Comparative dynamical analysis of trophic networks
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final report
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The key aim of this project was to make some improvement in the classical problem of linking structure to process in ecology. In particular, we were interested in the topological analysis of various ecological network (mostly trophic networks) and their functioning. The main question is how to use simple, static, structural models for predicting the behaviour of the ecological community: if we can make any progress here, we can contribute to predictive ecological modelling, and this strategy can be cheaper, faster and more efficient.

In some preliminary research, we compared carbon flows and the strength of interactions in several weighted trophic flow networks [1]. We studied a large set of weighted ecological networks by several topological indices and an index considered as a proxy to dynamical indices. We determined which topological indices are the best ones predicting the dynamics and ranked individual topological indices according to this evaluation. [6] This research, combined with trait databases, leads to a larger-scale research in preparation [21].

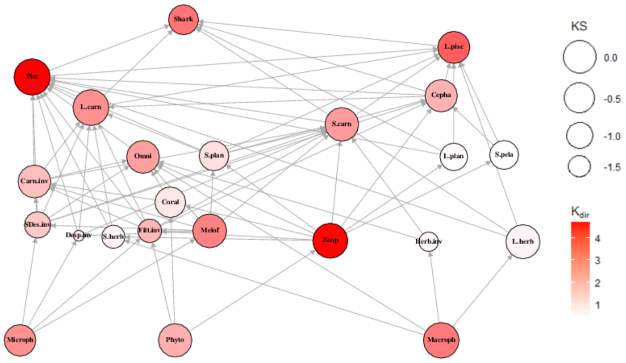

Figure 1. Larger nodes are dynamically more important, darker nodes are structurally more important. According to our main hypothesis, the larger the darker is.

Ideally, it is clear the real dynamical behaviour should be simulated instead of using some proxy. This is very hard to perform for large, real food web databases. We had to adapt our research plan and simulate hypothetical, small networks. Beyond studying the above questions, we were also interested in comparing single-species and pairwise in silico perturbation experiments [7]. We determined topological positions where pairwise perturbations are additive or non-additive (either escalating or dampening, Figure 2). These results depend on the actual community response function used, so we were looking also at comparing different functions [19]. Very importantly, instead of trying to rank individual indices for predictability, it is also possible to use machine learning techniques and evaluate many possible combinations of k indices, how do these correlate with dynamical importance simulated in this modelling framework [18].

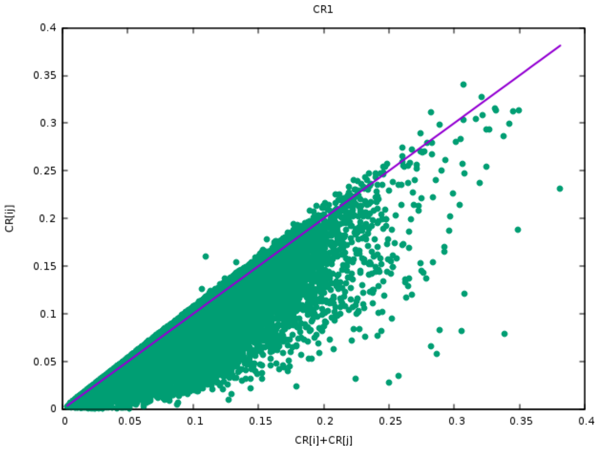

Figure 2. Additive effects around the line, non-additive effects are further.

A new direction of research, motivated by earlier studies in social network analysis, is to focus on the centrality of groups of nodes in networks. The key idea here is that the most central nodes can have similar, overlapping neighbourhood in a network, so, in a structural sense they mutually decrease each other's importance. If one is deleted, then the other one can maintain the structure (and, partly, also functioning). Thus, if k nodes can be deleted from the network, in order to maximize the damage to connectivity, the best solution is not to delete the k most central nodes in the centrality rank list of nodes, based on individual centrality values. Instead, there can be another set of k nodes whose deletion is worst for connectivity. Turning this argument upside down, in order to protect the connectivity of the network, we may maintain k nodes, in order to maximize connectivity, other than the k most central odes in the network.

First we tested this approach on spatial networks, habitat connectivity networks of forest patches, inhabited by several bird species. We adapted the methodology and quantified the solutions for various k values, for several species and for two kinds of approaches. We have found that protected areas are far from being optimally chosen, at least from this perspective [2, 4].

The same approach was applied to food webs. Here, the question is similar: which set of k species are the mostly central one in the network. If structure is relevant to functioning, then this approach can contribute to a more efficient and more predictable systems-based conservation management – in the future. We studied a large number of networks and the results are partly published [5, 8, 12], partly still in preparation [20]. The main result here is that for k = 3, we generally find three species, being connected, at different trophic levels. This means that a core food chain can be found in many food webs, and protecting this food chain can be a very efficient way to maintain the integrity and the functioning of the ecological community (Figure 3).

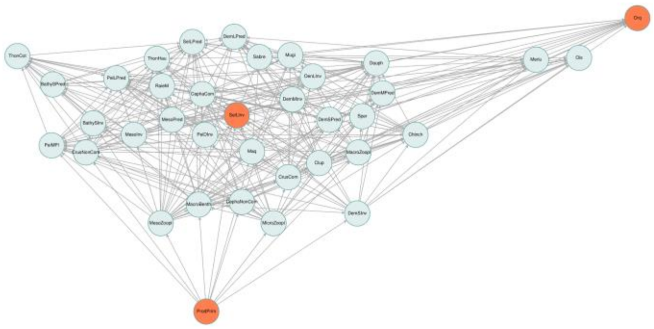

Figure 3. A core food chain.

Another old but still highly relevant issue is the aggregation of trophic data, i.e. how to represent trophic relationships, how the nodes of trophic networks should be defined. Every result of food web research, based on real data, is a function of the aggregation process, since various algorithms produce various networks. We used aggregation research to better interpret existing and missing data in the case of a real food web [3], and consideing the merits of trait-based approches [10], we also made research on comparing mathematical and trait-based aggregation algorithms [9]. A perspective for further research is to study highly-resoluted networks of microorganisms, at aggregation levels lower than ever in the literature [14]. This could provide a lot of information about processes never studied before in food webs (most food webs ave extremely high aggregation levels, especially at lower trophic levels).

One application of food eb research is the systemic description and monitoring of ecological processes [16]. We used a network analysis for describing succession and regime shifts in marine kelp forests.

Ecological models offer predictions that can or cannot be useful and applicable. For a more predictive and more applicable food web research, it is very much needed to test the results. This is not easy in the case of multispecies systems but the new mesocosm experimental facility at our Institute will offer this possibility. We performed some preliminary analysis on food web research in mesocosms [17].

As side-branches of our main research line, we studied the large-scale, global network structure of bipartite, plant-pollinator networks [11, 15] and social networks of marmot groups [13]. Checking and testing additional applications of network analysis always enrich the main research line, by offering alternatives and further inspirations.

References:

[1] Jordán, F., Sciarpetti, G. and Liu, W-C. 2016. Carbon flows and interaction strength in aquatic food web models. Life and Environment, 66: 325-331.

[2] Pereira, J., Saura, S. and Jordán, F. 2017. Single-node versus multi-node centrality in landscape graph analysis: key habitat patches and their protection for twenty birds in NE Spain. Methods in Ecology and Evolution, doi: 10.1111/2041-210X.12783.

[3] Patonai, K. and Jordán, F. 2017. Aggregation of incomplete food web data may help to suggest sampling strategies. Ecological Modelling, 352:77-89.

[4] Pereira, J. and Jordán, F. 2017. Multi-node selection of patches for protecting habitat connectivity: fragmentation versus reachability. Ecological Indicators, 81:192-200.

[5] Ortiz, M., Hermosillo-Nuñez, B., González, J., Rodríguez-Zaragoza, F., Gómez, I., Jordán, F. 2017. Quantifying keystone species complexes: ecosystem-based conservation management in the King George Island (Antarctic Peninsula). Ecological Indicators, 81:453–460.

[6] Endrédi, A., Senánszky, V., Libralato, S. and Jordán, F. 2018. Food web dynamics in trophic hierarchies. Ecological Modelling, 368:94-103.

[7] Móréh, Á., Endrédi, A. and Jordán, F. 2018. Additivity of pairwise perturbations in food webs: topological effects. Journal of Theoretical Biology, 448:112-121.

[8] Capocefalo, D., Pereira, J., Mazza, T., Jordán, F. 2018. Food web topology and nested keystone species complexes. Complexity, Article ID 1979214, 8 pages

[9] Jordán, F., Endrédi, A., Liu, W-C., D'Alelio, D. 2018. Aggregating a plankton food web: mathematical versus biological approaches. Mathematics, 6:336.

[10] Endrédi, A., Jordán, F., Abonyi, A. 2018. Trait-based paradise - or only feeding the computer with biology? Community Ecology, Forum, 19:319-321.

[11] Kovács-Hostyánszki, A., Földesi, R., Báldi, A., Endrédi, A., Jordán, F. 2019. The vulnerability of plant-pollinator communities to honeybee decline: a comparative network analysis in different habitat types. Ecological Indicators, 97:35-50.

[12] Jordán, F., Pereira, J., Ortiz, M. 2019. Mesoscale network properties in ecological system models. Current Opinion in Systems Biology, 13:122-128.

[13] Wey, T., Jordán, F., Blumstein, D. 2019. Transitivity and structural balance in animal social networks. Behav. Ecol. Sociobiol., 73:88.

[14] D'Alelio, D., Hay Mele, B., Libralato, S., Ribera d'Alcalà, M., Jordán, F. 2019. Rewiring and indirect effects underpin modularity reshuffling in a marine food web under environmental shifts. Ecology and Evolution, 00:1-16.

[15] Kovács-Hostyánszki, A., Jordán, F., Földesi, R., Báldi, A. Wild plant-pollinator networks support crop pollination in farmlands: important wild bees quantified. Scientific Reports, submitted.

[16] Uribe, R.A., Ortiz, M., Jordán, F. Different length in successional pathways of kelp and barren communities. Community Ecology, under revision.

[17] Póda, Cs., Jordán, F. Food web research in mesocosms: a literature survey. Food Webs, Short Communication, submitted.

[18] Gouveia, C., Móréh, Á., Jordán, F. Finding the most predictive cocktails of node centrality indices in ecological networks. PLoS Computational Biology, submitted.

[19] Móréh, Á., Jordán, F. Comparing community response indices in aquatic food web models. Advances in Oceanography and Limnology, submitted

[20] Pereira, J., Endrédi, A., Móréh, Á., Jordán, F. Keystone species complexes: the vertical core of food webs.

[21] Endrédi, A., Patonai, K., Jordán, F. Functional traits can make food web models more comparable. In preparation.