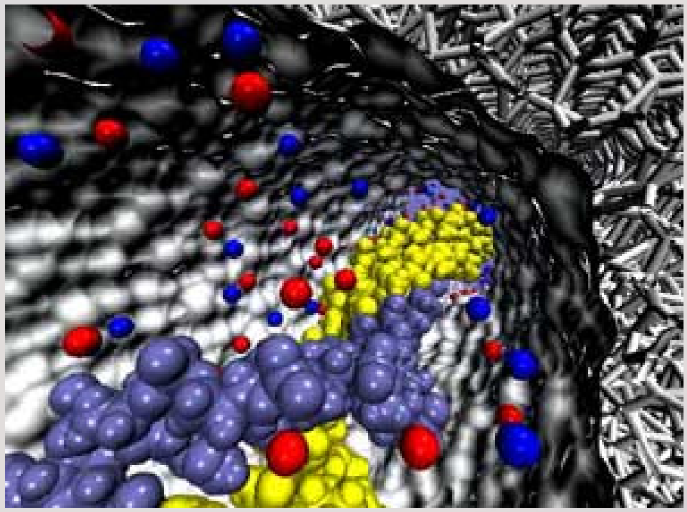
THE UNIVERSITY OF TEXAS AT AUSTIN
TEXAS ADVANCED COMPUTING CENTER

The Affordable "Personal" Genome

Ranger helps University of Illinois researchers simulate nanopore gene sequencer

The human genome was first decoded in 2003 after 13 years and $3 billion in research. Today, geneticists can produce the same information in a matter of months for a fraction of the cost. Transformational developments in technology and the methodology of DNA sequencing have made these advances possible.

As the medical community eagerly awaits the arrival of the $1,000 personal genome, Aleksei Aksimentiev, a computational physicist at the University of Illinois Urbana-Champaign, is helping develop the next generation of gene sequencers that will make this discovery possible. Using the Ranger supercomputer at the Texas Advanced Computing Center (TACC), Aksimentiev produced atom-by-atom models of a new "nanopore" gene sequencer that is smaller and faster than any previous device. Because of the extreme scale of the resolution involved, the simulations required more than seven million computing hours on Ranger.



Using TACC's Ranger supercomputer as a computational microscope, researchers from Illinois visualize DNA transport through synthetic nanopores. The image shows an atomic-scale model of a nanopore (gray surface), DNA (yellow and purple strands), and Cl– and K+ ions (red and blue spheres). Water molecules are not shown. [Courtesy of Aleksei Aksimentiev, University of Illinois at Urbana-Champaign]

Here's how the sequencers work: when DNA comes into contact with an electrical field, it stretches. This allows the strands to enter a smaller pore than they could usually fit into. Turning off the electrical field relaxes the strand and traps the DNA in the hole. By pulsing the electrical field, the DNA strands are able to move through the pore, and the sequence of each base pair can be deciphered.

"Aksimentiev's work is a brilliant example of how HPC is becoming a key tool of experimentalists from across a broad range of scientific disciplines," said Michael Gonzales, computational biology program director at TACC. "Advanced computing systems are no longer relegated to the analysis of experimental results. Rather, computing is in many ways driving the experimental design."

Aksimentiev's new nanopore sequencer promises a drastic reduction in cost and a commensurate increase in speed for DNA sequencing. "If we succeed, it will have a noticeable impact on the way we understand and treat human diseases," Aksimentiev said. "Everyone will be able to afford their DNA sequence."

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