

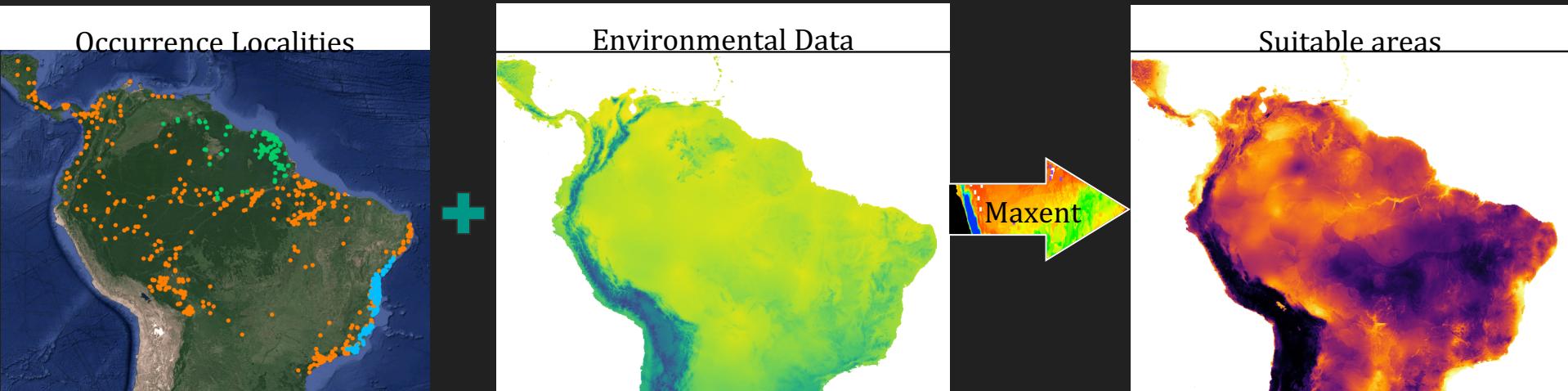


Delineating parapatric ranges using SDMs and SVMs:

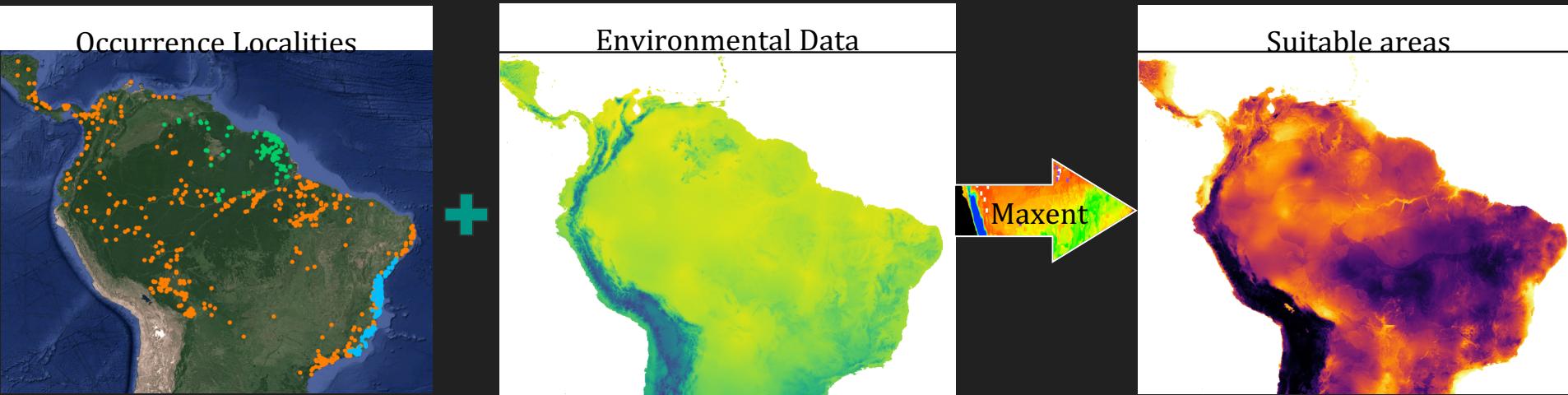
An example with three-toed sloths (*Bradypus*)

Cecina Babich Morrow, Jamie M. Kass, Peter J.
Galante, Robert P. Anderson, Mary E. Blair

Species distribution modeling in Wallace



Species distribution modeling in Wallace



Received: 9 October 2017 | Accepted: 16 November 2017

DOI: 10.1111/2041-210X.12945

APPLICATION

WALLACE: A flexible platform for reproducible modeling of species niches and distributions built for community expansion

Methods in Ecology and Evolution
BRITISH ECOLOGICAL SOCIETY

Jamie M. Kass^{1,2} | Bruno Vilela³ | Matthew E. Aiello-Lammens⁴ |
Robert Muscarella⁵ | Cory Merow⁶ | Robert P. Anderson^{1,2,7}

- Open source SDM software platform in R with Shiny
- Makes modeling techniques available to non-coders
- Reproducible and modular

Species distribution modeling in Wallace

Wallace v1.9.9.0

Intro

Occ Data

Env Data

Process Occs

Process Envs

Env Space

Partition Occs

Model

Visualize

Project

Post-Data(**)

Post-processing

Session Code

Obtain Occurrence Data

Modules Available:

- Query Database (Present)
- Query Database (Paleo)
- User-specified

Module: Query Database (Present)

spocc : Interface to Species Occurrence Data Sources

Choose Database

- GBIF
- VertNet
- BISON
- BIEN

Enter species scientific name

meles meles, martes martes

Set maximum number of occurrences

100

Query Database

Module Developers: Jamie M. Kass, Bruno Vilela, Gonzalo E. Pinilla-Buitrago, Hannah Owens, Cory Merow, Robert P. Anderson

spocc references

Package Developers: Scott Chamberlain, Karthik Ram, Ted Hart, rOpenSci

Current species

WELCOME TO WALLACE

Please find messages for the user in this log window.

Map

Table

Results

Component Guidance

Module Guidance

Download



<https://wallaceecomod.github.io>

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Wallace v1.9.9.0

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<https://wallaceecomod.github.io>

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Distribution modeling for parapatric species

Can adding biotic information improve range model predictions for parapatric species?

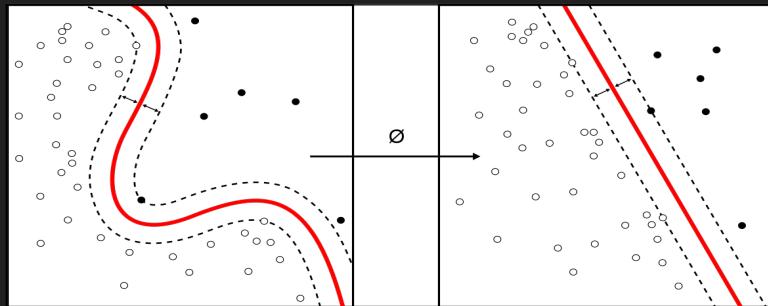


Distribution modeling for parapatric species

Can adding biotic information improve range model predictions for parapatric species?

How can we post-process species distribution models (SDMs) to account for competition?

Support vector machines (SVMs) to delineate ranges
maskRangeR package → extend this method to ≥ 2 species



Support vector machine (SVM)

Three-toed sloths: Genus *Bradypus*



Bradypus variegatus



Bradypus tridactylus



Bradypus torquatus



Bradypus variegatus

Most widespread species

Often mistaken for *B. tridactylus*

High phenotypic diversity



Bradypus tridactylus

Parapatric with *B. variegatus*

Possibility of hybrids with
B. variegatus near Manaus
(Corrêa 2015)



Bradypus torquatus

Parapatric/sympatric with
B. variegatus

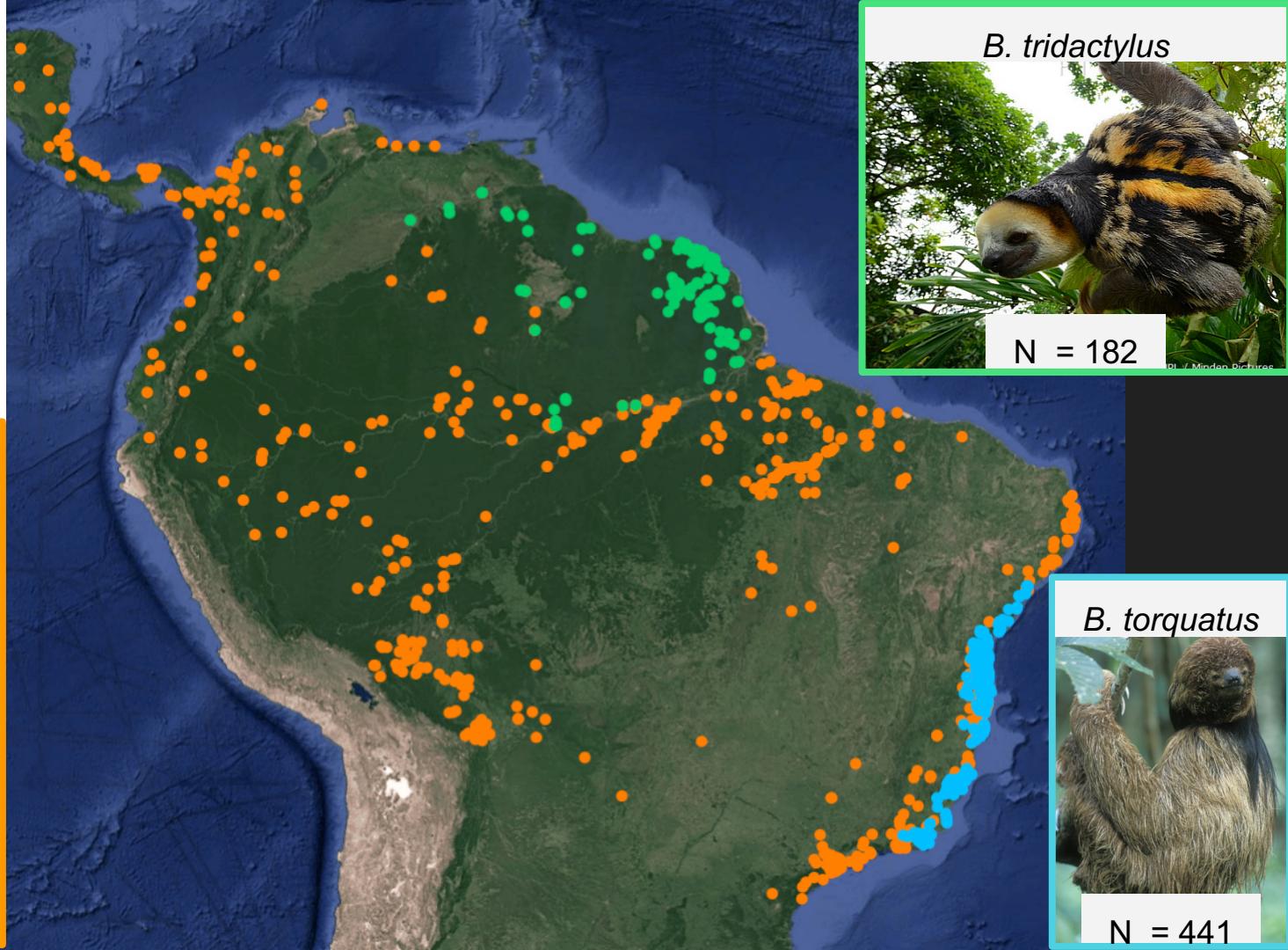
Distributional gaps with
strong genetic
differentiation



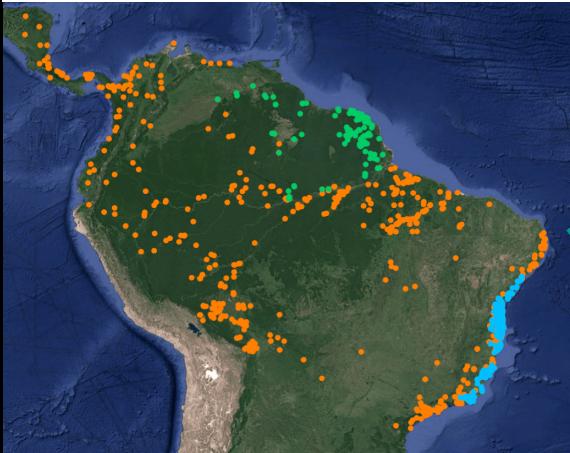
Database of Neotropical Xenarthrans (Santos et al. 2019) + other literature occurrences

(Anderson and Handley 2001; de Moraes-Barros et al. 2007, 2011;
Moreira et al. 2014; Silva et al. 2018)

B. variegatus

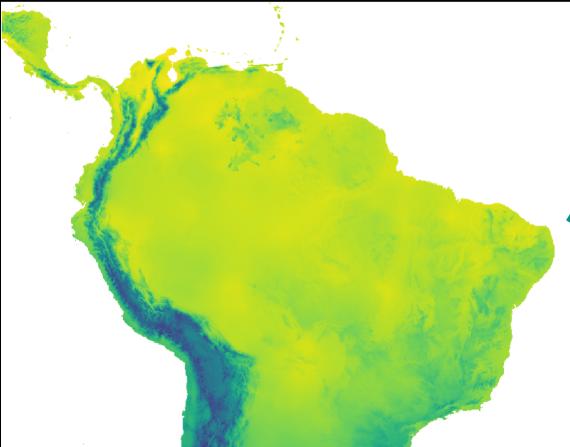


Occurrence Localities



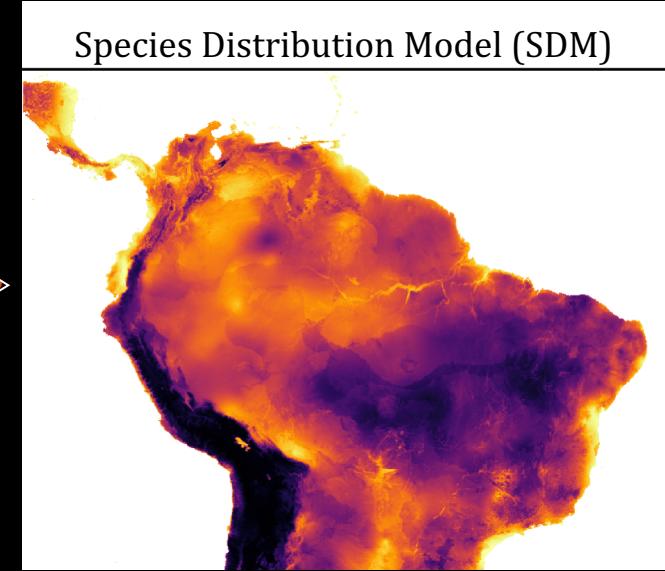
Building Species Distribution Models

Environmental Data



Maxent

Species Distribution Model (SDM)



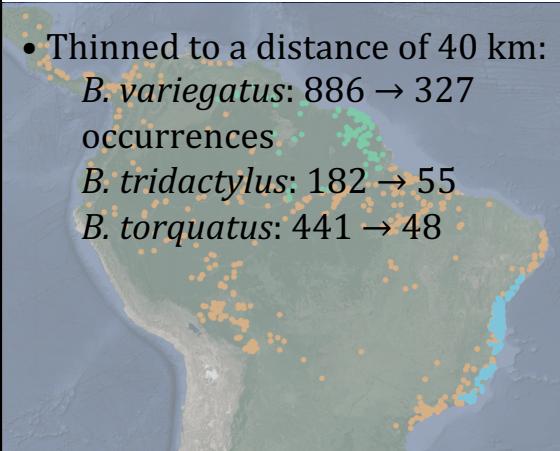
Occurrence Localities

- Thinned to a distance of 40 km:

B. variegatus: 886 → 327 occurrences

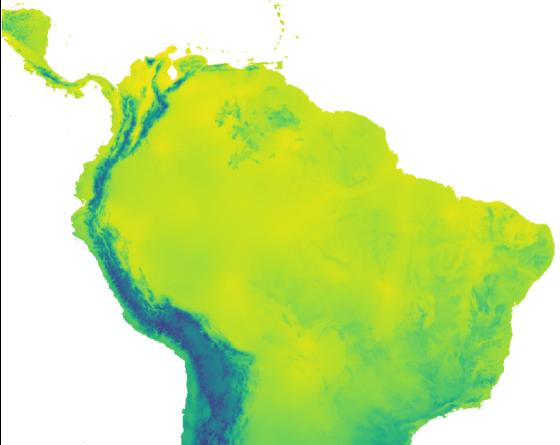
B. tridactylus: 182 → 55

B. torquatus: 441 → 48



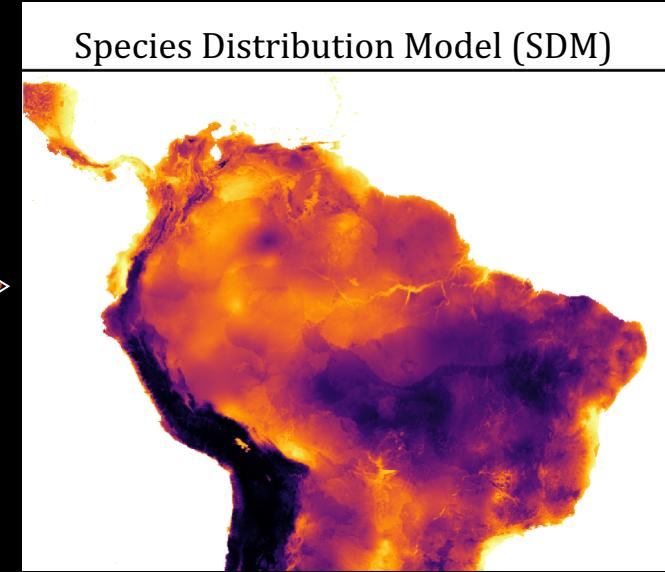
Building Species Distribution Models

Environmental Data



Maxent

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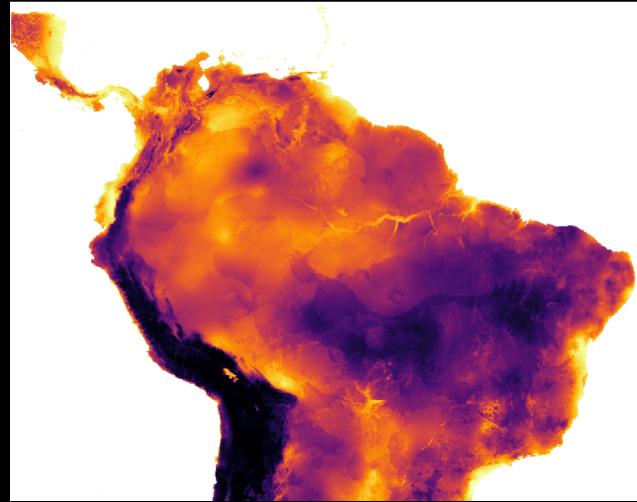
Building Species Distribution Models

Environmental Data

- 19 bioclimatic variables from WorldClim
- 2.5 arcminute resolution
- Background region of 4 degrees

Maxent

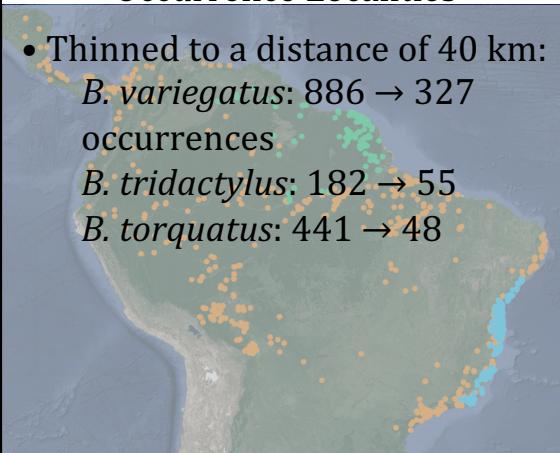
Species Distribution Model (SDM)



Building Species Distribution Models

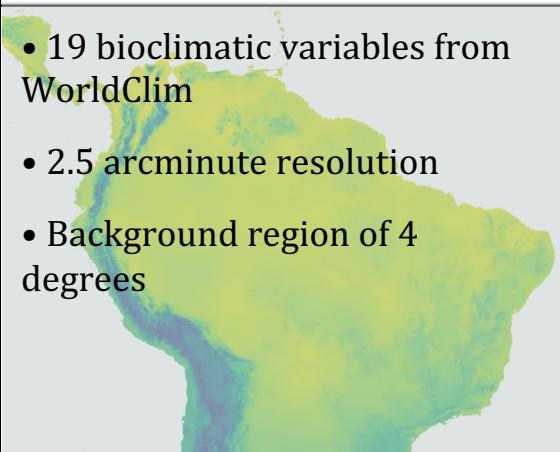
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Environmental Data

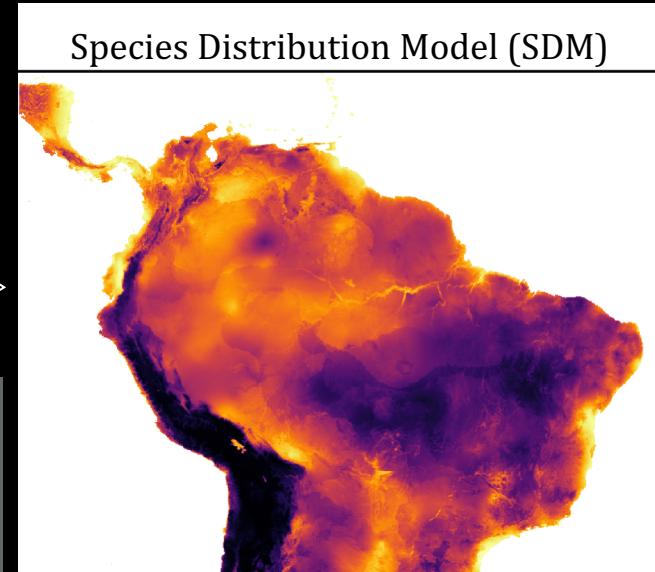
- 19 bioclimatic variables from WorldClim
- 2.5 arcminute resolution
- Background region of 4 degrees



Maxent

- Checkerboard partition
- Regularization multipliers: 0.5 to 5
- Feature classes: linear, quadratic, hinge, linear + quadratic, linear + quadratic + hinge

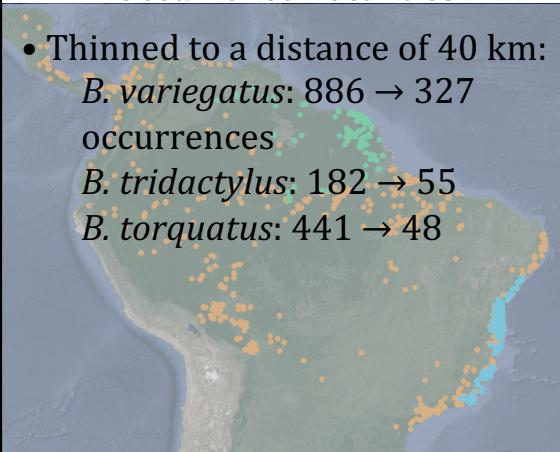
Species Distribution Model (SDM)



Building Species Distribution Models

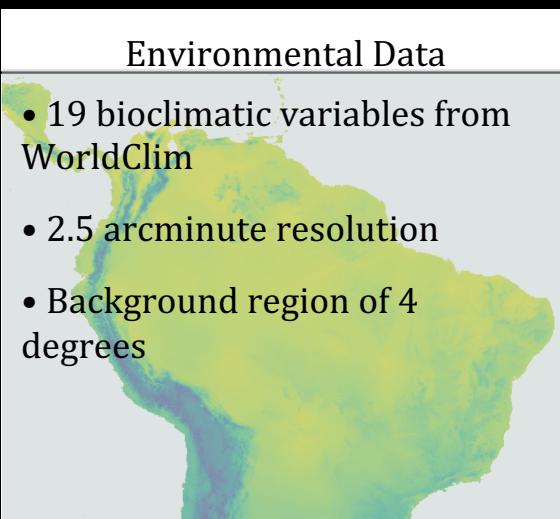
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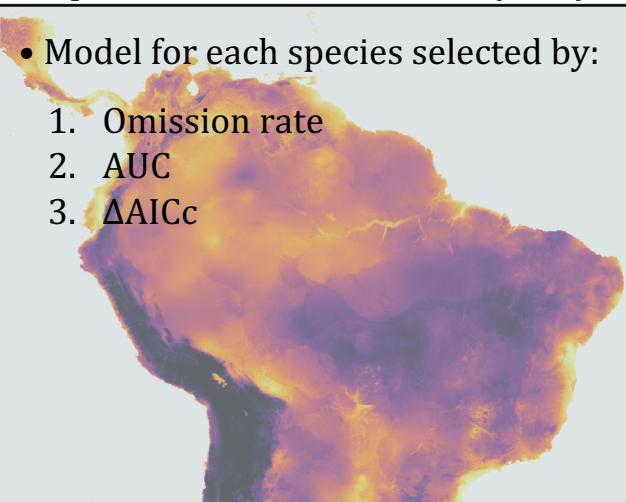


Maxent

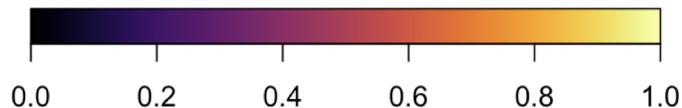
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Species Distribution Model (SDM)

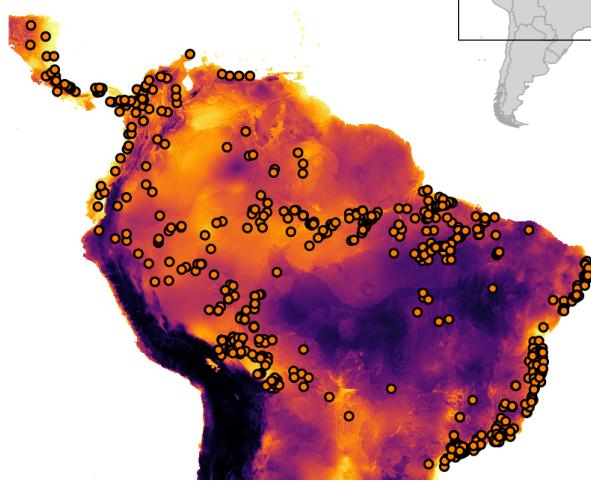
- Model for each species selected by:
 1. Omission rate
 2. AUC
 3. ΔAICc



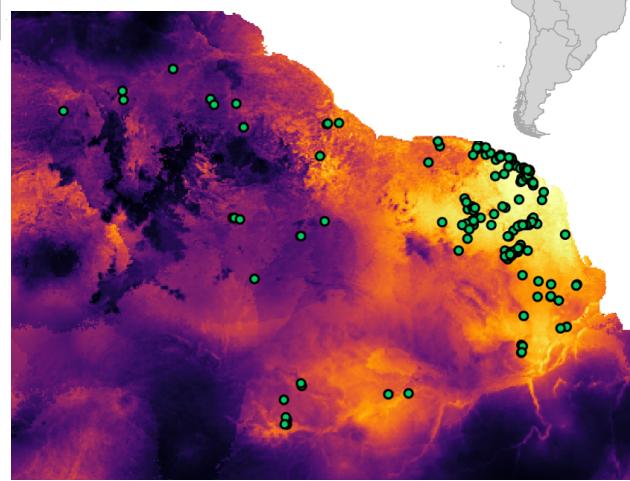
Species Distribution Models (SDMs)



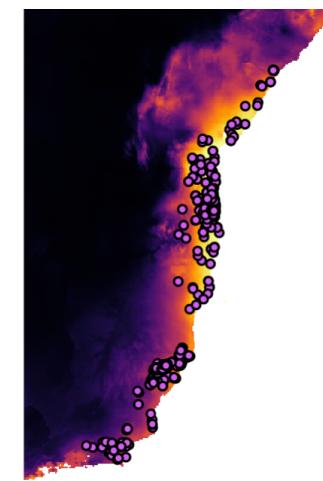
B. variegatus



B. tridactylus



B. torquatus



L 2.0: 11 parameters, 10% OR = 0.10,
AUC = 0.68, ΔAICc = 148.69

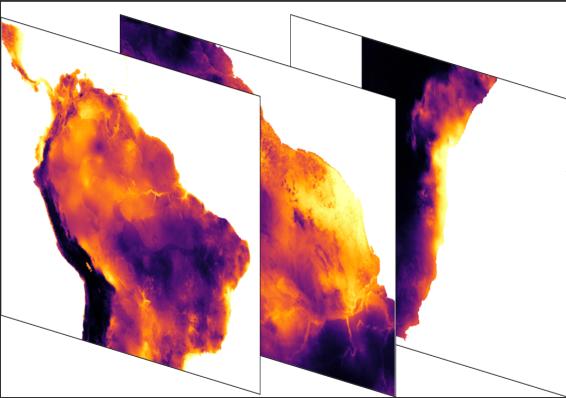
LH 3.0: 13 parameters, 10% OR =
0.15, AUC = 0.74, ΔAICc = 14.38

LQ 5.0: 11 parameters, 10% OR =
0.079, AUC = 0.88, ΔAICc = 30.83

Occurrence Localities



SDMs for 3 Species

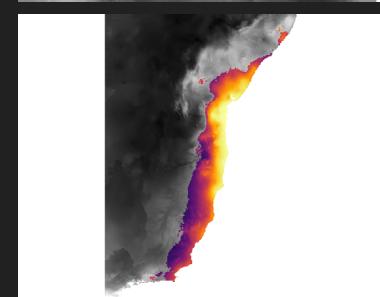
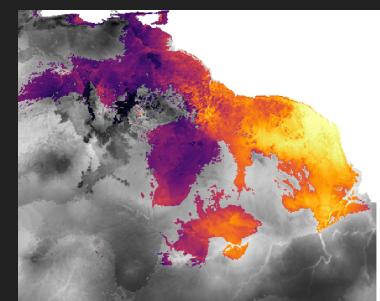


Masking with Support Vector Machines

Support Vector Machine (SVM)



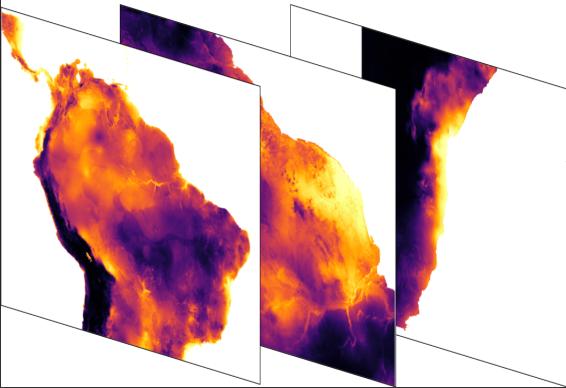
Masked SDMs



Occurrence Localities



SDMs for 3 Species

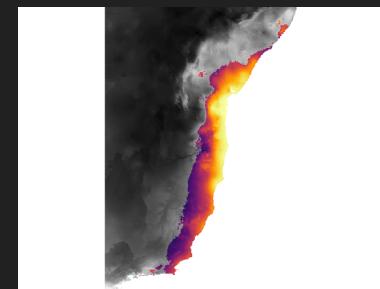
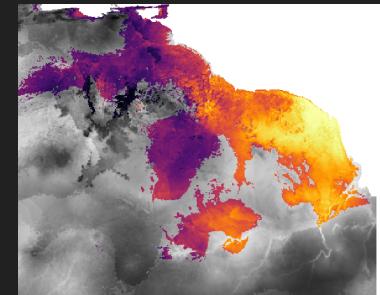


Masking with Support Vector Machines

Support Vector Machine (SVM)

- Spatial vs. spatial + environmental
- Weighted vs. unweighted

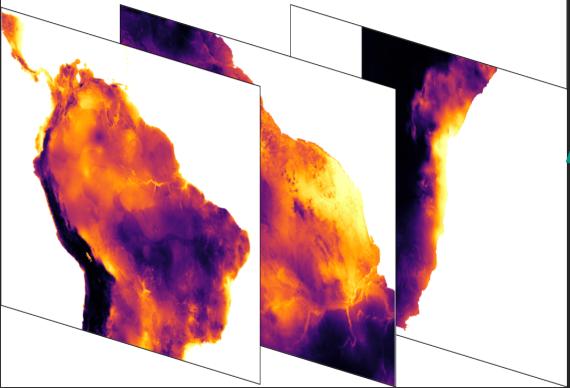
Masked SDMs



Occurrence Localities



SDMs for 3 Species

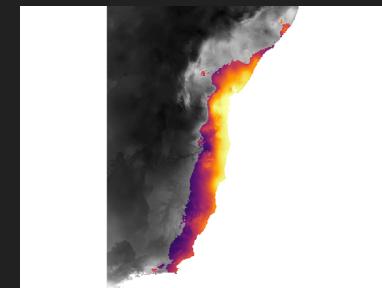
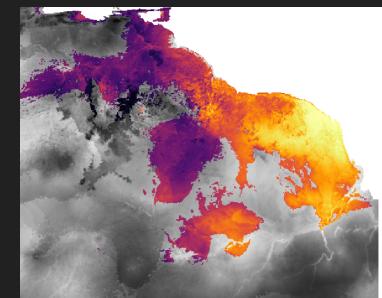
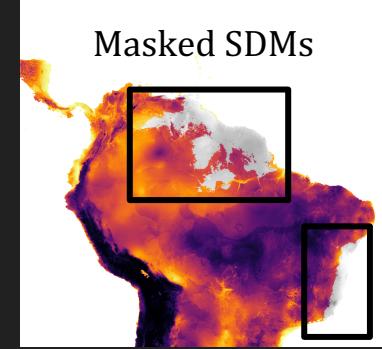


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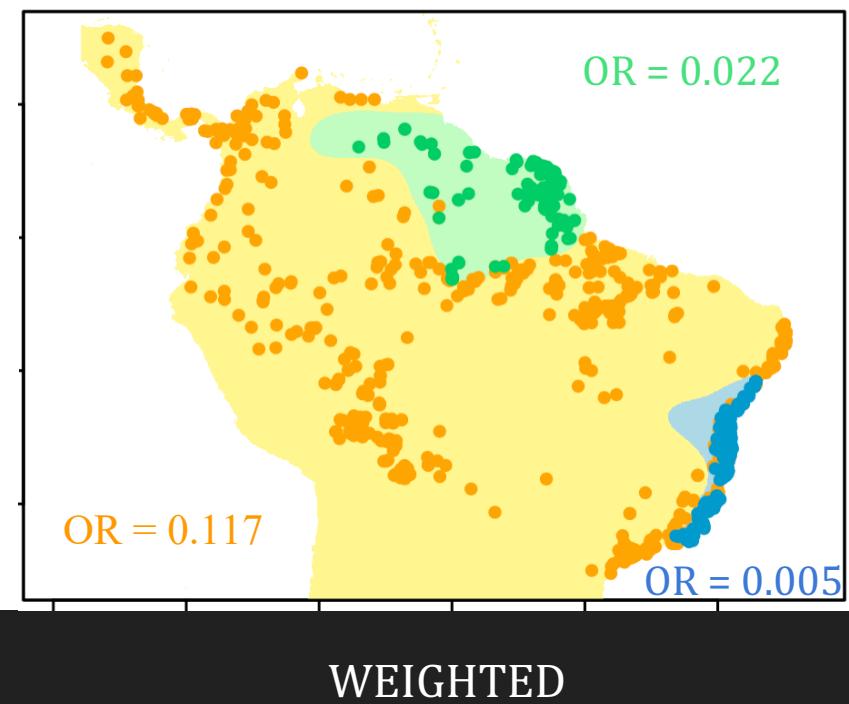
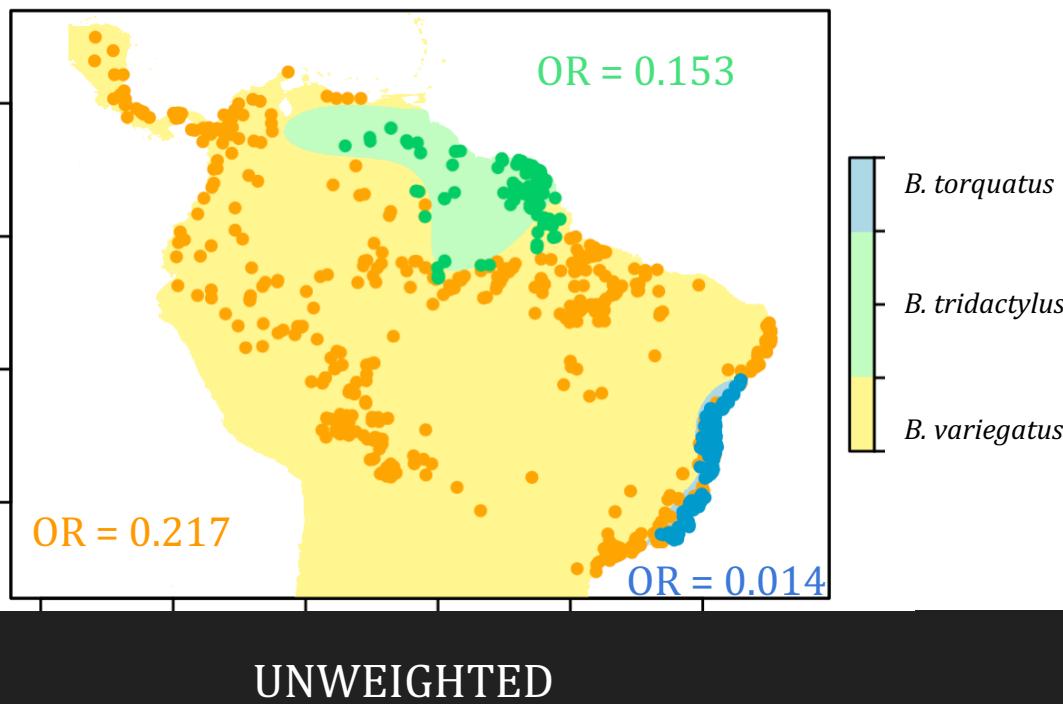
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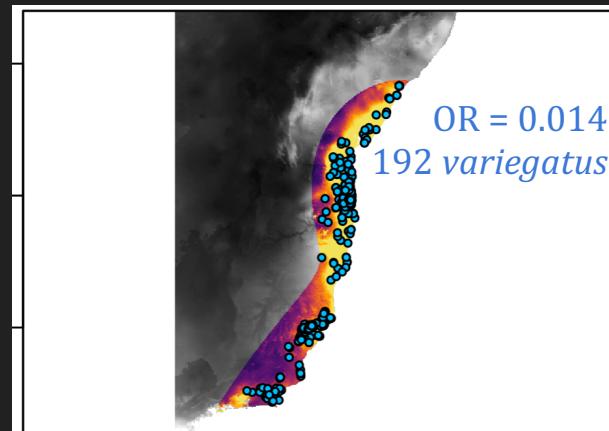
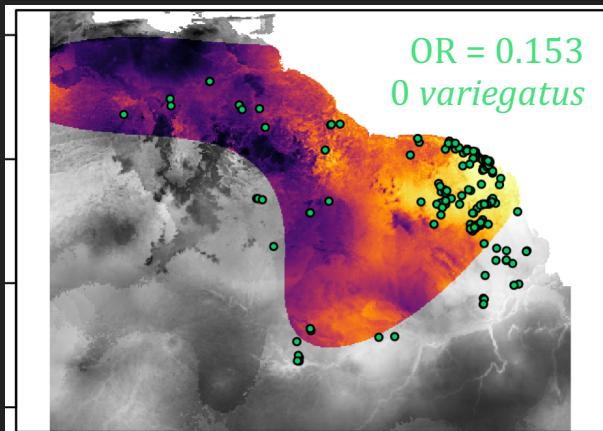
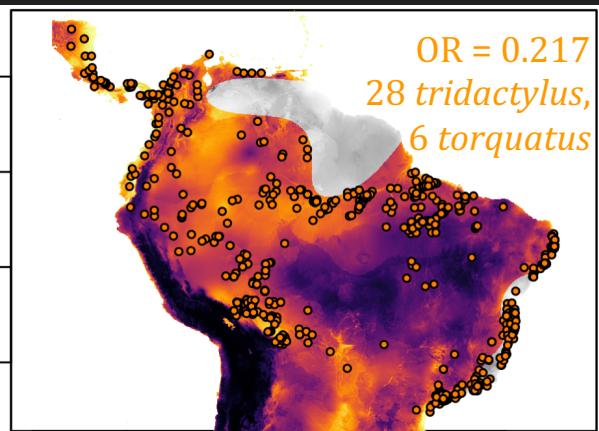
Masked SDMs



Spatial Only SVMs



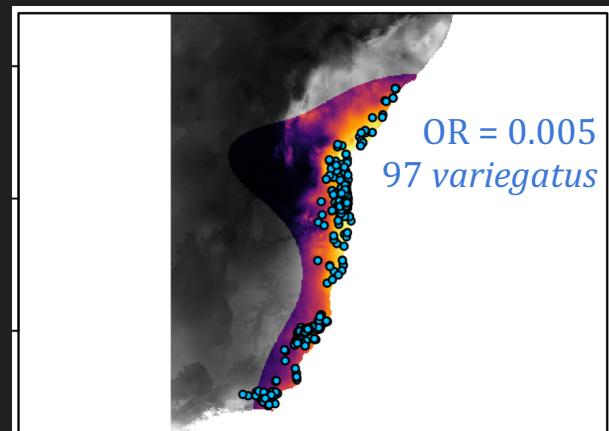
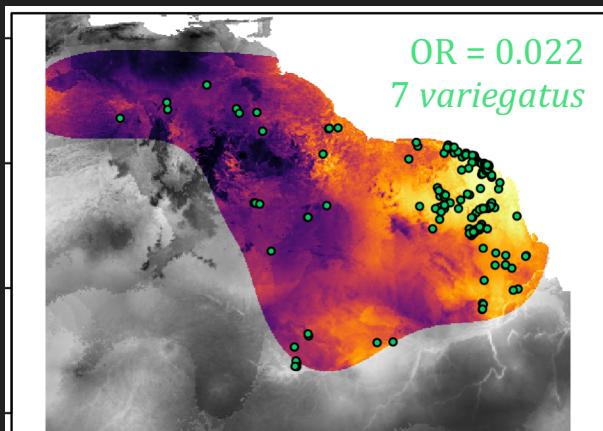
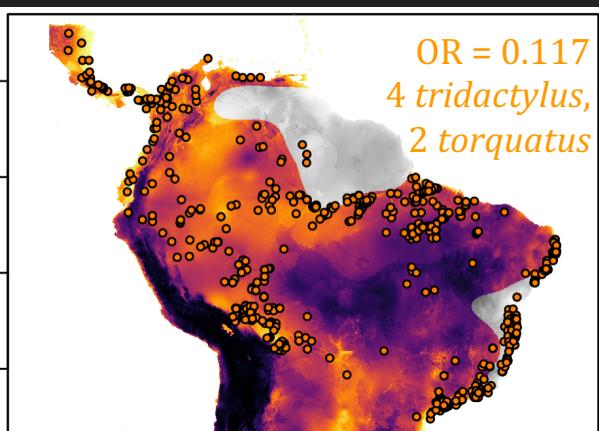
UNWEIGHTED



Bradypus variegatus

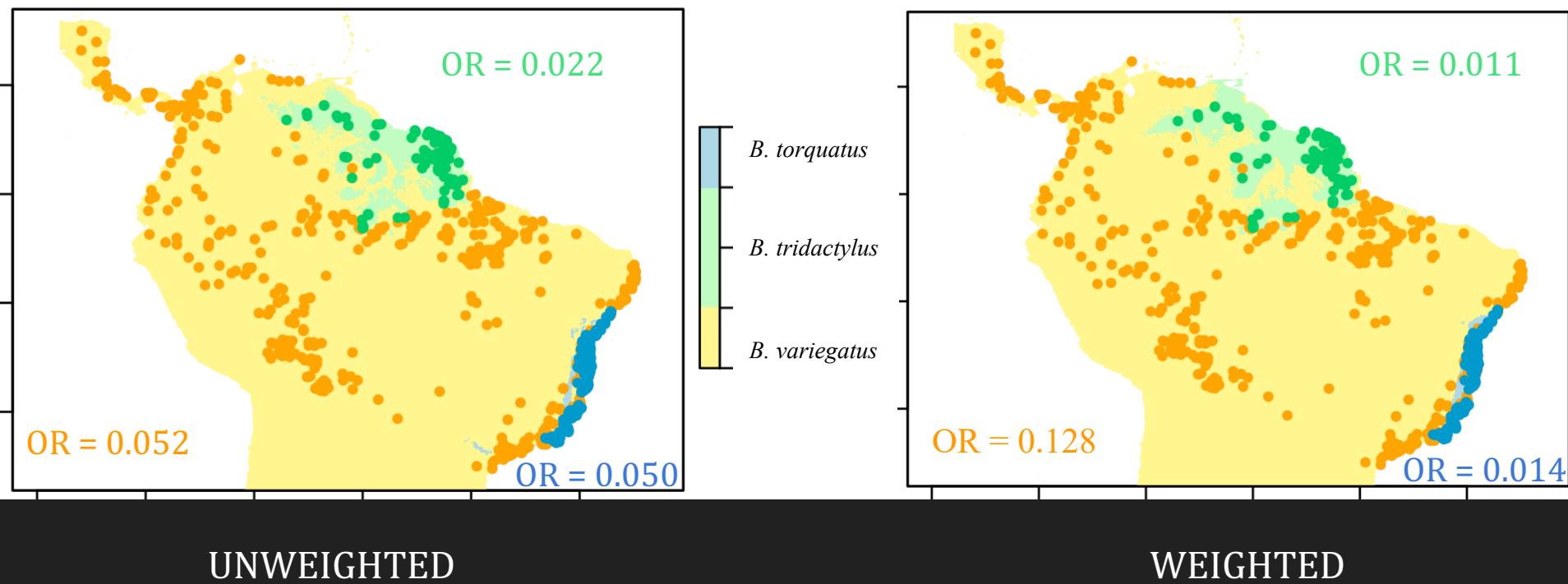
Bradypus tridactylus

Bradypus torquatus

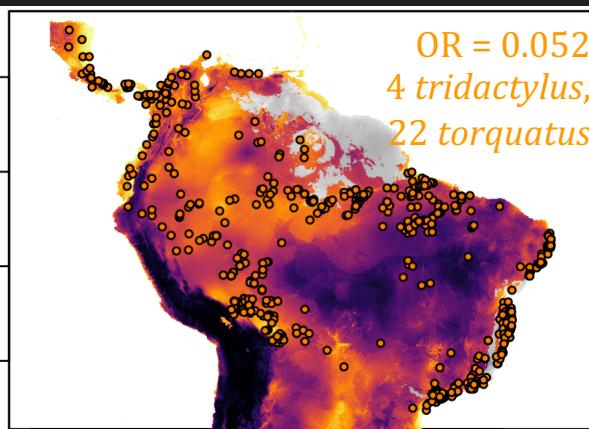


WEIGHTED

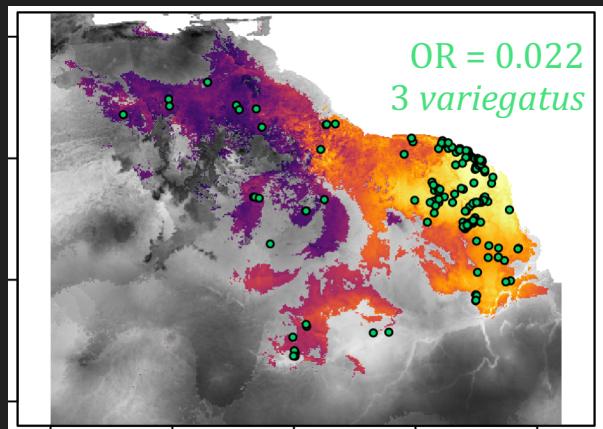
Spatial + Environmental SVMs



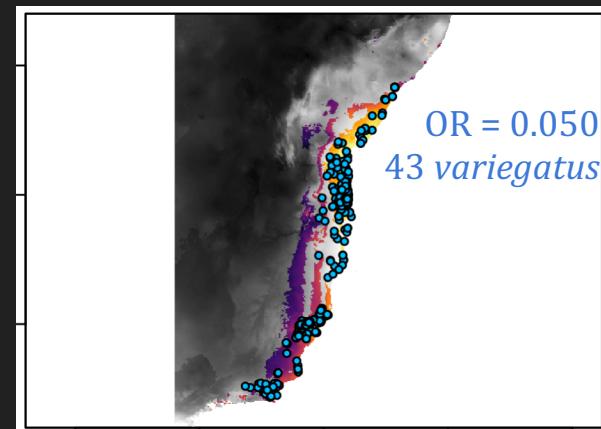
UNWEIGHTED



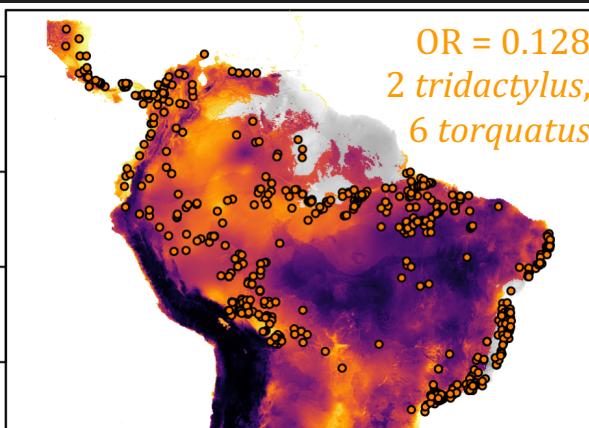
Bradypus variegatus



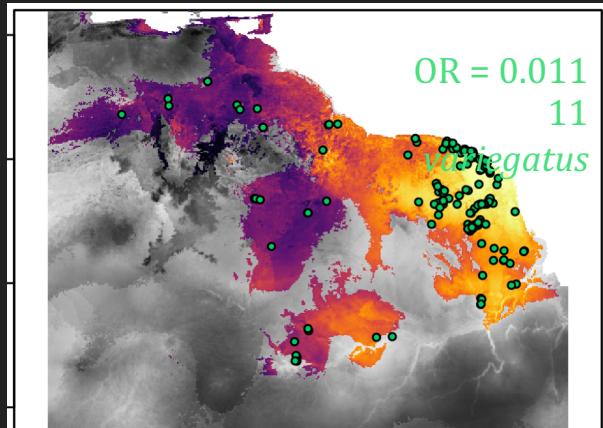
Bradypus tridactylus



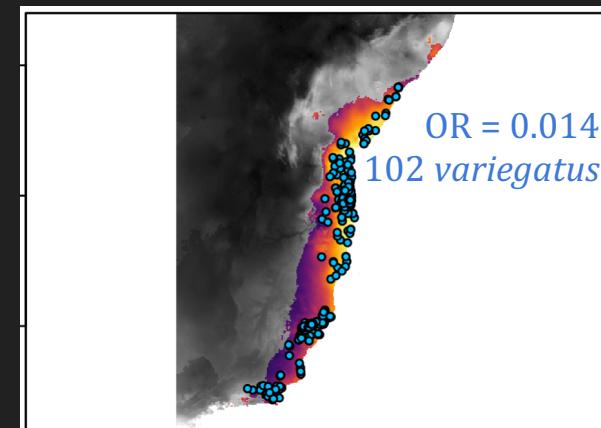
Bradypus torquatus



Bradypus variegatus



Bradypus tridactylus



WEIGHTED

Conclusions

Adding biotic information about the presence of congeneric species improves model predictions for *Bradypus*.

Spatial + Environmental SVMs better account for overlap zones between species and have ecologically relevant boundaries.

Weighting may improve predictions for undersampled species.

Next Steps

- Full incorporation of maskRangeR into Wallace
- Modeling of separate populations separately
- Forest cover masking
- Forest cover change “velocity”
 - Examining differential changes in forest cover across space and time
- “Fuzzy” boundaries to SVMs



Acknowledgments



- Gonzalo E. Pinilla-Buitrago & Valentina Grisales-Betancur at City College
- The BridgeUP:STEM team: Louise Crowley, Gabrielle Rabinowitz, Stephanie Lopez, & Yvonne De La Peña
- Camera Ford, Katy Abbott, Madelyne Xiao, and Colleen Cleary
- My Brown Scholar interns

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