

# Improving species range estimates for an arboreal species group with parapatric distributions

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OBJECTIVES
1. Post-process species distribution models (SDMs) to account for biotic interactions, e.g. competition between parapatric species.
2. Improve range predictions for three parapatric species of <i>Bradypus</i> .
3. Incorporate this tool into the new R package <code>maskRangeR</code> for $n \geq 2$ species.

DATA
<u>Occurrence data:</u> We thinned occurrences <sup>1,2,3,4,5,6</sup> by 40 km to mitigate the effects of spatial autocorrelation: <i>B. variegatus</i> : 886 → 327 thinned <i>B. tridactylus</i> : 182 → 55 thinned <i>B. torquatus</i> : 441 → 48 thinned
<u>Environmental data:</u> 19 bioclimatic variables from WorldClim at 2.5 arcminute resolution

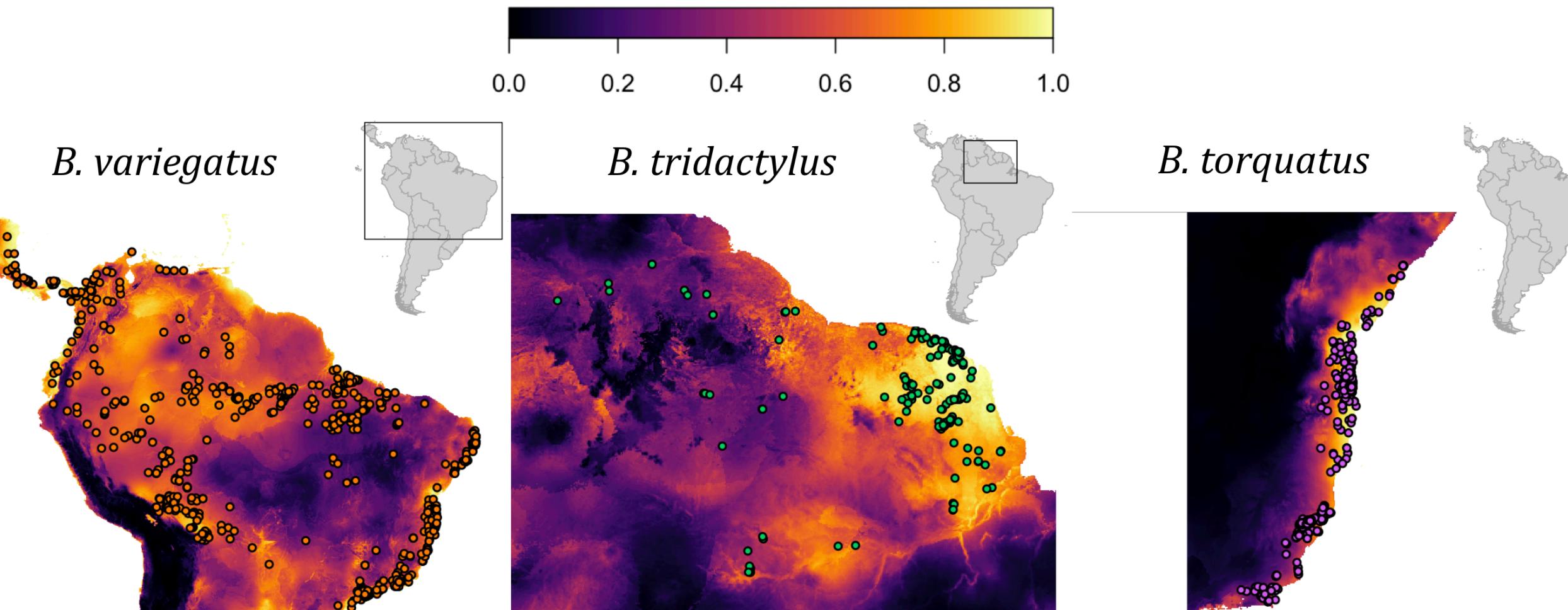
SPECIES DISTRIBUTION MODELING
We used ENMeval <sup>7</sup> to build Maxent <sup>8</sup> models: 4-degree buffered background region Regularization multipliers: 0.5 to 5 (by 0.5) Feature classes: L, Q, H, LQ, LQH Evaluated using cross-validation with a checkerboard partition
We selected models by average 10 percentile omission rate, followed by average test AUC, and finally $\Delta\text{AICc}$ to break ties.
  L 2.0: 11 parameters, 10% OR = 0.10, AUC = 0.68, $\Delta\text{AICc} = 148.69$ LH 3.0: 13 parameters, 10% OR = 0.15, AUC = 0.74, $\Delta\text{AICc} = 14.38$ LQ 5.0: 11 parameters, 10% OR = 0.079, AUC = 0.88, $\Delta\text{AICc} = 30.83$

Figure 1. Species distribution models.

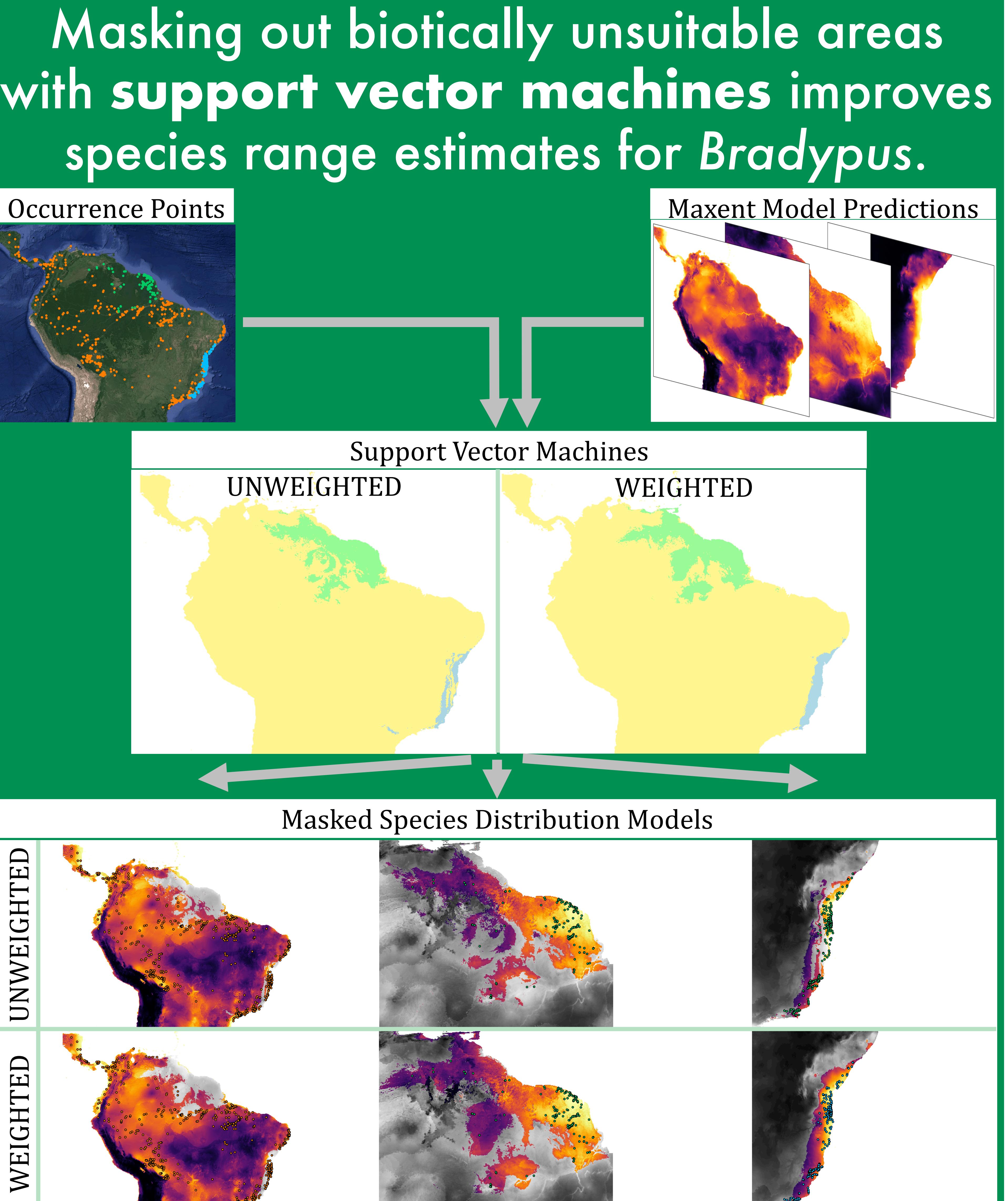


Figure 2. Occurrence points and SDM suitability values are used to train a support vector machine (SVM) classifier. The resulting predictions can be used as masks for removing potentially biotically unsuitable areas from species' ranges.

## SUPPORT VECTOR MACHINES

We used the `maskRangeR` package to implement machine learning classifiers called SVMs to delineate spatial boundaries between ranges.

Unweighted: all occurrence points are weighted equally

Weighted: occurrence points for each species are weighted inversely to the total number of occurrences for the species

## MASKED DISTRIBUTIONS

We used the SVMs to mask out the predicted ranges of the parapatric congeners.

**Table 1.** For each species: omission rates and number of occurrences from parapatric species within the predicted range.

	<i>B. variegatus</i>	<i>B. tridactylus</i>	<i>B. torquatus</i>
UNWEIGHTED	OR = 0.052 4 <i>B. tridactylus</i> , 22 <i>B. torquatus</i>	OR = 0.022 3 <i>B. variegatus</i>	OR = 0.050 43 <i>B. variegatus</i>
WEIGHTED	OR = 0.128 2 <i>B. tridactylus</i> , 6 <i>B. torquatus</i>	OR = 0.011 11 <i>B. variegatus</i>	OR = 0.014 102 <i>B. variegatus</i>

## CONCLUSIONS & FUTURE DIRECTIONS

- Adding biotic information improves range predictions for *Bradypus*.
- Weighted SVMs may improve predictions for undersampled species by decreasing omission rate.
- `maskRangeR` has been submitted to CRAN.  
How has deforestation affected these species?  
Can we model “fuzzy” borders in SVMs?

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Link: [babichmorrowc.github.io/talk/mammalogy\\_2019](http://babichmorrowc.github.io/talk/mammalogy_2019)

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