Cumulated implicit network connectivity and its application to marine sciences

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October 16, 2024

Abstract

Connectivity is a key feature of network's structure that determines how different nodes can be linked by consecutive edges. However, analytical expressions for connectivity probabilities that take into account connections realized by paths of different lengths in a *cumulated* manner were still lacking. Moreover, also the concept of connectivity by itself could be extended. Indeed, the usual *explicit* connectivity probabilities are conceptually associated with the pathway of a random walker that joins two nodes, symbolizing a kind of "parent-child" relationship (Figure, top panel). Nevertheless, each pair of nodes could be simultaneously influenced by a third node (or more than one) and such "sibling-sibling" relationships can determine similarities between nodes pairs that we could regard as a form of *implicit* connectivity (Figure, bottom panel).
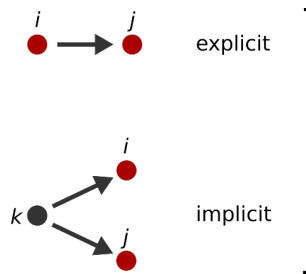
We show how we can derive expressions for explicit and implicit random-walk connectivity probabilities across any range of numbers of steps [1]. The multi-step expressions that we obtain are based on simple combinations of matrix and Hadamard products of the network adjacency matrices and can be computed efficiently within a sparse matrix approach [1]. Moreover, it is possible to link the probabilistic connectivity interpretation to transport dynamics. Indeed, we demonstrate that explicit connection probabilities are associated with processes of tagging or sampling a transported quantity across the network in single nodes, forward- or backward-in-time, respectively. Analogously, implicit connection probabilities are also related to tagging or sampling processes but in two nodes simultaneously [1].

Our theoretical approach can be applied to study any kind of temporal, weighted and directed network in which a random walk can be defined. This guarantees a broad applicability to various fields and could constitute a first step for future modeling efforts to characterize network connectivity from a probabilistic perspective.

Finally we illustrate how the aforementioned concepts and tools can be bring new insights to the study of marine ecology and biogeography. We use a compilation of ∼50 population studies of marine species over the Mediterranean basin to compare genetic distance observations against gene-flow predictions obtained from network models of oceanic connectivity [2]. We find that almost the 70% of observed variance in genetic differentiation is explained by implicit connectivity over multiple generations, significantly outperforming all other models [2].

Such results offer great promises to untangle the eco-evolutionary forces that shape marine population structure and to anticipate climate-driven redistributions, altogether improving spatial conservation planning.

References

[1] E. Ser-Giacomi et al. "Explicit and implicit network connectivity: Analytical formulation and application to transport processes" *Physical Review E* 103, 042309 (2021)

[2] T. Legrand et al. "Spatial coalescent connectivity through multi-generation dispersal modelling predicts gene flow across marine phyla" *Nature Communications* 13.1 (2022)