The covariance between any two species was a function of the phylogenetic distance.

Where η and ⍴ are the parameters for the L2-norm and P is the normalized phylogenetic distance between species i and j (only for cases where i≠j). We used the L2-norm, since it does not assume Brownian motion, and allows for a non-linear decline in covariance with distance.

We modeled the presence of VPL with a binomial model (logit link) with the following formula:

VPL ~ (1|genus) + sociality + longevity + relative brain size + body size

For a detailed model with all priors see supplemental materials.

We modeled the number of unique mimics Poisson model (log link) with the same formula as the VPL model. For a detailed model with all priors see supplemental materials.