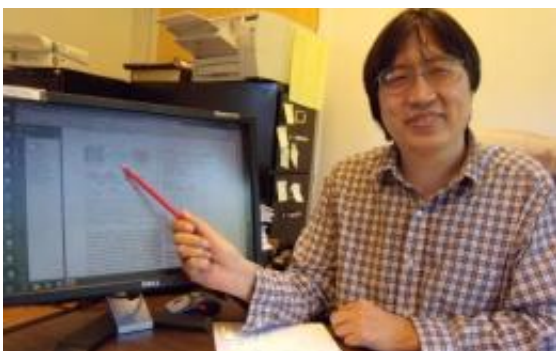


Researcher uses computer science to solve a genetic puzzle

June 15 2011, By Jennifer Donovan



Hairong Wei developed a novel algorithm for identifying clusters of genes that regulate biological processes.

(PhysOrg.com) -- Hairong Wei is a molecular biologist who turned to his other passion -- computer science -- to remove a major research roadblock. His cross-disciplinary efforts have produced a new computer-based tool for rapidly and accurately identifying the transcription factors (regulatory genes) that work together to control a biological process or trait.

In the latest issue of the journal *BMC [Systems Biology](#)*, Wei—an assistant professor in Michigan Technological University's School of Forest Resources and Environmental Science—reports how he built a conceptually novel co-expression network—a virtual map of the genes that have the greatest synchronicity and influence on a given biological

process—and used a novel algorithm he developed to break that network down into its separate components. This enabled him to efficiently identify a cluster of [transcription factors](#) that collectively control a biological process or a trait of interest.

Reviewers of Wei’s research call it “an article of importance in its field” and “work that will have a significant impact.”

Wei himself says the new tool can save time and money and speed progress in identifying key regulatory genes controlling a specific biological process from gene expression data. And “once these transcription factors are identified,” he explains, “scientists will know which genes to manipulate to get the results they want.”

Why do researchers want to identify the genes that regulate various biological processes anyway?

A few examples of biological processes make the answer abundantly clear.

- Cancer development is a biological process. Disruption of key transcription factors governing tumor growth could produce a cure for cancer.
- Crops trying to grow in salty or drought-ridden ground are battling a hostile environment. A biological process controlled by transcription factors enables those plants to survive
- Embryonic stem cells transform into skin, blood, bone—every kind of specialized cell in the body. That transformation is a biological process. Manipulation of key transcription factors enables stem cells to reprogram themselves and develop into different organs. Manipulation of transcription factors has shown potential for developing new avenues

for transplants.

It took biologists a decade and a least a few million dollars to identify 22 transcription factors that are necessary to maintain a stem cell in its ready-and-waiting state, says Wei. Now, using his computer algorithm and a microarray dataset, he was able to identify 24 transcription factors in less than one day. Among these 24 transcription factors, 17 matched the previously-identified 22.

“We were surprised,” he says. His group applied the technique to several data sets from Arabidopsis plants, poplar trees and the Axolotle salamander. They found that, based on already-existing research findings, many of the resulting TF clusters accurately represent a [biological process](#) of interest. The accuracy in prediction varied between 50 and 95%

The TF-Cluster is highly efficient, Wei notes. “This is a pipeline for quickly and accurately identifying functionally coordinated key transcription factors.” Once identified, these transcription factors can be used directly for genetic engineering or for gene network construction to give us a better understanding of how traits are regulated.

Provided by Michigan Technological University

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