**Supplementary Methods for The ecology of zoonotic parasites in the Carnivora**

Barbara A. Han, Adrian A. Castellanos, John Paul Schmidt, Ilya R. Fischhoff, John M. Drake

**Methods**

*Phylogenetic clustering*

To determine whether parasite transmission modes clustered within the carnivore tree, we used the phyloclust function in the R package RRphylo [(1)](https://paperpile.com/c/dodVGH/MO8v). Our phylogenetic tree data were the 10,000 birth-death node-dated trees subsetted to the Carnivora from [(2)](https://paperpile.com/c/dodVGH/sw2V). Transmission modes (used as our “state” data for the clustering analysis) for each were obtained from the Global Mammal Parasite Database ([(3)](https://paperpile.com/c/dodVGH/sfbq); see the Carnivore Parasite Records file for these data). We report the mean *p* values of 10,000 runs for each transmission mode.

*Boosted regression trees*

We used the gbm R package [(4)](https://paperpile.com/c/dodVGH/JKT4) to investigate the relationship between previously published species trait data [(5)](https://paperpile.com/c/dodVGH/Irl2) and zoonotic host status data [(6)](https://paperpile.com/c/dodVGH/VvIZ). Briefly, zoonotic host status and the number of zoonoses associated with each species were determined from the literature and cross-checked against the Global Infectious Diseases and Epidemiology Network (GIDEON; www.gideononline.com). Trait data were compiled from various existing databases or calculated from spatial data layers (see Carnivore Trait Data and Carnivore Trait Metadata files for more information). We used a hurdle model process that first fit a classification model to determine zoonotic host status followed by a regression model of all non-zero data regarding the number of zoonoses associated with each species ((7); see Zoonotic Host Status Code for more information). We used a Bernoulli error distribution for the classification model and a Poisson error distribution for modeling abundance of zoonoses. Model parameterization was done using a grid search of all appropriate parameters. The parameter combination with the best deviance curve and highest evaluation statistics was evaluated using 10 bootstrap iterations. The number of zoonoses model showed consistently low pseudo R2 from this bootstrap evaluation, so we only report results from the classification model of zoonotic host status.

**References**

1. [Castiglione S, Tesone G, Piccolo M, Melchionna M, Mondanaro A, Serio C, Di Febbraro M, Raia P. 2018. A new method for testing evolutionary rate variation and shifts in phenotypic evolution. Methods Ecol Evol 9:974–983.](http://paperpile.com/b/dodVGH/MO8v)

2. [Upham NS, Esselstyn JA, Jetz W. 2019. Inferring the mammal tree: Species-level sets of phylogenies for questions in ecology, evolution, and conservation. PLoS Biol 17:e3000494.](http://paperpile.com/b/dodVGH/sw2V)

3. [Stephens PR, Pappalardo P, Huang S, Byers JE, Farrell MJ, Gehman A, Ghai RR, Haas SE, Han B, Park AW, Schmidt JP, Altizer S, Ezenwa VO, Nunn CL. 2017. Global Mammal Parasite Database version 2.0. Ecology 98:1476.](http://paperpile.com/b/dodVGH/sfbq)

4. [Greenwell B, Boehmke B, Cunningham J, GBM Developers. 2020. gbm: Generalized Boosted Regression Models. R package version 2.1.8. Comprehensive R Archive Network (CRAN).](http://paperpile.com/b/dodVGH/JKT4)

5. [Fischhoff IR, Castellanos AA, Rodrigues JPGLM, Varsani A, Han BA. 2021. Predicting the zoonotic capacity of mammal species for SARS-CoV-2. bioRxiv 2021.02.18.431844.](http://paperpile.com/b/dodVGH/Irl2)

6. [Han BA, Kramer AM, Drake JM. 2016. Global Patterns of Zoonotic Disease in Mammals. Trends Parasitol 32:565–577.](http://paperpile.com/b/dodVGH/VvIZ)

7.     Cragg, J.G., 1971. Some statistical models for limited dependent variables with application to the demand for durable goods. Econometrica 39:829-844.