Oikos

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Appendix 1

Supplementary method

It was a major challenge to identify a metacommunity network that is ecologically relevant for all 25 taxa. Our premise was that for each taxon an ecologically relevant network structure would be one that maximizes the strength (absolute value) of the association between pond centrality and local diversity. To this end, we followed these four steps:

i. *Network construction*

Using a graph approach, we built a network for the whole system in which nodes represented the 52 pond communities and the links reflected the potential flow of individuals among them. We used a gradient of geographic distances with 400 break points from the minimum to the maximum edge-to-edge Euclidean distance between ponds to reflect the wide range of dispersal distances in a regional species pool that was composed of organisms from 25 different taxa. Thus, several networks were built taking into account the gradient of distances connecting two ponds. We identified a threshold distance and then linked all ponds in the network separated by a distance below this critical threshold. In this manner, we constructed 400 networks each defined by a threshold distance.

ii. *Pond centrality metrics*

For each of the 400 threshold networks, we calculated pond centrality for the whole metacommunity network using four centrality metrics: a) degree centrality, DC_i, which is defined as the number of direct connections between a patch and its neighbors; b) closeness centrality, CC_i, which is the reciprocal of the average length of the shortest path between the reference community (pond i) and all other communities in the metacommunity; c) betweenness centrality, BC_i, which describes how often the reference patch (i) acts as a mediator on the shortest path between two other patches in the network; and d) eigenvector centrality, EC_i, defined as the first eigenvector of the adjacency matrix whose scores are proportional to the centralities of those nodes to which a target node is connected. The centrality indices DC_i and EC_i best represent organism dispersal in the local neighborhood; BC_i and CC_i emphasize the bridging role of the patches in maintaining landscape connectivity beyond the local scale (Estrada and Bodin 2008). A detailed presentation of these metrics is provided elsewhere (Estrada and Bodin 2008, Economo and Keitt 2010).

iii. *Associations between pond centrality and local diversity*

We calculated a Pearson correlation between local diversity and the centrality index of a pond for almost all biological groups found in the metacommunity (25 taxa). If only one species was observed within a taxon, a logistic regression was fitted and the explained deviance of each model was used as an estimate of the degree of association (a pseudo-r^2). In order to obtain congruent patterns between correlation and logistic regression analyses when the logistic parameter (relating occurrence with centrality) was negative, we used the value $1–r^2$ in our calculations. In this analysis, 400 vectors of community centralities (with one vector for each linkage-distance network) were obtained for each index of centrality. In the next step, these vectors were related to those of local diversity among communities.

iv. *Local biodiversity–metacommunity structure association*

A linear segmented regression model was fitted to describe the relationship between the Pearson correlation coefficient or pseudo-r^2 and the gradient of link distances that defines the network structure (Muggeo, V. M. 2008. Segmented: an R package to fit regression models with broken-line relationships. – R news 8: 20–25). This analysis suggests a specific distance at which statistically significant maxima or minima in the diversity-centrality relationship may be located. In addition, we identified linkage distances with statistically significant association and the distance at which the maximum association occurred. These three criteria allowed identification of those linkage distances at which metacommunity networks were most congruent with local diversity. Our approach followed the logic of parameter estimation in statistical models.

It should be noted that we only considered species richness. However, the proposed approach could be used for any community attribute such as abundance, biomass, size structure, evenness, functional diversity, etc.

Figure A1. Identification of spatial scales associated with local diversity for the 25 taxa in the system studied. The associations (Pearson correlation or pseudo-r^2) between biodiversity and the four-centrality indices were calculated at different linkage distances for each taxon. Fitted lines (black) and breaking points were estimated with segmented regressions. Significant correlations are indicated in grey. In all cases, clear maxima or minima are observable. Extreme associations suggest a maximum congruence between biodiversity and the metacommunity network.

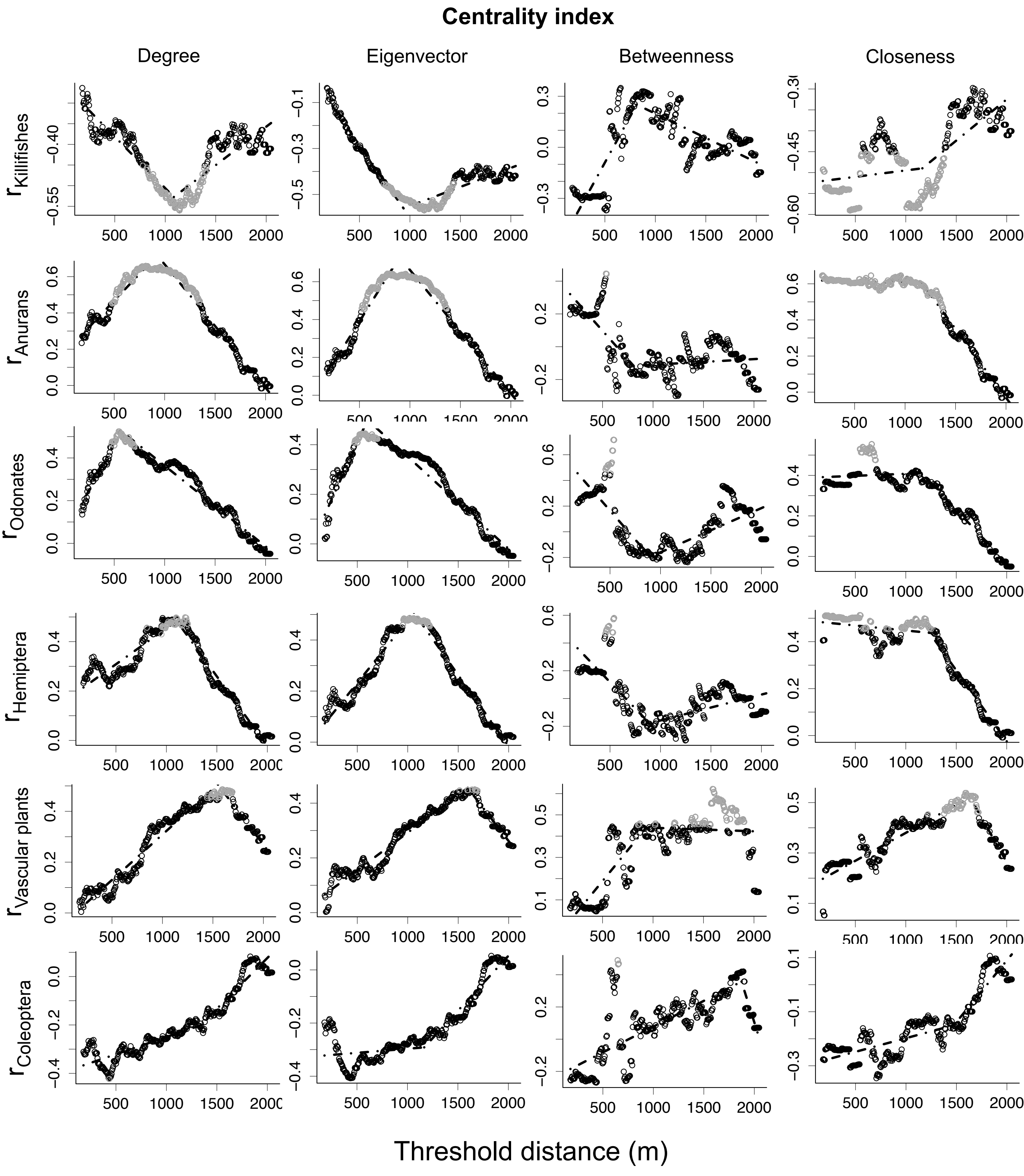


Figure A1. (continue)

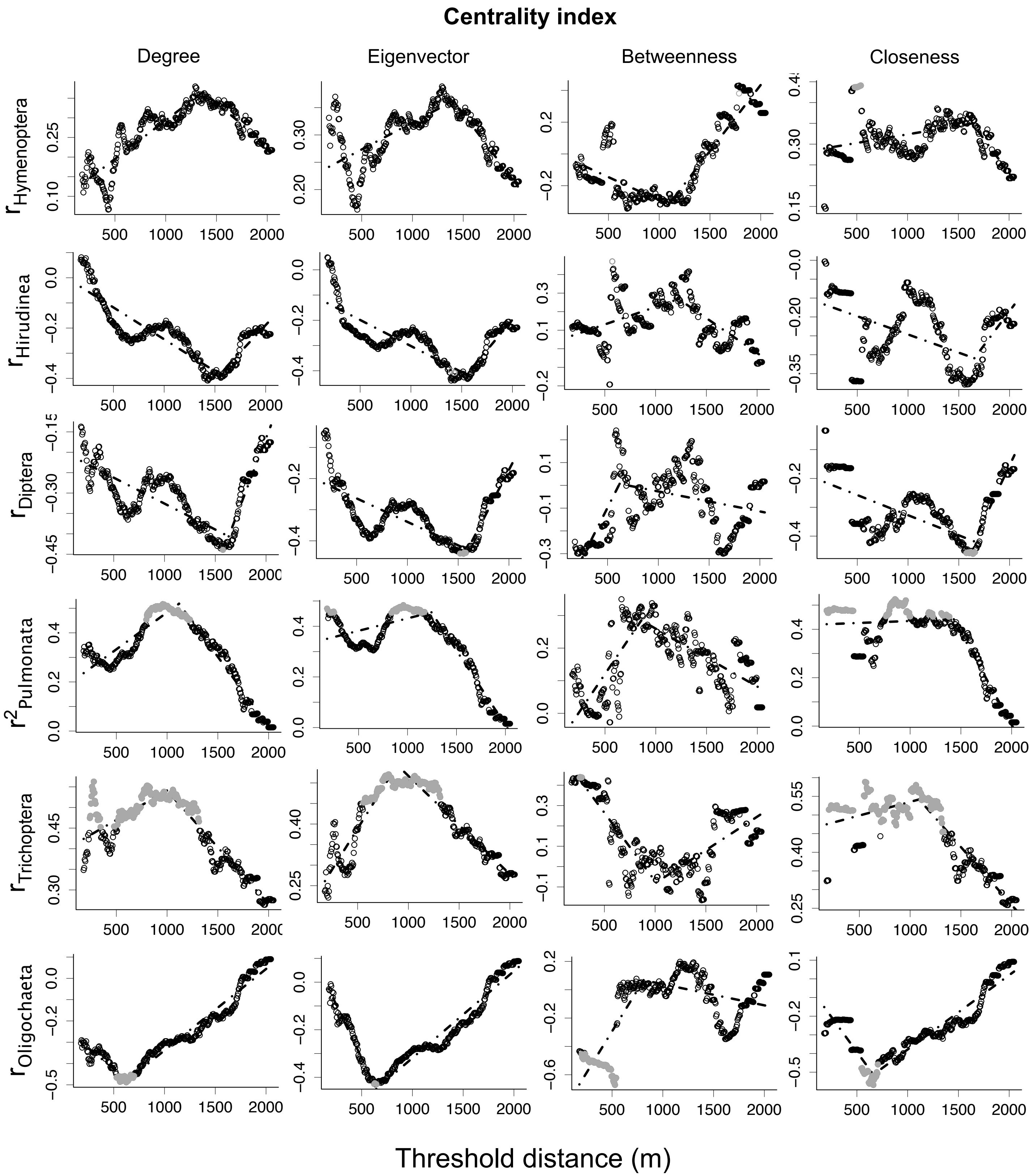
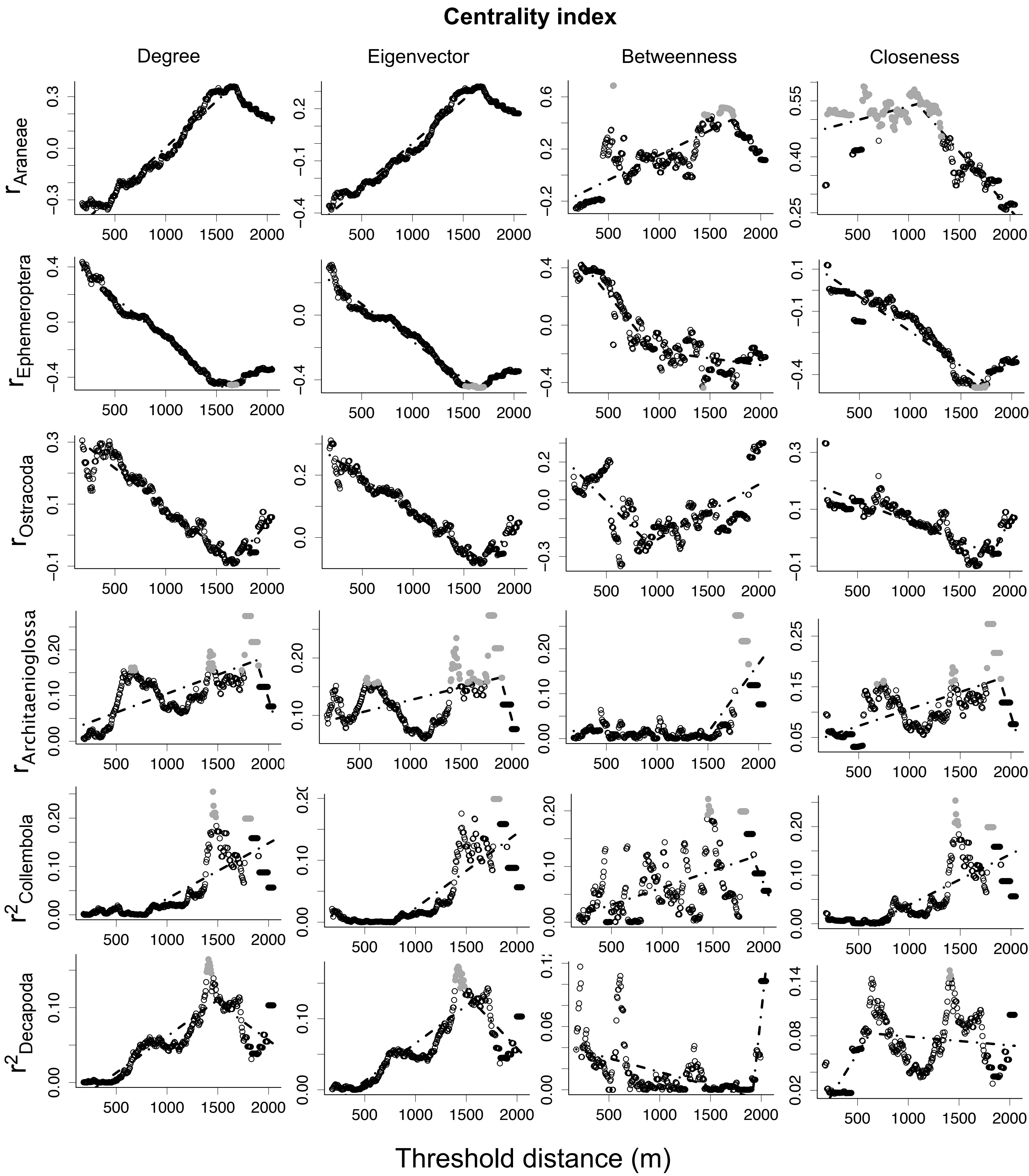


Figure A1. (continue)



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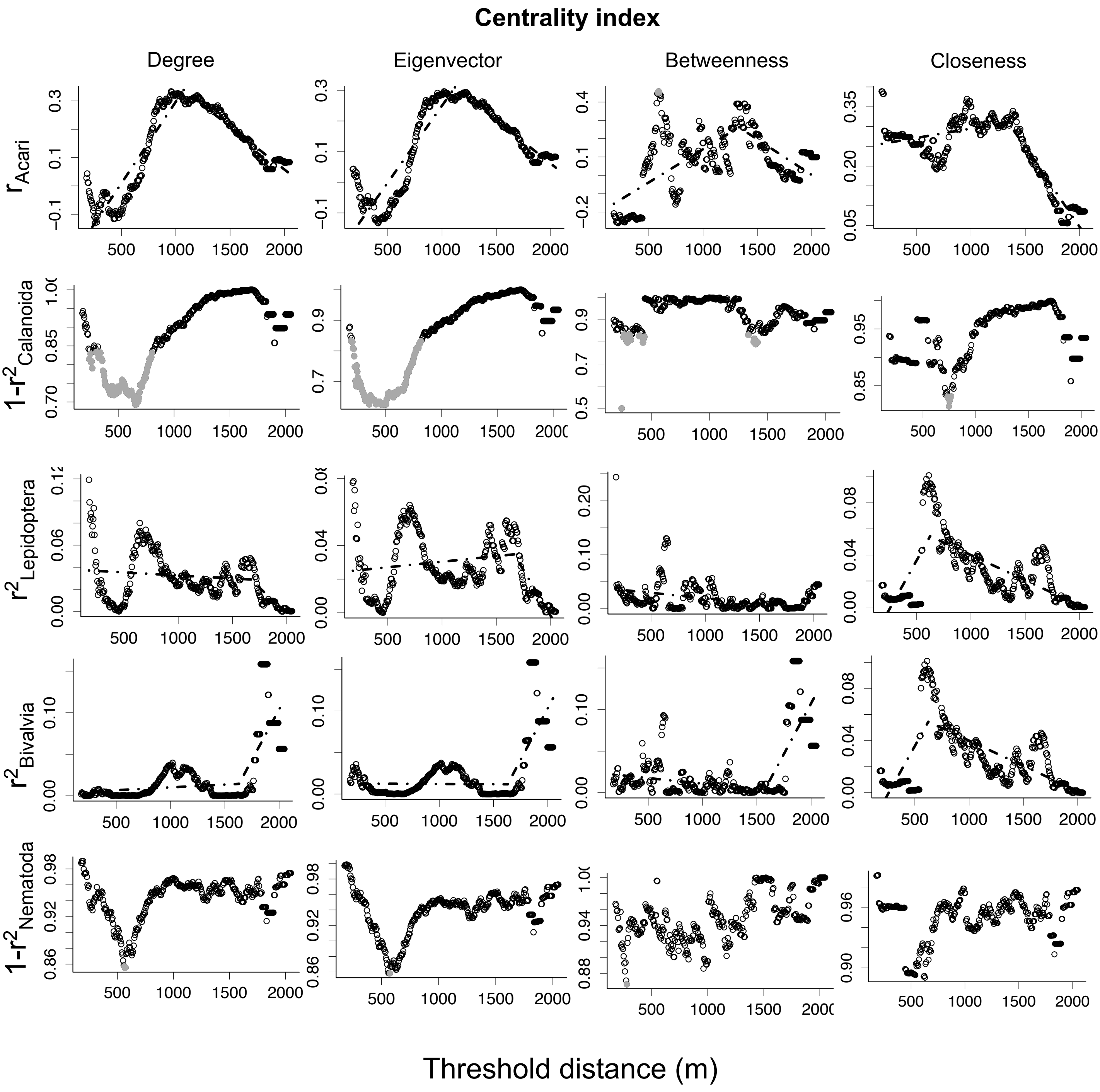
Centrality index
Degree
Eigenvector
Betweenness
Closeness
r_{Acari}
$1\text{-}r^2_{Calanoida}$
$r^2_{Lepidoptera}$
$r^2_{Bivalvia}$
$1\text{-}r^2_{Nematoda}$
Threshold distance (m)