ISSN: 1938-7024

American Museum of Natural History

Center for Biodiversity and Conservation
Network of Conservation Educators and Practitioners

LESSONS IN CONSERVATION

VOLUME 13
DECEMBER 2023

Monitoring and Modeling

American Museum of Natural History

Center for Biodiversity and Conservation
Network of Conservation Educators and Practitioners

Lessons in Conservation is the official journal of the Network of Conservation Educators and Practitioners (NCEP)—a collaborative project of the Center for Biodiversity and Conservation (CBC) at the American Museum of Natural History—and is published as issues become available. Teaching and learning modules presented here in ***Lessons in Conservation*** are available in modifiable form for teachers on the NCEP website (ncep.amnh.org). All materials are distributed free of charge. Any opinions, findings, and conclusions, or recommendations expressed in this material are those of the authors and do not necessarily reflect the views of the American Museum of Natural History or the funders of this project. All components of a module (e.g., Syntheses, Exercises, and Case Studies) have been peer-reviewed and approved for publication by NCEP.

Editorial team:

Suzanne K. Macey
CBC Assistant Director for Capacity Development

Nadav Gazit
CBC Visual Creative and Senior Research Assistant

Kristin E. Douglas
CBC Outreach and Production Coordinator

Ana L. Porzecanski
CBC Director

Lessons in Conservation
is available online at:
ncep.amnh.org/linc

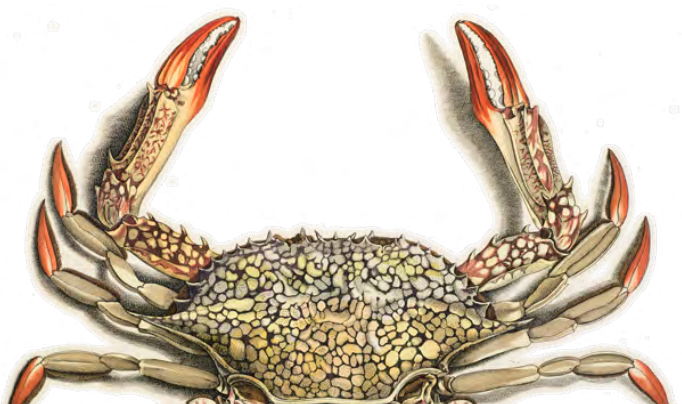
All reproduction or distribution must provide full citation of the original work and provide a copyright notice as follows:

"Copyright 2023, by the authors of the material and the Center for Biodiversity and Conservation of the American Museum of Natural History. All rights reserved."

Cover photo: "Ant" (common black ant, *Lasius sp.*)
Credit: Guy Streatfeild

Journal illustrations obtained from the American Museum of Natural History's library: images.library.amnh.org/digital/

And the Biodiversity Heritage Library:
www.flickr.com/photos/biodivlibrary/



Letter from the Editors

Dear Reader,

Welcome to Lessons in Conservation, the official journal of the Network of Conservation Educators and Practitioners (NCEP). NCEP is a collaborative project of the American Museum of Natural History's Center for Biodiversity and Conservation (CBC) and partners from around the world. This journal is designed to introduce NCEP's open-access teaching and learning resources (our "modules") to a broad audience. NCEP modules are written for undergraduate and professional level education. The modules featured in this issue—and many more on a variety of conservation related topics—are freely available for download on our website, ncep.amnh.org.

This issue of Lessons in Conservation is dedicated to the memory of the inspiring and sorely missed Dr. Eleanor J. Sterling (1960–2023). As a founder of NCEP, life-long teacher, mentor, and exceptional scientist, leader, and human, Eleanor shaped the discourse and practice of conservation education globally. In education, her vision and efforts strengthened curricula and teaching, connected teaching and practice, and fostered a holistic lens on conservation learning. In this issue's opening editorial, a small group of Eleanor's colleagues reflect on her visionary educational approaches and consider the needs and opportunities for the field of conservation education to continue to improve.

Under the umbrella of a *Monitoring and Modeling* theme, this issue includes five student-facing educational resources that support learners to contribute to the scientific process, collect data, and analyze and model existing datasets in the same ways that some communities and scientists do as part of conservation research. Four exercises engage learners with ongoing community science projects, monitoring of biodiversity in community-managed marine seascapes, evaluating the behavioral and evolutionary impacts of introduced species, and modeling distributions of species with cutting-edge software tools. Additionally, an updated and condensed synthesis document provides theoretical and practical guidance for the expanding field of species distribution modeling. Whether learning about cultural conservation practices or the adaptations of lizard populations, we hope these materials help illustrate the analytical and real-world challenges and excitement that are part of conservation science!

NCEP materials are meant to be modifiable for each educator's specific classroom or training needs; adaptable Microsoft Word versions of these modules are available for download through the NCEP module collection at https://ncep.amnh.org along with any available accompanying data files, appendices, presentations, teaching notes, and exercise solutions. We welcome any feedback on our materials and encourage those who are interested in becoming more involved to contact us for further information. We are grateful to our authors, our CBC colleagues, and our volunteer peer reviewers for their time and input.

We hope you enjoy this issue of Lessons in Conservation and encourage you to visit our website to start using the full collection of NCEP resources in your classroom!

Questions and feedback are welcome at ncep@amnh.org.

Suzanne Macey, Nadav Gazit, Kristin Douglas,
and Ana Luz Porzecanski

TABLE OF CONTENTS

Lessons from a Transformative Conservation Educator and Building the Future of Conservation Education 5

Ana L. Porzecanski, Sharon Akabas, Erin Betley, Mary Blair, Nora Bynum, Joshua R. Ginsberg, Martha J. Groom, Suzanne K. Macey, Alex C. Moore, Christian J. Rivera, and Paige West

Managing Marine Seascapes Through Community-based Conservation 15

Samantha K. Cunningham, Karina Murillo, Karen Chan, and Joleah B. Lamb

What is Community Science, and How Do I Get Involved? 38

J. Stephen Gosnell

Lessons from Lizards: Adaptation to Introduced Ants 44

Nicole A. Freidenfelds, Jennifer M. Deitloff, and Tracy Langkilde

A Brief Introduction to Species Distribution Modeling for Conservation Educators and Practitioners 61

Matthew E. Aiello-Lammens, Andrea Paz, Bethany A. Johnson, Mary E. Blair, and Richard G. Pearson

Creating and Optimizing Species Distribution Models: A Vignette for Wallace Ecological Modeling Application v2.0 76

Bethany A. Johnson, Gonzalo E. Pinilla-Buitrago, Andrea Paz, Jamie M. Kass, Sarah I. Meenan, Robert P. Anderson

Lessons from a Transformative Conservation Educator and Building the Future of Conservation Education

Ana L. Porzecanski[i], Sharon Akabas[ii], Erin Betley[i], Mary Blair[i], Nora Bynum[iii], Joshua R. Ginsberg[iv], Martha J. Groom[v], Suzanne K. Macey[i], Alex C. Moore[vi], Christian J. Rivera[vii], and Paige West[viii]

[i]Center for Biodiversity and Conservation, American Museum of Natural History, New York, New York, USA; [ii]Department of Pediatric, Columbia University Irving Medical Center, Columbia University, New York, USA (retired); [iii]Organization for Tropical Studies, Durham, North Carolina, USA; [iv]Cary Institute of Ecosystem Studies, Millbrook, New York, USA; [v]School of Interdisciplinary Arts and Sciences, University of Washington Bothell, Bothell, Washington, USA; [vi]Departments of Forest & Conservation Sciences and Botany, University of British Columbia, Vancouver, British Columbia, Canada; [vii]High Meadows Environmental Institute, Princeton University, Princeton, New Jersey, USA; [viii]Department of Anthropology, Barnard College and Columbia University, New York, USA

INTRODUCTION

Biodiversity conservation, as a discipline and a practice, is undergoing a major transformation, as it faces both intensifying trends and drivers of biodiversity loss (IPBES 2019) and its links to colonization, social injustices, and institutional racism (Tauli-Corpuz 2020; Cronin et al. 2021). Efforts are underway to promote deeper engagement with the full complexity of social-ecological systems by integrating social science (e.g., Bennett et al. 2017) and Indigenous perspectives and values (e.g., Price et al. 2021), among other perspectives and sources of knowledge. How can conservation education keep pace with this transformation? Here, we reflect on what we, as conservation researchers and practitioners, have learned and share our views on directions for the future.

The authors of this editorial all share something in common: we were all deeply influenced by our collaborations with the late Dr. Eleanor J. Sterling (1960–2023), a trail-blazing conservationist and innovative scientist of global influence. Eleanor guided and grew the conservation programs of the American Museum of Natural History's (AMNH) Center for Biodiversity and Conservation (CBC) for more than 20 years (Betley et al. 2023a; Blair et al. 2023) and multiple other higher education institutions, including Columbia University, the University of Hawai'i, Bard College, and Princeton University. Our collaborations with Eleanor were wide-ranging and included research on participatory and biocultural approaches to conservation (for example, see Sterling et al. 2017a, Sterling et al. 2017b), equitable and sustainable food systems education (Sterling et al. 2021), wildlife use (Rivera et al. 2021), ecology and conservation of sea turtles (Sterling et al. 2013), remote sensing and conservation (Horning et al. 2010), primate taxonomy, behavior, and conservation (Blair et al. 2023b), diversity and inclusion in conservation (Foster et al. 2014; Maas et al. 2020), student learning (Bravo et al. 2016a; Sterling et al. 2016; Porzecanski et al. 2021), and capacity development (Bravo et al. 2016b; Sterling et al. 2022; Porzecanski et al. 2022).

In particular, Eleanor's practice in conservation education profoundly shaped our views and approaches. Through multiple projects and activities, she articulated, implemented, and galvanized pathways for responsive, place- and needs-based conservation education and capacity building across scales from individuals to collectives. We see this editorial as a way to honor Eleanor and her work in education, reflect on its impact, and, as we look ahead, share our views on how the needs of conservation education are evolving.

RESPONSIVE CONSERVATION EDUCATION

How can education, in its diversity of approaches and levels, be responsive to the complex context in which it operates? How can conservation education respond to the multiple dimensions of the learners we engage with, who bring diverse personal histories, perspectives, passions, and values

to the learning experience? We discuss a few examples below to illustrate how Eleanor's approach worked in practice and distill the lessons we draw from them.

Strengthening curricula and teaching practice

Through many engagements around the world with conservation projects and educators in the 1980s and 1990s, Eleanor observed a startling lack of access to teaching materials and teaching know-how, particularly in the Global South. In a pre-digital world, both cost and logistical hurdles made accessing training materials very difficult. Once, in a Malagasy forest, Eleanor observed a teacher incorrectly telling her students that the boa they were observing was a mammal because it gave birth to live offspring rather than laying eggs. She later uncovered that the only preparation materials the teacher had access to were handwritten notes of university lectures handed down across generations of students. Many of these notes were sparse and focused on European biodiversity rather than Malagasy ecosystems or species. Informed by experiences like these, Eleanor joined forces with several colleagues to launch NCEP, the Network of Conservation Educators and Practitioners. For almost 25 years, NCEP has been a creative, responsive, needs-based model for co-creating open conservation education curricular materials that are relevant and designed to fit the context where they will be used (for an overview published in this journal, see Landrigan 2019).

With support from the National Science Foundation and the MacArthur Foundation, this work grew and ultimately broadened relevant content (what is being taught), promoted effective pedagogy and learning (how it is being taught and learned), and inclusive learning spaces (who is learning). More recently, this work has come to encompass efforts to develop students' capacities in systems thinking[i] and engage communities of educators in teaching innovations, as described below.

Connecting teaching, training, and conservation practice

Through innovative partnerships and convenings, Eleanor helped to inspire a revolution in NASA's earth science research and other remote sensing-based research efforts that broadened the use of satellites towards measurements of biodiversity (Turner et al. 2003; Horning et al. 2010). She expertly facilitated a collaboration among staff from the AMNH Library and NASA-trained scientists to apply state-of-the-art Remote Sensing and Geographic Information System (RS/GIS) tools and techniques to training materials, workshops, and effective visual tools that aid in conservation planning and decision-making. In the 2000s, Eleanor led efforts to advance the capacity of biodiversity conservation practitioners, researchers, and professionals in Southeast Asia in these techniques, with a focus on Vietnam and Laos. In addition to increasing access to the data needed by managers, planners, community members, and decision-makers on the ground, her efforts trained a large cohort of skilled and passionate researchers and practitioners in Southeast Asia, forming a vibrant network. This network is active to this day and has led to impactful work, updated conservation management plans and policies, and new collaborations and partnerships in the region related to transboundary conservation (Blair et al. 2022) and wildlife trade management (Blair et al. 2017).

Her work on biodiversity informatics also generated a course, GIS and Remote Sensing for Conservation and Evolutionary Biology, taught at the Richard Gilder Graduate School at AMNH. A favorite among students, the course features a hands-on inquiry-based approach that consistently contributes to students' dissertation chapters and peer-reviewed publications (e.g., Ingala et al. 2019;

[i]An introduction to systems thinking and other materials from these courses were published in NCEP's Lessons in Conservation issue on systems thinking; see Betley et al. 2021.

Musher et al. 2020; Provost et al. 2021).

Yet another example of how Eleanor strengthened curricula as well as teaching and learning was through her own teaching practice—primarily at Columbia University's Department of Ecology, Evolution, and Environmental Biology, where she was Director of Graduate Studies (2002–2012) and an Adjunct Professor (2017–2021). At Columbia, she and Joshua Ginsberg co-taught the two-term core course Conservation Biology for 13 years. With Eleanor always being an agent of change, the course quickly evolved a participatory learning approach that emphasized the role of student-led learning and collaborative work processes. In both terms, groups of four or five students chose a specific geography, and then studied the biodiversity, ecological challenges, social issues, and Indigenous rights, and finally worked to develop a conservation plan for the region. In the early years of the course, some students (and occasionally, faculty) pushed back on the collaborative nature of the experience, asking, "how can individual contributions to a group project be evaluated fairly?" With grace, Eleanor let the students figure out solutions to this challenge, and in the early 2010s, as the approach became more common, the emphasis on student-led learning was amplified by asking individuals and groups to pose questions to be examined in the readings and lead class discussion.

Fostering a holistic lens on conservation learning

Over the course of a decade of co-teaching with Paige West, Sharon Akabas, and Erin Betley, additional courses challenged students to think broadly and deeply, and evolved in how they incorporated systems thinking approaches and collaborative learning techniques. One of the subjects that most fascinated Eleanor was food, both as a bridge between culture and biodiversity, and for its ability to connect people to biodiversity in a very personal way. When Eleanor co-curated an AMNH exhibition on the topic of food, she found a way to feature Jane Austen's favorite frozen dessert—ice cream—to which she was also devoted. Building on research for that exhibition Eleanor co-developed, with West, two transdisciplinary courses, Food, Ecology and Globalization and Cultural, Biological, and Linguistic Diversity. These graduate-level courses were unique in how they brought together bodies of literature from the social and natural sciences. Undergraduate and graduate students with a range of interests, from ecology to music to law to journalism, found common ground while sampling and discussing the influence of local environment on the finest cheeses from around the world or working together to assess and reflect on what sustainability means in a globalized food system. While rigorous and challenging for the students, PW recalls these as "magically fun to teach" and "deeply transformative" for both her and Eleanor's approaches to conservation work.

Working with Akabas and Betley, Eleanor redesigned the food course as part of an expanded series of three new undergraduate food systems courses at Columbia University. The courses emphasized the relationship of our food system to our environment and were taken by a wide range of students, many of whom had little or no experience with ecology or environmental biology. Common to all of the courses was a focus on systems thinking, the inequities of access to healthy food, and the value of allowing students to approach "wicked" problems collaboratively.

Recognizing a pedagogical gap in support for sustainable food systems educators, Eleanor and collaborators group launched a Community of Practice of 26 colleges and universities across the U.S. and Canada centered around turning thought into action, particularly with regard to racial equity and food justice (Valley et al. 2020; Sterling et al. 2021). The Community of Practice has brought educators and students together to explore how food builds and sustains both human connections and connections with the natural world. This initiative illustrates Eleanor's intangible quality of being the center of gravity that held together and inspired growth in disparate groups of people.

Mentoring

Among her many accomplishments, perhaps Eleanor's most significant contribution was her devoted mentorship of others. Eleanor directly mentored some 80 students, including 37 Ph.D. and 22 Masters candidates. She also supported the careers of many other students and early-career professionals at AMNH through the CBC and the Richard Gilder Graduate School and at Columbia. Many students sought out her guidance because they were doing "radical" work, which was either interdisciplinary or weaving together knowledge systems, and they required mentorship that was not available in their programs. The lives of dozens of conservationists from around the world—from Brooklyn to Bolivia to Solomon Islands to Uruguay—have been profoundly changed by Eleanor. The best way to understand the impact of this mentoring is through the words of her past mentees who are co-authors of this editorial.

Christian Rivera recalls the robust and vibrant education and mentoring network he became part of once he met Eleanor. "I found myself an active part of it in unprecedented ways. I was a freshman when Eleanor gave me an opportunity to enroll in the Con Bio upper-level course she taught as a visiting professor at Princeton University in Spring 2011, and the exposure to biocultural diversity and conservation in the course changed my career trajectory. During my undergraduate studies, I did not have much opportunity to explore the linkages between biological and cultural diversity and often struggled when having to choose natural science courses over social science ones. Fast forward five years later to 2016, and I was now a master's student at Columbia, co-advised and mentored by Eleanor, Mary Blair (who was herself a former student of Eleanor's), and Suzanne Macey. Eleanor gave me the space and encouragement to engage in interdisciplinary conservation projects that allowed me to bridge together my passions. Her transformative applications of systems thinking and biocultural approaches to conservation were a common thread among our discussions and interactions in and outside of the classroom, and those conversations continue now in my day-to-day life. I am proud and privileged to now have returned to Princeton and help build on Eleanor's legacy of teaching and mentoring undergraduate students in interdisciplinary and systems approaches to conservation."

Alex Moore recalls how four months into their position as a postdoctoral fellow in the CBC, Eleanor extended an unexpected invitation to join her for a New York Philharmonic Orchestra concert. "I remember hesitating initially, still unsure of my place at the Museum and even more unsure of what boundaries I should establish between myself and my colleagues/supervisors. But I love the orchestra, and so I said yes. Even now, several years later, that night stands out as a core memory and an undeniable highlight, not just because of the beautiful performance but also because that night Eleanor showed me what good mentorship actually looks like: seeing me as a full person (not simply a mentee or employee) and finding ways to enrich my life. This was a pattern she continued to exhibit throughout our working relationship, providing opportunities for me to develop critical skills while also caring for my needs, modeling mentorship in a way that I had never experienced before and haven't experienced since. Now, as a new faculty member, I am driven to connect with my students and mentees beyond their academic interests because I understand firsthand how transformative it is to be seen. While I may never be able to replicate for others all of the ways that Eleanor enriched my life, every effort I make—asking my students about their weekends, checking in about challenging family matters—adds to the foundation of care and support that she built for me."

Paige West recalls how often, over the course of the twenty years that they were colleagues at Columbia University, Eleanor picked up students who had been treated poorly by other faculty and enveloped them with her support and love. "Eleanor collected mentee-orphans: people who could no longer bear the inattention or the abuse or the inability of a person in power to see them. Often, I

knew the person who had previously advised them, so there was no need to speak about the faculty member, but never, not once in all those years, did she center the failed mentor in our conversations; it was always about the student and their potential. This practice of taking on students who needed help and who needed kind mentorship, even when their interests are wildly different from my own, is something that Eleanor taught me, and I suspect many others."

Finally, Eleanor's leadership of the Society for Conservation Biology Education committee led her to champion the creation of the Diversity, Equity, and Inclusion Committee to address the ways in which conservation itself was failing to embrace and support the full membership of the Society. In all these endeavors, Eleanor was always at the forefront, leading necessary change in conservation education and practice.

EVOLVING CHALLENGES IN CONSERVATION EDUCATION

Eleanor's responsiveness, reciprocity, innovation, and horizon scanning continue to inspire us. As we look ahead, here are some of the areas and issues that, in our view, will—or should— become central concerns of conservation education.

The (still very real) challenges of integrating across natural and social sciences

In recent years, multiple frameworks have been proposed to guide the development of interdisciplinary conservation research (e.g., Pooley et al. 2014; Bennett et al. 2017). Significant challenges persist, however, in not only building interdisciplinary capacity for integrative approaches to conservation (e.g., Blair et al. 2017; Sterling et al. 2017b) but also in accessing and designing interdisciplinary courses. In the same way that setting up multi- and interdisciplinary research projects requires thoughtful planning and reflection, from recruitment of team members to developing a shared language (Pooley et al. 2014), so too must course development in conservation. Existing interdisciplinary frameworks can be used to guide syllabus development; this was recently done, for example, by building on the social-ecological systems framework of Blair et al. (2017) to analyze wildlife trade issues and develop a course that emphasizes the development of skills in systems thinking and synthesizing across natural and social sciences in the context of the wildlife trade (CJR, Princeton University, Fall 2023). Challenges associated with proposing such courses will vary across institutions and departments and may include 1) a perceived lack of disciplinary focus, 2) challenges to the "technical" and scientific credibility of the course given its equal emphasis on the social sciences, and 3) disparities in personal, departmental, and institutional interpretations of the goals of conservation science and related pedagogical approaches (e.g., the role of human cultural diversity in definitions of "biodiversity"). Perhaps we may begin to overcome the aforementioned challenges by emphasizing and advocating for the importance of developing skills in (social-ecological) systems thinking (Gray et al. 2019) and the implications for transformative innovation in the environmental and conservation arenas in the academy and beyond.

Embracing the "decolonial turn"—and putting it into practice

Contemporary conservation is in the midst of what we might call a "decolonial turn": a moment during which the field is looking back at its history and practices, and thinking about its role in dispossessions of many kinds. This effort should be celebrated. However, some of this disciplinary moment of transformation looks and feels like performance and not transformation because it is about discourse and optics, instead of practice, so examples of how to put this into practice as part of our scholarship and education are especially valuable.

Eleanor served as an early decolonial voice in conservation practice and education. PW believes that this stance went back to her time in Madagascar with the United States Peace Corps in the mid-1990s. She recalls: "Over the years, as we taught together and read conservation histories and critiques, an approach we came to think of as 'radical listening' came about. We noticed how rare it was for outsiders to really hear what people living with biodiversity were expressing in terms of their deep knowledge of socio-ecological assemblages and their careful attention to biocultural changes." By teaching these practices to her students, and to the scholars and practitioners reading her work (e.g., Pretty et al. 2009; Sterling et al. 2020; Sterling et al. 2022), her work was transformative in how it forced conservation to attend to Indigenous approaches to ecological futures. This attention to what Indigenous community members and community members living in richly biodiverse areas know, see, and feel can serve as the basis for learning how to work with communities and the conservation of their social-ecological places.

For many conservation researchers and practitioners, a way to put this into practice has been through a shift toward biocultural conservation, which acknowledges the reciprocal relationships among human and ecological communities, and emphasizes the myriad positive roles human cultures have played in supporting and managing biodiversity (e.g., Sterling et al. 2017b; Díaz et al. 2019). By adopting a biocultural lens to conservation, we are able to center the social-ecological contexts of species and ecosystem management explicitly and to attune our attention to local needs and values, in addition to their wider connections (Pretty et al. 2009).

Additionally, conservationists have begun to more fully recognize that the same systems that have led to the degradation and loss of biodiversity have been responsible for widespread marginalization, oppression, and loss of cultural diversity. When these connections are recognized, it becomes clear that conservation education must acknowledge and address the ways social justice issues are entwined with conservation ones (Cronin et al. 2021; Schell et al. 2020), and include environmental justice as a goal. This has been the focus of several professional development programs from high school through early career stages. For example, the Doris Duke Conservation Scholars Programs have supported undergraduates holding a wide range of identities across the USA in exploring the intersections of conservation and environmental justice. DDCSP students learn to analyze the historical and present-day cultural contexts of conservation practice and envision changes that better connect across communities to forward more effective conservation projects.

These approaches demand not only greater attention to Indigenous and local management approaches as part of curricular design (e.g., Kainer et al. 2019), but also to the capacities of academics and local actors to embrace multiple worldviews, and co-design and co-produce conservation research and actions, especially with communities most intimately related to their local biodiversity to maintain and enhance the resilience of their homelands and waters (e.g., Aini et al. 2023). A recent review of biocultural efforts in higher education (Saavedra 2023) has illuminated the need for closer ties between academic and Indigenous knowledge holders, with implications for curricula, faculty, and students, and the role that academia can play in linking traditional and local knowledge to policy and governance.

Making space for the affective domain

Engaging with the content from our discipline is as much an emotional experience as an intellectual one. For many learners, this is causing feelings of anxiety and grief, across generations and particularly in youth. The challenges and value of engaging the affective or emotional aspects of learning have been actively discussed in other fields, such as queer and feminist studies (e.g.,

Fawaz 2016). In conservation and environmental science, there is a growing awareness that we have emphasized the cognitive and behavioral domains of learning and neglected the affective domain.

Traditional taxonomies of learning (e.g., Bloom 1956) have guided our teaching and the levels of learning we target, from the ability to know and apply to the ability to analyze, synthesize, and evaluate. These taxonomies are being extended beyond their original emphasis and scope, in ways that could foster the kind of reflexivity, humility, intercultural literacy, and stamina needed to engage with wicked problems, and decolonizing and biocultural approaches. For example, Bloom's taxonomy has been extended to encompass "create" (Anderson and Krathwohl 2001). And Fink's Taxonomy of Significant Learning (Fink 2013) considers six dimensions of learning that combine to produce significant learning, including the more familiar dimensions of foundational knowledge, application, and integration, but now also including learning how to learn, learning about oneself and others, and developing new feelings and values ("caring").

Shifting our learning objectives to encompass, and center, the affective dimensions of conservation learning and practice will be important to build and maintain psychological resilience and develop agency in the face of climate change and biodiversity loss. The implications for conservation classrooms could be profound. Eleanor and collaborators demonstrated such transformations in the case of food systems education (Sterling et al. 2021). As scholarship and guidance for conservation educators begin to emerge (e.g., Atkinson and Ray 2021), it feels critical to create the spaces to explore and revise our curricula, syllabi, and teaching approaches, skills, and decisions and priorities accordingly. Communities of practice and interdisciplinary collaborative teaching, especially with experts in psychology and education seem promising avenues to explore.

Measuring what matters

Conservation is striving to become more rigorous, evidence-based, and evidence-informed, through more robust monitoring, evaluation, and learning (e.g., Baylis et al. 2016; Knight et al. 2019). Eleanor modeled a fierce commitment to the idea that "not everything important is measurable, and not everything measurable is important" (quote by Elliot Eisner). At the same time, recognizing that what is measured is what gets attention, her research pursued and illuminated new ways to measure what was previously considered unmeasurable—from students' systems thinking (Gray et al. 2019) to cultural ecosystem services (Sterling et al. 2017b; 2022).

This focus on efficacy has also taken place in education, and especially STEM education, as we aim to shift to evidence-based pedagogy and bring about diverse and significant learning outcomes (Freeman et al. 2014). Eleanor's co-instructors recall her attention to developing metrics and including evaluation, reflection, and improvement into every course. This commitment was manifest in her teaching in many ways, from rubrics that in lieu of grades assessed students from a scale of emerging to developing to mastering; to the use of peer review of both individual and group work; to student journals that elicited students' reflections on what and how learning occurred and how newly acquired knowledge or learning altered existing knowledge. Conservation education should embrace the power that is generated by a co-developed learning and assessment agenda; one that is co-developed and co-owned by teachers and learners. This has the potential to not only foster learning that flows both ways, but also to model the kind of co-production we aim to center in conservation practice.

CONCLUSION

Conservation education has evolved and must continue to evolve. Those of us who learned from Eleanor Sterling have been fortunate to see a truly interdisciplinary mind at work, asking exciting

new questions. We have seen what it looks like when one strives to see beyond the horizon, to face upcoming challenges and opportunities of all kinds, for research, for partnerships, for teaching and learning. We have a model for what it looks like to do leading work and lead the field forward. We hope this editorial provides inspiration for others to do so as well, as we question, diversify, and broaden conservation thinking, learning, and practice.

REFERENCES

Aini, J., P. West, Y. Amepou, M.L. Piskaut, C. Gasot, R.S. James, J.S. Roberts, P. Nason, and A.E. Brachey. 2023. Reimagining conservation practice: Indigenous self-determination and collaboration in Papua New Guinea. Oryx 57(3):50–359. https://doi.org/10.1017/S003060532200103X.

Anderson, L.W., and D.R. Krathwohl, editors. 2001. A Taxonomy for Learning, Teaching, and Assessing: A Revision of Bloom's Taxonomy of Educational Objectives. Addison Wesley Longman, Inc., New York, NY, USA.

Atkinson, J., and S.J. Ray. 2021. The emotional curriculum of climate justice education: An existential toolkit. CSU Journal of Sustainability and Climate Change 1(1):6. https://doi.org/10.55671/2771-5574.1003.

Baylis, K., J. Honey-Rosés, J. Börner, E. Corbera, D. Ezzine-de-Blas, P.J. Ferraro, R. Lapeyre, U.M. Persson, A. Pfaff, and S. Wunder. 2016. Mainstreaming impact evaluation in nature conservation. Conservation Letters 9:58–64. https://doi.org/10.1111/conl.12180.

Bennett, N.J., R. Roth, S.C. Klain, K.M. Chan, D.A. Clark, G. Cullman, G. Epstein, M.P. Nelson, R. Stedman, and T.L. Teel. 2017. Mainstreaming the social sciences in conservation. Conservation Biology 31(1):56–66. https://doi.org/10.1111/cobi.12788.

Betley, E., M.E. Blair, and G. Cullman. 2023. Eleanor Jane Sterling (1960–2023). Nature Ecology & Evolution 7:790–791. https://doi.org/10.1038/s41559-023-02054-4.

Blair, M.E., F. Arengo, N. Bynum, G. Cullman, L.R. Douglas, M.J. Groom, C.J. Rivera, and A.L. Porzecanski. 2023a. In memoriam: Eleanor Jane Sterling (1960–2023). Conservation Biology 37(3):e14099. https://doi.org/10.1111/cobi.14099.

Blair, M.E., G.T. Cao, E.H. López-Nandam, D.A. Veronese-Paniagua, M.G. Birchette, M. Kenyon, B.M. Md-Zain, R.A. Munds, K.A.-I. Nekaris, and V. Nijman. 2023b. Molecular phylogenetic relationships and unveiling novel genetic diversity among slow and pygmy lorises, including resurrection of *Xanthonycticebus intermedius*. Genes 14(3):643. https://doi.org/10.3390/genes14030643.

Blair, M.E., M.D. Le, G. Sethi, H.M. Thach, V.T. Nguyen, G. Amato, M. Birchette, and E.J. Sterling. 2017. The importance of an interdisciplinary research approach to inform wildlife trade management in Southeast Asia. BioScience 67(11):995–1003. https://doi.org/10.1093/biosci/bix113.

Blair, M.E., M.D. Le, and M. Xu. 2022. Species distribution modeling to inform transboundary species conservation and management under climate change: Promise and pitfalls. Frontiers of Biogeography 14(1). https://doi.org/10.21425/F5FBG54662.

Bloom, B., E. Engelhart, W. Hill, and D. Krathwohl. 1956. The Classification of Educational Goals, Handbook I: Cognitive Domain. David McKay, New York, NY, USA.

Bravo, A., A.L. Porzecanski, A. Valdés-Velásquez, L.F. Aguirre, G. Aguilera, A. Arrascue, N. Bynum, L. Castañeda, T.R. de Centurión, and C. Cortez. 2016b. Strengthening capacity for biodiversity conservation in the Southern Tropical Andes through partnerships of educators and practitioners. Pages 417–429 in R. Sukumar, and A.A Aguirre, editors. Tropical Conservation: Perspectives on Local and Global Priorities. Oxford University Press, Oxford, UK.

Bravo, A., A. Porzecanski, E. Sterling, N. Bynum, M. Cawthorn, D.S. Fernandez, L. Freeman, S. Ketcham, T. Leslie, and J. Mull. 2016a. Teaching for higher levels of thinking: Developing quantitative and analytical skills in environmental science courses. Ecosphere 7(4):e01290. https://doi.org/10.1002/ecs2.1290.

Cronin, M.R., S.H. Alonzo, S.K. Adamczak, D.N. Baker, R.S. Beltran, A.L. Borker, A.B. Favilla, R. Gatins, L.C. Goetz, and N. Hack. 2021. Anti-racist interventions to transform ecology, evolution and conservation biology departments. Nature Ecology & Evolution 5(9):1213–1223. https://doi.org/10.1038/s41559-021-01522-z.

Díaz, S., J. Settele, E.S. Brondízio, H.T. Ngo, J. Agard, A. Arneth, P. Balvanera, K.A. Brauman, S.H. Butchart, and K.M. Chan. 2019. Pervasive human-driven decline of life on Earth points to the need for transformative change. Science 366(6471):eaax3100. https://doi.org/10.1126/science.aax3100.

Fawaz, R. 2016. How to make a queer scene, or notes toward a practice of affective curation. Feminist Studies 42(3):757–768. https://doi.org/10.1353/fem.2016.0039.

Fink, L.D. 2013. Creating Significant Learning Experiences: An Integrated Approach to Designing College Courses. John Wiley & Sons, San Francisco, CA, USA.

Foster, M.J., M.E. Blair, C. Bennett, N. Bynum, and E.J. Sterling. 2014. Increasing the diversity of US conservation science professionals via the society for conservation biology. Conservation Biology 28(1):288–291. https://www.jstor.org/

stable/24479524.
Freeman, S., S.L. Eddy, M. McDonough, M.K. Smith, N. Okoroafor, H. Jordt, and M.P. Wenderoth. 2014. Active learning increases student performance in science, engineering, and mathematics. Proceedings of the National Academy of Sciences 111(23):8410–8415. https://doi.org/10.1073/pnas.131903011.
Gray, S., E.J. Sterling, P. Aminpour, L. Goralnik, A. Singer, C. Wei, S. Akabas, R.C. Jordan, P.J. Giabbanelli, and J. Hodbod. 2019. Assessing (social-ecological) systems thinking by evaluating cognitive maps. Sustainability 11(20):5753. https://doi.org/10.3390/su11205753.
Horning, N., J.A. Robinson, E.J. Sterling, and W. Turner. 2010. Remote Sensing for Ecology and Conservation: A Handbook of Techniques. Oxford University Press, Oxford, UK.
Ingala, M.R., D.J. Becker, J. Bak Holm, K. Kristiansen, and N.B. Simmons. 2019. Habitat fragmentation is associated with dietary shifts and microbiota variability in common vampire bats. Ecology and Evolution 9(11):6508–6523. https://doi.org/10.1002/ece3.5228.
IPBES. 2019. Global Assessment Report of the Intergovernmental Science-Policy Platform on Biodiversity and Ecosystem Services. E.S. Brondizio, J. Settele, S. Díaz, and H.T. Ngo, editors. IPBES secretariat, Bonn, Germany. 1148 pages. https://doi.org/10.5281/zenodo.3831673.
Kainer, K.A., C. López Binnqüist, J.L. Dain, B. Contreras Jaimes, P. Negreros Castillo, R. Gonzalez Basulto, E.A. Ellis, H.H. Covert, R. López Rodríguez, and I.U. Hernández Gómez. 2019. Leading by listening, learning by doing: Modeling democratic approaches to conservation leadership in graduate education. Journal of Environmental Studies and Sciences 9:206–217. https://doi.org/10.1007/s13412-019-00542-3.
Knight, A.T., C.N. Cook, K.H. Redford, D. Biggs, C. Romero, A. Ortega-Argueta, C. D. Norman, B. Parsons, M. Reynolds, and G. Eoyang. 2019. Improving conservation practice with principles and tools from systems thinking and evaluation. Sustainability Science 14:1531–1548. https://doi.org/10.1007/s11625-019-00676-x.
Landrigan, K. 2019. Building capacity for conservation through education: The what, how, why, & who of the Network of Conservation Educators and Practitioners. Lessons in Conservation 9(1):5–9.
Maas, B., K.E. Grogan, Y. Chirango, N. Harris, L.F. Liévano-Latorre, K.L. McGuire, A.C. Moore, C. Ocampo-Ariza, M.M. Palta, and I. Perfecto. 2020. Academic leaders must support inclusive scientific communities during COVID-19. Nature Ecology & Evolution 4(8):997–998. https://doi.org/10.1038/s41559-020-1233-3.
Musher, L.J., P.J. Galante, G. Thom, J.W. Huntley, and M.E. Blair. 2020. Shifting ecosystem connectivity during the Pleistocene drove diversification and gene-flow in a species complex of Neotropical birds (Tityridae: Pachyramphus). Journal of Biogeography 47(8):1714–1726. https://doi.org/10.1111/jbi.13862.
Pooley, S.P., J.A., Mendelsohn, and E. Milner-Gulland. 2014. Hunting down the chimera of multiple disciplinarity in conservation science. Conservation Biology 28(1):22–32. https://doi.org/10.1111/cobi.12183.
Porzecanski, A.L., A. Bravo, M.J. Groom, L.M. Dávalos, N. Bynum, B.J. Abraham, J.A. Cigliano, C. Griffiths, D.L. Stokes, and M. Cawthorn. 2021. Using case studies to improve the critical thinking skills of undergraduate conservation biology students. Case Studies in the Environment 5(1):1536396. https://doi.org/10.1525/cse.2021.1536396.
Porzecanski, A.L., E.J. Sterling, J.A. Copsey, M.R. Appleton, J.R. Barborak, B.L. Bruyere, N. Bynum, K.H. Farmer, R. Finchum, and D. Rakotobe. 2022. A systems framework for planning and evaluating capacity development in conservation: Recommendations for practitioners. Oryx 56(5):671–680. https://doi.org/10.1017/S003060532100154X.
Pretty, J., B. Adams, F. Berkes, S.F. De Athayde, N. Dudley, E. Hunn, L. Maffi, K. Milton, D. Rapport, and P. Robbins. 2009. The intersections of biological diversity and cultural diversity: Towards integration. Conservation and Society 7(2):100–112. https://doi.org/10.4103/0972-4923.58642.
Price, M., K.B. Winter, and A. Jackson. 2021. Towards resilience in the Anthropocene: Transforming conservation biology through Indigenous perspectives. Pacific Conservation Biology 27(4):309–319. https://doi.org/10.1071/PCv27n4_FO.
Provost, K.L., E.A. Myers, and B.T. Smith. 2021. Community phylogeographic patterns reveal how a barrier filters and structures taxa in North American warm deserts. Journal of Biogeography 48(6):1267–1283. https://doi.org/10.1111/jbi.14115.
Rivera, C.J., S.K. Macey, M.E. Blair, and E.J. Sterling. 2021. Assessing ecological and social dimensions of success in a community-based sustainable harvest program. Environmental Management 67:731–746. https://doi.org/10.1007/s00267-021-01425-6.
Saavedra, F. 2023. Biocultural Conservation in Higher Education: Organizational Review and Consultation. University of Florida, Tropical Conservation and Development Program. Available from: http://uftcd.org/wp-content/uploads/2023/10/Final-Report-Biocultural-Conservation-in-Higher-Ed-Saavedra-2023-Oct12.pdf (accessed December 2, 2023).
Schell, C.J., K. Dyson, T.L. Fuentes, S. Des Roches, N.C. Harris, D.S. Miller, C.A. Woelfle-Erskine, and M.R. Lambert. 2020. The ecological and evolutionary consequences of systemic racism in urban environments. Science 369(6510): eaay4497. https://doi.org/10.1126/science.aay4497.
Sterling, E.J. et al. 2021a. Centering equity in sustainable food systems education. Frontiers in Sustainable Food Systems 5. https://doi.org/10.3389/fsufs.2021.737434.

Sterling, E.J., et al. 2017a. Assessing the evidence for stakeholder engagement in biodiversity conservation. Biological Conservation 209:159–171. https://doi.org/10.1016/j.biocon.2017.02.008.

Sterling, E.J., et al. 2017b. Biocultural approaches to well-being and sustainability indicators across scales. Nature Ecology & Evolution 1(12):1798–1806. https://doi.org/10.1038/s41559-017-0349-6.

Sterling, E.J., A. Bravo, A.L. Porzecanski, R.L. Burks, J. Linder, T. Langen, D. Fernandez, D. Ruby, and N. Bynum. 2016. Think before (and after) you speak: Practice and self-reflection bolster oral communication skills. Journal of College Science Teaching 45(6):87–99. https://doi.org/10.2505/4/jcst16_045_06_87.

Sterling, E.J., K.W. McFadden, K.E. Holmes, E.C. Vintinner, F. Arengo, and E. Naro-Maciel. 2013. Ecology and conservation of marine turtles in a Central Pacific foraging ground. Chelonian Conservation and Biology 12(1):2–16. https://doi.org/10.2744/CCB-1014.1.

Sterling, E.J., et al. 2020. Creating a space for place and multidimensional well-being: Lessons learned from localizing the SDGs. Sustainability Science 15(4):1129–1147. https://doi.org/10.1007/s11625-020-00822-w.

Sterling, E.J., A. Sigouin, E. Betley, J.Z. Cheek, J.N. Solomon, K. Landrigan, A.L. Porzecanski, N. Bynum, B. Cadena, and S.H. Cheng. 2022. The state of capacity development evaluation in biodiversity conservation and natural resource management. Oryx 56(5):728–739. https://doi.org/10.1017/S0030605321000570.

Tauli-Corpuz, V., J. Alcorn, A. Molnar, C. Healy, and E. Barrow. 2020. Cornered by PAs: Adopting rights-based approaches to enable cost-effective conservation and climate action. World Development 130:104923. https://doi.org/10.1016/j.worlddev.2020.104923.

Turner, W., S. Spector, N. Gardiner, M. Fladeland, E. Sterling, and M. Steininger. 2003. Remote sensing for biodiversity science and conservation. Trends in Ecology & Evolution 18(6):306–314. https://doi.org/10.1016/S0169-5347(03)00070-3.

Valley, W., M. Anderson, N.T. Blackstone, E. Sterling, E. Betley, S. Akabas, P. Koch, C. Dring, J. Burke, and K. Spiller. 2020. Towards an equity competency model for sustainable food systems education programs. Elementa: Science of the Anthropocene 8:33. https://doi.org/10.1525/elementa.428.

Managing Marine Seascapes Through Community-based Conservation

Samantha K. Cunningham[i,ii], Karina Murillo[i], Karen Chan[iii], and Joleah B. Lamb[i]

[i]University of California, Irvine, Department of Ecology & Evolutionary Biology, Irvine, CA, USA; [ii]University of California, Irvine, School of Medicine, Irvine, CA, USA; [iii]Swarthmore College, Swarthmore, PA, USA

ABSTRACT

In this multi-component exercise, you have been recruited as community scientists to analyze real-world data collected in Vatu-i-Ra Seascape using non-destructive diver operated video (DOV) methods. These videos were previously collected by the Wildlife Conservation Society in collaboration with local divers in Fiji. Students will quantitatively analyze and use this data to assess the fisheries management efficacy of *tabu* areas—a traditional Fijian approach to create no-take, Marine Protected Areas—as a method of promoting marine biodiversity and improving overall ecosystem health using metrics such as fish abundance and coral reef complexity. During this exercise you will also learn about the importance and cultural significance of *tabu* areas in relation to ecosystem health and human livelihoods. You will be directed on how to visualize the results and summarize their conclusions through a written report in the style of a scientific journal article. In the discussion section of your scientific journal article, you are encouraged to critically think about study limitations and discuss future research directions to expand the project.

LEARNING OBJECTIVES

After completing this case-study based exercise, you will be able to:
1. Examine the ecological, cultural, economic, and social significance of fisheries management strategies.
2. Consider the strengths and weaknesses of the diver operated video (DOV) method.
3. Use DOV to assess the impact of *tabu* areas (MPA) on coral reef fish abundance and coral reef complexity.
4. Test hypotheses by analyzing and visualizing data.
5. Format research into the style of a scientific manuscript.

INTRODUCTION

Often referred to as the "rainforests of the sea", coral reefs are regarded as some of the most productive and biologically diverse ecosystems on the planet (Reaka-Kudla et al. 1996). Coral reefs provide a variety of ecosystem services to humans such as fisheries, coastal protection, water management, materials, and cultural benefits (Woodhead et al. 2019). However, coral reefs are susceptible to anthropogenic[1] disturbances such as climate change, pollution, habitat destruction, unsustainable fishing practices, and removal of keystone species[2] (Burke et al. 2011). These anthropogenic stressors disrupt critical ecosystem services coral reefs provide and are associated with global declines in fish populations, making conservation an international priority.

In response to coral reef degradation and global declines in fish populations, marine protected areas[3], or MPAs, are widely used to preserve marine biodiversity. MPAs are regions of the marine environment that have been designated to preserve nature (Grorud-Colvert et al. 2021). These areas are protected by various strategies, such as closures, management, or scientific study. There is substantial evidence to suggest that strictly enforced MPAs lead to increased biomass, fish size and density, biodiversity, resilience to natural disturbances, and livelihood security for fishing communities

(Edgar et al. 2014; Mellin et al. 2016; Roberts et al. 2001). In theory, MPAs are thought to positively affect adjacent fisheries through the "spillover effect," in which increases in biomass near the MPA borders move into fished areas (Di Lorenzo et al. 2020).

Located in the South Pacific region, the Fiji archipelago (1.3 million km^2 area) has one of the world's largest and most extensive coral reef systems. It is a critical site for marine conservation, home to an astounding 42 percent of all known coral species (Burke et al. 2011). Local communities in Fiji rely on the extensive ecosystem services of coral reefs for economic, cultural, and nutritional benefits—rendering it especially critical to ensure that marine protections are practical and beneficial (Mangubhai et al. 2019). The livelihoods of the local communities depend on the success of MPAs, therefore it is important to understand whether and how MPAs are effective for maintaining coral reef complexity and fish abundance. Much of the previously discussed research on protected areas has been conducted in areas with the highest level of protection, but locally managed marine areas (LMMAs) are an alternative where minimally destructive anthropogenic activity is allowed. Fiji is an example of a country that uses LMMAs to protect some of their coral reefs. Within the context of South Pacific culture, LMMAs are rooted in customary and traditional fisheries management practices designed to engage the community as stakeholders in the decision-making process (Doulman 1993). LMMAs with a definitive designation of areas that prohibit extractive uses are known as *tabu* areas (Robertson et al. 2020). The name *tabu*[4] (pronounced TAM-bo) comes from a customary Fijian fishery management tool in which fishing grounds (qoliqoli) are temporarily closed following the death of a community's chief.

The Vatu-i-Ra Conservation Park seascape

The Vatu-i-Ra Conservation Park covers over 100km^2 of marine and terrestrial ecosystems, including coral reefs, lagoons, and the island of Vatu-i-Ra (Figure 1). Management of the Conservation Park includes "no-take" zones (covering approximately 80% of the park) and "catch-and-release" zones, which allow sustainable, recreational fishing. The Conservation Park is home to over 100 species of fish, nine species of seabirds, and species of dolphins, whales, and sea turtles. Ideally, protection within the park encourages the growth of fish populations, causing a spillover effect in surrounding areas to support the adjacent traditional fishing ground (*qoliqoli*) of Cokovata Nakorotubu. Vatu-i-Ra Conservation Park is particularly vulnerable to impacts such as overfishing, invasive species, and climate change, and was damaged by Tropical Cyclone Winston in 2016.

OVERVIEW

In this assignment, you will generate data as a Community Scientist using previously collected Diver Operated Videos (DOVs; Figure 2) (Activity 1). Then, you will analyze the data your class produced (Activity 2) and draft a manuscript following the guidelines of the journal Conservation Biology (Activity 3).

ACTIVITY 1. DIVER OPERATED VIDEO DATA COLLECTION

Diver Operated Video (DOV): A non-invasive, non-destructive research method

The Wildlife Conservation Society, in collaboration with local divers in Fiji, created a series of diver operated videos (DOVs)[5] collected along transects[6] in the Vatu-i-Ra Marine Park. Through this activity, you will learn about the experimental design utilized by scientists and community members to collect the data. You will also assess the potential experimental errors of the study design and propose how to improve upon aspects of the experiment by considering the advantages and disadvantages of different underwater data collection methods. You will analyze the collected data and utilize numerical outputs to determine whether there is a difference in *tabu* and fished areas in the Vatu-i-Ra Seascape.

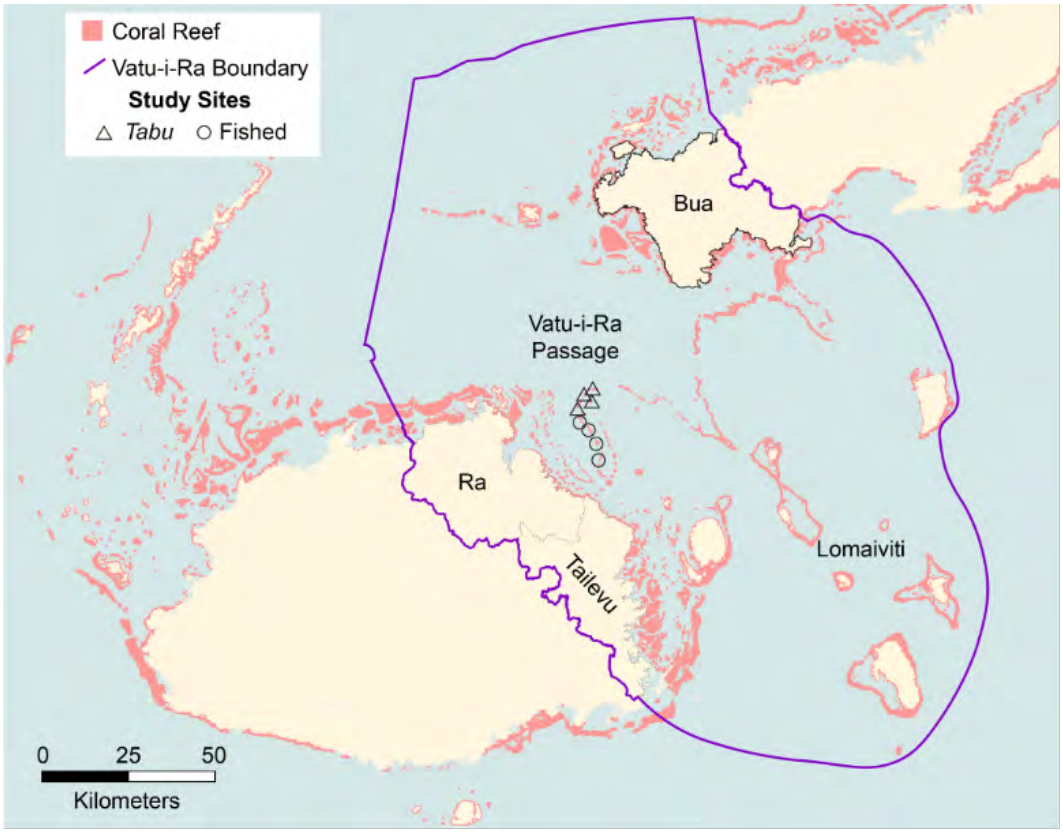


Figure 1. The Vatu-i-Ra Seascape is outlined in purple and includes four provinces in Fiji (Kastl and Gow 2014). Coral reefs are shown in pink (UNEP-WCMC et al. 2021), and study sites used in this exercise are represented by triangles and circles.

Figure 2. SCUBA diver conducting diver operated video (stereo-DOV) survey at Mo'orea, French Polynesia. Photo credit: Lauric Thiault/ Goetze et al. 2019.

Important links + resources

First, watch this ~7 minute DOV Methods video (https://methodsblog.com/2019/06/13/stereo-dov/) about advantages, methods, and applications of DOV in marine systems. (Note, you may be assigned to watch this video on your own, or watch it in class during the background lecture. Though the video describes two collection cameras, we will use only one of the two collection cameras in this assignment).

Then, review the journal article "A field and video analysis guide for diver operated stereo-video" (Goetze et al. 2019; https://doi.org/10.1111/2041-210X.13189) and especially pay attention to sections 1, 2, 7, and 9. Think about these questions: What are some advantages of DOVs? What are some limitations? How does standardizing collection methods help advance scientific knowledge?

Your instructor will assign specific DOV transects for you to analyze. Each video is an individual underwater transect.

The videos can be accessed here: YouTube—Diver-operated videos (DOV); https://www.youtube.com/playlist?list=PLc2xCMLuYq9asSAwIq7xQEDgQhGCk4MUE.

Part A. DOV transect protocol

- Download and use the DOV Data Entry Spreadsheet (provided by your instructor or downloaded from NCEP module collection at https://ncep.amnh.org) to add your data collected from the below protocol for each of your assigned video replicates: fish count and measurements of reef structural complexity.
- To submit: DOV data entry spreadsheet filled out for your videos.

For each video:

1. To enable more accurate counting, try to use a computer monitor or larger screen at eye level.
2. Set video to maximum quality (1080p) if possible.
3. Watch video at normal speed and write down the time where fish appear and group (no counting). At 5 timepoints every 20 seconds (0:20, 0:40, 1:00, 1:20, 1:40), pause the video and score the reef structural complexity from 1–5 using the categories described in Box 1 below, and enter the scores in the datasheet.
4. Watch the video a second time following these instructions:
   a. Slow the video by setting the speed to 0.25x.
   b. Start counting when the camera is stabilized after start. Use a counter with the app sound on (so you can hear it increase without looking at it)
   c. Use Pause when many fish quickly and suddenly appear in view
   d. For schooling pelagic fishes against blue water, count when you can clearly see the group of fishes
   e. For benthic fishes, look for movement against the reef background. Occasionally you may need to use Pause to count multiple fish in reef structures
   f. Use judgment to avoid double-counting: be mindful not to record anything that appears to come from behind the camera.
5. Submit the spreadsheet for this assignment to your instructor.

Part B. Structural complexity

- To submit: A Word document with a screenshot at each of the 5 timepoints and a complexity score for each screenshot.

Instructions:

1. For each DOV transect assigned, take screenshots at 5 timepoints (0:20, 0:40, 1:00, 1:20, 1:40) according to the protocol in Part A.
2. Create a Word document and, for each timepoint, paste in a screen shot from the video. On your document, type the video number, timepoint (0:20, 0:40, 1:00, 1:20, 1:40), and the structural complexity category for each timepoint.

Example for 1 timepoint screenshot at 1:00 for Video 6 with a Reef Complexity score of 5 (see Box 1):

- Submit the document that contains the 5 timepoint screenshots and associated information for each video you were assigned.

ACTIVITY 2. STATISTICAL ANALYSIS OF DATA

To share data with other researchers and the public, scientists must first make the data meaningful. One way scientists do this is by using statistics to determine whether there is a difference between averages of two groups of data. Here, you will use Excel to test the hypotheses that you will later write about in Activity 3. You will submit your three graphs and T-test[7] results to your instructor for grading. Note: Below instructions and screenshots may vary with different versions of Microsoft Excel. The functions required are relatively standard for many spreadsheet software versions, so use the Internet or help tools in the program to assist with variations.

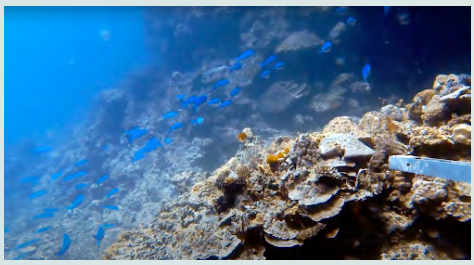
- To submit: Document with screenshot of coral complexity and fish count data, three graphs, and sample results sentences for each part (Appendix 1).

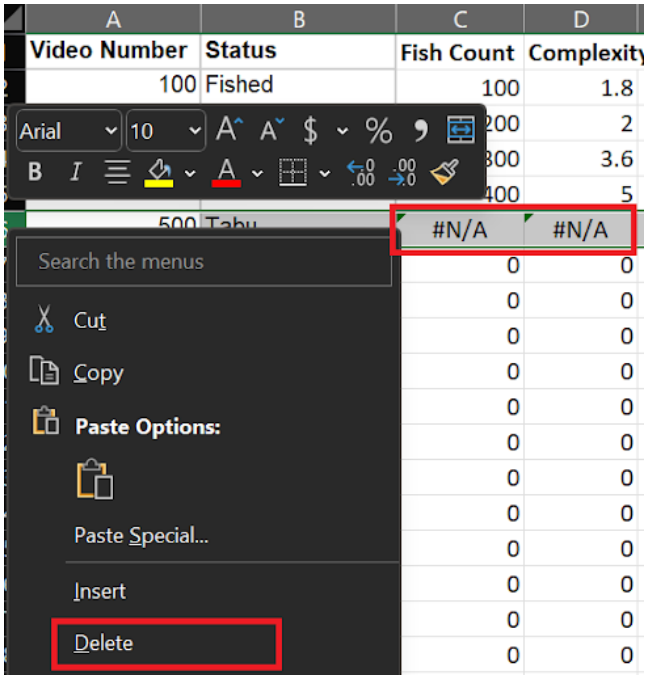
PART A. Test the hypothesis that *tabu* areas have different coral reef complexity compared to fished areas

1. Your instructor will provide you with an Excel spreadsheet that has combined all of the data from your class. Go to the tab titled "Video Data". This is the data you will be using to test your hypotheses.
2. Delete all video rows with missing data (shows as #N/A). These are the videos that your class did not analyze. To delete: highlight the row, right click, and select "Delete".

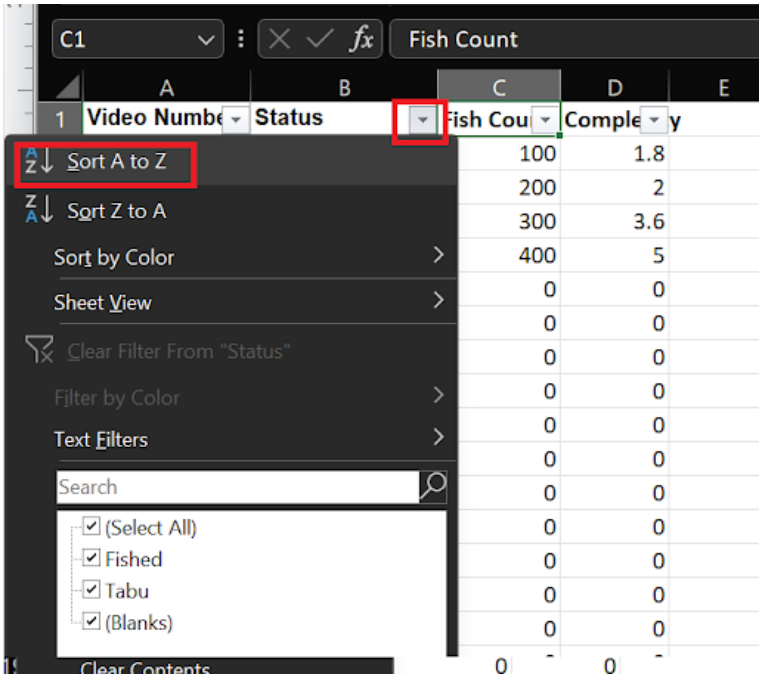
Box 1. Reef structural complexity

To measure structural complexity, you will be following the Williamson et al. 2004 categorical scaling system for coral reefs. As the observer, you will visually estimate the structural complexity of the reef slope for five timepoints in each video. See accompanying PowerPoint presentation for reference photos and additional examples.

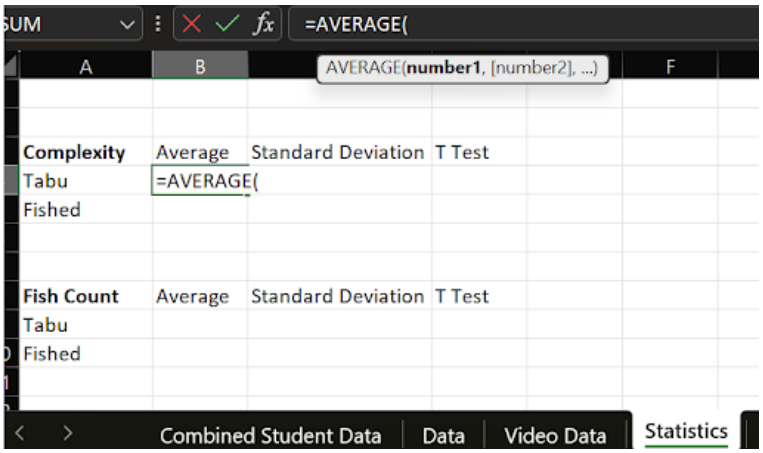
Category	Description	Example
1	Flat, sandy, expanses of rubble with some small scattered bommies (coral heads)	
2	Bommies amongst mostly rubble and sand. Reef slope < 45°	
3	Rubble amongst mostly coral bommies. Reef slope ~ 45°	
4	Good reef structure with some overhangs and holes. Reef slope >45°	
5	High reef complexity. Many overhangs, holes and caves. Large bommies. ~90° wall	

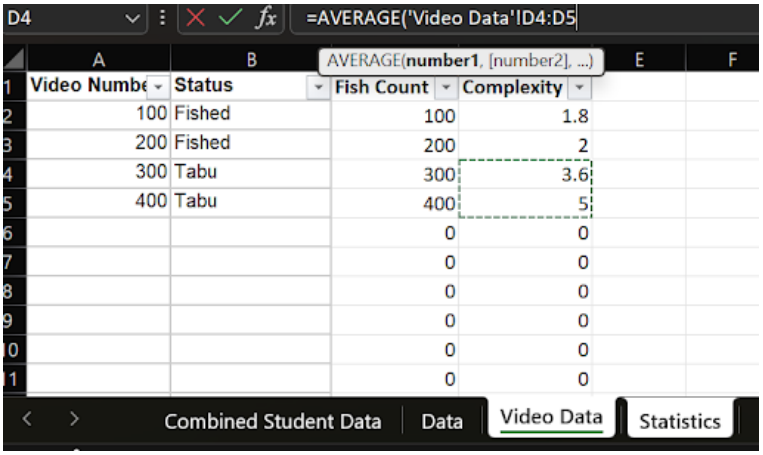


3. Sort by protection status. Click the dropdown arrow on "Status" and choose "Sort A to Z". Note: if there is not a dropdown arrow, highlight the first row and choose "Sort & Filter" > "Filter".

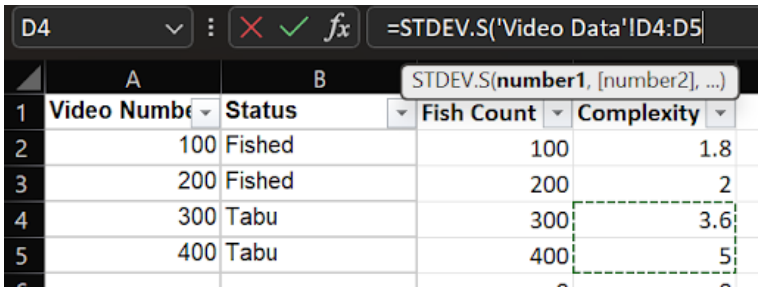


4. Go to the Statistics sheet. In the box for the average complexity of *tabu* areas, calculate the average complexity for the *tabu* areas from the Video Data sheet. To do so, type =AVERAGE(into the field. Then, navigate to the Video Data sheet and highlight the values to be averaged. Type) to close the formula and then hit enter.

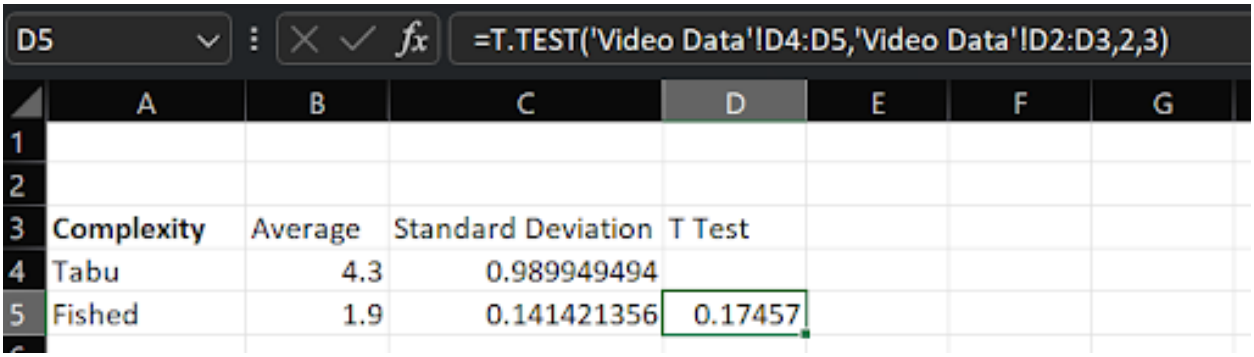




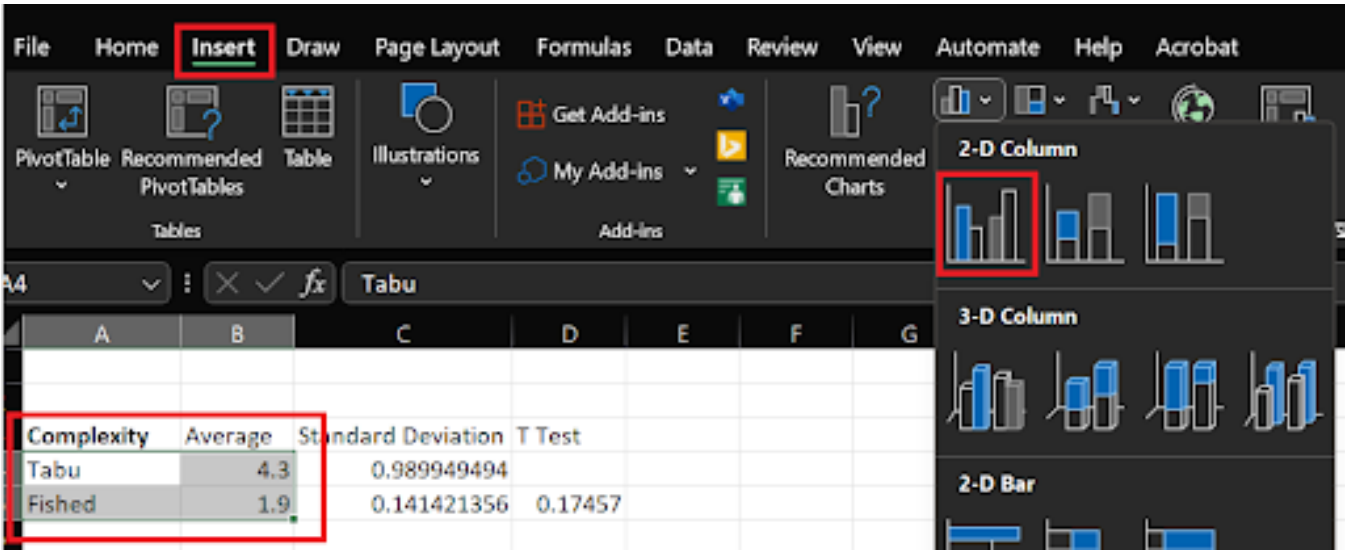
5. In the box for the standard deviation of complexity for *tabu* areas, calculate the standard deviation of the fields you used for the previous step. Type =STDEV.S(then highlight the complexity scores for *tabu* areas, and type) and hit enter.



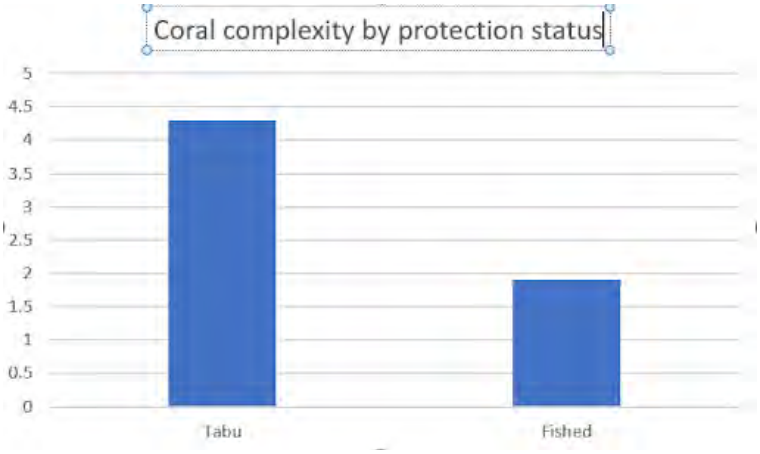
6. Repeat the previous two steps highlighting the complexity for the Fished videos to fill in the average and standard deviation for Fished areas.
7. Conduct a two-tailed T Test with unequal variance to compare the complexity of Fished versus *tabu* areas. Type =T.TEST(, highlight the *tabu* complexity values from Video Data (same as you highlighted for step 4), type comma ,, highlight the Fished complexity values from Video Data (same as you highlighted for Step 6), type comma ,, type 2, , type 3).



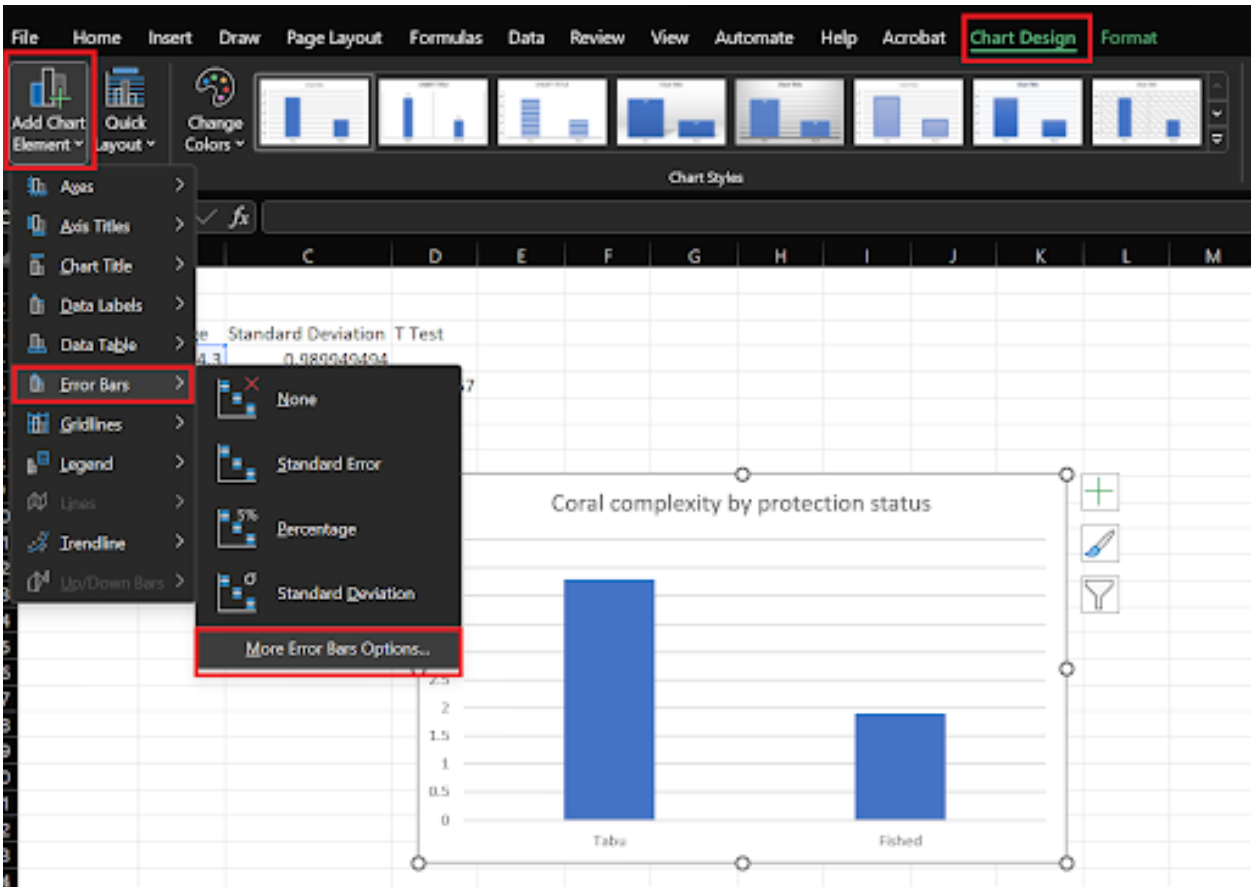
8. The number that the T test outputs is called a p value. It is the probability that the difference between the two averages is just by chance. As scientists, we say that if there is less than a 5% probability that the difference is by chance (meaning the p value is less than 0.05), the difference is statistically significant. For example, to write out the results for the example above, we would say: there is no significant difference in complexity between Fished (1.9+/-0.99) and *tabu* (4.3+/-0.14) areas (p=0.17). Example results sentences (replace the underlined green text with your own results):
   a. Fished areas (Average +/- Standard Deviation) have increased coral complexity compared to *tabu* areas (Average +/- Standard Deviation) (p=P VALUE)
   a. Fished areas (Average +/- Standard Deviation) have decreased coral complexity compared to *tabu* areas (Average +/- Standard Deviation) (p=P VALUE)
   a. There is no significant difference in coral complexity between Fished (Average +/- Standard Deviation) and *tabu* areas (Average +/- Standard Deviation) (p=P VALUE)
9. Generate a bar graph of your data. Highlight the protection status and average values > click Insert > 2-D Column > Clustered Column



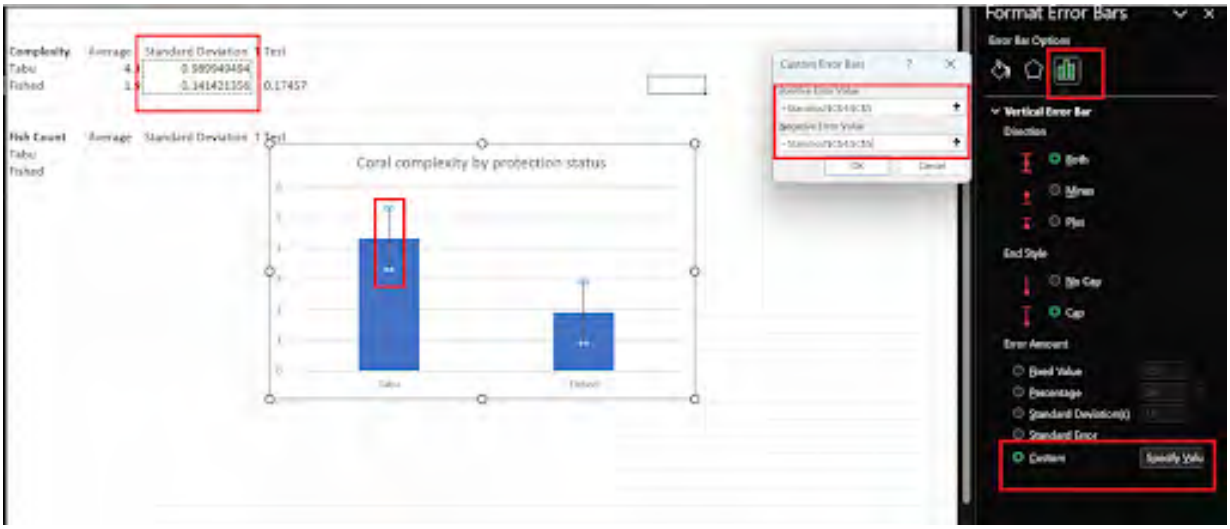
10. Change the Chart title by double clicking on it.



11. Insert error bars. With the chart selected, go to Chart Design > Add Chart Element > Error Bars > More Error Bars Options.



12. Set the Error Bars to the Standard Deviation you calculated: Double click on the Error Bars > Click the bars on the right menu > Select "Custom" at the bottom > Highlight the standard deviations for both "Positive Error Value" and "Negative Error Value".



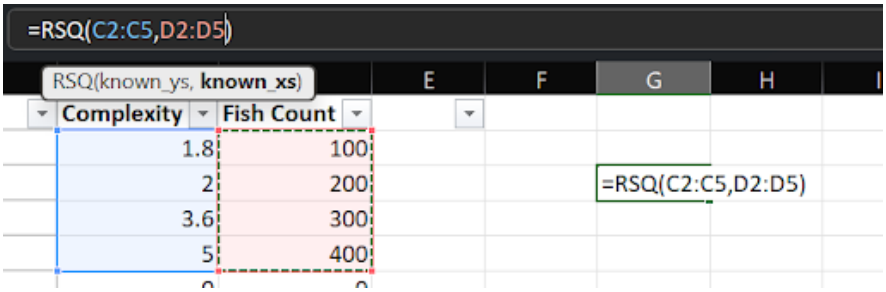
13. Play around with the colors, labels, and formatting to make the graph your own! Then, save a screenshot of the graph and of your data to a new document to be submitted to your instructor. In this document, also include an example results sentence with your results (Use the template from Step 8).

PART B. Test the hypothesis that *tabu* areas have different fish abundance compared to fished areas

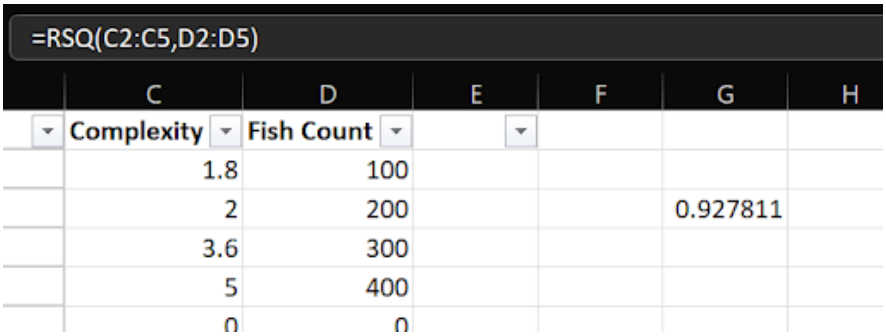
1. Use what you just learned in Part A to see if there is a difference in fish abundance between *tabu* and fished areas. Make a graph and fill in the table for fish count!
2. Save a screenshot of your graph and data, and write an example results sentence. Include these on your submission document.

PART C. Visualize the relationship between coral reef complexity and fish abundance

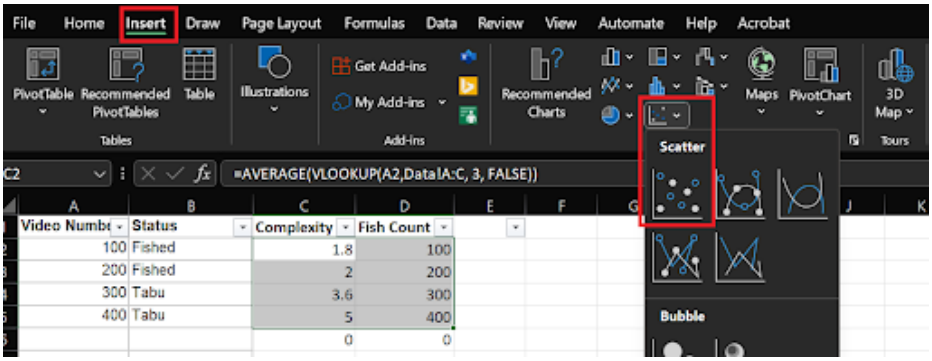
1. Calculate the relationship between fish abundance and coral complexity. We won't use a statistical test here, but will instead use an R-squared value[8]. This is a measure of how much of the variation in your variable is caused by the other variable. It can be between 0 and 1, meaning between none and 100 percent.
   a. In Excel, go to an open cell.
   b. Type =RSQ(, highlight the complexity data, type ,, highlight the fish count data, type) , hit enter.



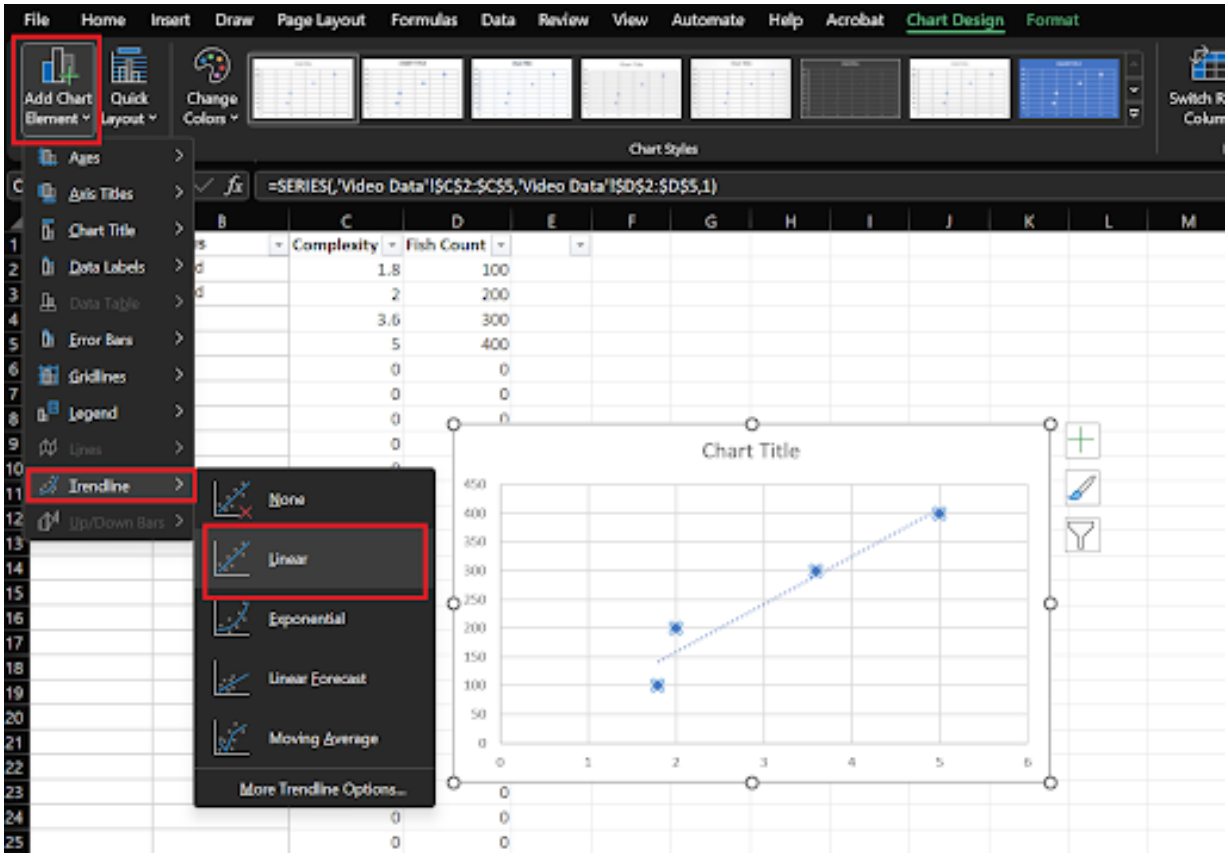
2. The number that is output is your R-squared. In this example, we would say that 92.8% of the variation in fish count is explained by complexity.



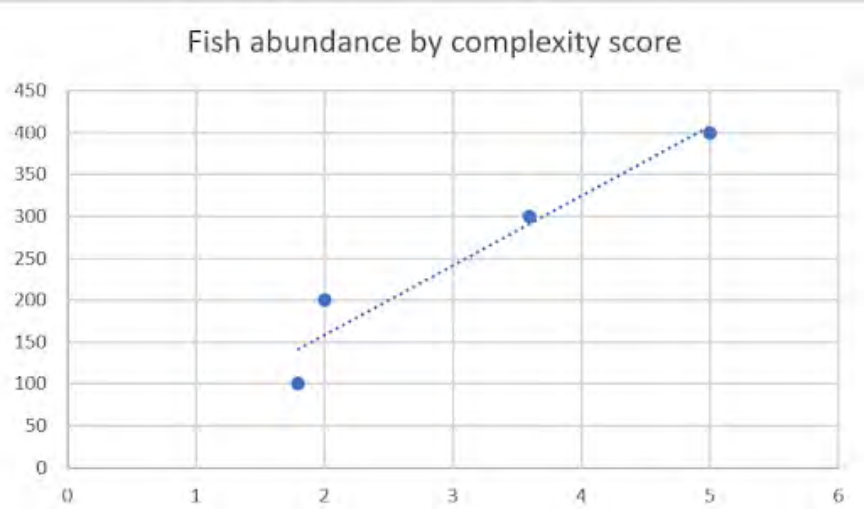
3. Highlight the fish count and complexity data from "Video Data".
4. Add a scatter plot. Choose Insert > Scatter > Scatter.



5. Add a trendline. Double click on the chart > Choose "Add Chart Element" > Trendline > Linear.



6. Change the graph title by double clicking.



7. Play around with the graph to make it your own!
8. Save a screenshot and add the screenshot to your document for submission. Submit the document, along with coral complexity and fish count, to your instructor.

ACTIVITY 3: CONSERVATION BIOLOGY MANUSCRIPT

Overview

After formulating your hypothesis and collecting data from Activity 1 and analyzing your data from Activity 2, the next steps are to reflect on your results and share your research findings in the form of a scientific manuscript. If your instructor assigns this as a group activity, please refer to instructions in Activity 4. The research you have conducted thus far is an example of the type of research that would be found in *Conservation Biology*.

Part A. Writing guideline for draft

- To submit: Complete manuscript draft, which will be graded.

To get an idea of the expectations for you as an author, read the Instruction Guide to Authors (provided by your instructor or downloaded from NCEP module collection at https://ncep.amnh.org) and use the checklist provided for each section.

1. Write the introduction

Describe the scientific question of interest. Start by describing the unknowns in this study and identify the population of interest that is being studied. Conclude the introduction section with your hypothesis statement(s) and predictions.
The introduction section of your manuscript should answer the following questions:

- Why is this study being conducted?
- Why is the study important?
- What is the aim of your study?
- What is your hypothesis/research question?

Journal format

Different research journals have different audiences, meaning the people who read your article will depend on the journal you choose. You will be drafting a research manuscript following the guidelines of *Conservation Biology*, a well-known peer reviewed journal that welcomes submissions that address the science and practice of conserving Earth's biological diversity. Manuscripts relevant to conservation that transcend the particular ecosystem, species, or situation described are prioritized for publication.

Grading format

Your manuscript will be graded by your instructor according to the *Conservation Biology* Manuscript Grading Rubric (Appendix 2). Each manuscript should resemble an article in *Conservation Biology* (headers, titles, author list and affiliations). You can submit the article as single spaced, double spaced or in 2 columns resembling a journal article (e.g., Lamb and Willis 2011; Kuempel et al. 2021). Follow your instructor's guidelines for submission. Note: your instructor may provide a manuscript template document.

2. Write the materials and methods

The materials and methods section should describe the study in detail so that it is replicable for any investigator. In this section you will answer the following questions:

- Where does the study take place?
- What is your study population?
- What methods were used to collect and review the data?
- What is the planned statistical analysis?

You should modify methods from (Goetze et al. 2019) to reflect how data was collected in this assignment.

3. Describe your results

Report your major findings in a systematic manner. This section should be organized such that the primary question of the study is addressed followed by the secondary research questions. Your results should be presented in an objective manner without overinterpretation. Use illustrations such as figures, tables, and graphs to showcase the results of your study. The illustrations should be mentioned in your text.

4. Discuss your findings

The discussion section is where you will interpret your data and draw conclusions. Start with a brief description of the main findings of the study answering the following questions:

- Do *tabu* areas (MPAs) have different coral reef fish abundance compared to fished areas?
- Do *tabu* areas (MPAs) have different coral reef complexity compared to fished areas?
- Is there a relationship between coral reef complexity and fish abundance?

The next step is to present your findings in scientific context. This is where you will be sharing what other investigators have observed, which can either support or refute your findings.

Following this, the next step is to discuss potential limitations to the study by answering the following questions:

- Think about the study design. Would there be a better way to test the impact of *tabu* areas on coral reef complexity and fish abundance? Hint: What if we could decide which areas were *tabu* areas and which were not?
- What are some benefits and limitations to the DOV methodology used in this study?
- In this study we used only one left camera and we did not use any special software since we were not measuring fish length or behavior. Given this methodology limitation, what modifications to your methodology would you propose?
- What are some confounding and uncontrolled variables that may be present in this study?

To end your discussion section, you will write one to two conclusion sentences about the study. Finally, you will write a few sentences about what next steps can continue this line of research.

5. References

The reference section should be up to date with the latest publications related to your line of research. It is recommended that you use a reference manager (e.g., Mendeley, Zotero, Papers, or others).

6. Writing the abstract

Word Count: Should not exceed 300 words.
The Abstract should summarize the Introduction, Methods, Results, and Discussion in that order. Key points should be identifiable however, do not make conclusions that are not supported by evidence reported in the abstract.

ACTIVITY 4: WORKING IN COLLABORATIVE TEAMS ASSESSMENT

Overview

Working as teams is an extremely important part of scientific research, particularly when working internationally on peer-reviewed manuscripts. If your instructor assigns Activity 3 as a group assignment, fill out and submit the Team Evaluation Form (Appendix 3).

Activity 4 is a Working in Collaborative Teams Assessment worth 25 points where you evaluate the contributions of each team member—you should review the information associated with that Activity so you are prepared to answer the questions and meet team expectations. The form includes Part A to be completed before beginning the manuscript and Parts B and C to complete after writing the manuscript.

Part A. Decide and agree upon roles for each team member. One way to divide the manuscript is to have each section assigned a "leader" and all other team members as "reviewers." Also, as a group, decide on a timeline for when you will have components completed and the final draft submitted.

Part B. Write the name of each group member in a separate column. For each group member, indicate the degree to which you agree with the statements under "Evaluation Criteria" using the following scale and total the number in each column: 1 = strongly disagree, 2 = disagree, 3 = agree, 4 = strongly agree

Part C. Feedback (please use full sentences and provide thoughtful responses):
1. Reflect about how effectively your group worked.
2. Identify any problems or disputes that occurred during your interactions and how were they solved or alleviated?
3. Did making a group plan and timeline have a positive effect on your learning and your manuscript assignment?

You will be graded as follows:
- Submission of the peer evaluation form with Part B and C completed in full (5 points),
- Average score from your team evaluators in Part C (20 points).

ACKNOWLEDGMENTS

We would like to thank the reviewers for their thoughtful comments and the Wildlife Conservation Society for providing the video footage for this module.

REFERENCES

Burke, L., K. Reytar, M. Spalding, and A. Perry. 2011. Reefs at risk revisited. World Resources Institute, Washington, DC, USA.

Di Lorenzo, M., P. Guidetti, A. Di Franco, A. Calò, and J. Claudet. 2020. Assessing spillover from marine protected areas and its drivers: A meta-analytical approach. Fish and Fisheries 21(5):906–915. https://doi.org/10.1111/faf.12469.

Doulman, D.J. 1993. Community-based fishery management: Towards the restoration of traditional practices in the South Pacific. Marine Policy 17(2):108–117. https://doi.org/10.1016/0308-597X(93)90025-X.

Edgar, G.J., et al. 2014. Global conservation outcomes depend on marine protected areas with five key features. Nature 506(7487): Article 7487. https://doi.org/10.1038/nature13022.

Goetze, J.S., et al. 2019. A field and video analysis guide for diver operated stereo- video. Methods in Ecology and Evolution 10(7):1083–1090. https://doi.org/10.1111/2041- 210X.13189.

Grorund-Colvert, K. et al. 2021. The MPA Guide: A framework to achieve global goals for the ocean. Science 373(6560). https://doi.org/10.1126/science.abf0861.

Kastl, B., and S. Gow. 2014. Economic valuation of tourism and fisheries in the Vatu-i-Ra Seascape. Wildlife Conservation Society, Bronx, NY, USA. https://doi.org/10.13140/RG.2.2.34480.87048.

Kuempel, C.D., V.J.D. Tulloch, A.L. Giffin, V. Hagger, C. Phua, and O. Hoegh-Guldberg. 2021. Identifying management opportunities to combat climate, land, and marine threats across less climate exposed coral reefs. Conservation Biology 36(3):1523-1739. https://doi.org/10.1111/cobi.13856.

Lamb, J.B., and B.L. Willis. 2011. Using coral disease prevalence to assess the effects of concentrating tourism activities on offshore reefs in a tropical marine park. Conservation Biology 25(5):1044-1054. https://doi.org/10.1111/j.1523-1739.2011.01724.x.

Mangubhai, S., et al. 2019. Fiji: Coastal and marine ecosystems. Pages 765-792 in C. Sheppard, editor. World Seas: An Environmental Evaluation (Second Edition). Academic Press, Cambridge, MA, USA. https://doi.org/10.1016/B978-0-08-100853- 9.00044-0.

Mellin, C., M. Aaron MacNeil, A.J. Cheal, M.J. Emslie, and M. Julian Caley. 2016. Marine protected areas increase resilience among coral reef communities. Ecology Letters 19(6):629–637. https://doi.org/10.1111/ele.12598.

Reaka-Kudla, M.L., D.E. Wilson, and E.O. Wilson. 1996. Biodiversity II: Understanding and Protecting Our Biological Resources. Joseph Henry Press, Washington, DC.

Roberts, C.M., J.A. Bohnsack, F. Gell, J.P. Hawkins, and R. Goodridge. 2001. Effects of Marine Reserves on Adjacent Fisheries. Science 294(5548):1920–1923. https://doi.org/10.1126/science.294.5548.1920.

Robertson, T., S. Greenhalgh, I. Korovulavula, T. Tikoibua, P. Radikedike, and P. Stahlmann-Brown. 2020. Locally managed marine areas: Implications for socio- economic impacts in Kadavu, Fiji. Marine Policy 117:103950. https://doi.org/10.1016/j.marpol.2020.103950.

UNEP-WCMC, WorldFish Centre, WRI, and TNC. 2021. Global distribution of warm- water coral reefs, compiled from multiple sources including the Millennium Coral Reef Mapping Project. Version 4.1. Includes contributions from IMaRS-USF and IRD (2005), IMaRS-USF (2005) and Spalding et al. (2001). Cambridge (UK): UN Environment World Conservation Monitoring Centre. Data DOI: https://doi.org/10.34892/t2wk-5t34.

Williamson, D.H, Russ, G.R., Ayling, A.M. 2004. No-take marine reserves increase abundance and biomass of reef fish on inshore fringing reefs of the Great Barrier Reef. Environmental Conservation 31(2):149–159. https://doi.org/10.1017/S0376892904001262.

Woodhead, A.J., C.C. Hicks, A.V. Norström, G.J. Williams, and N.A.J. Graham. 2019. Coral reef ecosystem services in the Anthropocene. Functional Ecology 33(6):1023–1034. https://doi.org/10.1111/1365-2435.13331.

GLOSSARY

1. Anthropogenic: caused by human activity
2. Keystone species: a species upon which the structure, functioning or productivity of a habitat or ecosystem depends (for example: coral in a coral reef)
3. Marine protected areas: areas of the marine environment protected by various strategies, such as closures, management, or scientific study
4. *Tabu*: a community-based management strategy in Fiji where fishing is prohibited; named for the customary closure of a fishing ground following a local Chief's death
5. Diver operated videos (DOVs): videos collected by divers along a transect that are later analyzed to provide data about the area
6. Transect: a predefined path that a scientist will follow to collect data
7. T-test: a statistical test used to determine whether there is a difference between two groups of data
8. R-squared value: a measure of how well the variation in one set of data can explain another set of data

NCEP materials are meant to be modifiable for each educator's specific classroom or training needs; adaptable Microsoft Word versions of modules are available for download through the NCEP module collection at https://ncep.amnh.org along with any available accompanying data files, appendices, presentations, teaching notes, and exercise solutions.

APPENDIX 1. STATISTICAL ANALYSIS SUBMISSION TEMPLATE

Name:

Part A. Is protection status related to coral reef complexity?

	Average	Standard Deviation
Tabu		
Fished		

P value:

Example results sentence:

Attach your graph.

Part B. Is protection status related to fish count?

	Average	Standard Deviation
Tabu		
Fished		

P value:

Example results sentence:

Attach your graph.

Part C. Is there a relationship between fish count and coral complexity?

P value:

Example results sentence:

Attach your graph.

APPENDIX 2. CONSERVATION BIOLOGY MANUSCRIPT GRADING RUBRIC

Criteria	Mastery	Proficient	Needs Improvement	Unsatisfactory
Title *Up to 5 points*	• Concise, specific, informative. • *5 points*	• Specific, but too wordy or jargon. • *4 points*	• Much too vague and/ or wordy. • *3 points*	• No title. • *0 points*
Abstract *Up to 7 points*	• Background/ big picture in 1-2 sentences. • Clear statement of question and/ or hypothesis. • Brief methods (2-3 sentences). • Major findings in no more than 2 or 3 sentences. • Concluding sentence related to statement of specific question or hypotheses. • *7 points*	• Background is too long. • Question and/or hypothesis are not clear. • Methods are excessive. • Too much detail about results. • Conclusion is vague. • *5 points*	• At least one element missing and the remainder are unclear. • Inadequate background. • No question or hypothesis. • Inadequate methods. • Not enough detail about results. • No conclusion. • *3 points*	• Multiple elements are missing. • *1 point*
Introduction Rationale of study *Up to 5 points*	• Justifies research in a compelling way to an audience of peers. • Demonstrates understanding of significance of the work. • Follows a clear, logical progression. • From what is known to what isn't known (i.e. "funnel shaped"). • Defines jargon and acronyms. • *5 points*	• Justification is too narrow or not geared to appropriate audience. • Logic occasionally is not clear or seems unorganized. • Student misunderstands some components of the work. • Some jargon and acronyms are not defined. • *4 points*	• Justification is too vague. • Significance of research is not demonstrated. • Logic is consistently unclear. • Most jargon and acronyms are not defined. • *3 points*	• Justification and significance are missing. • Logic is severely flawed. • Background is not appropriate for peers. • *2 points*
Introduction Questions, hypotheses, + predictions *Up to 7 points*	• Research question clearly stated and leads logically to hypothesis. • Hypotheses are clearly stated. • All variables that are part of the hypotheses are explained. • *7 points*	• Research question unclear or not sufficiently linked to hypotheses. • Hypotheses are present, but not in a logical place. • One of the variables that is part of the hypotheses is not discussed. • Irrelevant variable is introduced. • *5 points*	• Research question incorrectly posed or missing entirely. • Hypotheses are too vague. • More than one variable from the hypotheses is not discussed. • Multiple irrelevant variables are introduced. • *3 points*	• No research question. • No hypotheses. • Variables of interest are not discussed. • *1 point*

Materials and Methods Study system + location *Up to 5 points*	• Correctly describes study location, context, system. • *5 points*	• Too much or not enough detail provided. • Minor errors in details provided. • *4 points*	• Important details are absent. • *2 points*	• Does not include description of study location or system. • *0 points*
Materials and Methods Field and laboratory protocols used *Up to 5 points*	• Provides sufficient information for reader to repeat the work. • Clearly describes experimental design and sampling procedures with justification in relation to questions/ hypotheses/ predictions. • *5 points*	• Too much or not enough detail is provided. • Experimental design and sampling procedures are described but unclear and/or are not justified in relation to questions/hypotheses/ predictions. • *4 points*	• Excessive detail about experimental design and methods. • Design and methods not justified. • *2 points*	• Described methods are inaccurate and show a misunderstanding of the project. • No mention of experimental design. • *1 point*
Materials and Methods Data analysis *Up to 5 points*	• Graphing methods are appropriate to address the hypotheses posed and graphs are presented accurately. • *5 points*	• Graphing methods chosen are not ideal to address the hypotheses posed and/or graphs are presented with some inaccuracies. • *4 points*	• Graphing methods are not well-connected to hypotheses posed and are inaccurate. • *2 points*	• Graphing methods are not presented. • *0 points*
Results Description *Up to 7 points*	• Concisely and correctly summarizes all results. • Results statements are supported with reference to data and/ or statistics. • Results effectively address questions/ hypotheses posed. • Includes no in-depth analysis. • *7 points*	• Concisely and correctly summarizes most results. • Some results are unclear or unrelated to questions/ hypotheses posed. • Data are not used to support general statements. • Includes too much analysis/discussion. • *5 points*	• Some results are missing entirely and/ or results are mostly unclear. • Statements are not supported by data. • Includes frequent statements that should be in discussion. • *3 points*	• Results are not adequately explained or presented. • Results are unrelated to questions/ hypotheses. • More than half of the text belongs in the discussion. • *1 point*
Results Figures or Tables *Up to 7 points*	• Each figure/table makes an important contribution. • Figures/tables illustrate data correctly and with error bars. • Figures/tables have complete captions/legends and are formatted appropriately. • *7 points*	• Unnecessary table or figure. • Figures/tables may lack properly calculated error bars. • Figure captions/ legends are incomplete. • Occasional formatting errors. • *5 points*	• A necessary table or figure is missing entirely. • Data is presented inaccurately. • Many captions/ legends are incomplete. • Frequent formatting errors. • *3 points*	• Multiple figures or tables are missing. • Inadequate figures. • *1 point*

Discussion Introduction + data interpretation *Up to 5 points*	• Briefly restates the results within the context of the study. • Describes whether and how data support the hypothesis. • Effectively links findings to the research question/ objective. • Addresses unexpected anomalous results with specific ideas (not speculation). • *5 points*	• Restates too much detail from the results or does not interpret results clearly. • Whether the data supports the hypothesis is not clear. • Only partially links results to question/ objective. • Unexpected result is addressed with speculation. • *4 points*	• Restatement of results is too vague or has some misinterpretation. • The results are not linked to the hypothesis or research questions. • Interpretation of findings is weak or missing. • *3 points*	• No restatement of results. • Inadequate discussion of findings. • *2 points*
Discussion Main body *Up to 7 points*	• Interprets results in the context of primary literature. • Utilizes topic sentences to effectively structure discussion. • Effectively references results in relation to paragraph content and topic sentence thesis. • Explains similarities and differences to published results. • Accurately presents conservation theory in the interpretation of results. • *7 points*	• Some results are not discussed relative to primary literature. • Topic sentences are not wholly related to content within paragraphs. • Explains results without relation to topic sentence thesis. • Limitations of study or explanations of some findings are missing. • Conservation theory is presented but not related to results. • *5 points*	• More than one result is not discussed relative to primary literature. • Results are summarized but without interpretation and explanation. • Topic sentences are missing. • Explanations for several findings are missing. • Conservation theory is misrepresented. • *3 points*	• Results were not discussed relative to the primary literature. • Topic sentences are missing. • Conservation theory is absent. • *1 point*
References *Up to 15 points*	• Citations are appropriate and well chosen, showing adequate background research on the topic. • Citations are provided for background, justification, and any specific methods or claims. Correct formatting of citations within the text and literature cited section. • 5+ primary sources used. Zotero (or other reference manager) used properly. • *15 points*	• Some references are not relevant. • Some sections are missing references. • A couple of formatting issues. • A few references are not primary literature. • Incorrect reference format used. • *12 points*	• Several references are not relevant. • Frequent formatting issues. • Fewer than 5 references are included. • Zotero (or other reference manager) not used. • *8 points*	• Lack of relevant references. • *5 points*

Formatting *Up to 5 points*	• Appropriate length and structure for scientific manuscript. • Details are apportioned properly among the paper sections, which occur in the correct order. • 2-4 Figures and/or Tables presented. • *5 points*	• Paper is too short or too long. • Has some details placed in the wrong sections. • Sections are presented out of order. • Only 1 Figure or Table is presented. • *4 points*	• Paper is much too short or too long. • Completely missing a section. • *3 points*	• Paper does not follow formatting guidelines. • *2 points*
Readability *Up to 15 points*	• Writing is compelling and at an appropriate level. • Paper is organized around detailed topic sentences that provide a clear outline of the paper. • Contains few or no inaccurate statements. • Language is precise and scientific. • Writing is relatively free of grammar errors and typos. • *15 points*	• Writing is of high quality but at times vague or disorganized. • Some topic sentences are weak and/or do not forecast the paragraph contents. • A couple of inaccurate statements. • Occasional overuse of passive tense or jargon. • Occasional grammar errors and typos. • *12 points*	• Writing is frequently unclear or unscientific. • Paper is not organized around topic sentences. • Several inaccurate statements. • Language and grammar occasionally impede comprehension. • *8 points*	• Writing is mostly unclear. • Multiple inaccurate statements. • Much of the writing is difficult to understand because of grammar issues. • *5 points*

APPENDIX 3. CONSERVATION BIOLOGY MANUSCRIPT TEAM EVALUATION FORM

Part A. Prior to beginning the manuscript, agree upon roles for each team member. Write them here.

Group Member 1: _____

Group Member 2: _____

Group Member 3: _____

Group Member 4: _____

Part B. Write the name of each group member in a separate column. For each group member, indicate the degree to which you agree with the statements under *Evaluation Criteria* using the following scale and total the number in each column:

1 = strongly disagree, 2 = disagree, 3 = agree, 4 = strongly agree

Evaluation Criteria	**Example** AB Smith	**Group Member 1**	**Group Member 2**	**Group Member 3**	**Group Member 4**
Contributes meaningfully to group discussions	Score 1 - 4				
Completes group assignments on time	Score 1 - 4				
Prepares work in a quality manner	Score 1 - 4				
Demonstrates cooperative and supportive attitude	Score 1 - 4				
Contributes overall to the success of the project	Score 1 - 4				
TOTAL (out of 20 points possible)					

Part C. Write out responses to the following prompts. Please use full sentences and provide thoughtful responses.

1. Reflect about how effectively your group worked.
2. Identify any problems or disputes that occurred during your interactions and how were they solved or alleviated?
3. Did making a group plan and timeline have a positive effect on your learning and your manuscript assignment?

What is Community Science, and How Do I Get Involved?

J. Stephen Gosnell[i,ii]

[i]*Department of Natural Sciences, Baruch College CUNY, New York, NY, USA;* [ii]*The Graduate Center of the City University of New York, New York, NY, USA*

ABSTRACT

Community science allows individuals who are not professional scientists to contribute to active scientific research. In this exercise, students learn about the history and growth of community science efforts and how they connect participants to data. Defining traits of community science are discussed, along with examples and potential future directions. Students then have the opportunity to contribute as community scientists by working with projects hosted on the Zooniverse site. Follow-up questions have them reflect on this experience and relate their activity to the larger field.

LEARNING OBJECTIVES

After completing this exercise, students will be able to:
1. Identify key characteristics of community science.
2. Provide examples of how the public may be involved in community science through data collection.
3. Describe how the public may contribute to community science through data analysis, with a focus on participating in projects hosted on the Internet.
4. Contribute to a community science project hosted on Zooniverse.com.
5. Reflect on the project they participated in and consider how it exemplifies the characteristics of community science.

INTRODUCTION

The act of collecting and analyzing data in an attempt to answer questions about the natural world has long included individuals that are not trained or employed in scientific fields (Miller-Rushing et al. 2012). For example, many farmers and hunters have traditionally kept data on pest outbreaks and harvests. Members of the public have also contributed directly to research by providing observations and samples to scientists and collections (Miller-Rushing et al. 2012). These efforts allowed for data collection that would have not have been possible for anyone alone to accomplish and were early examples of what we now call community science.

Community science can be defined in multiple ways (National Academies of Sciences 2018; see Box 1 for more information on the term and related terms). Here we focus on efforts where individuals who are not professionally trained and are not employed by traditional research institutions, and who are often volunteers, play a vital role in the production of scientific knowledge (Miller-Rushing et al. 2012; National Academies of Sciences 2018). In other words, a "core feature" of these efforts is "nonscientists engaging in doing science"(National Academies of Sciences 2018). This focus on producing new scientific knowledge differentiates these activities from those focused purely on scientific outreach or training (Miller-Rushing et al. 2012), though community science efforts do serve to increase awareness of scientific issues and spread knowledge of scientific approaches (Bonney et al. 2016).

Community science projects may allow participants to engage in science by collecting or contributing data [Box 2]. This may take place in multiple ways. In some cases, project leaders may furnish community scientists with materials and/or instructions so they can conduct experiments and collect

Box 1. Community science: What's in a name?

Community science may also be known as citizen, neighborhood, or civic science. Here we use the term "community science" to define this range of efforts with a noted requirement that activities are connected to active research (National Academies of Sciences 2018), although others (Cooper et al. 2021) have noted potential issues with this "rebranding". Different groups have used these related terms in different, but often overlapping, ways (Eitzel et al. 2017; Cooper et al. 2021). While all involve projects where individuals without formal scientific training contribute to scientific activities (Miller-Rushing et al. 2012; National Academies of Sciences 2018), they may differ in goals, leadership, scale, and scope. For example, some efforts are led by professional scientists or affiliated institutions who are involving the public in data collection or analysis focused on traditional scientific products (e.g., articles, presentations); others, including those more historically known as community science, focus on efforts that are not led by scientists affiliated with professional research institutions that may have goals that are more community-focused (Cooper et al. 2021). However, over the past several years multiple groups [e.g., Audubon ("Why We're Changing From 'Citizen Science' to 'Community Science'" 2018)], Great Smoky Mountains Institute at Tremont (Staff 2019) have specifically changed the name of their volunteer-focused efforts to "community science" in an effort to become more inclusive. This is in response to issues regarding the geographic and political connotations associated with the term "citizen" and the fact that most participants in community-science endeavors are white, college-educated adults (National Academies of Sciences 2018; Cooper et al. 2021). Similarly, the use of the term "amateur" or "project-relevant" (National Academies of Sciences 2018) scientist creates a power imbalance that may be inappropriate, especially as many of these projects would not be possible without the public's participation. Also, while most projects rely on volunteers, some projects do financially compensate participants (Kaartinen et al. 2013).

data. For example, efforts to consider oyster enhancement potential of three sites in North Carolina were aided by community members (Anderson et al. 2019). Community members grew oysters on their docks for 6-12 months before transporting them to one of the three sites. Oysters were deployed within 2 hours of collection, enabling community members to observe the full experimental process, and subsequently monitored for eighteen months as part of a pilot program. As another example, in Chicago, community scientists deployed and monitored a playback experiment kit to study the impacts of predator calls on bird behavior (Zuckerberg et al. 2022).

Other projects may have community scientists collect observations in focused efforts. In New York, volunteers help monitor oyster growth and reef biodiversity at restored sites (McCann 2019). Other examples include the Christmas Bird Count and North American Breeding Bird Survey, both organized events where volunteers collect data on bird diversity, and bioblitzes, where volunteers work in teams alongside taxonomic experts to rapidly document diversity in multiple groups during a specified period at a focal site (Parker et al. 2018).

Volunteer connections with data may also include opportunistic efforts where collected data (e.g., observations of species) are not directly connected to a research project but are later harnessed by researchers. For example, websites and apps such as iNaturalist, where members can post geo-tagged photos of organisms they have observed, or eBird, where birders can submit bird checklists, may be used to provide data for future scientific studies (Bonney 2021). All of these efforts may increase the temporal and spatial range of observations (Cohn 2008).

Box 2. Examples of community science

Although community science projects go beyond outreach, civic engagement, or training, they all do offer chances for education and outreach. As a result, many efforts are focused on or include children or young adult contributors.

Measuring manure

Student members of 4H Federation of Finland, a youth organization with a focus on agriculture, helped with a project focused on determining the importance of invertebrate communities to waste removal via decomposition (Kaartinen et al. 2013). For each focal farm, students collected manure from a cattle barn and formed it into 15 standardized "pats". Five pats were used to sample dung beetle diversity, with students sending samples to scientists leading the project. The remaining ten were assigned to five treatments that limited access by different decomposers.

Restoring oysters in New York Harbor

The Billion Oyster Project of New York, United States, is a group committed to restoring oyster reefs in the New York Harbor in order to improve water quality and protect shorelines. Many of their projects involve volunteers. School-age participants and teachers from the local area are directly involved in data collection as they deploy and monitor oyster research stations, or floating mini-reefs containing approximately 300 oysters. Students check the research stations regularly and collect and share data on oyster growth, water quality, and biodiversity (see related NCEP exercise in Gosnell and Schreiber in review). Other community members can join similar efforts at several community oyster reefs throughout the city. Volunteers also help in building and filling the cages and other structures used to house oysters at restoration sites, and local restaurants can contribute discarded oyster shells for use in future restoration work.

Students across Finland conducted field experiments focused on quantifying dung beetle diversity and impacts of beetle communities on decomposition. Photo credit: Timo Marttila.

Students measure oyster growth and invertebrate diversity in an oyster research station. Photo used with permission of Billion Oyster Project. Photo credit: Billion Oyster Project.

Community scientists may also engage with data synthesis or analysis. For example, multiple websites such as Zooniverse now allow participants to contribute to projects by processing records or samples. Volunteers may transcribe data from handwritten notes to digital format or analyze camera trap data. These projects take advantage of the fact humans are innately good at tasks that are hard to

automate, such as pattern and hand-writing recognition.

In order for community science efforts to be used towards the production of scientific knowledge, projects must use systematic approaches in regard to data collection, synthesis, and analysis. For example, projects posted on Zooniverse typically have clear instructions and tutorials to train volunteers, and projects that ask community scientists to deploy experiments and/or collect data must provide clear guidance [e.g., species identification information (Pavía et al. 2023)]. Since community science projects are producing real research, these projects must also meet widely recognized standards of scientific integrity. Community science efforts now play a key role in many studies published in academic journals and may also be used to construct reports or management plans. The integrity of these outputs requires ensuring the data used are of the highest quality.

Quality checks and assurances may be carried out in multiple ways. Projects may have data-based efforts randomly checked by staff, or the same data may be analyzed or transcribed by multiple participants in order to ensure accuracy (Gura 2013). Projects relying on opportunistic data, like that generated by iNaturalist, also need to consider how human behavior may influence collections (Knape et al. 2021). For example, weekend increases in sightings of organisms are more likely due to observer schedules than organism traits or phenology. Evidence indicates, however, that opportunistic data may be useful for research and management, especially alongside (and not as a replacement for) other biomonitoring tools and approaches employed in planned, standardized surveys (Rapacciuolo et al. 2021; Zulian et al. 2021; van Tongeren et al. 2023)

One reason for the recent growth of community science projects is the availability of technology. Internet access and smartphone prevalence give many people the ability to collect, share, and analyze data (Bonney et al. 2014; Bonney 2021). Advances in technology will only continue to increase these connections. For example, recent advances have been developed that allow photos of footprints to be automatically matched to individual organisms using software; this technology, known as Wildtrack, combined with community scientist input via photos of footprints, has the potential to allow large carnivores and other organisms to be monitored at greatly reduced costs (Alibhai et al. 2017).

Involving community scientists in projects can also allow projects to grow beyond boundaries that might be set by traditional research ventures due to constraints related to finances or human resources. Volunteer contributions at any point may make a project less expensive (Kaartinen et al. 2013), and in many cases will actually make a project feasible. In fact, estimates suggest volunteers may be providing value to science that rivals that of major funding agencies (Theobald et al. 2015). These projects have other benefits as well. For example, they may increase effort on topics related to local concerns (Miller-Rushing et al. 2012).

The ability to focus on local concerns and involve a large number of participants also means community science projects may play a key role in diversifying who participates in science. These projects may expand the public's perception of who can be a scientist and what science looks like. Integrating community science projects into early (e.g., K-12 or primary and secondary) educational settings may be especially useful. Researchers are also considering how community science projects can be structured to offer maximal learning outcomes or other benefits for participants (National Academies of Sciences 2018; Bonney 2021; Peter et al. 2021) while also minimizing negative environmental impacts related to habitat visitation or reliance on personal vehicles and associated fuel usage (Gillings and Harris 2022).

EXERCISE

Zooniverse (https://www.zooniverse.org/) is one of the world's largest portals for community science projects. You can learn more about the site by looking at the FAQ (https://www.zooniverse.org/about/faq) and information (https://www.zooniverse.org/about) sections. Although Zooniverse has projects on topics ranging from history to astronomy, for this exercise you'll select one project from the Climate or Nature tab. You may register for the site so you can track your work, but few projects require it.

First, survey the range of projects available for the public to participate in. Go to the Projects tab and select "Climate" or "Nature".

1. Use the tabs to learn more about 3 projects. Briefly describe each.
2. How do they differ, and how are they similar? List at least 3 similarities and 3 differences among the projects.

Choose one that you find the most interesting and would like to contribute to.

3. Which project did you choose and why?
4. What are the goals of the project, and why do you think it is important?

Spend at least 30 minutes collecting or analyzing data for the project.

5. Save a screenshot showing what you did as a community scientist and include in the submission of your assignment. Explain what the image shows and briefly describe what you did for the project as a community scientist.
6. How did the project exemplify the use of "systematic approaches" (clear, standardized methods) to data collection or analysis?
7. What is a hypothesis that could be tested using the data that you worked with?
8. Did you find working on the project interesting? Why or why not?
9. Were you surprised by what research can look like? What did you expect, and how did your experience meet your expectations?
10. Would you volunteer your time on the site again? Why or why not?

EXTENDED ACTIVITIES

- Use the information you find on Zooniverse to prepare a short "commercial" or social media post for the project you worked on. You should focus on what the project is trying to accomplish, what you did, and why someone should want to contribute.
- Identify a local opportunity to contribute to data collection as a community scientist and take part!

ACKNOWLEDGEMENTS

This exercise was originally developed with funding provided by Baruch College as part of New York's Open NYS initiative. Module development was further supported by a grant from the National Science Foundation (Award # 1839656).

REFERENCES

Alibhai, S., I.Z. Jewel, and J. Evans, J. 2017. The challenge of monitoring elusive large carnivores: An accurate and cost-effective tool to identify and sex pumas (*Puma concolor*) from footprints. PLOS ONE 12:e0172065. Public Library of Science.

Anderson, L., P. Sacks, M. Donnelly, V. Barker, S. Anderson, and L. Walters. 2019. Oyster reef enhancement utilizing gardened oysters in a subtropical estuary. Restoration Ecology 27:966–973.

Bonney, R. 2021. Expanding the impact of citizen science. BioScience 71:448–451.
Bonney, R., T.B. Phillips, H.L. Ballard, and J.W. Enck. 2016. Can citizen science enhance public understanding of science? Public Understanding of Science 25:2–16.
Bonney, R., J.L. Shirk, T.B. Phillips, A. Wiggins, H.L. Ballard, A.J. Miller-Rushing, and J.K. Parrish. 2014. Next steps for citizen science. Science 343:1436–1437.
Cohn, J.P. 2008. Citizen science: Can volunteers do real research? BioScience 58:192–197.
Cooper, C.B. et al. 2021. Inclusion in citizen science: The conundrum of rebranding. Science 372:1386–1388.
Eitzel, M.V. et al. 2017. Citizen science terminology matters: Exploring key terms. Citizen Science: Theory and Practice 2017:1–20.
Gillings, S., and S.J. Harris. 2022. Estimating the carbon footprint of citizen science biodiversity monitoring. People and Nature 4:996–1006.
Gosnell, J.S., and K. Schreiber. In review. Using data to support oyster restoration in New York City. Lessons in Conservation. Network of Conservation Educators and Practitioners, Center for Biodiversity and Conservation, American Museum of Natural History, New York, NY.
Gura, T. 2013. Citizen science: Amateur experts. Nature 496:259–261.
Kaartinen, R., B. Hardwick, and T. Roslin. 2013. Using citizen scientists to measure an ecosystem service nationwide. Ecology 94:2645–2652.
Knape, J., S.J. Coulson, R. van der Wal, and D. Arlt. 2021. Temporal trends in opportunistic citizen science reports across multiple taxa. Ambio 51:183–198.
McCann, M. 2019. Restoring oysters to urban waters: Lessons Learned and Future Opportunities in NY/NJ Harbor. The Nature Conservancy, New York, NY. Available from: https://www.nature.org/content/dam/tnc/nature/en/documents/new-york-city-restoring-oysters-lessons-learned-2019.pdf (accessed December 2, 2023).
Miller-Rushing, A., R. Primack, and R. Bonney. 2012. The history of public participation in ecological research. Frontiers in Ecology and the Environment 10:285–290.
National Academies of Sciences E. 2018. Learning through citizen science: Enhancing opportunities by design. Available from: https://nap.nationalacademies.org/catalog/25183/learning-through-citizen-science-enhancing-opportunities-by-design (accessed July 3, 2022).
Parker, S.S., G.B. Pauly, J. Moore, N.S. Fraga, J.J. Knapp, Z. Principe, B.V. Brown, J.M. Randall, B.S. Cohen, T.A. Wake. 2018. Adapting the bioblitz to meet conservation needs. Conservation Biology 32:1007–1019.
Pavía, C.E.C., F. Mascareño Suárez, J. Brunetti, M. Eliceche, and K.A. Ayres. 2023. Seasonal occurrence and environmental drivers of pelagic shark species in Los Cabos, Mexico, assessed using citizen science. Environmental Biology of Fishes. Available from https://doi.org/10.1007/s10641-023-01434-w (accessed June 22, 2023).
Peter, M., T. Diekötter, K. Kremer, and T. Höffler. 2021. Citizen science project characteristics: Connection to participants' gains in knowledge and skills. PLOS ONE 16:e0253692.
Rapacciuolo, G., A. Young, and R. Johnson. 2021. Deriving indicators of biodiversity change from unstructured community-contributed data. Oikos 130:1225–1239.
Staff, T. 2019, October 8. Why we are changing "Citizen Science" to "Community Science." Available from: https://gsmit.org/why-we-are-changing-citizen-science-to-community-science/ (accessed July 3, 2022).
Theobald, E.J. et al. 2015. Global change and local solutions: Tapping the unrealized potential of citizen science for biodiversity research. Biological Conservation 181:236–244.
van Tongeren, E. et al. 2023. Unstructured citizen science reduces the perception of butterfly local extinctions: The interplay between species traits and user effort. Biodiversity and Conservation. Available from: https://doi.org/10.1007/s10531-023-02721-9 (accessed October 11, 2023).
Why we're changing from "Citizen Science" to "Community Science." 2018, May 3. Available from: https://debspark.audubon.org/news/why-were-changing-citizen-science-community-science (accessed July 3, 2022).
Zuckerberg, B., J.D. McCabe, and N.A. Gilbert. 2022. Antipredator behaviors in urban settings: Ecological experimentation powered by citizen science. Ecology and Evolution 12:e9269.
Zulian, V., D.A.W. Miller, and G. Ferraz. 2021. Integrating citizen-science and planned-survey data improves species distribution estimates. Diversity and Distributions 27:2498–2509.

NCEP materials are meant to be modifiable for each educator's specific classroom or training needs; adaptable Microsoft Word versions of modules are available for download through the NCEP module collection at https://ncep.amnh.org along with any available accompanying data files, appendices, presentations, teaching notes, and exercise solutions.

Lessons from Lizards: Adaptation to Introduced Ants

Nicole A. Freidenfelds[i], Jennifer M. Deitloff[ii], and Tracy Langkilde[iii]

[i]Department of Natural Resources and the Environment, University of Connecticut, CT, USA; [ii]Department of Biological Sciences, Commonwealth University of Pennsylvania, PA, USA; [iii]Department of Biology, Eberly College of Science, Pennsylvania State University, PA, USA

ABSTRACT

The fence lizard and fire ant ecological system provides an excellent real-world case study for students to examine the impacts of nuisance introduced species on native organisms, with particular emphasis on the topic of adaptation. In this exercise, students are tasked with making predictions, analyzing real scientific data, and applying critical-thinking strategies to interpret their results. A reflection component at the end of the exercise involves the creation of a concept map to synthesize and integrate ideas from the lesson within the broader context of natural selection.

LEARNING OBJECTIVES

After this case study and exercise, students will be able to:
1. Identify the negative impacts that red imported fire ants can have on people and native organisms.
2. Predict and interpret the behavioral response of native lizards to attack by red imported fire ants.
3. Use evidence to explain how native fence lizard populations can respond, through different kinds of adaption processes, to the presence of red imported fire ants.
4. Apply statistical analysis to support an explanation that lizards with an advantageous trait tend to increase in proportion to those lacking this trait.

INTRODUCTION

William Buren described the red imported fire ant with the specific epithet name invicta*, meaning invincible, because of its resilient nature and the belief that it would be difficult to manage. The ant has proven to be appropriately named.*

- Department of Entomology and Plant Pathology, Auburn University

How can introduced species impact native organisms? Can populations of native organisms change in response to the establishment of introduced species? These important questions have implications for the conservation of ecological communities on scales from local to global, to which humans are intricately linked. In this module, you will engage and explore these questions and background concepts. Then you will take on the role of a research scientist working in the Southeastern United States and studying the ecology and behavior of native eastern fence lizards and red imported fire ants, an introduced species that is considered a nuisance. You will make predictions based on your observations, statistically analyze your data, and explain your results in the context of natural selection and adaptation.

PART A: ENGAGE AND EXPLORE

Background concepts: Natural selection

The purpose of this section is to generate curiosity and elicit responses that uncover what you know or think about natural selection. To begin, record your observations and any questions that come to mind in the graphic organizer below while watching this short video: https://youtu.be/X9VqF5xF8os?si=a0aLWpwGLaLcyrOC&t=3 (note: you might need to watch it more than once).

Provide as many detailed observations as possible in the *I notice* column and aim for at least three questions in the *I wonder* column.

I notice...	**I wonder...**
Example: something crawling on the lizard	*Example: what kind of lizard is that?*

Next, in small groups and using a large sheet of paper (or another approach recommended by your instructor), take about five minutes to create a drawing that illustrates *natural selection*—the process whereby organisms better adapted to their environment tend to survive longer and produce more offspring (Figure 1). The drawing can include labels, if necessary, but should have limited text. After five minutes, share and view the other groups' drawings. Discuss as a class what your group drew and the drawings you saw.

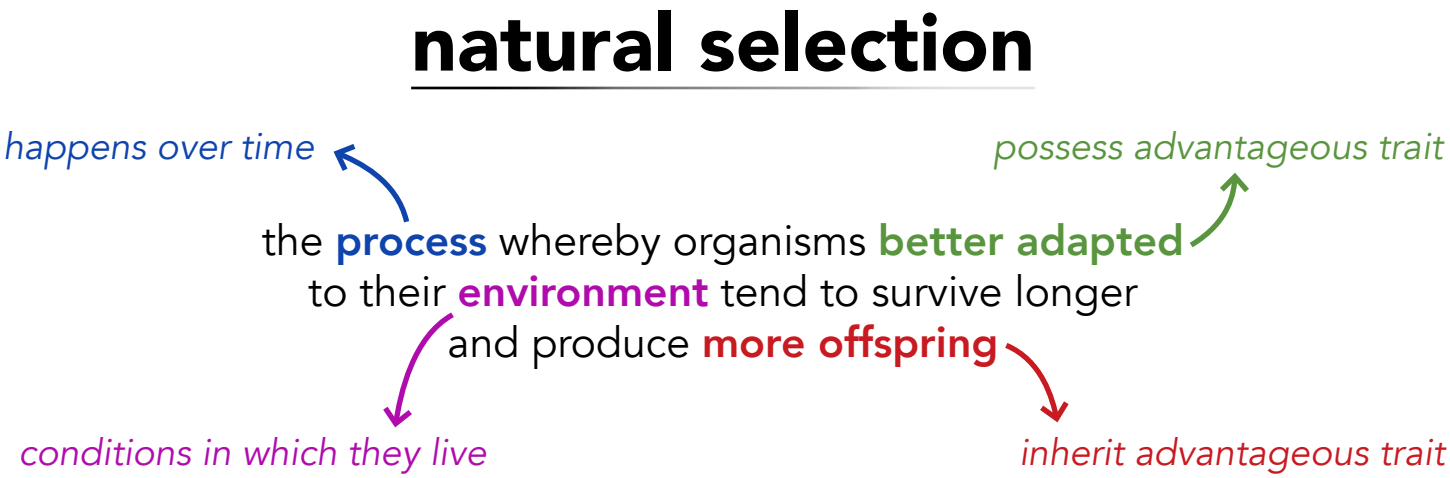


Figure 1. Expanded definition of *natural selection*.

Background concepts: Adaptation

Adaptation, as pointed out by Begon and colleagues (1996), is "a confusing word used to mean quite different things.

i. Characteristics of organisms evolved as a consequence of natural selection in its evolutionary past and which result in a close match with features of the environment and/or constrain the organism to life in a narrow range of environments.
ii. Changes in the form or behavior of an organism during its life as a response to environmental stimuli.
iii. Changes in the excitability of a sense organ as a result of continuous stimulation."

This case study and exercise explores adaptation as described in the first two definitions above. Focusing on definition (i) to start, an organism's evolved characteristics can be structural (physical), behavioral, or physiological (internal body process). Using the North American beaver (*Castor canadensis*) as an example, some of their evolved characteristics include:

- Webbed hind feet,
- Oil produced in special glands that they rub into their fur,
- Transparent inner eyelids,
- Ear and nose valves that close when submerged (e.g., under water), and
- Oxygen storage capacity in muscles is almost twice that of terrestrial mammals.

Discuss: Categorize each evolved characteristic as structural, behavioral, and/or physiological. How do you think these characteristics helped beavers, over time, survive better in their aquatic environment (e.g., ponds, wetlands)?

Elaborating on definition (ii) above, some organisms can respond behaviorally or physically to different environmental stimuli such as temperature. For example, the tree swallow (*Tachycineta bicolor*), a common and widespread bird species in northern North America, breeds earlier in warmer spring seasons (Dunn and Winkler 1999).

Discuss: What other environmental stimuli might trigger adaptive behavioral changes in an organism?

Species information: Eastern fence lizard

The eastern fence lizard (*Sceloporus undulatus*) is a medium-sized lizard (10–18.5 cm) native to eastern North America and occurs from the Atlantic coast to as far west as Texas (Conant and Collins 1998; Figure 2). Their average lifespan is uncertain but likely under five years. Belonging to the family of North American spiny lizards, eastern fence lizards have rough, pointed scales on their backs. They are gray to brown in color with a chevron pattern on their backs that can help them blend into their background. Most mature males, and some females, have patches of bright blue scales on their bellies and throats. Male eastern fence lizards establish and defend their territory by doing 'push-ups' to flash their blue scales and scare off other males.

Figure 2. Left: A juvenile eastern fence lizard (*Sceloporus undulatus*). Photo credit: Nicole Freidenfelds. Right: Can you spot the adult eastern fence lizard on the tree bark? Photo credit: Tracy Langkilde.

Eastern fence lizards are sit-and-wait predators that eat a wide variety of insects, spiders, and other invertebrates, including ants. They are common in many habitats, particularly open forests and field edges. Eastern fence lizards occasionally spend time on the ground foraging and moving between both natural and human-made basking/perch sites, such as tree stumps and tree trunks, rock piles, dead logs, and fence posts. Their cryptic coloration (i.e., camouflage) can reduce visual detection by some of their main predators including birds and domestic cats.

Species information: Red imported fire ant

Solenopsis invicta, commonly known as the red imported fire ant in the United States, is a species of fire ant native to tropical and subtropical South America; Figure 3). These ants thrive in ecologically disturbed areas and live in a wide variety of habitats such as rain forests, deserts, grasslands, alongside roads and buildings, and in electrical equipment (Callcott and Collins 1996). The red imported fire ant is one of the most successful nuisance species in parts of the world where humans accidentally introduced it: Australia, New Zealand, several Asian and Caribbean countries and the United States. See Box 1 for more information on introduced species.

Red imported fire ants have spread considerably throughout the southeastern United States since accidentally introduced into the port of Mobile, Alabama via cargo ship during the 1930s. They currently inhabit nearly 370 million acres in the U.S. and Puerto Rico. Counties throughout Texas, Arkansas, Oklahoma, Mississippi, Louisiana, Tennessee, Alabama, Georgia, Florida, South Carolina, and North Carolina are under Federal Quarantine, which restricts the interstate movement of regulated articles (e.g., hay, plants, soil) to prevent the human-assisted spread of fire ants (Figure 4).

Solenopsis invitca, like other ant species, perform valuable ecosystem functions such as nutrient turnover and soil modification, and serve as prey and detritivores within the system. As omnivores their diet consists of dead mammals, invertebrates (e.g., arthropods, earthworms), vertebrates, seeds, and sweet liquid substances from plants or honeydew-producing insects. In their native South American range, their abundance is moderated by competition with other ant species (Buren et al. 1974) and the presence of co-evolved predators (Porter et al. 1997). They often become the dominant ant species in introduced areas outside of their native range due to their aggressive foraging behavior, high reproductive capability and lack of predators and competitors (Allen et al. 2004).

Figure 3. Left: Red imported fire ants on a cotton swab. Right: Red imported fire ant mound in Covington County, Alabama. Photo credit: Nicole Freidenfelds.

Box 1: What's the problem with introduced species?

Introduced species are organisms non-indigenous to a specific region. While many introduced species are not destructive, some cause substantial damage to the ecosystem, economy, and/or public health in their new environment. There are several mechanisms through which introduced species can spread and establish themselves:

Introduction through human activities: This can happen accidentally through international trade, tourism, escape from captivity, or transportation. Organisms can "hitchhike" on goods, vehicles, or in ballast water from ships, or be introduced to an area by release of unwanted pets or live bait.

Intentional introduction: In some cases, species are deliberately introduced for specific purposes, such as agriculture, hunting, or ornament. However, these introduced species can become problematic if they have no natural predators, competitors, or pathogens in their new environment.

Climate change: As climates change, certain areas may become more hospitable to species that were previously limited by temperature or other factors. This can lead to species expanding their ranges and becoming problematic in new areas.

Lack of natural predators: Introduced species often lack natural predators or diseases that would normally keep their populations in check in their native ecosystems. This allows them to reproduce and spread rapidly in their new environment.

Rapid reproduction and adaptation: Introduced species often have high reproductive rates and adapt well to different conditions. This gives them a competitive advantage over native species in their new habitat.

Altered ecosystem dynamics: In some cases, introduced species can alter the ecosystem dynamics of their new habitat by outcompeting native species for resources like food, water, and shelter.

Where introduced, red imported fire ants can negatively impact people, agriculture, natural resources, and native organisms. They can damage crops by feeding on the buds and fruits of plants, especially corn, soybean, okra, and citrus. They sometimes chew through irrigation tubing and cause physical damage to other farm equipment from their mounds or through electrical shorts. A single fire ant can sting repeatedly, causing injury to, or killing livestock either intentionally to obtain prey or in fierce defense of their mound; young and newborn animals are especially susceptible to the ants' venom. All these actions can result in substantial economic losses. They can also harm wildlife by reducing native ant and other invertebrate biodiversity and injuring or killing native birds, reptiles, amphibians, and mammals (Allen et al. 2004). Because of their painful, venomous sting, red imported fire ants are a nuisance introduced species, particularly in urban areas, and can even cause allergic reactions including rare instances of anaphylactic shock in humans (Potiwat and Sitcharungsi 2015).

Species information: Fire ant-fence lizard interactions

These two species co-occur and overlap in habitat over much of the southern distribution of the fence lizards' range (Callcott and Collins 1996; Conant and Collins 1998; Langkilde 2009a). Fire ants build extensive underground tunnels to help them forage tens of meters away from their distinctive mounds, of which as many as 400 can be found on a single acre of land (Markin et al. 1975; Buhs

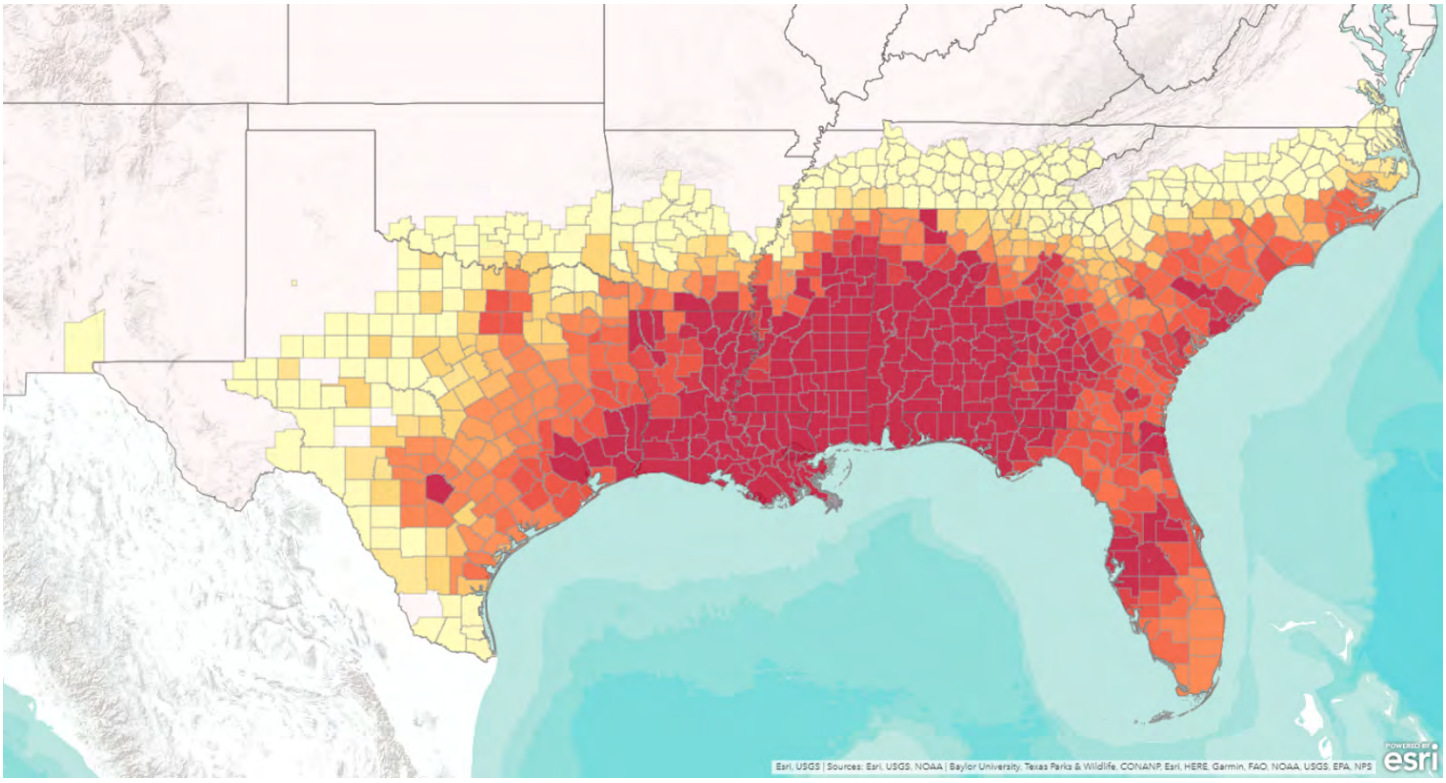


Figure 4. Map showing imported fire ant quarantined areas as of August 12, 2023. Color corresponds to the length of time since the quarantine was established in that county (dark = greater time). Visit the interactive online map (https://www.aphis.usda.gov/aphis/maps/plant-health/ifa-quarantine-mapping) to see if imported fire ants are expanding their range—are there new quarantine areas? You can also explore maps of other pests and diseases (https://www.aphis.usda.gov/aphis/newsroom/interactive-maps) surveyed by the United States Department of Agriculture Animal and Plant Health Inspection Service.

2005). Constantly using their efficient tracking capabilities to locate food sources, once fire ants find potential live prey, they use odor trails and chemical signals to quickly recruit other ants to join the attack (Vander Meer et al. 1988; Tschinkel 2006). This communication and cooperative behavior allows them to overcome and kill animals much larger than themselves, including fence lizards (Figure 5; also see: www.youtube.com/watch?v=F60agY1IpmU).

Researchers are studying how fence lizards and other native species respond to the threat of red imported fire ants. When fire ants and fence lizards come into contact, the lizards' behavior can determine whether or not they survive. Scientists discovered lizards that exhibit a behavioral response such as body twitching or fleeing can reduce their venom exposure and survive the attack. While it is possible that there exists a genetic basis to these behaviors and that lizard populations may adapt to exhibit higher frequencies of these behaviors, it is important to point out that not all behavioral responses are inherited and contribute to a population's evolution. As seen in adaptation's second definition (ii) above, some adaptive behaviors that improve an individual's longevity are environmentally induced and learned throughout an organisms' lifetime. Another factor to consider is that some behaviors may be adaptive and may be non-adaptive (i.e., counterproductive to an individual's survival or reproductive success), depending on the context or conditions.

Given the high frequency of encounters between fence lizards and red imported fire ants (Freidenfelds et al. 2012), there should be strong pressure for lizards to exhibit behavior that increases their survival. By understanding how animals at the edge of the fire ant inhabited area can protect themselves, scientists could aid the management of introduced species by providing insight into the

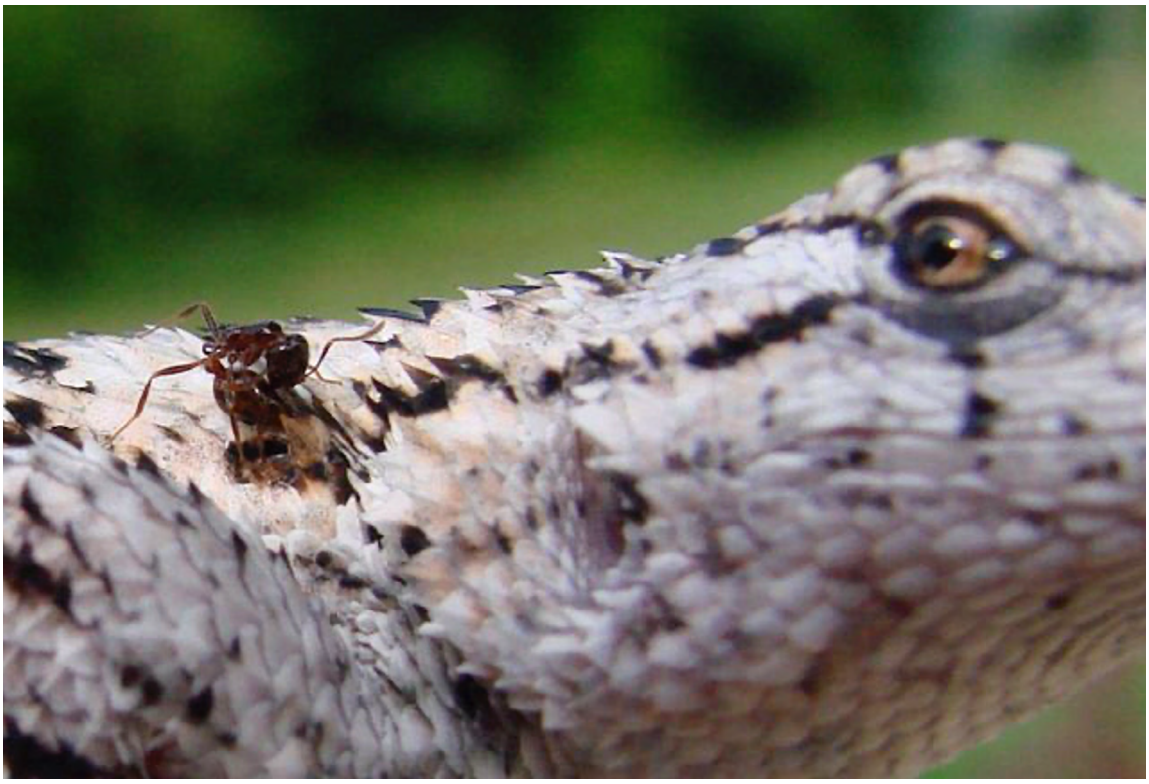


Figure 5. A red imported fire ant (*Solenopsis invicta*) attacking an eastern fence lizard (*Sceloporus undulatus*). The fire ant uses its mandibles to attach to the lizard and then pries up a scale to sting beneath it. Photo credit: Tracy Langkilde.

process and rate of behavioral adaptation both within and across generations of a population (e.g., Losos et al. 2004; Greenlees et al. 2010).

PART B: EXPLAIN

Key terms and misconceptions

Before continuing this exercise, read through and make sure you are familiar with these other key terms:

1. Advantageous: involving favorable circumstances that increase the chances of success.
2. Ecosystem: a biological community of interacting organisms and their physical environment.
3. Introduced Species: organisms non-indigenous to a specific region.
4. Native Species: a species that evolved to occupy a particular ecosystem without human assistance.
5. Nuisance Species: organisms that cause substantial damage to the ecosystem, economy, and/or public health, where introduced.
6. Population: group of organisms of the same species that live in the same area.
7. Proportion: a number considered in comparative relation to a whole.
8. Response: a reaction to something.
9. Statistically Significant: the likelihood that a relationship between two or more variables is caused by something other than chance.
10. Trait: distinguishing quality or characteristic.

Natural selection and adaptation are components of evolution, a complicated and often misunderstood process.

Pair and Share: Review and reflect on the misconceptions and realities about evolution highlighted in the table below.

Table 1. Common misconceptions, and corresponding realities, about evolution and evolutionary processes.

Misconception	Reality
Except for minor fluctuations from year to year, environmental conditions have stayed the same throughout the history of the earth.	The earth's history contains a rich past of significant and often dramatic changing environmental conditions and shifting land masses over millions of years.
Individual organisms can deliberately develop new heritable traits because they need them for survival.	Evolution does not occur through deliberate or conscious efforts of individual organisms. It operates through processes of variation, selection, and inheritance over long periods of time.
Sudden environmental change is required for evolution to occur.	While sudden environmental changes can sometimes drive rapid evolutionary responses, they are not a requirement for evolution to take place. Evolution is a continuous process that occurs in response to a variety of environmental conditions, both gradual and sudden.
Changes in a whole population cannot occur from the enhanced survival and reproduction of a few individuals.	Evolution is driven by the differential reproductive success of individuals with certain traits. This process of natural selection involves the preferential survival and reproduction of individuals with advantageous traits, leading to changes in the population over time.
Evolution happens when individual organisms acclimate or "get used to" new conditions gradually.	Evolution involves changes in the genetic makeup of populations over generations, not individuals over their lifetime, in response to environmental pressures.
Change occurs in the inherited characteristics of a population of organisms over time because of the use or disuse of a particular characteristic.	This "use/disuse" concept has been largely disproven by modern genetics. Evolution operates primarily through genetic variation, natural selection, and the accumulation of beneficial traits over generations.
Change to the characteristics of populations (i.e., the proportion of individuals in the population having certain traits) of organisms is always random and is not influenced by the favorability of that change in a given environment.	While variability in a population can arise by random chance, the process of evolution is driven by natural selection, where traits that enhance survival and reproduction in a given environment become more common over time. This results in a non-random change in the proportion of individuals with certain traits within a population.
Except for differences between males and females, and between young and old, all organisms of the same species look and act the same.	While individuals of the same species share certain common characteristics, there is inherent variation within populations due to genetic diversity that plays a crucial role in evolution and adaptation to changing environments.
The internal chemistry, appearance, and behavior of individuals of a species do not change, even over long periods of time.	Evolution is a continuous process that leads to changes in the internal chemistry, appearance, and behavior of individuals of a species over long periods of time.

Making predictions & analyzing results

Penn State biologist Dr. Tracy Langkilde conducts research on native fence lizards and their adaptive responses to the presence of red imported fire ants. The fire ants' well-documented spread through the southern U.S., and the fact that they are currently restricted to just a portion of the lizards' range, allows Dr. Langkilde's team to compare how lizards from ecologically similar areas differ behaviorally and physically based on the presence or absence of these fire ants.

Written Response: You have been given access to Dr. Langkilde's data in the associated Student Data Excel file provided by your instructor or downloaded from NCEP module collection at https://ncep.amnh.org. Read the Part B research study notes below (Table 2). Work individually or in pairs through the comprehension questions and then make predictions and analyze the results using online statistical software.

Table 2. Research study notes (Part B) from Langkilde, T. 2009. Invasive fire ants alter behavior and morphology of native lizards. Ecology 90:208–217.

Overview	Adult fence lizards were placed on fire ant mounds for 60 seconds and their behavior was recorded. If a lizard ran off the mound (fled) before 60 seconds, the trial was ended at the time recorded. Lizards were closely monitored to make sure they did not get stung by too many ants.
Trial #	The experiment was conducted on 80 lizards total, 40 from each location.
Location	Alabama: Southern part of the state where fire ants were introduced in the 1930s. Arkansas: Eastern part of the state which has not yet been inhabited by red imported fire ants.
# Twitches	Number of times a lizard twitched its body while being exposed to fire ants for 60 seconds.
Time to Flee (sec)	Lizards that did not flee off the fire ant mound within 60 seconds were removed and scored as "61" (this is a conservative estimate because they may never have fled off the mound).

This study adhered to federal requirements for the humane care and use of animals in research and was approved by Yale University's Institutional Animal Care and Use Committee.

1. How many different locations were the fence lizards in this study from and where were they?
2. How long ago were fire ants introduced in Alabama?
3. How were *Time to Flee* data recorded for lizards that did not flee (run) off the fire ant mound in 60 seconds?
4. How many lizards were tested from each location?
5. Complete the prediction based on background information that you have previously been provided: Lizards from _____ twitch _____ than lizards from _____ when exposed to red imported fire ants.

You will now test your prediction. Open the Excel file, click the *Data* tab and familiarize yourself with the information provided. (Note: you may use a spreadsheet software other than Microsoft Excel, but specific formula instructions or locations of functions may differ than what is provided here.)

To compare the two groups of lizards, those from Alabama versus those from Arkansas, you need to first calculate the average values for each. You do not need to do this with a calculator—Excel can do it for you. In the *Calculations* box under *Average # Twitches*, type the following for Alabama: =AVERAGE(C2:C41)

6. What is the average number of times that lizards from Alabama twitched in response to fire ants?

In the *Calculations* box under *Average # Twitches*, type the following for Arkansas: =AVERAGE(C42:C81)

7. What is the average number of times that lizards from Arkansas twitched in response to fire ants?

So what? Are these averages considered different from each other, or are they pretty much the same? Scientists will use statistical tests to support these types of determinations. You will now analyze the data using what is called an unpaired T-test. The unpaired T- test compares the averages of two groups.

8. What are the two groups you are comparing?
9. What variable did you calculate the average for?

Click the *GraphPad: unpaired T-test* link below the *Calculations* box in the Data tab of the Excel file. It should open the webpage shown in Figure 6 (left).

In the *1. Choose data entry format* box, make sure *Enter or paste up to 2000 rows* is selected.

In the *2. Choose a test* box, select *Unpaired t test*.

In the *3. Enter data box*, change the QuickCalcs data label text to *Alabama* and *Arkansas*. Then, in Excel, use your mouse to select the data in the *# Twitches* column (C) for only the Alabama lizards. Copy what you selected and paste it into the QuickCalcs box. Repeat for the Arkansas lizards. Your data should look like what is shown in Figure 6 (right).

Click the *Calculate Now* button.

Let's examine the results.

P value and statistical significance:

10. The two-tailed P value equals _____.
By conventional criteria, this difference is considered to be _____ statistically significant. What does this mean? A P value less than 0.05 means that the difference you observed would happen rarely due to random sampling, and most likely there is a difference that is large enough to be explained by the hypothesis you are testing. In short, the analysis tells us that there is a significant difference in the number of _____ between the two groups of lizards.

You will now visualize the data graphically in Excel. Type the average number of twitches you calculated earlier for each group in the *Part B Summary* tab where appropriate. Your first graph should have been generated automatically. It already includes error bars that indicate the uncertainty

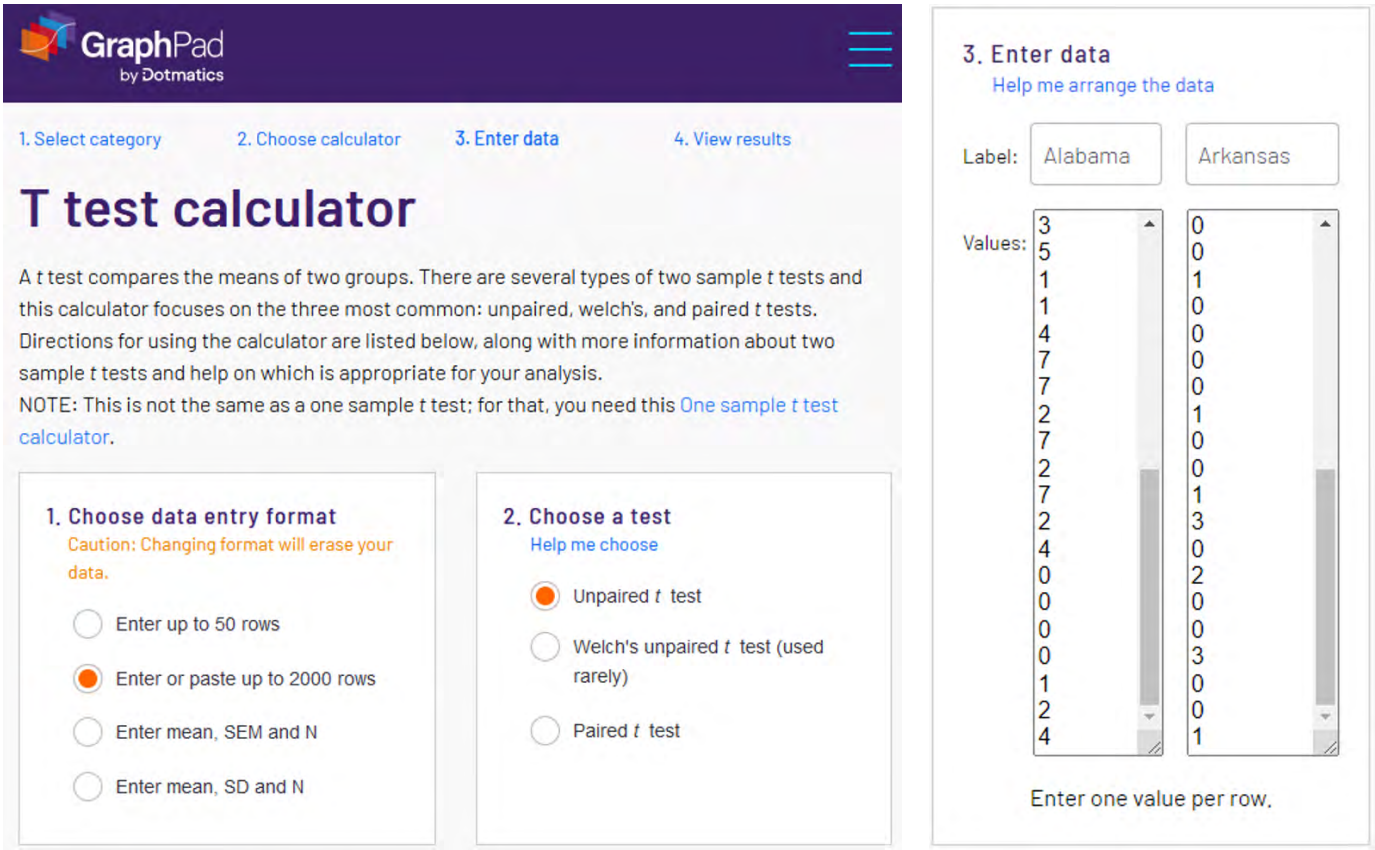


Figure 6. Screenshots of the GraphPad T test calculator webpage (https://www.graphpad.com/quickcalcs/ttest1/?Format=C).

in a reported measurement. Small error bars are good!

11. Describe the graph. Be as detailed as possible.
12. Was your earlier prediction correct? Explain why or why not.
13. Recall the second definition of adaptation in Part A: changes in the form or behavior of an organism during its life as a response to environmental stimuli. Why do you think the lizards from Alabama twitched more than those from Arkansas?
14. Now think about the data Dr. Langkilde measured for how long it took lizards to flee in response to fire ants. Make a prediction based on the background information that you have previously been provided: Lizards from _____ flee _____ than lizards from _____ when exposed to red imported fire ants.

In the *Calculations* box under *Average Time to Flee*, type the following for Alabama:
=AVERAGE(D2:D41)

15. What is the average time to flee for lizards from the Alabama site when exposed to fire ants?

In the *Calculations* box under *Average Time to Flee*, type the following for Arkansas:
=AVERAGE(D42:D81)

16. What is the average time to flee for lizards from the Arkansas site when exposed to fire ants?
17. What unit is *Time to Flee* reported in?

Again, we need to analyze these values to see if they are statistically different. Highlight, copy and paste into QuickCalcs the same way you did before and then click the *Calculate Now* button.

P value and statistical significance:

18. The two-tailed P value is less than _____.
    By conventional criteria, this difference is considered to be _____ statistically significant.
    What does that mean? Write out a result statement in your own words.

Create a graph of the *Time to Flee* data by typing the average values into the appropriate boxes in the *Part B Summary* tab. The graph with error bars should have been generated for you (if you don't see it, scroll down!).

19. Describe the graph. Be as detailed as possible.
20. Was your prediction correct? Explain why or why not.
21. How many seconds faster, on average, did lizards from Alabama flee from fire ants than lizards from Arkansas?
22. Why do you think the lizards from Alabama fled faster than those from Arkansas?
23. What can happen if a lizard does not twitch or flee (run away) in response to fire ants?
24. Based on the data you analyzed, which population of lizards, those from Alabama or Arkansas, do you think would survive better in the presence of fire ants? Explain why.

Read the following excerpt modified from Tylan and Langkilde (2023, The Conversation).

This [twitching/fleeing] behavior is common in baby fence lizards, which are vulnerable even to native ants, but is usually lost in adults as they outgrow threats from native ants by getting larger. However, in areas with fire ants, adult lizards retain this behavior that better enables them to survive fire ant attack.

Dr. Langkilde's research suggest that the higher percentage of behaviorally responsive adult lizards in fire ant areas could be the result of selection acting against unresponsive adults (e.g., if you don't twitch, you have a higher chance of dying from fire ant attack, and hence reproducing) and/or it could also be due to lifetime exposure that leads lizards to benefit from continuing some of their juvenile behaviors into adulthood.

What this means is that the fence lizard's twitching behavior is complicated! It may be that natural selection acts on a heritable twitching trait across generations for all lizards, even those that haven't been exposed to fire ants, because babies that twitch are more likely to survive into adulthood and reproduce. And, as lizards that live where fire ants have been introduced grow into adults, they learn to "keep twitching" because that behavioral response removes attacking fire ants.

Tylan and Langkilde continue…

Lizards can't tell whether they have a potentially deadly fire ant crawling on them or if it's something harmless like a fly. So, to be safe, they respond in the same way to anything that they feel climbing on their scales. Unfortunately, this shake-it-off behavior doesn't solve all the lizards' problems, since it breaks their usual camouflage, making them more obvious to visual predators like birds. We have observed more evidence of wounds in fire ant-adapted lizards.

25. Do you think adult lizards from Alabama twitched and fled in response to fire ants when they were

first introduced to the area in the 1930s? Explain why or why not.
26. Under what conditions could twitching and fleeing be non-adaptive lizard behaviors?

PART C: ELABORATE

Beyond behavior

Watch the lizard video again: https://youtu.be/X9VqF5xF8os?si=a0aLWpwGLaLcyrOC&t=3.

Pair and Share: Which physical trait or characteristic is most important in helping lizards remove fire ants? Focus on physical (body) traits that are easily measurable.

Written Response: You will again be using Dr. Langkilde's data in the associated Student Data Excel file. Read the Part C research study notes (Table 3) and examine Figure 7 below. Then, work through the following questions individually or in pairs.

Table 3. Research study notes (Part C) from Langkilde, T. 2009. Invasive fire ants alter behavior and morphology of native lizards. Ecology 90:208–217.

Overview	Adult fence lizards were placed on fire ant mounds for 60 seconds and their behavior was recorded. If a lizard ran off the mound (fled) before 60 seconds lapsed, the trial was ended at the time recorded. Lizards were closely monitored to make sure they did not get stung by too many ants.
BL (cm)	Body Length: measure of lizard body length from tip of snout (nose) to base of tail (Figure 6)
HLL (cm)	Hind Limb Length: measure of lizard hind limb length (Figure 6)
REL HLL (cm)	Relative Hind Limb Length: longer lizards have longer hind limbs; to account for differences in lizard size, it is important to compare the relative hind limb length, that is the length of the hind limb as a ratio of body length (REL HLL = HLL / BL)

1. All the data you have analyzed up until now have been behavioral data—how the lizards from different populations responded behaviorally to fire ants. Think back to the video you just watched. What physical (body) trait would best help a lizard remove fire ants crawling on it? You may want to watch the video again.
2. There are two types of physical trait data that Dr. Langkilde measured for each lizard, BL and HLL. What do these abbreviations stand for?
3. Why was it important to calculate a relative hind limb length?
4. What is the formula that Dr. Langkilde used to calculate the lizards' Relative Hind Limb Length (REL HLL)?

In the *Data* tab, type the following formula into the first empty box of the REL HLL column of the data table: =F2/E2

Click that box and while holding down the mouse button, highlight the rest of the empty boxes in that column. Release the mouse button and press CTRL+D (or Command+D on Mac) to autofill the formula into the rest of the boxes. There should now be data in the entire table.

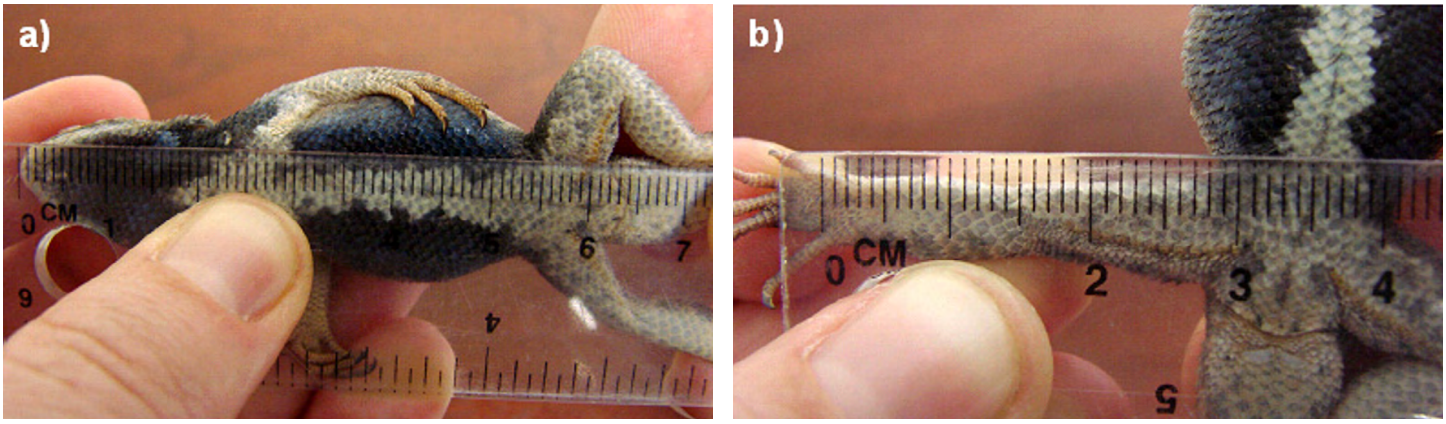


Figure 7. Demonstration of how eastern fence lizard a) Body Length and b) Hind Limb Length were measured in Dr. Tracy Langkilde's study. Photo credit: Nisha Ligon (photographer), Langkilde, T. 2009. Invasive fire ants alter behavior and morphology of native lizards. Ecology 90:208–217.

5. What unit of measure is REL HLL recorded in?
6. Make a prediction based on the background information that you have previously been provided: Lizards from _____ have _____ hind limbs than lizards from _____.

In the *Calculations* box under *Average REL HLL*, type the following for Alabama: =AVERAGE(G2:G41)

7. What is the average relative hind limb length of lizards from Alabama?

In the *Calculations* box under *Average REL HLL*, type the following for Arkansas: =AVERAGE(G42:G81)

8. What is the average relative hind limb length of lizards from Arkansas?
9. Do these two values seem very different, yes or no? What is the mathematical (i.e., numerical) difference between them?

You will again perform an unpaired T-test to statistically compare the averages of the two groups. Highlight, copy and paste into QuickCalcs the same way you did before and then click the *Calculate now* button.

P value and statistical significance:

10. The two-tailed P value is less than _____
    By conventional criteria, this difference is considered to be _____ statistically significant. How can a difference of only 0.013 cm be significant? For scale, most cell phones are slightly smaller than 1 cm thick.

Examine the data visually. Create a graph of the REL HLL data by typing the average values into the appropriate boxes in the *Part C Summary* tab. The graph with error bars should have been generated for you.

11. Describe the graph. Be as detailed as possible.
12. Was your earlier prediction correct? Explain why or why not.

It is hypothesized that there is a genetic basis to these differences in relative hind limb length. Read another excerpt from Tylan and Langkilde (2023, The Conversation):

We find lizard populations that have been living with fire ants have adapted [over generations] to have longer legs, which are better at removing fire ants when a lizard twitches and flees. This is a big shift for this species, reversing the latitudinal pattern we see in museum specimens—lizards tend to have shorter limbs the closer the population is to the equator.

The graph (Figure 8) shows data from the same two lizard populations in Dr. Langkilde's study. Use the graph and evidence from your statistical analyses from Part B and Part C to support the explanation that lizards with advantageous traits against fire ants tend to increase in proportion to those lacking these traits.

Putting the pieces together

Watch a brief video from Penn State Eberly College of Science for insights on additional research from Dr. Langkilde's team: "Lizards adapt to invasive fire ants, reversing geographical patterns in traits" (https://youtu.be/2jL6qOGV2BI).

Written Response: In pairs, create a concept map to illustrate how the fence lizard and fire ant system fits into the broader context of natural selection and adaptation (for guidance on concept maps, visit: https://scarfedigitalsandbox.teach.educ.ubc.ca/concept-maps-for-teaching-and-learning/ or https://creately.com/guides/how-to-create-concept-maps/).

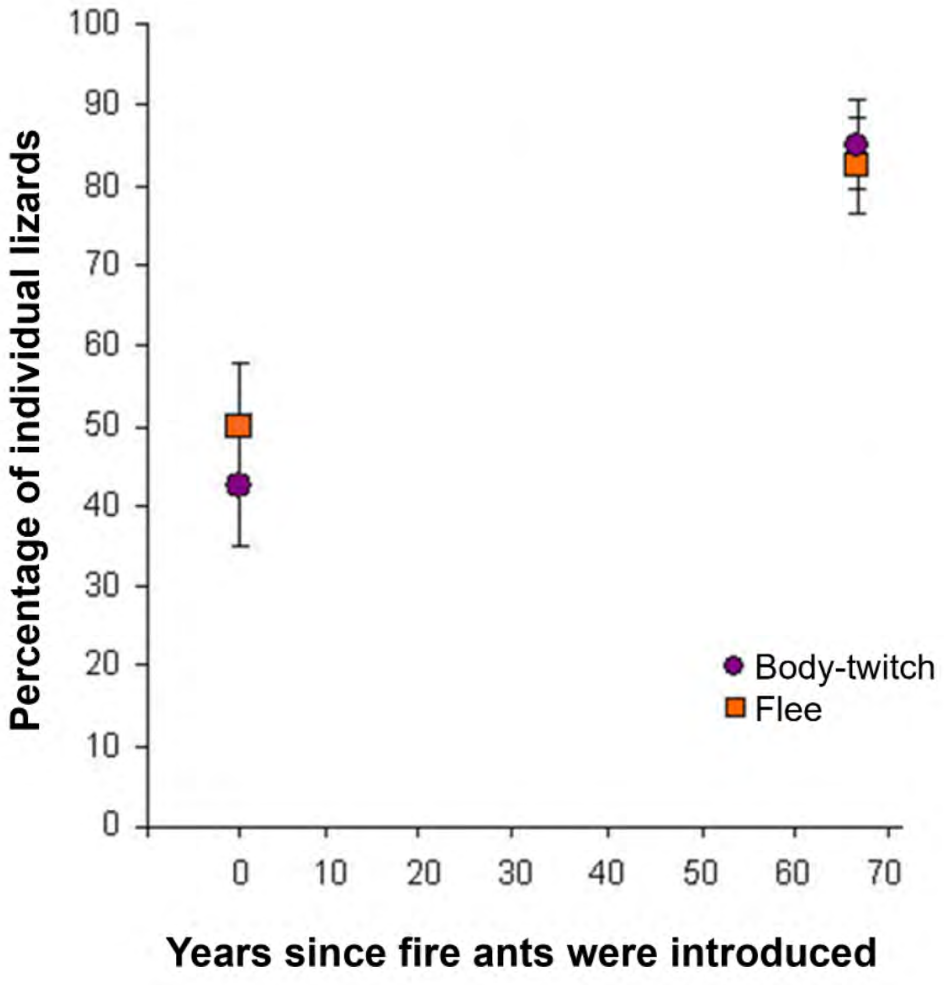


Figure 8. The proportion of eastern fence lizards that behaviorally responded during exposure to invasive fire ants at two sites with different time since invasion. Photo credit: Modified from Langkilde, T. 2009. Invasive fire ants alter behavior and morphology of native lizards. Ecology 90, 208–217.

PART D: EVALUATE

Final synthesis

Written Response: Your instructor might assign the following individual prompt as a form of assessment for this exercise: First, identify the negative impacts that introduced fire ants can have on people and native wildlife. Then, construct an explanation based on evidence for how native fence lizard populations are able to respond to red imported fire ants. Are there aspects of their response that you would consider a behavioral response that can develop within an individual's lifetime? Are there aspects of their response that you feel are compatible with adaptation via natural selection? Why?

ACKNOWLEDGMENTS

Support for this project was provided, in part, by an Education and Outreach grant from the Society for the Study of Evolution.

REFERENCES

Allen, C.R., D.M. Epperson, and A.S. Garmestani. 2004. Red imported fire ant impacts on wildlife: A decade of research. American Midland Naturalist 152:88–103.

Begon, M., J.L. Harper, and C.R. Townsend. 1996. Ecology. Individuals, Populations and Communities. 3rd Edition. Blackwell Scientific Publications, Oxford, UK.

Boronow, K.E., and T. Langkilde. 2010. Sublethal effects of invasive fire ant venom on a native lizard. Journal of Experimental Zoology Part A: Ecological Genetics and Physiology 313:17–23.

Brown G.P., B.L. Phillips, and R. Shine. 2011. The ecological impact of invasive cane toads on tropical snakes: Field data do not support laboratory-based predictions. Ecology 92:422–431.

Buhs, J.B. 2005. The Fire Ant Wars: Nature, Science and Public Policy in Twentieth Century America. University of Chicago Press, Chicago, IL, USA.

Buren, W.F., G.E. Allen, W.H. Whitcomb, F.E. Lennartz, and R.N. Williams. 1974. Zoogeography of the imported fire ants. Journal of the New York Entomological Society 82:113–124.

Bybee, R.W., and N.M. Landes. 1990. Science for life & living: An elementary school science program from biological sciences curriculum study. The American Biology Teacher 52:92–98.

Callcott, A.A., and H.L. Collins. 1996. Invasion and range expansion of imported fire ants Hymenoptera: Formicidae in North America from 1918–1995. Florida Entomologist 79:240–251.

Conant, R., and J.T. Collins. 1998. A Field Guide to Reptiles and Amphibians of Eastern and Central North America. 3rd ed. Houghton Mifflin Company. Boston, MA, USA.

Dunn, P.O. and D.W. Winkler. 1999. Climate change has affected the breeding date of tree swallows throughout North America. Proceedings of the Royal Society B 266:2487–2490.

Duran, L.B., and E. Duran. 2004. The 5E instructional model: A learning cycle approach for inquiry-based science teaching. Science Education Review 3:49–58.

Freidenfelds, N.A., T.R. Robbins, and T. Langkilde. 2012. Evading invaders: The effectiveness of a behavioral response acquired through lifetime exposure. Behavioral Ecology 23:659–664.

Greenlees, M., B.L. Phillips, and R. Shine. 2021. Adjusting to a toxic invader: Native Australian frog learns not to prey on cane toads. Behavioral Ecology 21:966–971.

Langkilde T. 2009a. Invasive fire ants alter behavior and morphology of native lizards. Ecology 90:208–217.

Langkilde T. 2009b. Holding ground in the face of invasion: Native fence lizards (*Sceloporus undulatus*) do not alter their habitat use in response to introduced fire ants (*Solenopsis invicta*). Canadian Journal of Zoology 87:626–635.

Langkilde, T., and N.A. Freidenfelds. 2010. Consequences of envenomation: Red imported fire ants have delayed effects on survival but not growth of native fence lizards. Wildlife Research 37:566–573.

Losos, J.B., T.W. Schoener, and D.A. Spiller. 2004. Predator-induced behaviour shifts and natural selection in field–experimental lizard populations. Nature 432:505–508.

Markin, G.P., J. O'Neal, and J. Dillier. 1975. Foraging tunnels of the red imported fire ant, *Solenopsis invicta* (Hymenoptera: Formicidae). Journal of the Kansas Entomological Society 48:83–89.

Porter, S.D., D.F. Williams, R.S. Patterson, and H.G. Fowler. 1997. Intercontinental differences in the abundance of *Solenopsis* fire ants (Hymenoptera: Formicidae): Escape from natural enemies? Environmental Entomology 26:373–384.

Potiwat, R., and R. Sitcharungsi. 2015. Ant allergens and hypersensitivity reactions in response to ant stings. Asian Pacific Journal of Allergy and Immunology 33:267–275.

Tylan, C., and T. Langkilde. 2023. Native eastern fence lizards changed their bodies and behavior in response to invasive red imported fire ants. The Conversation. Available from: https://theconversation.com/native-eastern-fence-lizards-changed-their-bodies-and-behavior-in-response-to-invasive-red-imported-fire-ants-186275 (accessed December 2, 2023).

Tschinkel, W.R. 2006. The Fire Ants. Harvard University/Belknap Press, Cambridge, MA, USA.

Vander Meer, R.K., F. Alvarez, and C.S. Lofgren. 1988. Isolation of the trail recruitment pheromone of *Solenopsis invicta*. Journal of Chemical Ecology 14:825–838.

NCEP materials are meant to be modifiable for each educator's specific classroom or training needs; adaptable Microsoft Word versions of modules are available for download through the NCEP module collection at https://ncep.amnh.org along with any available accompanying data files, appendices, presentations, teaching notes, and exercise solutions.

A Brief Introduction to Species Distribution Modeling for Conservation Educators and Practitioners

Matthew E. Aiello-Lammens[i], Andrea Paz[ii], Bethany A. Johnson[iii], Mary E. Blair[iv], and Richard G. Pearson[v]

[i]Pace University, Pleasantville-Briarcliff Campus, Environmental Studies and Science, Pleasantville, NY, USA; [ii]Department of Environmental Systems Science, Institute of Integrative Biology, ETH Zürich, Switzerland; [iii]City College of the City University of New York, Biology, New York, NY, USA; [iv]Center for Biodiversity and Conservation, American Museum of Natural History, New York, NY, USA; [v]University College London, London, UK

This Synthesis is an update of "Pearson, R.G. 2008. Species' Distribution Modeling for Conservation Educators and Practitioners. Synthesis. American Museum of Natural History. Available at https://ncep.amnh.org."

This update is a condensed version of the original, with updated references, and a streamlined introduction and framing to reflect recent developments in the field, and especially to provide further emphasis on machine learning approaches to species distribution modeling.

Author contributions: Aiello-Lammens led the update. Paz, Johnson, and Blair contributed to the update. Pearson wrote the original version.

LEARNING OBJECTIVES

Through use of this synthesis, teachers will enable students to:

1. Identify and describe important theoretical underpinnings of species distribution models.
2. Identify key components of distribution models, including appropriate data and methods / algorithms.
3. Be prepared to apply algorithms to train a species distribution model and test its predictive performance.
4. Identify applications of distribution models in addressing a range of conservation questions.

INTRODUCTION

Predicting species' distributions has become an important component of conservation planning in recent years, and a wide variety of modeling techniques have been developed for this purpose (Guisan and Thuiller 2005; Elith and Leathwick 2009; Peterson et al. 2011). These models commonly utilize associations between environmental variables and known species' occurrence records to identify environmental conditions within which populations can be maintained. The spatial distribution of environments that are suitable for the species can then be estimated across a study region. This approach has proven valuable for generating biogeographical information that can be applied across a broad range of fields, including conservation biology, ecology and evolutionary biology. This synthesis aims to provide an overview of the theory and key components of species distribution modeling. Through use of the synthesis, teachers will enable students to understand the theoretical basis of distribution models, understand the techniques and steps required to run models using a variety of approaches, test the predictive ability of models, and apply the models to address a range of questions.

What is a species distribution model?

A common strategy for estimating the actual or potential geographic distribution of a species is to characterize the environmental conditions that are suitable for the species, and to then identify where suitable environments are distributed in space. For example, if we are interested in modeling the distribution of a plant that is known to thrive in wet clay soils, then simply identifying locations with clay soils and high precipitation can generate an estimate of the species' distribution. There are a number

of reasons why the species may not actually occupy all suitable sites (e.g., geographic barriers that limit dispersal, competition from other species), which we will discuss later. However, this is the fundamental strategy common to most species distribution models (SDMs).

The environmental conditions that are suitable for a species may be characterized using either a *mechanistic* or a *correlative* approach. Mechanistic models aim to incorporate physiologically limiting mechanisms in a species' tolerance to environmental conditions (Kearney and Porter 2009). For example, (Chuine and Beaubien 2001) modeled distributions of North American tree species by estimating responses to environmental variables (including mean daily temperature, daily precipitation, and night length) using mechanistic models of factors including frost injury, phenology, and reproductive success. Such mechanistic models require detailed understanding of the physiological response of species to environmental factors and are therefore difficult to develop for all but the most well understood species.

Correlative models aim to estimate the environmental conditions that are suitable for a species by associating known species' occurrence records with suites of environmental variables that can reasonably be expected to affect the species' physiology and probability of persistence. The central premise of this approach is that the observed distribution of a species provides useful information as to the environmental requirements of that species. For example, we may assume that our plant species of interest favors wet clay soils because it has been observed growing in these soils. The limitations of this approach are discussed later in the synthesis, but it has been demonstrated that this method can yield valuable biogeographical information (e.g., Raxworthy et al. 2003; Bourg et al. 2005). Since spatially explicit occurrence records are available for a large number of species, the vast majority of species distribution models are correlative. The correlative approach to distribution modeling is the focus of this synthesis.

What data are needed to build an SDM?

The principal steps required to build and validate a correlative species distribution model are outlined in Figure 1. Two types of model input data are needed: 1) known species' occurrence records; and 2) a suite of environmental variables. "Raw" environmental variables, such as daily precipitation records collected from weather stations, are often processed to generate model inputs that are thought to have a direct physiological role in limiting the ability of the species to survive (see Nix 1986 for early examples of such processing). Another important advancement involved spatial interpolation of these bioclimate factors (a brief history of these processes can be found in Booth et al. 2014). Presently there are several environmental data sets focusing on bioclimatic variables that are readily available (e.g., CliMond - Kriticos et al. 2011; WorldClim 2.0 - Fick and Hijmans 2017; ENVIREM - Title and Bemmels 2018). Additionally, environmental variables derived from remote sensing products are increasingly becoming available and being applied at local (e.g., Pasetto et al. 2018), regional (e.g., Paz et al. 2022), and global spatial scales (e.g., Deblauwe et al. 2016). Importantly, these remote-sensed environmental data are allowing researchers to move beyond relationships between presence and climate conditions only, which has been the dominant approach for many years.

The species occurrence records and environmental variables are entered into an algorithm that aims to identify environmental conditions that are associated with species occurrence. If just one or two environmental variables were used, then this task would be relatively straightforward. For example, we may readily discover that our plant species has only been recorded at localities where mean monthly precipitation is above 60mm and soil clay content is above 40%. In practice, we usually seek algorithms that are able to integrate more than two environmental variables, since species are in reality likely to respond to multiple factors. Algorithms that can incorporate interactions among variables are also preferable (Elith et al. 2006; Franklin 2010; Valavi et al. 2022). For example, a more

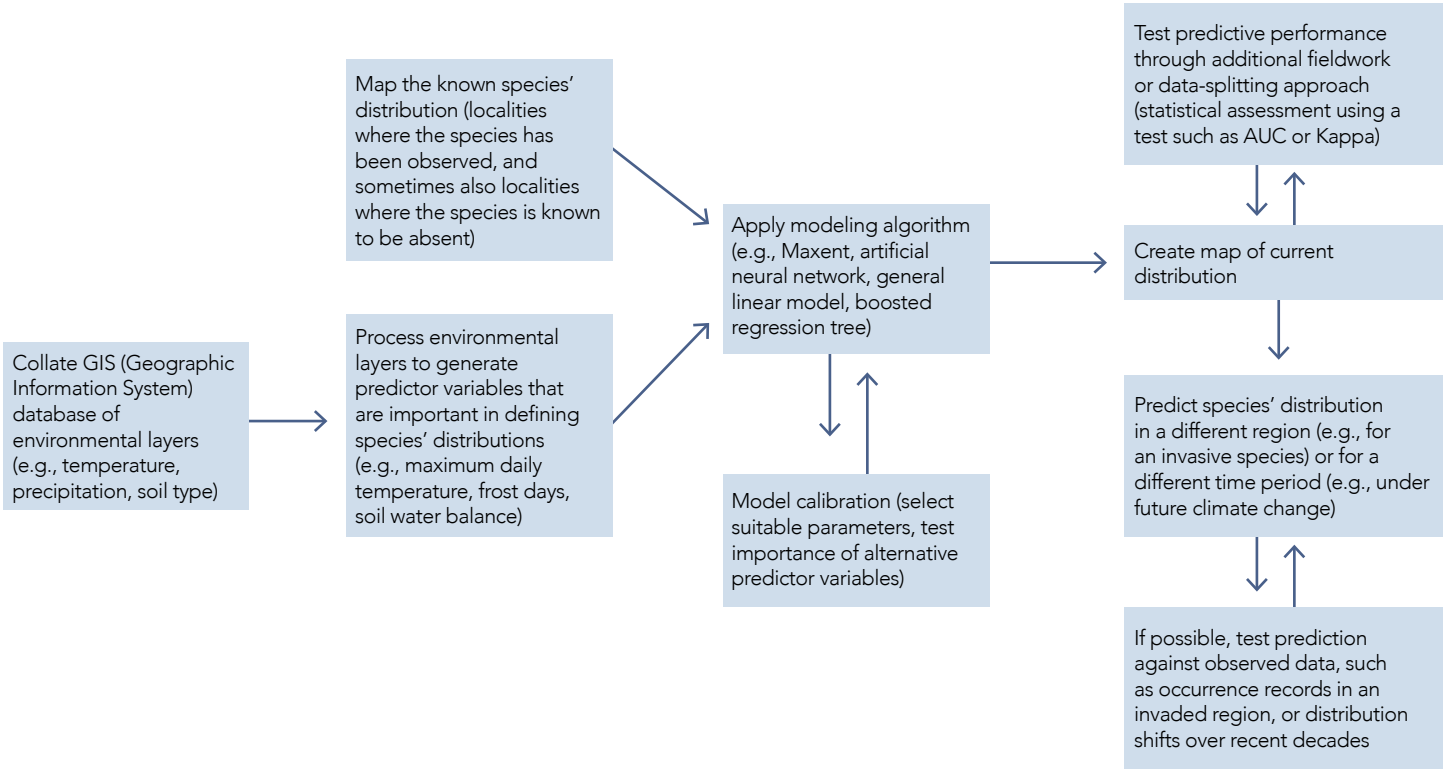


Figure 1. Flow diagram detailing the main steps required for building and validating a correlative species distribution model.

accurate description of our plant's requirements may be that it can occur at localities with mean monthly precipitation between 60mm and 70mm if soil clay content is above 60%, and in wetter areas (>70mm) if clay content is as low as 40%.

Multiple modeling algorithms are available to determine relationships between species presence and environmental conditions (see Valavi et al. 2022 for one overview of multiple methods). Possible appropriate algorithms include those based on foundational frequentist statistics (e.g., logistic regression, generalized linear models, and generalized additive models), Bayesian statistics (e.g., hierarchical Bayesian models), or machine learning principles (e.g., Maxent, random forest, and artificial neural networks; see Box 1 for more information on machine learning). Depending on the method used, various decisions and tests will need to be made to ensure the algorithm gives optimal results. For example, a suitable "regularization" parameter will need to be selected if applying the Maxent method (see Phillips et al. 2006; Elith et al. 2010; Merow et al. 2013; and the Wallace - Module Guidance for the Maxent module in software described in Kass et al. 2023), or the degrees of freedom must be selected if running a generalized additive model (see Guisan et al. 2002). The relative importance and/or correlation of alternative environmental predictor variables may also be assessed at this stage so as to select which variables are used in the final model.

After running a modeling algorithm, the resulting estimated mathematical relationships between species occurrence and environmental conditions can be used to construct a map showing the predicted species' distribution. The ability of the model to predict the known species' distribution should be evaluated, or tested, at this stage. A YouTube video providing an overview of model evaluation is available here: ENM2020 - W22T1 - Evaluation Overview; https://youtu.be/jG5bcr3jzmA. A set of species occurrence records that have not previously been used in the modeling should be used as independent testing data. The ability of the model to predict the independent data is assessed using a suitable test statistic. Different approaches to generating test datasets and

Box 1. Machine learning algorithms

Machine learning algorithms are increasingly being applied to species distribution modeling (Lucas 2014). This is primarily due to the abilities of many machine learning algorithms to fit complex and non-linear relationships that are common in natural systems, and because computational advances have made these algorithms fast and efficient (Olden et al. 2008; Peters et al. 2014).

At a high level, machine learning algorithms can be divided into three categories: supervised learning, unsupervised learning, and reinforcement learning. Supervised learning involves training a model using input data associated with known outputs (e.g., climatic and/or environmental conditions at known locations of species presence or absence). Unsupervised learning, on the other hand, involves finding patterns in data without known outcomes (i.e., no response variable is identified). Reinforcement learning involves training a model to make decisions based on feedback from data collected from a dynamic system or environment. As of 2023, machine learning approaches using supervised learning were most commonly applied in SDMs (e.g., Maxent, random forests, support vector machine, artificial neural networks; Lucas 2014; Peters et al. 2014), though some unsupervised learning algorithms are also used (e.g., k-means clustering, Guassian mixture models; Christin et al. 2019). While reinforcement algorithms are beginning to be applied in conservation sciences (e.g., Lapeyrolerie et al. 2022), we know of no applications to SDMs at this time.

The success of machine learning algorithms depends on the quality and quantity of the training data. To train a model, the data is split into a training set and a testing set, where the training set is used to train the model, and the testing set is used to evaluate its performance on unseen data. There are several approaches an analyst can take to splitting the data, which are discussed in the model evaluation section below.

alternative statistical tests are discussed in detail in Pearson's Species' Distribution Modeling for Conservation Educators and Practitioners synthesis (2008, Section 5; available from the NCEP module collection at https://ncep.amnh.org). Since a number of modeling algorithms predict a continuous distribution of environmental suitability (i.e., a prediction between 0 and 1, as opposed to a binary prediction of "suitable" or "unsuitable"), it is sometimes useful to convert model output into a prediction of suitable (1) or unsuitable (0). This is a necessary step before applying many test statistics; thus, methods for setting a threshold probability, above which the species is predicted as present, are also outlined in Section 5, with additional information available in Liu et al. 2005 and Liu et al. 2016.

Once these steps have been completed, and if model validation is successful, the model can be used to predict species' occurrence in areas where the distribution is unknown. Thus, a set of environmental variables for the area of interest is input into the model and the suitability of conditions at a given locality is predicted. In many cases the model is used to "fill the gaps" around known occurrences (e.g., Anderson et al. 2002; Ferrier et al. 2002). In other cases, the model may be used to predict species' distributions in new regions (e.g., to study invasion potential, for review see Peterson 2003; Srivastava 2019) or for a different time period (e.g., to estimate the potential impacts of future climate change, for review see Anderson 2013). Ideally, model predictions into different regions or different time periods should be tested against observed data; for example, Thuiller et al. 2005 tested predictions of invasion potential using occurrence records from the invaded distribution, whilst Araújo et al. 2005a tested predictions of distribution shifts under climate change using observed records from different decades.

This modeling approach has been variously termed "species distribution," "ecological niche,"

"environmental niche," "habitat suitability," and "bioclimate envelope" modeling. Use of the term "species distribution modeling" is widespread but it should be noted that the term is somewhat misleading since it is actually the distribution of suitable environments that is being modeled, rather than the species' distribution *per se*. Regardless of the name used, the basic modeling process is essentially the same and the theoretical underpinnings of the models are similar. It is essential that these theoretical underpinnings are properly understood in order to interpret model outputs accurately. The following section describes this theoretical framework.

THEORETICAL FRAMEWORK

This section outlines some of the fundamental concepts that are crucial for understanding how species distribution models work, what types of questions they are suitable for addressing, and how model output should be interpreted.

Geographical versus environmental space

We are used to thinking about the occurrence of species in geographical space; that is, the species' distribution as plotted on a map. To understand species distribution models it is important to also think about species occurring in environmental space, which is a conceptual space defined by the environmental variables to which the species responds. The concept of environmental space has its foundations in ecological niche theory. The term "niche" has a long and varied history of use in ecology (Chase and Leibold 2003), but the definition proposed by (Hutchinson 1957) is most useful in the current context. Hutchinson defined the *fundamental niche* of a species as the set of environmental conditions within which a species can survive and persist. The fundamental niche may be thought of as an "*n*-dimensional hypervolume", every point in which corresponds to a state of the environment that would permit the species to exist indefinitely (Hutchinson 1957, p. 416). It is the axes of this *n*-dimensional hypervolume that define environmental space.

Visualizing a species' distribution in both geographical and environmental space helps us to define some basic concepts that are crucial for species distribution modeling (Figure 2). Notice that the observed localities constitute all that is known about the species' *actual distribution*; the species is likely to occur in other areas in which it has not yet been detected (e.g., Figure 2, area A). If the *actual distribution* is plotted in environmental space then we identify that part of environmental space that is occupied by the species, which we can define as the *occupied niche*.

The distinction between the occupied niche and the fundamental niche is similar, but not identical, to Hutchinson's (1957) distinction between the realized niche and the fundamental niche. With reference to the case of two species utilizing a common resource, Hutchinson described the realized niche as comprising that portion of the fundamental niche from which a species is not excluded due to biotic competition. The definition of the occupied niche used in this synthesis broadens this concept to include geographical and historical constraints resulting from a species' limited ability to reach or re-occupy all suitable areas, along with biotic interactions of all forms (competition, predation, symbiosis, and parasitism). Thus, the occupied niche reflects all constraints imposed on the actual distribution, including spatial constraints due to limited dispersal ability, and multiple interactions with other organisms.

If the environmental conditions encapsulated within the fundamental niche are plotted in geographical space then we have the *potential distribution*. Notice that some regions of the potential distribution may not be inhabited by the species (Figure 2, areas B and C), either because the species is excluded from the area by biotic interactions (e.g., presence of a competitor or absence of a food

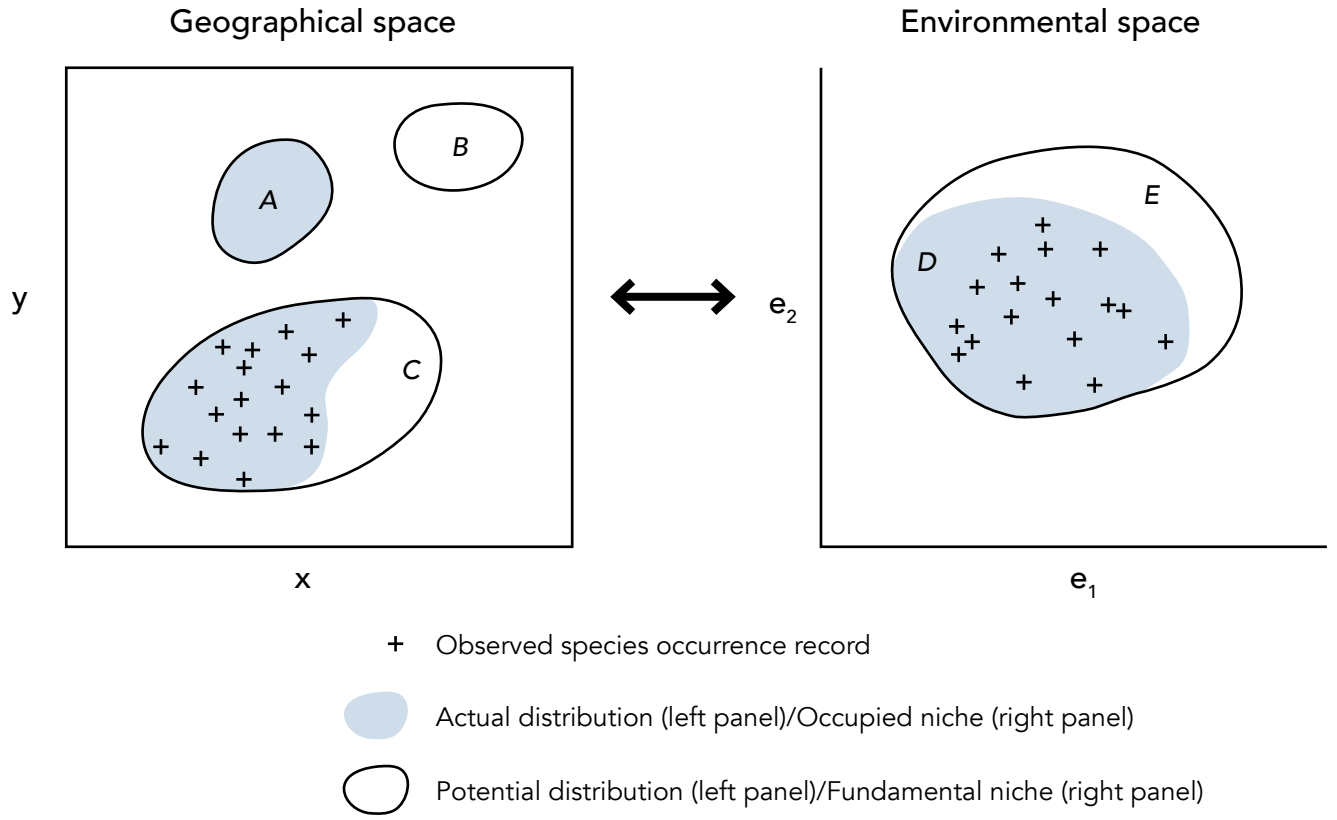


Figure 2. Illustration of the relationship between a hypothetical species' distribution in geographical space and environmental space. Geographical space refers to spatial location as commonly referenced using x and y coordinates. Environmental space refers to Hutchinson's n-dimensional niche, illustrated here for simplicity in only two dimensions (defined by two environmental factors, e_1 and e_2). Crosses represent observed species occurrence records. Grey shading in geographical space represents the species' actual distribution (i.e., those areas that are truly occupied by the species). Notice that some areas of actual distribution may be unknown (e.g., area A is occupied but the species has not been detected there). The grey area in environmental space represents that part of the niche that is occupied by the species: the occupied niche. Again, notice that the observed occurrence records may not identify the full extent of the occupied niche (e.g., the shaded area immediately around label D does not include any known localities). The solid line in environmental space depicts the species' fundamental niche, which represents the full range of abiotic conditions within which the species is viable. In geographical space, the solid lines depict areas with abiotic conditions that fall within the fundamental niche; this is the species' potential distribution. Some regions of the potential distribution may not be inhabited by the species due to biotic interactions or dispersal limitations. For example, area B is environmentally suitable for the species, but is not part of the actual distribution, perhaps because the species has been unable to disperse across unsuitable environments to reach this area. Similarly, the non-shaded area around label C is within the species' potential distribution, but is not inhabited, perhaps due to competition from another species. Thus, the non-shaded area around label E identifies those parts of the fundamental niche that are unoccupied, for example due to biotic interactions or geographical constraints on species dispersal.

source), because the species has not dispersed into the area (e.g., there is a geographic barrier to dispersal, such as a mountain range, or there has been insufficient time for dispersal), or because the species has been extirpated from the area (e.g., due to human modification of the landscape).

Before we go on to discuss how these concepts are used in distribution modeling, it is important to appreciate that the environmental variables used in a distribution model are unlikely to define all possible dimensions of environmental space. Hutchinson originally proposed that all variables, "both physical and biological" (1957, p. 416), are required to define the fundamental niche. However, the variables available for modeling are likely to represent only a subset of possible environmental factors that influence the distribution of the species. Variables used in modeling most commonly describe the physical environment (e.g., temperature, precipitation, soil type), though aspects of the biological

environment are sometimes incorporated (e.g., Araújo and Luoto 2007; Heikkinen et al. 2007). However, the distinction between biotic and abiotic variables is often problematic; for example, land cover type is likely to incorporate both abiotic (e.g., urban) and biotic (e.g., deciduous forest) classes.

Another important factor that we must be aware of is source-sink dynamics, which may cause a species to be observed in unsuitable environments. "Source-sink" refers to the situation whereby an area (the "sink") may not provide the necessary environmental conditions to support a viable population, yet may be frequently visited by individuals that have dispersed from a nearby area that does support a viable population (the "source"). In this situation, species occurrence may be recorded in sink areas that do not represent suitable habitat, meaning that the species is present outside its fundamental niche (Pulliam 2000). We can logically expect this situation to occur most frequently in species with high dispersal ability, such as birds. In such cases it is useful to only utilize records for modeling that are known to be from breeding distributions, rather than migrating individuals. Because correlative species distribution models utilize observed species occurrence records to identify suitable habitat, inclusion of occurrence localities from sink populations is problematic. However, it is often assumed that observations from source areas will be much more frequent than observations from sink areas, so this source of potential error is commonly overlooked.

One more thing to be aware of before we move on is that some studies explicitly aim to only investigate one part of the fundamental niche, by using a limited set of predictor variables. For example, it is common when investigating the potential impacts of future climate change to focus only on how climate variables impact species' distributions. A species' niche defined only in terms of climate variables may be termed the *climatic niche* (Pearson and Dawson 2003), which represents the climatic conditions that are suitable for species existence. An approximation of the climatic niche may then be mapped in geographical space, giving what is commonly termed the *bioclimate envelope* (Huntley et al. 1995; Pearson and Dawson 2003).

Estimating niches and distributions

Let us now consider the extent to which species distribution models can be used to estimate the niche and distribution of a species. We will assume in this section that the chosen model algorithm is excellent at defining the relationship between observed occurrence localities and environmental variables; this will enable us to focus on understanding the ecological assumptions underlying distribution models.

Let us first ask what the aim of the modeling is: what element of a species' distribution are we trying to estimate? There are many potential uses of the approach (Table 1) and these require modeling either the *actual distribution* or the *potential distribution*. For example, if a model is being used with the purpose of selecting sites that should be given high conservation priority, then modeling the actual distribution will be the aim (since there would be less priority given to conserving sites where the environment is suitable for the species, but the species is not present). In contrast, if the purpose is to identify sites that may be suitable for the reintroduction of an endangered species, then modeling the potential distribution is an appropriate aim. We will now consider the degree to which alternative aims are achievable using the species distribution modeling approach.

Correlative species distribution models rely on observed occurrence records for providing information on the niche and distribution of a species. Two key factors are important when considering the degree to which observed species occurrence records can be used to estimate the niche and distribution of a species:

Table 1. Some published uses of species distribution models in conservation biology (Based in part on Guisan and Thuiller 2005).

Type of use	Example reference(s)
Guiding field surveys to find populations of known species	Bourg et al. 2005; Guisan et al. 2006
Guiding field surveys to accelerate the discovery of unknown species	Raxworthy et al. 2003
Projecting potential impacts of climate change	For review see Stanton et al. 2015; Blair et al. 2022
Predicting species' invasion	Higgins et al. 1999; Thuiller et al. 2005; Barbosa et al. 2012
Exploring speciation mechanisms	Graham et al. 2004; Kozak and Wiens 2006; Musher et al. 2020
Supporting conservation prioritization and reserve selection	Villero et al. 2017
Species delimitation	Raxworthy et al. 2007; Bett et al. 2012
Assessing the impacts of land cover change on species' distributions	Gavrutenko et al. 2021
Testing ecological theory	Anderson et al. 2002; Graham et al. 2006
Comparing paleodistributions and phylogeography	Hugall et al. 2002; Musher et al. 2020
Guiding reintroduction or re-establishment of endangered species	Pearce and Lindenmayer 1998; Trinh-Dinh et al. 2022
Assessing disease risk	Peterson et al. 2006, 2007
Assessing ecosystem services	Manhães et al. 2018

1. *The degree to which the species is at "equilibrium" with current environmental conditions.* A species is said to be at equilibrium with the physical environment if it occurs in all suitable areas, while being absent from all unsuitable areas. The degree of equilibrium depends both on biotic interactions (for example, competitive exclusion from an area) and dispersal ability (organisms with higher dispersal ability are expected to be closer to equilibrium than organisms with lower dispersal ability; Araújo et al. 2005b). When using the concept of "equilibrium" we should remember that species distributions change over time, so the term should not be used to imply stasis. However, the concept is useful for us here to help understand that some species are more likely than others to occupy areas that are abiotically suitable.

2. *The extent to which observed occurrence records provide a sample of the environmental space occupied by the species.* In cases where very few occurrence records are available, perhaps due to limited survey effort (Anderson and Martínez-Meyer 2004) or low probability of detection (Pearson et al. 2007), the available records are unlikely to provide a sufficient sample to enable the full range of environmental conditions occupied by the species to be identified. In other cases, surveys may provide extensive occurrence records that provide an accurate picture as to the environments inhabited by a species in a particular region (for example, breeding bird distributions in the United Kingdom and Ireland are well known; Gibbons et al. 1993). It should be noted that there is not necessarily a direct relationship between sampling in geographical space and in environmental space. It is quite possible that poor sampling in geographical space could still result in good sampling in environmental space.

Each of these factors should be carefully considered to ensure appropriate use of a species distribution model (see Box 2). In reality, species are unlikely to be at equilibrium (as illustrated by area B in Figure 2, which is environmentally suitable but is not part of the actual distribution) and occurrence records will not completely reflect the range of environments occupied by the species (illustrated by that part of the occupied niche that has not been sampled around label D in Figure 2). Figure 3 illustrates how a species distribution model may be fit under these circumstances. Notice that the model is calibrated (i.e., trained) in environmental space and then projected into geographical space. In environmental space, the model identifies neither the occupied niche nor the fundamental niche; instead, the model fits only to that portion of the niche that is represented by the observed records. Similarly, the model identifies only some parts of the actual and potential distributions when projected back into geographical space. Therefore, it should not be expected that species distribution models are able to predict the full extent of either the actual distribution or the potential distribution.

This observation may be regarded as a failure of the modeling approach (Lawton 2000; Woodward and Beerling 1997; Hampe 2004). However, we can identify three types of model prediction that yield important biogeographical information: species distribution models may identify 1) the area around the observed occurrence records that is expected to be occupied (Figure 3, area 1); 2) a part of the actual distribution that is currently unknown (Figure 3, area 2); and/or 3) part of the potential distribution that is not occupied (Figure 3, area 3). Prediction types 2 and 3 can prove very useful in a range of applications, as we will see in the following section.

Uses of species distribution models

Consider modeled area 2 in Figure 3, which identifies part of the actual distribution for which no occurrence records have been collected. Although the model does not predict the full extent of the actual distribution, additional sampling in the area identified may yield new occurrence records. A number of studies have demonstrated the utility of species distribution modeling for guiding field surveys toward regions where there is an increased probability of finding new populations of a known species (Fleishman et al. 2003; Bourg et al. 2005; Guisan et al. 2006). Accelerating the discovery of new populations in this way may prove extremely useful for conservation planning, especially in poorly known and highly threatened landscapes.

Consider now predicted area 3 in Figure 3. Here, the model identifies an area of potential distribution that is environmentally similar to where the species is known to occur, but which is not inhabited. The full extent of the potential distribution is not predicted, but the model can be useful for identifying sites that may be suitable for reintroduction of a species (Pearce and Lindenmayer 1998) or sites

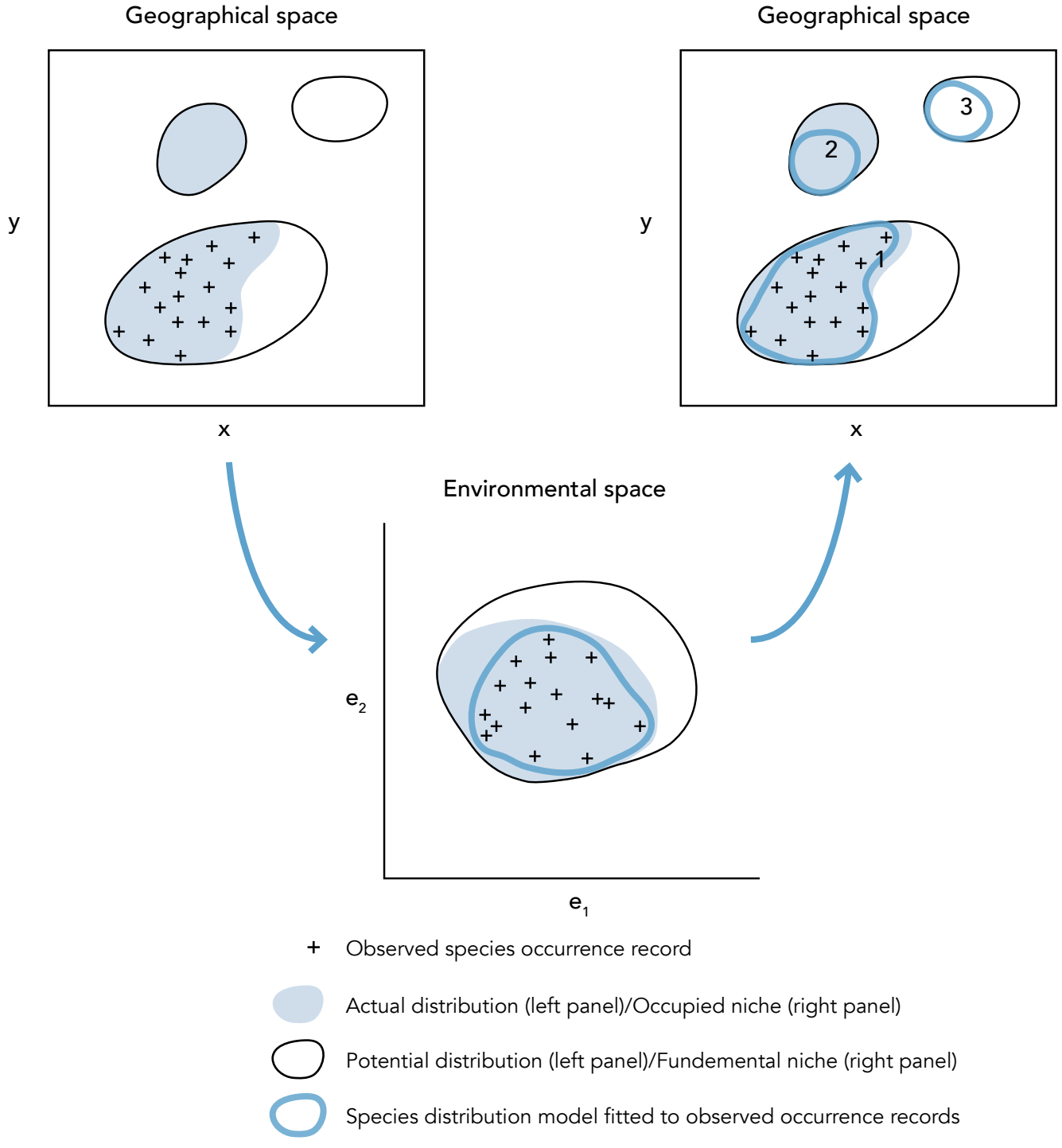


Figure 3. Diagram illustrating how a hypothetical species distribution model may be fitted to observed species occurrence records (using the same hypothetical case as in Figure 2). A modelling technique (e.g., GARP, Maxent) is used to characterize the species' niche in environmental space by relating observed occurrence localities to a suite of environmental variables. Notice that, in environmental space, the model may not identify either the species' occupied niche or fundamental niche; rather, the model identifies only that part of the niche defined by the observed records. When projected back into geographical space, the model will identify parts of the actual distribution and potential distribution. For example, the model projection labeled 1 identifies the known distributional area. Projected area 2 identifies part of the actual distribution that is currently unknown; however, a portion of the actual distribution is not predicted because the observed occurrence records do not identify the full extent of the occupied niche (i.e., there is incomplete sampling; see area D in Figure 2). Similarly, modeled area 3 identifies an area of potential distribution that is not inhabited (the full extent of the potential distribution is not identified because the observed occurrence records do not identify the full extent of the fundamental niche due to, for example, incomplete sampling, biotic interactions, or constraints on species dispersal; see areas D and E in Figure 2).

where a species is most likely to become invasive (if it overcomes dispersal barriers and if biotic competition does not prevent establishment; Peterson 2003). Model predictions of this type also have the potential to accelerate the discovery of previously unknown species that are closely related to the modeled species and that occupy similar environmental space but different geographical space (Raxworthy et al. 2003).

Model predictions as illustrated in Figure 3 therefore have the potential to yield useful information, even though species are not expected to inhabit all suitable locations and sampling may be poor. Additional uses of species distribution modeling include identifying potential areas for disease outbreaks (Peterson et al. 2006), examining niche evolution (Peterson et al. 1999; Kozak and Wiens 2006) and informing taxonomy (Raxworthy et al. 2007). However, some potential applications require an estimation of the actual distribution of a species. For example, if a model is being used with the purpose of selecting priority sites for conservation, then an estimate of the actual species' distribution is desired since it would be inefficient to conserve sites where the species is not present (Loiselle et al. 2003). In such cases, it should be remembered that modeled distributions represent environmentally suitable regions but do not necessarily correspond closely with the actual distribution. Additional processing of model output may be required to improve predictions of the actual distribution (Merow et al. 2022). For example, predicted areas that are isolated from observed occurrence records by a dispersal barrier may be removed (Peterson et al. 2002) and the influence of competing species may be incorporated (Anderson 2002; Kass et al. 2021; Merow et al. 2022).

It is useful to note that mechanistic distribution models (e.g., Chuine and Beaubien 2001; Kearney and Porter 2009) are subject to the same basic caveat as correlative approaches: the models aim to identify areas with suitable environmental conditions, but do not inform us which areas are actually occupied. Mechanistic models are ideally suited to identifying a species' fundamental niche, and hence its potential distribution. This is because mechanistic approaches model physiological limitations in a species' environmental tolerance, without relying on known occurrence records to define suitable environments. However, the detailed understanding of species' physiology that is required to build mechanistic models prohibits their use in many instances.

The discussion in this section should help clarify the theoretical basis of the species distribution modeling approach. It is crucial that any application of these models has a sound theoretical basis and that model outputs are interpreted in the context of this framework (see Box 2). It should now be apparent why the terminology used to describe these models is so varied throughout the literature. The terms "ecological niche model," "environmental niche model," "bioclimate envelope model," and "environmental suitability model" usually refer to attempts to estimate the potential distribution of a species. Use of the term "species distribution model" implies that the aim is to simulate the actual distribution of the species. Nevertheless, each of these terms refers to the same basic approach, which can be summarized as follows: 1) the study area is modeled as a raster map composed of grid cells at a specified resolution, 2) the dependent variable is the known species' distribution, 3) a suite of environmental variables are collated to characterize each cell, 4) a function of the environmental variables is generated so as to classify the degree to which each cell is suitable for the species (Hirzel et al. 2002).

Box 2. Caution! On the use and misuse of models

Garbage in, garbage out: This old adage is as relevant to distribution modeling as it is to other fields. Put simply, a model is only as good as the data it contains. Thus, if the occurrence records used to build a correlative species distribution model do not provide useful information as to the environmental requirements of the species, then the model cannot provide useful output. If you put garbage into the model, you will get garbage out.

Model extrapolation: "Extrapolation" refers to the use of a model to make predictions for areas with environmental values that are beyond the range of the data used to calibrate (i.e., develop) the model. For example, suppose a distribution model was calibrated using occurrence records that spanned a temperature range of 10–20°C. If the model is used to predict the species' distribution in a different region (or perhaps under a future climate scenario) where the temperature reaches 25°C, then the model is extrapolating. In this case, because the model has no prior information regarding the probability of the species' occurrence at 25°C, the prediction may be extremely uncertain (see Pearson et al. 2006). Model extrapolation should be treated with a great deal of caution.

The lure of complicated technology: Many approaches to modeling species' distributions utilize complex computational technology (e.g., machine learning tools such as artificial neural networks and genetic algorithms) along with huge GIS (Geographic Information Systems) databases of digital environmental layers. In some cases, these approaches can yield highly successful predictions. However, there is a risk that model users will be swayed by the apparent complexity of the technology: "it is so complicated, it must be correct"! Always remember that a model can only be useful if the theoretical underpinnings on which it is based are sound. For additional discussion of the limitations of ecological models, see the NCEP module "Applications of Remote Sensing to Ecological Modeling" available in NCEP module collection at https://ncep.amnh.org.

REFERENCES

Anderson, R.P. 2013. A framework for using niche models to estimate impacts of climate change on species distributions. Annals of the New York Academy of Sciences, Sep 1297(2013):8-28. https://doi.org/10.1111/nyas.12264.

Anderson, R.P., M. Gómez-Laverde, and A.T. Peterson. 2002. Geographical distributions of spiny pocket mice in South America: Insights from predictive models. Global Ecology and Biogeography 11(2):131–141. https://doi.org/10.1046/j.1466-822X.2002.00275.x.

Anderson, R.P., and E. Martínez-Meyer. 2004. Modeling species' geographic distributions for preliminary conservation assessments: An implementation with the spiny pocket mice (*Heteromys*) of Ecuador. Biological Conservation 116(2):167–179. https://doi.org/10.1016/S0006-3207(03)00187-3.

Anderson, R.P., A.T. Peterson, and M. Gómez-Laverde. 2002. Using niche-based GIS modeling to test geographic predictions of competitive exclusion and competitive release in South American pocket mice. Oikos 98(1):3–16. https://doi.org/10.1034/j.1600-0706.2002.t01-1-980116.x.

Araújo, M.B., and M. Luoto. 2007. The importance of biotic interactions for modelling species distributions under climate change. Global Ecology and Biogeography 16(6):743–753. https://doi.org/10.1111/j.1466-8238.2007.00359.x.

Araújo, M.B., R.G. Pearson, and C. Rahbek. 2005b. Equilibrium of species' distributions with climate. Ecography 28(5):693–695. https://www.jstor.org/stable/3683759.

Araújo, M.B., R.G. Pearson, W. Thuiller, and M. Erhard. 2005a. Validation of species–climate impact models under climate change. Global Change Biology 11(9):1504–1513. https://doi.org/10.1111/j.1365-2486.2005.01000.x.

Barbosa, F.G., F. Schneck, and A.S. Melo. 2012. Use of ecological niche models to predict the distribution of invasive species: A scientometric analysis. Brazilian Journal of Biology 72:821–829. https://doi.org/10.1590/S1519-69842012000500007.

Bett, N.N., M.E. Blair, and E.J. Sterling. 2012. Ecological niche conservatism in doucs (Genus *Pygathrix*). International Journal of Primatology 33(4):972–988. https://doi.org/10.1007/s10764-012-9622-3.

Blair, M.E., M.D. Le, and M. Xu. 2022. Species distribution modeling to inform transboundary species conservation

and management under climate change: Promise and pitfalls. Frontiers of Biogeography 14(1). https://doi.org/10.21425/F5FBG54662.

Booth, T.H., H.A. Nix, J.R. Busby, and M.F. Hutchinson. 2014. bioclim: The first species distribution modelling package, its early applications and relevance to most current MaxEnt studies. Diversity and Distributions 20(1):1–9. https://doi.org/10.1111/ddi.12144.

Bourg, N.A., W.J. McShea, and D.E. Gill. 2005. Putting a cart before the search: Successful habitat prediction for a rare forest herb. Ecology 86(10):2793–2804. https://doi.org/10.1890/04-1666.

Chase, J.M., and M.A. Leibold. 2003. Ecological Niches: Linking Classical and Contemporary Approaches. University of Chicago Press, Chicago, IL, USA.

Chuine, I., and E.G. Beaubien. 2001. Phenology is a major determinant of tree species range. Ecology Letters 4(5):500–510. https://doi.org/10.1046/j.1461-0248.2001.00261.x.

Christin, S., É. Hervet, and N. Lecomte. 2019. Applications for deep learning in ecology. Methods in Ecology and Evolution 10(10):1632–1644. https://doi.org/10.1111/2041-210X.13256.

Deblauwe, V., et al. 2016. Remotely sensed temperature and precipitation data improve species distribution modelling in the tropics. Global Ecology and Biogeography 25(4):443–454. https://doi.org/10.1111/geb.12426.

Elith, J., et al. 2006. Novel methods improve prediction of species' distributions from occurrence data. Ecography 29(2):129–151. https://doi.org/10.1111/j.2006.0906-7590.04596.x.

Elith, J., and J.R. Leathwick. 2009. Species distribution models: Ecological explanation and prediction across space and time. Annual Review of Ecology, Evolution, and Systematics 40(1):677–697. https://doi.org/10.1146/annurev.ecolsys.110308.120159.

Elith, J., S.J. Phillips, T. Hastie, M. Dudík, Y.E. Chee, and C.J. Yates. 2010. A statistical explanation of MaxEnt for ecologists. Diversity and Distributions 17(1):43–57. https://doi.org/10.1111/j.1472-4642.2010.00725.x.

Ferrier, S., G. Watson, J. Pearce, and M. Drielsma. 2002. Extended statistical approaches to modelling spatial pattern in biodiversity in northeast New South Wales. I. Species-level modelling. Biodiversity & Conservation 11(12):2275–2307. https://doi.org/10.1023/A:1021302930424.

Fleishman, E., R.M. Nally, and J.P. Fay. 2003. Validation tests of predictive models of butterfly occurrence based on environmental variables. Conservation Biology 17(3):806–817. https://doi.org/10.1046/j.1523-1739.2003.02113.x.

Franklin, J. 2010. Mapping Species Distributions: Spatial Inference and Prediction. Cambridge University Press, Cambridge, UK.

Gavrutenko, M., B.E. Gerstner, J.M. Kass, S.M. Goodman, and R.P. Anderson. 2021. Temporal matching of occurrence localities and forest cover data helps improve range estimates and predict climate change vulnerabilities. Global Ecology and Conservation 27:e01569. https://doi.org/10.1016/j.gecco.2021.e01569.

Gibbons, D.W., J.B. Reid, and R.A. Chapman. 1993. The New Atlas of Breeding Birds in Britain and Ireland: 1988-1991. Poyser, UK.

Graham, C.H., C. Moritz, and S.E. Williams. 2006. Habitat history improves prediction of biodiversity in rainforest fauna. Proceedings of the National Academy of Sciences 103(3):632–636. https://doi.org/10.1073/pnas.0505754103.

Graham, C.H., S.R. Ron, J.C. Santos, C.J. Schneider, and C. Moritz. 2004. Integrating phylogenetics and environmental niche models to explore speciation mechanisms in dendrobatid frogs. Evolution 58(8):1781–1793. https://doi.org/10.1111/j.0014-3820.2004.tb00461.x.

Guisan, A., O. Broennimann, R. Engler, M. Vust, N.G. Yoccoz, A. Lehmann, and N.E. Zimmermann. 2006. Using niche-based models to improve the sampling of rare species. Conservation Biology 20(2):501–511. https://doi.org/10.1111/j.1523-1739.2006.00354.x.

Guisan, A., T.C. Edwards, and T. Hastie. 2002. Generalized linear and generalized additive models in studies of species distributions: Setting the scene. Ecological Modelling 157(2–3):89–100. https://doi.org/10.1016/S0304-3800(02)00204-1.

Guisan, A., and W. Thuiller. 2005. Predicting species distribution: Offering more than simple habitat models. Ecology Letters 8(9):993–1009. https://doi.org/10.1111/j.1461-0248.2005.00792.x.

Hampe, A. 2004. Bioclimate envelope models: What they detect and what they hide. Global Ecology and Biogeography 13(5):469–471. https://www.jstor.org/stable/3697578.

Heikkinen, R.K., M. Luoto, R. Virkkala, R.G. Pearson, and J.-H. Körber. 2007. Biotic interactions improve prediction of boreal bird distributions at macro-scales. Global Ecology and Biogeography 16(6):754–763. https://doi.org/10.1111/j.1466-8238.2007.00345.x.

Higgins, S.I., D.M. Richardson, R.M. Cowling, and T.H. Trinder-Smith. 1999. Predicting the landscape-scale distribution of alien plants and their threat to plant diversity. Conservation Biology 13(2):303–313. https://doi.org/10.1046/j.1523-1739.1999.013002303.x.

Hirzel, A.H., J. Hausser, D. Chessel, and N. Perrin. 2002. Ecological-niche factor analysis: How to compute habitat-suitability maps without absence data? Ecology 83(7):2027–2036. https://doi.org/10.1890/0012-9658(2002)083[2027:ENFAHT]2.0.CO;2.

Hugall, A., C. Moritz, A. Moussalli, and J. Stanisic, J. 2002. Reconciling paleodistribution models and comparative phylogeography in the Wet Tropics rainforest land snail *Gnarosophia bellendenkerensis* (Brazier 1875). Proceedings of the National Academy of Sciences 99(9):6112–6117. https://doi.org/10.1073/pnas.092538699.

Huntley, B., P.M. Berry, W. Cramer, and A.P. McDonald. 1995. Special paper: Modelling present and potential future ranges of some European higher plants using climate response surfaces. Journal of Biogeography 22(6):967–1001. https://doi.org/10.2307/2845830.

Hutchinson, G.H. 1957. Concluding remarks. Cold Spring Harbor Symposium on Quantitative Biology 22:415–457.

Kass, J.M., S.I. Meenan, N. Tinoco, S.F. Burneo, and R.P. Anderson. 2021. Improving area of occupancy estimates for parapatric species using distribution models and support vector machines. Ecological Applications 31(1):e02228. https://doi.org/10.1002/eap.2228.

Kass, J.M., et al. 2023. wallace 2: A shiny app for modeling species niches and distributions redesigned to facilitate expansion via module contributions. Ecography 2023(3):e06547. http://doi.org/10.1111/ecog.06547.

Kearney, M., and W. Porter. 2009. Mechanistic niche modelling: Combining physiological and spatial data to predict species' ranges. Ecology Letters 12(4):334–350. https://doi.org/10.1111/j.1461-0248.2008.01277.x.

Kozak, K.H., and J. Wiens. 2006. Does niche conservatism promote speciation? A case study in North American salamanders. Evolution 60(12):2604–2621. https://doi.org/10.1111/j.0014-3820.2006.tb01893.x.

Lapeyrolerie, M., M.S. Chapman, K.E.A. Norman, and C. Boettiger. 2022. Deep reinforcement learning for conservation decisions. Methods in Ecology and Evolution 13(11):2649–2662. https://doi.org/10.1111/2041-210X.13954.

Lawton, J. 2000. Concluding remarks: A review of some open questions. Ecological Consequences of Heterogeneity. Pages 401–424 in M. Hutchings, E. John, and A.J.A. Stewart, editors. Cambridge University Press, Cambridge, UK.

Liu, C., P.M. Berry, T.P. Dawson, and R.G. Pearson. 2005. Selecting thresholds of occurrence in the prediction of species distributions. Ecography 28(3):385–393. https://doi.org/10.1111/j.0906-7590.2005.03957.x.

Liu, C., G. Newell, and M. White. 2016. On the selection of thresholds for predicting species occurrence with presence-only data. Ecology and Evolution 6(1):337–348. https://doi.org/10.1002/ece3.1878.

Loiselle, B.A., C.A. Howell, C.H. Graham, J.M. Goerck, T. Brooks, K.G. Smith, and P.H. Williams. 2003. Avoiding pitfalls of using species distribution models in conservation planning. Conservation Biology 17(6):1591–1600. https://doi.org/10.1111/j.1523-1739.2003.00233.x.

Lucas, T.C.D. 2020. A translucent box: Interpretable machine learning in ecology. Ecological Monographs 90(4):e01422. https://doi.org/10.1002/ecm.1422.

Manhães, A.P., R. Loyola, G.G. Mazzochini, G. Ganade, A.T. Oliveira-Filho, and A.R. Carvalho. 2018. Low-cost strategies for protecting ecosystem services and biodiversity. Biological Conservation 217:187–194. https://doi.org/10.1016/j.biocon.2017.11.009.

Merow, C., M.J. Smith, and J.A. Silander, Jr. 2013. A practical guide to MaxEnt for modeling species' distributions: What it does, and why inputs and settings matter. Ecography 36(10):1058–1069. https://doi.org/10.1111/j.1600-0587.2013.07872.x.

Merow, C., et al. 2022. Operationalizing expert knowledge in species' range estimates using diverse data types. Frontiers of Biogeography 14(2). https://doi.org/10.21425/F5FBG53589.

Musher, L.J., P.J. Galante, G. Thom, J.W. Huntley, and M.E. Blair. 2020. Shifting ecosystem connectivity during the Pleistocene drove diversification and gene-flow in a species complex of Neotropical birds (*Tityridae*: *Pachyramphus*). Journal of Biogeography 47(8):1714–1726. https://doi.org/10.1111/jbi.13862.

Nix, H.A. 1986. A biogeographic analysis of Australian elapid snakes. Pages 4–15 in R. Longmore, editor. Atlas of Elapid Snakes of Australia. Australian Flora and Fauna Series No. 7, Australian Government Publishing Service, Canberra, Australia.

Olden, J.D., J.J. Lawler, and N.L. Poff. 2008. Machine learning methods without tears: A primer for ecologists. The Quarterly Review of Biology 83(2):171–193. https://doi.org/10.1086/587826.

Pasetto, D. et al. 2018. Integration of satellite remote sensing data in ecosystem modelling at local scales: Practices and trends. Methods in Ecology and Evolution 9(8):1810–1821. https://doi.org/10.1111/2041-210X.13018.

Paz, A., T.S. Silva, and A.C. Carnaval. 2022. A framework for near-real time monitoring of diversity patterns based on indirect remote sensing, with an application in the Brazilian Atlantic rainforest. PeerJ 10:e13534. https://doi.org/10.7717/peerj.13534.

Pearce, J., and D. Lindenmayer. 1998. Bioclimatic analysis to enhance reintroduction biology of the endangered helmeted honeyeater (*Lichenostomus melanops cassidix*) in Southeastern Australia. Restoration Ecology 6(3):238–243. https://doi.org/10.1046/j.1526-100X.1998.00636.x.

Pearson, R.G., and T.P. Dawson. 2003. Predicting the impacts of climate change on the distribution of species: Are bioclimate envelope models useful? Global Ecology and Biogeography 12(5):361–371. https://doi.org/10.1046/j.1466-822X.2003.00042.x.

Pearson, R.G., C.J. Raxworthy, M. Nakamura, and A. Townsend Peterson. 2007. Predicting species distributions from small numbers of occurrence records: a test case using cryptic geckos in Madagascar. Journal of Biogeography

34(1):102–117. https://doi.org/10.1111/j.1365-2699.2006.01594.x.
Peters, D.P.C., K.M. Havstad, J. Cushing, C. Tweedie, O. Fuentes, and N. Villanueva-Rosales. 2014. Harnessing the power of big data: Infusing the scientific method with machine learning to transform ecology. Ecosphere 5(6):art67. https://doi.org/10.1890/ES13-00359.1.
Peterson, A.T. 2003. Predicting the geography of species' invasions via ecological niche modeling. The Quarterly Review of Biology 78(4):419–433. https://doi.org/10.1086/378926.
Peterson, A.T., B.W. Benz, and M. Papeş. 2007. Highly pathogenic H5N1 avian influenza: Entry pathways into North America via bird migration. PLOS ONE 2(2):e261. https://doi.org/10.1371/journal.pone.0000261.
Peterson, A.T., R.R. Lash, D.S. Carroll, and K.M. Johnson. 2006. Geographic potential for outbreaks of Marburg hemorrhagic fever. American Journal of Tropical Medicine & Hygiene 75:9–15.
Peterson, A.T., M.A. Ortega-Huerta, J. Bartley, V. Sánchez-Cordero, J. Soberón, R.H. Buddemeier, and D.R.B. Stockwell. 2002. Future projections for Mexican faunas under global climate change scenarios. Nature 416(6881):Article 6881. https://doi.org/10.1038/416626a.
Peterson, A.T., J. Soberón, R.G. Pearson, R.P. Anderson, E. Martínez-Meyer, M. Nakamura, and M.B. Araújo. 2011. Ecological niches and geographic distributions (MPB-49). Princeton University Press, Princeton, NJ, USA.
Peterson, A.T., J. Soberón, and V. Sánchez-Cordero. 1999. Conservatism of ecological niches in evolutionary time. Science 285(5431):1265–1267.
Phillips, S.J., R.P. Anderson, and R.E. Schapire. 2006. Maximum entropy modeling of species geographic distributions. Ecological Modelling 190(3–4):231–259. https://doi.org/10.1016/j.ecolmodel.2005.03.026.
Pulliam, H.R. 2000. On the relationship between niche and distribution. Ecology Letters 3(4):349–361. https://doi.org/10.1126/science.285.5431.1265.
Raxworthy, C., C. Ingram, and R. Pearson. 2007. Species delimitation applications for ecological niche modeling: A review and empirical evaluation using *Phelsuma* day gecko groups from Madagascar. Systematic Biology 56(6):907–923. https://doi.org/10.1080/10635150701775111.
Raxworthy, C J., E. Martinez-Meyer, N. Horning, R.A. Nussbaum, G.E. Schneider, M.A. Ortega-Huerta, and A. Townsend Peterson. 2003. Predicting distributions of known and unknown reptile species in Madagascar. Nature 426(6968):Article 6968. https://doi.org/10.1038/nature02205.
Srivastava, V. 2019. Species distribution models (SDM): Applications, benefits and challenges in invasive species management. CAB Reviews: Perspectives in Agriculture, Veterinary Science, Nutrition and Natural Resources:14(020). https://doi.org/10.1079/PAVSNNR201914020.
Stanton, J.C., K.T. Shoemaker, R.G. Pearson, and H.R. Akçakaya. 2015. Warning times for species extinctions due to climate change. Global Change Biology 21(3):1066–1077. https://doi.org/10.1111/gcb.12721.
Thuiller, W., D.M. Richardson, P. Pyšek, G.F. Midgley, G.O. Hughes, and M. Rouget. 2005. Niche-based modelling as a tool for predicting the risk of alien plant invasions at a global scale. Global Change Biology 11(12):2234–2250.
Trinh-Dinh, H., A.T. Nguyen, M.D. Le, X. Li, N.T.H. Cao, and M.E. Blair. 2022. Assessment of climate change impacts on one of the rarest apes on Earth, the Cao Vit Gibbon *Nomascus nasutus*. Frontiers of Biogeography 14(1). https://doi.org/10.21425/F5FBG53320.
Valavi, R., G. Guillera-Arroita, J.J. Lahoz-Monfort, and J. Elith. 2022. Predictive performance of presence-only species distribution models: a benchmark study with reproducible code. Ecological Monographs 92(1):e01486. https://doi.org/10.1002/ecm.1486.
Villero, D., M. Pla, D. Camps, J. Ruiz-Olmo, and L. Brotons. 2017. Integrating species distribution modelling into decision-making to inform conservation actions. Biodiversity and Conservation 26(2):251–271. https://doi.org/10.1007/s10531-016-1243-2.
Woodward, F.I., and D.J. Beerling. 1997. The dynamics of vegetation change: Health warnings for equilibrium "dodo" models. Global Ecology and Biogeography Letters 6(6):413–418. https://doi.org/10.2307/2997350

NCEP materials are meant to be modifiable for each educator's specific classroom or training needs; adaptable Microsoft Word versions of modules are available for download through the NCEP module collection at https://ncep.amnh.org along with any available accompanying data files, appendices, presentations, teaching notes, and exercise solutions.

Creating and Optimizing Species Distribution Models: A Vignette for Wallace Ecological Modeling Application v2.0

Bethany A. Johnson[i], Gonzalo E. Pinilla-Buitrago[i,ii], Andrea Paz[iii], Jamie M. Kass[iv], Sarah I. Meenan[iv], Robert P. Anderson[i,ii,iv]

[i]City College of the City University of New York, Biology, New York, NY, USA; [ii]Graduate Center of the City University of New York, Biology, New York, NY, USA; [iii]Department of Environmental Systems Science, Institute of Integrative Biology, ETH Zürich, Switzerland; [iv]Graduate School of Life Sciences, Tohoku University, Sendai, Miyagi, Japan; [v]American Museum of Natural History, Division of Vertebrate Zoology, New York, NY, USA

ABSTRACT

Species distribution modeling (SDM) enables ecologists and conservation scientists to make range estimates for species of concern, as well as predictions of potential range in unsampled areas and for different time periods. Although advances in model building and evaluation are widespread in the ecology and evolution literature, most cutting-edge modeling methods are inaccessible to those who cannot read and write computer code, resulting in a "barrier to use" for many who would like to apply SDM to their research or to conservation efforts. The Wallace ecological modeling application, implemented in the R programming language as the CRAN package "**wallace**," provides a graphical user interface that allows any user to implement advanced SDM methods. Each Wallace module provides extensive guidance text and references key papers from the literature to help both new and experienced users learn best practices. In this exercise, we will introduce you to the Wallace software and its key features and learn how to create optimized SDMs for a species.

PREFACE

Welcome to the Wallace EcoMod v2.0 vignette. This vignette was written specifically for Wallace v2.0, so if you are using a different version of Wallace, some text and images in this vignette may not match up exactly with the version you use. For other versions of this vignette and other vignettes, go to: https://wallaceecomod.github.io/wallace/index.html and select from the "Vignettes" dropdown menu.

INTRODUCTION

Wallace is an R-based GUI (Graphical User Interface) application (R package **wallace**) for ecological modeling that currently focuses on building, evaluating, and visualizing models of species niches and distributions. We will refer to these models as species distribution models (SDMs), and we will not explain them at length here—as you read through, you will be pointed to some sources of detailed information within the application (such as the "Component Guidance" and "Module Guidance" tabs) for reference. Additionally, we highly recommend you read NCEP Synthesis "A Brief Introduction to Species Distribution Modeling for Conservation Educators and Practitioners" (available in the NCEP Module Collection at https://ncep.amnh.org) for additional background information.

Wallace has many qualities which we think make it a good example of next-generation scientific software: it's 1) accessible, 2) open, 3) expandable, 4) flexible, 5) interactive, 6) instructive, and 7) reproducible.

The application, which is constructed with the R package **shiny**, features a pannable/zoomable map and dynamic plots and tables. Data for the models can be downloaded from online databases or uploaded by the user. Most results can be downloaded, including the option to save R code that can reproduce your analysis. For more details, including on SDMs, please see our initial publication[1] in *Methods in Ecology and Evolution* and our follow-up publication[2] in *Ecography*.

1. Kass, J.M., B. Vilela, M.E. Aiello-Lammens, R. Muscarella, C. Merow, and R.P. Anderson. 2018. Wallace: A flexible platform for reproducible modeling of species niches and distributions built for community expansion. Methods in Ecology and Evolution 9(4):1151–1156. https://doi.org/10.1111/2041-210X.12945.
2. Kass, J.M., et al. 2022. Wallace 2: A shiny app for modeling species niches and distributions redesigned to facilitate expansion via module contributions. Ecography, 2023(3):e06547. https://doi.org/10.1111/ecog.06547.

Helpful Links

- Wallace project's main page: https://wallaceecomod.github.io/
- Wallace Google Group: https://groups.google.com/forum/#!forum/wallaceecomod
- Official email: wallaceecomod@gmail.com
- CRAN page (https://cran.r-project.org/package=wallace) hosts the stable version
- GitHub development page: https://github.com/wallaceEcoMod/wallace
- YouTube channel (https://www.youtube.com/@WallaceEcoMod) with various tutorial videos and recorded seminars

1. SETUP

Installing the package

For the **wallace** package to work, you should be using **R** version 3.5.0 or later. Download for Windows (https://cran.r-project.org/bin/windows/base/) or Mac (https://cran.r-project.org/bin/macosx/).

To install and load Wallace v2.0.5, open either the **R** GUI or RStudio (https://posit.co/download/rstudio-desktop/) and run the code below. It's the only code you'll have to run to use **wallace**.

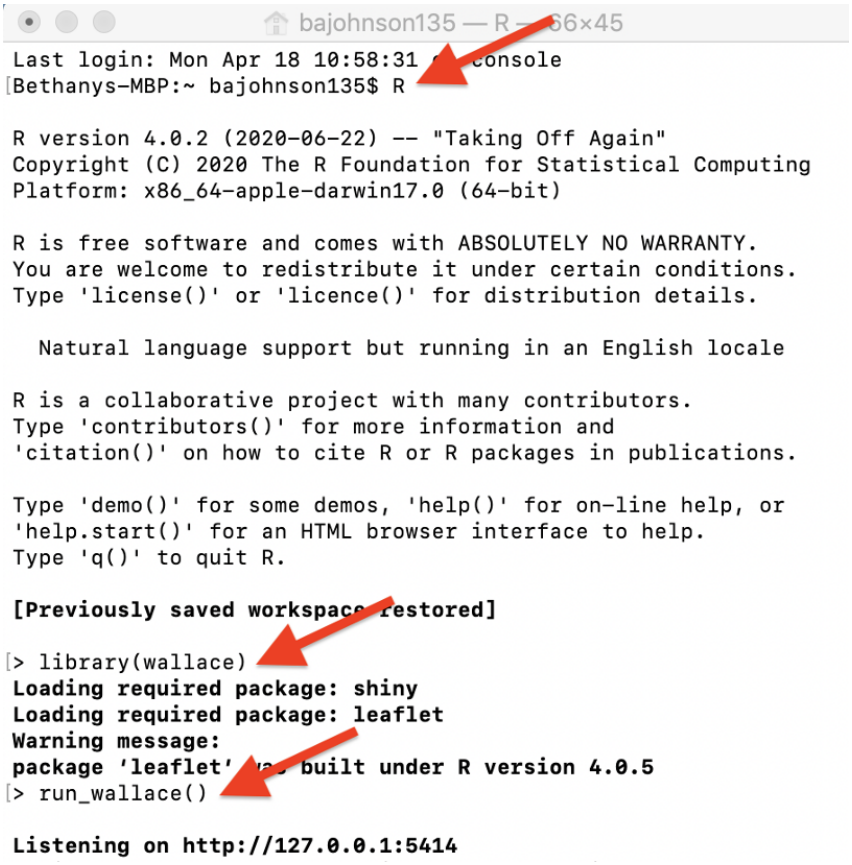
```
# Install Wallace from CRAN
install.packages("wallace")

# OR install Wallace from GitHub
install.packages("remotes")
remotes::install_github("wallaceEcoMod/wallace")

# THEN load Wallace
library(wallace)
# AND Run Wallace
run_wallace()
```

The Wallace GUI will open in your default web browser, and the **R** console will be occupied while Wallace is running.

The **R** console displays messages regarding **R**-package information or any error messages if complications arise, including valuable information for troubleshooting. If you intend to ask a question in the Google Group (preferred) or by email, please include any error messages from the console.

If you'd like to use the **R** console while running Wallace, open another **R** session, or alternatively a terminal window (MacOS/Linux) or command prompt (Windows) and initialize **R**, then run the lines above.

An example screenshot of running in Terminal in MacOS appears below.



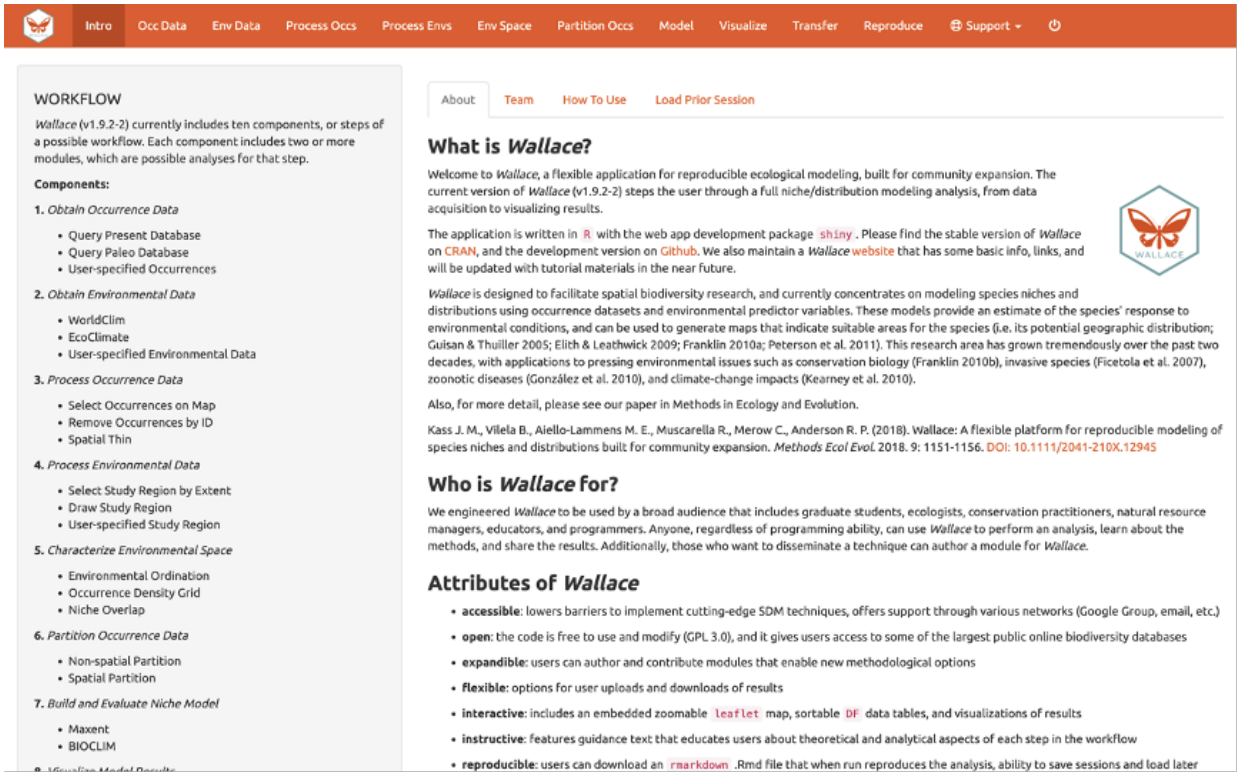
To exit Wallace, hit 'Escape' while in the R console and close the browser window, or click the quit button in the top right corner of the GUI. Note: If you close the browser window running Wallace, *your session will be over and all progress will be lost*. See section 9. Save & Load Session for how to save your work and be able to restart your analysis.

Setting up Java version of Maxent

Wallace v2.0 includes two options to run Maxent models: maxnet and maxent.jar. The former, which is an R implementation of Maxent and fits the model leveraging the package **glmnet**, is now the default and does not require running Java (see Phillips et al. 2017). The latter, which is the original Java implementation, runs the **maxent()** function in the package **dismo**, which in turn relies on tools from the package **rJava**. When using **dismo** to run maxent.jar, the user must place the maxent.jar file in the /java directory of the **dismo** package root folder. You can download Maxent (https://biodiversityinformatics.amnh.org/open_source/maxent/) and find maxent.jar, which runs Maxent, in the downloaded folder. You can find the directory path to dismo/java by running **system.file('java', package="dismo")** in the R console. Simply copy maxent.jar and paste it into the /java directory of the **dismo** package root folder. If you try to run Maxent in Wallace without the file in place, you will get a warning message in the log window and Maxent will not run. Also, if you have trouble installing **rJava** and making it work, there is a bit of troubleshooting on the Wallace Github repository README (https://github.com/wallaceEcoMod/wallace/blob/master/README.md) that hopefully should help.

2. ORIENTATION

We'll begin with an orientation of the Wallace interface. After running **run_wallace()** in the R console, Wallace opens to the "Intro" page. The "About" tab contains background information about the program. The "Team" tab has details about the developers and collaborators who contributed to Wallace. The "How to Use" tab contains a brief user manual, which is an abridged version of this



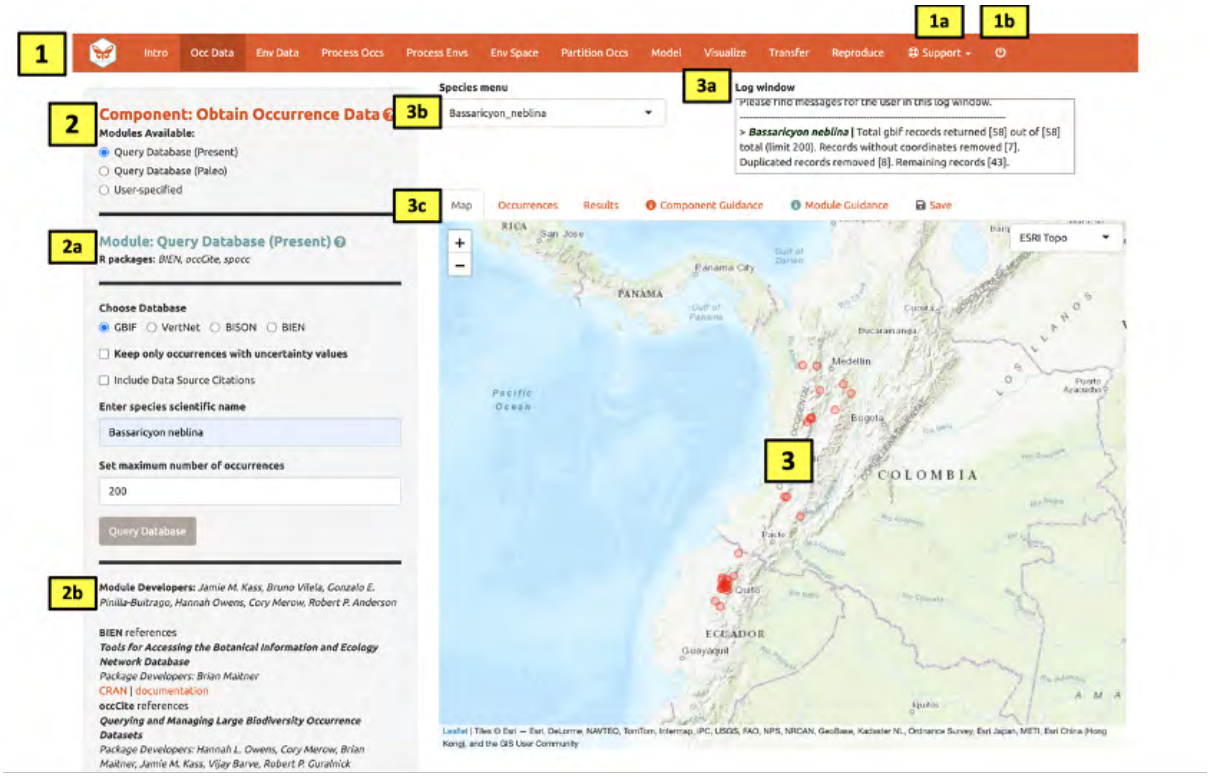
vignette without a worked example. The "Load Prior Session" tab is for loading a prior session, which we will cover later in section 9. Save & Load Session of this exercise.

At the top in the orange panel are the "Components", which represent the steps of analysis. Each of these component tabs opens to the corresponding step. Within each component are several "Modules", which are discrete analysis options within the components. To the left in the gray panel is the Wallace WORKFLOW, outlining the version number, components (numbered), and modules (bulleted) currently included. Click on the component tab "Occ Data", select a module, and consult the schematic below showing the different parts of the Wallace interface.

(1) These are the components. You will be stepping sequentially through them. Wallace v2 includes a Support button (1a), which links to the Google Group, email, website, and the Github page to report issues, as well as the quit button (1b), which will end the session. (2) This is the toolbar with all the user interface controls, such as buttons, text inputs, etc. You can see that the module "Query Database (Present)" is currently selected. You'll see that two other modules exist for this component: Query Database (Paleo) and User-specified. This last module lets you upload your own occurrence data. Try choosing it instead and notice that the toolbar changes, then click back to "Query Database (Present)".

Both the "Component" and "Module" have question mark buttons (?) next to the title text. Clicking these will link to the respective guidance texts.

Within this toolbar, you can find the module name and the R packages it uses (2a), as well as the control panel for the selected module (2b). Modules can be contributed by other researchers and the developers; CRAN links and documentation are at the bottom. (3) The right side is the visualization space. Any functions performed will trigger a message in the log window (3a). This window will also display any error messages. Wallace v2.0.5 allows the user to load multiple species. If multiple species are loaded, toggle and select between species using the species drop-down menu (3b).



The visualization space includes several tabs (3c), including an interactive map, occurrence records table, results window, model and component guidance text windows, and a tab for saving outputs and the current session.

At this stage of the analysis, no results exist, and you have no data yet for the table, but you can view the "Component Guidance" and "Module Guidance" text now. This text was written by the developers to prepare users for each component and module theoretically (why we should use the tools) and methodologically (what the tools do). The guidance text also references scientific papers from the literature for more detailed reading. Please get into the habit of consulting these before undertaking analyses—and discussing them with your peers—as this should give you a more solid foundation for moving forward.

The next tab in the visualization space is "Save". At any point along the workflow, selecting "Save session" within this tab will save the progress as a .rds file. This file can be loaded back into `wallace` to resume analysis. If at any point during the vignette you need to pause, jump to section 9. Save & Load Session in this exercise to learn how to save and load your Wallace session. This tab is also where you will be able to download and save results. The session code, metadata, and package citations can be downloaded within "Component: Reproduce" (section 13. Reproduce in this exercise).

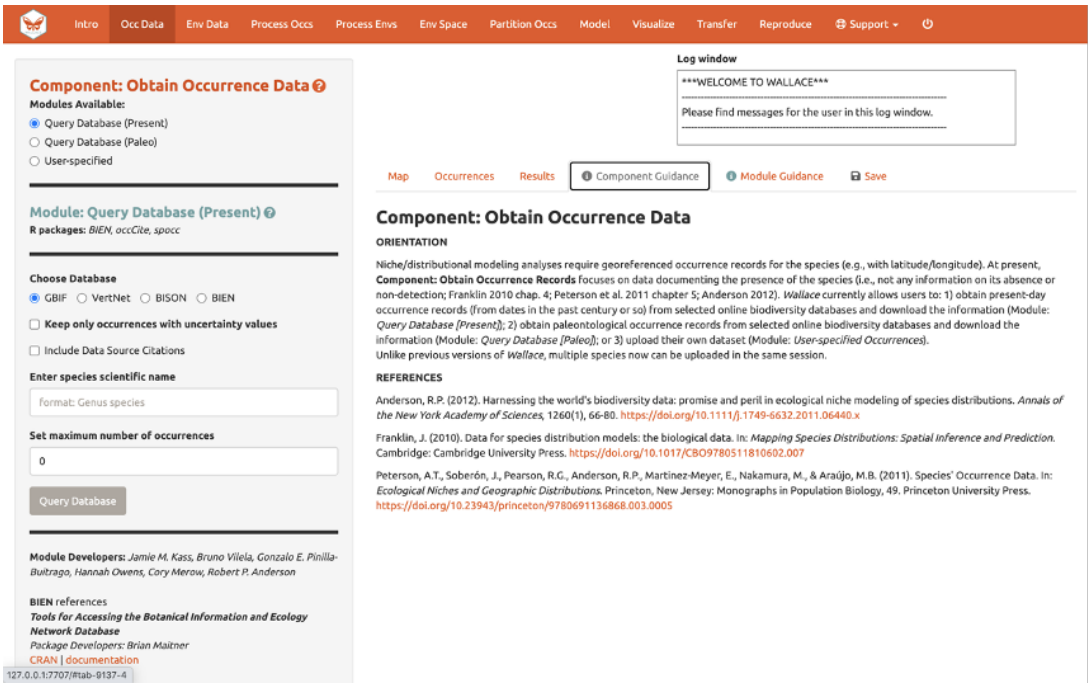
Now let's begin our analysis.

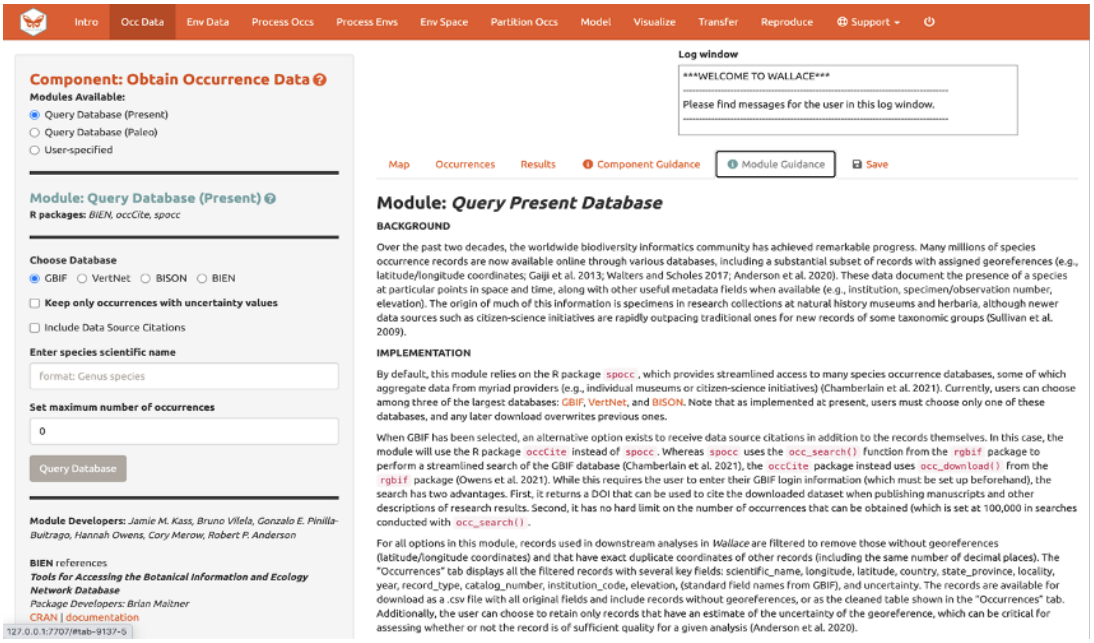
We'll be modeling the ranges of two mammal species of the genus *Bassaricyon*, which are members of the family Procyonidae that includes raccoons. *Bassaricyon neblina*, or the olinguito, is found in tropical montane areas of western Colombia and Ecuador in South America. The olinguito gained species status in 2013 when it was identified from existing museum specimens and is currently a species of concern listed as "Near Threatened" by the IUCN (Helgen et al. 2020). *Bassaricyon alleni*, or the eastern lowland

olingo, is a relative of the olinguito and has a broader range throughout northern South America; it is currently listed as "Least Concern" by the IUCN (Helgen et al. 2016).

3. OBTAIN OCCURRENCE DATA

Make sure you are in the first component ("Obtain Occurrence Data") and click to read the component guidance text. There are three modules available for obtaining occurrence data: "Query Database (Present)", "Query Database (Paleo)", and "User-Specified". Choose a module and click on the module guidance text. Notice the module guidance text changes as you select among the three modules. Read through these to get a better understanding of how occurrence data is typically obtained and how Wallace implements it.

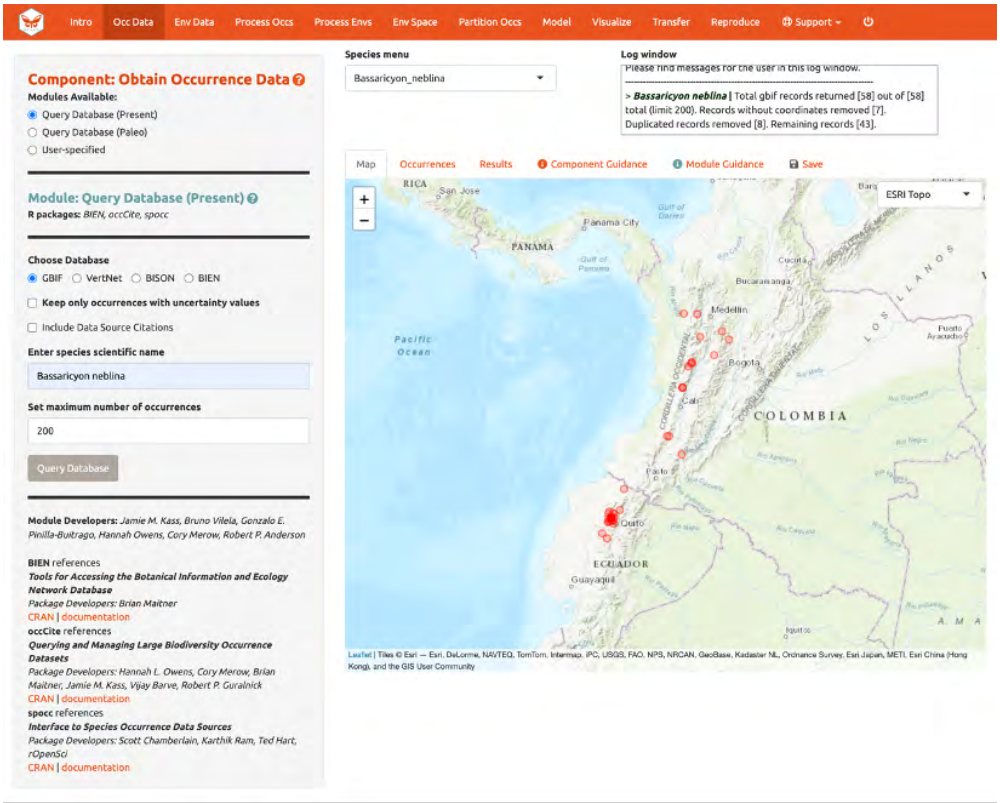




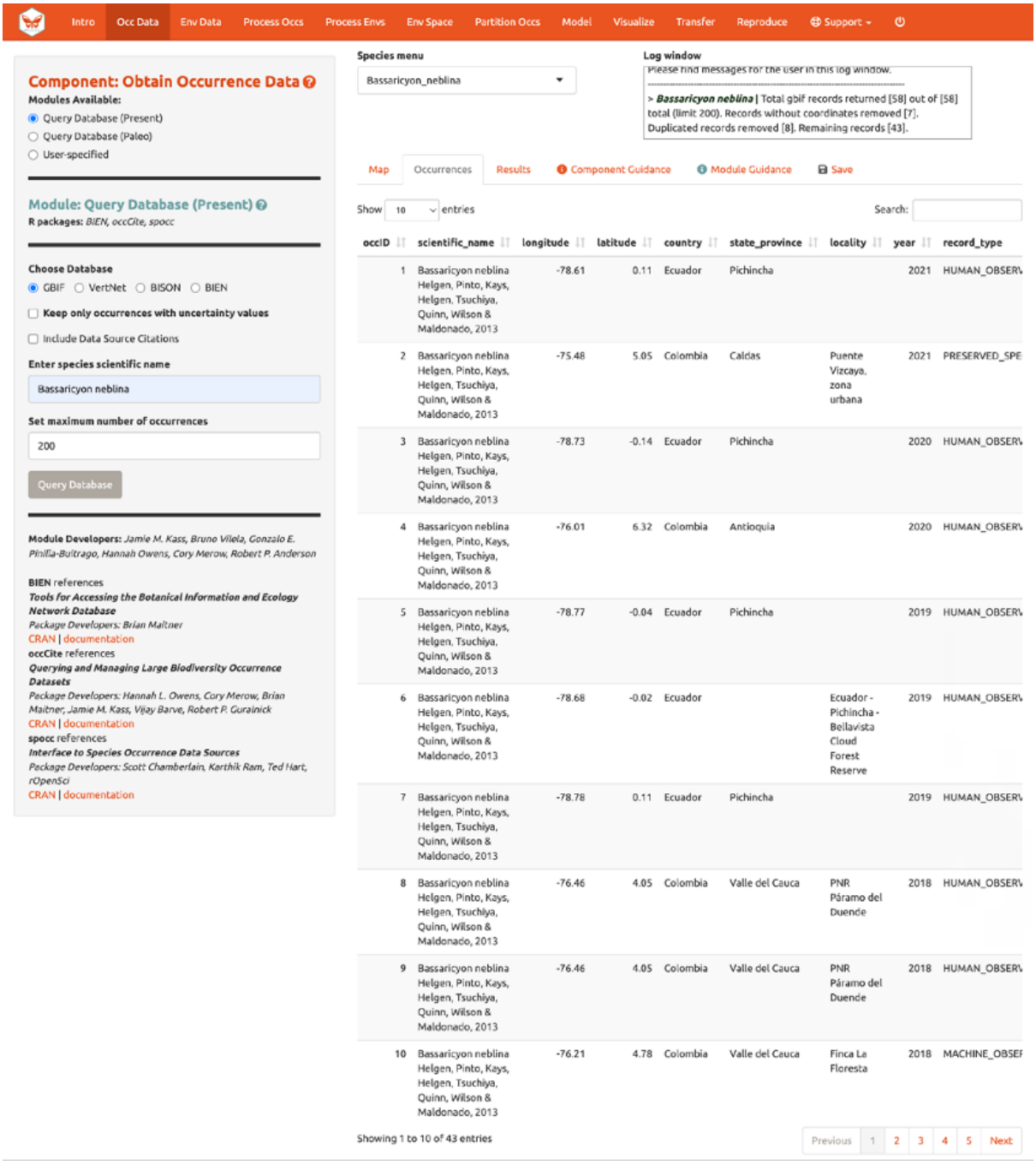
Let's proceed to get some occurrence data. We'll be using present occurrences (as opposed to those from the deep past via fossil data, etc.) and therefore use Module: "Query Database (Present)". There is a selection of databases to choose from, as well as the option to return only those occurrences that contain information on coordinate uncertainty (which can be useful to filter by later). Optional: If you have a GBIF User ID, checking the "Include Data Source" box will allow you to log in with your username and password to download a DOI for the dataset. In order for this to work, you will need to install the R-package **`occCite`** from RStudio or **`R`** prior to running Wallace. Since **`occCite`** is a suggested package, it will not install automatically like the other package dependencies. If this is the case, you will see a notification to install `occCite` in the log window. If you don't already have a GBIF account, you can create a user ID login at https://www.gbif.org.

Choose GBIF (the Global Biodiversity Information Facility—one of the largest storehouses for biodiversity data), keep uncertainty unchecked, type in *Bassaricyon neblina* into the scientific name box, set the maximum number of occurrences to 200, and click "Query Database".

After the download is complete, the log window will contain information on the analysis performed. Your search should return at least 58 records (numbers recorded at the time of writing), but after accounting for records without coordinate information (latitude, longitude) and removing duplicate records, at least 43 should remain. This species has relatively few records, so setting the maximum to 200 is sufficient, but for modeling with data-rich species, 200 may not be enough for adequately sampling the known range, and the maximum can be increased. ***Numbers may be different as more records are added to GBIF*.

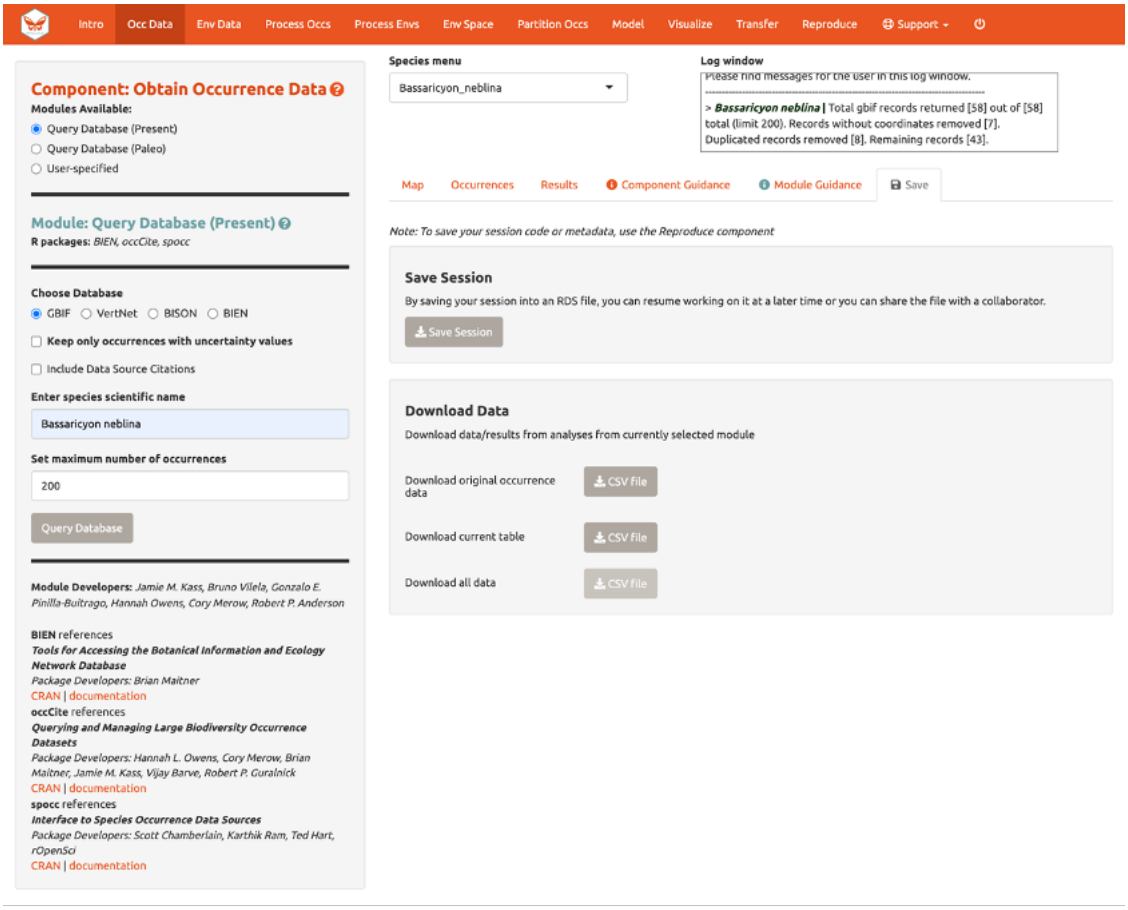


Now click on the "Occurrences" tab to view more information on the records. The developers chose the fields that are displayed based on their general relevance to studies on species ranges. Note that you can download the full table with all fields.



Click the "Save" tab. The first save box allows you to download your session. It is available in all the components and modules (See section 9. Save & Load Session for more details). The download options below the Save Session box change depending on which component is selected. Here, you can get a .csv file of the records just acquired. The first option will download the original database fields for every downloaded record (before any filtering). The second option downloads the current table. The third option, "Download all data", is unavailable at this point, but that will change after we include our second species.

Note to Chrome users: If you find the map is loading incorrectly after downloading an object, specifically the corner tile loads but the rest of the map is gray, closing the download bar at the bottom of the page should reset the map and fix the problem.



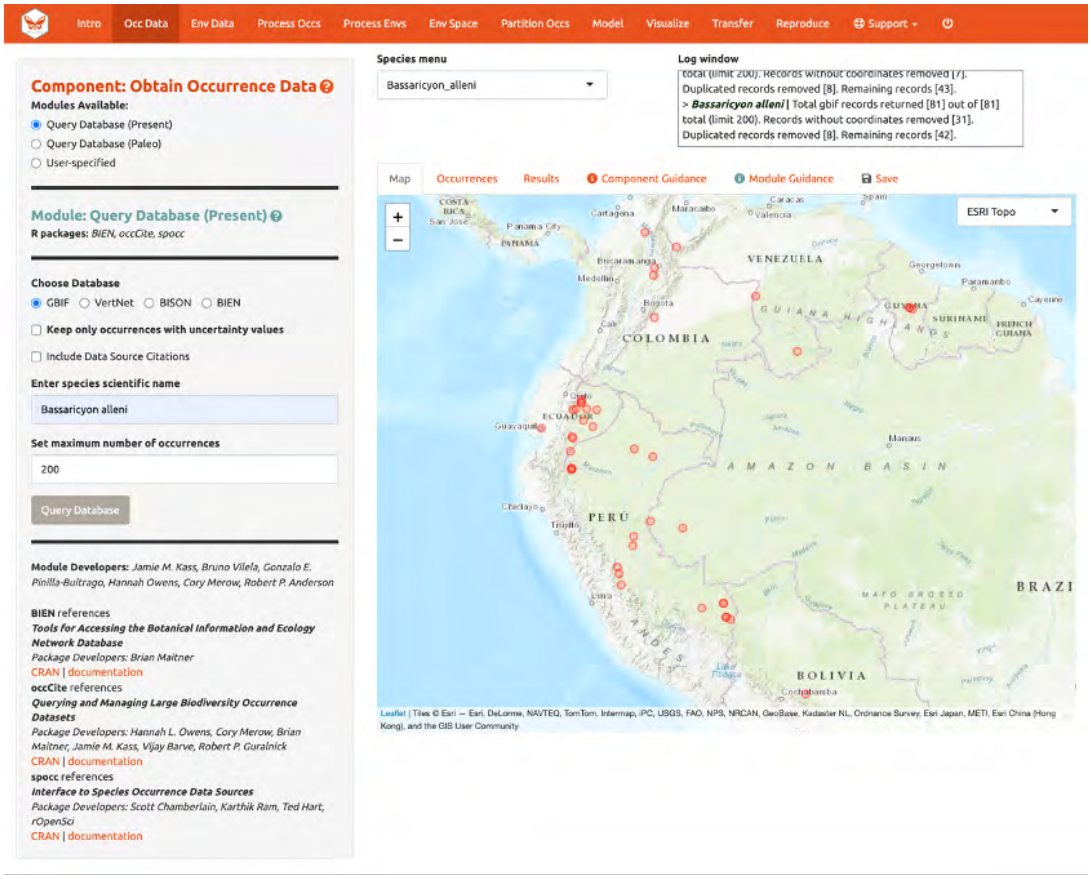
A major improvement in Wallace v2.0 from previous versions is the ability to consider multiple species (separately) in the same session. Let's add another species to model.

Aside from GBIF, you can query the Vertnet (for vertebrate data) and BIEN (for botantical data) for species occurrence records. In the second module "Query Database (Paleo)", you can query PaleobioDB databases for fossil records by selecting a time interval and species. Specific packages may have to be downloaded prior to loading Wallace to use these (e.g., `BIEN` and `paleobioDB`). Reminder: depending on the version of Wallace you are using and the availability of associated packages or databases, you may see variations between these instructions and your application options.

If you have your own occurrence data, you can import it using the third module, "User-specified". Your occurrence data file must be a .csv with the columns "scientific_name", "longitude", and "latitude", explicitly named and in that order. It may have other columns, but those must be the first three. You also have the option to specify the delimiter and separator of your file.

We'll continue with GBIF occurrence data. Search the database for *Bassaricyon alleni* (eastern lowland olingo), keeping the max set at 200. This should return at least 81 records and after cleaning should come to at least 42 records. You might have noticed that the log window was updated, but the map remains the same. The map will not change automatically, as *Bassaricyon neblina* is still selected in the Species menu. Toggle between species to show the map for Bassarricyon alleni.

Click back to the "Save" tab. Notice that the third option is now available.



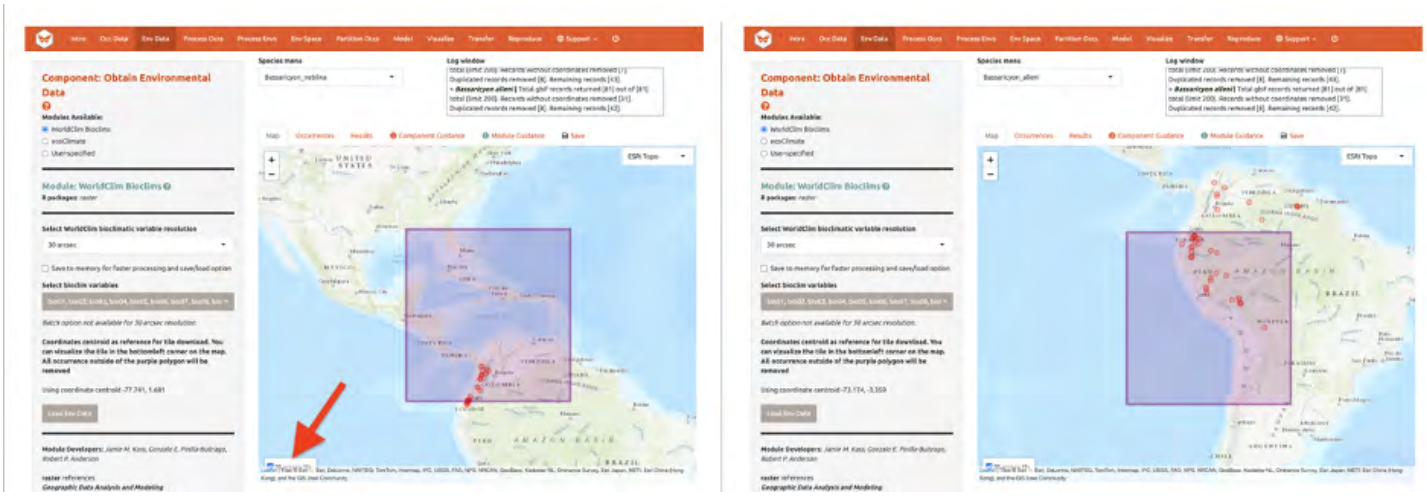
4. OBTAIN ENVIRONMENTAL DATA

Next, you will need to obtain environmental variables for the analysis. The values of the variables are extracted for the occurrence records, and this information is provided to the model. These data are in raster form, which simply means a large grid where each grid cell specifies a value. Rasters can be displayed as colored grids on maps (we'll see this later). Click on the component "Env Data". The first module, "WorldClim Bioclims", lets you download bioclimatic variables from WorldClim, a global climate database of interpolated climate surfaces derived from weather station data at multiple resolutions. The interpolation is better for areas with more weather stations, and more uncertainty exists in areas with fewer stations. The "bioclim variables" are summaries of temperature and precipitation that have been proposed to have general biological significance. You have the option to specify a subset of the 19 total variables to use in the analysis.

The second module, "ecoClimate", is a module included with v2 that includes paleoclimate reconstructions. It accesses climatic layers from the PMIP3 – CMIP5 projects from ecoClimate. Users can select from Atmospheric Oceanic General Circulation Models and choose a temporal scenario to use. All ecoClimate layers have a resolution of 0.5 degrees, whereas WorldClim allows resolution options of 30 arcsec, 2.5 arcmin, 5 arcmin, or 10 arcmin.

The third module, "User-specified", is for uploading your own rasters into Wallace. These can be continuous, numerical, or categorical variables to provide to the model. We'll be using WorldClim. The first time you use Wallace, these data are downloaded to a temporary folder on your hard drive; after that, they will simply be loaded from this local directory (which will be quicker than downloading from the web). You also have the option to save to memory for faster processing—this saves the data temporarily as a RasterBrick in your RAM for Wallace to access. Finer resolution

rasters will take longer to download. The finest resolution data (30 arcsec) is served in large global tiles when downloading through R with the raster package (which `wallace` uses) and a single tile that corresponds to the map center will be downloaded. Set the resolution to 30 arcsec and the latitude and longitude of the map center will be given. To visualize how well the tile will cover the occurrence points, click the "30 arcsec tile" box in the bottom left corner of the map. The points outside the tile will be excluded; you may need to zoom out to see fully.

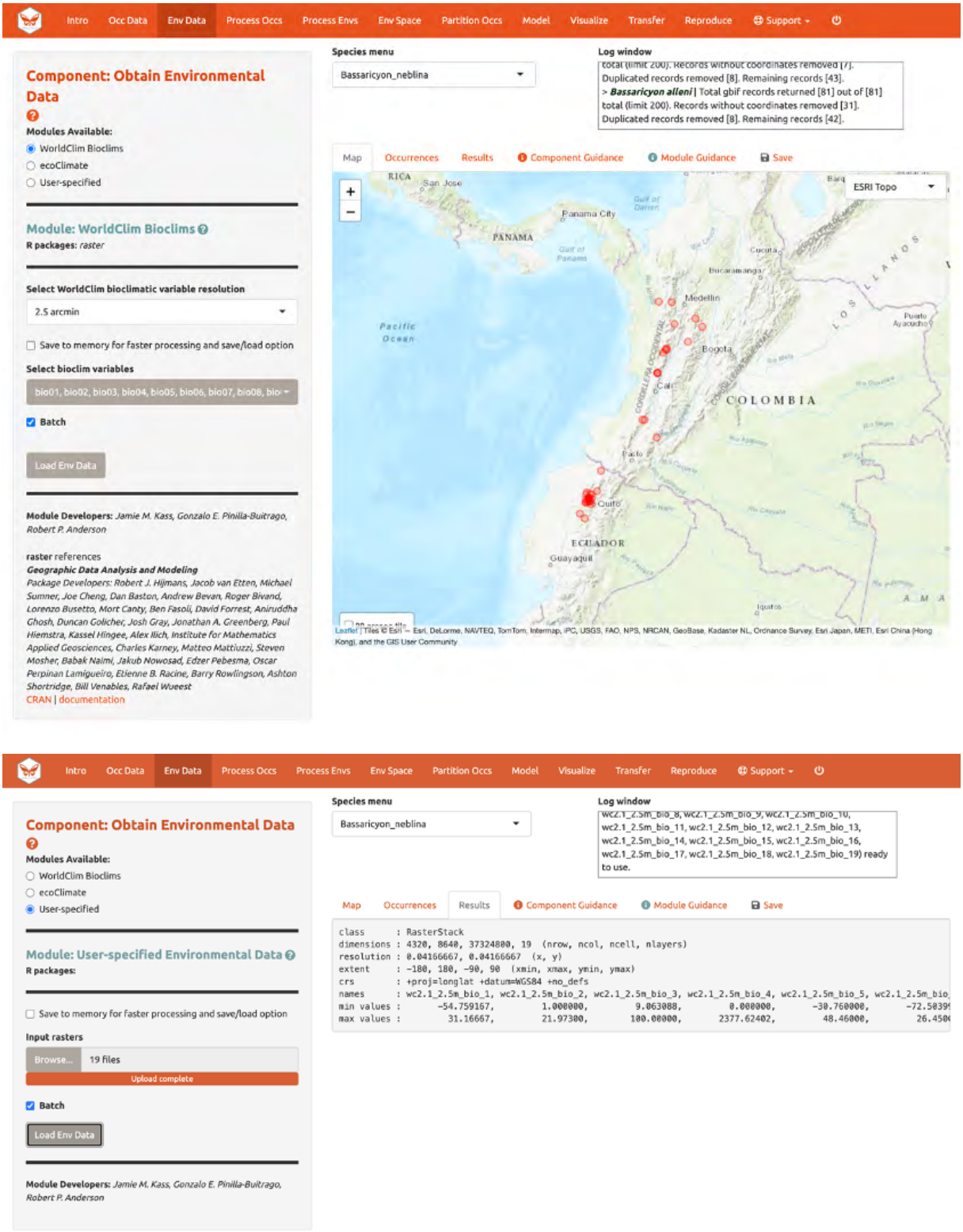


Although you could download the (very big) 30 arcsec global raster from the WorldClim website and load it into Wallace (preferably after cropping it with GIS software or in R), we will instead choose the 2.5 arcmin bioclimatic variable resolution that Wallace serves in a global extent to cover all our occurrence points, and we will keep all 19 bioclimatic variables checked. Note that the selections made will be performed only for the species selected in the Species Menu box, unless the "Batch" box is checked. The "Batch" button will perform the analysis you've set up in the module for all the species you have uploaded. You'll notice this option in many of the modules. If you want to perform individualized analyses for each species (in this case, different environmental variables), leave "Batch" unchecked. Note: The batch option is not available for 30 arcsec resolution since different tiles may need to be accessed.

Check "Batch" and click "Load Env Data". Notice the progress bar in the bottom-right corner.

After the rasters have loaded, the "Results" tab will display summary information about them (e.g., resolution, extent, cell number, etc.). In addition to downloading the rasters, Wallace will also remove any occurrence points with no environmental values (i.e., points that did not overlap with grid cells with data in the rasters).

You can download your environmental variables from within the Download Data section of the "Save" tab.



5. PROCESS OCCURRENCE DATA

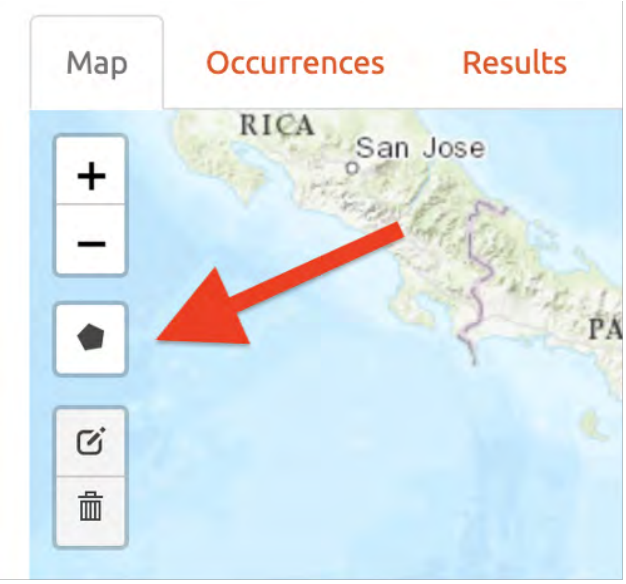
The next component, "Process Occs", gives you access to some data-cleaning tools. The data you retrieved from GBIF are raw, and there will almost always be some erroneous points. Some basic knowledge of the species' range can help us remove the most obvious errors. For databases like GBIF that accumulate lots of data from various sources, there are inevitably some dubious localities. For example, coordinates might specify a museum location instead of those associated with the specimen,

or the latitude and longitude might be inverted. In order to eliminate these obviously erroneous records, select only the points you want to keep for analysis with the module "Select Occurrences On Map". Alternatively, you can also remove specific occurrences by ID with the module "Remove Occurrences by ID". Even after removing problematic points, those you have left may be clustered due to sampling bias. This often leads to artifactually inflated spatial autocorrelation, which can bias the environmental signal for the occurrence data that the model will attempt to fit. For example, there might be clustering of points near cities because the data are mostly from citizen scientists who live in or near them. Or, the points can cluster around roads because the field biologists who took the data were either making observations while driving or gained access to sites from them. The last module, "Spatial Thin" will help reduce the effects of sampling bias. Unlike other components, in Process Occs the modules are not exclusive, and all can be used in any order.

Make sure *Bassaricyon alleni* is in the species menu.

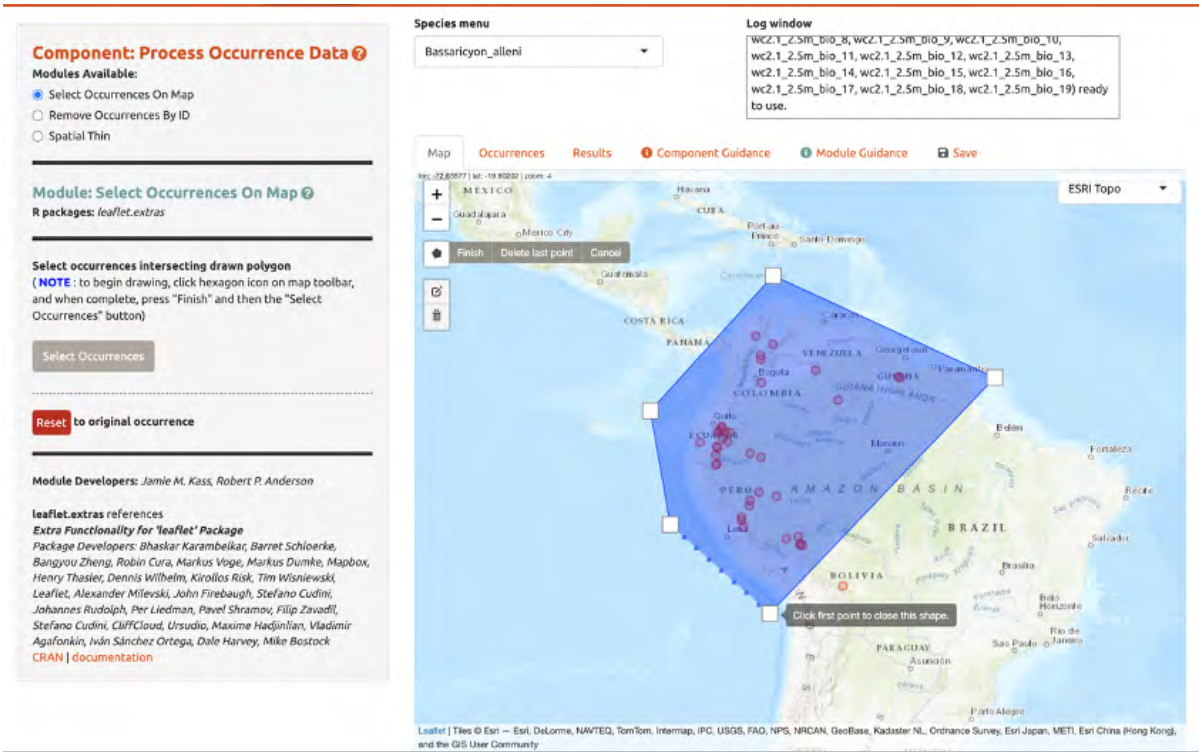
We will practice using the first two modules with this species. In the first module, we will use the polygon-drawing tool to select occurrences. The polygon drawing tool is useful to draw extents and will be seen in other modules later on as well.

Click on the polygon icon on the map toolbar.

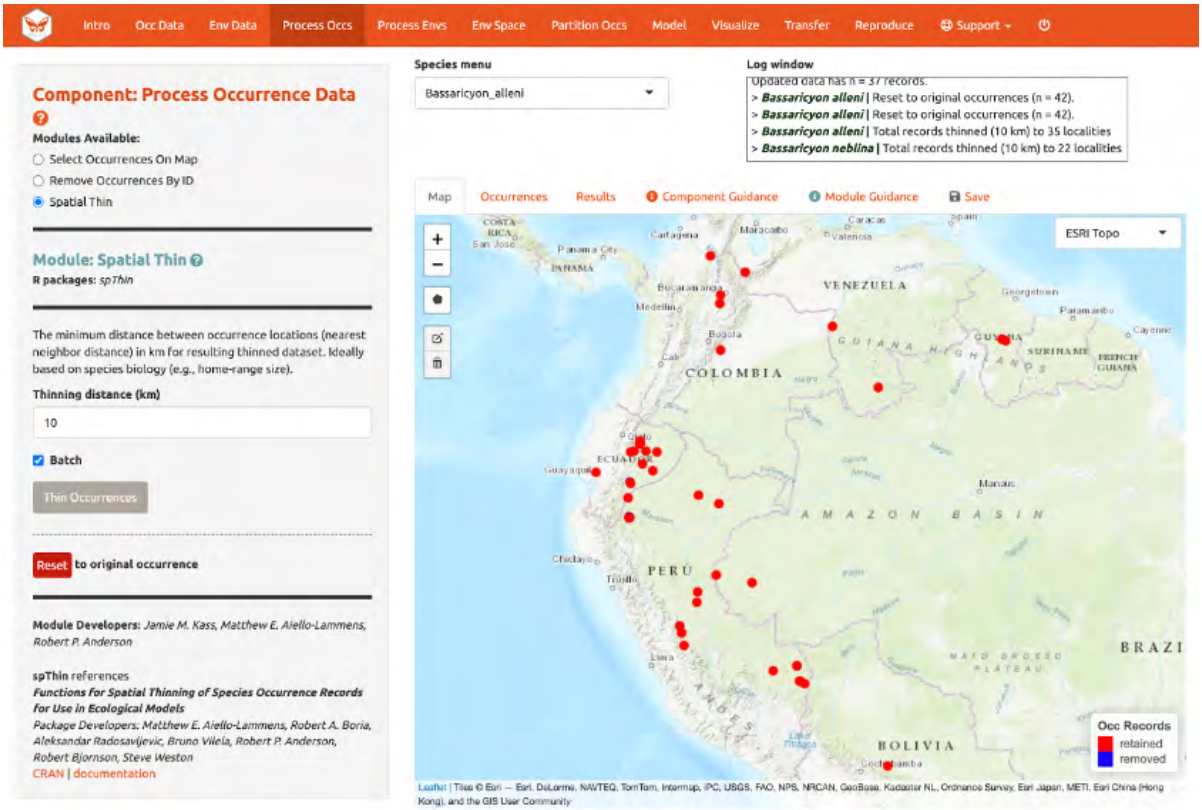


This opens the drawing tool. Click to begin drawing—each click connects to the last with a line. Draw a shape around South America, omitting the record in Bolivia. If you make a mistake in drawing, you can click "Delete last point" or "Cancel" to start over. To finish drawing, click again on the first point you made, or click "Finish" in the drawing tool. This finalizes the shape to use in analysis. Now click "Select Occurrences" and you will see the point in Bolivia disappear. To remove the blue shaded polygon, click on the trashcan icon on the map toolbar and hit "Clear All". If you are displeased or have made an error, the red "Reset" button in the module interface will revert back to the original points. Since we arbitrarily removed the record in Bolivia, click reset to return to our original dataset.

We will now remove it again, this time using the second module, "Remove Occurrences by ID". With the pointer, click on the record in Bolivia. Information on the record will pop up, starting with the OccID.



In this case it is OccID #18 (it may be a different number for you). Other information from the attribute table will be available. For example, the record has no information (NA) on the institution code, state/province, or basis. Since we know the OccID number, we can find the full information associated in the Occurrences tab. Click there and find the record. Here we can see it is a preserved specimen from the Museum of Southwestern Biology (MSB). Go back to the map. Enter "18" for the ID to be removed and "Remove Occurrence". You will see the point disappear again. Click reset to get it back again.



We are now left with 35 points for *Bassaricyon alleni* and 21 for *Bassaricyon neblina* (your numbers may be different). You can zoom in to see what the function did. Red points were retained and blue ones were removed. Download the processed occurrence datasets as a .csv file by clicking on the button in the "Save" tab. Reminder: the data downloaded are only for the species currently in the species menu.

6. PROCESS ENVIRONMENTAL DATA

Now we will need to choose the study extent for modeling. This will define the region from which "background" points are drawn for model fitting. Background points are meant to sample the environments in the total area available to the study species. Methods like Maxent are known as presence-background techniques because they compare the predictor variable values at background points to those at the occurrence points (as opposed to presence-absence techniques, which require absence data). In making decisions about the study extent, we want to avoid areas the species has historically been unable to move to—for example, regions beyond a barrier like a mountain range or large river that the species cannot cross. Including these areas may send a false signal to the model that these areas are not environmentally suitable. Like every other step of the analysis, please see the relevant guidance text for more details.

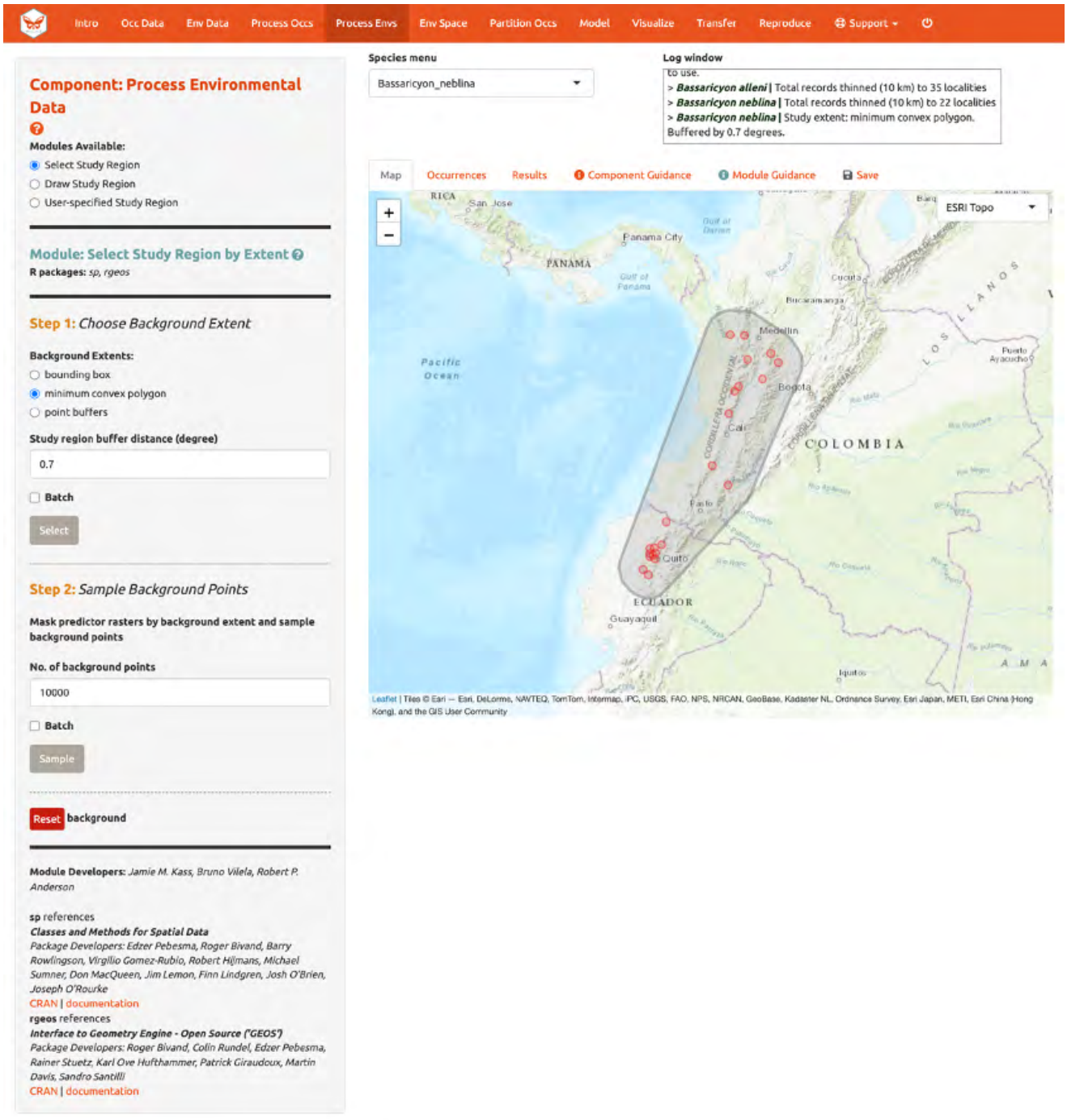
You can explore the different options for delineating the study extent here. Each module has two steps: 1) choosing the shape of the background extent, and 2) sampling the background points. To begin, go to the module "Select Study Region". Under "Step 1", try out the different options and see how each one draws the background shape. Try increasing and decreasing the buffer to see how the shape is affected. Now set the species to *B. neblina* and use "Select study region" to a minimum convex polygon with a 0.7° buffer distance. Then switch to *B. alleni* and use point buffers with a 0.7° buffer.

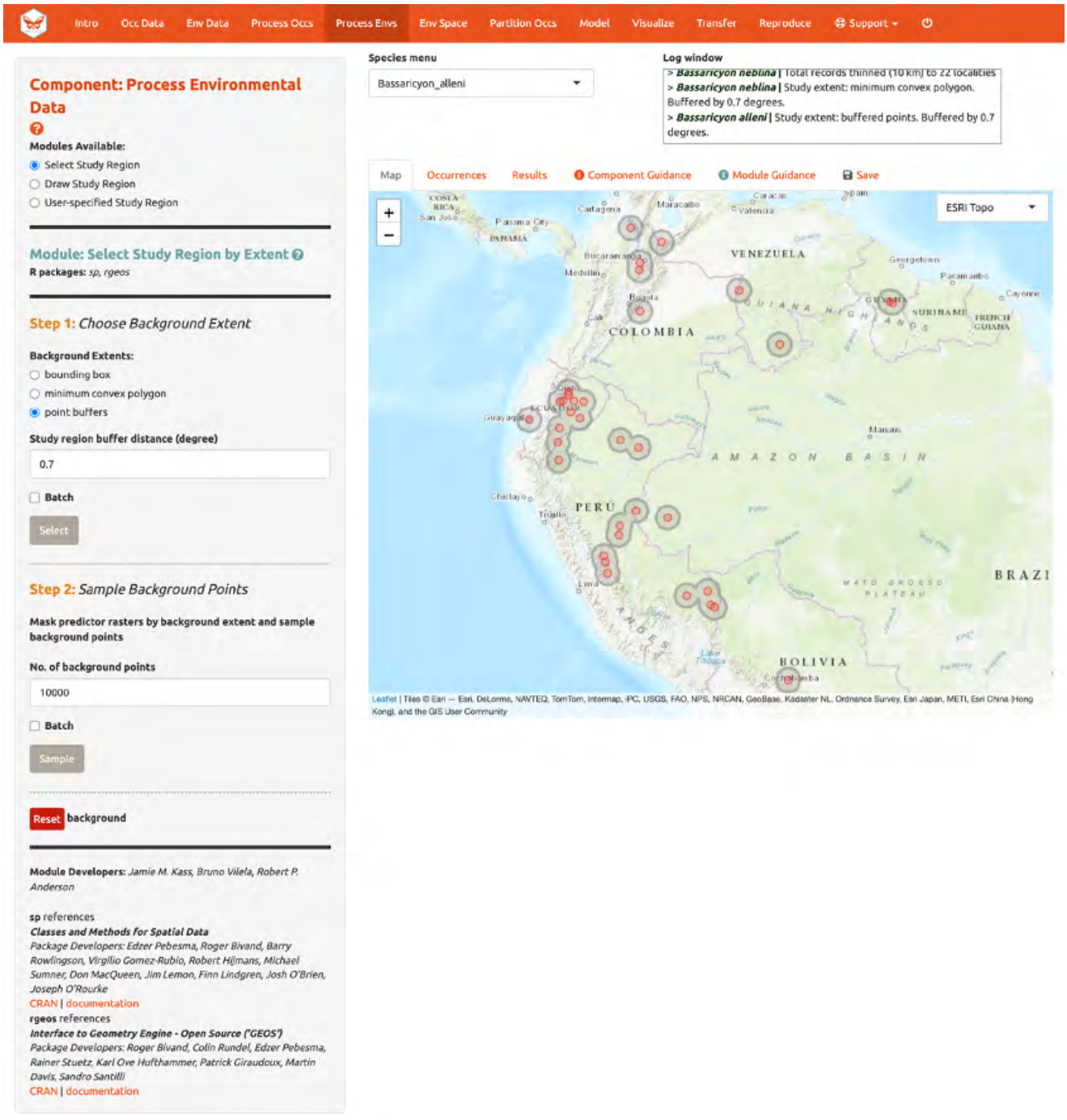
Alternatively, you can draw your own polygon (using the same polygon drawing tool we tested in "Component: Process occs"). If you have a file specifying the background extent, you can upload it with the "User-specified Study Region" module. This module can accept a shapefile (must include .shp, .shx, and .dbf files) or a .csv file of polygon vertex coordinates with the field order: longitude, latitude. Note that the polygon you draw or shape you upload needs to contain all the occurrence points.

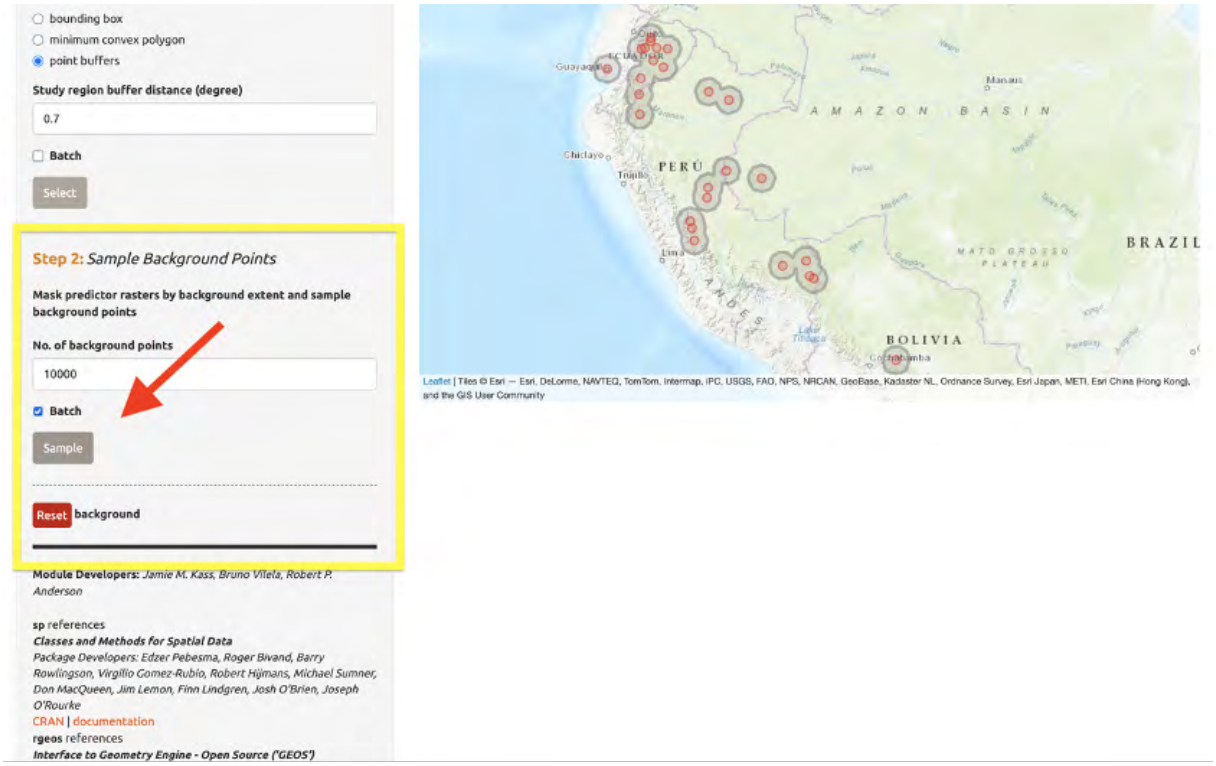
Next, complete "Step 2", which both clips the rasters by the study extent and samples the background points. Set the number of background points to 10,000 (larger samples can be appropriate for larger extents or those with finer resolution; see component guidance text), check "Batch", and click the "Sample" button.

You may find that requesting 10,000 background points exceeds the number of grid cells in the background extent. The available number of points will be given in the log window, and that amount can be used instead of 10,000.

A .zip file of the clipped rasters (e.g., the environmental data clipped to the extent of the background you just created) is available to download in the "Save" tab. Make sure to toggle the species to download the file for each one.


Intro
Occ Data
Env Data
Process Occs
Process Envs
Env Space
Partition Occs
Model
Visualize
Transfer
Reproduce
Support
Component: Process Environmental Data
Modules Available:
Select Study Region
Draw Study Region
User-specified Study Region
Module: Select Study Region by Extent
R packages: sp, rgeos
Step 1: Choose Background Extent
Background Extents:
bounding box
minimum convex polygon
point buffers
Study region buffer distance (degree)
0.7
Batch
Select
Step 2: Sample Background Points
Mask predictor rasters by background extent and sample background points
No. of background points
10000
Batch
Sample
Reset background
Module Developers: Jamie M. Kass, Bruno Vilela, Robert P. Anderson
sp references
Classes and Methods for Spatial Data
Package Developers: Edzer Pebesma, Roger Bivand, Barry Rowlingson, Virgilio Gomez-Rubio, Robert Hijmans, Michael Sumner, Don MacQueen, Jim Lemon, Finn Lindgren, Josh O'Brien, Joseph O'Rourke
CRAN | documentation
rgeos references
Interface to Geometry Engine - Open Source ('GEOS')
Package Developers: Roger Bivand, Colin Rundel, Edzer Pebesma, Rainer Stuetz, Karl Ove Hufthammer, Patrick Giraudoux, Martin Davis, Sandro Santilli
CRAN | documentation
Species menu
Bassaricyon_neblina
Log window
to use.
> Bassaricyon alleni | Total records thinned (10 km) to 35 localities
> Bassaricyon neblina | Total records thinned (10 km) to 22 localities
> Bassaricyon neblina | Study extent: minimum convex polygon. Buffered by 0.7 degrees.
Map
Occurrences
Results
Component Guidance
Module Guidance
Save
ESRI Topo
COSTA RICA
San Jose
Panama City
PANAMA
Gulf of Panama
Gulf of Darien
Pacific Ocean
Cucuta
Bucaramanga
Medellin
Bogota
Cali
COLOMBIA
LOS LLANOS
Puerto Ayacucho
Pasto
Quito
ECUADOR
Guayaquil
Iquitos
AMA
Leaflet | Tiles © Esri — Esri, DeLorme, NAVTEQ, TomTom, Intermap, iPC, USGS, FAO, NPS, NRCAN, GeoBase, Kadaster NL, Ordnance Survey, Esri Japan, METI, Esri China (Hong Kong), and the GIS User Community

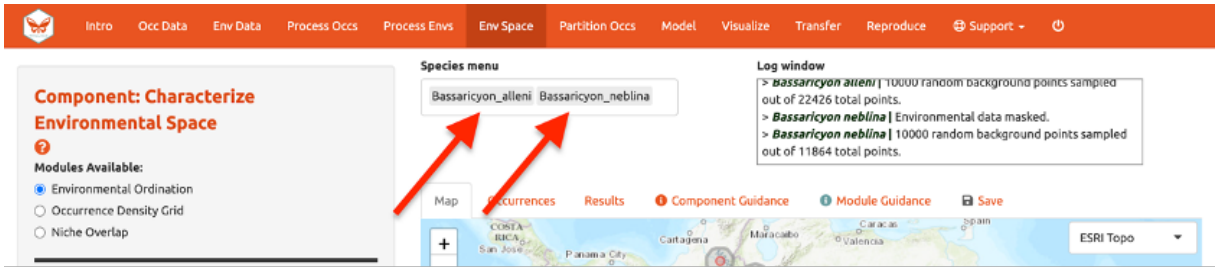

Intro
Occ Data
Env Data
Process Occs
Process Envs
Env Space
Partition Occs
Model
Visualize
Transfer
Reproduce
Support
Component: Process Environmental Data
Modules Available:
Select Study Region
Draw Study Region
User-specified Study Region
Module: Select Study Region by Extent
R packages: sp, rgeos
Step 1: Choose Background Extent
Background Extents:
bounding box
minimum convex polygon
point buffers
Study region buffer distance (degree)
0.7
Batch
Select
Step 2: Sample Background Points
Mask predictor rasters by background extent and sample background points
No. of background points
10000
Batch
Sample
Reset background
Module Developers: Jamie M. Kass, Bruno Vilela, Robert P. Anderson
sp references
Classes and Methods for Spatial Data
Package Developers: Edzer Pebesma, Roger Bivand, Barry Rowlingson, Virgilio Gomez-Rubio, Robert Hijmans, Michael Sumner, Don MacQueen, Jim Lemon, Finn Lindgren, Josh O'Brien, Joseph O'Rourke
CRAN | documentation
rgeos references
Interface to Geometry Engine - Open Source ('GEOS')
Package Developers: Roger Bivand, Colin Rundel, Edzer Pebesma, Rainer Stuetz, Karl Ove Hufthammer, Patrick Giraudoux, Martin Davis, Sandro Santilli
CRAN | documentation
Species menu
Bassaricyon_alleni
Log window
> Bassaricyon neblina | Total records thinned (10 km) to 22 localities
> Bassaricyon neblina | Study extent: minimum convex polygon. Buffered by 0.7 degrees.
> Bassaricyon alleni | Study extent: buffered points. Buffered by 0.7 degrees.
Map
Occurrences
Results
Component Guidance
Module Guidance
Save
ESRI Topo
VENEZUELA
COLOMBIA
PERU
BOLIVIA
AMAZON BASIN
GUIANA HIGHLANDS
SURINAME
FRENCH GUIANA
Leaflet | Tiles © Esri — Esri, DeLorme, NAVTEQ, TomTom, Intermap, iPC, USGS, FAO, NPS, NRCAN, GeoBase, Kadaster NL, Ordnance Survey, Esri Japan, METI, Esri China (Hong Kong), and the GIS User Community



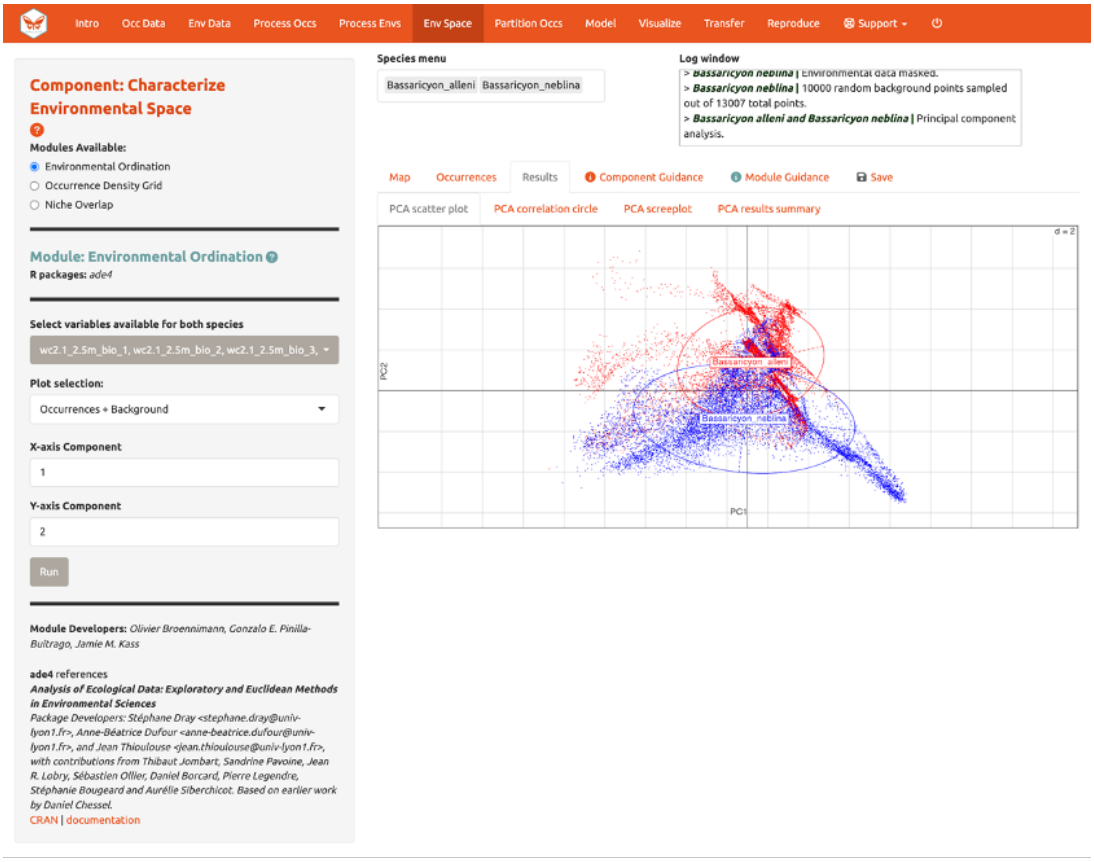
7. CHARACTERIZE ENVIRONMENTAL SPACE

"Component: Characterize Environmental Space" contains multi-species analyses and is optional. Unlike some other components which let you perform the modules in any order, the modules within "Characterize Environmental Space" are sequential and thus need to be performed consecutively (i.e., you can't get an "Occurrence Density Grid" without first performing an "Environmental Ordination").

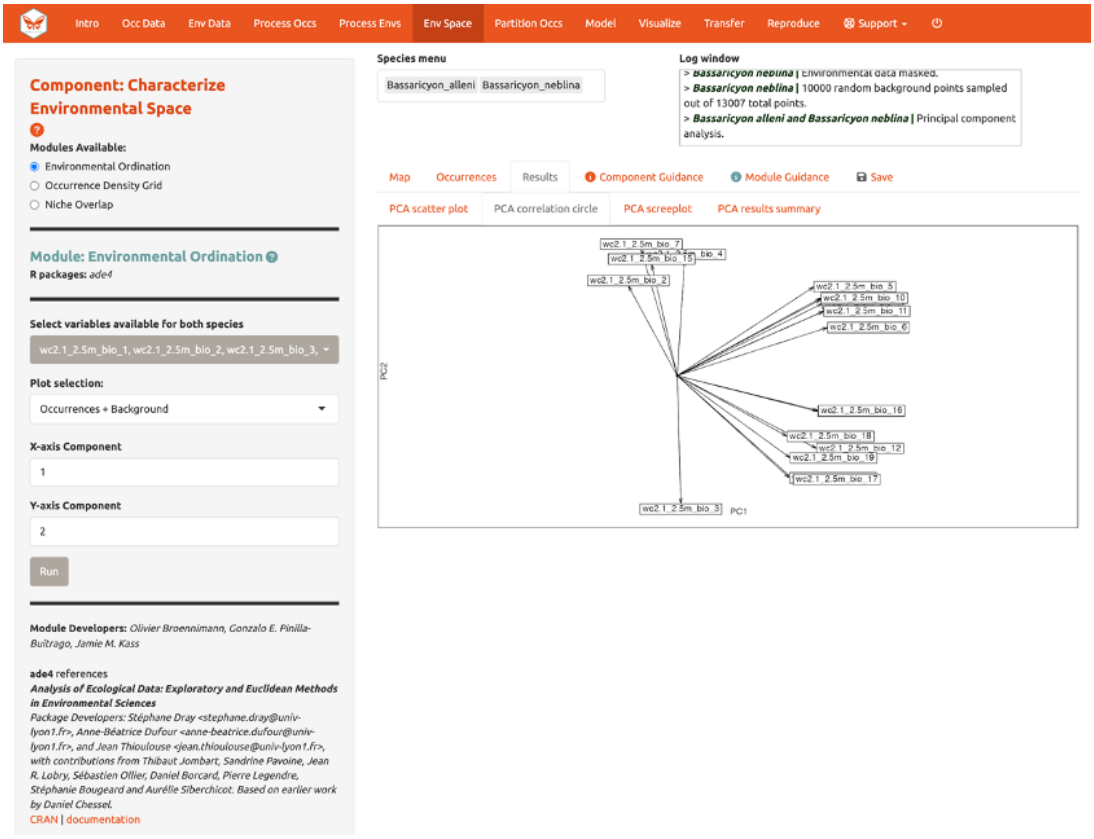
Before we begin the Module: "Environmental Ordination" analysis, you need to select two species to work with. If you had more than two species uploaded, select two from the species menu drop-down. Since we only have two uploaded, click in the species menu box and select the second species. Both names will appear in the box simultaneously—this functionality is currently only available for the "Characterize Environmental Space" component.

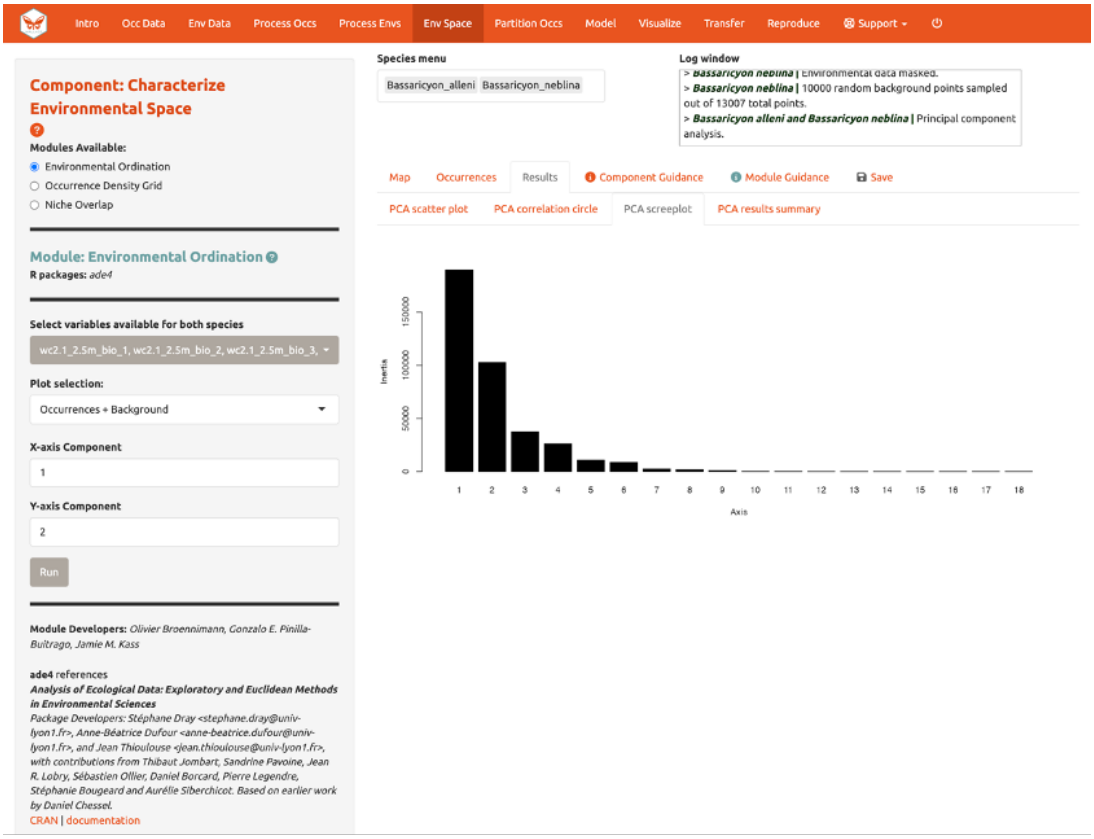


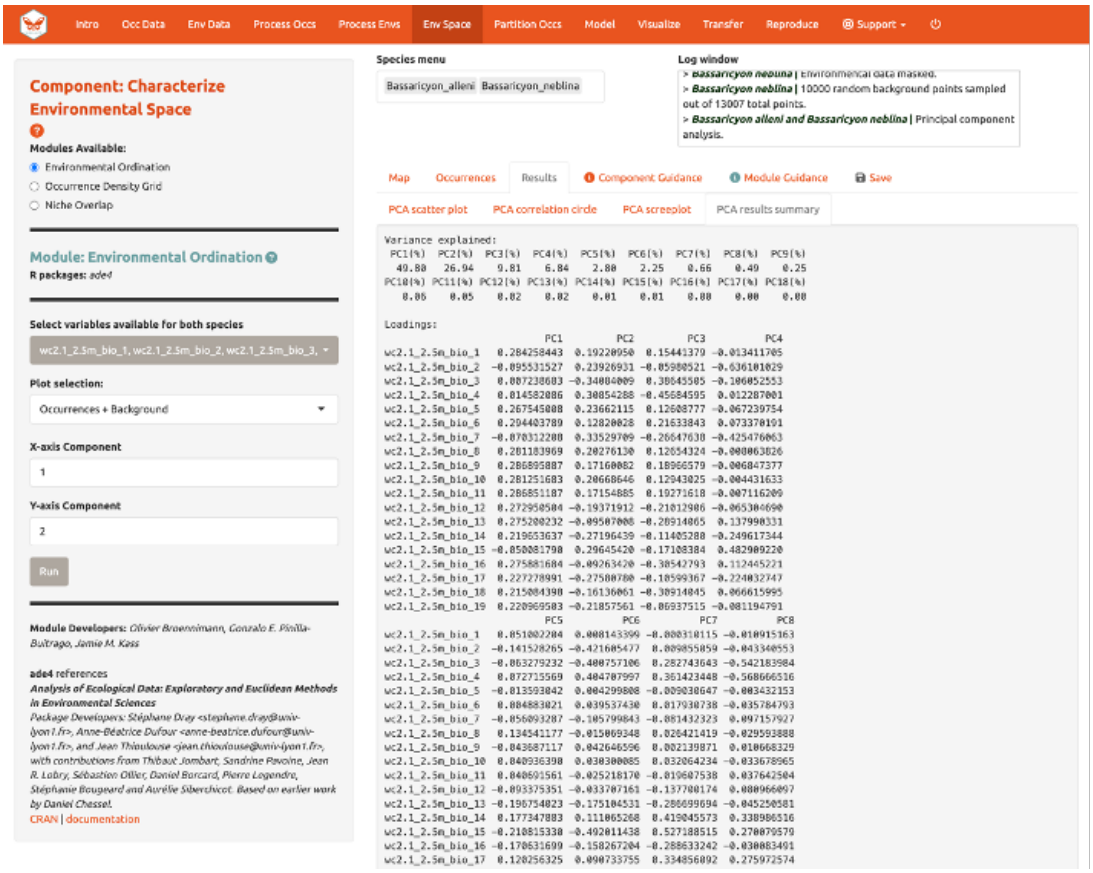
Module: "Environmental Ordination" is for conducting an ordination approach called Principal Component Analysis (PCA), that maximizes the variation contained in the predictor variables into fewer ones. To perform a PCA, select the variables available for both species by checking/unchecking the bioclimatic variables. Choose between "Occurrences Only" or "Occurrences & Background" for the plot selection and set the x- and y-axis components. The PCA Scatter Plot appears in the Results tab.



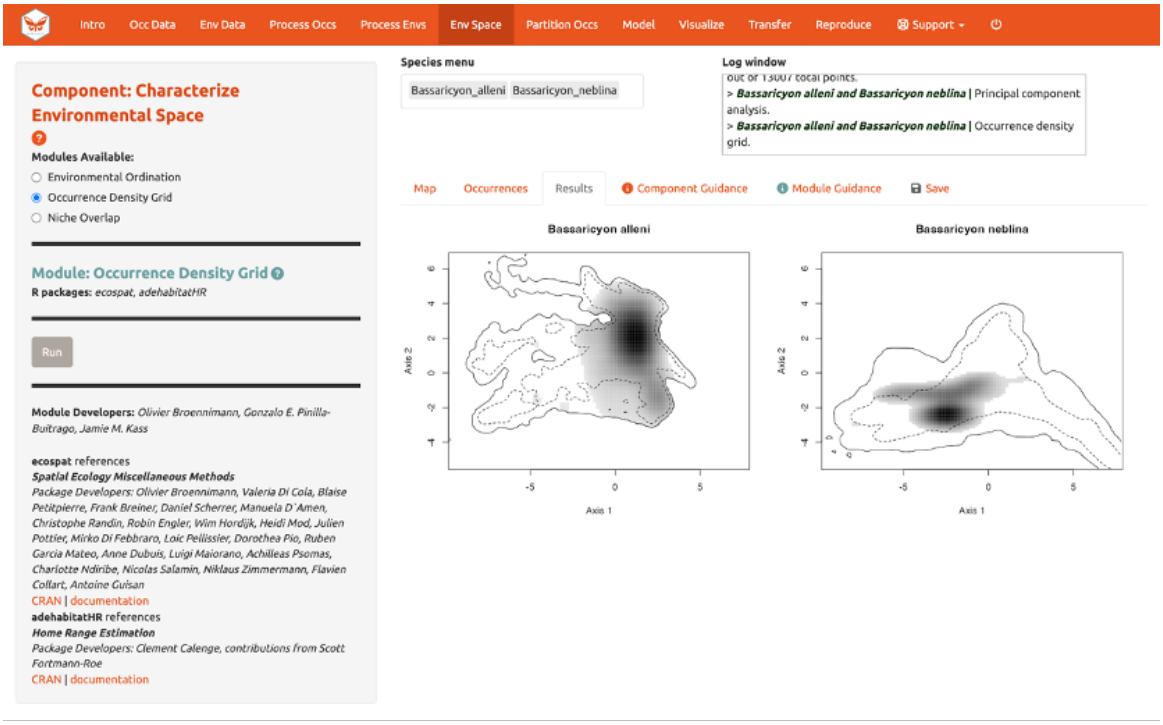
You can also view the PCA correlation circle, PCA screeplot, and the PCA results summary. For more information on these statistics and how to evaluate the results, consult the module guidance text.



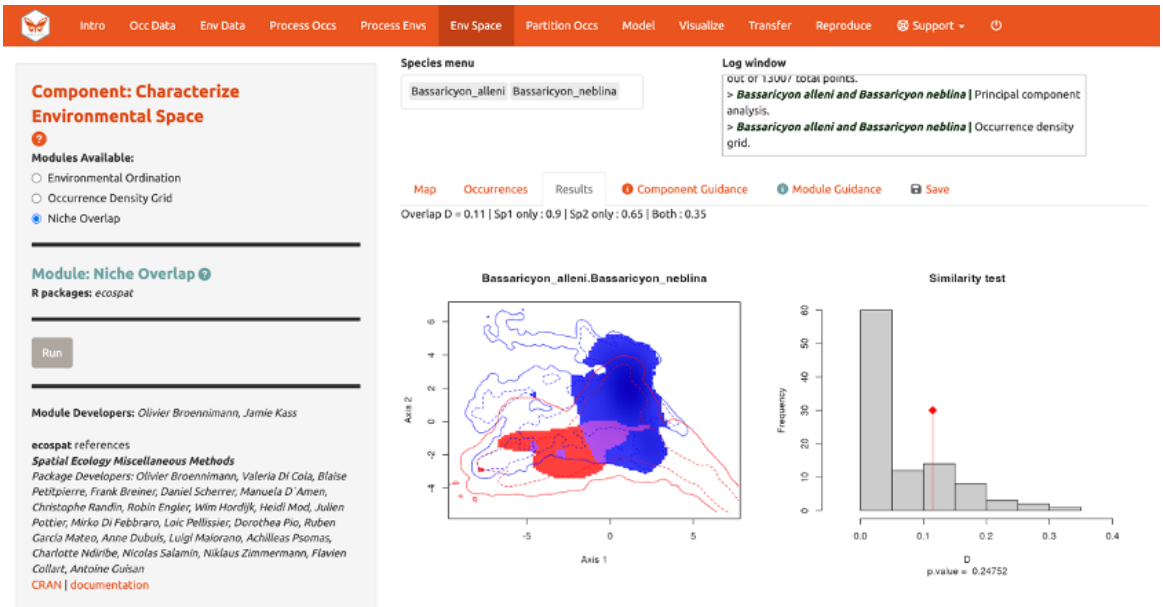

Intro
Occ Data
Env Data
Process Occs
Process Envs
Env Space
Partition Occs
Model
Visualize
Transfer
Reproduce
Support
Component: Characterize Environmental Space
Modules Available:
Environmental Ordination
Occurrence Density Grid
Niche Overlap
Module: Environmental Ordination
R packages: ade4
Select variables available for both species
wc2.1_2.5m_bio_1, wc2.1_2.5m_bio_2, wc2.1_2.5m_bio_3,
Plot selection:
Occurrences + Background
X-axis Component
1
Y-axis Component
2
Run
Module Developers: Olivier Broennimann, Gonzalo E. Pinilla-Buitrago, Jamie M. Kass
ade4 references
Analysis of Ecological Data: Exploratory and Euclidean Methods in Environmental Sciences
Package Developers: Stéphane Dray <stephane.dray@univ-lyon1.fr>, Anne-Béatrice Dufour <anne-beatrice.dufour@univ-lyon1.fr>, and Jean Thioulouse <jean.thioulouse@univ-lyon1.fr>, with contributions from Thibaut Jombart, Sandrine Pavoine, Jean R. Lobry, Sébastien Ollier, Daniel Borcard, Pierre Legendre, Stéphanie Bougeard and Aurélie Siberchicot. Based on earlier work by Daniel Chessel.
CRAN | documentation
Species menu
Bassaricyon_alleni
Bassaricyon_neblina
Log window
> Bassaricyon neblina | Environmental data masked.
> Bassaricyon neblina | 10000 random background points sampled out of 13007 total points.
> Bassaricyon alleni and Bassaricyon neblina | Principal component analysis.
Map
Occurrences
Results
Component Guidance
Module Guidance
Save
PCA scatter plot
PCA correlation circle
PCA screeplot
PCA results summary
Inertia
Axis


Intro
Occ Data
Env Data
Process Occs
Process Envs
Env Space
Partition Occs
Model
Visualize
Transfer
Reproduce
Support
Component: Characterize Environmental Space
Modules Available:
Environmental Ordination
Occurrence Density Grid
Niche Overlap
Module: Environmental Ordination
R packages: ade4
Select variables available for both species
wc2.1_2.5m_bio_1, wc2.1_2.5m_bio_2, wc2.1_2.5m_bio_3,
Plot selection:
Occurrences + Background
X-axis Component
1
Y-axis Component
2
Run
Module Developers: Olivier Broennimann, Gonzalo E. Pinilla-Buitrago, Jamie M. Kass
ade4 references
Analysis of Ecological Data: Exploratory and Euclidean Methods in Environmental Sciences
Package Developers: Stéphane Dray <stephane.dray@univ-lyon1.fr>, Anne-Béatrice Dufour <anne-beatrice.dufour@univ-lyon1.fr>, and Jean Thioulouse <jean.thioulouse@univ-lyon1.fr>, with contributions from Thibaut Jombart, Sandrine Pavoine, Jean R. Lobry, Sébastien Ollier, Daniel Borcard, Pierre Legendre, Stéphanie Bougeard and Aurélie Siberchicot. Based on earlier work by Daniel Chessel.
CRAN | documentation
Species menu
Bassaricyon_alleni
Bassaricyon_neblina
Log window
> Bassaricyon neblina | Environmental data masked.
> Bassaricyon neblina | 10000 random background points sampled out of 13007 total points.
> Bassaricyon alleni and Bassaricyon neblina | Principal component analysis.
Map
Occurrences
Results
Component Guidance
Module Guidance
Save
PCA scatter plot
PCA correlation circle
PCA screeplot
PCA results summary
Variance explained:
PC1(%) PC2(%) PC3(%) PC4(%) PC5(%) PC6(%) PC7(%) PC8(%) PC9(%)
49.80 26.94 9.81 6.84 2.80 2.25 0.66 0.49 0.25
PC10(%) PC11(%) PC12(%) PC13(%) PC14(%) PC15(%) PC16(%) PC17(%) PC18(%)
0.06 0.05 0.02 0.02 0.01 0.01 0.00 0.00 0.00
Loadings:
PC1 PC2 PC3 PC4
wc2.1_2.5m_bio_1 0.284258443 0.19220950 0.15441379 -0.013411705
wc2.1_2.5m_bio_2 -0.095531527 0.23926931 -0.05980521 -0.636101029
wc2.1_2.5m_bio_3 0.087238603 -0.34004009 0.38045505 -0.106052553
wc2.1_2.5m_bio_4 0.014582086 0.30054288 -0.45684595 0.012287001
wc2.1_2.5m_bio_5 0.267545088 0.23662115 0.12608777 -0.067239754
wc2.1_2.5m_bio_6 0.294403789 0.12820028 0.21633843 0.073370191
wc2.1_2.5m_bio_7 -0.070312280 0.33529709 -0.26647630 -0.425476063
wc2.1_2.5m_bio_8 0.281183969 0.20276130 0.12654324 -0.000063826
wc2.1_2.5m_bio_9 0.286895887 0.17160082 0.18966579 -0.006847377
wc2.1_2.5m_bio_10 0.281251683 0.20668646 0.12943025 -0.004431633
wc2.1_2.5m_bio_11 0.286851187 0.17154885 0.19271618 -0.007116209
wc2.1_2.5m_bio_12 0.272950504 -0.19371912 -0.21012986 -0.065304690
wc2.1_2.5m_bio_13 0.275200232 -0.09507008 -0.20914065 0.137990331
wc2.1_2.5m_bio_14 0.219653637 -0.27196439 -0.11405288 -0.249617344
wc2.1_2.5m_bio_15 -0.050081798 0.29645420 -0.17108384 0.482989220
wc2.1_2.5m_bio_16 0.275881684 -0.09263420 -0.30542793 0.112445221
wc2.1_2.5m_bio_17 0.227278991 -0.27580780 -0.10599367 -0.224032747
wc2.1_2.5m_bio_18 0.215084398 -0.16136061 -0.30914045 0.066615995
wc2.1_2.5m_bio_19 0.220969503 -0.21857561 -0.06937515 -0.081194791
PC5 PC6 PC7 PC8
wc2.1_2.5m_bio_1 0.051002284 0.008143399 -0.000310115 -0.010915163
wc2.1_2.5m_bio_2 -0.141528265 -0.421605477 0.009855859 -0.043340553
wc2.1_2.5m_bio_3 -0.063279232 -0.400757106 0.282743643 -0.542183984
wc2.1_2.5m_bio_4 0.072715569 0.404707997 0.361423448 -0.568666516
wc2.1_2.5m_bio_5 -0.013593842 0.004299808 -0.009038647 -0.003432153
wc2.1_2.5m_bio_6 0.004883021 0.039537430 0.017930738 -0.035784793
wc2.1_2.5m_bio_7 -0.056093287 -0.105799843 -0.081432323 0.097157927
wc2.1_2.5m_bio_8 0.134541177 -0.015069348 0.026421419 -0.029593888
wc2.1_2.5m_bio_9 -0.043687117 0.042646596 0.002139871 0.010668329
wc2.1_2.5m_bio_10 0.040936398 0.038300085 0.032064234 -0.033678965
wc2.1_2.5m_bio_11 0.040691561 -0.025218170 -0.019607538 0.037642504
wc2.1_2.5m_bio_12 -0.093375351 -0.033707161 -0.137700174 0.080966097
wc2.1_2.5m_bio_13 -0.196754023 -0.175104531 -0.286099694 -0.045250581
wc2.1_2.5m_bio_14 0.177347883 0.111065268 0.419045573 0.338986516
wc2.1_2.5m_bio_15 -0.210815330 -0.492011438 0.527188515 0.270079579
wc2.1_2.5m_bio_16 -0.170631699 -0.158267204 -0.288633242 -0.030083491
wc2.1_2.5m_bio_17 0.120256325 0.090733755 0.334856092 0.275972574

Next, run an "Occurrence Density Grid". This calculates and plots which part of the environmental space is occupied more densely by the species and the availability of environmental conditions present within the background extent. Darker areas represent higher occurrence density. Areas within solid lines represent all environmental conditions available in the background extent, and areas within dashed lines represent the 50% most frequent ones.



And calculate "Niche Overlap"…



The niche overlap quantification is based on the occurrence and background densities in the available environmental space estimated in Module: "Occurrence Density Grid". The overlap is quantified using Schoener's D metric. The environmental conditions covered only by the niche of species 1 are shown in blue, the environmental conditions covered only by the niche of species 2

are shown in red, and the environmental conditions covered by both species, or the niche overlap, is shown in purple. In the Similarity Test, if the observed overlap (red line) is higher than 95% of the simulated overlaps (p-value < 0.05), we can consider the two species to be more similar than random, which is not what we see here. Again, consult the module guidance texts for more help to understand the analyses and help on evaluating the results.

Download the PCA results (.zip), density grid (.png), and overlap plot (.png) from the "Save" tab.

8. PARTITION OCCURRENCES

We have not built any distribution models yet, but before we do, we will make decisions on how to partition our data for evaluation. In order to determine the strength of the model's predictive ability, you theoretically need independent data to test it. When no independent datasets exist, one solution is to partition your data into subsets that we assume are independent of each other, then sequentially build a model on all the subsets but one and evaluate the performance of this model on the left-out subset. This is known as k-fold cross-validation (where "k" is the total number of subsets, or "folds"), which is quite prevalent in statistics, especially the fields of machine learning and data science. After this sequential model-building exercise is complete, Wallace averages the model performance statistics over all the itinerations and then builds a model using *all* the data.

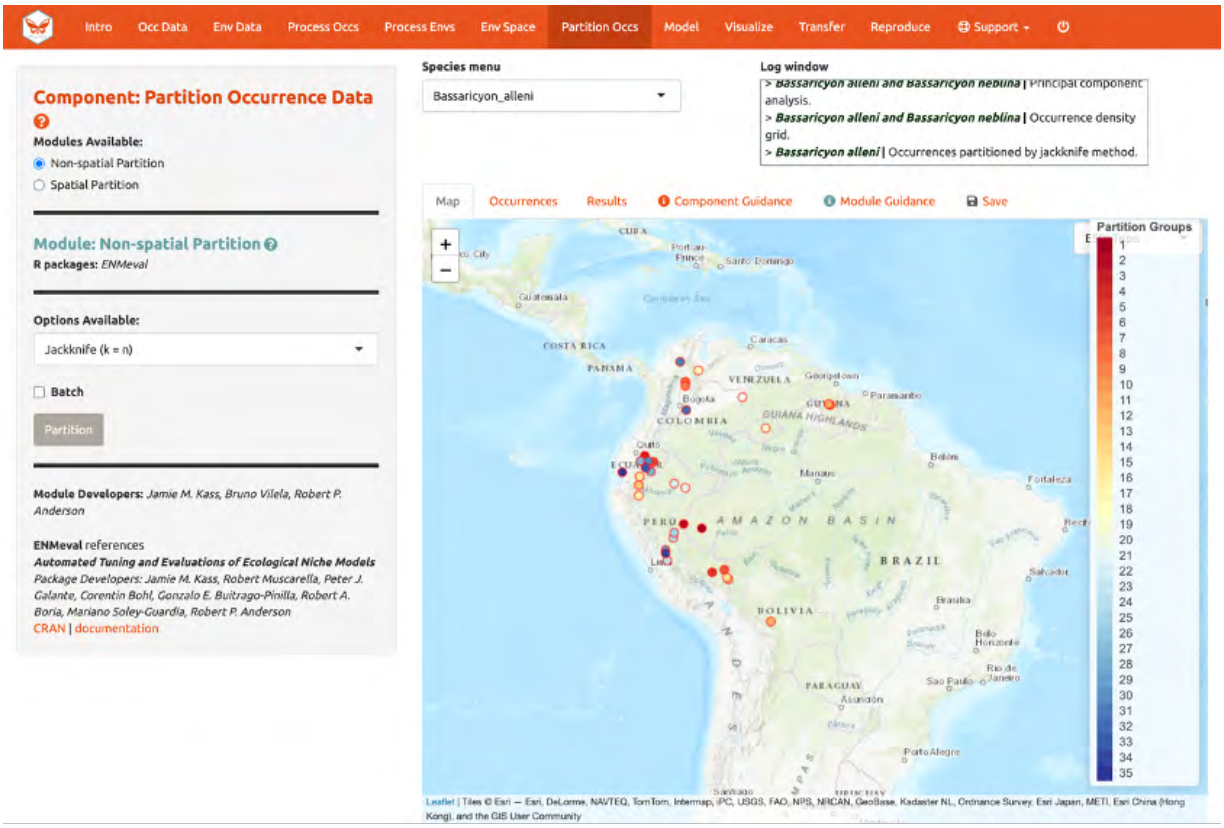
There is a whole literature on how to best partition data for evaluating models. One option is to simply partition randomly, but with spatial data we run the risk that the groups are not spatially independent of each other. The jackknife method ("leave-one-out") is recommended for species with small sample sizes and has previously been used for modeling *Bassaricyon neblina* (Gerstner et al. 2018) but may have long computational times.

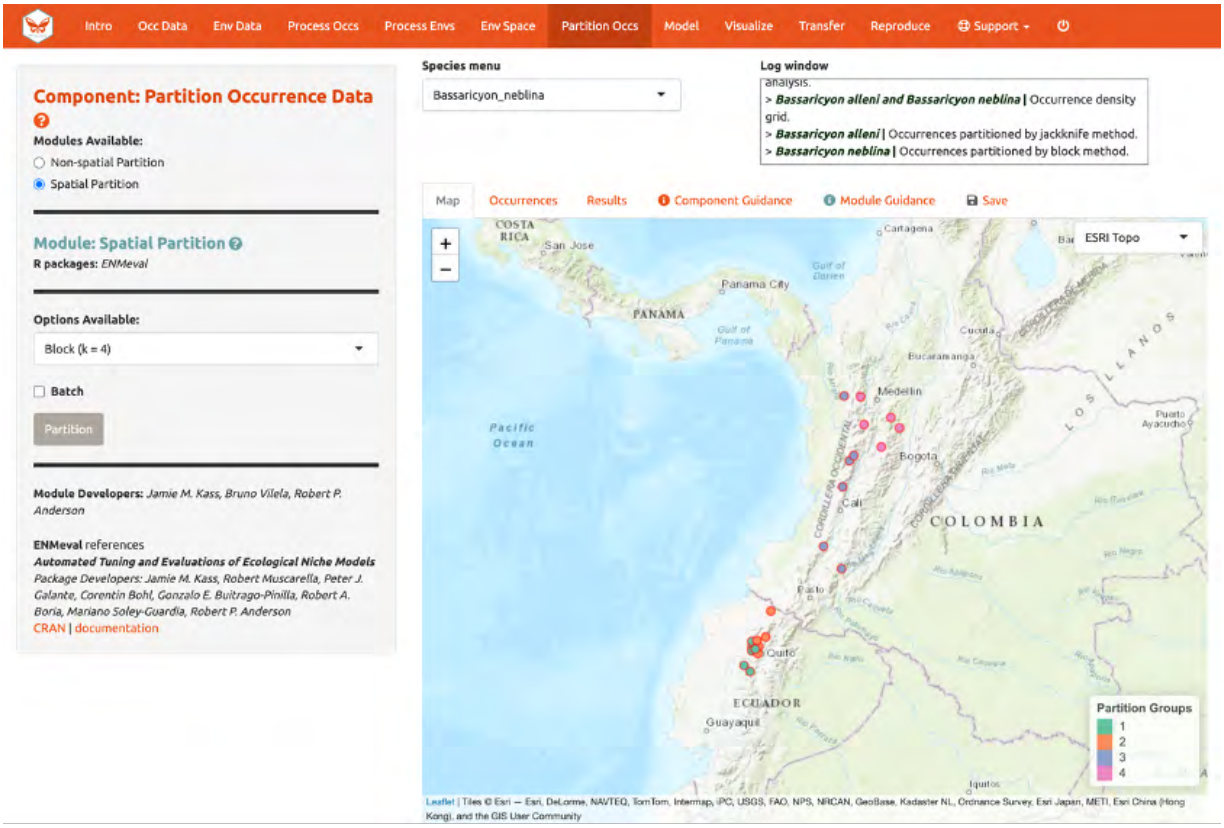
Another option is to partition spatially—for example, by drawing lines on a map to divide the data. Spatial partitioning with k-fold cross-validation forces the model to predict into regions that are distant from those used to train the model (note that Wallace also excludes background points from regions corresponding to the withheld partition). For *Bassaricyon alleni*, environmental conditions in Colombia and Ecuador may differ considerably from conditions in Bolivia. If the model has accurate predictions on average on withheld spatially partitioned data, it likely has good transferability, which means it can transfer well to the new values of predictor variables (because distant areas are usually more environmentally different than close ones). As always, please refer to the guidance text for more details on all the types of partitioning offered in Wallace. The first image on the next page is an example of jacknife (k = n), which assigns each point to its own partition group, so the number of bins equals the number of occurrences.

The second image on the next page is an example of spatial blocking, which assigns each point to one of four spatially separate partition groups.

We'll use this last method now for faster computation, but it is recommended to review the guidance text and other literature—and talk to your peers!—to make an informed decision on partition methods.

Partition both species using Module: "Spatial Partition Block" (k = 4) option.


Intro
Occ Data
Env Data
Process Occs
Process Envs
Env Space
Partition Occs
Model
Visualize
Transfer
Reproduce
Support
Component: Partition Occurrence Data
Modules Available:
Non-spatial Partition
Spatial Partition
Module: Non-spatial Partition
R packages: ENMeval
Options Available:
Jackknife (k = n)
Batch
Partition
Module Developers: Jamie M. Kass, Bruno Vilela, Robert P. Anderson
ENMeval references
Automated Tuning and Evaluations of Ecological Niche Models
Package Developers: Jamie M. Kass, Robert Muscarella, Peter J. Galante, Corentin Bohl, Gonzalo E. Buitrago-Pinilla, Robert A. Boria, Mariano Soley-Guardia, Robert P. Anderson
CRAN | documentation
Species menu
Bassaricyon_alleni
Log window
> Bassaricyon alleni and Bassaricyon neblina | Principal component analysis.
> Bassaricyon alleni and Bassaricyon neblina | Occurrence density grid.
> Bassaricyon alleni | Occurrences partitioned by jackknife method.
Map
Occurrences
Results
Component Guidance
Module Guidance
Save
Partition Groups
1
2
3
4
5
6
7
8
9
10
11
12
13
14
15
16
17
18
19
20
21
22
23
24
25
26
27
28
29
30
31
32
33
34
35
COSTA RICA
PANAMA
COLOMBIA
VENEZUELA
GUYANA
ECUADOR
PERU
BRAZIL
BOLIVIA
PARAGUAY
AMAZON BASIN
GUIANA HIGHLANDS
Caracas
Georgetown
Paramaribo
Bogotá
Quito
Manaus
Belém
Fortaleza
Salvador
Brasília
Belo Horizonte
Rio de Janeiro
São Paulo
Asunción
Porto Alegre
Lima
Guatemala
Santo Domingo
Leaflet | Tiles © Esri — Esri, DeLorme, NAVTEQ, TomTom, Intermap, iPC, USGS, FAO, NPS, NRCAN, GeoBase, Kadaster NL, Ordnance Survey, Esri Japan, METI, Esri China (Hong Kong), and the GIS User Community


Intro
Occ Data
Env Data
Process Occs
Process Envs
Env Space
Partition Occs
Model
Visualize
Transfer
Reproduce
Support
Component: Partition Occurrence Data
Modules Available:
Non-spatial Partition
Spatial Partition
Module: Spatial Partition
R packages: ENMeval
Options Available:
Block (k = 4)
Batch
Partition
Module Developers: Jamie M. Kass, Bruno Vilela, Robert P. Anderson
ENMeval references
Automated Tuning and Evaluations of Ecological Niche Models
Package Developers: Jamie M. Kass, Robert Muscarella, Peter J. Galante, Corentin Bohl, Gonzalo E. Buitrago-Pinilla, Robert A. Boria, Mariano Soley-Guardia, Robert P. Anderson
CRAN | documentation
Species menu
Bassaricyon_neblina
Log window
analysis.
> Bassaricyon alleni and Bassaricyon neblina | Occurrence density grid.
> Bassaricyon alleni | Occurrences partitioned by jackknife method.
> Bassaricyon neblina | Occurrences partitioned by block method.
Map
Occurrences
Results
Component Guidance
Module Guidance
Save
ESRI Topo
Partition Groups
1
2
3
4
COSTA RICA
PANAMA
COLOMBIA
ECUADOR
San José
Panamá City
Cartagena
Medellín
Bucaramanga
Cúcuta
Bogotá
Cali
Pasto
Quito
Guayaquil
Iquitos
Puerto Ayacucho
Pacific Ocean
Gulf of Darien
Gulf of Panama
LOS LLANOS
Leaflet | Tiles © Esri — Esri, DeLorme, NAVTEQ, TomTom, Intermap, iPC, USGS, FAO, NPS, NRCAN, GeoBase, Kadaster NL, Ordnance Survey, Esri Japan, METI, Esri China (Hong Kong), and the GIS User Community

9. SAVE & LOAD SESSION

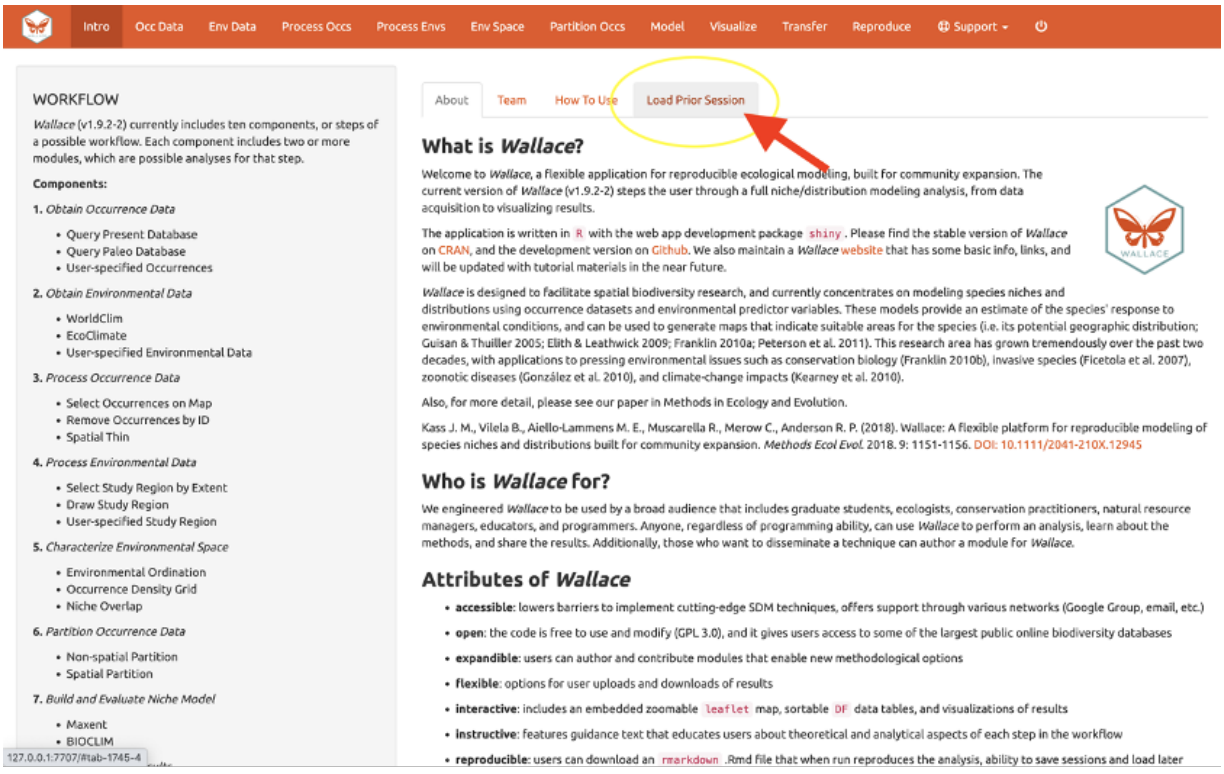
Before we go into "Modeling", let's explore one of the great features of Wallace v2, which is the ability to stop and save your progress to be continued later. If you want to skip this step (and risk losing everything if an error occurs except the data or results you have downloaded), you can move on to "Model".

Click "Save Session" within the "Save" tab. This tab is available from any of the Components. This will save your progress as an RDS (.rds) file, a file type used to save R objects. After it is saved, you can hit the stop sign in the upper right corner or close the browser window and exit R/RStudio. *Note: if the Wallace session is closed before saving results and/or the session, all work will be lost.*

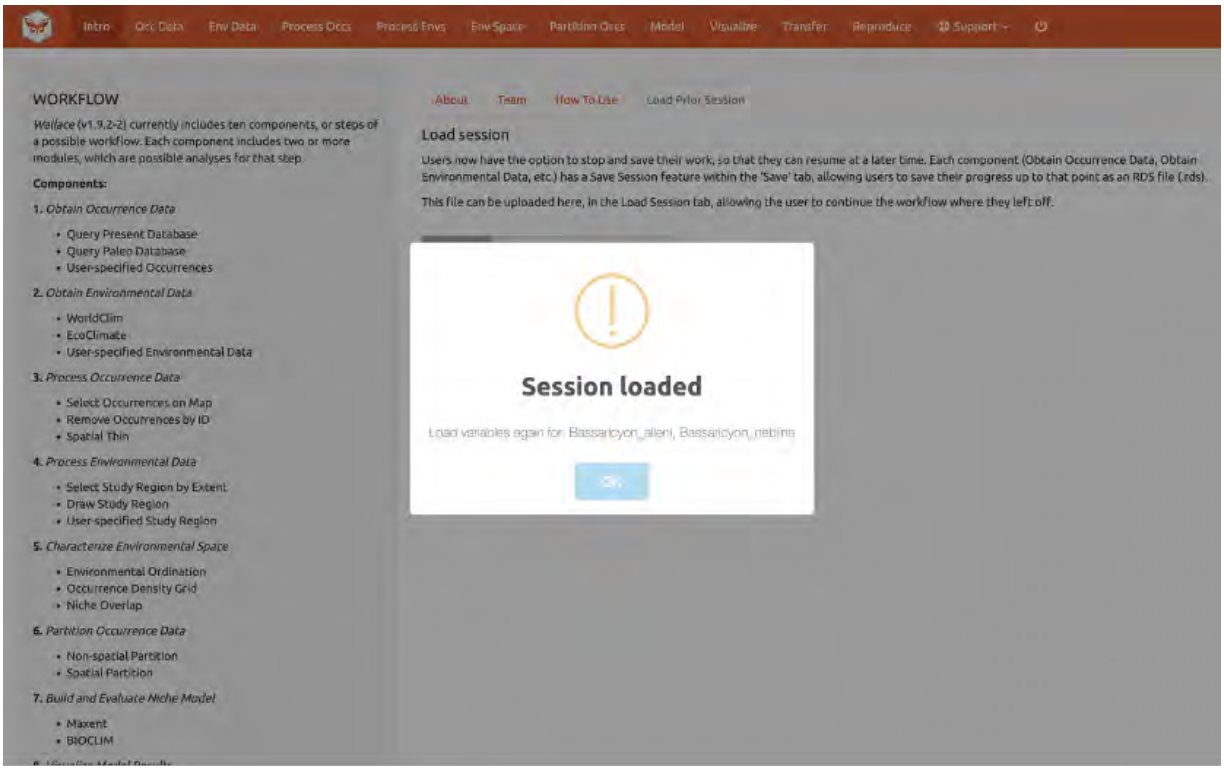
When you are ready to resume, load `wallace` again.

```
library(wallace)
run_wallace()
```

In the "Intro" component, use the "Load Prior Session" tab to import your .rds session file.



A box will pop up—it looks like other Wallace warning messages, but in this case it is indicating the session is loaded. It may be necessary to reload your variables, using "Occ Data" and "Env Data" as previously carried out. You can now carry on with the previous analysis.



10. MODEL

We are now ready to build a distribution model. Wallace v2.0 provides two algorithm options; Maxent and BIOCLIM. For this vignette, we'll use Maxent, a machine learning method that can fit a range of functions to patterns in the data, from simple (i.e., straight lines) to complex (i.e., curvy or with lines that can change direction; these can get jagged if complexity is not controlled). For more details on Maxent, please consult the Maxent website and guidance text.

Maxent is available to run through `maxnet` package or through Java with the `maxent.jar` option. In the interest of time and to avoid Java-related issues, let's choose the following modeling options:

- Choose maxnet
- Select L, LQ, and H feature classes. These are the shapes that can be fit to the data:
  - L = Linear, e.g. temp + precip
  - Q = Quadratic, e.g. temp^2 + precip^2
  - H = Hinge, e.g. piecewise linear functions, like splines (think of a series of lines that are connected together)

- Select regularization multipliers between 0.5 and 4 with a step value of 0.5.
  - Regularization is a penalty on model complexity.
  - Higher values = smoother, less complex models. Basically, all predictor variable coefficients are shrunk progressively until some reach 0, when they drop out of the model. Only those variables with the greatest predictive contribution remain in the model.

- Keep "NO" selected for categorical variables. This option is to indicate if any of your predictor variables are categorical, like soil or vegetation classes.
  - Had you loaded categorical variables, you would check here and then indicate which of the rasters is categorical.

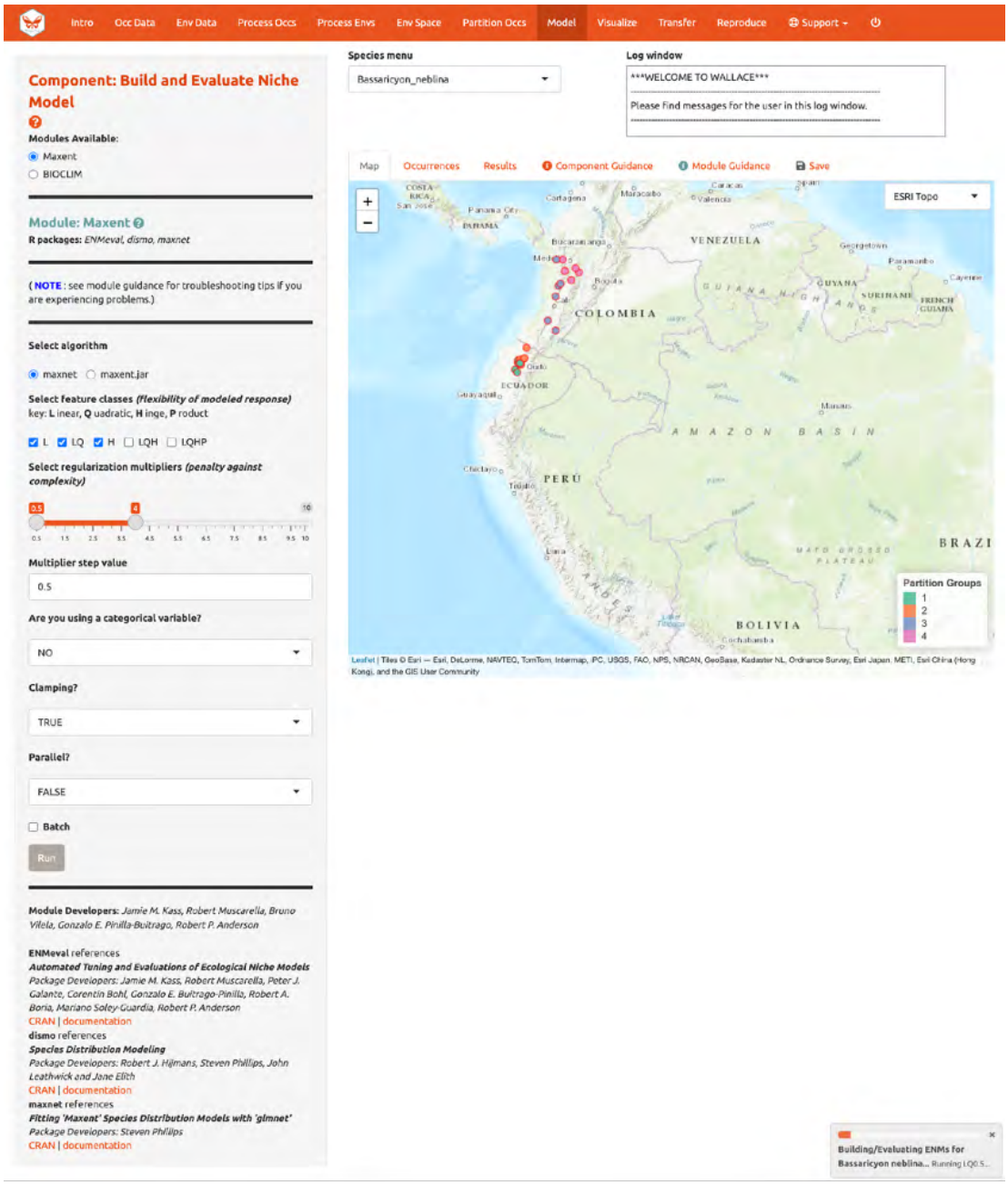
- Set Clamping? to "TRUE". This will clamp the model predictions (i.e., keep the environmental values more extreme than those present in the background data to within the bounds of the background data).

- If you set Parallel? to "TRUE", you can indicate the number of cores for parallel processing.

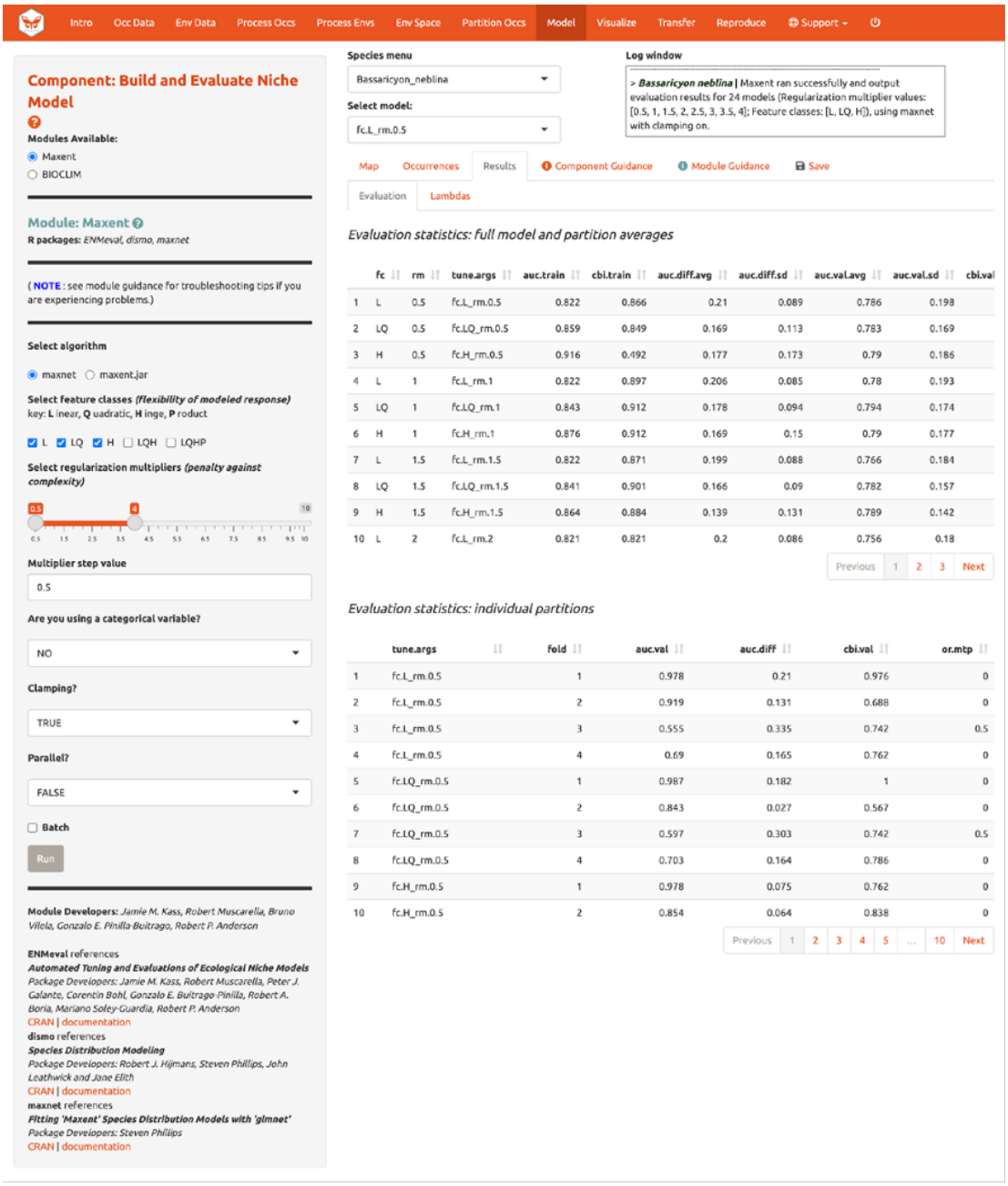
We will construct a model for *Bassaricyon neblina*, but note that the Batch feature can be checked to run these selections for all species you have uploaded.

Make sure *Bassaricyon neblina* is selected in the species menu and Batch is unchecked before hitting "Run".

The 3 feature class combinations (L, LQ, H) x 8 regularization multipliers (0.5, 1, 1.5, 2, 2.5, 3, 3.5, 4) = 24 candidate models. The hinge feature class (H) will enable substantial complexity in the response, so it takes a bit longer to run than the simpler models.



The results appear in two tables of evaluation statistics, allowing comparison of the different models you just built. The first table shows the statistics for the full model and partition averages. There should be 24 rows: one for each of the feature class / regularization multiplier combinations. In the first table, statistics from the models built from the 4 occurrence data partition groups (one withheld for each iteration) are averaged. In the second table, the partition group statistics averaged in the first table are shown, and thus it contains 96 rows (each of the 4 folds for each of the 24 models).

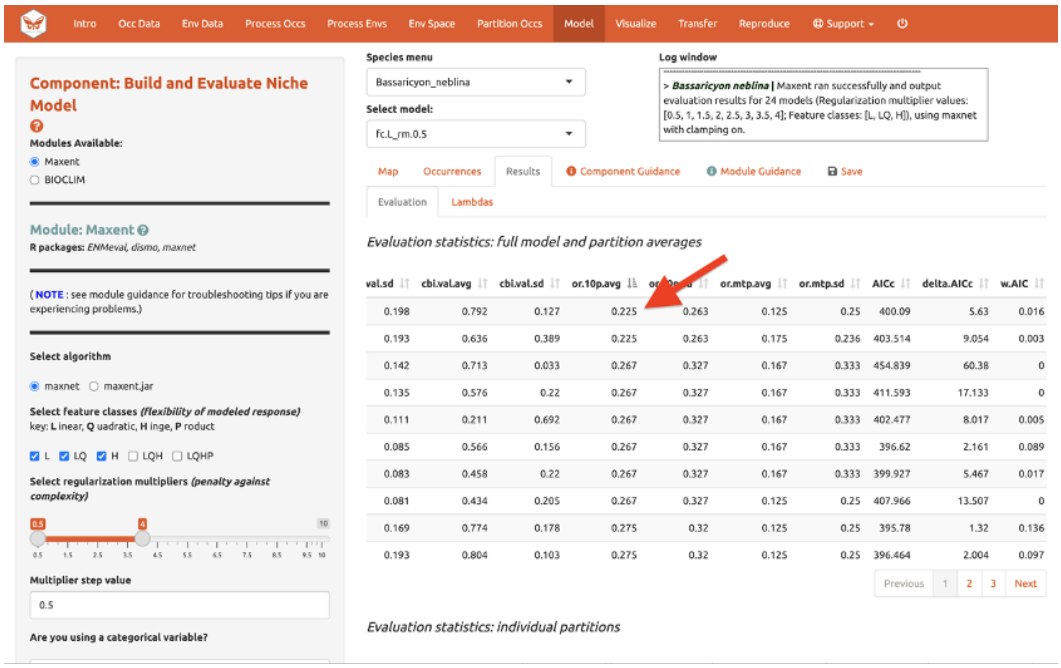


How do we choose the "best" model?

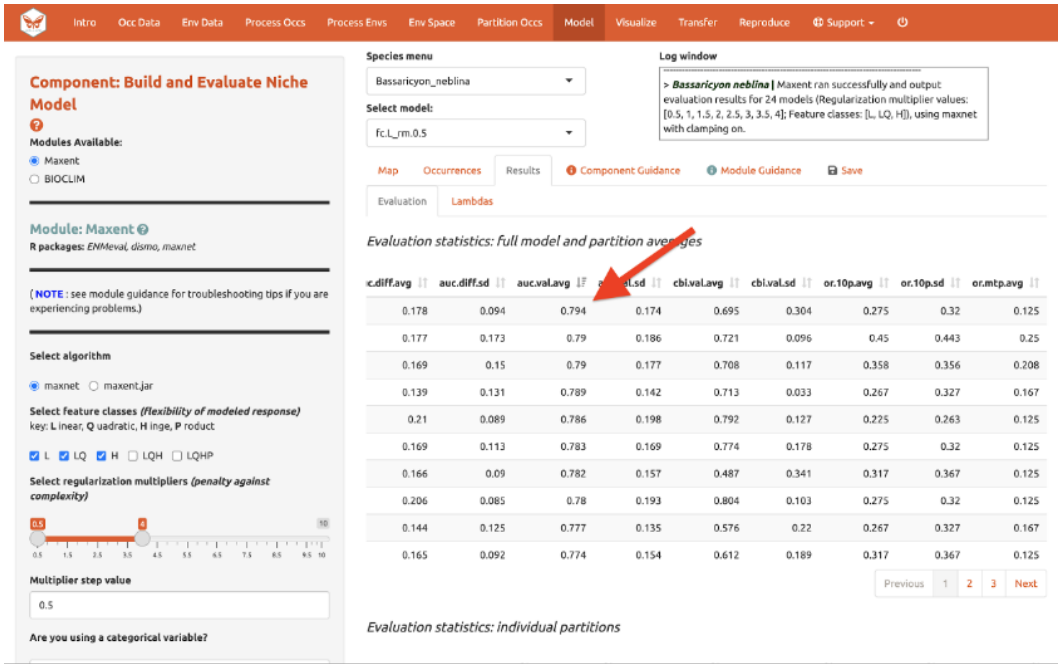
There is a mountain of literature about this, and there is really no single answer for all datasets. The model performance statistics AUC (Area Under the Curve), OR (Omission Rate), and CBI (Continuous Boyce Index) were calculated and averaged across our partitions, and AICc (corrected Akaike information criterion) was instead calculated using the model prediction of the full background extent (and all of the thinned occurrence points). Although AICc does not incorporate the cross-validation

results, it does explicitly penalize model complexity—hence, models with more parameters tend to have a worse AICc score. It's really up to the user to decide, and the guidance text has some references which should help you learn more.

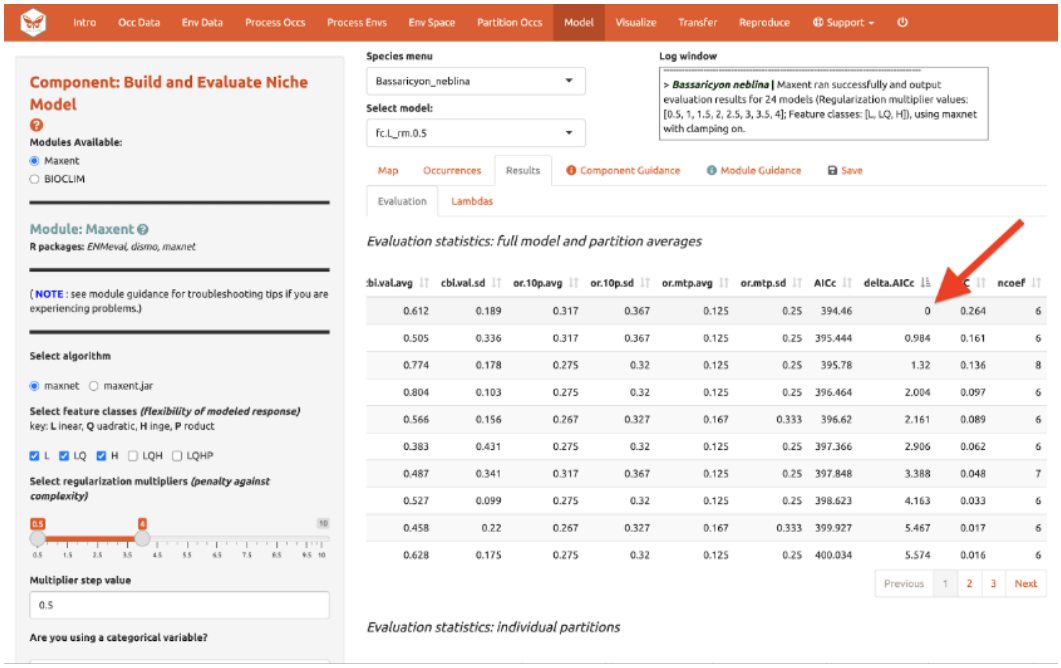
The evaluation metrics table can be sorted. First, we will prioritize models that omitted few occurrence points in the predicted area during cross-validation. Sort the results table in ascending order by "or.10p.avg", or the average omission rate when applying a 10-percentile training presence threshold to the (withheld) validation data (see guidance text for details). As we would prefer a model that does not omit many withheld occurrences when it makes a range prediction, we are prioritizing low values of "or.10p.avg". Note: your values may be different than shown here.



Let's also look at average validation AUC values (where higher values are better).

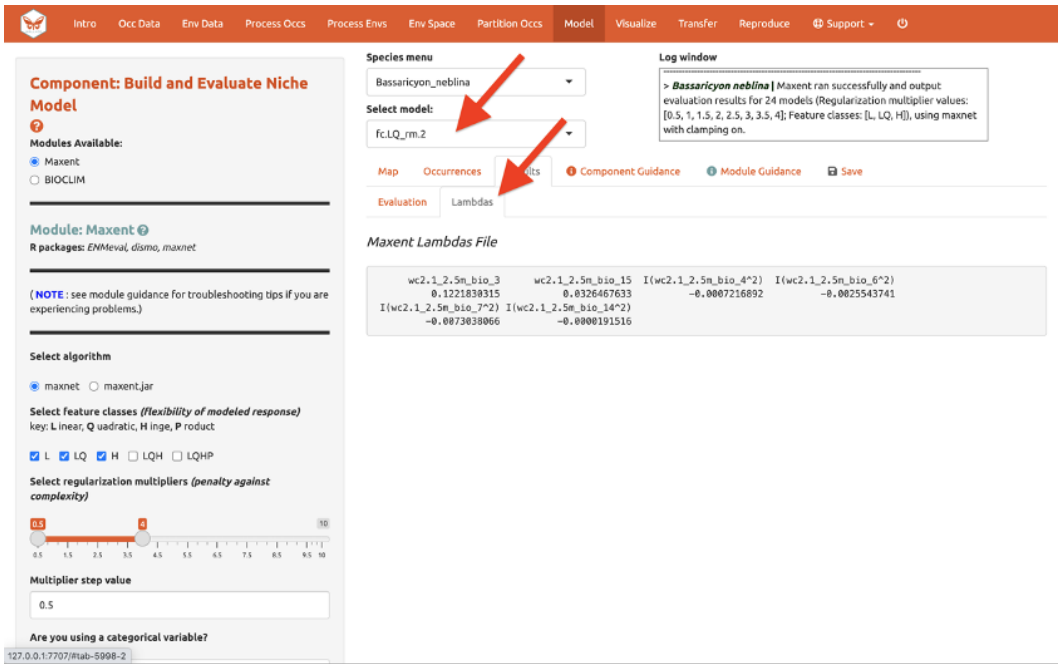


And AICc (where lower values are better)…



In our example, if we had chosen the model with the lowest AICc score, we would have ended up with LQ_2. Note: your values may be different.

Next to the "Evaluation" results, you can access the Maxent "Lambdas" file (which describe the weights for feature classes of each variable) for each of the models (changing the candidate model in the drop-down box changes the output).

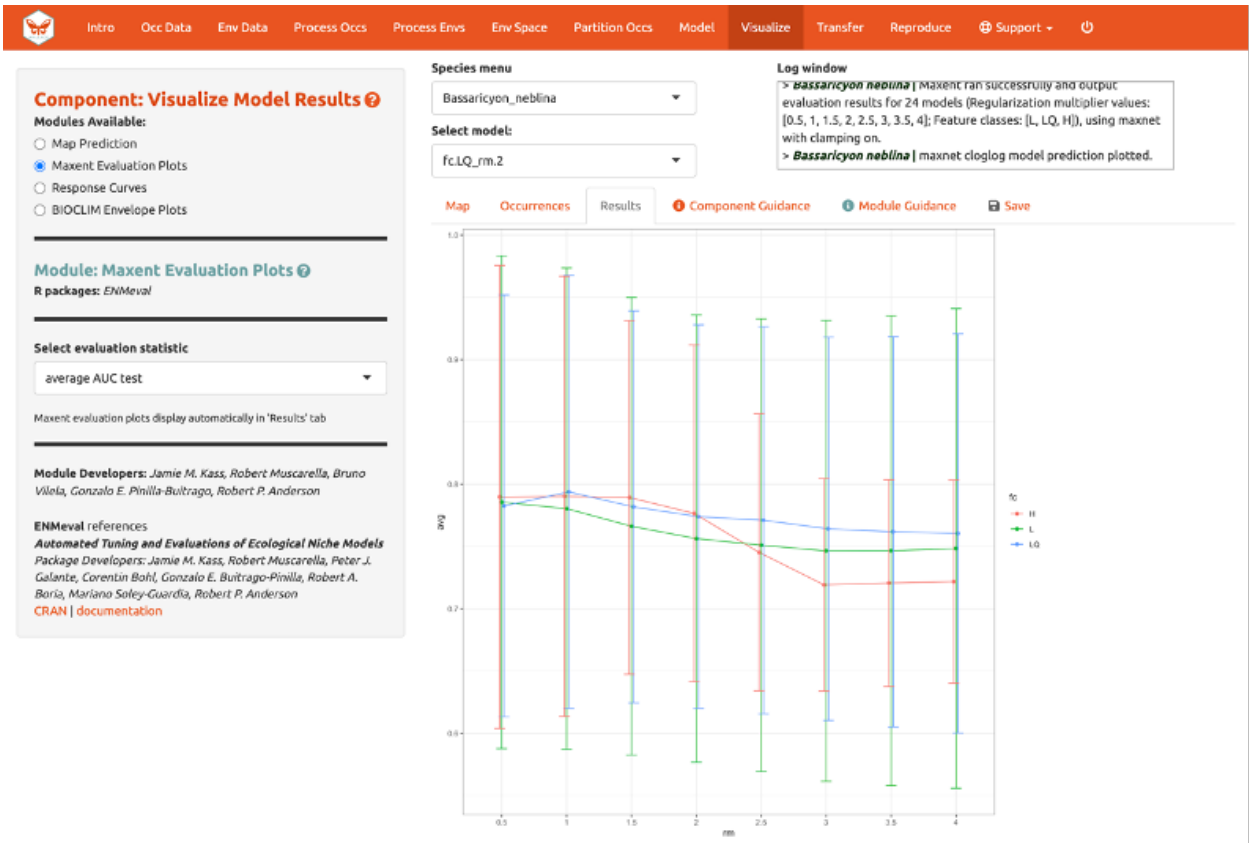


Use the "Save" tab to download the evaluation tables.

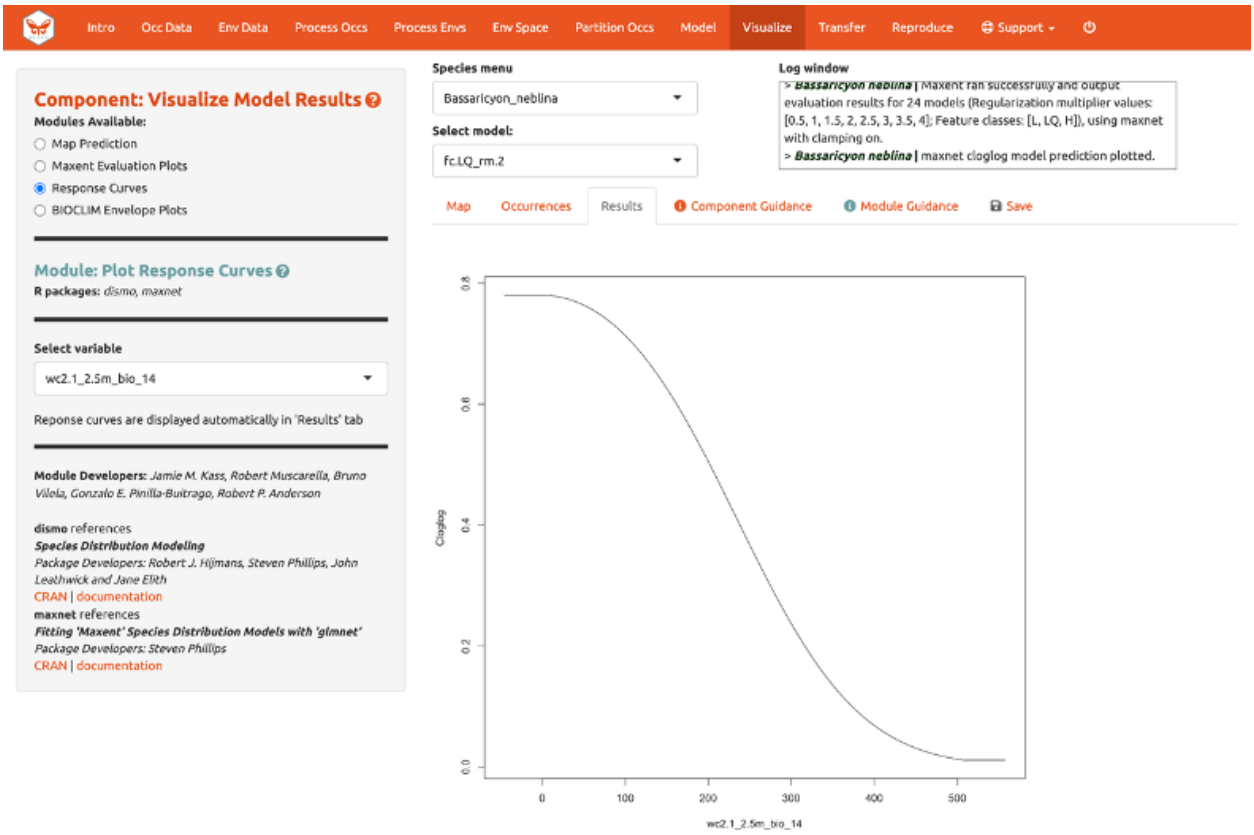
11. VISUALIZE

There are four modules for Visualization. We'll save the first, "Map Prediction", for last. We'll skip the fourth module, "BIOCLIM Envelope Plot", since we used Maxent instead of BIOCLIM.

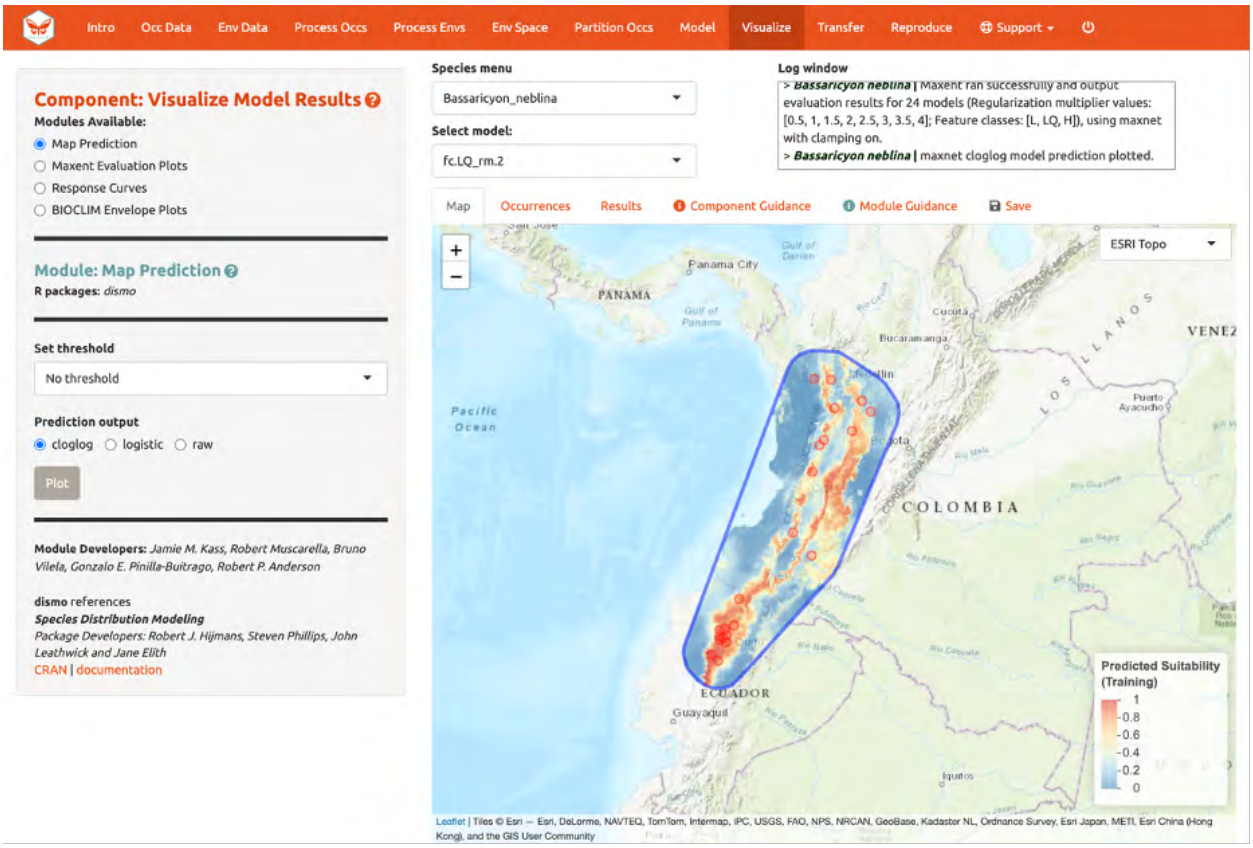
The module "Maxent Evaluation Plots", enables users to evaluate the performance statistics across models. Graphs appear in the Results tab. Below, see how the feature class and regularization multiplier selections affect average validation AUC values.



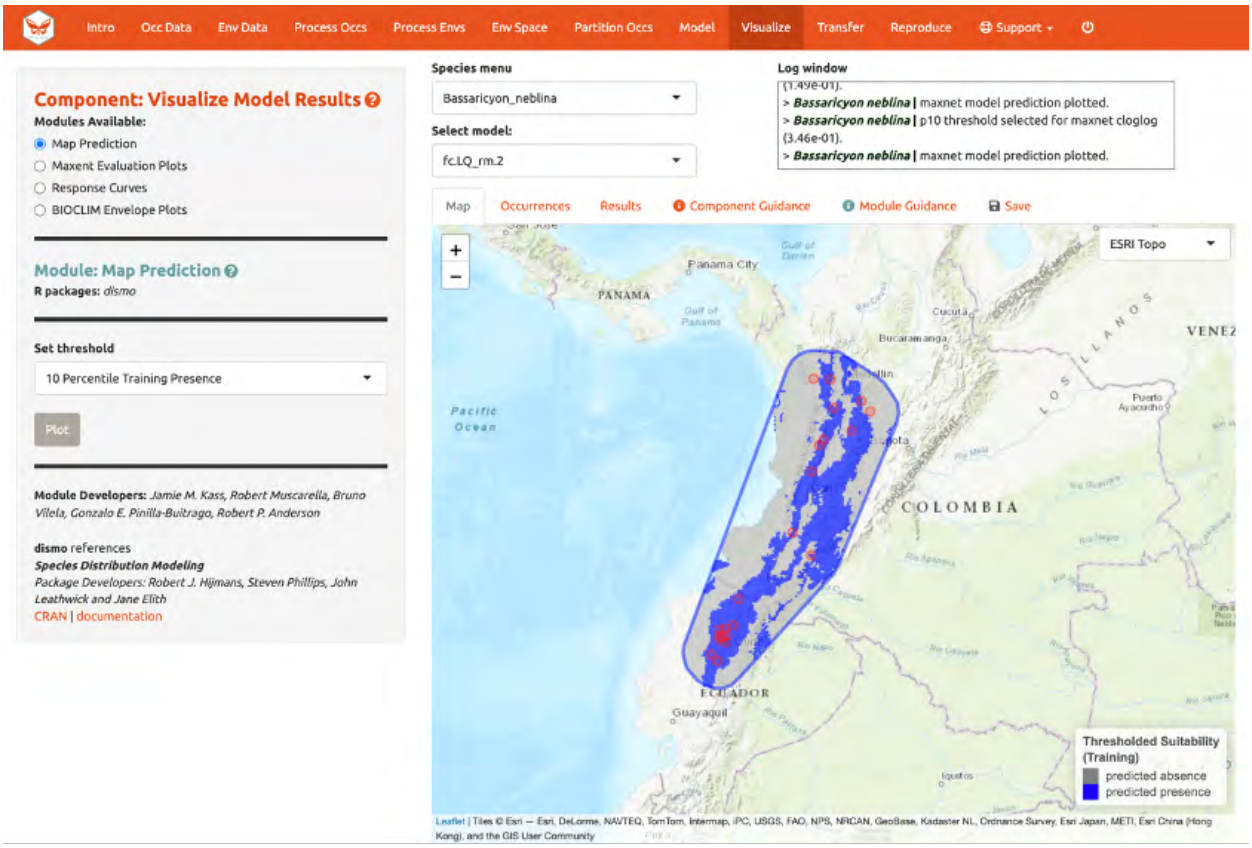
We should also examine the "Response Curves," which show how the predicted suitability (y-axis) changes based on different values of each variable (x-axis). For these curves, the marginal response of one variable is shown while the other variables are held at their mean values. If you want to see the results for a particular model, select it by using the dropdown menu below the species box. Below is a response curve for model LQ_2 for the mean precipitation of the driest month (bio14).



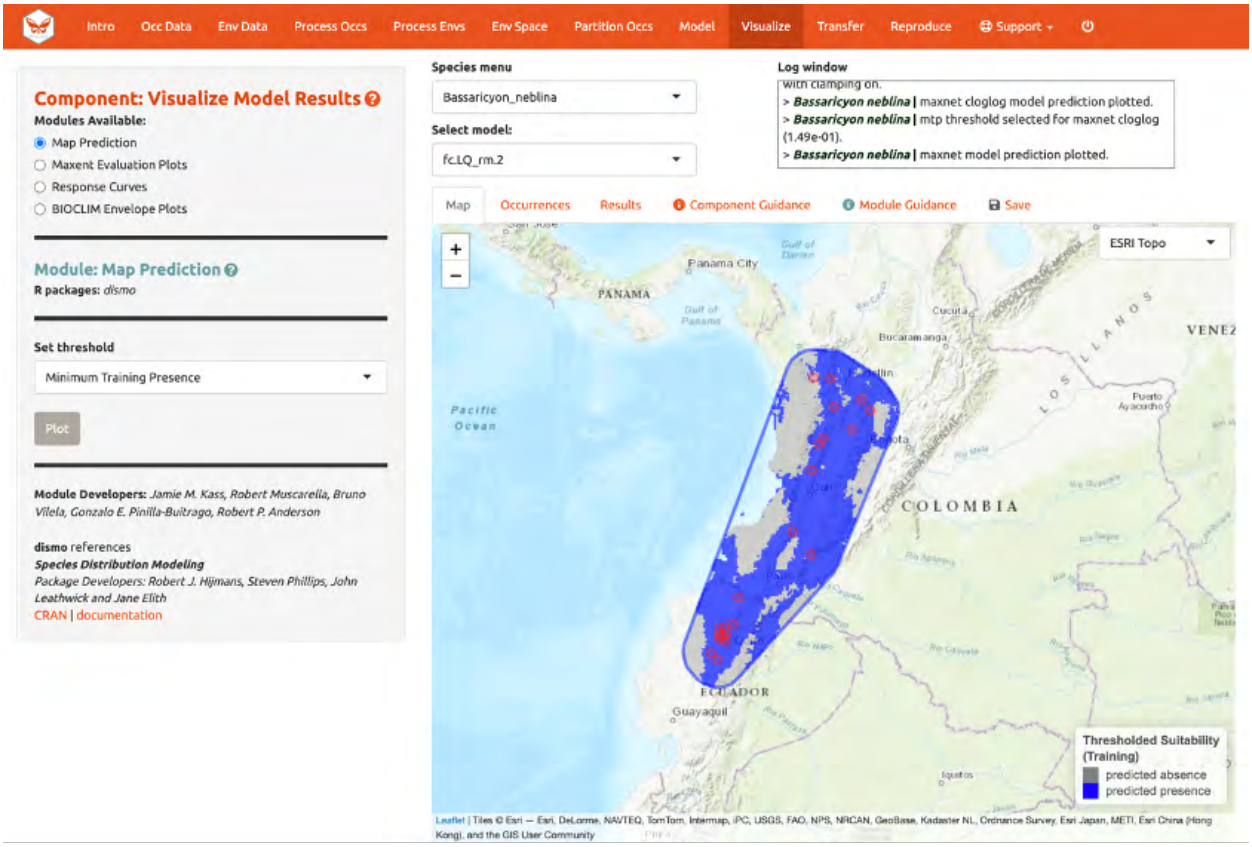
Of course, you can also visualize model predictions on the map. Predictions of suitability can be continuous (a range of values from low to high) or binary (thresholded to two values: 0, unsuitable and 1, suitable). We are visualizing predictions made with the "cloglog" transformation, which converts the raw Maxent output (relative occurrence rate) to a probabilistic scale between 0 and 1 to approximate probability of presence (given key assumptions). Please see the module guidance for information about Maxent model output scalings and thresholding rules. Here is the mapped prediction for model LQ_2, no threshold, in cloglog output.



Below is the mapped prediction of the same model, this time with the threshold set to the 10-percentile training presence value (the occurrence suitability value we used to calculate omission rates above to help us select models). Some of the occurrence points will fall outside the blue regions that represent suitable areas for *Bassaricyon neblina*. For the 10-percentile training presence value, as it represents not the lowest predicted suitability, but the value greater than the 10% lowest, the expected omission would be 0.1 (i.e., 10% omitted).



Try mapping the prediction with the threshold set to the less strict "Minimum Training Presence" and notice the difference. You can also threshold by a quantile of training presences that are omitted. Try setting the quantile to different values and notice the change in prediction.



You may have noticed the batch option is not available for this component. Users need to select optimal models relative to each species, therefore predictions can only be mapped individually. You can download your Maxent or BIOCLIM evaluation plots, response curves, and map predictions from the "Save" tab. Note that this will download the current plot. For instance, if you wanted to download the continuous prediction, you'll have to plot again, since we last plotted the threshold map.

12. MODEL TRANSFER

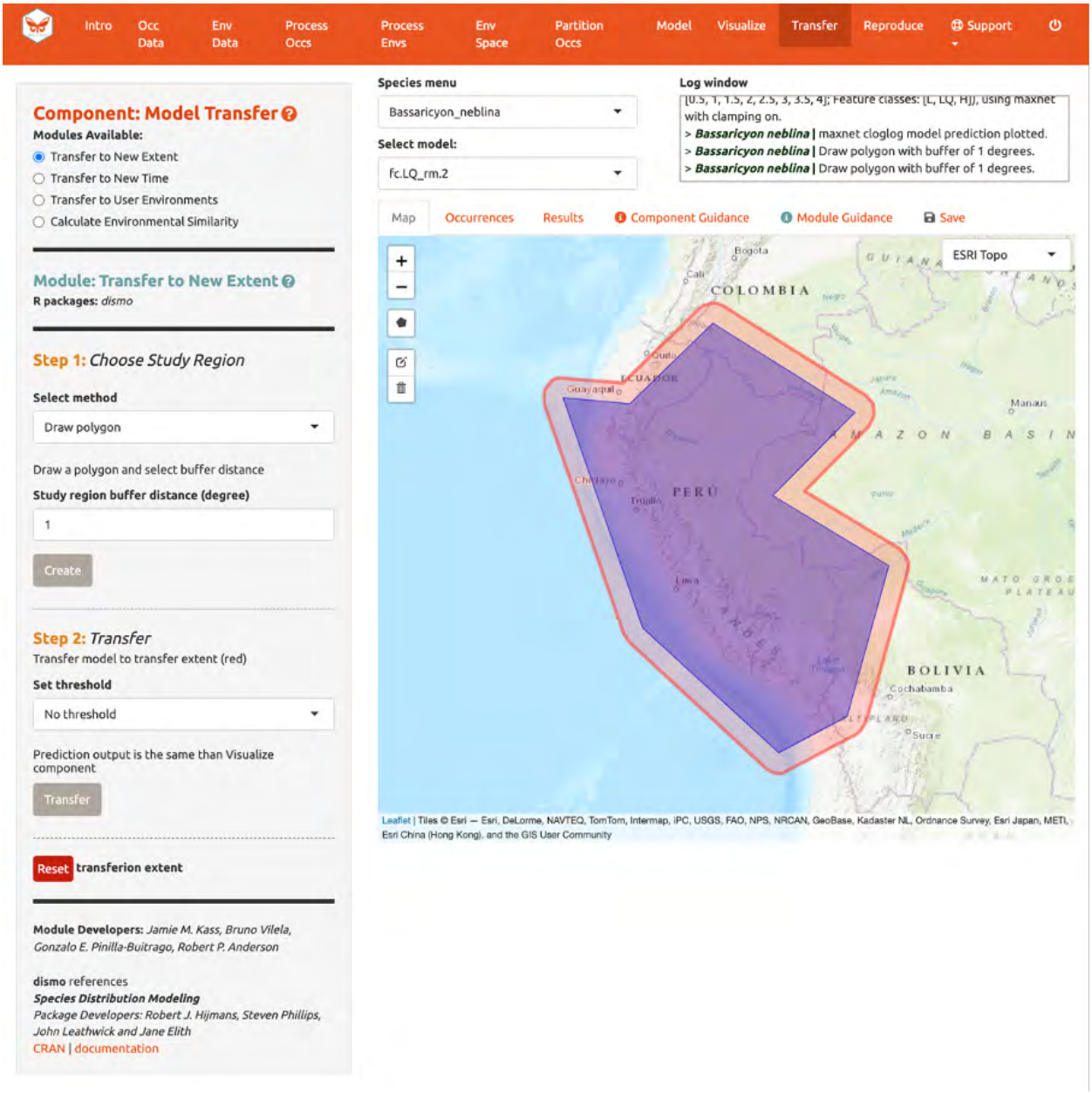
Next, you can transfer the model to new locations and past/future climate scenarios. "Transferring" simply means making predictions with the selected model using new environmental values (i.e., those not used for model building) and getting suitability predictions for new variable ranges. Note: This can also be referred to as "projecting" a model, but do not confuse this with the GIS term typically used for changing the coordinate reference system of a map.

This is potentially confusing because the cross-validation step we used also transferred to new conditions. The spatial cross-validation step iteratively forced models to predict to new areas (and thus likely new environments), and the evaluation statistics summarized the ability of the particular model settings to result in models that transfer accurately. However, the final model that we used to make the predictions we are visualizing was built with all the data (it did not exclude any partition groups or the geographic areas they correspond to). So the variable ranges associated with all of the background points in our dataset were used in the model-building process.

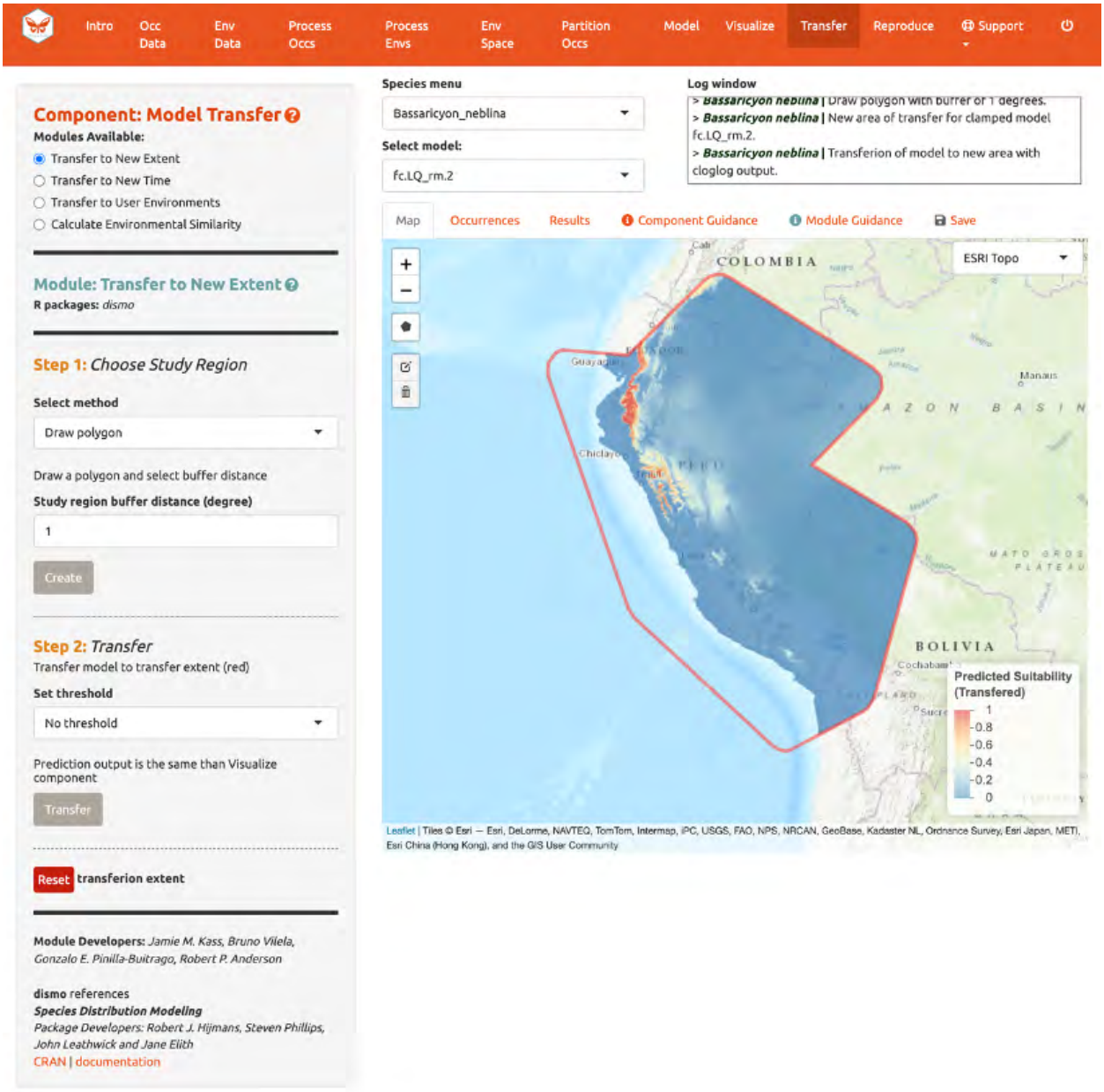
We are now taking this model and transferring it to variable ranges that might not have been used in

model-building (i.e., not represented in the training data). Thus, these environmental values for different places and times could be completely new to our model, even potentially so different that we may be uncertain in the accuracy of our prediction. This is because although the modeled variable responses remain the same, predictions for variable values more extreme than the training data can result in unexpected suitability predictions. For this reason, clamping is often used to constrain model transfers (see below). Please see the guidance text for more orientation regarding these "non-analog conditions".

Let's begin with "Transfer to New Extent" and see if Peru has suitable areas for the olinguito. In Step 1, use the polygon drawing tool to draw around Peru with a 1-degree buffer and hit "Create". Alternatively, you can upload a shapefile or .csv file with records for vertices with fields "longitude, latitude" to use as a study region.



In Step 2, choose a threshold to make a binary prediction or "No Threshold" for a continuous one and click "Transfer". Here, we see very low suitability for most of Peru for the olinguito.



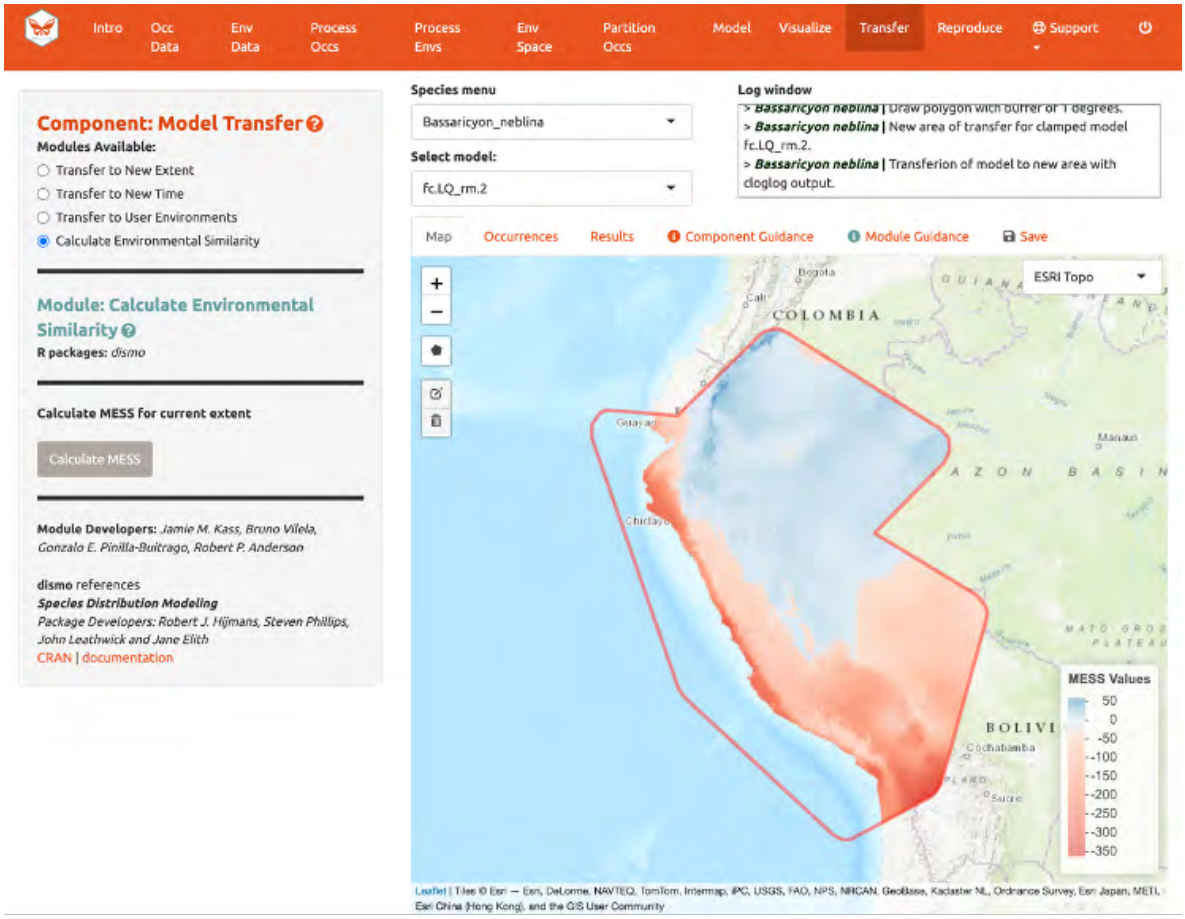
Note: to remove the outline of the polygon from the prediction, click the Trashcan icon and "Clear all".

If you initially used WorldClim or ecoClimate as environmental variables, you can use "Transfer to New Time". In Step 1, there are three options to choose a study region; to draw a polygon, use the same extent, or upload a polygon. In Step 2, you have the choice of WorldClim or Ecoclimate for source variables. The choice depends on your initial selection of environmental variables in "Component: Env Data". For WorldClim, select a time period, a global circulation model, a representative concentration pathway (RCP), and a threshold. Notice also that there are several global circulation models (GCMs) to choose from—these all represent different efforts to model future climate. Not all GCMs have raster data for each RCP. See the module guidance text for more on RCPs and GCMs. Note: some databases have phased out RCPs for Shared Socioeconomic Pathways (SSPs), so be advised that some literature might use SSP terminology instead of RCP. For ecoClimate, you can select a Atmospheric Oceanic General Circulation Model (AOGCM), temporal scenario, and threshold.

The third module, "Transfer to User Environments", gives users the option to project their model to their own uploaded environmental data. The first step is the same as before (select the study region), but in the second step users can upload single-format rasters (.tif, .asc) to use as new data for model projection. The rasters must have the same extent and resolution (cell size), and the names of the files must correspond to the environmental variables used in modeling. To assist, there is a message "Your files must be named as: …" indicating the correct file names to use.

We will skip the "Transfer to New Time" and "Transfer to User Environments" and move on to to "Calculate Environmental Similarity".

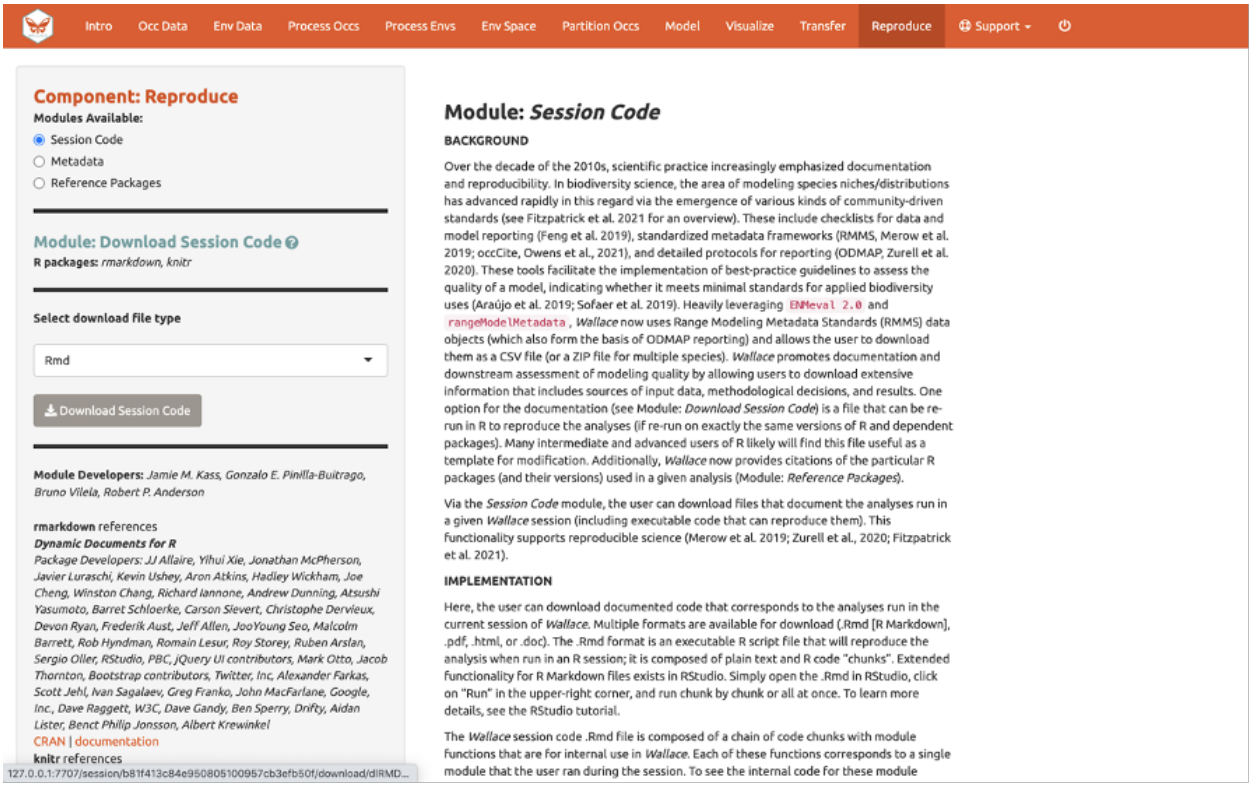
When transferring a model, there may be areas within our new ranges of values that have high uncertainty because they are very different from the values used in model-building. In order to visualize where these areas are, we can use the fourth module, "Calculate Environmental Similarity", to plot a MESS map. MESS stands for (M)ultivariate (E)nvironmental (S)imilarity (S)urface, and the map shows a continuous scale of environmental difference from the training data used for model-building, where increasing positive values mean more similar (blue), and decreasing negative values mean more different (red); please see the module guidance text for details. We can see that future climate values at high elevation are more similar to our training data, whereas those at lower elevations towards the coast are very different in some places. We may therefore interpret that predicted suitability in these areas has higher uncertainty.



13. REPRODUCE

A major advantage of Wallace is reproducibility. The first option within this component is downloading code to run the analysis. While we were using Wallace, **R** code has been running in the background, evident from the messages printed to the **R** console. This option allows you to download a simplified version of this code in the form of a condensed and annotated **R** script. This script serves as documentation for the analysis and can be shared. It can also be run to reproduce the analysis, or edited to change aspects of it. The script can be downloaded as several file types, but the R Markdown format (.Rmd), which is a convenient format for combining **R** code and notation text, can be run directly in **R**. For .pdf downloads, the software TeX is necessary to be installed on your system. Please see the text on this page for more details.

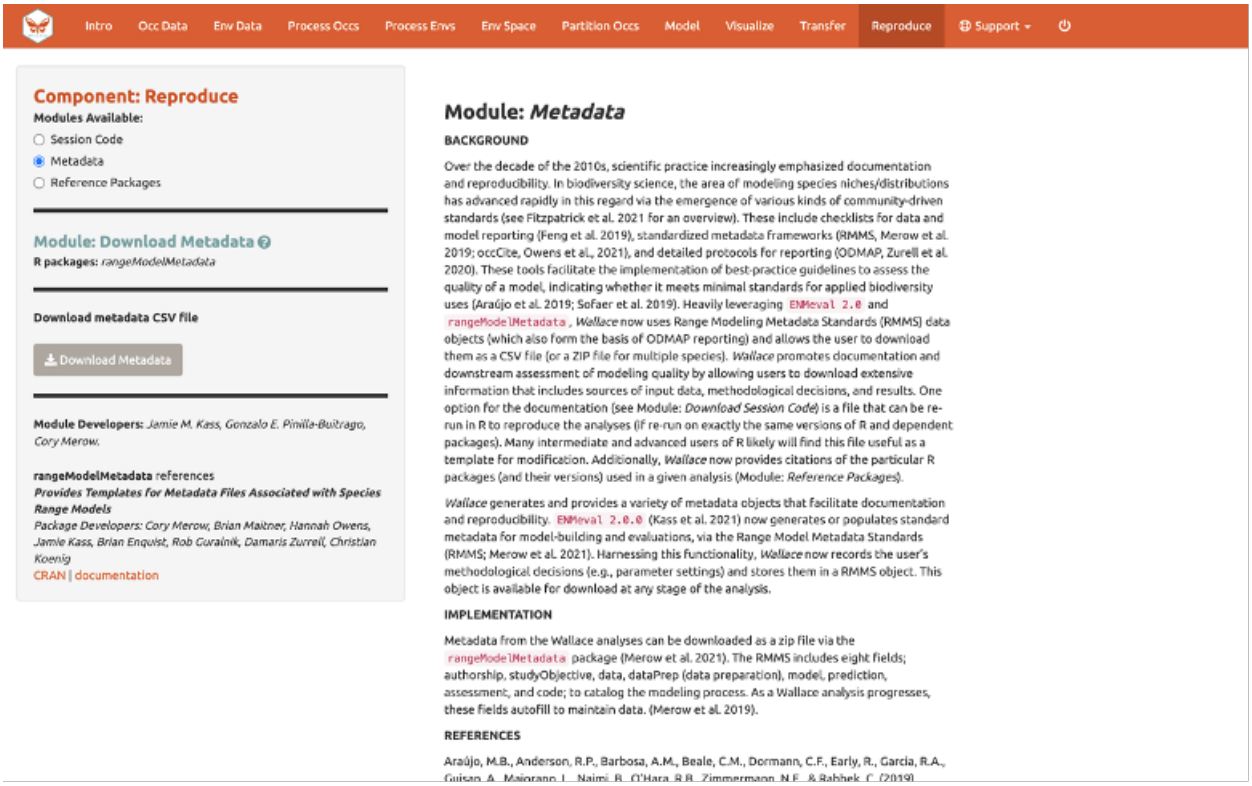
To download the script, select "Rmd" and click "Download".

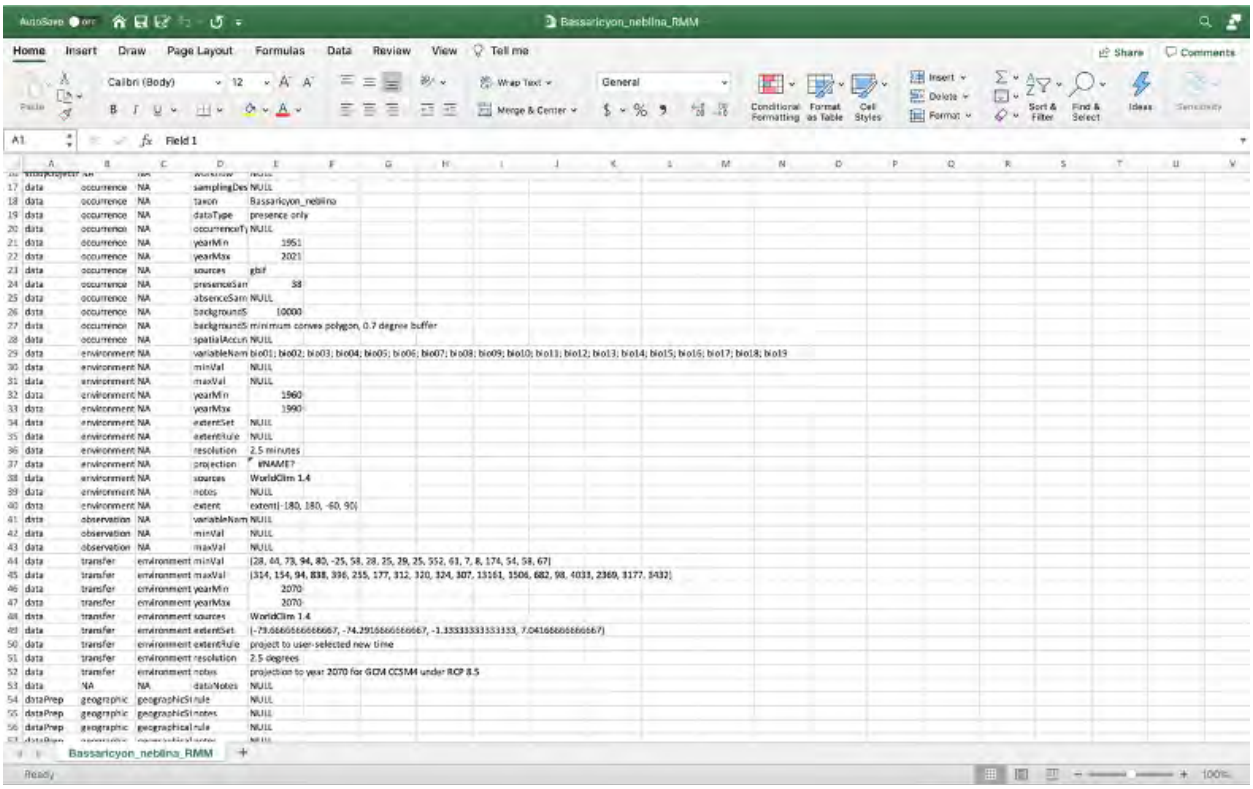


Now, you should have an .Rmd file that contains your complete analysis. Modules from Wallace are indicated as headers denoted by ###.

You might want to open a new **R** window and try running some of this code. Remember that later sections of code may depend on things that were done earlier, so they may not all run if you skip ahead. Note that any “Env Space” analysis will appear at the end of the file. Also remember that if you close your Wallace session you’ll lose your progress in the web browser (but your .Rmd will be unaffected). If you use RStudio, you can open this Rmd and click “knit” to compile your workflow into a shareable html document.

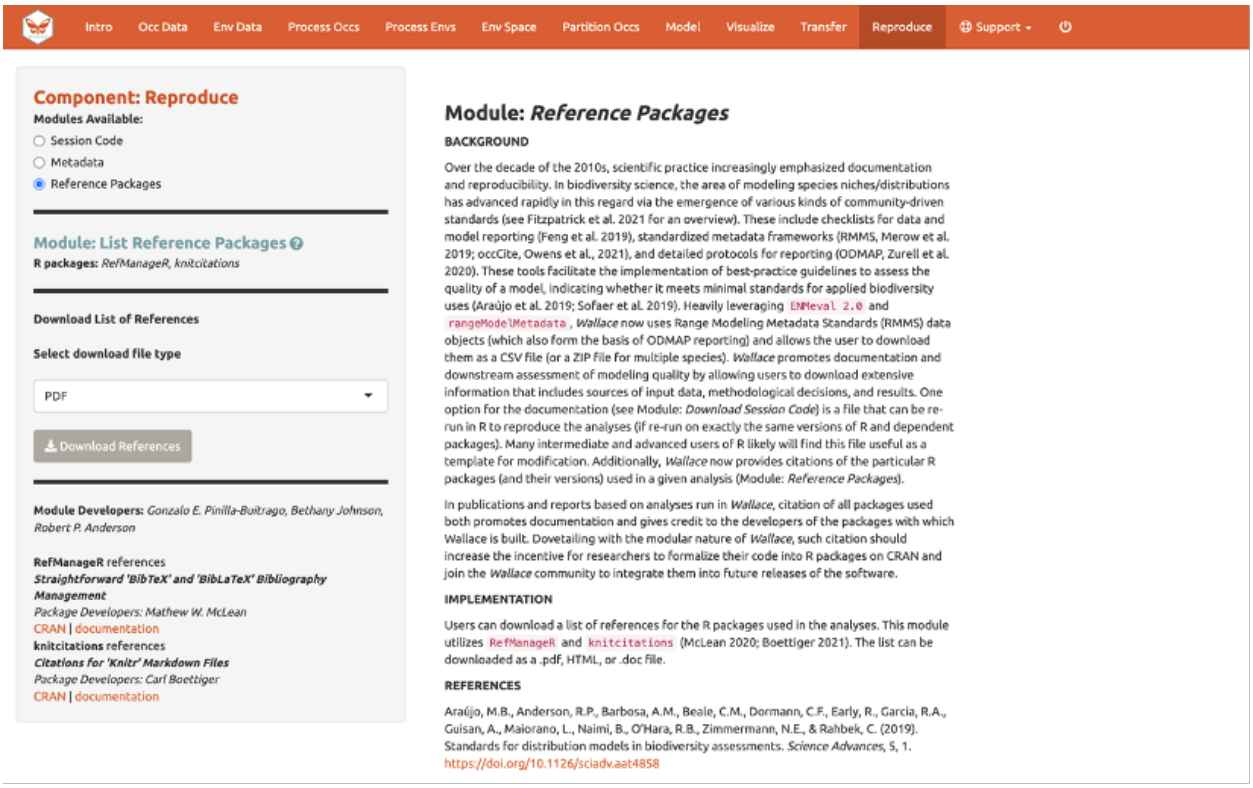
You can also download the Metadata. Wallace generates and provides a variety of metadata objects that facilitate documentation and reproducibility by recording the user’s methodological decisions (e.g., parameter settings) and stores them in a Range Model Metadata Standards object. This will download as a zip and contain a .csv file for each species.

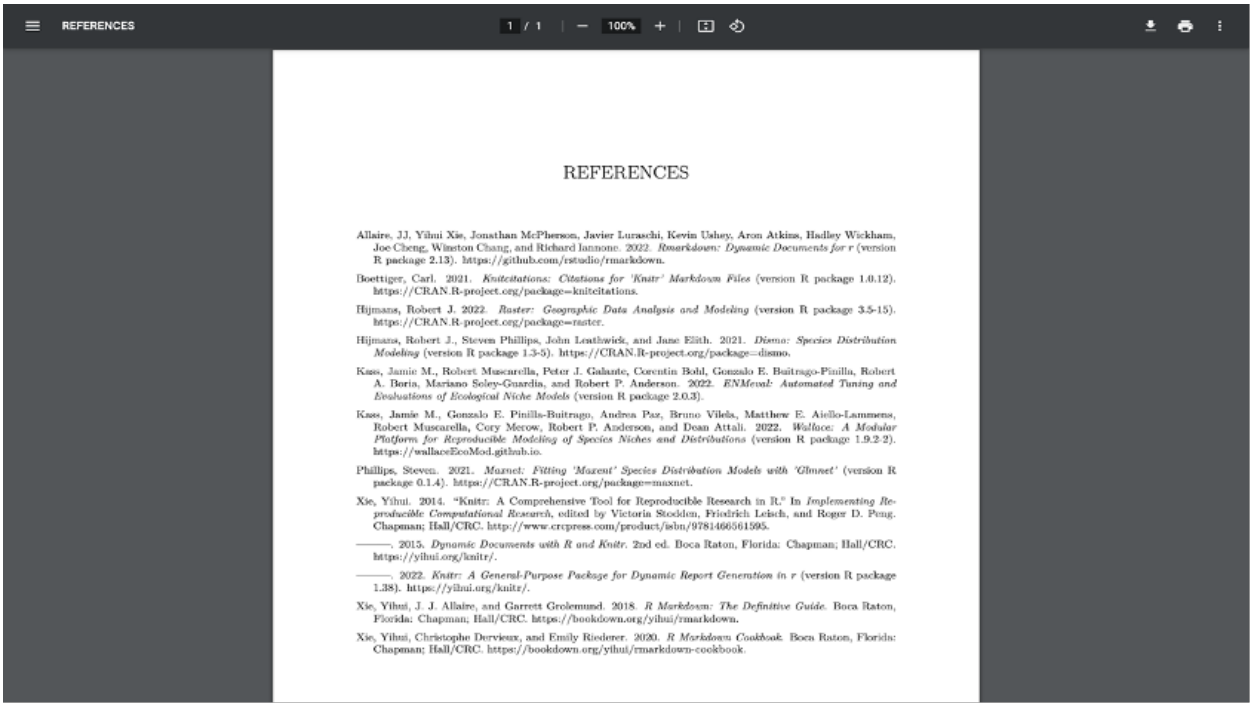




The last module available in the "Reproduce" component is "Reference packages". Here, you can download the citations for all the R-packages used in the analysis. To give people credit for the underlying packages that make Wallace possible (and to document your analyses properly), it is critical to cite the packages and their version number. Remember, Wallace is modular and aims to facilitate access to and use of many R packages being produced by the biogeography research community. Please promote developer credit and reproducible science by citing packages… and think about

making one of your own R packages and adding it to a future version of Wallace someday!





CONCLUSION

Thank you for following the Wallace v2 vignette. We hope you learned more about the updated application, its features, and modeling of species distributions and niches in general. We hate to be repetitive, but we highly encourage you to read the guidance text, follow up on the recommended publications, and hopefully let them lead you to other relevant publications that can inform you further. Also, remember to discuss these topics with your peers.

We encourage you to join the Wallace Google Group: https://groups.google.com/g/wallaceecomod. We'd love to hear your thoughts, opinions, or suggestions on how to make Wallace better for all users. Members can post to the community and be updated on any future announcements.

If you find a bug in the software, it can be reported on the GitHub issues page: https://github.com/wallaceEcoMod/wallace/issues, or using the bug reporting form: https://forms.gle/UffoBCQnMZjWYjfk9.

We are currently working with various partners on exciting additions, so stay tuned for future versions of Wallace.

ACKNOWLEDGMENTS

Wallace was recognized as a finalist for the 2015 Ebbe Nielsen Challenge of the Global Biodiversity Information Facility (GBIF), and received prize funding.

This material is based upon work supported by the National Science Foundation under Grant Numbers DBI-1661510 (RPA; Robert P. Anderson), DBI-1650241 (RPA), DEB-1119915 (RPA), DEB-1046328 (MEA; Matthew E. Aiello-Lammens), DBI-1401312 (RM; Robert Muscarella), and funding from the National Aeronautics and Space Administration grant 80NSSC18K0406 (MEB; Mary E. Blair). Any opinions, findings, and conclusions or recommendations expressed in this material are those of the author(s) and do not necessarily reflect the views of the NSF or NASA.

RESOURCES

- Wallace website: https://wallaceecomod.github.io/
- ENM2020 W19T2 Online open access Ecological Niche Modeling Course by A.T. Peterson, summary of modeling, includes Walkthrough of Wallace V1: https://www.youtube.com/watch?v=kWNyNd2X1uo&t=1226s
- Learn more about Olingos and the Olinguito: https://www.ncbi.nlm.nih.gov/pmc/articles/PMC3760134/
- Gerstner et al. 2018. Revised distributional estimates for the recently discovered olinguito (*Bassaricyon neblina*), with comments on natural and taxonomic history. https://doi.org/10.1093/jmammal/gyy012.
- Aiello-Lammens, M.E., R.A. Boria, A. Radosavljevic, B. Vilela, and R.P. Anderson. 2015. spThin: an R package for spatial thinning of species occurrence records for use in ecological niche models. Ecography 38(5):541–545. https://doi.org/10.1111/ecog.01132.
- Hijmans, R.J., S.E. Cameron, J.L. Parra, P.G. Jones, and A. Jarvis. 2005. Very high resolution interpolated climate surfaces for global land areas. International Journal of Climatology 25(15):1965–1978. https://doi.org/10.1002/joc.1276.
- Lima-Ribeiro, M.S., S. Varela, J. González-Hernández, G. Oliveira, J.A.F. Diniz-Filho, and L.C. Terribile. 2015. ecoClimate: A database of climate data from multiple models for past, present, and future for Macroecologists and Biogeographers. Biodiversity Informatics 10:1–21. Available from: https://www.ecoclimate.org/ (accessed December 2, 2023).
- Kass, J., R. Muscarella, P.J. Galante, C.L. Bohl, G.E. Pinilla-Buitrago, R.A. Boria, M. Soley-Guardia, and R.P. Anderson. 2021. ENMeval 2.0: Redesigned for customizable and reproducible modeling of species' niches and distributions. Methods in Ecology and Evolution,12(9):1602–1608. https://doi.org/10.1111/2041-210X.13628.

- Merow, C., M.J. Smith, and J.A. Silander. 2013. A practical guide to MaxEnt for modeling species' distributions: What it does, and why inputs and settings matter. Ecography 36(10):1058–1069. https://doi.org/10.1111/j.1600-0587.2013.07872.x.

REFERENCES

GBIF.org (2022). GBIF Home Page. Available from: https://www.gbif.org (accessed April 2022).

Gerstner, B.E., J.M. Kass, R. Kays, K.M. Helgen, and R.P. Anderson. 2018. Revised distributional estimates for the recently discovered olinguito (*Bassaricyon neblina*), with comments on natural and taxonomic history. Journal of Mammalogy 99(2,3):321–332. https://doi.org/10.1093/jmammal/gyy012.

Helgen, K., R. Kays, C. Pinto, and J. Schipper. 2016. Bassaricyon alleni. The IUCN Red List of Threatened Species 2016:e. T48637566A45215534. Available from: https://www.iucnredlist.org/species/48637566/45215534 (accessed December 2, 2023).

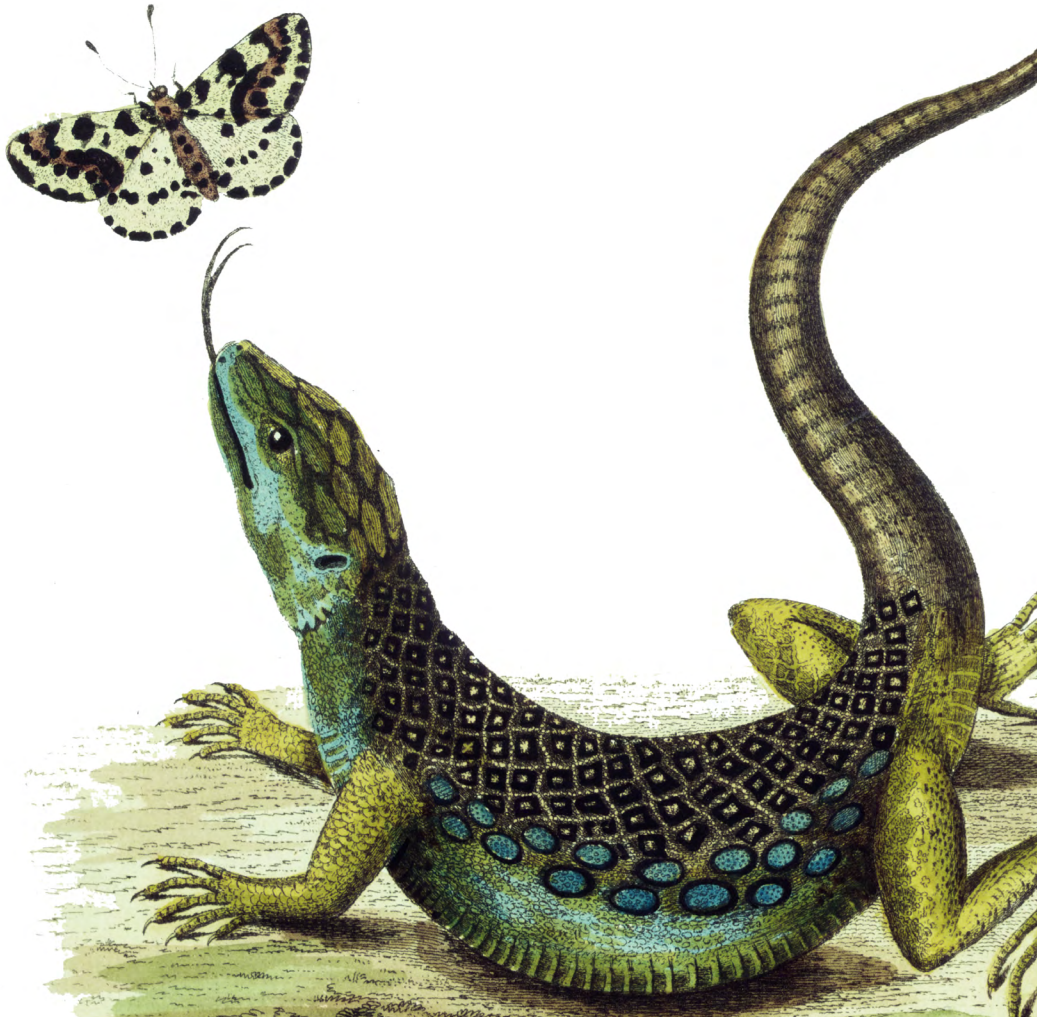
Helgen, K., R. Kays, C. Pinto, J. Schipper, and J.F. González-Maya. 2020. *Bassaricyon neblina* (amended version of 2016 assessment). The IUCN Red List of Threatened Species 2020:e.T48637280A166523067. Available from: https://www.iucnredlist.org/species/48637280/166523067 (accessed December 2, 2023).

Phillips, S.J., R.P. Anderson, M. Dudík, R.E. Schapire, and M.E. Blair. 2017. Opening the black box: An open-source release of Maxent. Ecography 40(7):887–893. https://doi.org/10.1111/ecog.03049.

NCEP materials are meant to be modifiable for each educator's specific classroom or training needs; adaptable Microsoft Word versions of modules are available for download through the NCEP module collection at https://ncep.amnh.org along with any available accompanying data files, appendices, presentations, teaching notes, and exercise solutions.

We welcome your comments and feedback. To write to NCEP or for more information, contact the Network of Conservation Educators and Practitioners at:

American Museum of Natural History
Center for Biodiversity and Conservation
200 Central Park West
New York, New York 10024
ncep@amnh.org

Lessons in Conservation
is available electronically at
ncep.amnh.org/linc

Adaptable Microsoft Word versions of these modules are available for download from the NCEP module collection at ncep.amnh.org along with accompanying presentations, teaching notes, exercise solutions, supplementary files, and links to other relevant open educational resources.