

## Genome Map Heralds Cheap Drugs

Sep 13 2000

Top genomics researchers from around the world are gathering in Miami this week to explore ways of using the mountains of information created by the Human Genome Project.

The main thrust of this research is to discover new drugs faster and cheaper. To do that, scientists need to find innovative ways to combine biology with information technology, a field dubbed bioinformatics.

"If you want to successfully use the new paradigm for drug discovery, you really have to take biology into account," said Cyrus Harmon, CEO of [Neomorphic](#), a genomics company in Berkeley, California.

"The molecular biology revolution changed the game and now we suddenly have the ability to go into much greater detail and (to) speed the understanding of the nature of biology and utilize the information to treat diseases that were intractable before," Harmon said.

Researchers predict that the time and cost it takes to develop drugs will be significantly reduced by biology-based approaches. It now takes about 12 years and \$500 million to bring a drug to market.

"We think we can reduce this by about six years," said William Haseltine, CEO of [Human Genome Sciences \(HGS\)](#), a genomics company in Rockville, Maryland. "By both increasing the success rates and shortening the trial period, we think we can dramatically improve cost efficiency in drug discovery."

Discussion on those themes figure to be lively this week.

One company participating in the [Gene Sequencing and Analysis Conference](#), [Lion Bioscience \(LEON\)](#), said on Tuesday it would add a strategic drug-discovery tool to its bioinformatics platform.

Lion will incorporate the tool, called Stackpack, into its data integration platform to more quickly identify genes responsible for disease.

"I think the real challenge in these days is not to come up with stand-alone eclectic solutions, because there is such diversity and such a tremendous amount of data -- think of the Human Genome Project and the overwhelming amount of data," said Dr. Friedrich Von Bohlen, chairman and CEO of Lion.

Lion launched the most successful biotech IPO ever earlier this year in Germany, and also launched one in the United States that held its own, garnering \$182 million in funding.

The working draft of the human genome map in June promises to provide scientists with the biological foundation of human life. Researchers say the complete map may herald a revolution in medicine, giving physicians the material they need to predict, prevent, and even treat disease.

But in its present state, it tells researchers little about disease, which is where bioinformatics comes in. Using information technology to mine tons of biological information, scientists hope to discover the secrets of the human body.

The Stackpack technology is an Expressed Sequence Tag analysis technology invented by Electric Genetics of Cape Town, South Africa. The Stackpack tool can look at small bits of genes, instead of sequencing an entire gene.

ESTs contain enough information about a gene to allow investigators to search databases for similar genes -- the standard method used by researchers to get a better idea of what type of gene they've found.

By studying these bits of genetic sequence, researchers can eventually learn which tissues in the body the gene controls.

Lion researchers say they've taken bioinformatics to a new level, which they call . According to Von Bohlen, i-biology is the key to allowing companies to access and search the plethora of types of data used by biotech researchers.

"The challenge for industry is to come up with support for not only biology but also chemistry and medicine. That is the i-biology concept," Von Bohlen said.

The concept is based on a platform that Lion calls the Sequence Retrieval System, which has been adopted by over 400 private and academic institutions.

Approaches like Lion's could help the large pharmaceutical companies, which are based mainly on chemistry, to adapt to the biology age.