

Mining higher-order triadic interactions in gene-expression data

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Higher-order networks [1] are attracting large scientific interest in recent years. However, a key challenge is to infer higher-order interactions from data. Triadic interactions [2] are a fundamental type of higher-order interactions that occur when one node regulates the interaction between two other nodes. Triadic interactions are known to be key in ecosystems, in neuronal networks, and in gene regulation networks. However, information theory approaches to mine triadic interactions are still lacking.

In this work we explore the fundamental dynamical properties of networks with triadic interactions between continuous variables. We formulate a general model of networks with triadic interactions. Moreover we propose an information theory framework and an algorithm, validated on the triadic model, that we call Triaction, that is able to mine triadic interactions from data.

This algorithm is applied on synthetic data as well as Acute Myeloid Leukemia gene expression data finding new candidates for triadic interactions as well as validating already established biological results.

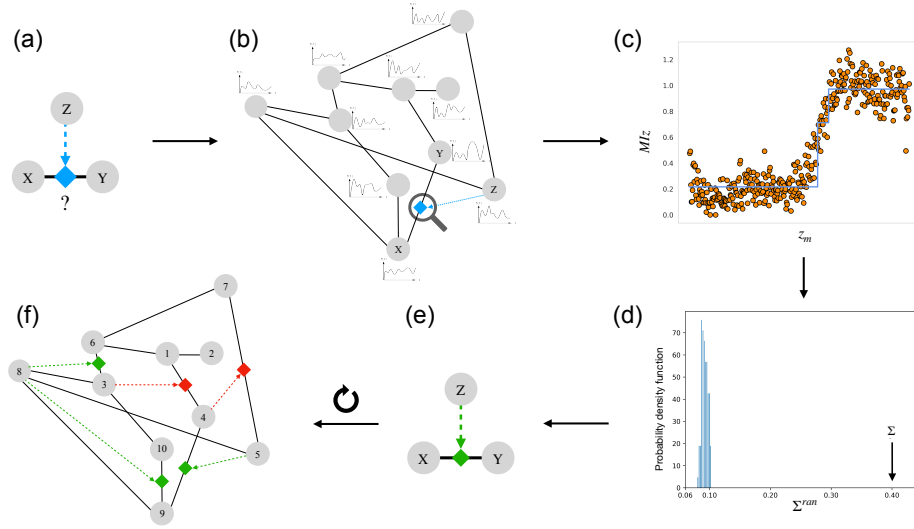


Figure 1: Schematic description of the Triaction algorithm pipeline.

In conclusion, our work proposes a new information theoretic approach to mine triadic interactions. In the future, the method could be applied to other types of data including structured missingness.

References

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- [2] Sun, H., et al.: The dynamic nature of percolation on networks with triadic interactions. Nature Communications, 14(1):1308 (2023).
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