

# Accepted Manuscript

Biological mechanisms beyond network analysis via mathematical modeling

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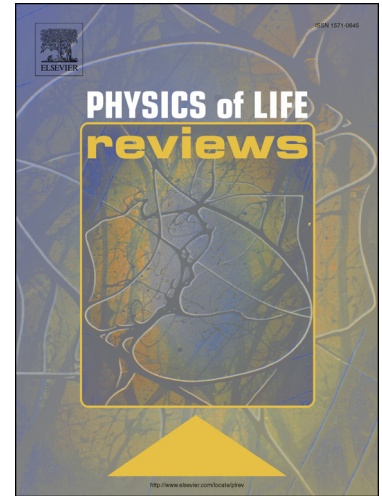
PII: S1571-0645(17)30187-2  
DOI: <https://doi.org/10.1016/j.plrev.2017.12.001>  
Reference: PLREV 954

To appear in: *Physics of Life Reviews*

Received date: 30 November 2017  
Accepted date: 5 December 2017

Please cite this article in press as: Pedersen MG. Biological mechanisms beyond network analysis via mathematical modeling. *Phys Life Rev* (2017), <https://doi.org/10.1016/j.plrev.2017.12.001>

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Biological mechanisms beyond network analysis via mathematical modeling:

Comment on “Network Science of Biological Systems at Different Scales: A Review” by Marko Gosak et al.

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Methods from network theory are increasingly used in research spanning from engineering and computer science to psychology and the social sciences. In this issue, Gosak et al. [1] provide a thorough review of network science applications to biological systems ranging from the subcellular world via neuroscience to ecosystems, with special attention to the insulin-secreting beta-cells in pancreatic islets.

Such applications typically investigate whether a suitably defined network present particular structure, such as being scale-free, small-world, random, etc. Having identified the network structure, the researchers can then apply known results from network science to conclude that the biological system under study possesses certain properties. For example, small-world networks are known to transmit information efficiently, and scale-free networks are insensitive to random failure, but sensitive to targeted attacks [2].

Biological systems are unique compared to engineered or social networks since their underlying structures are often unknown. For example, the worlds’ air transportation network is well described: it has certain major hubs connected by scheduled flights to other hubs (long-range links), as well as to minor airports locally. It is therefore quite straightforward to define and analyze the resulting network (which is a small-world network [3]). Similarly, social-media connections [4] or co-starring actors [5] unambiguously define social networks, which can be analyzed with the tools of network science.

In contrast, understanding biological interactions is often a task of reverse engineering: we can observe activity in units such as certain brain areas, or individual cells, but we may only have a vague idea about how these units communicate with each other. Some exceptions include ecological food webs [6], and the anatomical connectivity of the nervous system of *C. Elegans* [5].

Researchers have therefore resorted to constructing functional networks where two units (nodes) are considered linked if their activity is sufficiently correlated. Interestingly, such functional networks often present small-world properties; this is the case for example for the human brain [7] or pancreatic islets [8]. Such insight tells us something about how these biological systems function: do they relay information efficiently from one unit to another? Are they prone to attacks, e.g. cell death, in case of disease? This kind of information is important for understanding how the system works in health, and how to interact to treat the system when it does not function properly in disease. A word of caution may be

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