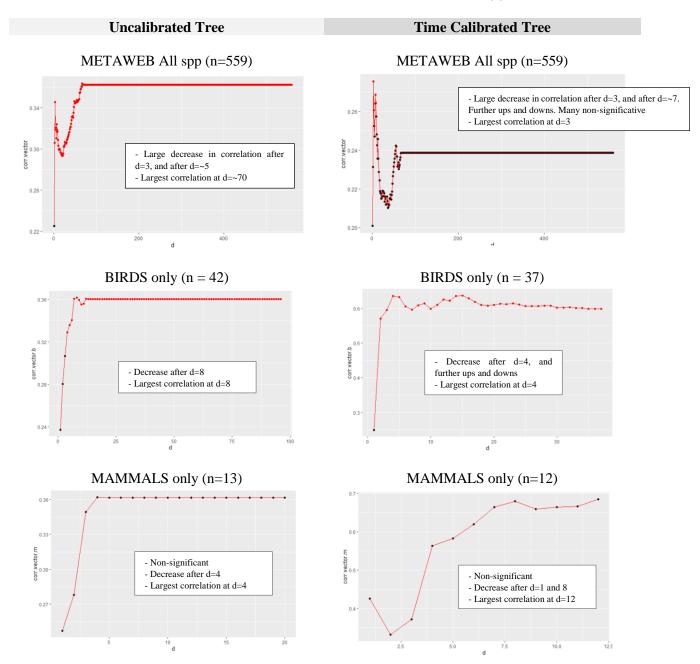
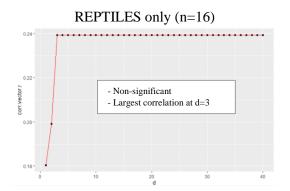
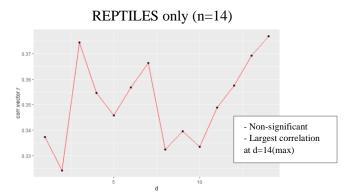
Investigating correlations between network dimensionality and phylogenetic signal in Galapagos food-metaweb

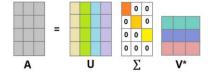
Plotting Procrustes correlations (between phylogenetic and foraging traits distances of predators) vs the number of dimensions (d) or latent traits considered for the foraging traits' distance matrix of predators. Dots in red or black indicate a significant ($P \le 0.05$) or non-significant correlation, respectively. Axes: X is the correlation value from Procrustes test, and Y is the number of dimensions (d).







The Foraging Traits' matrix is obtained from the decomposition of the adjacency matrix of the metaweb (SXS).

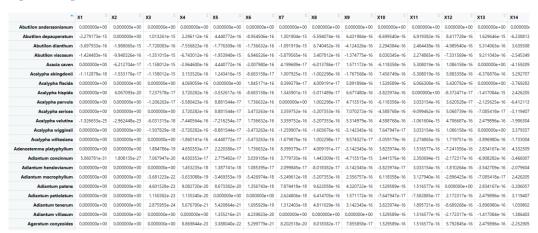


A -> Species x Species food web Adjacency Matrix

U -> Foraging Traits

V -> Vulnerability Traits

Example of a piece of "U" matrix from the Metaweb:



To compute distance matrices based on increasing number of dimensions [,1:i], we can't use Jaccard distances since we have continue and negative values that resulted from the decomposition. Therefore, I used **Euclidean distances** to compute the Foraging traits' distance matrix for each given dimension.

Madelaine Proulx (Master student at Dominiqur Gravel's lab, Univ.Sherbrooke) used Jaccard distances to compute dissimilarity matrix od predator's diets. Our results largely differ for the Uncalibrated Tree, but are quite similar for the Time-Calibrated Tree.