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Press Release

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June 4, 2007

Who's with whom?

Göttingen scientist develops a method to identify circuitry structures of networks.

The mathematical analysis of regulatory networks is becoming increasingly important in different fields of biology – since such networks exist everywhere in nature. Species of animals and plants in an ecosystem, genes and proteins in a cell or neurons in the brain constitute networks of interacting units. Marc Timme, researcher at the Bernstein Center for Computational Neuroscience and at the Max Planck Institute for Dynamics and Self-Organization in Göttingen, has now developed a mathematical method to infer the circuitry structure of a regulatory network from its dynamical response properties. The implementation of this theoretical method can make it possible to determine the exact connections between the units of a network – for example, the interaction between the molecules of a cell or the connections in a neuronal network. The study will appear in June in the scientific journal “Physical Review Letters”.

As a precondition, Timme’s method requires that the network is in a stable, balanced equilibrium, similar to that of a mobile toy in a balanced state. If a small weight is carefully attached to a figure of the mobile, can one infer information about the structure of the mobile from the altered up- and downwards positions of the other figures? And if so, how many times would one have to place weights onto the mobile in different variations before it is possible to reliably determine the connections between all its figures? Timme pursued these questions – not for mobiles but for balanced regulatory networks in general.

In nature, we find many regulatory network systems, for example, for generating the recurring pattern of activity when breathing or when the heart beats. If in such a network the dynamics of one component is altered, the other components respond to it. If a neuronal network is fed somewhere with an external signal, a new, slightly shifted balance is restored – that is, some neurons now transmit signals later, some earlier than previously. “The dynamical response of the network not only depends on the type of signal applied but also characteristically on the structure of the network", Timme explains. This fact was successfully demonstrated in a previous work published in the journal "Europhysics Letters" in November 2006. In his latest work, Timme showed how the structure of a network can be determined by studying its response and how the connectivity can be reconstructed on a mathematical level. With the help of his method, it is not only possible to determine which elements of a network are connected with one another, but also how strong the connections are.

Precisely determining every connection within a network requires the recording of a vast amount of data. "To reconstruct the entire network we need to collect sufficient information", Timme explains, "in general this means that the number of different experiments needs to equal the number of all components of a network." Only few researchers have dared to draw conclusions about the structure of a network from its dynamic responses. Up to now such mathematical analysis methods have mainly allowed for statistical assertions, e.g. about the percentage of connected units or the expected strengths of the connections. Timme's approach is different in that his mathematical model determines every single connection of the network. He has tested the validity of this theory with the help of computer simulations of different networks.

In reality, regulatory networks consist of thousands or millions of components, making a recording of the responses of a network to a large number of signals practically impossible. A further significant step in Timme's method nonetheless allows to determine the structure of even very large networks with just a moderate number of experiments. Nature normally arranges its network units very efficiently such that a desired function can be accomplished with a minimal number of connections. In his method, Timme makes use of nature's principle of sparseness as a feature beneficial for finding the structure of larger networks. He shows how to reconstruct the structure of a sparsely connected network with a number of experiments far fewer than the number of components represented in a network. The novel method provides researchers with the basic principles for a tool to systematically investigate the interdependences between structure and function of regulatory networks.

Original publications:

Marc Timme. Revealing Network Connectivity From Response Dynamics. Physical Review Letter, 98:224101 (2007)

Marc Timme. Does dynamics reflect topology in directed networks? Europhysics Letters 76 (3), 367–373 (2006)

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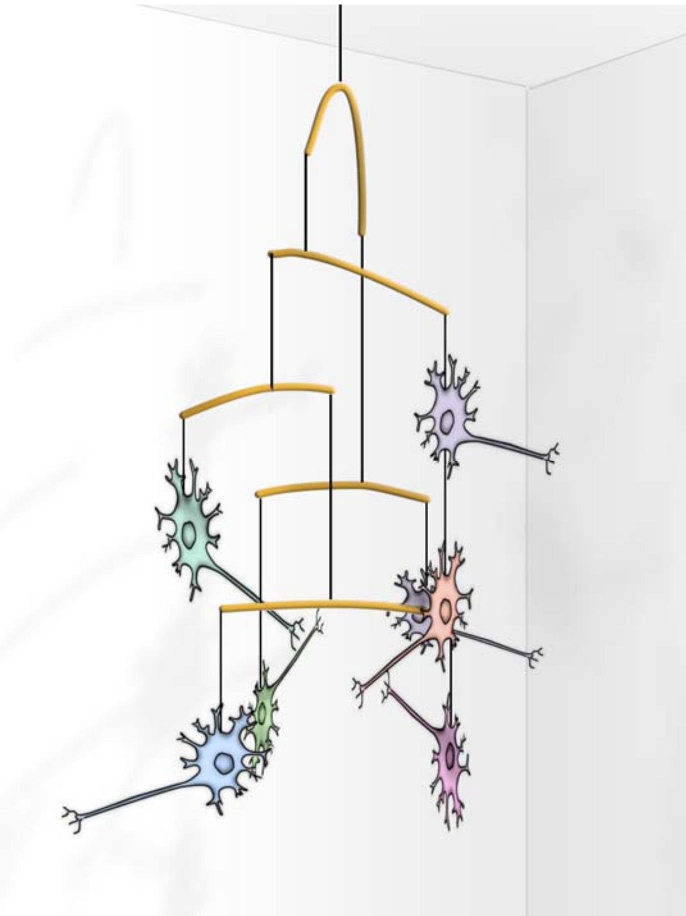

Caption:
A mobile toy constitutes a simple example of a network in which individual units are connected to others in a non-trivial way. Timme has now developed a method to determine the connectivity structures of networks that are in stable equilibrium – just as a balanced mobile toy.
Source: Max Planck Institute for Dynamics and Self-Organization

The Federal Ministry of Education and Science (BMBF) has founded four Bernstein Centers for Computational Neuroscience (BCCN) in Berlin, Freiburg, Göttingen, and Munich. The interdisciplinary field of research combines experiments with data analysis and computer simulation on the basis of well-defined theoretical concepts. The central aim of Computational Neuroscience is to identify the neuronal basis of brain performance.

The BCCN Göttingen is a joint center of the Georg-August-University Göttingen, the Max Planck Institute for Dynamics and Self-Organization, the Max Planck Institute for Biophysical Chemistry, the Max Planck Institute for Experimental Medicine, the German Primate Center, and Otto Bock HealthCare GmbH.