

Inference of the interactions within the pathobiome of *Erysiphe alphitoides*

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Introduction

Plant-inhabiting micro-organisms interact directly with each other, forming complex microbial interaction networks. The arrival of a new species such as a pathogen can lead to a disruption in such networks. Here we are interested in *Erysiphe alphitoides*, a species of fungus which causes powdery mildew on oak trees. This is one of the most common diseases affecting European forests. The pathogenicity of this fungus follows from specific interactions with its microbial environment. It is thus necessary to study its pathobiome, *i.e.* all the microbes interacting with the pathogen and their influence on pathogenesis. Nonetheless, these interactions can be concealed by indirect relationships resulting from the environment, hence the need to account for environmental covariates in the inference of these links.

Data

The data were collected from leaves taken from three oaks with different observed susceptibility to mildew (from highly susceptible to strongly resistant). These trees were located very close to each other, so that their global environmental conditions could be considered similar. For each leaf, the distances to the base of the branch, the tree trunk and the ground were measured, along with the orientation of the branch (SW or NE) where the leaf was taken. The abundances of foliar fungal and bacterial operational taxonomic units (OTUs) were obtained by metagenomic sequencing. Here we only consider a subset of the most abundant OTUs made of 48 bacterial OTUs and 66 fungal OTUs (including *Erysiphe alphitoides*).

Inference of Direct Ecological Interactions

The inference of the graph summing up the interactions of the 114 involved species was performed in a tree-based framework [Schwaller et al., 2015]. The idea is to explore a

subset of undirected decomposable graphs made up of connected graphs with no cycles. Such graphs are called spanning trees. The existence of any particular edge is then assessed by looking at the probability of its belonging to a random spanning tree given the observations.

As the environmental covariates could not directly be integrated in the model, the number of reads for each OTU was previously fitted with a Negative Binomial generalized linear model with environmental variables as predictors and the total number of reads per sample (log-transformed) as an offset.

The Pearson residuals obtained from the fitted models were used to infer the direct interactions between the OTUs. As we wanted to model the bivariate links between OTUs with Gaussian copulas, the residuals were transformed using empirical cumulative density functions.

Hindsight on the sign of the interactions, which is of interest to better understand their nature, is obtain by looking at the maximum a posteriori estimates for the correlations of the bivariate Gaussian copulas.

Results

The whole network for the susceptible tree had 1099 edges, 65% of which were positive. Within-kingdom interactions were predominantly positive (71% for interactions between bacteria and 63% for interactions between fungi), as were cross-kingdom interactions (60%). The other two networks were also dominated by positive edges. The network for the tree with intermediate resistance had 1112 edges, 66% of which were positive. The network for the resistant tree had 1082 edges, 65% of which were positive. In total, 95 positive interactions and five negative interactions were common to all three networks.

References

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