

Nurturing a seed of discovery

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(PhysOrg.com) -- Network scientists at Northeastern University have collaborated with an interdisciplinary team of colleagues in cell biology and interactive data acquisition to create the first large-scale map of a plant's protein network.

The results of the study were published in the July 29 issue of *Science* magazine.

The team's research findings — which could eventually be applied to treating human diseases, such as cancer — shed light on the interactions among proteins in *Arabidopsis thaliana*, which serves as a model organism in plant biology.

“Creating this [map](#) is a significant building block to understanding plants in general and learning more about the biological similarities between plants and animals,” said world-renowned network scientist Albert-László Barabási, a Distinguished Professor of Physics with joint appointments in biology and the College of Computer and Information Science. Barabási is also the founding director of Northeastern's world-leading Center for Complex Network Research.

Barabási, and three postdoctoral research associates in his lab — Yong-Yeol Ahn, Gourab Ghoshal and Sabrina Rabello — were part of the project's bioinformatics and analysis group. Researchers at Harvard Medical School, the Dana-Farber Cancer Institute, the Salk Institute for Biological Studies, the United States Department of Agriculture and the Department of Computing at Imperial College in London also

contributed to the study.

Northeastern's contribution to the paper builds upon earlier research featured in a June 2010 issue of *Nature* magazine, in which postdoctoral research associates in Barabási's lab developed a mathematical algorithm to identify communities in complex networks, including major biological networks and large-scale social networks.

In this case, Barabási and his colleagues used the algorithm to comb the map for communities of interconnected proteins that share in the same biological function. Researchers found more than two-dozen such communities.

The findings offer researchers a sneak peak at the evolutionary process within networks of plant proteins. As Barabási put it, "The communities were not random and each had a dominant function that did not emerge by chance."

Provided by Northeastern University

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