The Bioinformatics Revolution

by *David Sigfredo Angulo*

Computers have revolutionized the sciences, biology in particular. With the aid of massively parallel instruments, scientists can now sequence the entire human genome, a string of over four billion characters. This huge data set would be unusable without methods to organize, search, and interpret it.

This month, Crossroads brings you a special issue devoted to bioinformatics - the computational analysis of biological data. Included in this issue is an interview with one of the field's foremost visionaries, Dr. Lee Hood of the Institute of Systems Biology and inventor of the DNA sequencer. Dr. Hood discusses the history of bioinformatics and its recent challenges, including the difficulties of funding in the current political climate. We also present four articles covering recent research:

In "Jump-Starting Your Bioinformatics Career as an Undergraduate: One Student's Approach," a recent graduate from Arizona State University describes the rigors of a bioinformatics education. His insights into joining a research project funded by the Fulton Undergraduate Research Initiative and developing the ArrayViz software are sure to be of interest to students considering a similar path.

The second article, "Modeling Protein Dependency Networks Using CoCoA," covers modeling protein dependencies in signaling networks. In order to make hypothetical predictions of relationships in such pathways, the author calculates statistical correlations between the expression levels of various proteins. For this task, he uses CoCoA - an interpreted programming language designed for algebraic computations. Exploiting the unique memory utilization features of CoCoA, the author overcomes

impediments encountered while using Maple.

In our third article, Eric Rouchka explains one approach to a fundamental bioinformatics problem: sequencing DNA. "Aligning DNA Sequences Using Dynamic Programming," gives students a firm basis from which to tackle more difficult algorithms.

The next article in this issue describes exporting proteomic mass spectrometry data from an XML encoding into a database that allows researchers to study proteins. This article offers an intriguing look into how biologists use mass spectrometry to further medical research. It also describes computational techniques for determining spectral similarity.

"Becoming a Virtual Organism to Learn about Genetics" demonstrates how handheld personal digital assistants (PDAs) can be used as tools for evolutionary modeling. The author focuses on a game in which thinking tag devices - wearable computers the size of nametags - were used to simulate the spread of viruses. The author shows how more powerful PDAs can be employed to set up a virtual population and examine its evolution over time.

What other area of study combines rapid scientific discovery, cutting-edge technology, and the secrets of life itself? I hope this special issue inspires you to consider this increasingly important field.

Biography

David Sigfredo Angulo spent 20 years in the computer industry at various software companies, including Datalogics and SPSS. A leader in object-oriented technology, web technology, web services, grids, XML, and bioinformatics, David founded the Illinois Bio-Grid in 2002. He currently serves on the faculty of the Computer Science, Telecommunications, and Information Systems (CTI) department at DePaul University in Chicago.