

Disordered networks synchronise faster than small world networks

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Synchronization occurs when individual elements in a complex network behave in line with each other. This applies to real-life examples such as the way neurons fire during an epileptic seizure or the phenomenon of crickets falling into step with one another.

In this study, Carsten Grabow and colleagues from the Max Planck Institute for Dynamics and Self-Organization in Göttingen, Germany, created a model to test the speed of synchronisation of complex networks in collaboration with the Warwick Complexity Centre, UK. They tested this model using three very different oscillators acting on complex networks, which are known as Kuramoto, Rössler and pulse-coupled oscillators. As a result, for all tested networks they showed that the structure of the coupling between [network](#) nodes determines the speed of synchronisation.

In short: the higher the disorder in the network, the faster the synchronisation. They subsequently verified this observation in real-life networks including an air-transported network, a social net-work and a human travel network. Given the great variety of networks used, the increase in the speed of synchronisation in line with increased disorder can be considered universal.

This result goes against previous observations, which showed that so-called small-world net-works, which consist of an intermediate structure of fully ordered and fully disordered networks, favour synchronisation. The small-world effect was famously applied to analysing social

networks and gave rise to the theory that there are only six degrees of separation between people in a given country.

The authors are currently working on deriving a mathematical formula to predict which [complex network](#) would synchronise and how fast. Such an approach would require integrating parameters, including the network size and typical number of links per node, as well as the spread of the disorder introduced. This work could have real-life applications, for example, in measuring the robustness of the relaxation process in gene regulatory networks.

More information: C. Grabow, S. Grosskinsky and M. Timme (2011). Speed of complex network synchronization. European Physical Journal B. [DOI: 10.1140/epjb/e2011-20038-9](https://doi.org/10.1140/epjb/e2011-20038-9)

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