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SES 598: Fundamentals of Complexity
Peer review

C. Elegans GRN Network (*Kelle Dhein*)

This paper applies informational dynamics measurements to a biological network: the gene and protein network that regulates the early embryonic cell cycle of C. Elegans. The purpose of the paper is to analyze how biological networks differ from non-biological ones and more specifically if the non-functional pathways of the network process information in a different way than the functional ones.

This paper provides a complete and well-rounded introduction to both the network studied and the motivation behind the study. This introduction is written in a simple, yet accurate vocabulary, making it ideal for people who are not experts in the topic. However, the informational measurements employed are not fully explained. A qualitative explanation of the concepts and differences between transfer entropy and active information would help the reader understand the results presented.

The model as a whole is also described in a clear and concise way. The explanation of the phases of the process helps the non-biology expert understand the reality behind the network. However, some details are confusing, such as the explanation of why under certain circumstances two of the phases are skipped.

The paper includes plenty of informative figures that make the text clearer and easy to understand. However, there are several formatting problems that prevent the reader from a careful understanding of said plots. In the first place, the figures are not clearly labeled. A brief description of each figure right underneath it would make it easier to know what the figure is plotting without having to go back to the text. Also, in some of the figures, the axes are not labeled, making it hard to understand the figure. In some others, tilting the labels in the X axis would make the reading easier. For aesthetic purposes, the legend could be included in the figure instead of as footnote.

The summary and discussion section of the paper clearly explains some of the results, however it is incomplete. All the interpretations that the author has done on the data and the results should be included in this section, even the more speculative ones (but clearly stating the less confident nature of the result in this circumstance).

In summary, this paper stands out for being a useful introduction to the world of biological networks for non-experts. It provides clear explanations and background on the topics discussed without getting lost in unnecessary technical details. In its current version the main flaw of the paper are some major formatting problems that should be easily fixed before its final version.

Note: The paper in its current state is actually an annotated draft, specifically written to obtain feedback before writing a definite version. I've tried to address all the concerns stated on the paper in this review.