Disentangling Microbial Association Networks in the Ocean

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Microbial ecosystems are composed of many interacting species, yet most of these interactions are still unknown. Omics allow us to start analyzing associations of species or functions over spatiotemporal scales. Microbial associations can be represented as networks. In the ocean, constructed association networks are often dense and static, despite the biological system being highly dynamic. Here, we explore strategies to disentangle marine microbial association networks aiming to generate improved networks that can lead to a better understanding of the oceans microbial ecosystems.

Problem: dense network (hairball)



Dynamic network: monthly networks for one year

- ~ node represents a microbe
- ~ edge represents an association between two microbes
- ~ one monthly network is a subnetwork of the static network. A network for a given month is obtained by filtering the edges. An edge is present in a monthly network if both nodes and the association are present in the given month





- ~ node size = abundance in given month
- ~ color represents detected modules of static network,



Evaluation and Evidence

An association predicted through the network may be evaluated by a literature based database. Moreover, additional evidence may be obtained by using Single Cell Amplified Genomes (co-occurrence in one SAG) or finding the same association in several networks constructed from different datasets. If two interaction partners show same environmental preference / niche, they are more likley to be true interaction partners. Further evidence can be obtained if two species have complementary genes suggesting that there is a dependency between them.

Biological interpretation

What are the microbes environmental preference, niche? Who are the keystone species? Which groups of microbes interact with each other? What are the predicted interactions for microbes of interest? The network approach generates microbial interaction hypotheses.

Outlook

While we concentrate here on taxonomic networks, the next step will be to look at metabolic networks. Comparing these networks over time, are metabolic networks more stable in time than the taxonomic networks?

Network constructed from Blanes Bay Microbial Observatory data 2004 - 2013: Anders K. Krabberød, Ina M. Deutschmann, Marit F. M. Bjorbækmo, Vanessa Balagué, Caterina R. Giner, Isabel Ferrera, Gipsi Lima-Mendez, Esther Garcés, Josep M. Gasol, Ramon Massana, Ramiro Logares, Dynamics in the core marine interactome over a decade, in preparation Program aiming to detect environmentally-driven associations: Ina Maria Deutschmann, Gipsi Lima-Mendez, Anders K. Krabberød, Jeroen Raes, Karoline Faust and Ramiro Logares (2019). EnDED - Environmentally-Driven Edge Detection Program https://doi.org/10.5281/zenodo.3271730

Network visualization with Gephi: Bastian M., Heymann S., Jacomy M. (2009). Gephi: an open source software for exploring and manipulating networks. International AAAI Conference on Weblogs and Social Media. Module search as implemented in Gephi, Algorithm: Vincent D Blondel, Jean-Loup Guillaume, Renaud Lambiotte, Etienne Lefebvre, Fast unfolding of communities in large networks, in Journal of Statistical Mechanics: Theory and Experiment 2008 (10), P1000

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