

Influential few predict behaviour of the many

Technique helps to untangle complexity in systems from metabolism to social networks.

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To completely understand how a living organism works one would have to take it apart, the great physicist Niels Bohr once observed — but then the organism would certainly be dead¹. In general, systems of high complexity, including living things but ranging from the Internet to social networks, are often impossible to track in all their details.

But what if you didn't have to? Network-theory researchers now have come up with some clever mathematics that reveals complex systems by tracking a selected few of their components.

Say, for example, that you wanted to find a biological marker that identifies people with a certain disease. You can track down all the genes that are expressed differently in people with the disease and assemble a network that shows their interactions, but how do you then pick out those that are specific to the illness?

The new work may help researchers to identify the key nodes in a network that determine the state of every other node, greatly simplifying the search.

To demonstrate their technique, Yang-Yu Liu of Northeastern University in Boston and his colleagues looked at the entire human metabolic network and found that concentrations of about 10% of the body's 2,763 metabolites could be used to determine the levels of all the rest.

But the method could also be used in social networks to identify the people whose opinions determine everyone else's, helping to predict the outcome of, say, a presidential election. Or it could help ecologists to single out the particular species to track to follow changes in an entire ecosystem, to name just a few potential applications.

Needle-like nodes

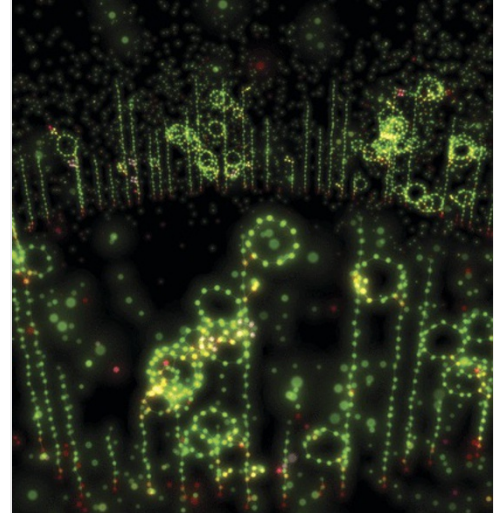
To imagine how this works, start with a simple network in which a chemical A becomes chemical B. Because any changes in B are exclusively determined by A, monitoring B over time will also enable you to determine the state of A. The same would not be true if you monitored only A: Without knowing the initial level of B, changes in A aren't enough to determine the level of B. The team pictured the situation above as a pair of nodes, A and B, with an arrow going from B to A to represent how information about B leads to information about A but not vice versa.

More complex reaction systems don't yield such obvious results. Liu's team tackled the problem by examining clusters of strongly connected components in a network, again represented by nodes with arrows connecting them. For clusters that have no incoming arrows, as is the case of B above, the researchers freely picked a single node from each cluster.

They found that most of the time (and almost always in real-world networks), these selected nodes alone are sufficient to determine the state of every other node in the network. The team published its results in the *Proceedings of the National Academy of Sciences*².

Although theoretically possible, it is extremely difficult to reconstruct the entire network from these nodes. In many applications, however, that will not be necessary, because the needle-like nodes in the haystack of links should reveal the network's most important properties.

"This paper shows how you can reduce a network to the really important component parts that drive the system's behaviour," says Joseph Loscalzo of Harvard Medical School in Boston, Massachusetts. "It begins to make the system more tractable," adds Loscalzo,



Mauro Martino

The complex behaviour of a network can be fully captured by tracking a few crucial nodes, here pictured in red.

who would like to apply the technique to medicine.

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References

1. Bohr, N., *Nature* **131**, 457–459 (1933).
2. Liu, Y.-Y., Slotine, J.-J. & Barabási, A.-L. *Proc. Natl Acad. Sci. USA* **110**, 2460–2465 (2013).