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

Jamie M. Kass, Bruno Vilela, Matthew E. Aiello-Lammens, Robert Muscarella, Cory Merow & Robert P. Anderson ...

... and Jenna Rios, Sara Varela, Hannah L., Owens, Brian S. Maintner, Olivier Broennimann, Mary E. Blair, Ned Horning, Jorge Velásquez-Tibatá, Gonzalo E. Pinilla-Buitrago, Beth E. Gerstner, Peter J. Galante, Sarah I. Meenan, Valentina Grisales-Betancur, Cecina Babich-Morrow, Erica E. Johnson ...















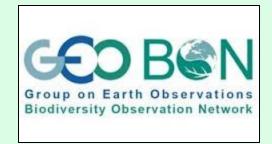
and many collaborating institutions!

Range estimates needed









Applied biodiversity informatics

Anderson (2012)

ANNALS OF THE NEW YORK ACADEMY OF SCIENCES

Issue: Blavatnik Awards for Young Scientists

Harnessing the world's biodiversity data: promise and peril in ecological niche modeling of species distributions

Robert P. Anderson^{1,2,3,4}

Agenda: Making data and modeling ready to address critical environmental issues of the 21st century

Agenda: applied biodiversity informatics

ANNALS OF THE NEW YORK ACADEMY OF SCIENCES

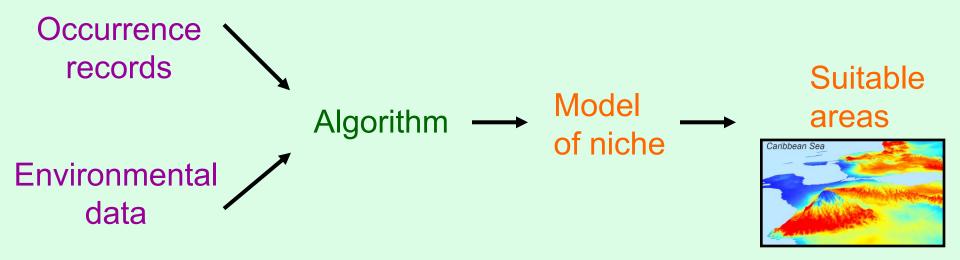
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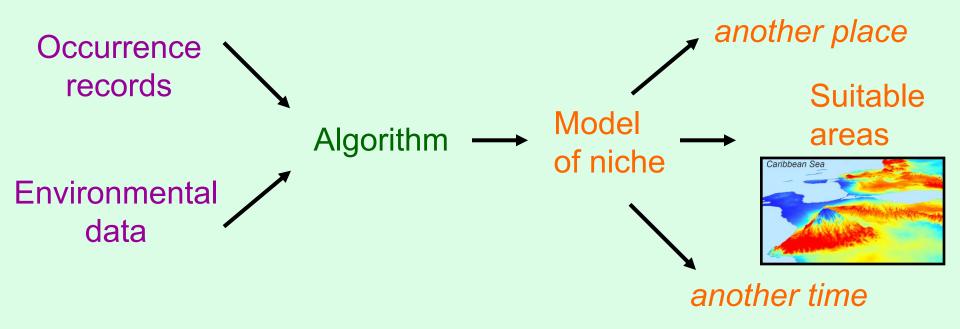
Robert P. Anderson^{1,2,3,4}

- 1. High-quality data, ready to be accessed when the particular problem presents itself
- 2. Software that achieves an appropriate balance between automation and supervision
- 3. Scientists capable of building, applying, and appraising high-quality models

Correlative modeling of species niches and ranges



Correlative modeling of species niches and ranges



Conservation, invasive species, zoonotic diseases, climate change



Anderson (2015)

Biogeografía 8

LEAD ARTICLE

EL MODELADO DE NICHOS Y DISTRIBUCIONES: NO ES SIMPLEMENTE "CLIC, CLIC, CLIC"

Robert P. Anderson

Biogeografía 8

MODELING NICHES AND DISTRIBUTIONS: IT'S NOT JUST "CLICK, CLICK, CLICK"

Robert P. Anderson

Biogeografía 8

LA MODÉLISATION DE NICHE ET DE DISTRIBUTIONS:

CE N'EST PAS JUSTE "CLIC, CLIC, CLIC"

Robert P. Anderson

Agenda: applied biodiversity informatics

Anderson (2012)

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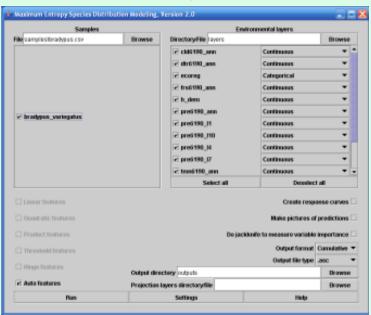
Robert P. Anderson 1,2,3,4

Software that achieves an appropriate balance between automation and supervision

- automates repetitive aspects
- forces user to make critical biological and conceptual decisions
- general with respect to algorithms used

Problems with existing analyses

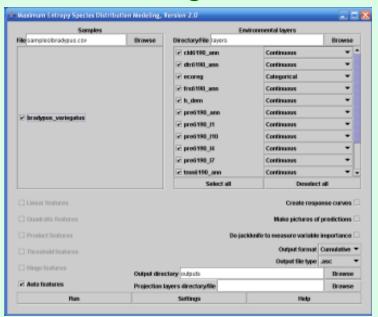
Existing GUIs



- (too) easy
- default settings
- inflexible
- infrequently updated
- strings of applications

Problems with existing analyses

Existing GUIs



- (too) easy
- default settings
- inflexible
- infrequently updated
- strings of applications

Code

- error-prone
- not easily generalizable
- slow to be taken up

From R to a web app



Innovative use of GBIF occurrence data

Wallace (beta v0.1):
Harnessing Digital
Biodiversity Data for
Predictive Modeling,
Fueled by R

This team has created a GUI interface for R packages related to biodiversity informatics and predictive modeling.

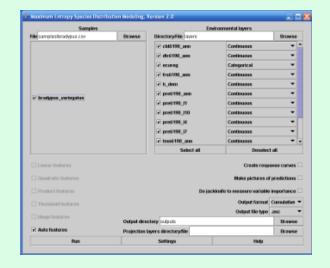




Combine code-based methods with GUI

Foreground:

Flexible, interactive, expandable GUI



Background:

R code from new packages: reproducible

APPLICATION



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

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





















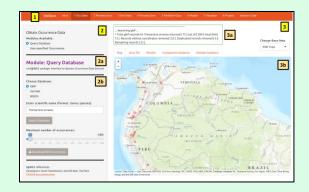
Wallace: currently under expansion ...

Jamie M. Kass, Bruno Vilela, Matthew E. Aiello-Lammens, Robert Muscarella, Cory Merow & Robert P. Anderson

... and Jenna Rios, Sara Varela, Hannah L., Owens, Brian S. Maintner, Olivier Broennimann, Mary E. Blair, Ned Horning, Jorge Velásquez-Tibatá, Gonzalo E. Pinilla-Buitrago, Beth E. Gerstner, Peter J. Galante, Sarah I. Meenan, Valentina Grisales-Betancur, Cecina Babich-Morrow, Erica E. Johnson ...



What is Wallace?



Point-and-click (GUI) application that includes most steps of a niche/distribution modeling workflow

Harnesses R packages and gives credit to their authors

R packages on the inside



Ecography 38: 001–005, 2015 doi: 10.1111/ecog.01132

© 2015 The Authors. Ecography © 2015 Nordic Society Oikos Subject Editor: Thiago Rangel. Editor-in-Chief: Miguel Araújo. Accepted 18 November 2014

spThin: an R package for spatial thinning of species occurrence records for use in ecological niche models

Matt Robe

and D Dept of North

Methods in Ecology and Evolution



doi: 10.1111/2041-210X.12261

APPLICATION

ENMeval: An R package for conducting spatially independent evaluations and estimating optimal model complexity for MAXENT ecological niche models

Robert Muscarella^{1*}, Peter J. Galante², Mariano Soley-Guardia^{2,3}, Robert A. Boria², Jamie M. Kass^{2,3}, María Uriarte¹ and Robert P. Anderson^{2,3,4}

¹Department of Ecology, Evolution and Environmental Biology, Columbia University, 1200 Amsterdam Ave., New York, NY 10027, USA; ²Department of Biology, City College of the City University of New York, 160 Convent Ave., New York, NY 10031, USA; ³Graduate Center of the City University of New York, 365 5th Ave., New York, NY 10016, USA; and ⁴Division of Vertebrate Zoology (Mammalogy), American Museum of Natural History, Central Park West & 79th Street, New York, NY 10024, USA

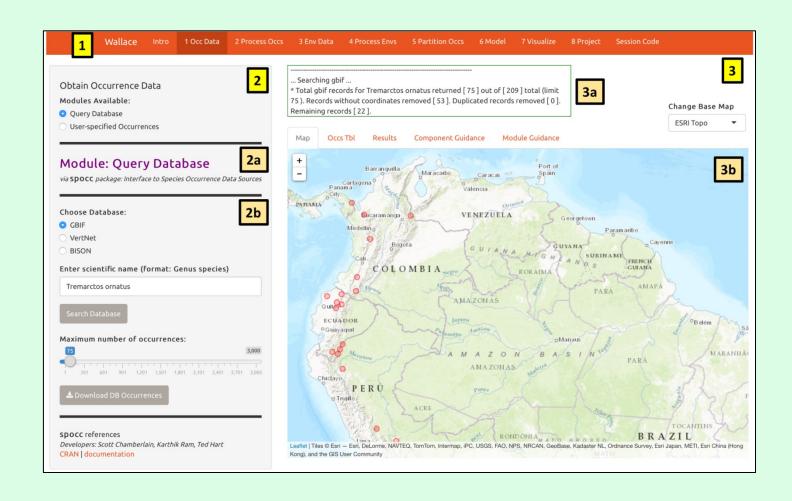






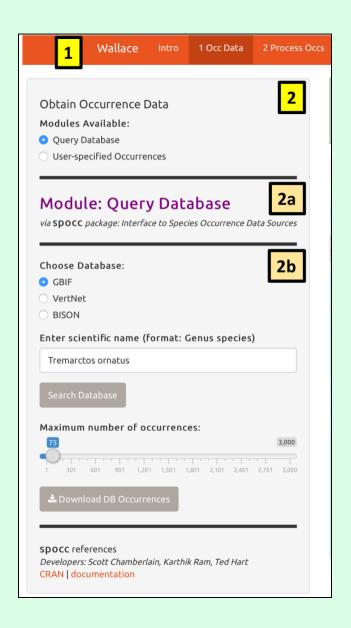


Wallace



Wallace's code is free and **OPEN**

(& users can download data from online databases.)



Wallace provides GUIDANCE

that addresses conceptual and methodological issues.

 Map
 Occs Tbl
 Results
 Component Guidance
 Module Guidance

Module: Query Database

BACKGROUND

Over the past two decades, the worldwide biodiversity informatics community has achie available online through various databases—including a substantial subset of records wit Peterson et al. 2015). These data document the presence of a species at particular point institution, specimen/observation number, elevation, etc.). The origin of much of this infalthough newer data sources such as citizen-science initiatives are growing contributors

IMPLEMENTATION

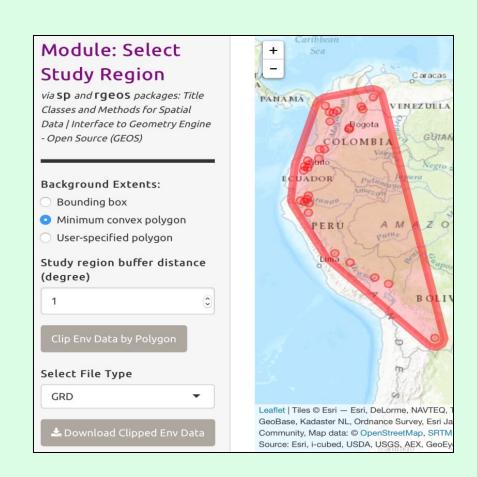
The R package spoce provides streamlined access to many species occurrence databas **Database** users can choose between three of the largest databases: GBIF, VertNet, and any later download overwrites previous ones. The resulting table includes several key figure georeferences. The table displays all such records (and allows their download), but record downstream components of *Wallace*. Users can download a .csv file with all the original

REFERENCES

Peterson, A. T., Soberón, J., & Krishtalka, L. (2015). A global perspective on decadal chall

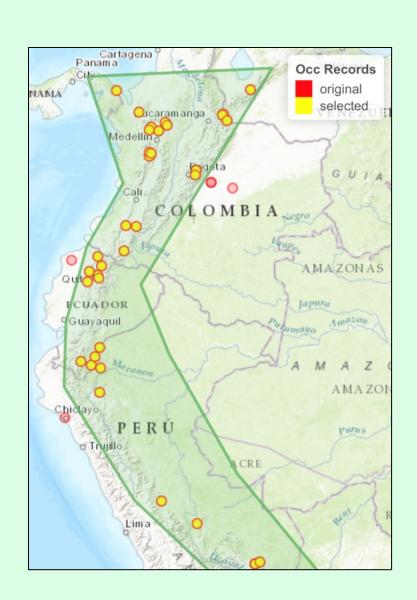
Wallace is **FLEXIBLE**

by providing multiple options, and allowing user inputs and downloads for most components.



Wallace features INTERACTIVE

maps, tables, and graphs to explore data and model predictions.



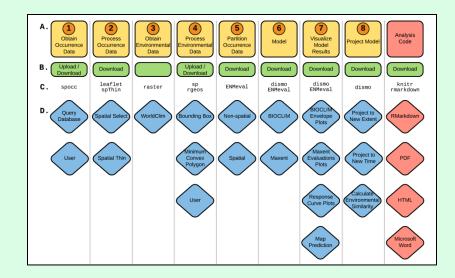
Wallace is **REPRODUCIBLE**

by providing executable code for documenting and rerunning the analysis.

```
Please find below the R code history from your *Wallace* session. You can reproduce your session
    file in RStudio (for more information see <a href="http://rmarkdown.rstudio.com">http://rmarkdown.rstudio.com</a>).
    ### Package installation
    Wallace uses the following R packages that must be installed and loaded before starting.
    library(devtools)
    library(spocc)
    library(maptools)
    library(spThin)
    library(dismo)
    library(rgeos)
    library(repmis)
    library(ENMeval)
    Wallace also includes several functions developed to help integrate different packages and some a
    this reason, it is necessary to load the file 'functions.R', which can be found on Wallace's GitHi
    (<a href="https://github.com/wallaceEcoMod/wallace">https://github.com/wallaceEcoMod/wallace</a>). Download the file, place it in your working director
    and then load it:
    source(file.path("/Users/musasabi/Documents/github/wallace", 'functions.R'))
    Record of analysis for *Tremarctos ornatus*.
    ### Obtain Occurrence Data
    The search for occurrences was limited to 81 records. Obtain occurrence records of the selected s
    results <- occ(query = "Tremarctos ornatus", from = "gbif", limit = 81, has_coords = TRUE)
    results.data <- results[["gbif"]]$data[[formatSpName("Tremarctos ornatus")]]</pre>
    occs <- remDups(results.data) # remove rows with duplicate coordinates
B8 - ### Process Occurrence Data
    You chose 42 of 51 total occurrence localities via polygon selection to keep in the analysis.
    occs <- occs[c(1, 2, 3, 5, 6, 8, 9, 10, 11, 12, 13, 14, 15, 16, 17, 18, 20, 21, 22, 24, 25, 26, 2
    40, 41, 42, 43, 44, 45, 46, 47, 48, 49, 50, 51), ] # subset occs by selected rows
```

Wallace is EXPANDABLE!

by featuring different methodological options (modules) that researchers can contribute to advance functionality.



Wallace: software for niche/distribution modeling

Qualities:

open
instructive
flexible
interactive
reproducible
expandable
broadening
human diversity

Female and minority-student coder-biologists



External partners, undergraduates, and interns/fellows:

Sara Varela, Hannah L. Owens, Cecina Babich-Morrow, Jenna Rios, Sarah I. Meenan, Valentina Grisales-Betancur

Installing Wallace

- Install R and (optionally) Rstudio
- For Maxent java version, install maxent.jar
 (https://biodiversityinformatics.amnh.org/open_sourc
 e/maxent/ and appropriate Java version for your
 system, then place maxent.jar in dismo folder
- Install the wallace package from CRAN

```
# install the package
install.packages('wallace')
# load the package
library(wallace)
# run the app
run_wallace()
```

 Troubleshooting on Github page (https://github.com/wallaceEcoMod/wallace)

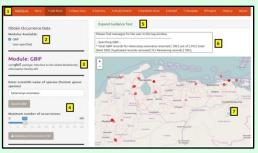
Wallace today

- 1. Full Release 1.0.6 (Kass et al. 2018, Methods in Ecology & Evolution software note; Google group; Wallace e-mail)
- 2. Ongoing NSF funding to work with external partners to add new modules

3. Ongoing NASA funding, led by Mary Blair (AMNH), to develop new R packages and add them to Wallace and interface with BioModelos



Mary E. Blair



NSF DEB-1119915 & DBI-1650241



NSF DBI-1661510



NASA 80NSSC18K0406

Acknowledgments



https://wallaceecomod.github.io/

http://www.andersonlab.ccny.cuny.edu























Anderson lab (chronosequence)







