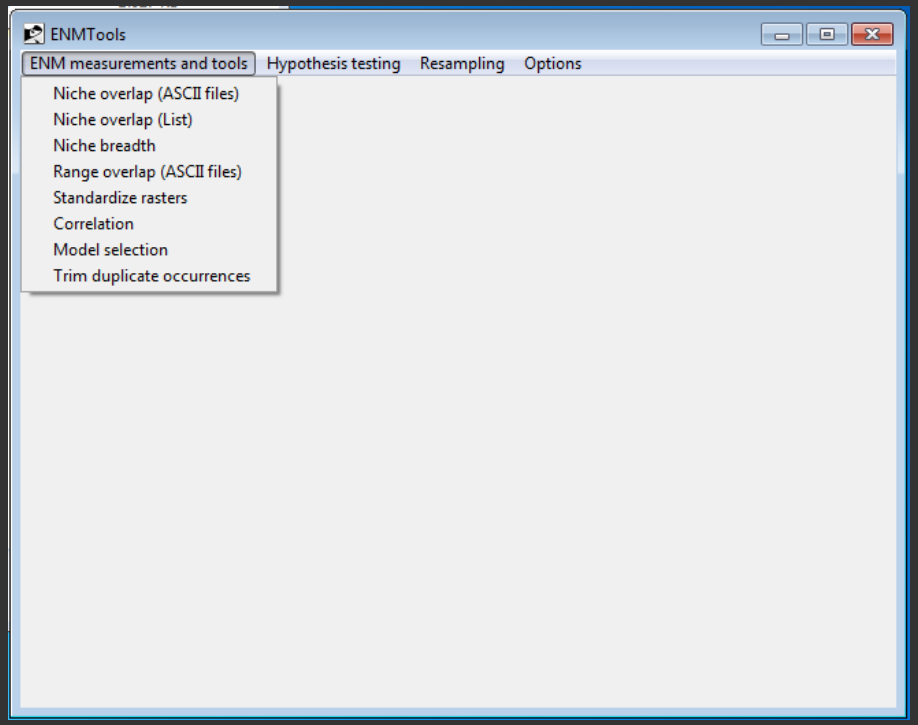
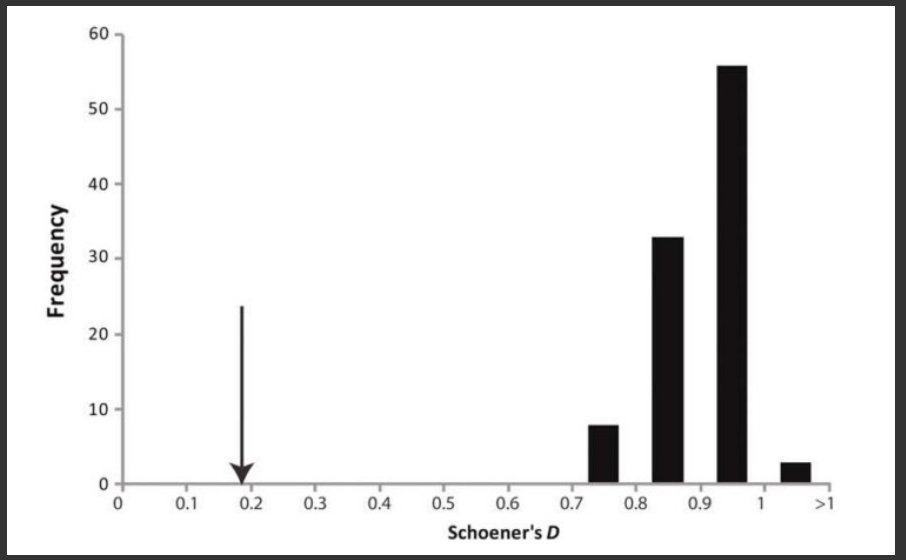
INTRODUCTION TO ECOSPAT

CICGE
SBL Spatial Biology Lab
U.PORTO
FACULDADE DE CIÊNCIAS UNIVERSIDADE DO PORTO

Neftalí Sillero
CICGE/SBLab/FCUP
neftali.sillero@gmail.com

- Program for analysing niche similarity among species.
- Analysis are performed using Maxent.
- Writen on Perl.
- Only for Windows and Mac.
- http://enmtools.blogspot.com.es/





ENVIRONMENTAL NICHE EQUIVALENCY VERSUS CONSERVATISM: QUANTITATIVE APPROACHES TO NICHE EVOLUTION

Dan L. Warren,[1,2] Richard E. Glor,[3,4] and Michael Turelli[1,5]

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Evolution 62-11: 2868–2883

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Software notes

Ecography 33: 607–611, 2010
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Subject Editor: Thiago Rangel. Accepted 4 September 2009

ENMTools: a toolbox for comparative studies of environmental niche models

Dan L. Warren, Richard E. Glor and Michael Turelli

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American Journal of Botany

American Journal of Botany 97(4): 680–693. 2010.

ECOLOGICAL AND GEOGRAPHIC MODES OF SPECIES DIVERGENCE IN WILD TOMATOES[1]

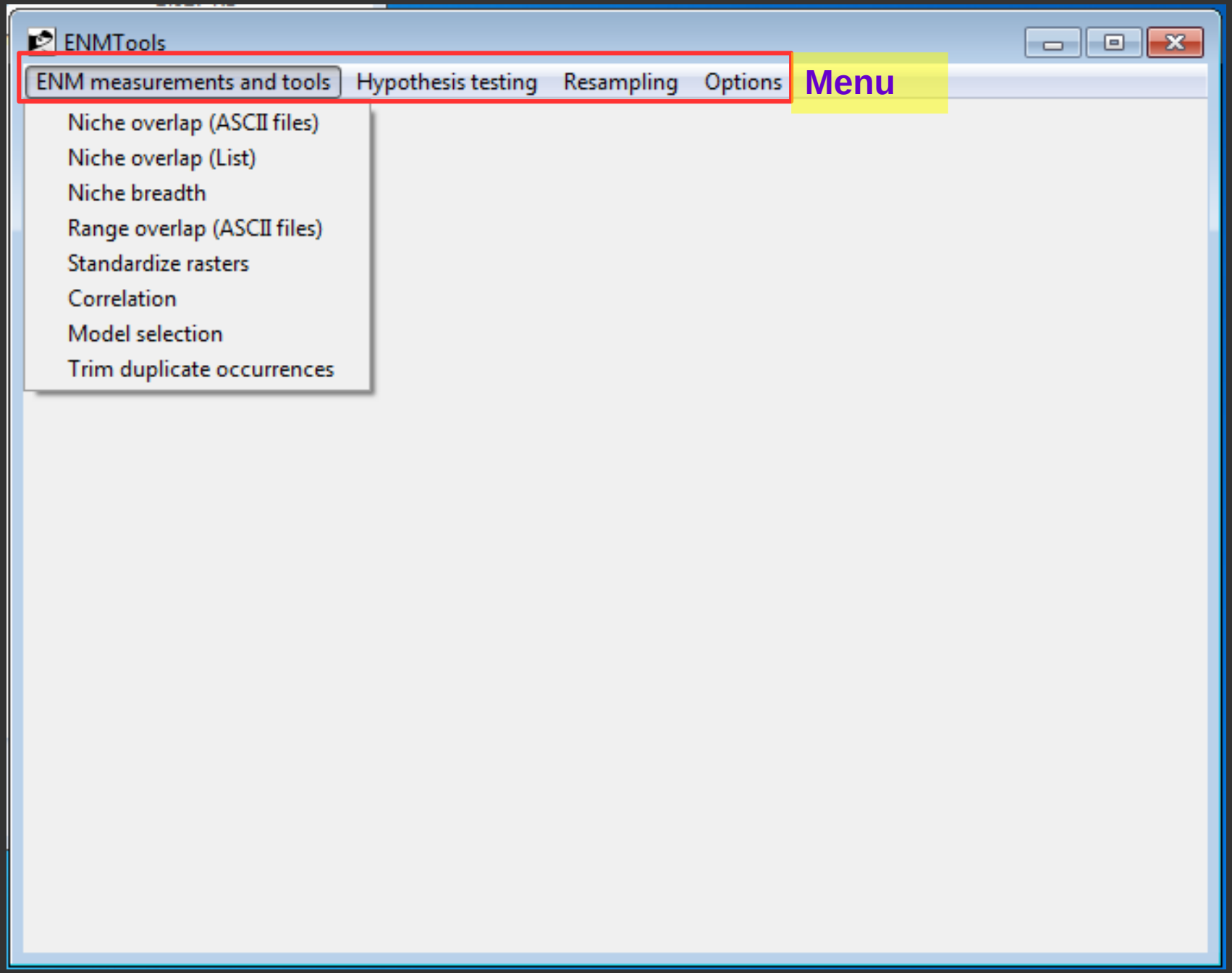
TAKUYA NAKAZATO[2,5], DAN L. WARREN[3], AND LEONIE C. MOYLE[4]

[2]Department of Biology, The University of Memphis, Memphis, Tennessee 38152 USA;
[3]Population Biology Graduate Group, University of California, Davis, California 95616 USA; and
[4]Department of Biology, Indiana University, Bloomington, Indiana 47405 USA

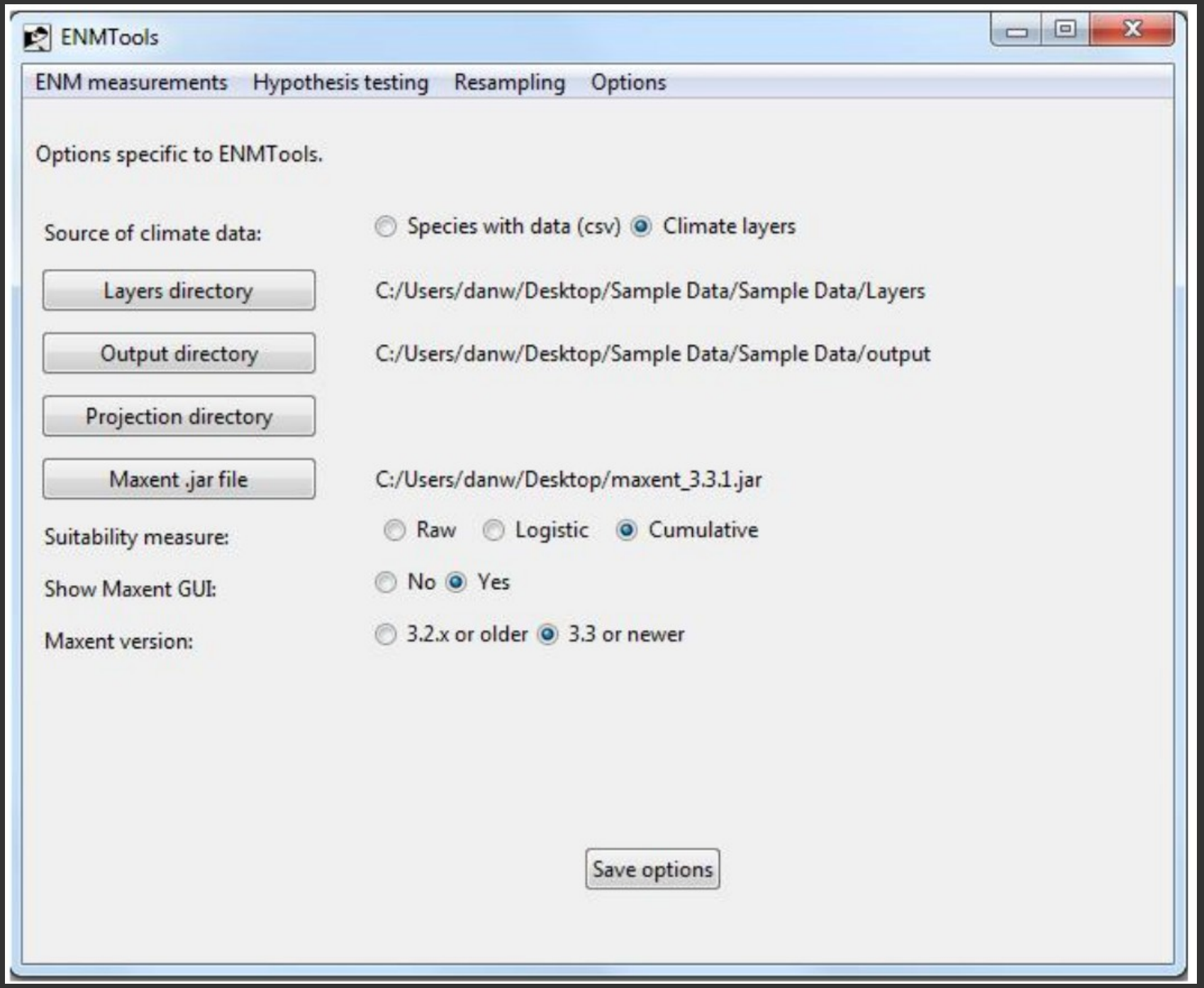
Understanding the role of geography and ecology in species divergence is central to the study of evolutionary diversification. We used climatic, geographic, and biological data from nine wild Andean tomato species to describe each species' ecological niche and to evaluate the likely ecological and geographical modes of speciation in this clade. Using data from >1000 wild accessions and publicly available data derived from geographic information systems for various environmental variables, we found most species pairs were significantly differentiated for one or more environmental variables. By comparing species' predicted niches generated by species distribution modeling (SDM), we found significant niche differentiation among three of four sister-species pairs, suggesting ecological divergence is consistently associated with recent divergence. In comparison, based on age-range correlation (ARC) analysis, there was no evidence for a predominant geographical (allopatric vs. sympatric) context for speciation in this group. Overall, our results suggest an important role for environmentally mediated differentiation, rather than simply geographical isolation, in species divergence.

Key words: age range; allopatric; *Lycopersicon*; species distribution model; Solanaceae; sympatric; wild tomato.

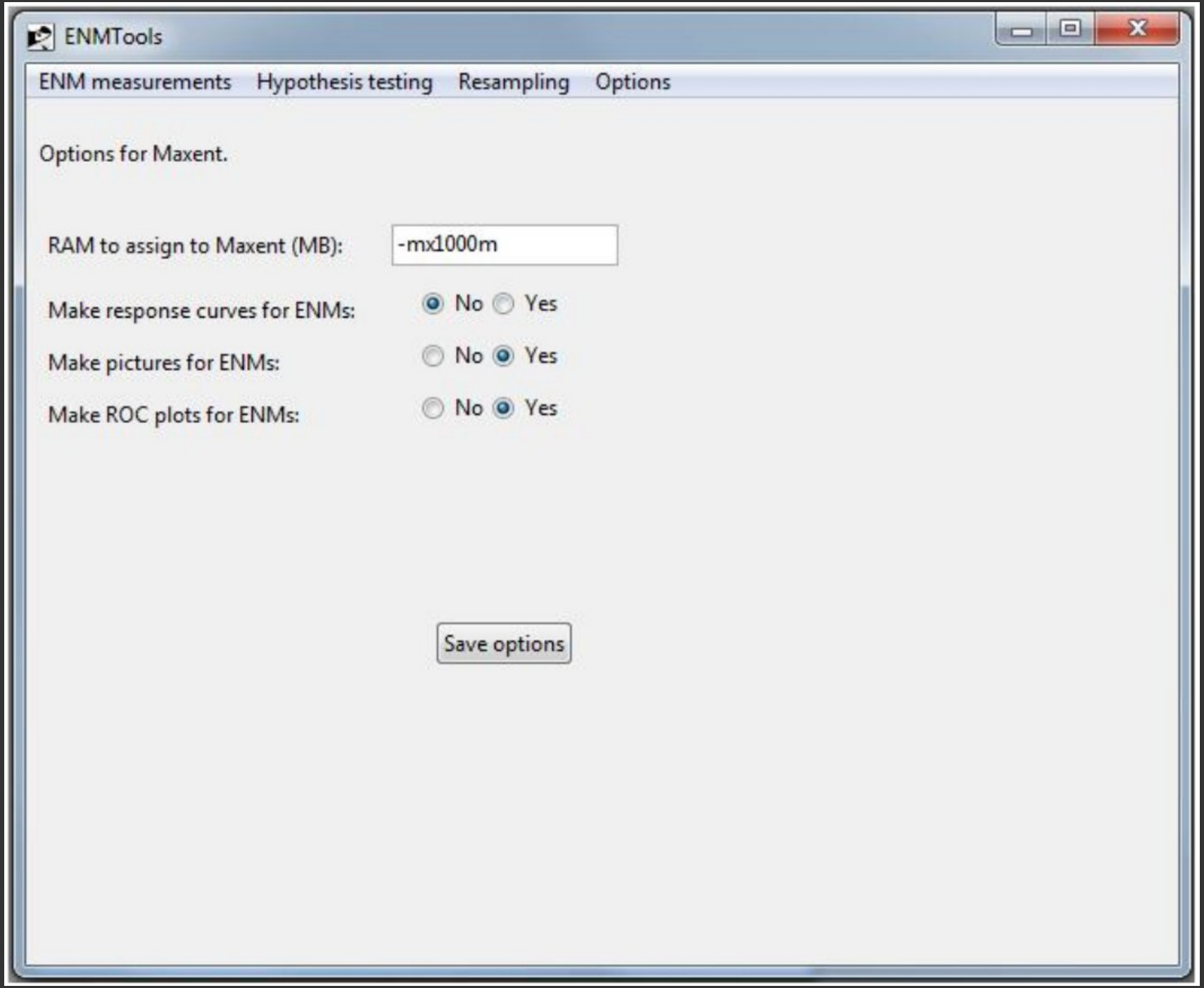
1. Designed exclusively to run with Maxent.
2. You must indicate where is Maxent program files.
3. Environmental layers as ASCII ESRI layers.
4. Species' dataset as txt or csv file, separated with COMMAS.
5. Niche overlap.
6. Niche breadth.
7. Identity test.
8. Background test.
9. Resampling tools.


ENMTools
ENM measurements and tools
Hypothesis testing
Resampling
Options
Menu
Niche overlap (ASCII files)
Niche overlap (List)
Niche breadth
Range overlap (ASCII files)
Standardize rasters
Correlation
Model selection
Trim duplicate occurrences

ENMTools OPTIONS



ENMTools OPTIONS



Schoener's D index

$$D(p_X, p_Y) = 1 - \frac{1}{2} \sum_i |p_{X,i} - p_{Y,i}|,$$

Hellinger's I index

$$I(p_X, p_Y) = 1 - \frac{1}{2} \sqrt{\sum_i \left(\sqrt{p_{X,i}} - \sqrt{p_{Y,i}} \right)^2}.$$

From 0 (discordant ENMs) to 1 (identical ENMs)

IDENTITY TEST

- Whether the ENMs produced by two populations are **identical**.
- Pooling datasets of two species and extracting randomly two new population samples with the same sizes as the two original samples.
- This process is repeated to generate a user-specified number of pseudoreplicated data sets.
- Maxent is called to generate an ENM from each pseudoreplicated data sets.
- Niche similarity indices (e.g. I and Schoener's D) are calculated from each pseudoreplicated data sets.
- ENMTools obtains a distribution of overlap scores between populations drawn from a shared distribution, assuming that the populations are interchangeable in their use of niche space.

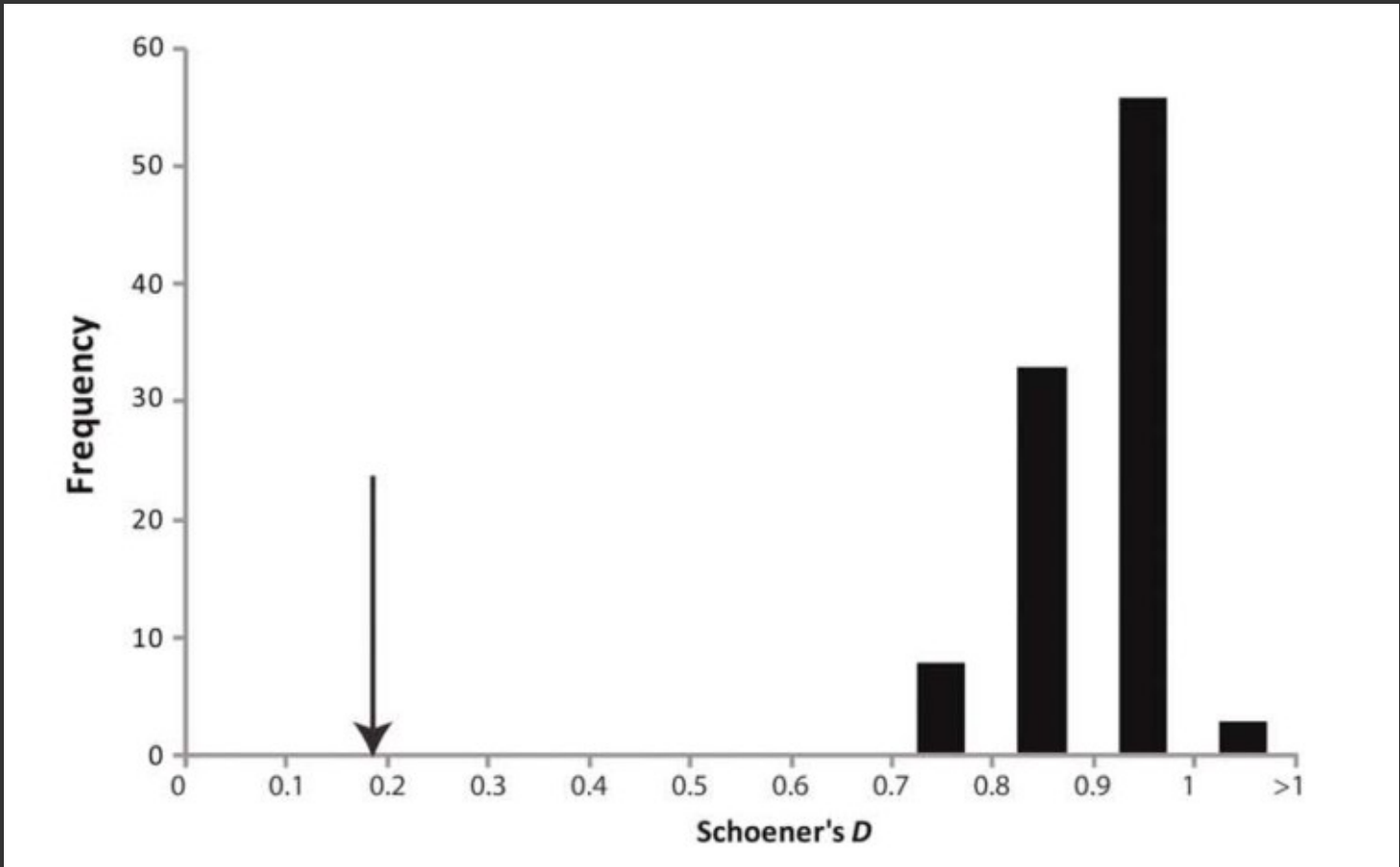
IDENTITY TEST

- Whether the ENMs produced by two populations are identical.
- From 0 (discordant ENMs) to 1 (identical ENMs)

  - Ho: Both populations are similar
    D → 1
  - Ha: Both populations are dissimilar
    D → 0

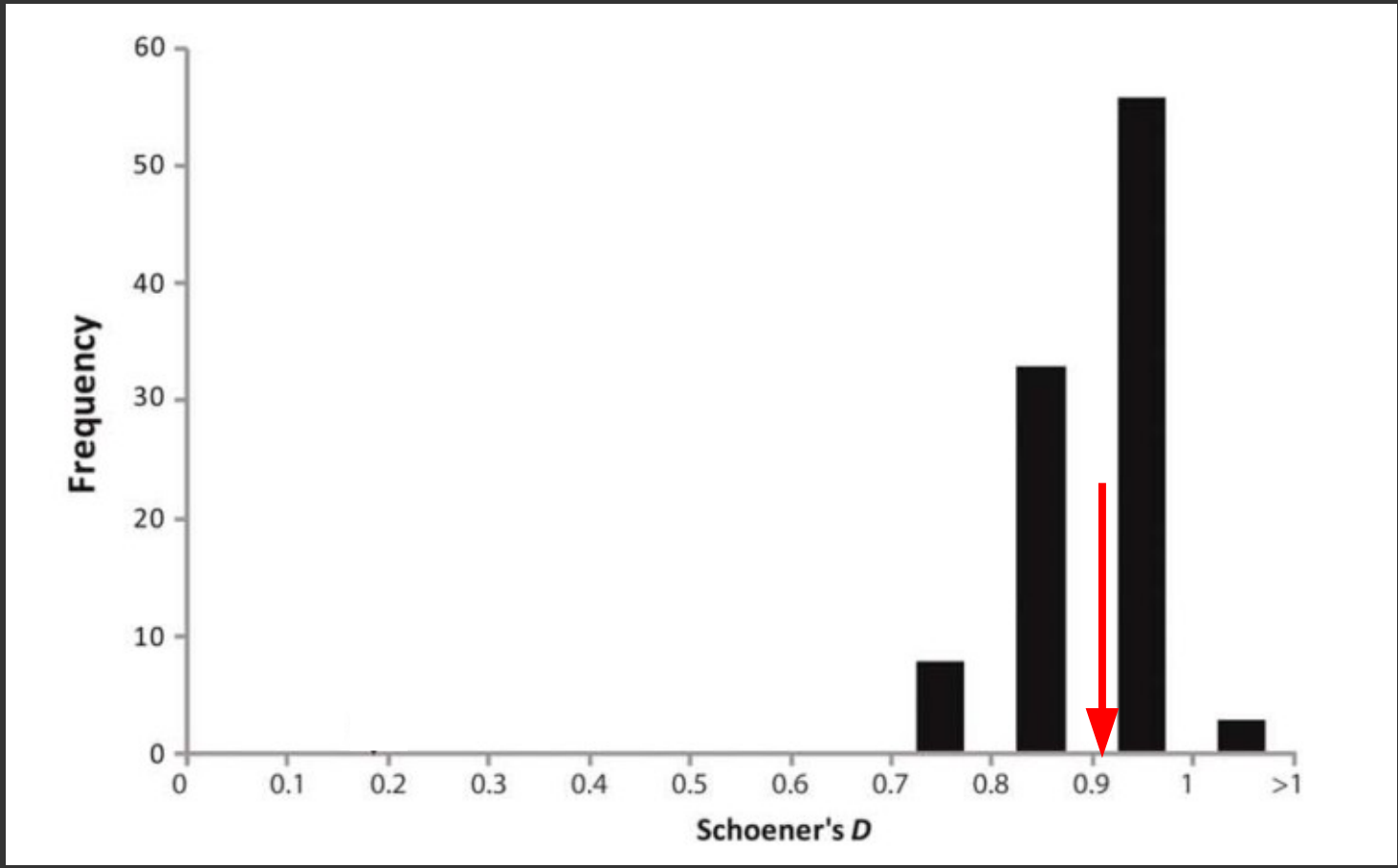
- The hypothesis of niche identity is rejected (both populations are dissimilar) when the empirically observed value for I/D is significantly lower than the values expected from the pseudo-replicated data sets.

- **The hypothesis of niche identity is rejected when the empirically observed value for I/D is significantly lower than the values expected from the pseudo-replicated data sets.**



From 0 (discordant ENMs) to 1 (identical ENMs)

- The hypothesis of niche identity is **accepted** when the empirically observed value for I/D is significantly **not** lower than the values expected from the pseudo-replicated data sets.



From 0 (discordant ENMs) to 1 (identical ENMs)

BACKGROUND TEST

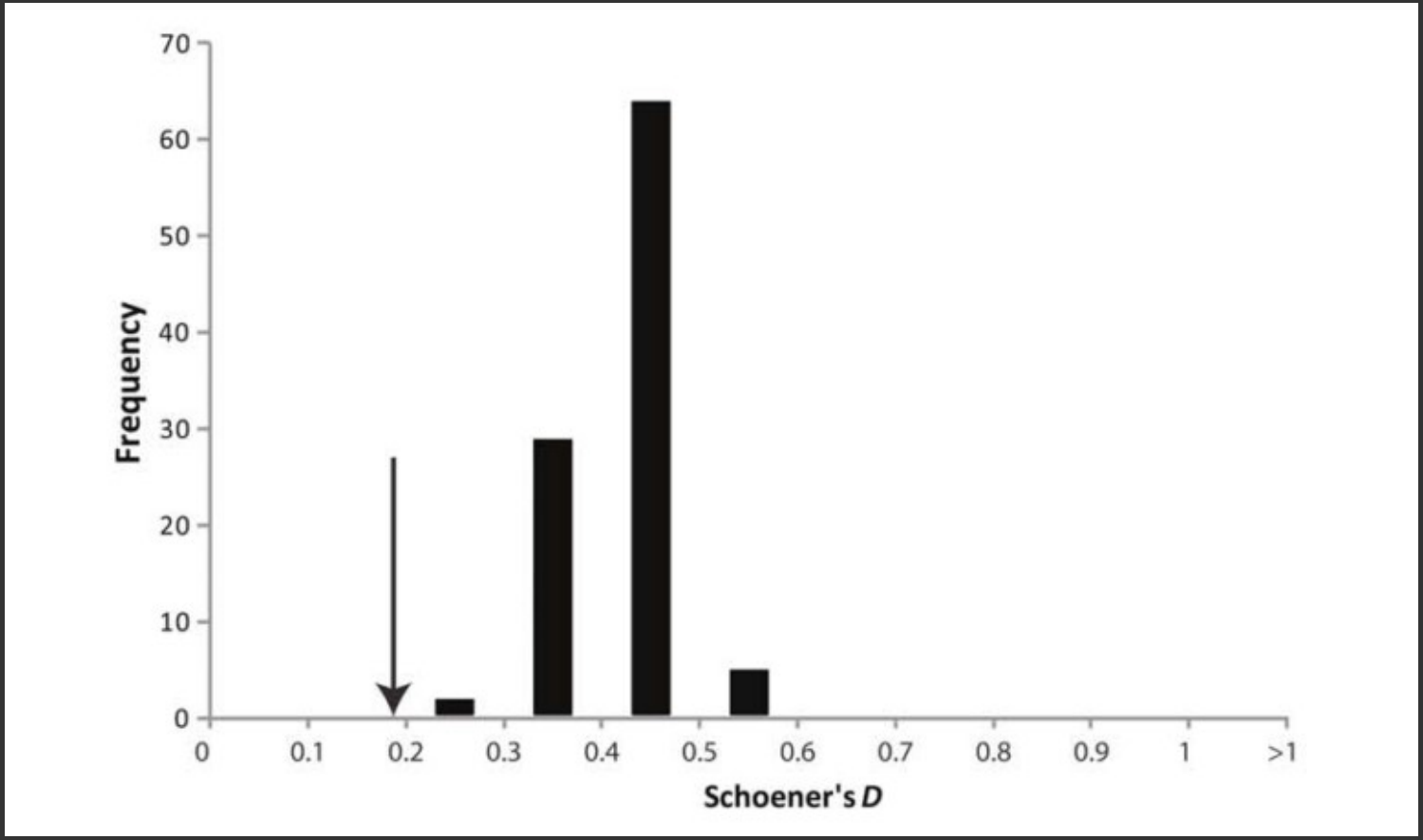
- Whether ENMs are **more similar** than expected by chance, based on the geographical regions in which they occur.
- Whether the ENMs obtained from two allopatrically distributed populations are more different than would be expected given the underlying environmental differences between the regions in which they occur.
- A null distribution is generated for the ENM difference expected between one population and occurrence points placed at random within the range of another population.
- The points to be treated as environmental background can either be specified as a set of comma- separated coordinates, or can be sampled from an ASCII raster file.

BACKGROUND TEST

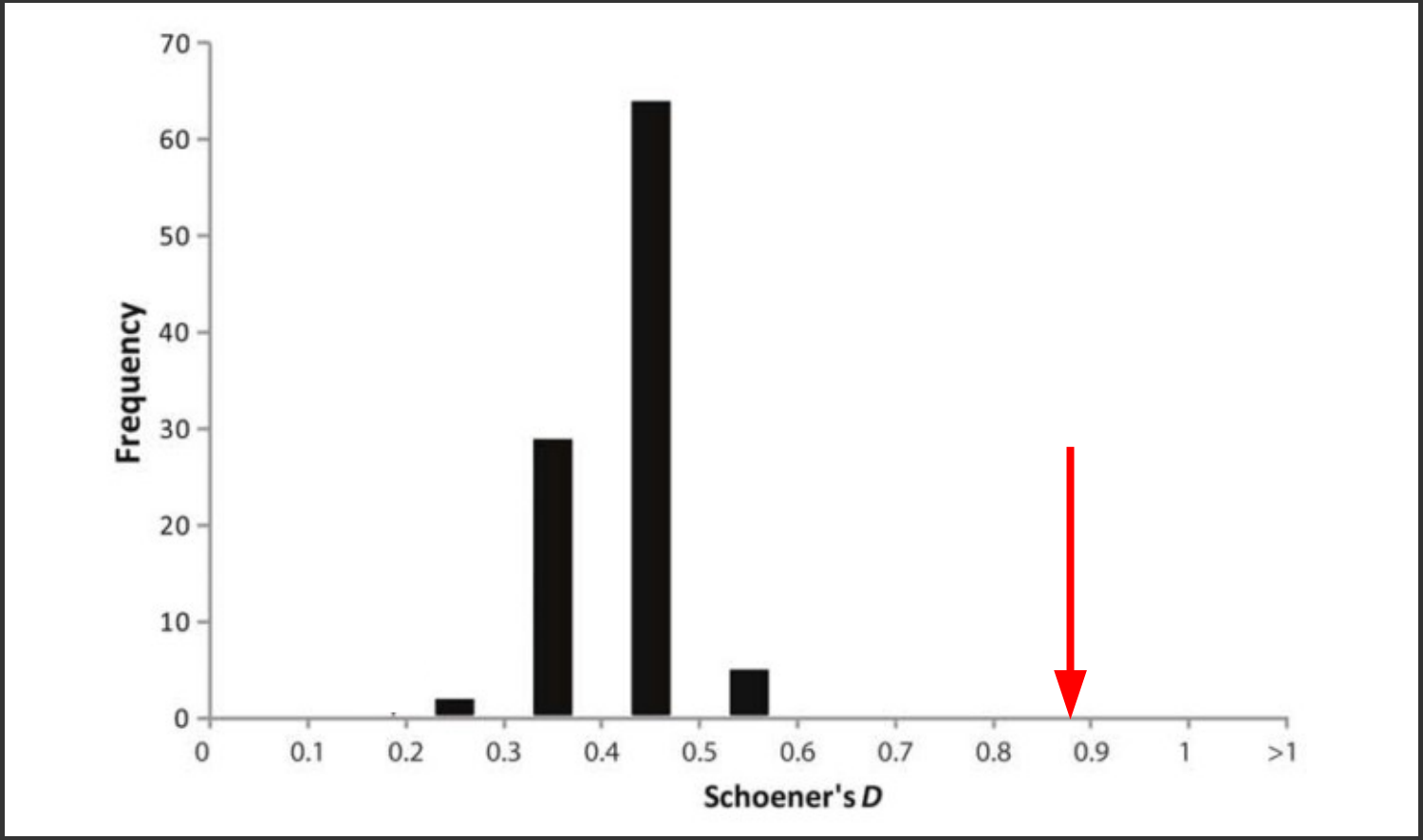
- First file is a .csv file with occurrences for a single species – the focal species for this particular test.
- Second file is either a .csv file of points (lat-long) from the designated “background” region or an ASCII raster file to use as a mask to generate random background points.
- The number of background points you use should be the number of points you have for species B (if you have 25 points for A and 50 for B, you compare the actual occurrences for A to 50 randomly chosen background points from the area of species B).

- Whether ENMs are more similar than expected by chance, based on the geographical regions in which they occur.
  - Ho: Both populations are more similar than expected
    - D → 1
  - Ha: Both populations are less similar (dissimilar) than expected
    - D → 0
- If the observed values of the niche similarity measures obtained from the two original populations are significantly higher (or lower) than expected from this null distribution, the null hypothesis that similarity (or divergence) between species is no more than expected based on the availability of habitat is rejected: both populations are then dissimilar.

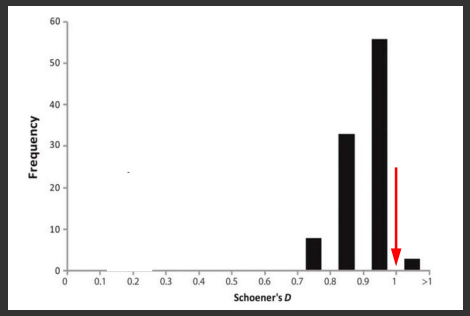
- The observed overlap between the two species is **lower** than expected under the null hypothesis, indicating that the two species are more divergent than expected.

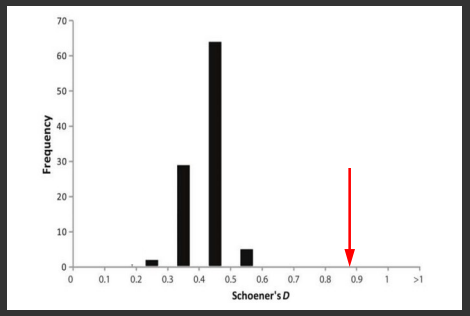


- The observed overlap between the two species is **higher** than expected under the null hypothesis, indicating that the two species are more similar than expected.

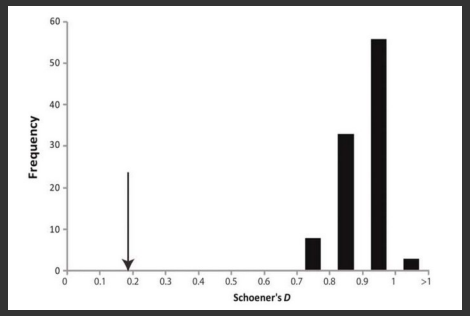


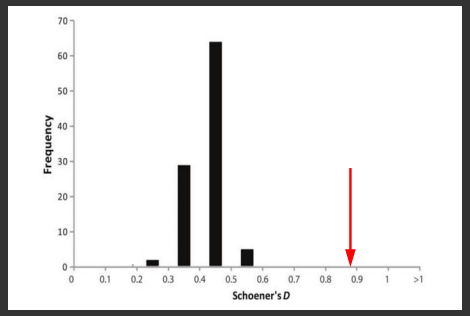
IT: similar niches; BT: similar niches



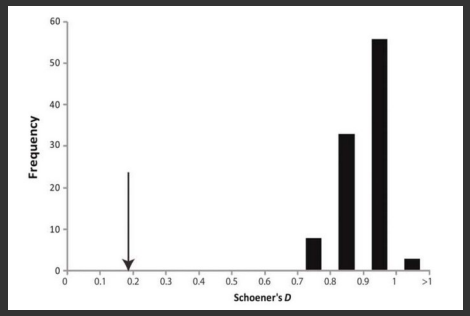


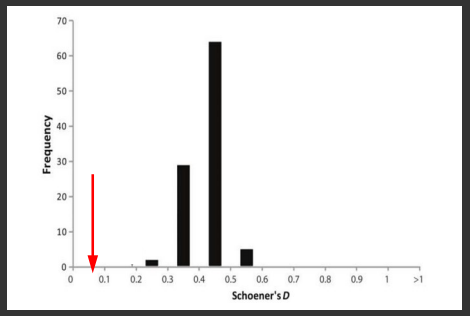
IT: different niches; BT: similar niches



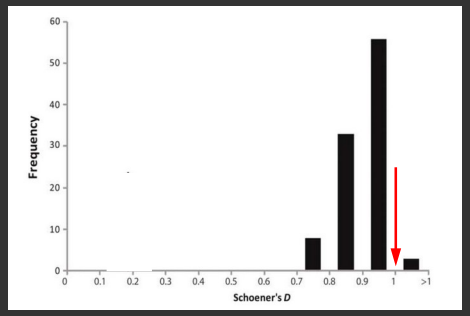


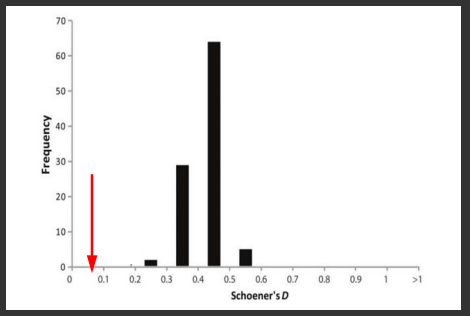
IT: different niches; BT: different niches





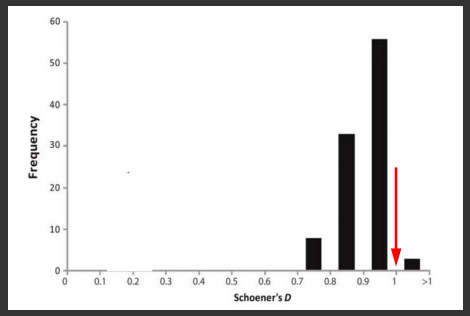
IT: similar niches; BT: different niches

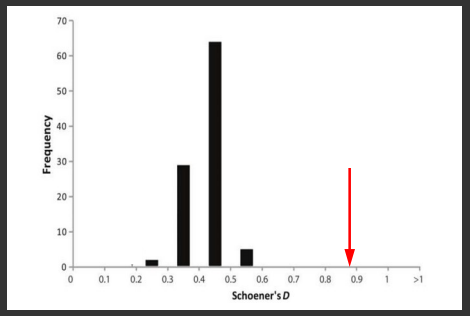




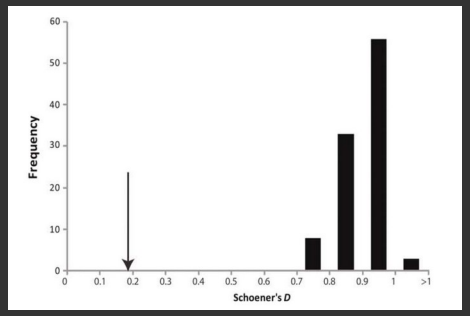
From 0 (discordant niches) to 1 (identical niches)

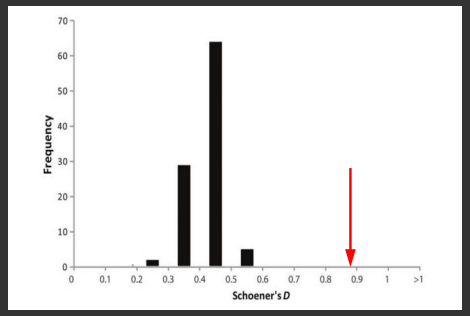
IT: similar niches; BT: similar niches





IT: different niches; BT: similar niches





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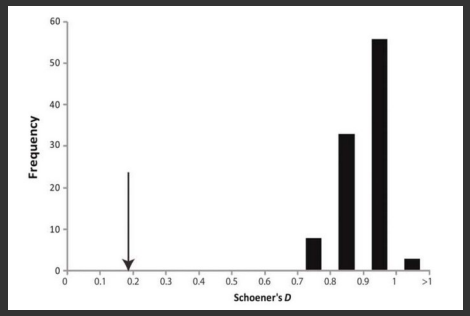
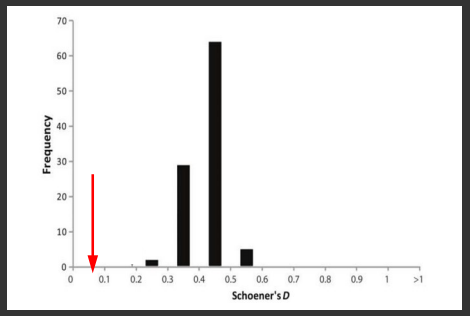
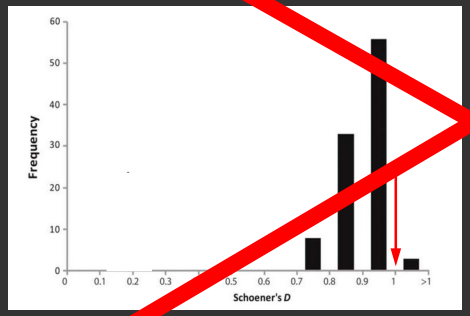
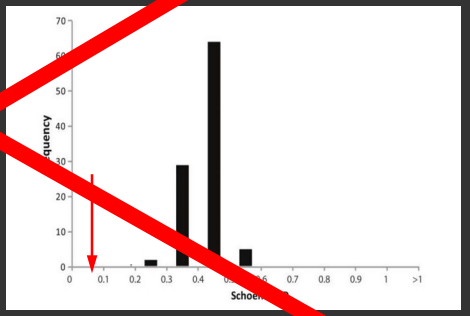




IT: similar niches; BT: different niches





From 0 (discordant niches) to 1 (identical niches)

Global Ecology and Biogeography, (Global Ecol. Biogeogr.) (2012) **21**, 481–497

RESEARCH PAPER

Measuring ecological niche overlap from occurrence and spatial environmental data

Olivier Broennimann[1*,†], Matthew C. Fitzpatrick[2†], Peter B. Pearman[3†], Blaise Petitpierre[1], Loïc Pellissier[1], Nigel G. Yoccoz[4], Wilfried Thuiller[5], Marie-Josée Fortin[6], Christophe Randin[7], Niklaus E. Zimmermann[3], Catherine H. Graham[8] and Antoine Guisan[1]

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Software notes

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© 2016 The Authors. Ecography © 2016 Nordic Society Oikos
Subject Editor: Thiago Rangel. Editor-in-Chief: Miguel Araújo. Accepted 17 November 2016

ecospat: an R package to support spatial analyses and modeling of species niches and distributions

Valeria Di Cola, Olivier Broennimann, Blaise Petitpierre, Frank T. Breiner, Manuela D'Amen, Christophe Randin, Robin Engler, Julien Pottier, Dorothea Pio, Anne Dubuis, Loic Pellissier, Rubén G. Mateo, Wim Hordijk, Nicolas Salamin and Antoine Guisan

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CRAN - Package ecospat - Mozilla Firefox

https://cran.r-project.org/web/packages/ecospat/index.html

Search

all | package eco... | CRAN - Pack...

ecospat: Spatial Ecology Miscellaneous Methods

Colection of R functions and data sets for the support of spatial ecology analyses with a focus on pre-, core and post- modelling analyses of species distribution, niche quantification and community assembly., written by current and former members and collaborators of the ecospat group of Antoine Guisan, Department of Ecology and Evolution (DEE) & Institute of Earth Surface Dynamics (IDYST), University of Lausanne, Switzerland.

Version:	2.0
Depends:	ade4 (≥ 1.6-2), ape (≥ 3.2), gbm (≥ 2.1), sp (≥ 1.0-15)
Imports:	adehabitatHR (≥ 0.4.11), adehabitatMA (≥ 0.3.8), biomod2 (≥ 3.1-64), dismo (≥ 0.9-3), ecodist (≥ 1.2.9), maptools (≥ 0.8-39), randomForest (≥ 4.6-7), spatstat (≥ 1.37-0), raster (≥ 2.2-31), rms (≥ 4.5-0), MigClim (≥ 1.6), gtools (≥ 3.4.1), PresenceAbsence (≥ 1.1.9), methods (≥ 3.1.1), doParallel (≥ 1.0.10), foreach (≥ 1.4.3), iterators (≥ 1.0.8), parallel
Suggests:	rgdal (≥ 0.8-16), rJava (≥ 0.9-6), XML (≥ 3.98-1.1)
Published:	2016-05-26
Author:	Olivier Broennimann [aut], Valeria Di Cola [cre, aut], Blaise Petitpierre [ctb], Frank Breiner [ctb], Manuela D`Amen [ctb], Christophe Randin [ctb], Robin Engler [ctb], Wim Hordijk [ctb], Julien Pottier [ctb], Mirko Di Febbraro [ctb], Loic Pellissier [ctb], Dorothea Pio [ctb], Ruben Garcia Mateo [ctb], Anne Dubuis [ctb], Daniel Scherrer [ctb], Luigi Maiorano [ctb], Achilleas Psomas [ctb], Charlotte Ndiribe [ctb], Nicolas Salamin [ctb], Niklaus Zimmermann [ctb], Antoine Guisan [aut]
Maintainer:	Valeria Di Cola <valeria.dicola at unil.ch>
BugReports:	NA
License:	GPL-2 | GPL-3 [expanded from: GPL]
URL:	http://www.unil.ch/ecospat/home/menuguid/ecospat-resources/tools.html
NeedsCompilation:	no
Materials:	NEWS
CRAN checks:	ecospat results

Downloads:

Reference manual:	ecospat.pdf
Package source:	ecospat_2.0.tar.gz
Windows binaries:	r-devel: ecospat_2.0.zip, r-release: ecospat_2.0.zip, r-oldrel: ecospat_2.0.zip
OS X Mavericks binaries:	r-release: ecospat_2.0.tgz, r-oldrel: ecospat_2.0.tgz
Old sources:	ecospat archive

Reverse dependencies:

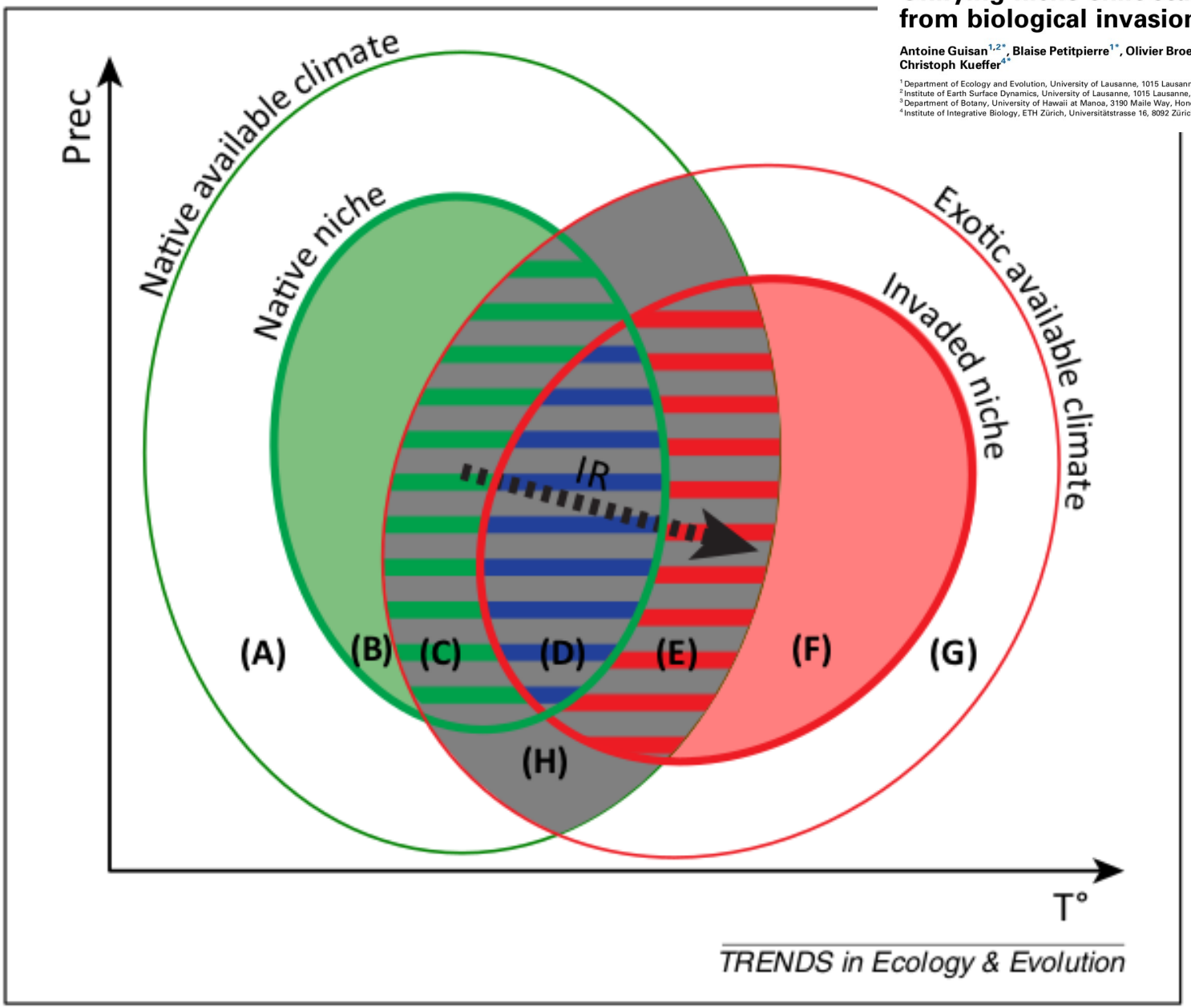
Reverse suggests: biomod2

Review
CellPress

Unifying niche shift studies: insights from biological invasions

Antoine Guisan[1,2*], Blaise Petitpierre[1*], Olivier Broennimann[1*], Curtis Daehler[3*], and Christoph Kueffer[4*]

[1] Department of Ecology and Evolution, University of Lausanne, 1015 Lausanne, Switzerland
[2] Institute of Earth Surface Dynamics, University of Lausanne, 1015 Lausanne, Switzerland
[3] Department of Botany, University of Hawaii at Manoa, 3190 Maile Way, Honolulu, HI 96822, USA
[4] Institute of Integrative Biology, ETH Zürich, Universitätstrasse 16, 8092 Zürich, Switzerland



- Extracts environmental values for presence records
- Estimates each climatic niche by kernel smoothers
- Calculates a PCA to quantify niche overlap between both niches

IDENTITY TEST = EQUIVALENCY TEST
BACKGROUND TEST = SIMILARITY TEST

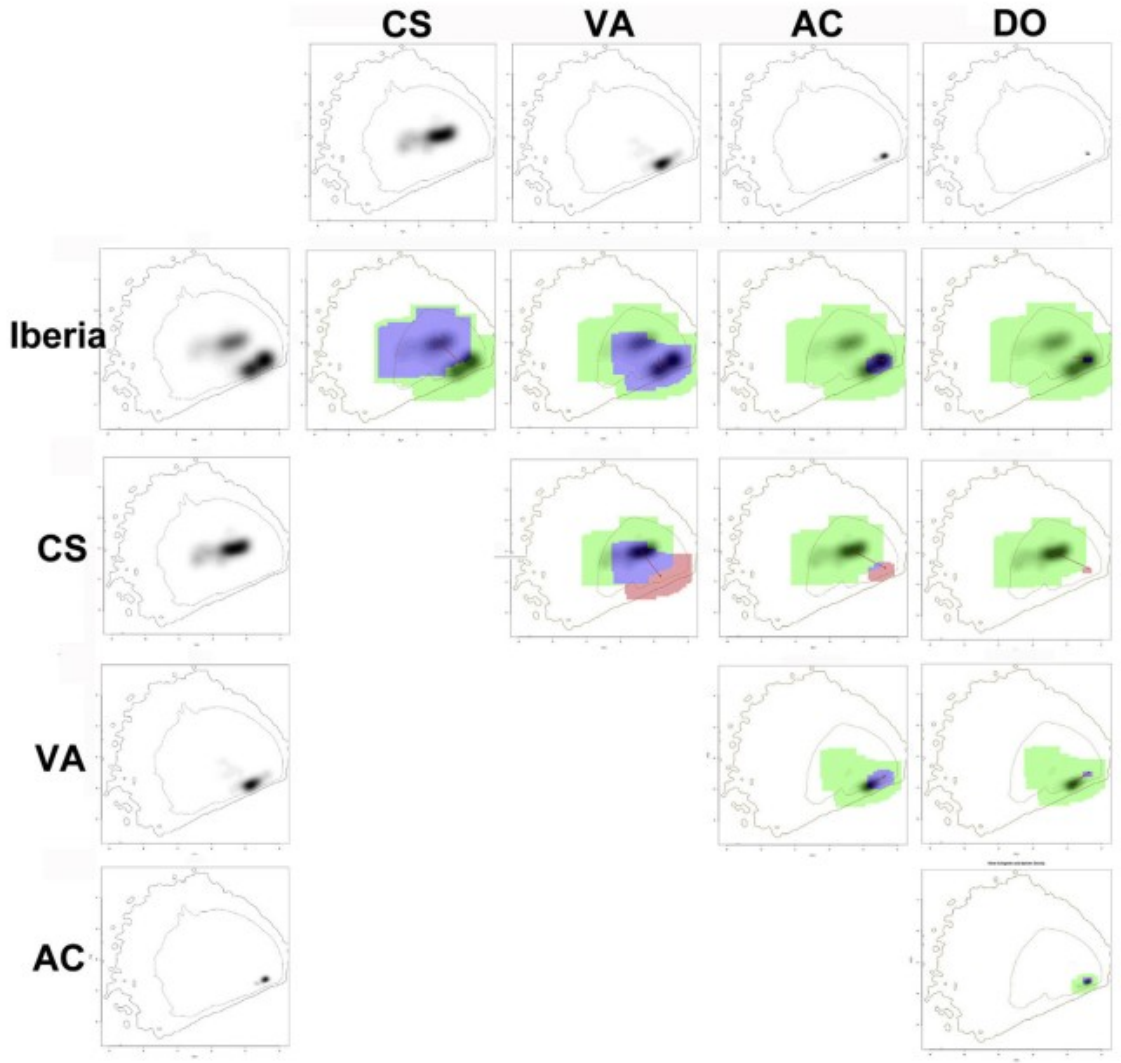


Fig. 4. On the first column, density plots of the subranges of *Podarcis carbonelli* projected on the first two principal components (PCA1: 45.22% var; PCA2: 24.98% var.) of the environmental space. The remaining plots indicate the pairwise comparisons between subranges and associated expansion (red), stability (blue) and unfilling (green). Density of the occurrences of each subrange by cell is grey-shaded; solid and dashed contour lines illustrate 100% and 50% of the available environmental space, respectively. See Table 1 for dataset abbreviations. (For interpretation of the references to colour in this figure legend, the reader is referred to the web version of this article.)

QUESTIONS?