

Supplementary Information 4. Regularization multiplier and spatial cross-validation

We determined the values of regularization multiplier per species by fitting single-variable models with regularization multiplier one, three, five, seven and nine, and then inspecting the smoothness of response curves (Elith et al., 2011; Radosavljevic & Anderson, 2014). Abrupt / multimodal response curves for many variables were considered to be an indicator of overfitting (Zhu & Qiao, 2016); regularization multiplier values that produced smooth response curves were chosen.

We divided all points into five spatial clusters using the function `cv_cluster()` with the 'blockCV' package (Valavi et al., 2019) and held out each cluster once for model evaluation. Only two species (i.e., *Ph. papatasi* and *Ph. perfiliewi*) were observed in widespread areas (after environmental thinning) that allowed for cross-validation with five spatial blocks. Three species had four folds cross-validation, five species were cross-validated with three spatial blocks, and two species (i.e., *Ph. tobbi*, *Ph. ariasi*) could only be cross-validated with two folds due to paucity of species occurrence records.

Table. The chosen regularization multiplier for model fitting and the folds of spatial cross-validation per *Phlebotomus* species.

Species Name	Regularization multiplier	Folds
<i>Ph. papatasi</i>	9	5
<i>Ph. perniciosus</i>	9	3
<i>S. minuta</i>	9	4
<i>Ph. sergenti</i>	9	4
<i>Ph. tobbi</i>	9	2
<i>Ph. mascittii</i>	9	3
<i>Ph. neglectus</i>	7	3
<i>Ph. perfiliewi</i>	7	5
<i>Ph. ariasi</i>	9	2
<i>S. dentata</i>	9	3
<i>Ph. simici</i>	7	3
<i>Ph. alexandri</i>	5	4

Reference

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- Valavi, R., Elith, J., Lahoz-Monfort, J. J., & Guillera-Aroita, G. (2019). blockCV: An r package for generating spatially or environmentally separated folds for k-fold cross-validation of species distribution models. *Methods in Ecology and Evolution*, 10(2), 225–232. <https://doi.org/10.1111/2041-210X.13107>

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