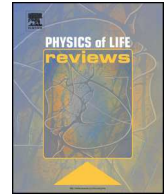


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Comment

Causal inference from high-dimensional static data in soil microbiota networks

Comment on “Topological change of soil microbiota networks for forest resilience under global warming” by Gong et al.

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ARTICLE INFO

Communicated by M. Frank-Kamenetskii

In their insightful review article, Gong et al. [1] present a broad framework that bridges abstract mathematical concepts from topology with practical network analysis in the study of soil microbiota. By integrating advanced methodologies such as functional mapping, quasi-dynamic modeling, and GLMY homology, they offer novel insights into how soil microbial communities respond to global warming and forest management practices, particularly thinning.

Professor Rongling Wu and his collaborators have a rich history of developing interdisciplinary methods to unravel complex biological systems. Building on the concept of functional mapping [2], they have progressively expanded their toolkit to include functional clustering [3] and more advanced mathematical constructs involving differential equations [4] and game theory [5]. Their previous works, detailed in numerous manuscripts and the seminal texts *Statistical Genetics of Quantitative Traits* [6], *Statistical and Computational Pharmacogenomics* [7], and *Quantitative Methods for Precision Medicine* [8], lay the foundation for the innovative approaches applied in this study.

One of the most intriguing aspects of the current work is the application of *informative, dynamic, omnidirectional, and personalized networks* (idopNetworks) [9] that leverage a relatively new digraph topology theory—GLMY homology theory [10]. This represents a novel application of idopNetworks in the context of soil microbiota. The authors demonstrate how idopNetworks can infer interactions from high-dimensional static data without relying on predefined causal models, a challenging feat in ecological studies where temporal data may be scarce.

Gong et al. employ allometric scaling laws to model the relationship between individual microbial abundance and the overall habitat index, effectively transforming static data into quasi-dynamic representations. This methodology, rooted in the principles of functional mapping, allows for the reconstruction of dynamic networks from static datasets, addressing a critical limitation in traditional network analysis.

In Section 3.2 of their article, the authors apply functional clustering to categorize thousands of microbial operational taxonomic units (OTUs) into distinct modules based on abundance patterns. The application of modularity [11] reduces complexity and facilitates the reconstruction of multilayer networks, capturing interactions at different biological scales. Such hierarchical modeling echoes the principles of developmental modularity and extends its applicability across a wide range of disciplines.

Further advancing their analytical framework, Sections 3.3, 4, and 5 introduce more sophisticated mathematical concepts, including quasi-dynamic mixed ordinary differential equations (qdMODEs) and evolutionary game theory. These methods allow for

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<https://doi.org/10.1016/j.plrev.2024.10.012>

Received 21 October 2024; Accepted 23 October 2024

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1 the modeling of independent and dependent components of microbial abundance, capturing both intrinsic growth and interspecies 1
 2 interactions. The incorporation of GLMY homology theory provides a topological perspective on network structures, enabling the 2
 3 identification of key features that influence network stability and functionality [10]. 3

4 Importantly, the study moves beyond the design and implementation of the field trial—previously addressed in Wang et al.'s work 4
 5 [12]—to focus on the innovative methodologies for network reconstruction and causal inference. By integrating soil physical and 5
 6 chemical properties into their models, the authors underscore the intricate feedback mechanisms governing ecosystem responses to 6
 7 environmental changes. 7

8 This research brings together deep, complex topics from many different disciplines—statistical genetics, network analysis, digraph 8
 9 topology, soil microbiota, and more. A further description of the methodology, applied to metabolomic networks in complex diseases, 9
 10 can be found in the recent article “The metabolomic physics of complex diseases” [13]. By leveraging advanced mathematical theories, 10
 11 the authors provide valuable insights into the mechanisms underpinning complex biological systems. 11

12 This work exemplifies an excellent effort to translate abstract mathematical theories into practical tools for analyzing real-world 12
 13 network problems. The ability to derive interactions from high-dimensional static data is particularly noteworthy and has the po- 13
 14 tential to revolutionize studies in ecology and beyond. However, the practical implications of these complex models warrant further 14
 15 exploration. While the theoretical framework is robust, translating these findings into actionable strategies for forest management re- 15
 16 mains an area for future research. For instance, identifying specific microbial interactions that enhance forest resilience could inform 16
 17 targeted interventions, but applying such insights in practice requires additional steps. 17

18 In conclusion, Gong et al.'s article makes a substantial contribution to our understanding of soil microbiota dynamics under 18
 19 environmental stress. By bridging the gap between abstract mathematical concepts and practical network analysis, they offer valuable 19
 20 insights into the mechanisms underpinning forest resilience and set the stage for future interdisciplinary research. The advancements 20
 21 in network analysis methodologies showcased in this work represent significant progress toward unraveling the complexities of 21
 22 ecological networks and their responses to global challenges. 22

23 Declaration of competing interest 24

25 The authors declare that they have no known competing financial interests or personal relationships that could have appeared to 25
 26 influence the work reported in this paper. 26
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