Appendix E. Besag-York-Mollie (BYM) models for human-carnivore relations.

We used INLA's Bayesian modeling framework (Rue et al 2009) for running generalized linear models assuming a BYM specification (Besag et al 1991). The BYM model is one of the most popular approaches to account for spatial dependency of residuals (Blangiardo and Cameletti 2015). We apply the log-link to model mean number of (1) mentions of coexistence, (2) mentions or evaluations of tolerance of carnivores, (3) ecosystem services mentioned and, (4) conflicts mentioned in studies at a state *i*, as linear functions of covariates and two BYM components:

$$y_i \sim Poisson(\lambda_i)$$
 [1]

$$log(\lambda_i) = b_0 + \beta_k \times variable_{ki} + \beta_{n_studies} \times numberof studies_i + u_i + v_i$$
[2]

In expressions [1] and [2] y_i and λ_i represent the number of human-carnivore relations and ecosystem services mentioned in studies at state *i* and the average number of relations and services, $\lambda_i = E(y_i)$, respectively. Additive parameters included intercept b_0 , and slope terms for the effects of *k*th variable and number of studies (β_k and $\beta_{n_studies}$). We separately estimated the effects of 17 variables, i.e., percentage of federal and private land, three carnivore families (i.e., Canidae, Felidae, and Ursidae), three social actors (i.e., local, non-local, and manager/academia), three management actions (i.e., non-lethal actions, community development programs, and lethal control interventions), two ecosystem services (i.e., regulating and cultural), and four conflicts (i.e., damage to human food, damage to human property, damage to human safety, and humanhuman conflicts) on the mention of coexistence and the mention or evaluation of tolerance of carnivores. We also estimated the effects of the first 11 variables on the number of ecosystem services and conflicts mentioned. Finally, we included in the models two BYM components (u_i and v_i) to account for spatial autocorrelation in residuals. u_i is a state-specific spatially structured random effect and v_i is a state-specific unstructured random effect:

$$u_i | u_{-i} \sim Normal\left(\frac{1}{N_i} \sum_{j=1}^n a_{ji} \times u_j, s_i^2\right)$$
[3]

$$v_i \sim Normal(0, \sigma_v^2)$$
[4]

where u_{-i} indicates all the states but the *i*th, N_i is the set of neighbors of state *i*, a_{ji} is 1 if state *i* and *j* are neighbors and 0 otherwise, s_i^2 is the variance for the state *i*, and σ_v^2 is the variance of the unstructured residuals modeled among the 12 states. We specified a symmetric adjacency matrix *M*, to assign the set of neighbors for each state (figure E1(b)), so that $M_{ij} \neq 0$ if and only if *i* and *j* states are neighbors. The adjacency matrix was based on the map of states of the West (figure E1(a)).

We used the default prior distributions provided by the R-INLA package for the parameters (Martino & Rue, 2010). Thus, minimally informative priors were specified on: the log of the

structured effect precision $log(\tau_u) \sim logGamma(1, 5e - 05)$ and the log of the unstructured effect precision $log(\tau_v) \sim logGamma(1, 5e - 05)$, where the precision is the inverse of the variance. The prior specification for the intercept and fixed effects were *Normal*(0, 1) and *Normal*(0, 0.001), respectively. The second term of the prior distributions refers to precision.



Figure E1. (a) Map of states of the west used to produce the adjacency matrix (b) Adjacency matrix for human-carnivore relations and ecosystem services mentioned in studies aggregated by states. Rows and columns identify states; black squares identify neighbors. For example, Alaska (1st row) has no neighbors, while California (2nd row) has 3 neighbors.

References

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