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 divided by 3.92

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:
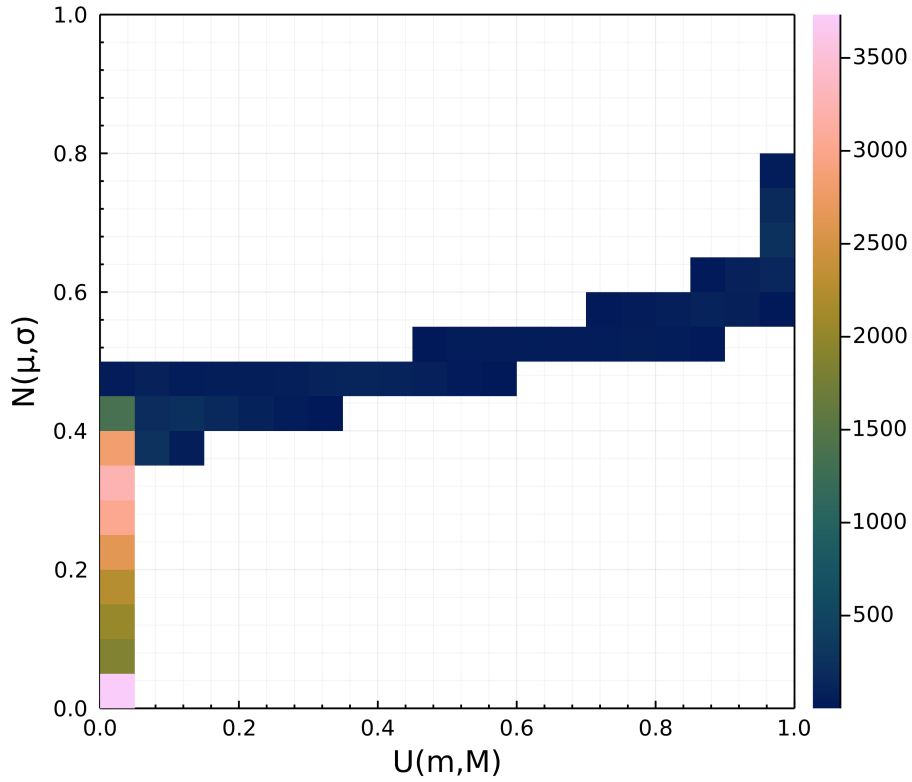

Figure 1: Here the color scale shows the number of interactions for each bin (where a bin is the combination of the uniform and normal score)

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.
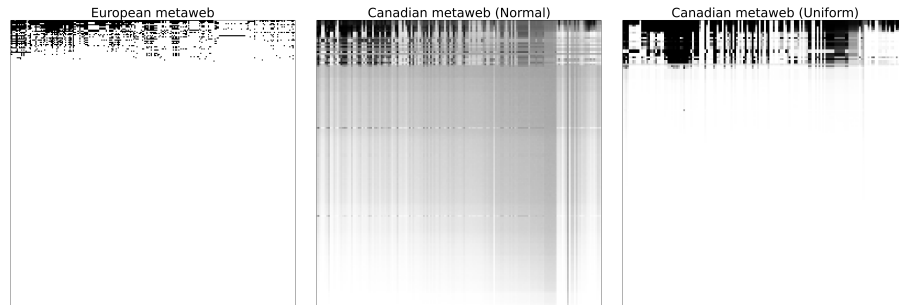

This can be further revealed by looking at the connectance of the networks under different thresholds:
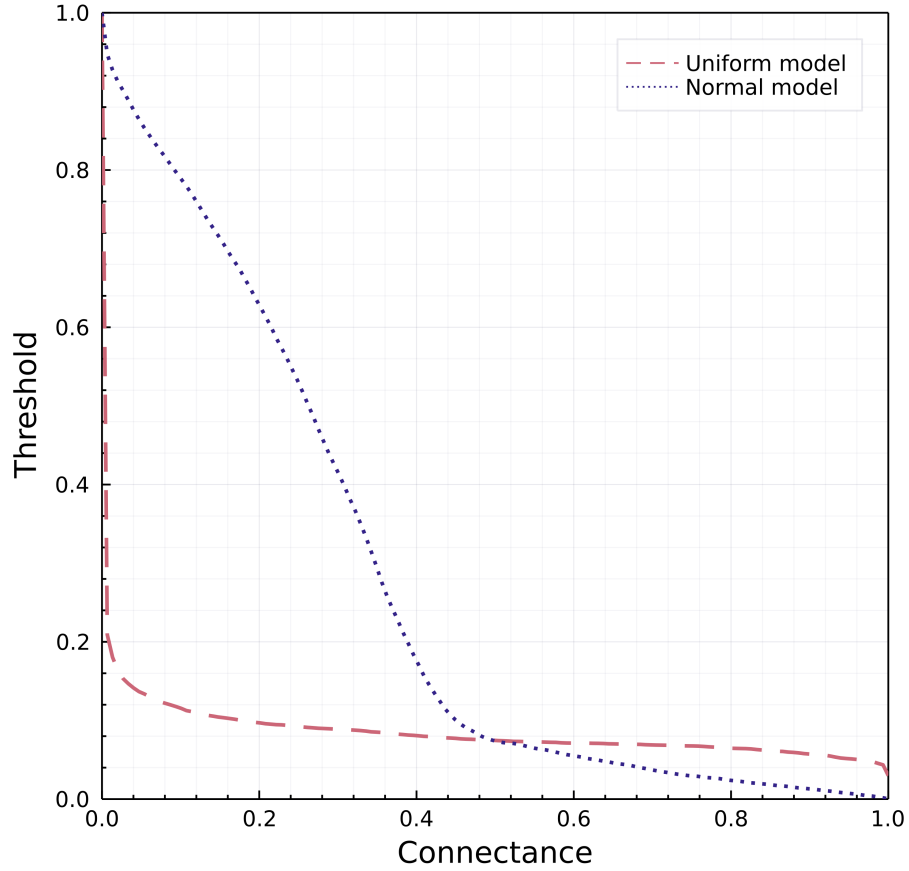
Although the Uniform model predicts a lot of interactions with extremely low probability, that are removed at a low threshold, the distribution of probabilities under the Normal model leads to extremely (abnormally) high connectances even for thresholds that are over twice as large as the optimal threshold determined in main text and Supp. Mat. 1.

This has consequences for the overall network *structure*: specifically, the Normal model predicts a lot more top predators than we expect under the uniform model; rather than there being a progressive change in top-intermediate-bottom proportions as the threshold changes, there is an abrupt shift at a threshold of about 0.6, which suggests that the Normal model is biased towards over-predicting most interactions with probabilities in the range $[0, 0.6]$.
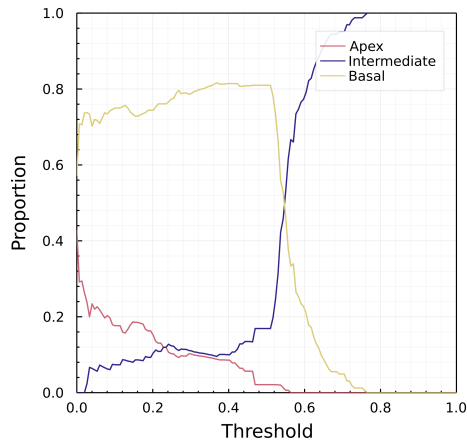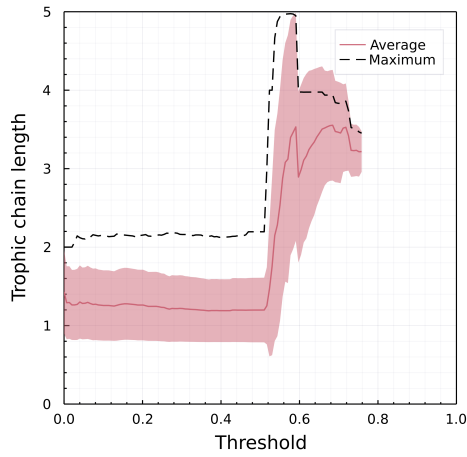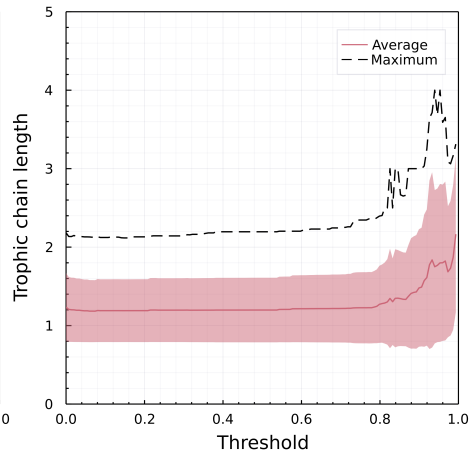
Normal model   Uniform model
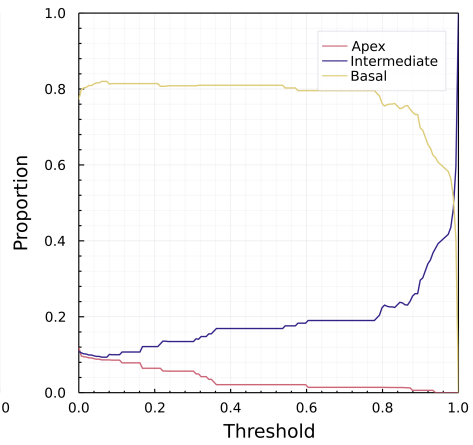
The same "jump" can be observed when looking at the distribution of food chain lengths:

Normal model   Uniform model

For these reasons, we only use predictions from the Uniform model in the main text.

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