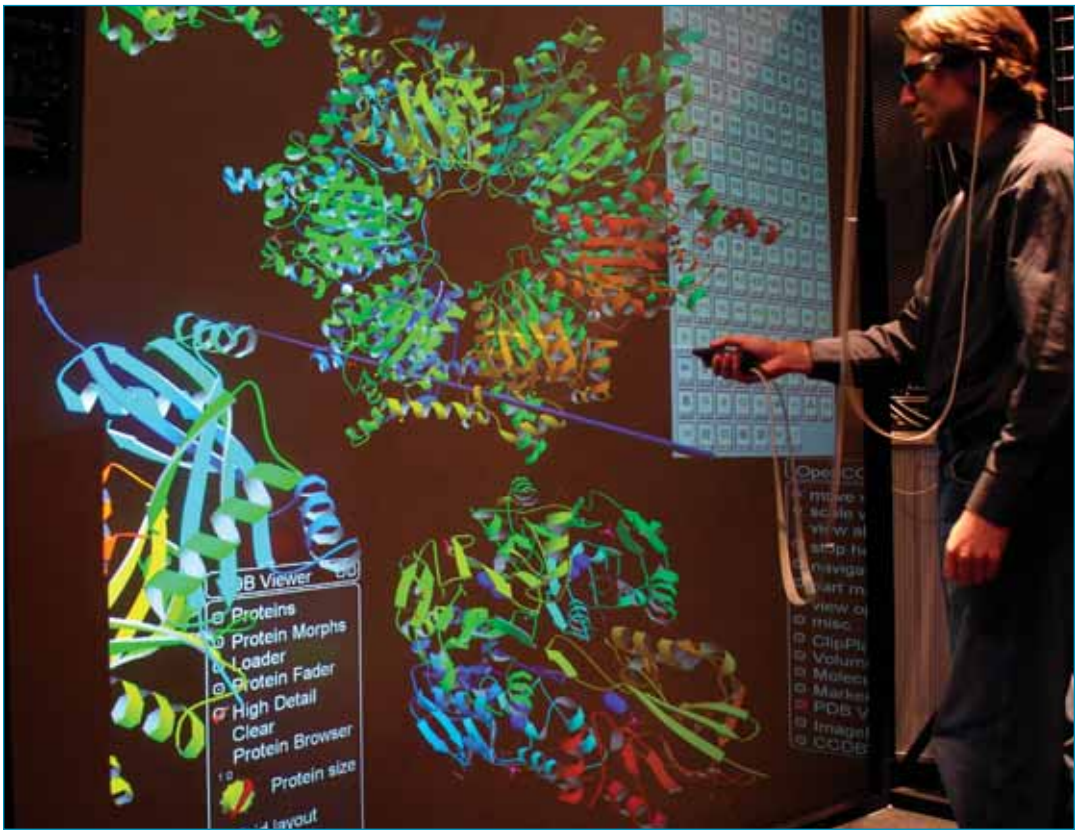
For decades, biochemists have tried to solve the riddle of what individual proteins do. They've done this in the lab, painstakingly slowly. But scientists now sequence genomes far faster than they can assign functions to the corresponding proteins. When there were only a few sequenced genomes, this problem was relatively small in scale and seemed manageable. But, says **Iddo Friedberg, PhD**, the conference organizer and a postdoctoral associate in Godzik's lab, "By sheer scale the problem has changed."

Now, using computational methods, researchers can tease through to answers much more quickly. At the AFP conference, those adept at the process charted the future of this discipline.

Their approach weaves together methods biologists have used for years. They include physical analysis of a protein's structure; genomic context, in which researchers compare a protein's position in a gene to those of similar genes elsewhere with known functions; and what Friedberg calls "guilt by association," or information gleaned in the laboratory about what the protein does when a cell undergoes a particular process. But because they're using computers and high-level algorithms, AFP researchers can now analyze more information faster and come to more robust conclusions about the workings of previously mysterious proteins. Visit http://BioFunctionPrediction.org for more information.

Godzik was pleased with the progress the conference made in crystallizing the field. "Until now," he says, "automated function prediction has been a black art."

—Brittany Grayson



AFP conference participant* Jurgen Schulze, PhD*, receiving an immersive experience of protein functional sites in the virtual reality cave at California Institute for Telecommunications and Information Technology. The software supports collaborative viewing of proteins at multiple sites on the internet. Courtesy of Jurgen P. Schulze.

Neurons Seek Their Own Solution

Each cell in our nervous system is an instrument in a complex symphony of electrophysiologic communication. A neuron's signaling abilities arise from its array of ion channels—tunnels within the cell's membrane that act as gatekeepers of electrical charge. But how does a cell determine the types of channels it needs and where in its membrane they should sit? The results of a new computer model suggest that even with markedly different patterns of ion channels, neurons still can come to play the same tune.

The work supports a growing paradigm shift in neurophysiology, says **Erik De Schutter, MD, PhD**, professor of neurobiology at the University of Antwerp, Belgium, lead author of the study. "We used to think of [ion channels] as LEGO blocks," he explains—with a predetermined number, type and position regulating how the neuron fires.

More recently, physiological experiments have suggested that cells with wildly different ion channel compositions could have similar firing patterns. But researchers have consistently attributed such variability to