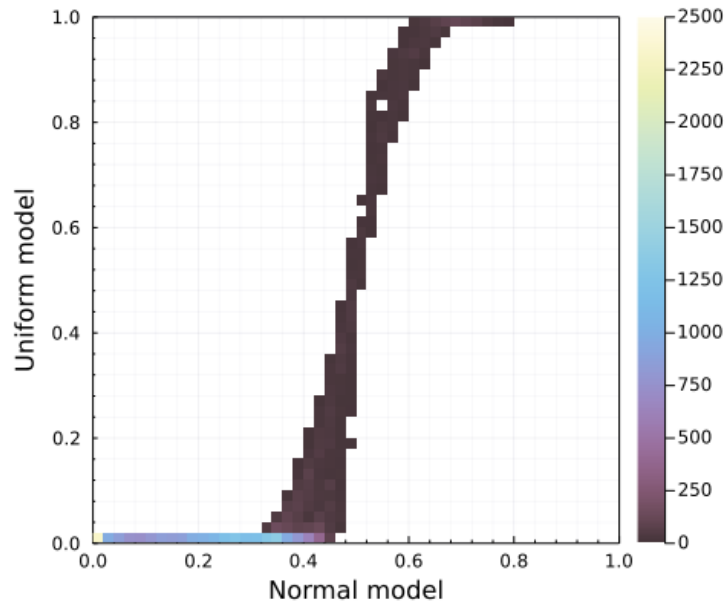


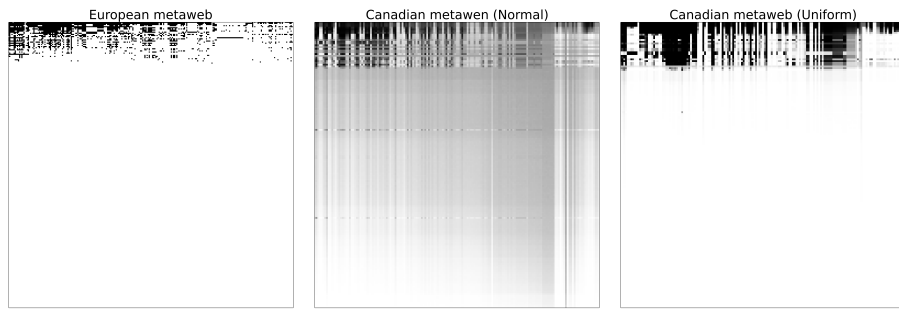
S.M.2 - the Normal model of latent variable evolution over-predicts

In this appendix, we compare the raw predictions made by the Normal and Uniform models of latent variable evolution. The Normal model was created by (i) getting the average μ of the simulated values for each species/variable combination, and (ii) estimating the standard deviation as $(\mu + c - \mu - c)/3.92$, where c is one half of the 95% confidence interval around μ .

As can be seen on the following figure, the Normal model tends to assign high probabilities (up to $p \approx 0.4$) for interactions that the Uniform model essentially rules out:



This can lead to severe over-estimation of the number of interactions. In fact, the consequences of using a Normal model are obvious from looking at the adjacency matrices below: most of the interactions are predicted between species that occupy the lower trophic level, and are ecologically unrealistic.



For this reason, we only use predictions from the Uniform model in the main text.