Whether plant or animal, new genetic model can predict its future

July 18 2007

Rongling Wu is out to prove Mark Twain clearly didn't know a darn thing about genetics.

"Lies and damn lies" notwithstanding, Twain's much-maligned statistics are our best shot at reading the truth within the coded messages of DNA — whether that of a person or a poplar tree.

Wu is developing a technique that will help farmers predict how fast crops will grow. And thanks to an $855,000 grant from the National Science Foundation, he will soon use the same technology to speed the process of creating new lifesaving drugs.

Using massive amounts of statistical data, he's built a computer modeling technique that helps predict how a plant or animal's bodily functions and growth are affected by complex genetic interactions.

"The very important thing about this approach is how universal it is," said Wu, a professor of statistical genetics at the University of Florida's Institute of Food and Agricultural Sciences.

Every day, thousands of researchers toil away at uncovering the process by which genes control and create life. Every discovery brings understanding, but the search will be virtually unending — life's processes bring chemical structures and actions that are nearly boundless in their variety.

So Wu’s process focuses on the big picture. In short, he watches what happens on a large scale, and then statistically correlates that with genetic interactions he knows are taking place on a small scale.

“You can look at one gene and one result,” Wu said. “But we need to know more—we know that genes play together.”

Wu’s technique, called functional mapping, produces a computer model that uses known gene interactions along with expected environmental conditions.

He began his research more than a decade ago with plant variations. For example, he examined how soil nutrients interacted with genetic traits of black cottonwood trees to produce differing growth rates.

Over the years, he expanded his tinkering of functional analysis, publishing a comprehensive explanation in the March 2006 issue of the journal Nature Genetics.

His work eventually looked at how drugs interplay with human genomics, a field known as pharmacogenetics. He began to use data from the University of Florida’s Health Science Center and the Duke University’s Institute for Genome Sciences and Policy.

In May, he and colleagues published the first major analysis of functional mapping models of human drug responses in the journal Bioinformatics. The work examined how different genes affected heart rate when exposed to the drug Dobutamine.

“This model means that we can get a very important part of the big picture for drug trials,” said Min Lin, a research colleague of Wu’s at Duke University. That big picture, she said, could limit human trials for experimental drugs or help weed out unnecessarily risky drugs earlier.

The process, of course, has a margin of error.

“There are many strange things that can arise with any process this complicated,” Lin said. “This is just predicting what will most likely happen. Not how it will happen.”

“Still, all clinical trials use statistics that take the greatest results,” she added. “This is a tool that will just enhance the process.”

The program designed by Wu’s team during its heart research can be downloaded from the University of Florida’s Statistical Genetics Group Web site at www.stat.ufl.edu/genetics/software.html .

However, this program will be paltry compared to Wu’s next endeavor. Shortly after the publication of his latest work in Bioinformatics, Wu received an $855,000 NSF grant to construct a user-friendly functional model for anyone pursing pharmacogenetic research.

The programming may be especially useful in light of worldwide efforts to match genetic profiles with physical traits, such as The Pharmacogenetics and Pharmacogenomics Knowledge Base (PharmGKB).

“I am excited that we can help bring this process to more people at a time where we are able to collect enough information to make it useful,” Wu said. “Hopefully, this will become used all over the world.”

Source: University of Florida

Citation: Whether plant or animal, new genetic model can predict its future (2007, July 18) retrieved 23 April 2024 from https://phys.org/news/2007-07-animal-genetic-future.html