

8. Analysis of nestedness and modularity. Bacteriophage-host adjacency matrix re-arranged with BiMAT (Flores et al., arXiv:1406.6732v2 [q-bio.QM], 2014) to visualize modularity and nestedness. The adjacency matrix consists of positive associations between 816 bacteriophages and 451 hosts predicted for the surface and deep chlorophyll maximum layers.

