

# APPLICATIONS OF ECOLOGICAL NICHE MODELS

- Ecological niche identification
- Identification of contact zones
- Integration with genetic data
- Species expansions
- Species invasions
- Dispersion hypotheses
- Species conservation status
- Prediction of future conservation problems
- Projection to future and past climate change scenarios
- Modelling past species
- High spatial resolution models
- Modelling species richness
- Road-kills
- Diseases
- Windmills
- Location of protected areas
- Snake bites
- Human settlements

Estuaries and Coasts  
DOI 10.1007/s12237-015-9966-y

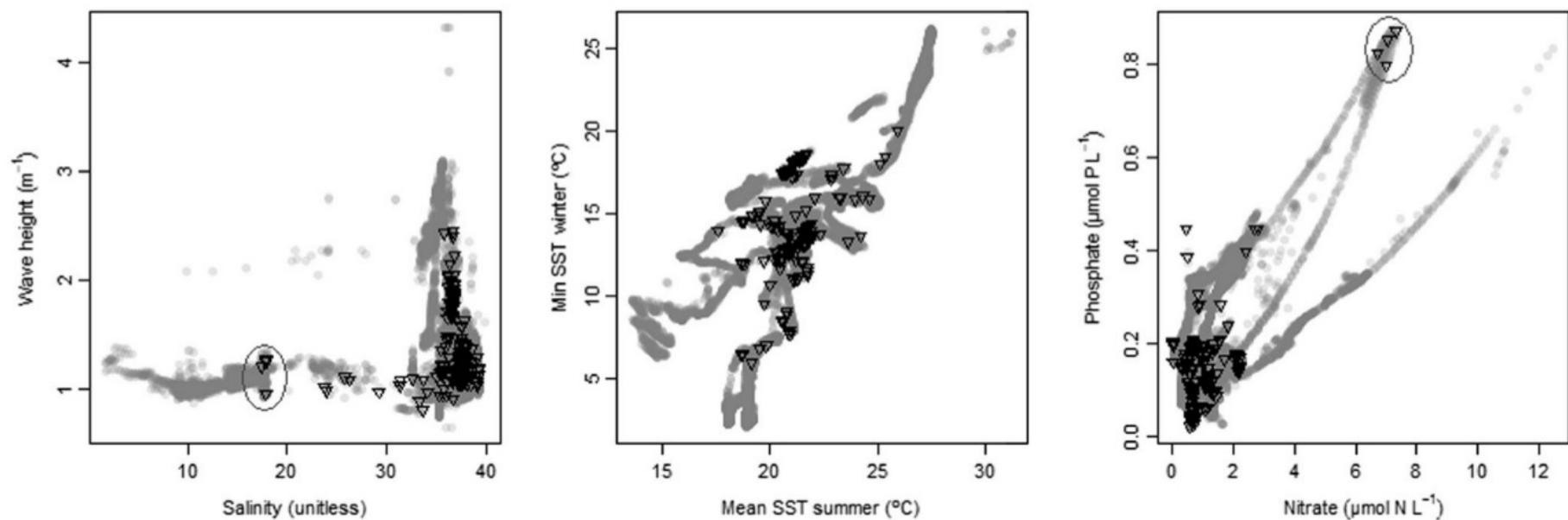
## Large-Scale Prediction of Seagrass Distribution Integrating Landscape Metrics and Environmental Factors: The Case of *Cymodocea nodosa* (Mediterranean–Atlantic)

Rosa M. Chefaoui<sup>1</sup> · Jorge Assis<sup>1</sup> · Carlos M. Duarte<sup>2</sup> · Ester A. Serrão<sup>1</sup>

- Identification of realised niche of a marine grass
- Biomod2.
- Multiple modelling methods: GLM, GAM, GBM, DA, RF, MARS.

# ECOLOGICAL NICHE IDENTIFICATION

Estuaries and Coasts



**Fig. 4** Distribution of values of environmental variables found among the most important for ensemble of generalized additive models (GAMs) and environmental niche factor analysis (ENFA). Grey dots represent all

the cells of the study area. Triangles correspond to presences of *C. nodosa*. Ellipse in the left includes Black Sea records, while ellipse in the right includes Mauritanian records (SST: sea surface temperature)

# ECOLOGICAL NICHE IDENTIFICATION

**Table 4** Mean validation scores of the 30 models obtained using each technique and the three sets of predictors

Model	AUC mean ( $\pm SD$ )	TSS mean ( $\pm SD$ )	Sensitivity ( $\pm SD$ )	Specificity ( $\pm SD$ )
All variables (ENV+MET)				
GLM	0.839 ( $\pm 0.008$ )	0.547 ( $\pm 0.008$ )	76.939 ( $\pm 4.377$ )	78.630 ( $\pm 4.167$ )
GBM	0.874 ( $\pm 0.013$ )	0.587 ( $\pm 0.025$ )	79.398 ( $\pm 4.417$ )	80.501 ( $\pm 3.458$ )
GAM	<b>0.957</b> ( $\pm 0.006$ )	<b>0.805</b> ( $\pm 0.021$ )	<b>91.858</b> ( $\pm 1.678$ )	<b>89.450</b> ( $\pm 1.237$ )
FDA	0.836 ( $\pm 0.016$ )	0.524 ( $\pm 0.028$ )	76.885 ( $\pm 5.719$ )	76.650 ( $\pm 5.395$ )
MARS	0.843 ( $\pm 0.019$ )	0.573 ( $\pm 0.032$ )	78.525 ( $\pm 3.821$ )	79.532 ( $\pm 4.589$ )
RF	0.891 ( $\pm 0.011$ )	0.624 ( $\pm 0.018$ )	80.819 ( $\pm 2.645$ )	82.596 ( $\pm 2.398$ )
Environmental (ENV)				
GLM	0.829 ( $\pm 0.009$ )	0.527 ( $\pm 0.022$ )	77.268 ( $\pm 4.529$ )	76.259 ( $\pm 3.896$ )
GBM	0.871 ( $\pm 0.013$ )	0.579 ( $\pm 0.026$ )	80.437 ( $\pm 4.699$ )	78.883 ( $\pm 3.823$ )
GAM	<b>0.928</b> ( $\pm 0.007$ )	<b>0.725</b> ( $\pm 0.019$ )	<b>89.399</b> ( $\pm 2.292$ )	<b>83.883</b> ( $\pm 1.399$ )
FDA	0.832 ( $\pm 0.020$ )	0.511 ( $\pm 0.032$ )	78.524 ( $\pm 5.519$ )	74.411 ( $\pm 4.899$ )
MARS	0.846 ( $\pm 0.013$ )	0.576 ( $\pm 0.033$ )	80.710 ( $\pm 2.914$ )	77.953 ( $\pm 2.601$ )
RF	0.889 ( $\pm 0.010$ )	0.626 ( $\pm 0.024$ )	81.257 ( $\pm 3.991$ )	82.046 ( $\pm 3.704$ )
Landscape metrics (MET)				
GLM	0.672 ( $\pm 0.013$ )	0.281 ( $\pm 0.025$ )	64.863 ( $\pm 7.923$ )	65.429 ( $\pm 6.598$ )
GBM	0.731 ( $\pm 0.015$ )	<b>0.395</b> ( $\pm 0.036$ )	59.344 ( $\pm 4.588$ )	<b>81.160</b> ( $\pm 4.194$ )
GAM	0.714 ( $\pm 0.011$ )	0.323 ( $\pm 0.020$ )	<b>68.852</b> ( $\pm 9.541$ )	64.774 ( $\pm 8.614$ )
FDA	0.714 ( $\pm 0.014$ )	0.361 ( $\pm 0.020$ )	66.885 ( $\pm 4.529$ )	70.401 ( $\pm 4.146$ )
MARS	0.710 ( $\pm 0.015$ )	0.357 ( $\pm 0.030$ )	65.737 ( $\pm 3.932$ )	70.968 ( $\pm 3.265$ )
RF	<b>0.744</b> ( $\pm 0.018$ )	<b>0.395</b> ( $\pm 0.037$ )	63.442 ( $\pm 7.089$ )	76.991 ( $\pm 7.370$ )

The best models are highlighted in bold

*SD* standard deviation, *GLM* generalized linear model, *GBM* generalized boosting model, *GAM* generalized additive model, *FDA* flexible discriminant analysis, *MARS* multiple adaptive regression splines, *RF* randomForest

# IDENTIFICATION OF CONTACT ZONES

Diversity and Distributions, (Diversity Distrib.) (2008) 14, 452–461

BIODIVERSITY  
RESEARCH



## GIS-based niche models identify environmental correlates sustaining a contact zone between three species of European vipers

F. Martínez-Freiría<sup>1\*</sup>, N. Sillero<sup>2,3</sup>, M. Lizana<sup>1</sup> and J. C. Brito<sup>2</sup>

- Identification of hybrid zones among three species of Iberian vipers.
- Maxent.

# IDENTIFICATION OF CONTACT ZONES

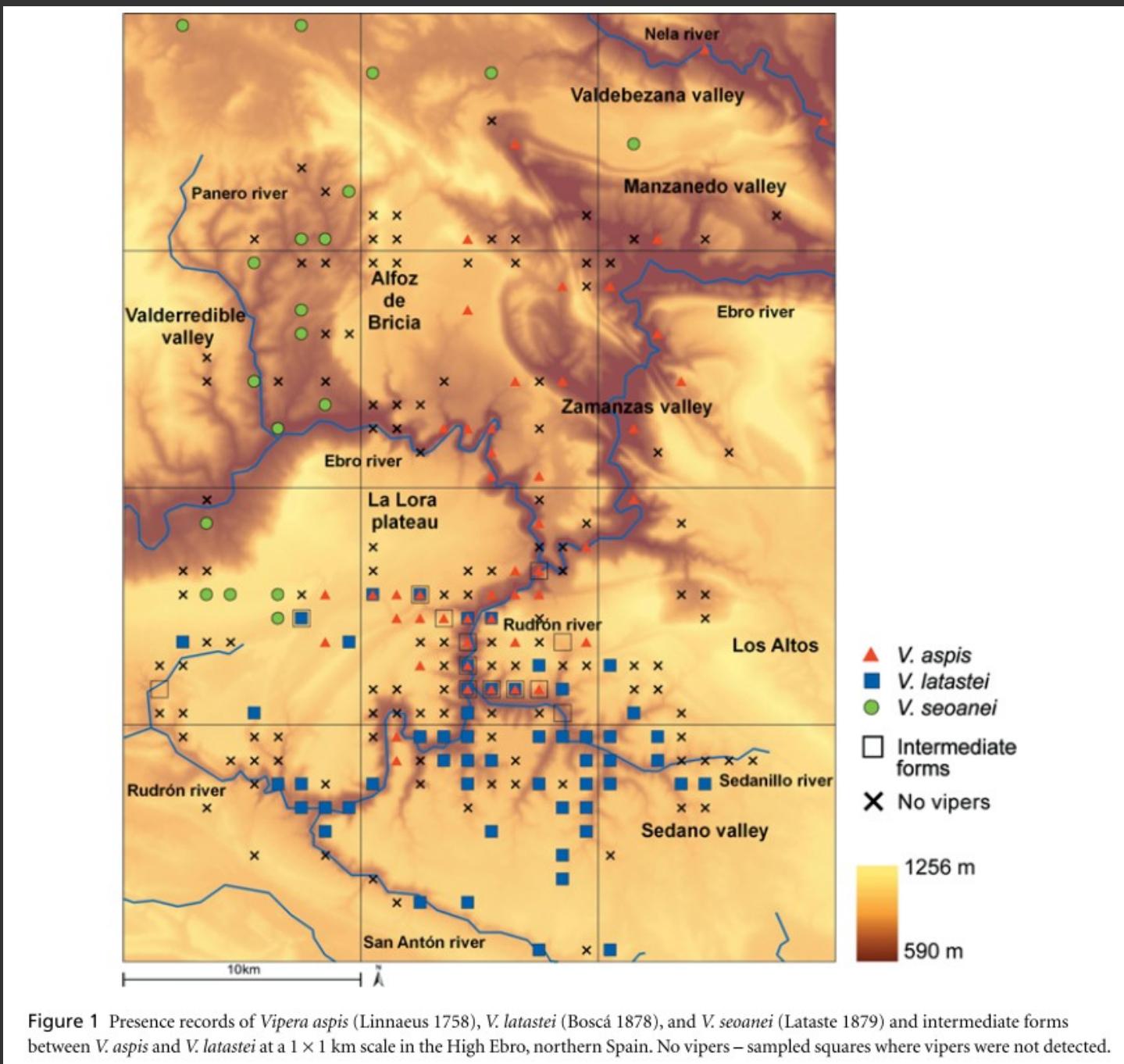
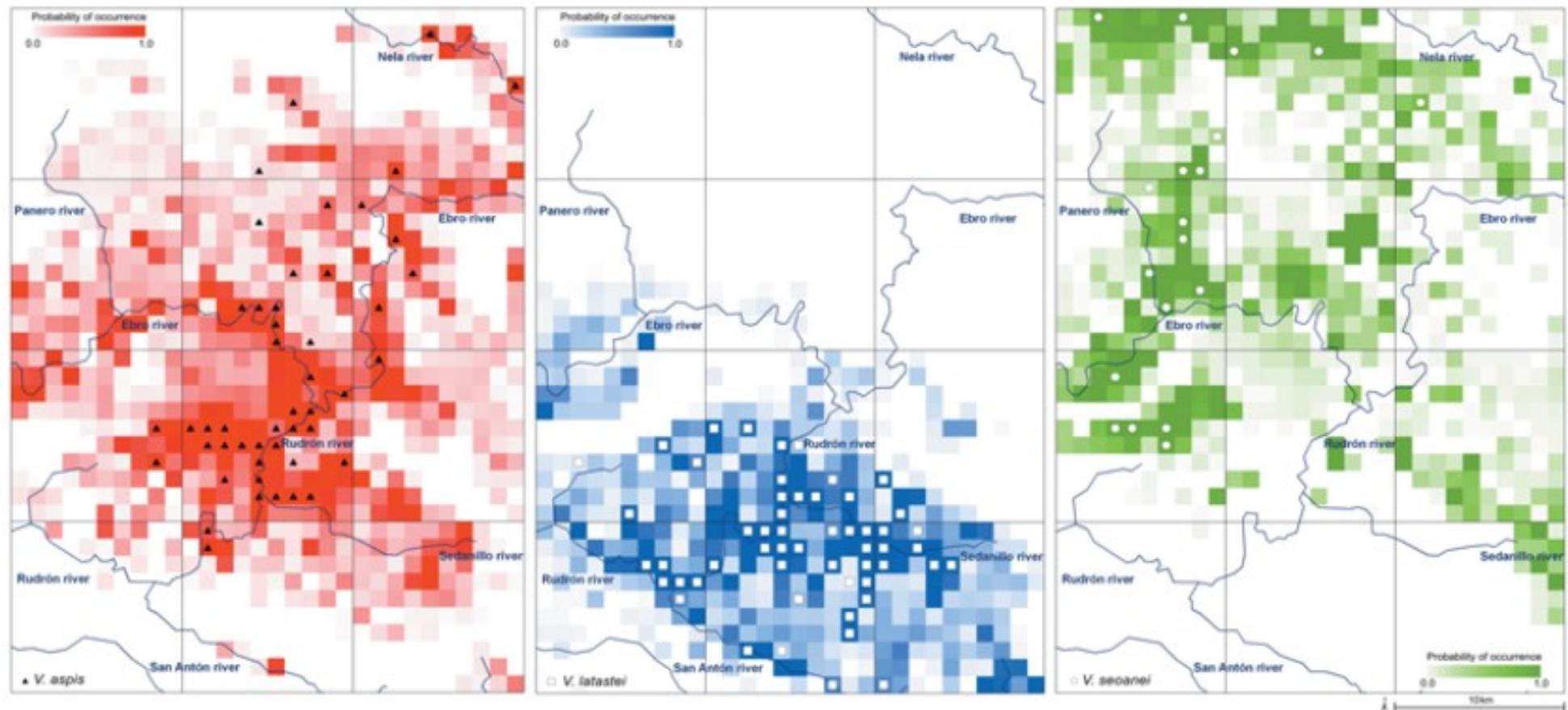


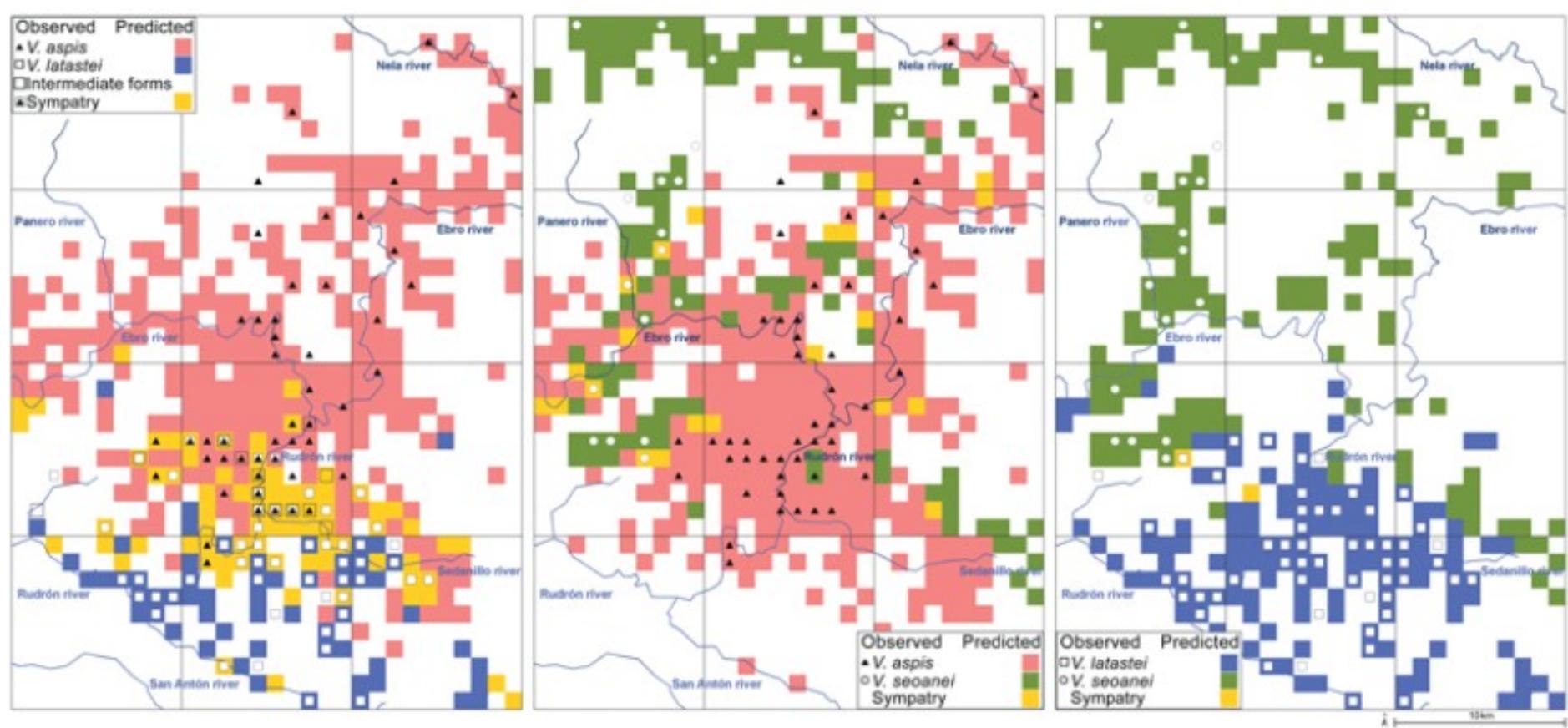
Figure 1 Presence records of *Vipera aspis* (Linnaeus 1758), *V. latastei* (Boscá 1878), and *V. seoanei* (Lataste 1879) and intermediate forms between *V. aspis* and *V. latastei* at a  $1 \times 1$  km scale in the High Ebro, northern Spain. No vipers – sampled squares where vipers were not detected.

# IDENTIFICATION OF CONTACT ZONES



**Figure 4** Probability density function with the likelihood of occurrence of *Vipera aspis*, *V. latastei*, and *V. seoanei* in the High Ebro, northern Spain, at a 1 × 1 km scale estimated by the ensemble of 10 Maximum Entropy models.

# IDENTIFICATION OF CONTACT ZONES



**Figure 5** Consensus forecast showing the area where at least half (the mean) of the 10 Maximum Entropy models predict the presence of vipers in the High Ebro, northern Spain, at a  $1 \times 1$  km scale. Areas of probable sympatry (*Vipera aspis*–*V. latastei*, *V. aspis*–*V. seoanei*, and *V. latastei*–*V. seoanei*) were estimated by the ensemble of 15–20 forecasts, i.e. sympatry areas ranged from a minimum of five forecasts for one species and 10 for the other to a maximum of 10 forecasts for each species.

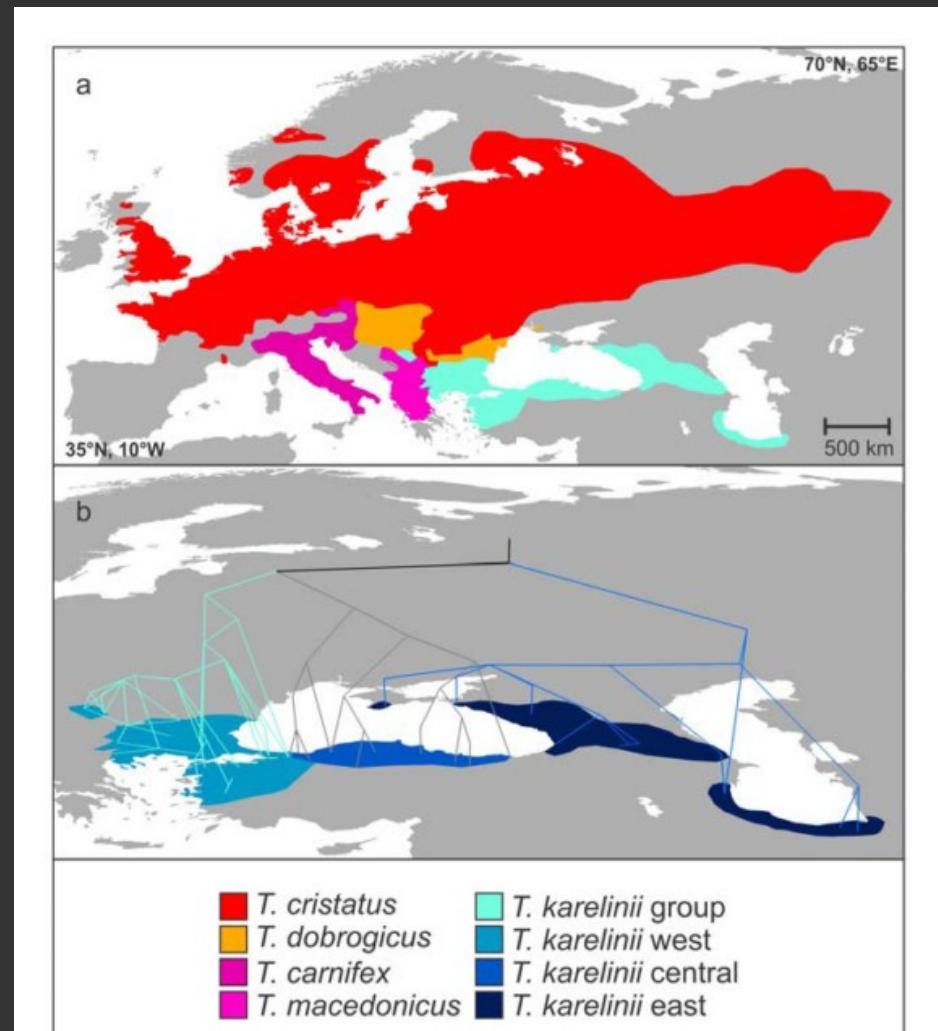
# Corresponding Mitochondrial DNA and Niche Divergence for Crested Newt Candidate Species

**Ben Wielstra<sup>1,2\*</sup>, Wouter Beukema<sup>2</sup>, Jan W. Arntzen<sup>1</sup>, Andrew K. Skidmore<sup>2</sup>, Albertus G. Toxopeus<sup>2</sup>, Niels Raes<sup>1</sup>**

**1** Naturalis Biodiversity Center, Leiden, The Netherlands, **2** University of Twente, Faculty of Geo-Information Science and Earth Observation – ITC, Enschede, The Netherlands

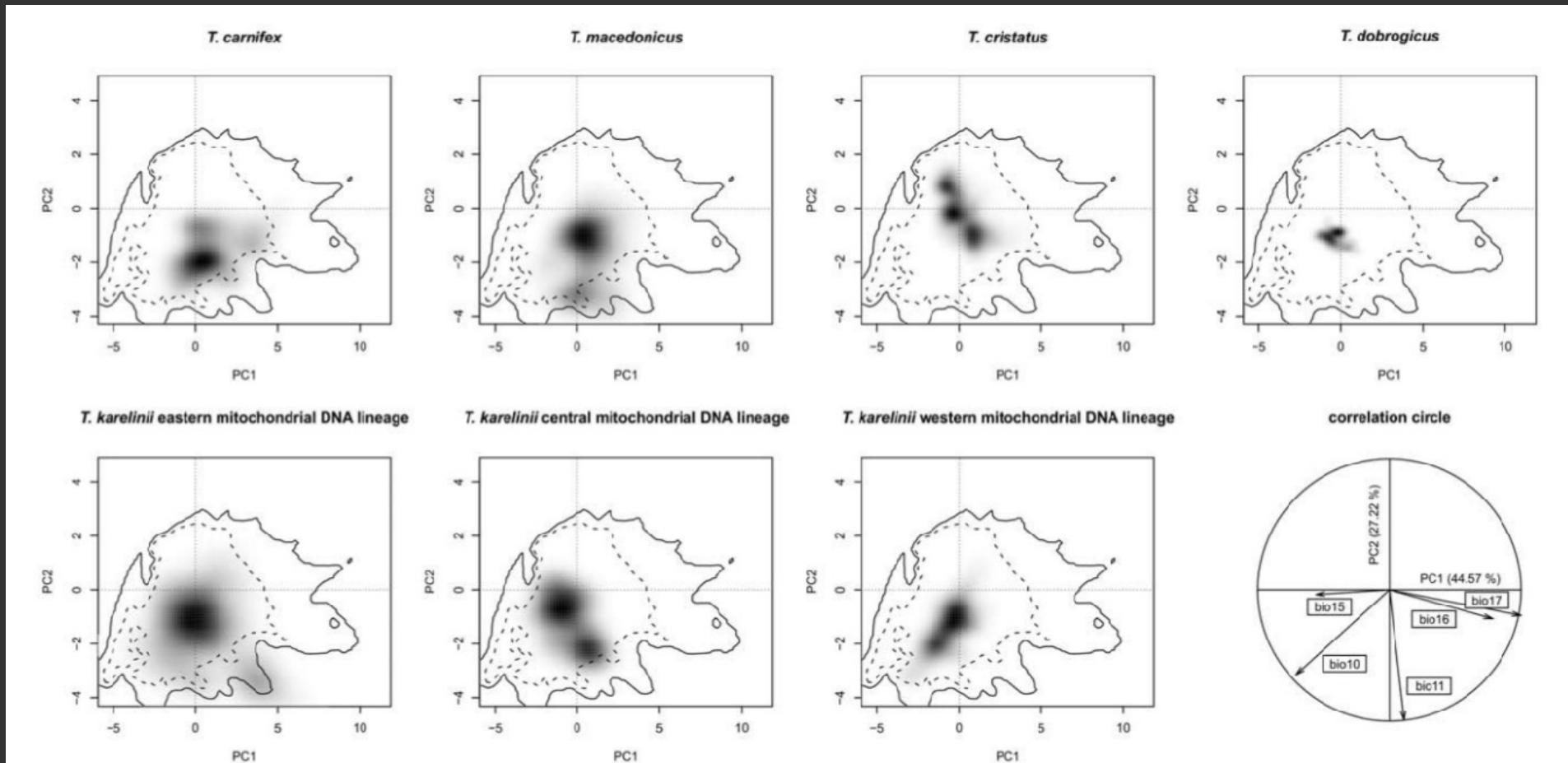
- To distinguish the niches of several species.
- Integration with genetic data.
- Ecological Niche Factor Analysis (ENFA).

# INTEGRATION WITH GENETICAL DATA



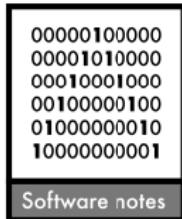
**Figure 1. The distribution of the crested newt *Triturus cristatus* superspecies.** Fig. 1a shows the distribution of the four recognized crested newt species and the *Triturus karelinskii* group. Fig. 1b shows the distribution of the distinct eastern, central and western mitochondrial DNA lineages comprising the *Triturus karelinskii* group (sensu [11]), with a phylogeny superimposed (created with GeoPhyloBuilder [31]).  
doi:10.1371/journal.pone.0046671.g001

# INTEGRATION WITH GENETICAL DATA



**Figure 2. Niches of the different crested newt (candidate) species based on PCA-env.** Each (candidate) species' niche is displayed on the same referential: a multi-dimensional scale represented by the first two axes of a principal component analyses summarizing the entire study area. Grey shading reflects the density of the occurrences of each (candidate) species in each cell. The solid and dashes contour lines illustrate 100% and 50% of the available environment in the study area. The correlation circle (bottom left) shows the contribution of the climatic variables on the two axes of the PCA and the percentage of inertia explained by the two axes.  
doi:10.1371/journal.pone.0046671.g002

Comparison of species' niches (Broennimann et al 2012)



Software notes

**Ecography 33: 607–611, 2010**

doi: 10.1111/j.1600-0587.2009.06142.x

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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**

*D. L. Warren (dan.l.warren@gmail.com) and M. Turelli, Dept of Evolution and Ecology, Univ. of California, Davis, CA 95616, USA.  
– R. E. Glor, Dept of Biology, Univ. of Rochester, Rochester, NY 14627, USA.*

- Description of ENMTools software.
- Tools for statistical comparison of species' niches.
- Software for Windows OS.
- For Maxent models.

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

## Hellinger's distance I

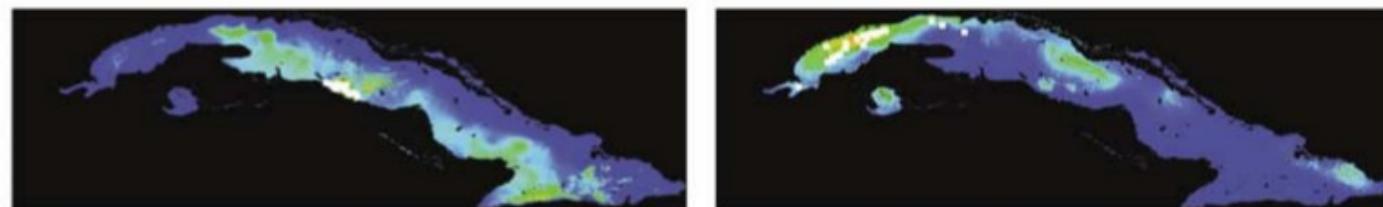
$$D(p_X, p_Y) = 1 - \frac{1}{2} \sum_i |p_{X,i} - p_{Y,i}|,$$

## Schoener's D index

- 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.

# COMPARING NICHE MODELS

A

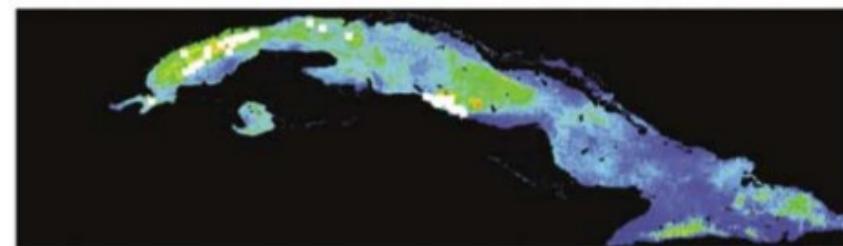


*Anolis ahli*

*Anolis allogus (west)*

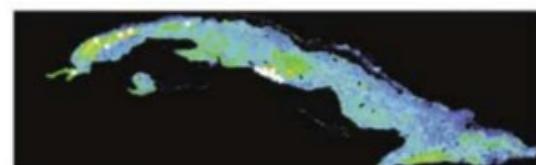
Niche Similarity:  $I = 0.47, D = 0.19$

B

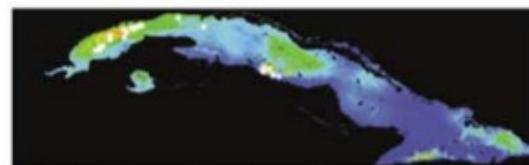


Pooled Sample from *A. ahli* + *A. allogus (west)*

C

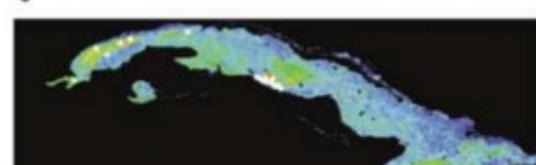


Pseudoreplicate 1A

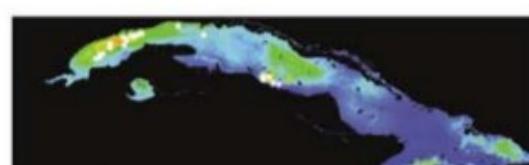


Pseudoreplicate 1B

$I = 0.87, D = 0.76$



Pseudoreplicate 1000A



Pseudoreplicate 1000B

$I = 0.91, D = 0.84$

# COMPARING NICHE MODELS

D

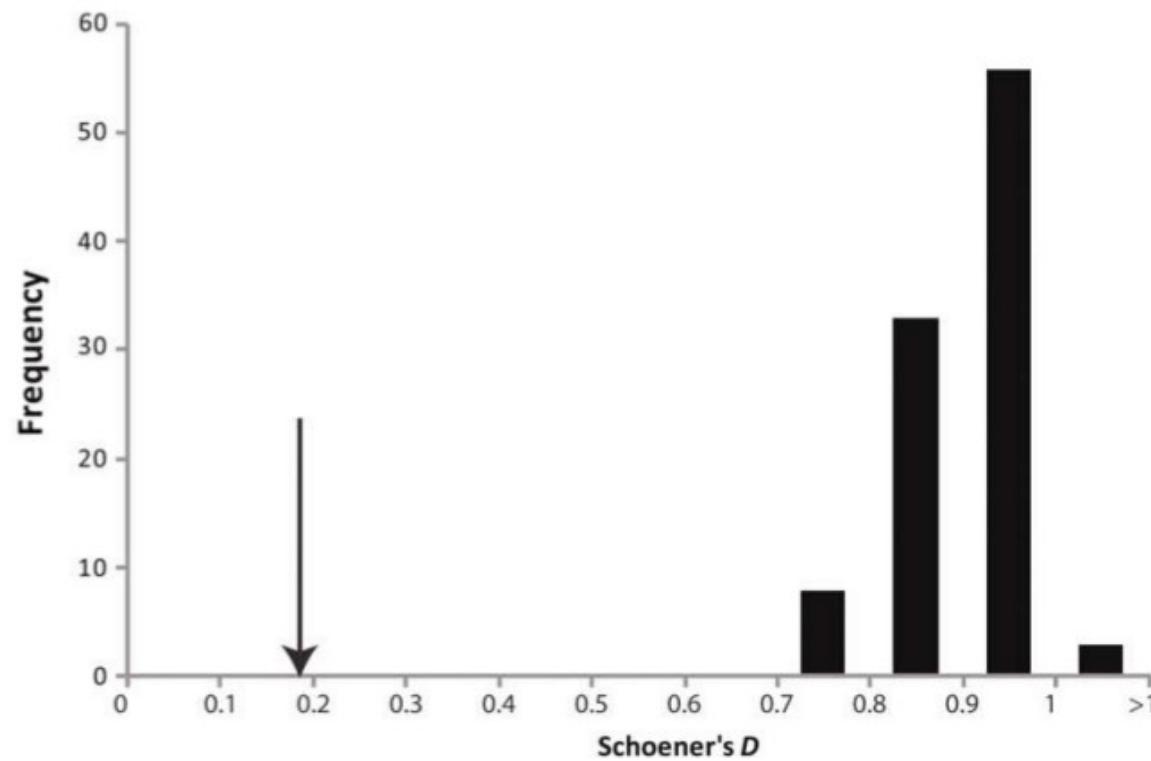
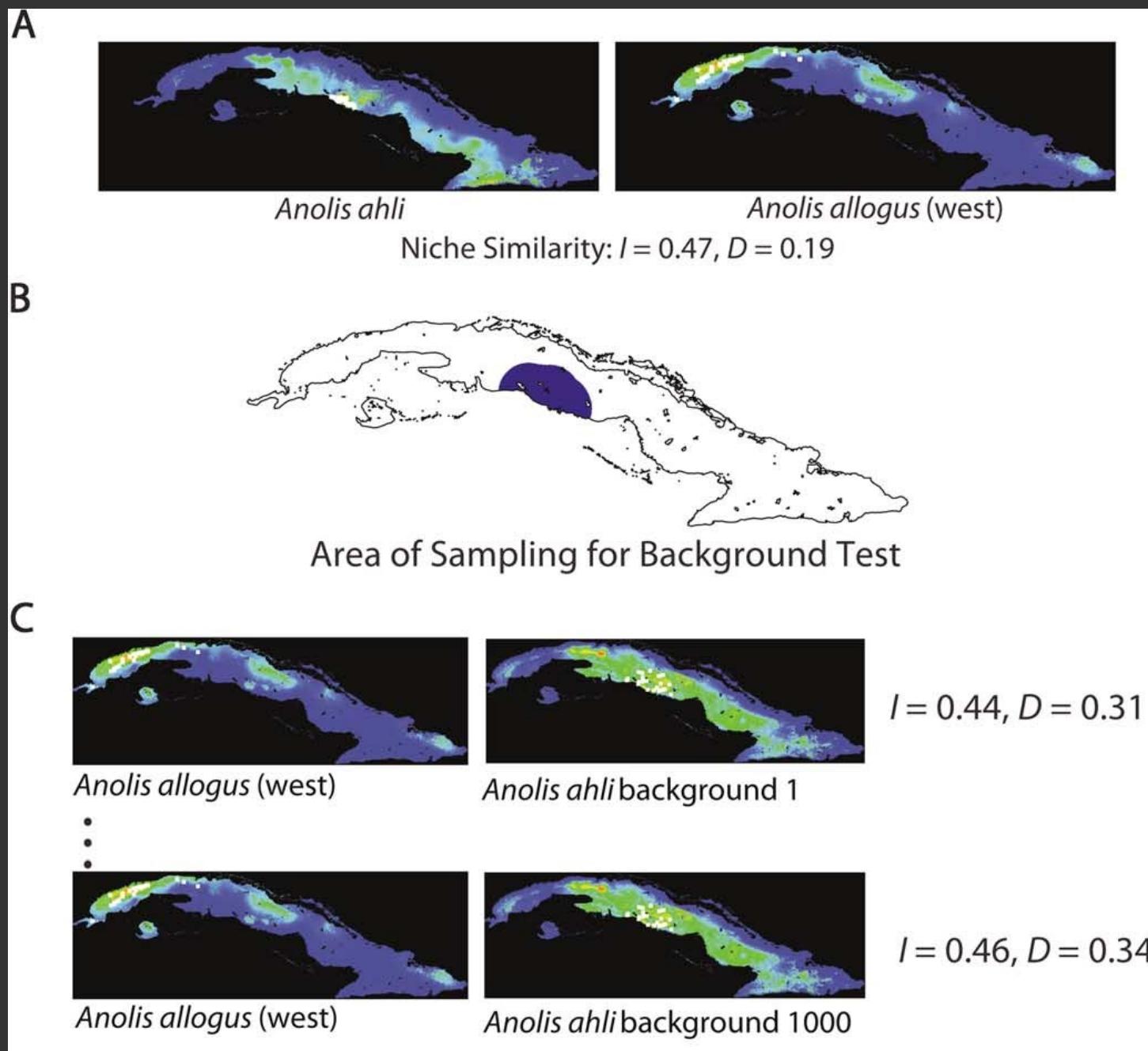


Figure 1. Sampling for identity test. In the identity test, the similarity score for ENMs built from known occurrences of two species (panel A) is compared to the distribution of similarity scores between ENMs built from occurrences drawn randomly from the pooled occurrences for the two species (panels B–D). The entirety of Cuba was treated as the study area for ENM construction. This example compares the environmental niches of *Anolis allogus* (west) and *Anolis ahli*. As seen in panel D, the similarity score for ENMs built for the actual occurrences of the two species (black arrow) is much lower than expected based on the null hypothesis of niche equivalency, indicating that the two species' environmental niches are not equivalent.

- 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.

# COMPARING NICHE MODELS



# COMPARING NICHE MODELS

D

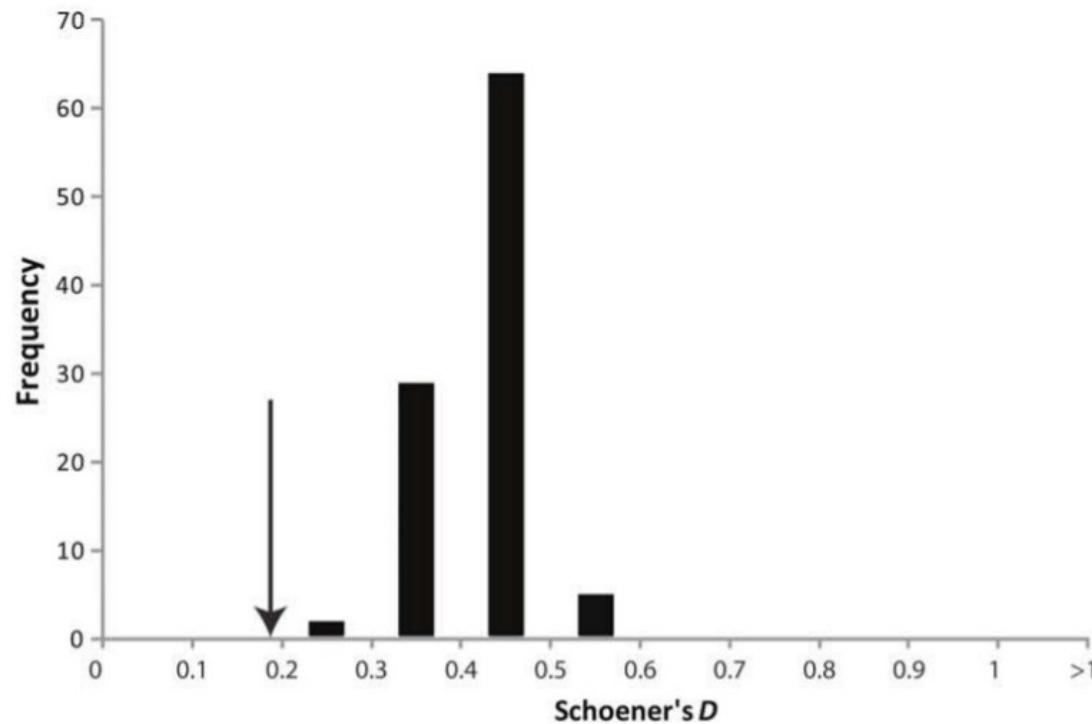


Figure 2. Sampling for background test. In the background test, the similarity score for ENMs built from known occurrences of two species (panel A) is compared to similarity scores for ENMs constructed using points drawn at random from the region defined as “environmental background” for one of the species (panels B–D). In this example, occurrence points for *Anolis allogus* (west) are being compared to points drawn at random from the environmental background that has been chosen for *Anolis ahli*. In this case, the background (blue region, panel B) was chosen arbitrarily to be all points within 0.5 decimal degrees of a known occurrence of *A. ahli*. As seen in panel D, the observed overlap between the two species (black arrow) is lower than expected under the null hypothesis, indicating that the two species are more divergent than expected based on the habitat available to *A. ahli*.

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



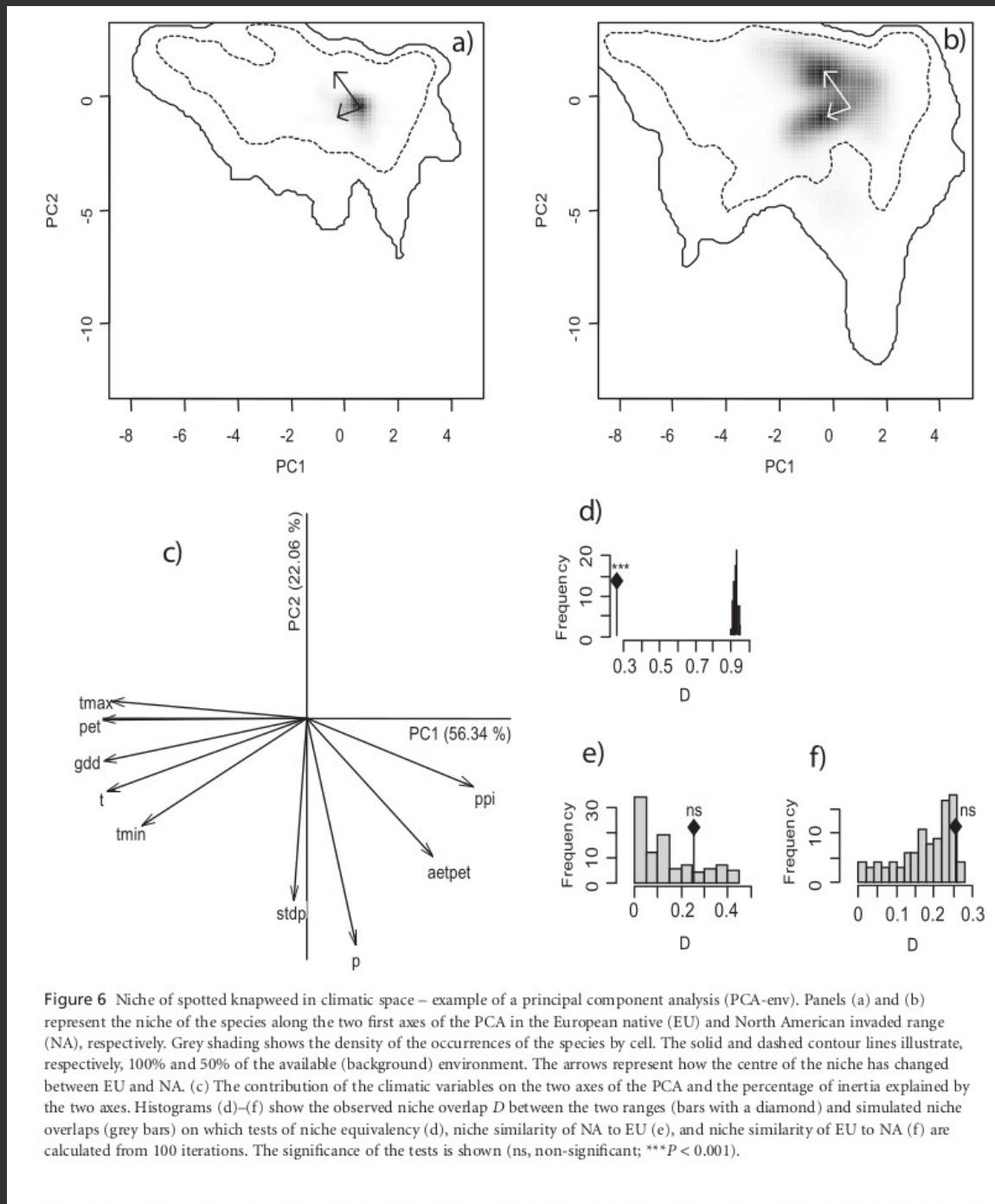
RESEARCH  
PAPER

## Measuring ecological niche overlap from occurrence and spatial environmental data

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

- Tools for statistical comparison of species' niches.
- Based on ENMTools indexes.
- Script for R.
- For Biomod and Maxent models.
- Principal Component Analysis.
- Ecological Niche Factor Analysis.
- Linear Discriminant Analysis.
- Multidimensional Scaling Analysis.

# COMPARING NICHE MODELS



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Software notes

**Ecography 40: 774–787, 2017**

doi: 10.1111/ecog.02671

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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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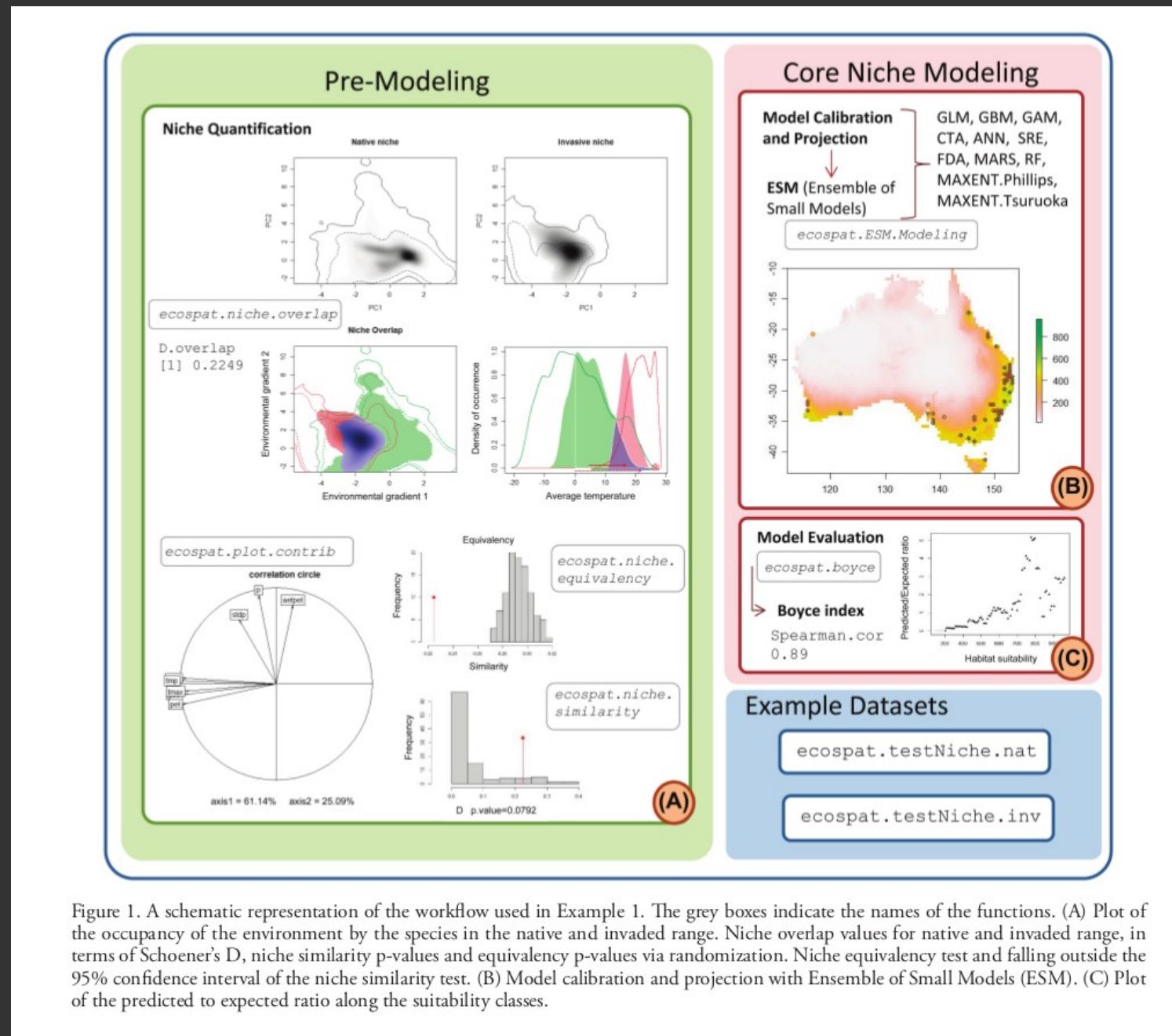


Figure 1. A schematic representation of the workflow used in Example 1. The grey boxes indicate the names of the functions. (A) Plot of the occupancy of the environment by the species in the native and invaded range. Niche overlap values for native and invaded range, in terms of Schoener's D, niche similarity p-values and equivalency p-values via randomization. Niche equivalency test and falling outside the 95% confidence interval of the niche similarity test. (B) Model calibration and projection with Ensemble of Small Models (ESM). (C) Plot of the predicted to expected ratio along the suitability classes.

# R PACKAGE ECOSPAT

CRAN - Package ecospat - Mozilla Firefox

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

ecospat: Spatial Ecology Miscellaneous Methods

Collection 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 (DÉE) & 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.dcola 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](#)

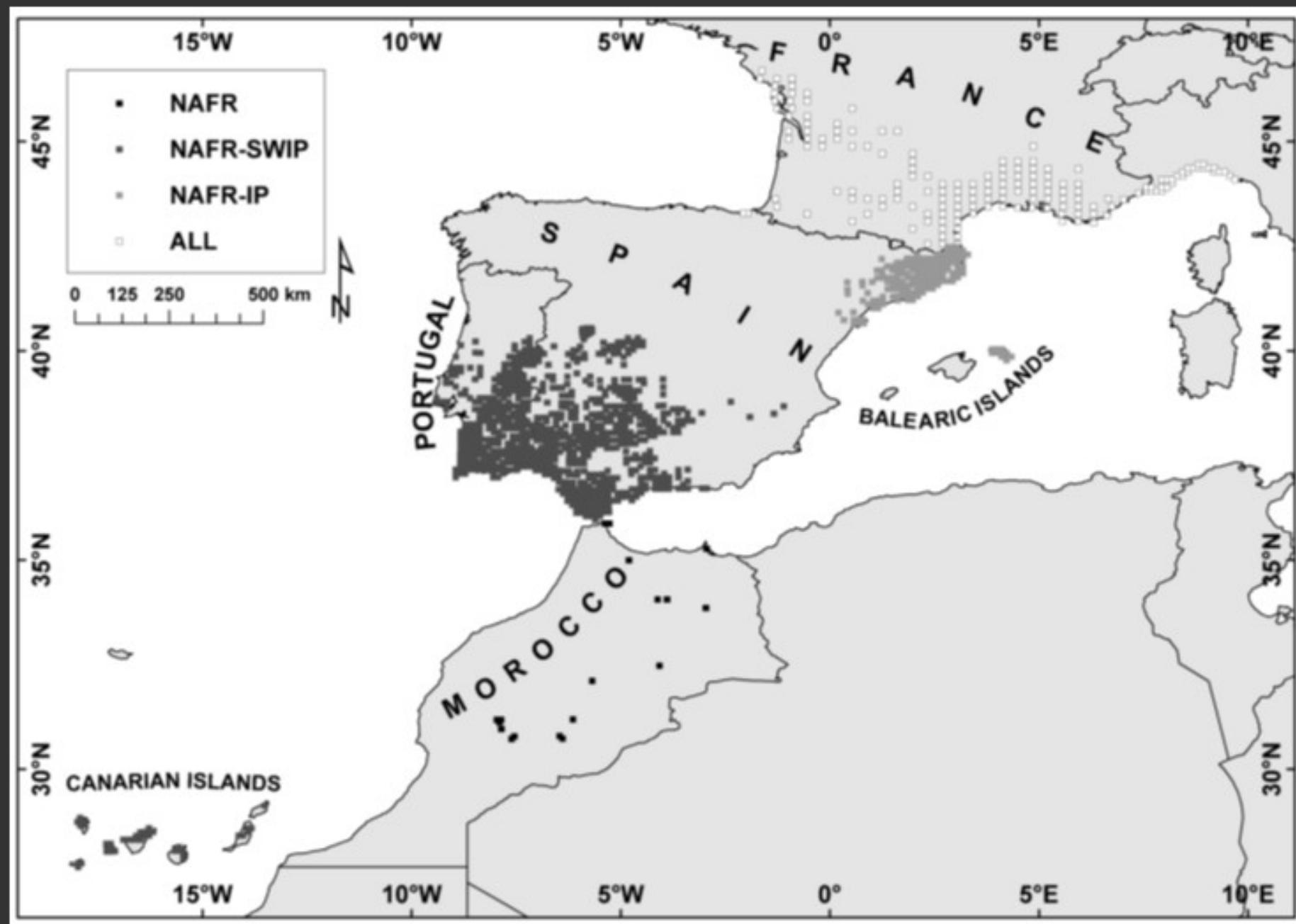
Amphibia-Reptilia 31 (2010): 37-50

## Modelling suitable areas for *Hyla meridionalis* under current and future hypothetical expansion scenarios

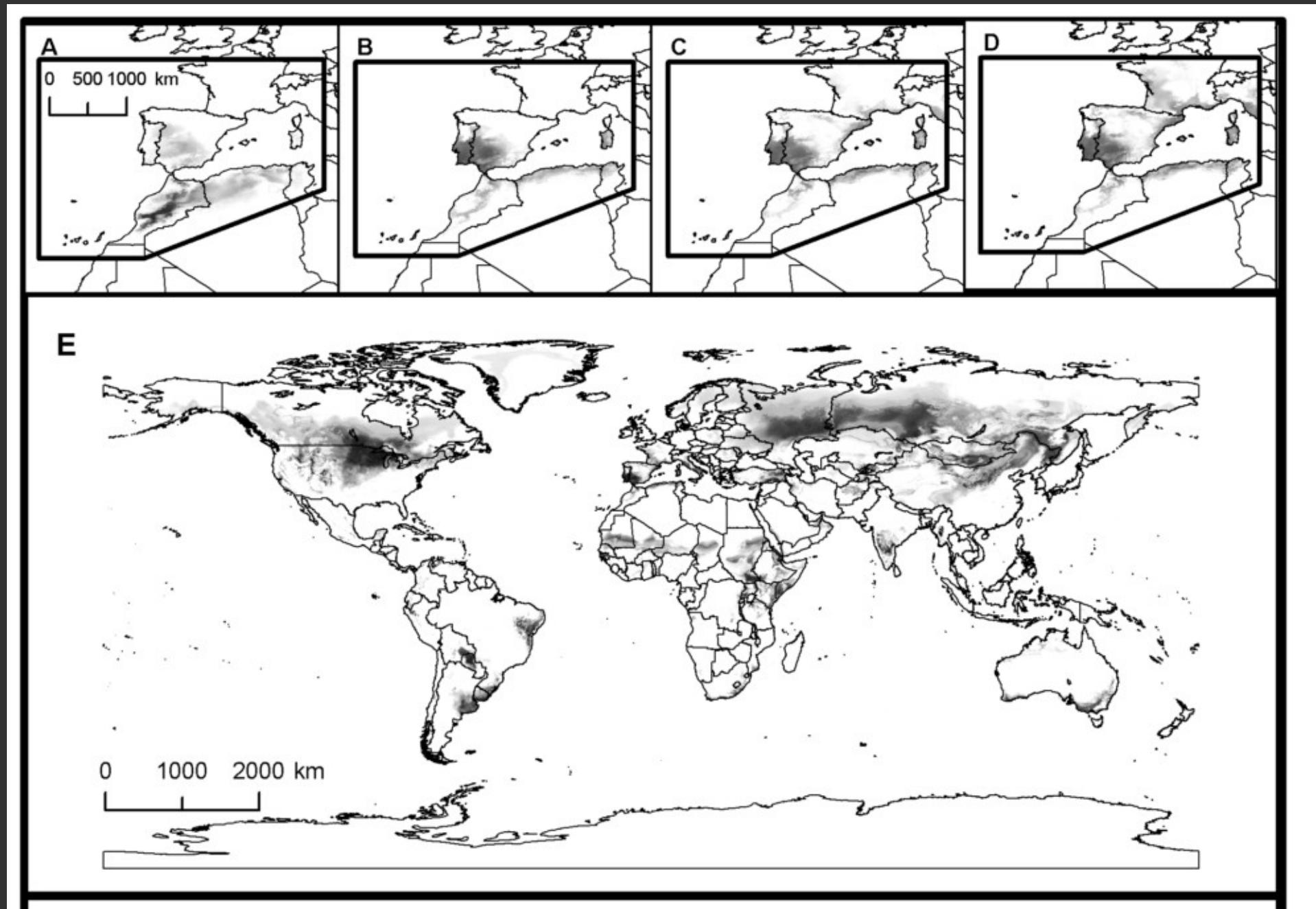
Neftalí Sillero

- To determine if the species is in expansion.
- Modelling the possible expansion process.
- Maxent.

# SPECIES EXPANSIONS

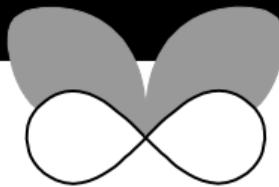


# SPECIES EXPANSIONS



Diversity and Distributions, (Diversity Distrib.) (2007) 13, 476–485

BIODIVERSITY  
RESEARCH

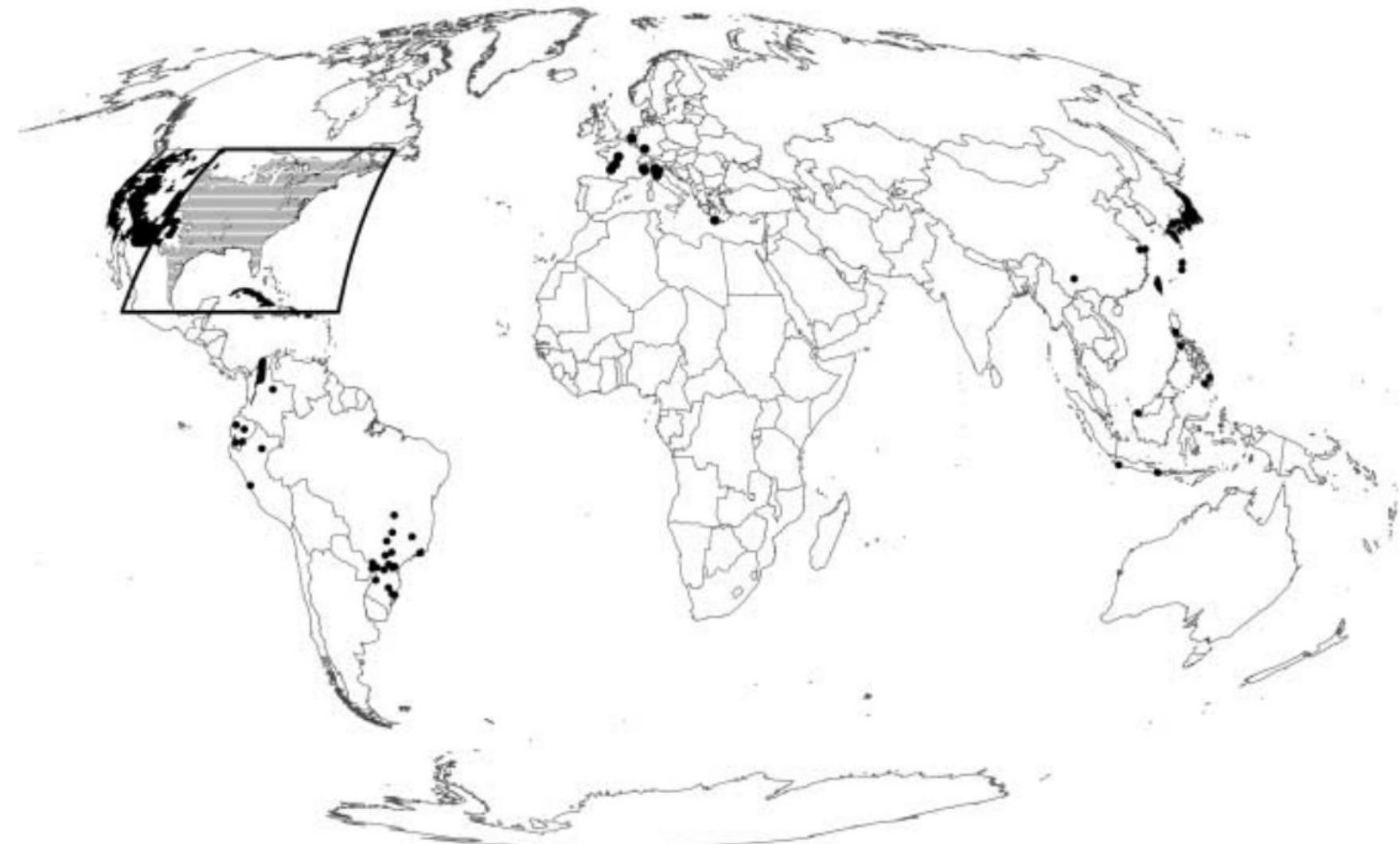


## Prediction and validation of the potential global distribution of a problematic alien invasive species — the American bullfrog

Gentile Francesco Ficetola<sup>1\*</sup>, Wilfried Thuiller<sup>2</sup> and Claude Miaud<sup>1</sup>

- To build a model predicting which areas are more susceptible to a successful invasion of bullfrog at the global scale.
- To evaluate if the model correctly predicts the outcome of introductions, by using data on historical introduction attempts performed in Europe.
- American Bullfrog: *Rana catesbeiana*
- Maxent and Logistic Regression
- Modelling the native distribution.
- Projection to the invaded region.

# SPECIES INVASIONS



**Figure 1** Distribution of native (barred) and non-native (black) populations of the American bullfrog. The inset represents the area of calibration of the suitability model. Distribution maps are from the Global Amphibian Assessment (Santos-Barrera *et al.*, 2004).

# SPECIES INVASIONS

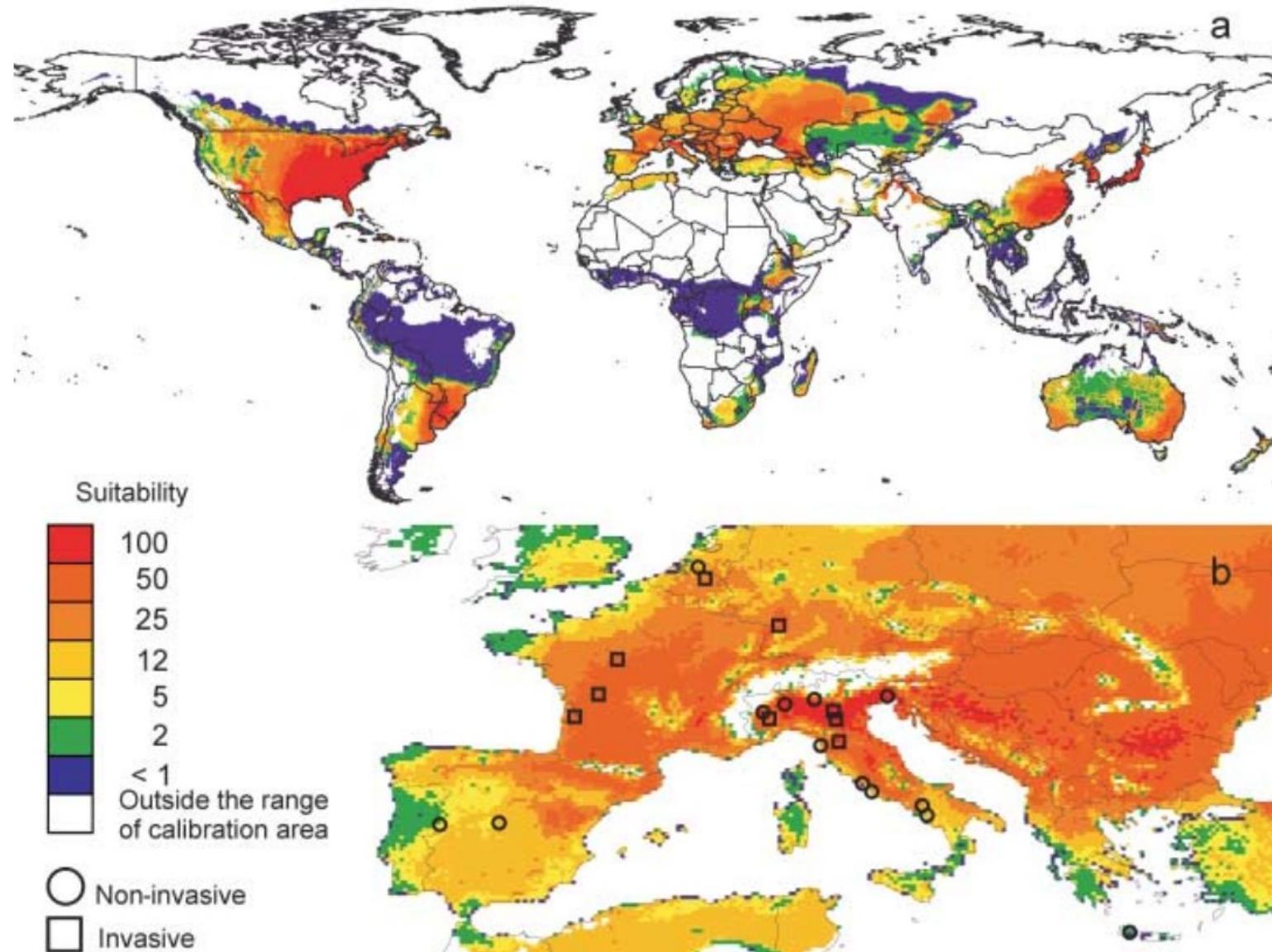


Figure 3 (a) Worldwide projection for the environmental suitability for bullfrogs. (b) Projected suitability in the areas of Europe where bullfrog introductions occurred. Squares: invasive populations; circles: non-invasive populations.

# SPECIES INVASIONS

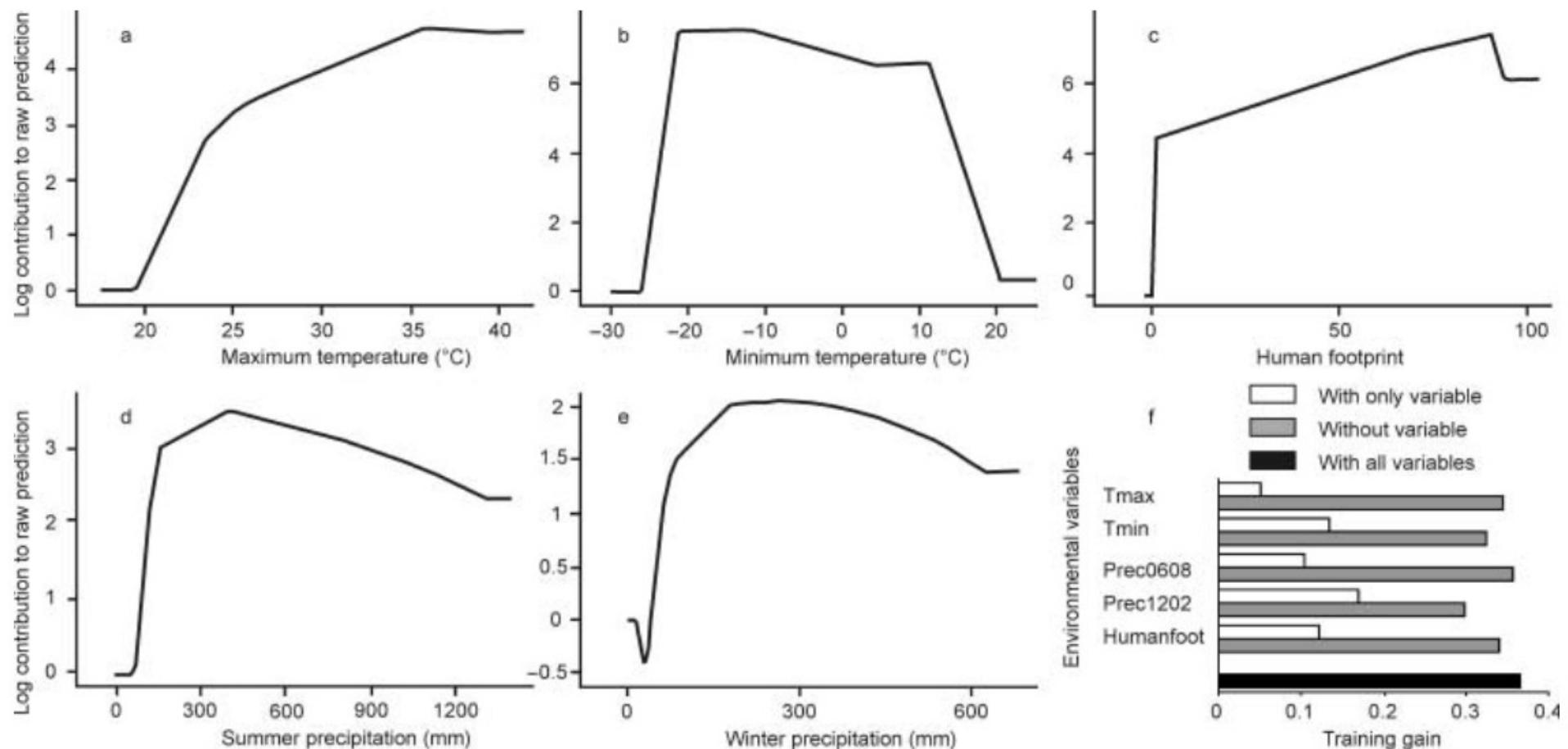


Figure 2 Results of environmental suitability model. (a–e) Relationships between environmental features and suitability for bullfrogs. (f) Results of jack-knife evaluation of relative importance of predictors.

## RESEARCH ARTICLE

# Snakes on the Balearic Islands: An Invasion Tale with Implications for Native Biodiversity Conservation

Iolanda Silva-Rocha<sup>1</sup>\*, Daniele Salvi<sup>1</sup>\*, Neftalí Sillero<sup>2</sup>, Jose A. Mateo<sup>3</sup>, Miguel A. Carretero<sup>1</sup>

**1** CIBIO Research Centre in Biodiversity and Genetic Resources, InBIO, Universidade do Porto, Vairão, Vila do Conde, Portugal, **2** CICGE, Centro de Investigação em Ciências Geo-Espaciais, Faculdade de Ciências da Universidade do Porto, Observatório Astronómico Prof. Manuel de Barros, Vila Nova de Gaia, Portugal, **3** Servei de Protecció d'Espècies, Govern de les Illes Balears, Palma de Mallorca, Spain

• These authors contributed equally to this work.

\* [danielesalvi.bio@gmail.com](mailto:danielesalvi.bio@gmail.com)

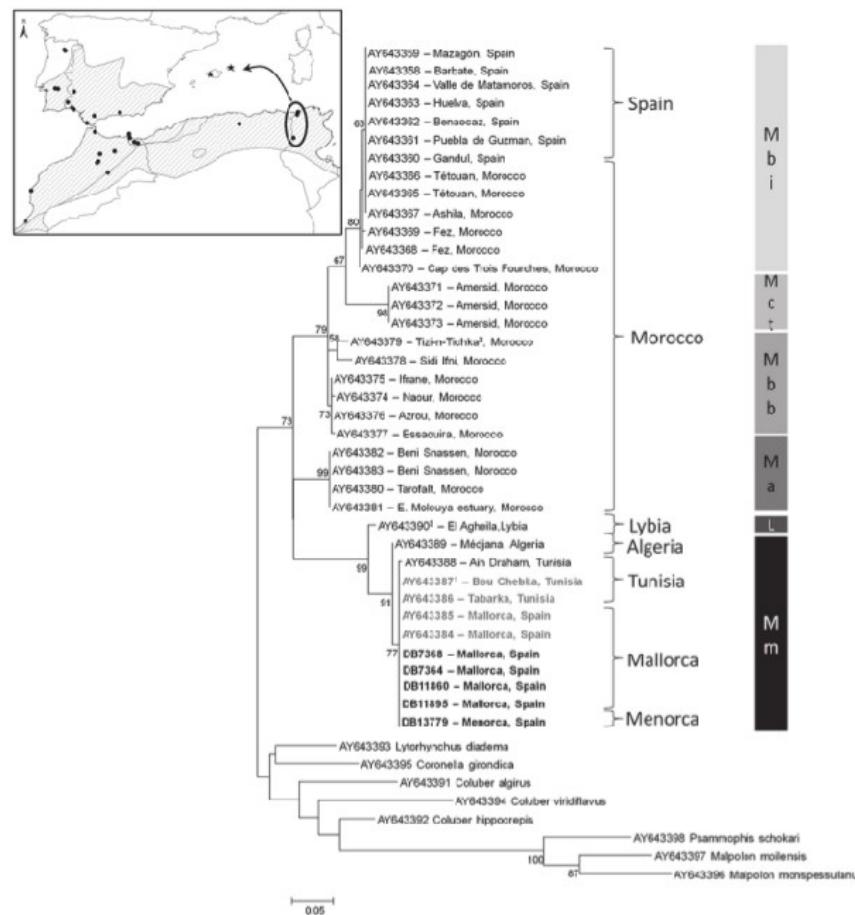


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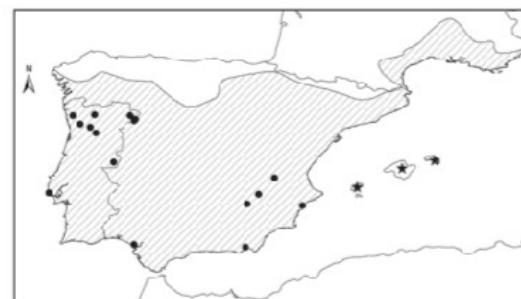
- Four species of snakes in Balearic islands
- Maxent and genetic analyses
- Modelling the native distribution.
- Projection to the invaded region and future climate change scenarios.

# SPECIES INVASIONS AND PHYLOGEOGRAPHY

C *Macroprotodon sp.*



D *Rhinechis scalaris*



**Fig 2. Results from genetic analysis and geographic origin of the introduced populations.** Numbers on branches indicate ML bootstrap values (BP) over 1000 replicates (BP<50 are not reported). (2A): ML tree based on the combined 12S+cytb dataset depicting the relationships between haplotypes of the native range of *Hemorrhois hippocrepis* from Carranza et al. [23] and those from the introduced populations from Mallorca and Ibiza Islands. MSA: Morocco+Iberia+Algeria; T: Tunisia. (2B) ML tree based on the cytb dataset depicting the relationships between haplotypes of native range of *Malpolon*

# SPECIES INVASIONS AND PHYLOGEOGRAPHY

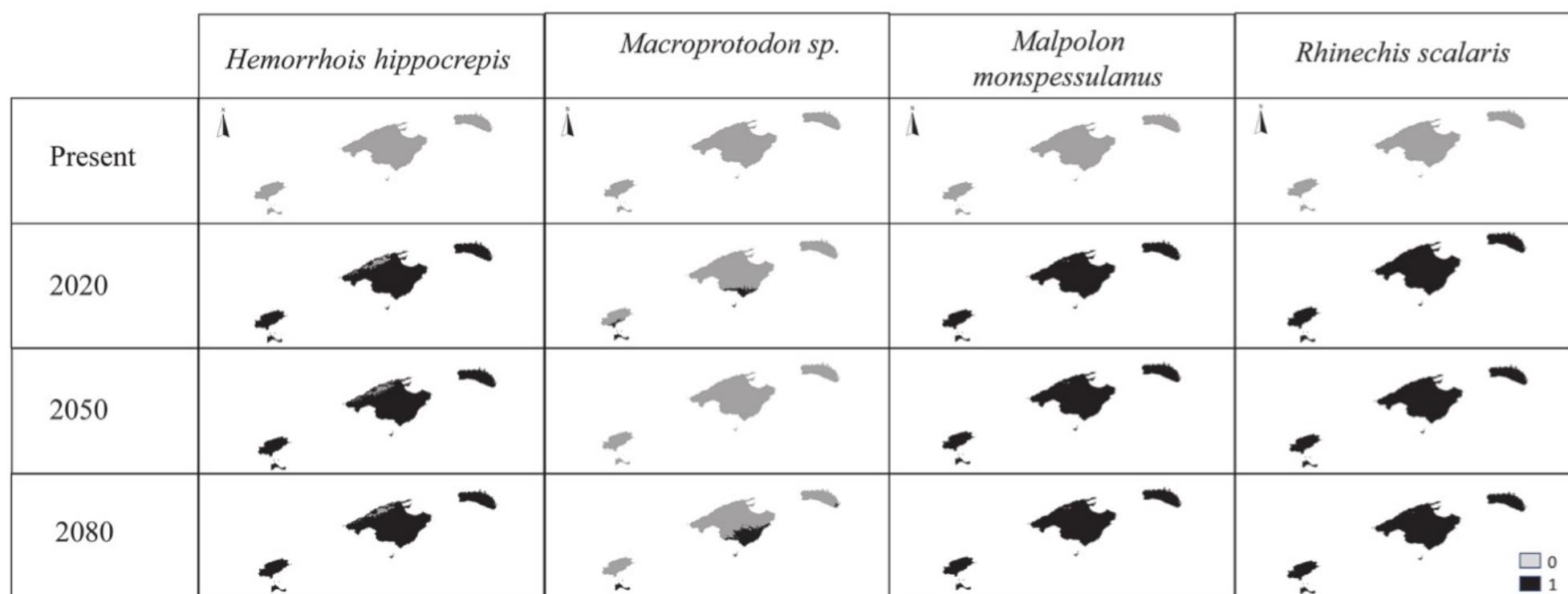
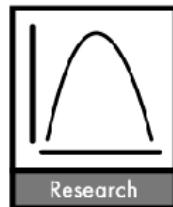


Fig 3. Habitat suitability models for the present and for the future (2020, 2050 and 2080) of all the study species.

doi:10.1371/journal.pone.0121026.g003



**Ecography 32: 34–45, 2009**

doi: 10.1111/j.1600-0587.2009.05789.x

© 2009 The Authors. Journal compilation © 2009 Ecography

Subject Editor: Jens-Christian Svenning. Accepted 6 February 2009

## Predicting future distributions of mountain plants under climate change: does dispersal capacity matter?

Robin Engler\*, Christophe F. Randin\*, Pascal Vittoz, Thomas Czáká, Martin Beniston,  
Niklaus E. Zimmermann and Antoine Guisan

- Inclusion of dispersion hypotheses in ENMs.
- GLM, GAM, Gradient Boosting Machine and Random Forest
- Dispersion is modelled with MigClim software.
- Four dispersal scenarios (unlimited dispersal, no dispersal, realistic dispersal, and realistic dispersal with long-distance dispersal events).
- Four climate change scenarios.
- Models with unlimited dispersion were similar to real dispersion.

# DISPERSION HYPOTHESES

Table 2. Parameters used in the MigClim model for each dispersal category (1–7).

	Dispersal categories						
	1	2	3	4	5	6	7
Max disp. dist.	1 m	5 m	15 m	150 m	500 m	1500 m	5000 m
MaxLDD disp. dist.	1 km	1 km	1 km	1 km	5 km	5 km	10 km
LDD frequency*	0.002	0.002	0.0004	0.01	0.04	0.04	0.04
Disp. event freq.**	5 yr	5 yr	1 yr	1 yr	1 yr	1 yr	1 yr
Generation time	Parameter set individually for each species (Supplementary material Appendix S3)						
Resilience time	Parameter set individually for each species (Supplementary material Appendix S3)						
Barriers	Forests or nothing						
Filters	Urban areas, lakes, rivers, glaciers+grassland and/or rock and/or scree						
No. of species	53	10	55	21	24	83	41
Pixel size	5 m	5 m	5 m	25 m	50 m	50 m	50 m
No. of pixels	30 000 000		4 800 000		1 200 000		

\*Variations in LDD event frequencies reflect the corrections applied for pixel size and dispersal event frequency to maintain the 0.01 frequency assigned to 25 m pixels constant over all categories.

\*\*Dispersal event frequency indicates the time between two successive dispersal events.

- MigClim uses several dispersal parameters.

$$\text{Migration rate index} = \log_{10} \left( \frac{\text{MaxDispersal}_{99\% \text{ of Seeds}}}{\text{Generation Time}} \right) + 1$$

# DISPERSION HYPOTHESES

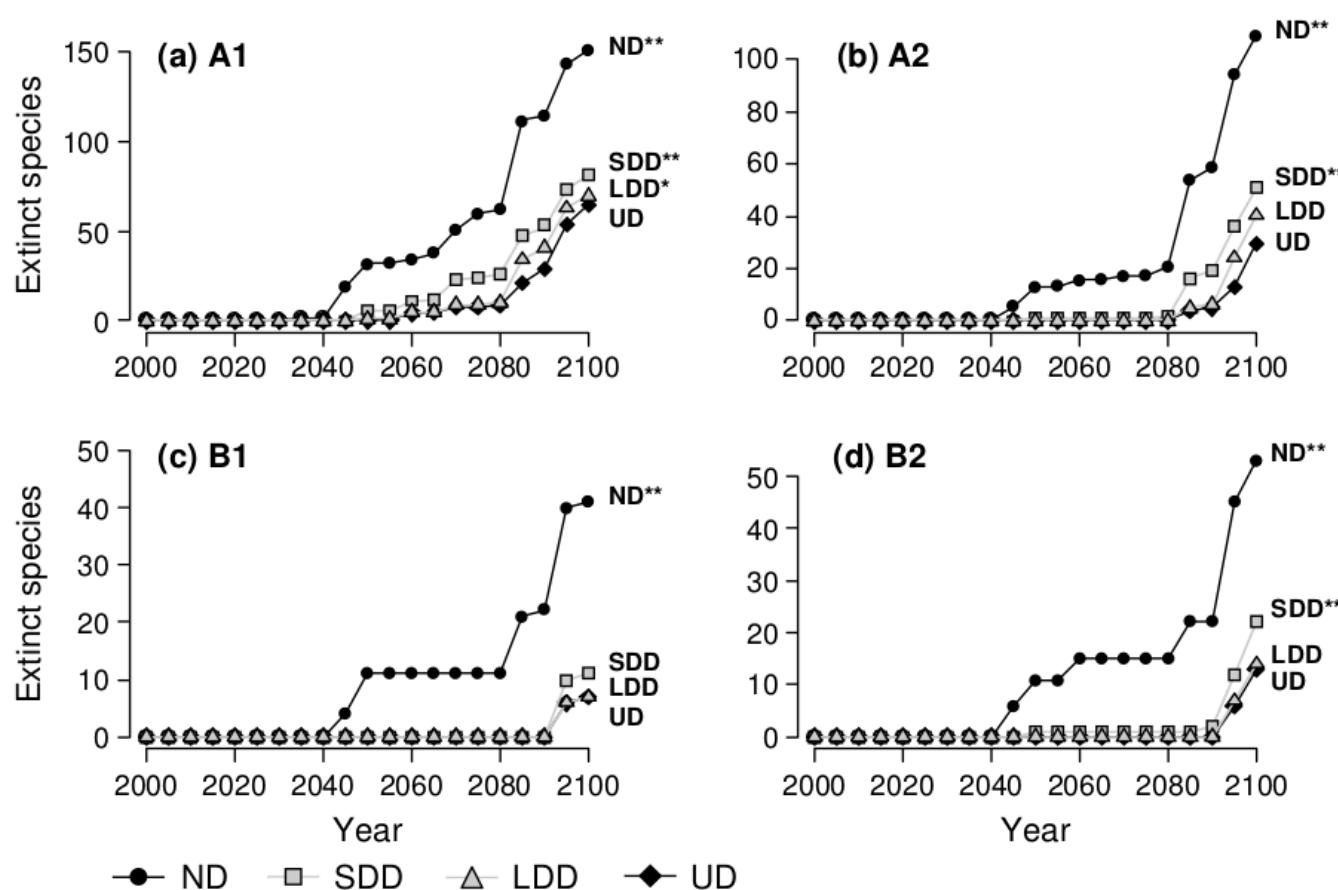


Figure 4. Cumulative number of species going extinct from 2000 to 2100 under the four climate change and four dispersal scenarios. \*\* = series is significantly different from the series immediately below with  $p < 0.01$ , \* = series is significantly different from the series immediately below with  $p < 0.05$ . Abbreviations as in Fig. 2.

00000100000  
00001010000  
00010001000  
00100000100  
01000000010  
10000000001

Software notes

**Ecography 35: 872–878, 2012**

doi: 10.1111/j.1600-0587.2012.07608.x

© 2012 The Authors. Ecography © 2012 Nordic Society Oikos

Subject Editor: Thiago Rangel. Accepted 11 May 2012

## The MIGCLIM R package – seamless integration of dispersal constraints into projections of species distribution models

**Robin Engler, Wim Hordijk and Antoine Guisan**

*R. Engler (robin.engler@gmail.com), W. Hordijk and A. Guisan, Dept of Ecology and Evolution, Univ. of Lausanne, CH-1015 Lausanne, Switzerland.*

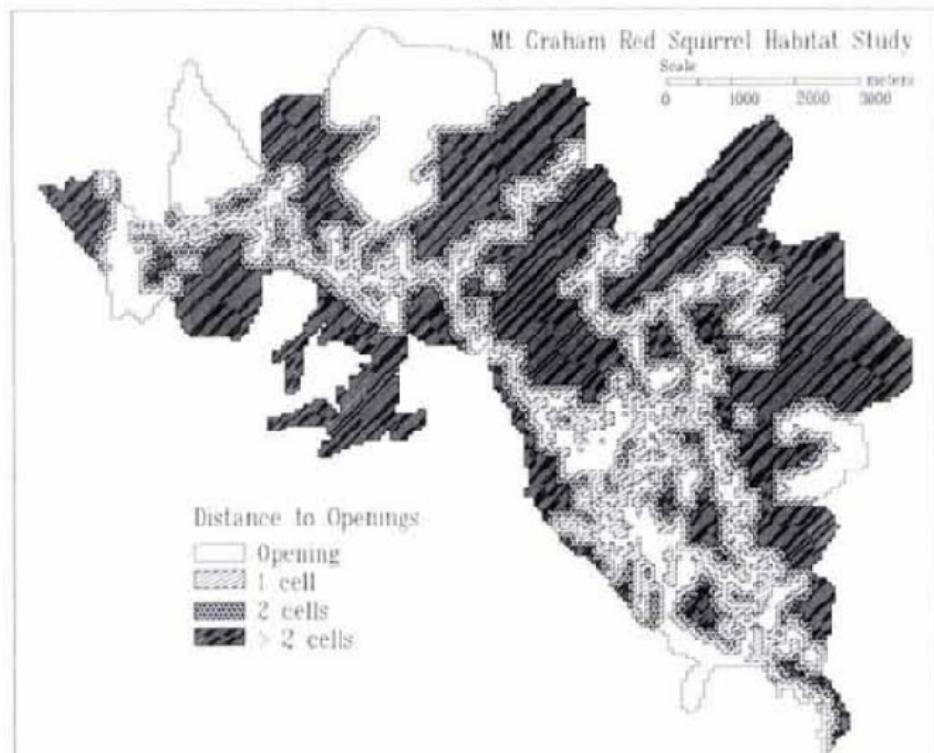
## GIS-Based Habitat Modeling Using Logistic Multiple Regression: A Study of the Mt. Graham Red Squirrel

*José M. C. Pereira\* and Robert M. Itami*

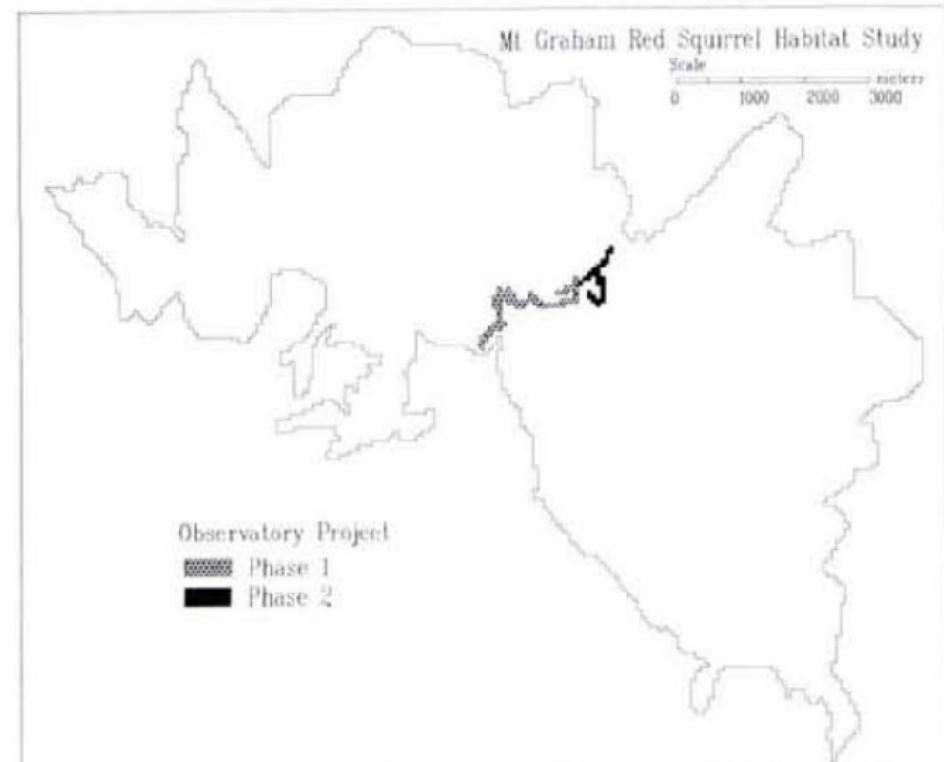
School of Renewable Natural Resources, University of Arizona, Tucson, AZ 85721

- To measure the habitat loss of the squirrel after astronomical observatory building.
- Remote Sensing as data source.
- Logistic regression.

# SPECIES CONSERVATION STATUS



(e)



(f)

FIG. 4. Database maps of (a) land-cover types, (b) food productivity, (c) canopy cover, (d) tree diameter at breast height (d.b.h.), (e) distance to clearings, and (f) project location.

# SPECIES CONSERVATION STATUS

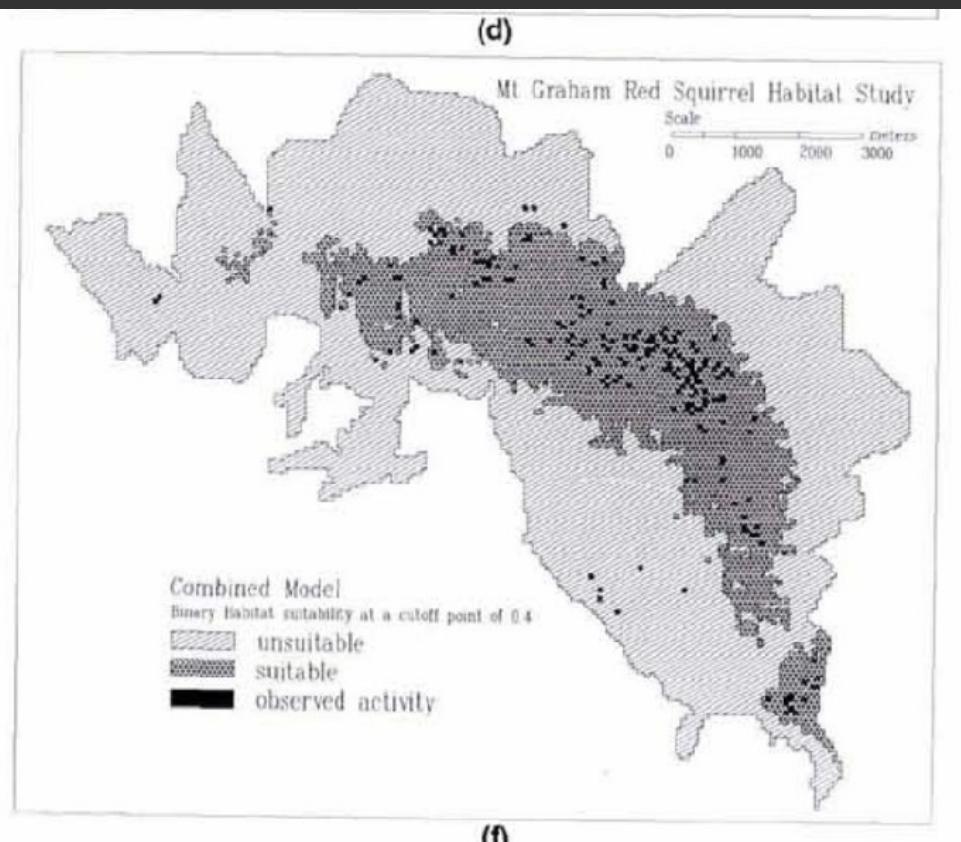
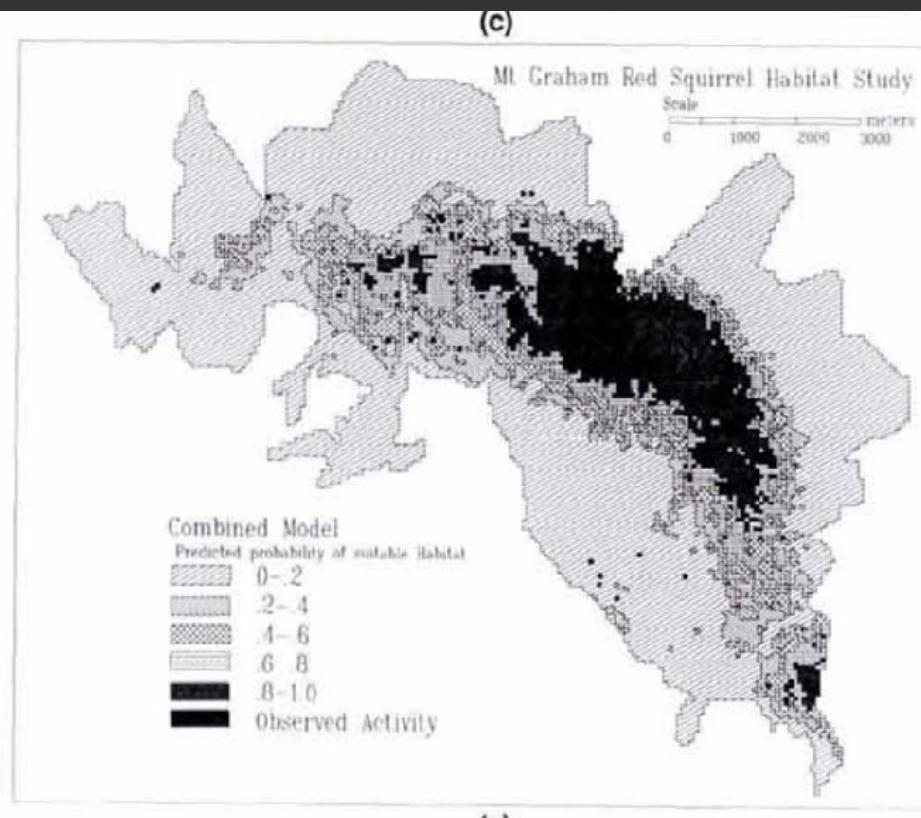


FIG. 7. Five class map representation of (a) environmental, (c) trend surface, and (e) Bayesian models, and binary habitat classification at optimal cut-off points for (b) environmental, (d) trend surface, and (f) Bayesian models.

BIOLOGICAL CONSERVATION 142 (2009) 344–352



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journal homepage: [www.elsevier.com/locate/biocon](http://www.elsevier.com/locate/biocon)



## Habitat suitability, threats and conservation of isolated populations of the smooth snake (*Coronella austriaca*) in the southern Iberian Peninsula

Xavier Santos<sup>a,b,\*</sup>, José C. Brito<sup>c</sup>, Jesús Caro<sup>d</sup>, Antonio J. Abril<sup>d</sup>,  
Marcial Lorenzo<sup>e</sup>, Neftalí Sillero<sup>f</sup>, Juan M. Pleguezuelos<sup>d</sup>

<sup>a</sup>Parc Natural de Sant Llorenç del Munt i l'Obac, Oficina Tècnica de Parcs Naturals, Diputació de Barcelona, c/ Urgell 187, E-08036 Barcelona, Spain

<sup>b</sup>Dep. Biología Animal, Universitat de Barcelona, Avgda. Diagonal 645, E-08028 Barcelona, Spain

<sup>c</sup>CIBIO, Centro de Investigação em Biodiversidade e Recursos Genéticos, Instituto de Ciências Agrárias de Vairão, R. Padre Armando Quintas, 4485-661 Vairão, Portugal

<sup>d</sup>Dep. Biología Animal, Fac. Biología, Univ. Granada, E-18071 Granada, Spain

<sup>e</sup>Pías 12, E-36770 O Rosal, Pontevedra, Spain

<sup>f</sup>Centro de Investigação em Ciências Geo-Espaciais (CICGE), Dep. de Matemática Aplicada, Univ. Porto, Rua do Campo Alegre, 687, 4169-007 Porto, Portugal

- To use ENMs to explain the current conservation status of the southern isolated populations of the snake *Coronella austriaca*.
- Ecological Niche Factor Analysis (ENFA).
- Definition of Marginality and Specialisation

# SPECIES CONSERVATION STATUS

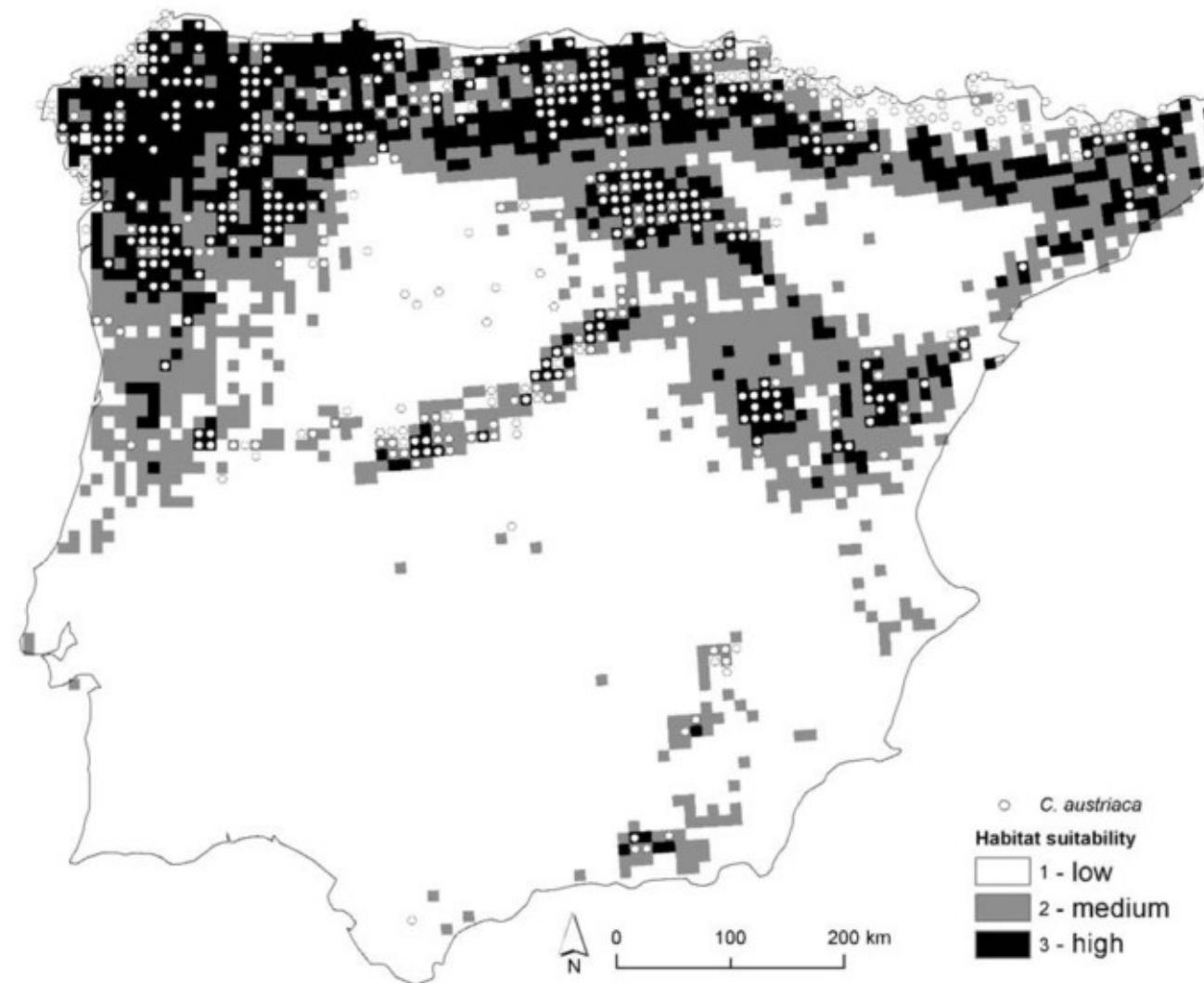


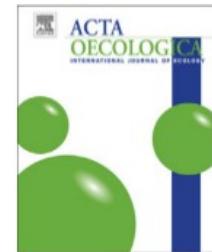
Fig. 4 – Habitat suitability for *C. austriaca* in the Iberian Peninsula. The map is derived from ecological-Niche factor analysis (see Section 2 for details) according to UTM 10 × 10 km grid size.

Acta Oecologica 77 (2016) 207–216



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Original article

## Evaluating how species niche modelling is affected by partial distributions with an empirical case



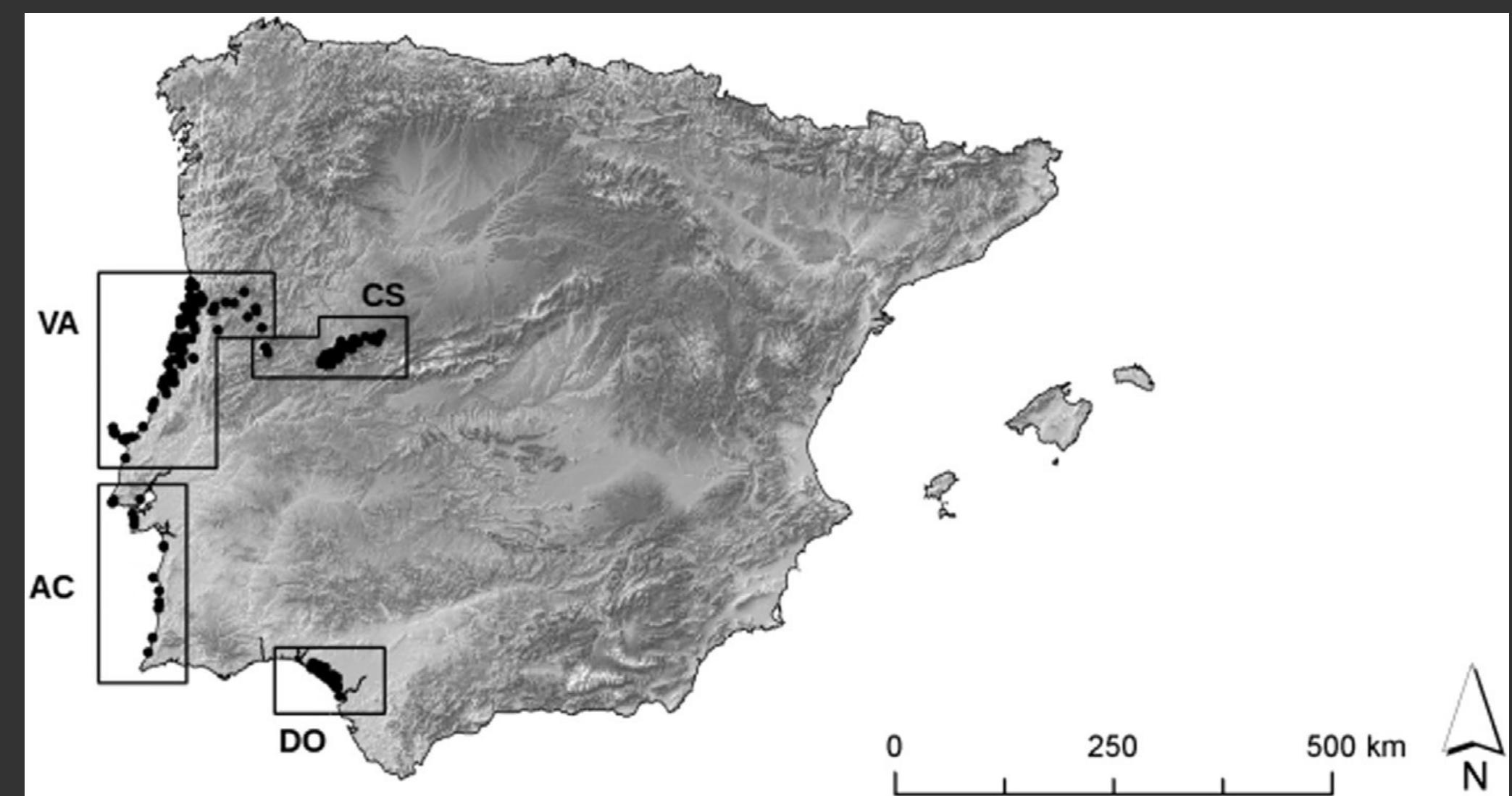
Miguel A. Carretero <sup>a,\*</sup>, Neftalí Sillero <sup>b</sup>

<sup>a</sup> CIBIO - Research Centre in Biodiversity and Genetic Resources, InBIO, Universidade do Porto, Campus de Vairão, Rua Padre Armando Quintas, Nº 7, 4485-661, Vairão, Vila do Conde, Portugal

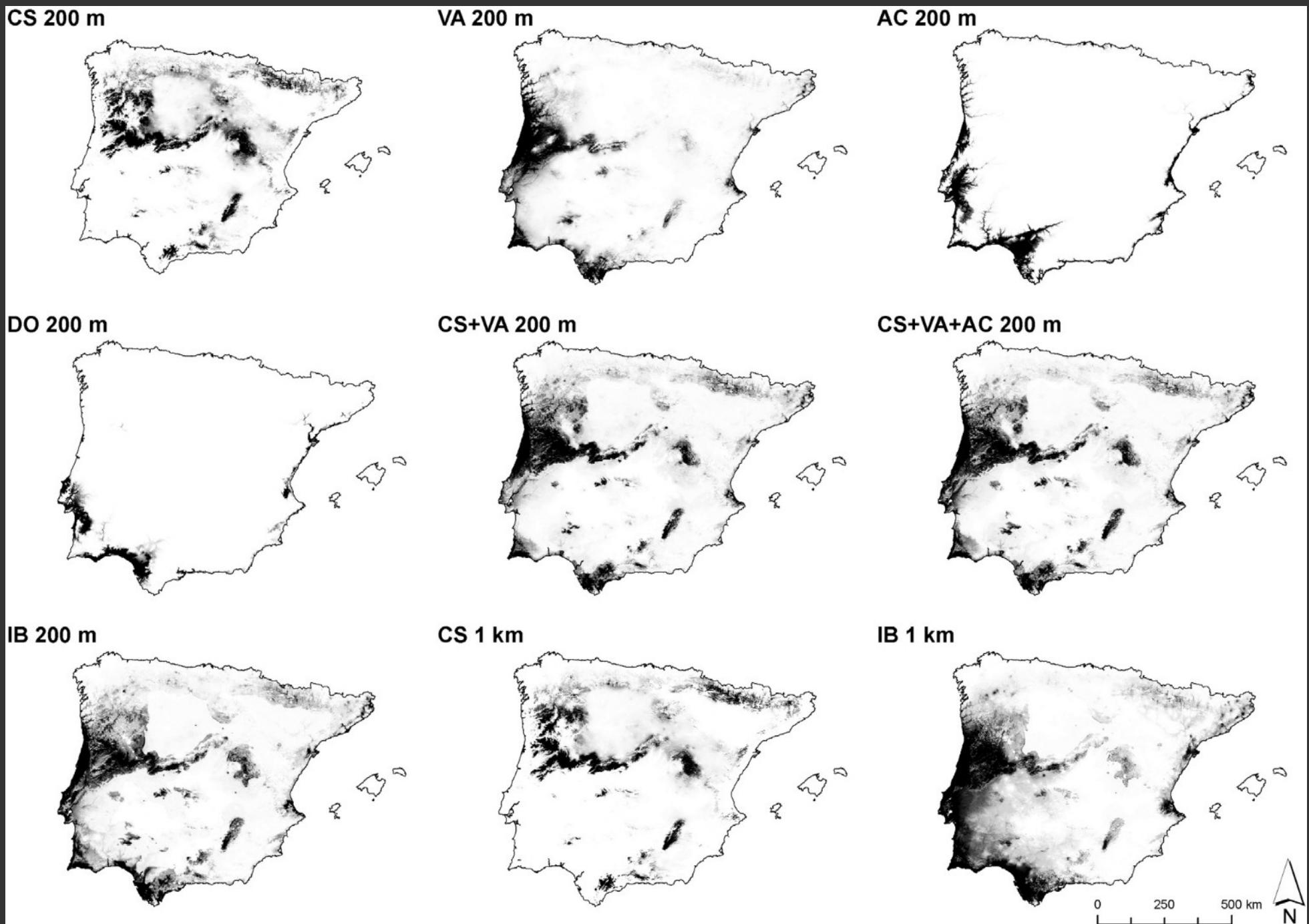
<sup>b</sup> CICGE - Centro de Investigação em Ciências Geo-Espaciais, Faculdade de Ciências da Universidade do Porto (FCUP), Observatório Astronómico Prof. Manuel de Barros, Alameda do Monte da Virgem, 4430-146, Vila Nova de Gaia, Portugal

- Can we model a species' range from partial distributions?
- Maxent, ENFA, Bioclim, and Domain
- Species with a fragmented distribution
- Conservation consequences

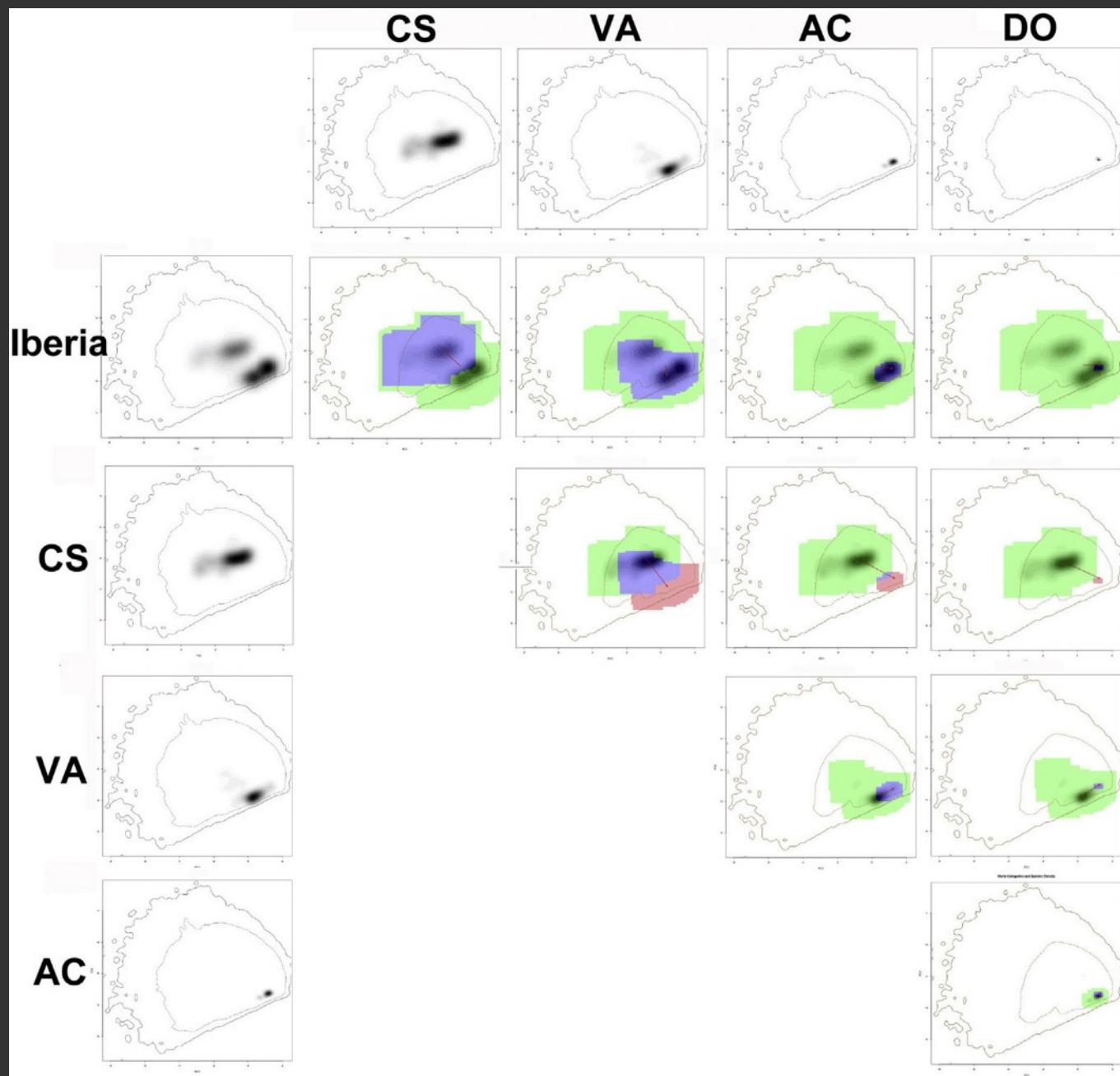
# SPECIES WITH MULTI-MODAL NICHES



# SPECIES WITH MULTI-MODAL NICHES



# SPECIES WITH MULTI-MODAL NICHES





Global Change Biology (2010) 16, 3257–3270, doi: 10.1111/j.1365-2486.2010.02212.x

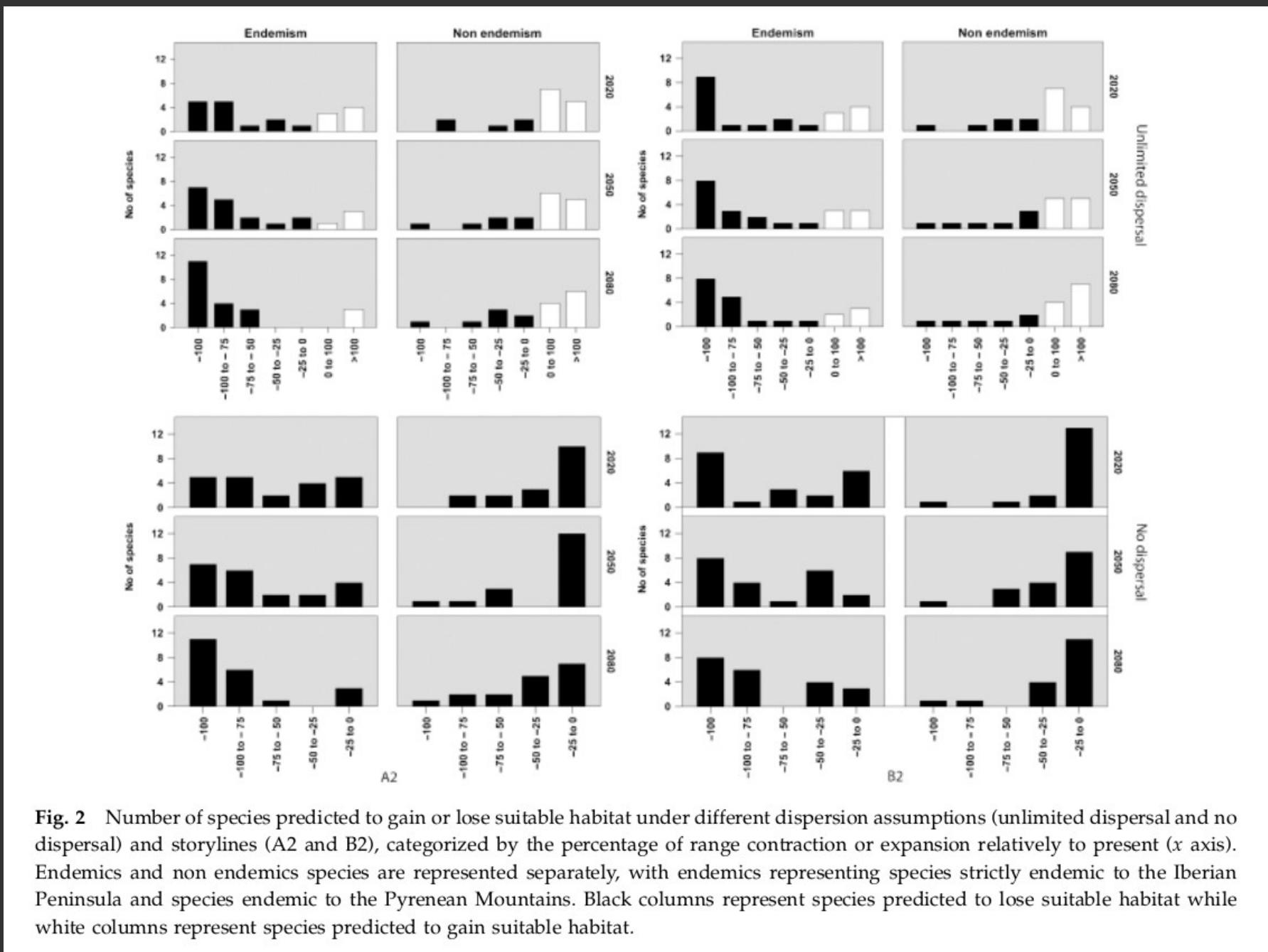
# From climate change predictions to actions – conserving vulnerable animal groups in hotspots at a regional scale

SÍLVIA B. CARVALHO\*†‡, JOSÉ C. BRITO\*, EDUARDO J. CRESPO†§  
and HUGH P. POSSINGHAM†¶

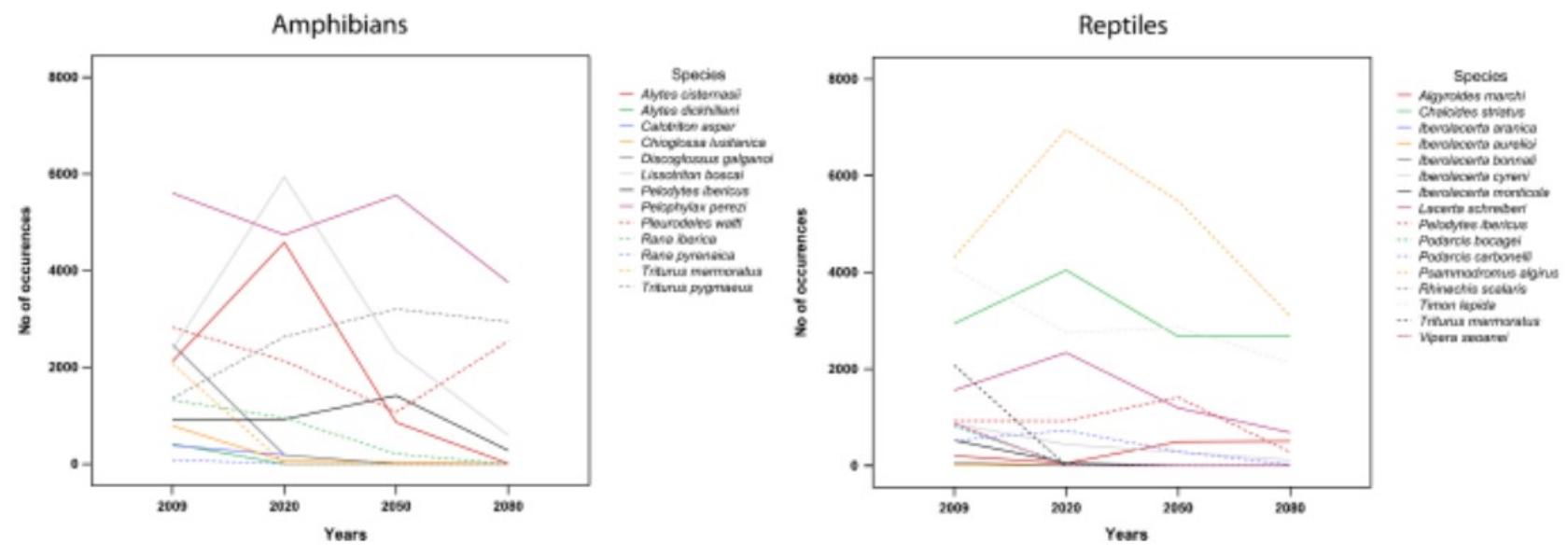
\*CIBIO – Centro de Investigação em Biodiversidade e Recursos Genéticos da Universidade do Porto, R. Padre Armando Quintas, 4485-661 Vairão, Portugal, †Departamento de Biologia Animal, Faculdade de Ciências da Universidade de Lisboa, Campo Grande, 1749-016 Lisboa, Portugal, ‡The Ecology Centre, The University of Queensland, St. Lucia, Qld 4072, Australia, §CBA, Centro de Biologia Ambiental da Universidade de Lisboa, Campo Grande, 1749-016 Lisboa, Portugal, ¶The School of Maths and Physics, The University of Queensland, St. Lucia, Qld 4072, Australia

- To evaluate future extinction risks of Iberian herp species.
- Modelling species richness.
- Maxent and Biomod.
- Two climate change scenarios.
- Two dispersal scenarios: unlimited and no dispersal.

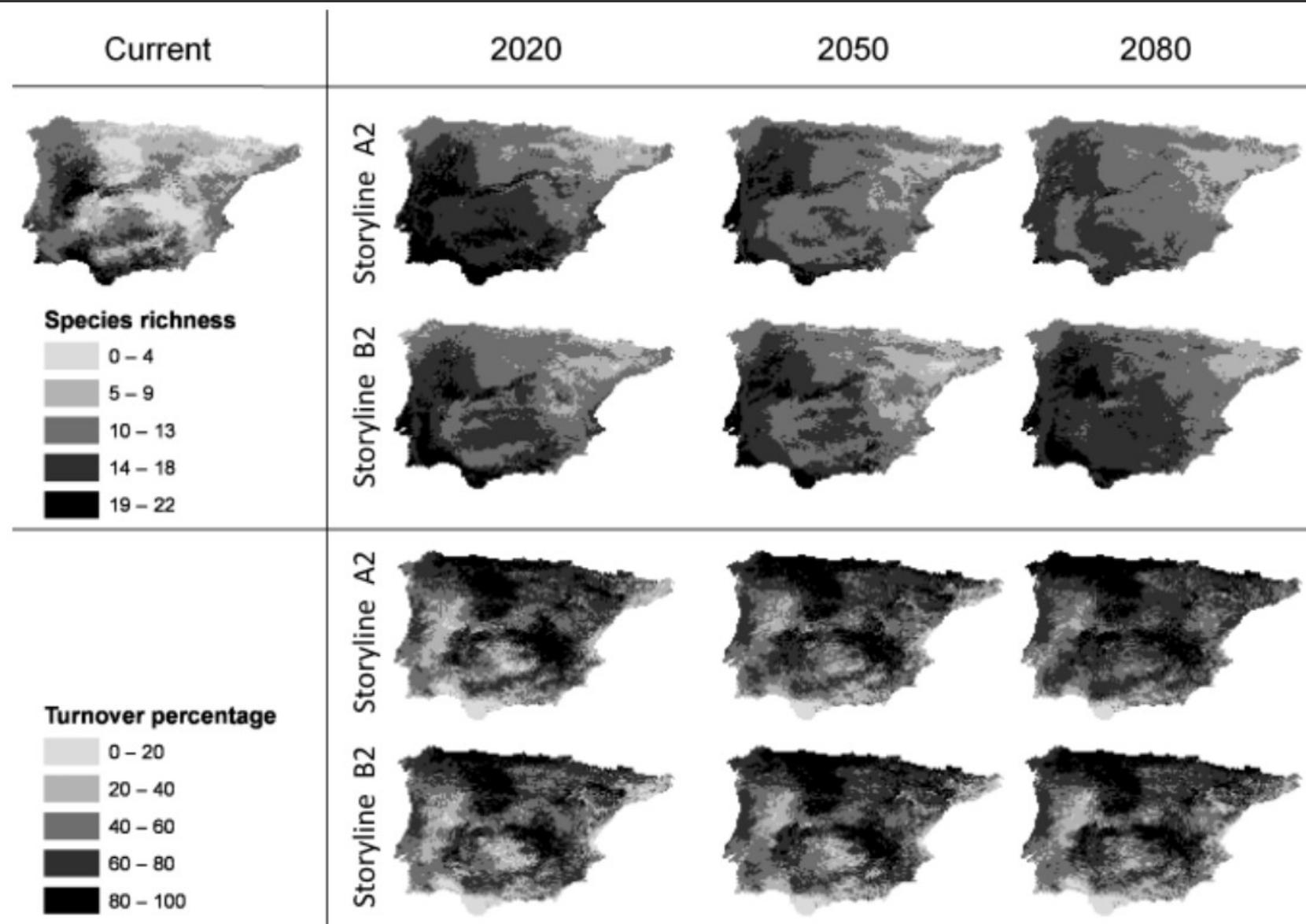
# CLIMATE CHANGE



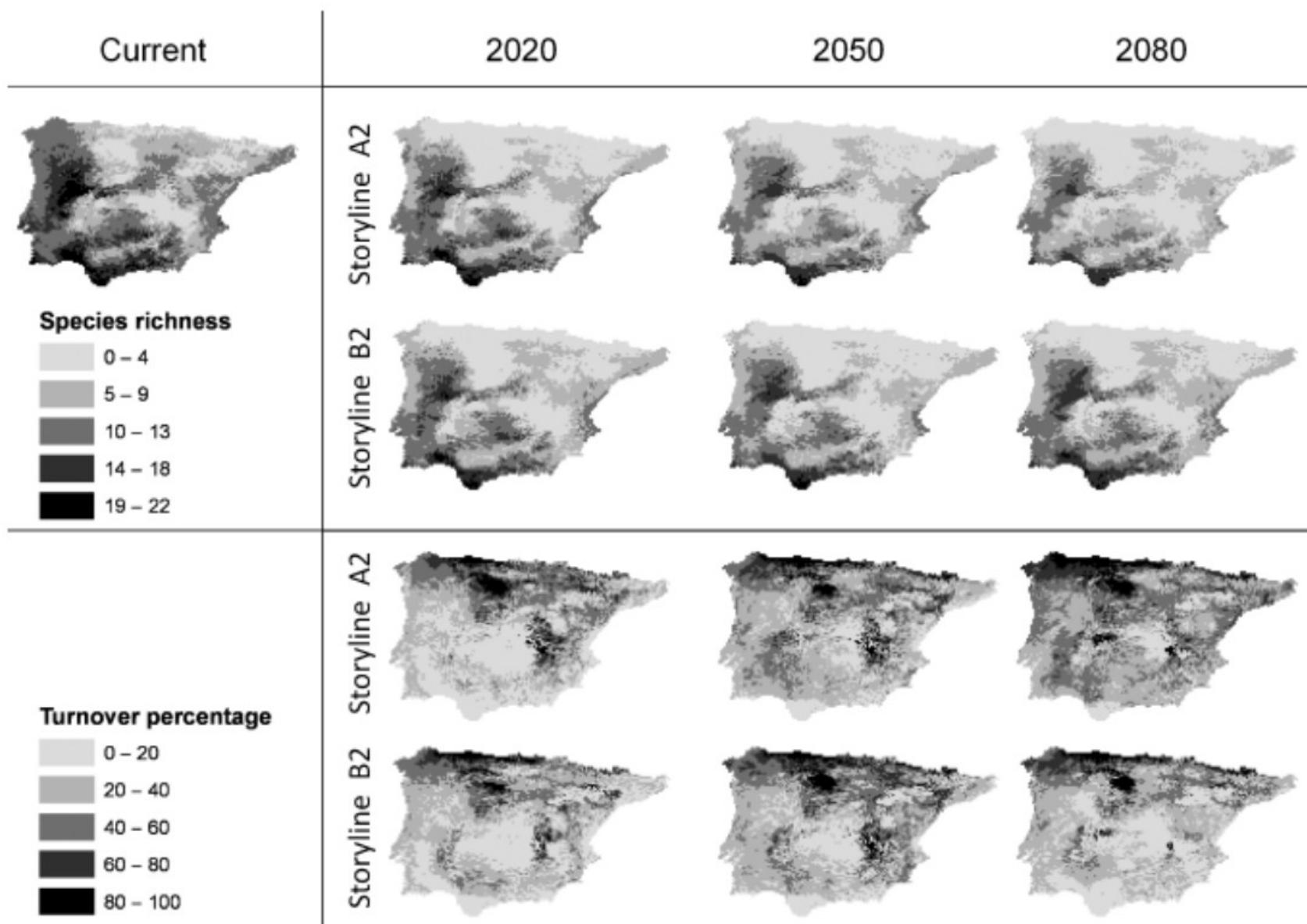
**Fig. 2** Number of species predicted to gain or lose suitable habitat under different dispersion assumptions (unlimited dispersal and no dispersal) and storylines (A2 and B2), categorized by the percentage of range contraction or expansion relatively to present ( $x$  axis). Endemics and non endemics species are represented separately, with endemics representing species strictly endemic to the Iberian Peninsula and species endemic to the Pyrenean Mountains. Black columns represent species predicted to lose suitable habitat while white columns represent species predicted to gain suitable habitat.



**Fig. 3** Variation in the predicted number of occurrences through time for species predicted to lose suitable habitat according to the unlimited dispersion scenario and storyline A2.



**Fig. 4** Spatial distribution of predicted current and future (2020, 2050 and 2080) species richness and turnover percentage according to storylines A2 and B2 and under the unlimited dispersion scenario.



**Fig. 5** Spatial distribution of predicted current and future (2020, 2050 and 2080) species richness and turnover percentage according to storylines A2 and B2 and under the no dispersion scenario.

Zoologischer Anzeiger 252 (2013) 289–298



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Zoologischer Anzeiger

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# Zoologischer Anzeiger

Modelling the past and future distribution of contracting species. The Iberian lizard *Podarcis carbonelli* (Squamata: Lacertidae) as a case study

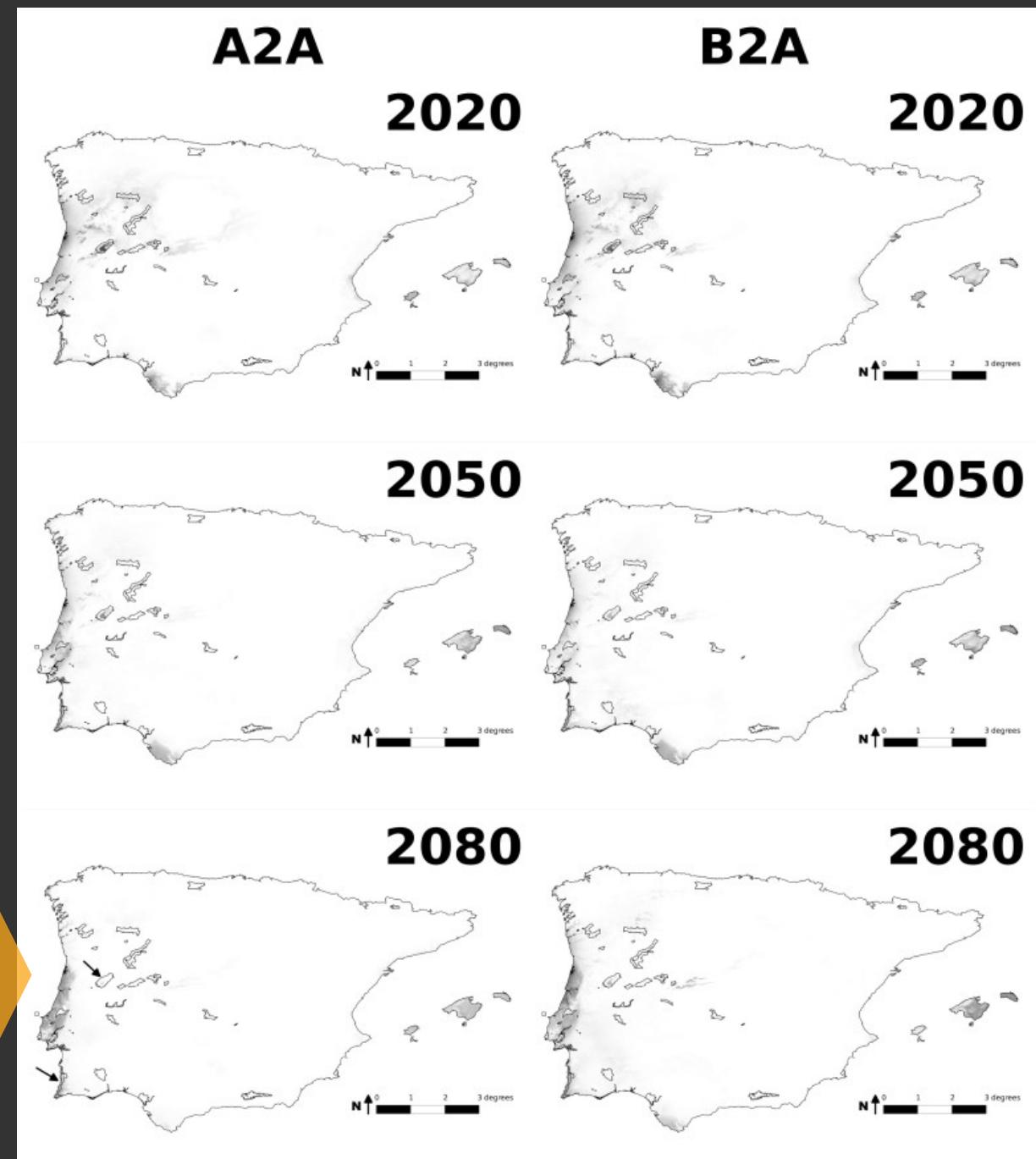
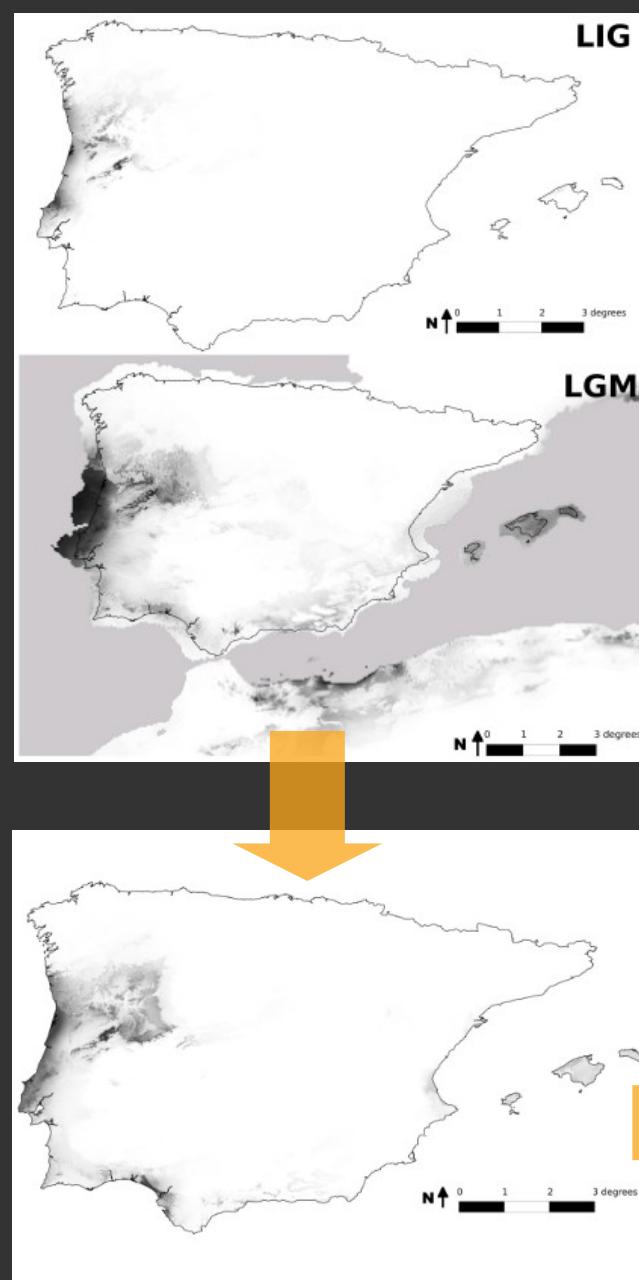
Neftalí Sillero<sup>a,\*</sup>, Miguel A. Carretero<sup>b</sup>

<sup>a</sup> Centro de Investigação em Ciências Geo-Espaciais (CICGE) da Universidade do Porto, Departamento de Matemática Aplicada, R. Campo Alegre 687, 4169-007 Porto, Portugal

<sup>b</sup> CIBIO, Centro de Investigação em Biodiversidade e Recursos Genéticos, Universidade do Porto, Campus Agrário de Vairão, 4485-661 Vairão, Portugal

- To describe the past, current, and future realised niche of the lizard *Podarcis carbonelli*.
- Maxent.

# CLIMATE CHANGE: FROM PAST TO FUTURE



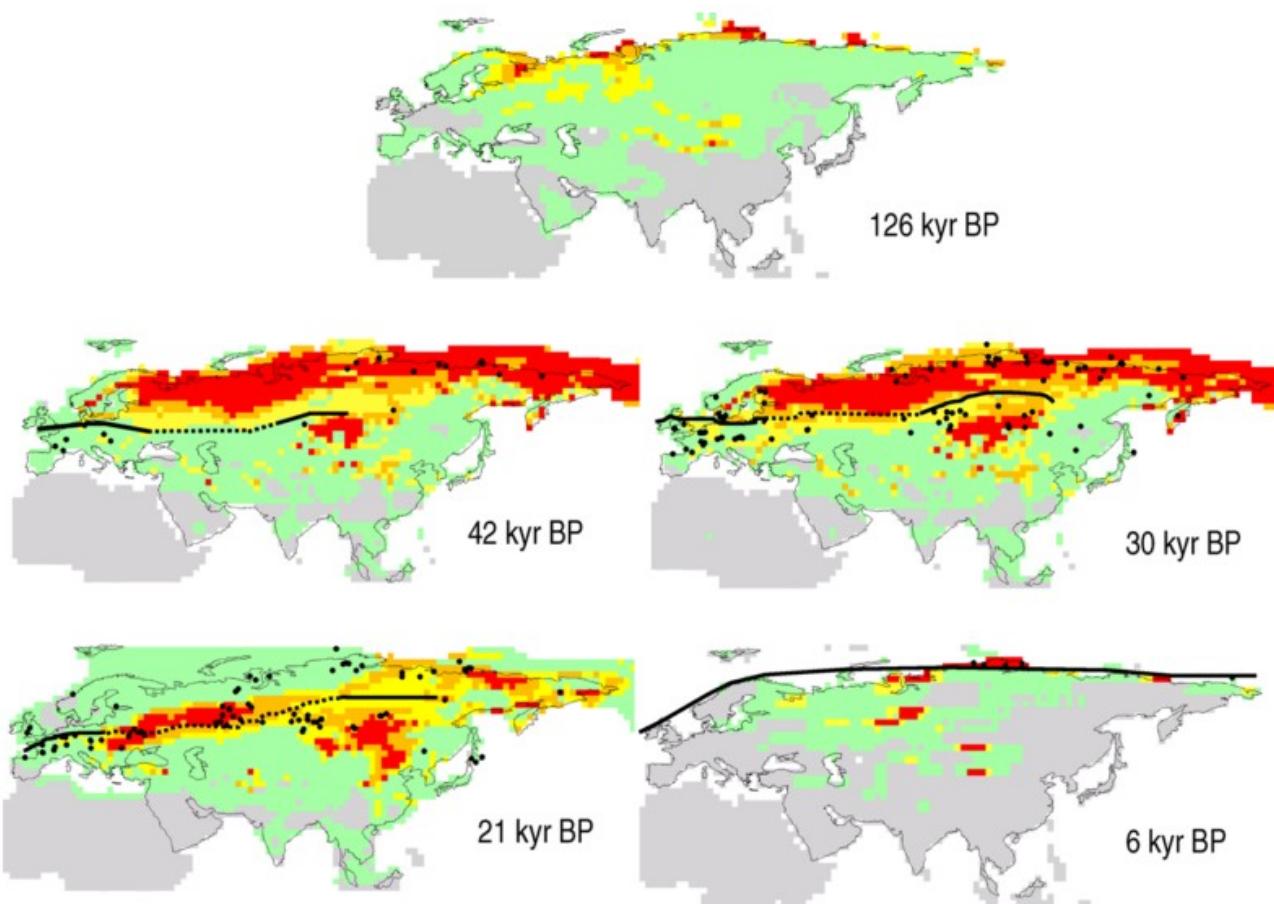
# Climate Change, Humans, and the Extinction of the Woolly Mammoth

David Nogués-Bravo<sup>1\*</sup>, Jesús Rodríguez<sup>2</sup>, Joaquín Hortal<sup>3</sup>, Persaram Batra<sup>4</sup>, Miguel B. Araújo<sup>1</sup>

**1** Department of Biodiversity and Evolutionary Biology, National Museum of Natural Sciences, Consejo Superior de Investigaciones Científicas, Madrid, Spain, **2** National Research Center on Human Evolution, Centro Nacional De Investigación Sobre La Evolución Humana, Burgos, Spain, **3** Natural Environment Research Council Centre for Population Biology, Imperial College London, Ascot, Berkshire, United Kingdom, **4** Department of Earth and Environment, Mount Holyoke College, South Hadley, Massachusetts, United States of America

- To investigate the extent to which the extinction of the woolly mammoth might have been driven by the collapse of its suitable climate conditions and the intensification of human hunting.
- The climate envelope of the woolly mammoth was characterised based on statistical associations.
- Mahalanobis distance.

# FOSSIL SPECIES



**Figure 3.** Maps of Projected Climatic Suitability for the Woolly Mammoths in the Late Pleistocene and Holocene

Suitability scores are divided into four colour-scale classes (quartiles 1 [more suitable] to 4 [less suitable] of the MD), where increasing intensities of red represent increasing suitability of the climate and increasing intensities of green represent decreasing suitability. Black points are the records of mammoth presence for each of the periods. Black lines represent the northern limit of modern humans [59]. Black dotted lines indicate uncertainty in the limit of modern humans.

doi:10.1371/journal.pbio.0060079.g003

## Spatial structure analysis of a reptile community with airborne LiDAR data

N. Sillero<sup>a\*</sup> and Luís Gonçalves-Seco<sup>a,b,c</sup>

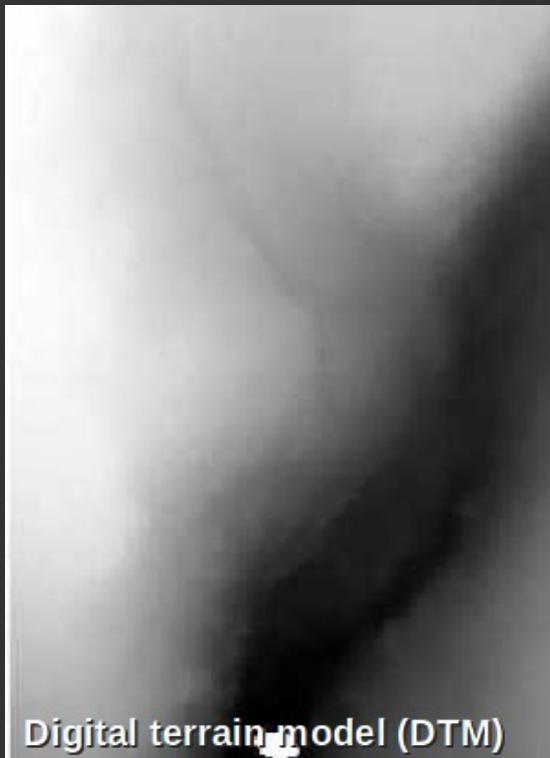
<sup>a</sup>*Centro de Investigação em Ciências Geo-Espaciais (CICGE), Alameda do Monte da Virgem, Vila Nova de Gaia, Portugal;* <sup>b</sup>*ISMAI Instituto Superior da Maia (ISMAI), Castelo da Maia, Avioso S. Pedro, Porto, Portugal;* <sup>c</sup>*Instituto de Ciencias del Patrimonio, Consejo Superior de Investigaciones Científicas, Santiago de Compostela, Spain*

(Received 24 July 2013; accepted 3 March 2014)

- Identification of realised niches of several species.
- Remote sensing as data source.
- Environmental variables of very high spatial resolution.
- Maxent.

# HIGH SPATIAL RESOLUTION MODELS

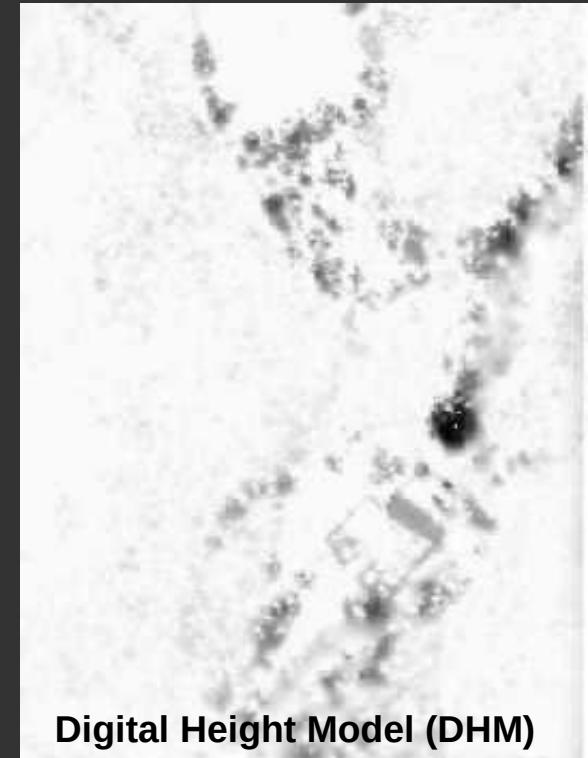
1m spatial resolution



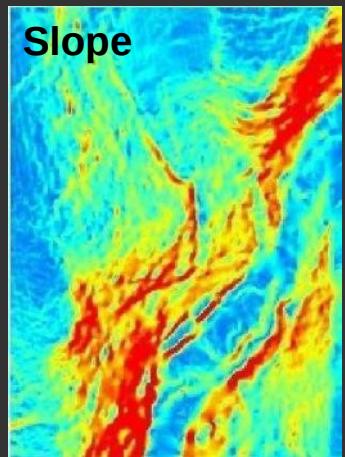
Digital terrain model (DTM)



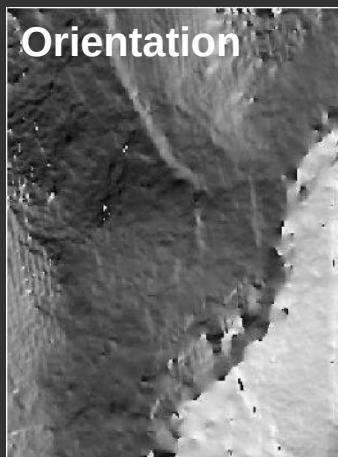
Digital surface model (DSM)



Digital Height Model (DHM)



Slope



Orientation

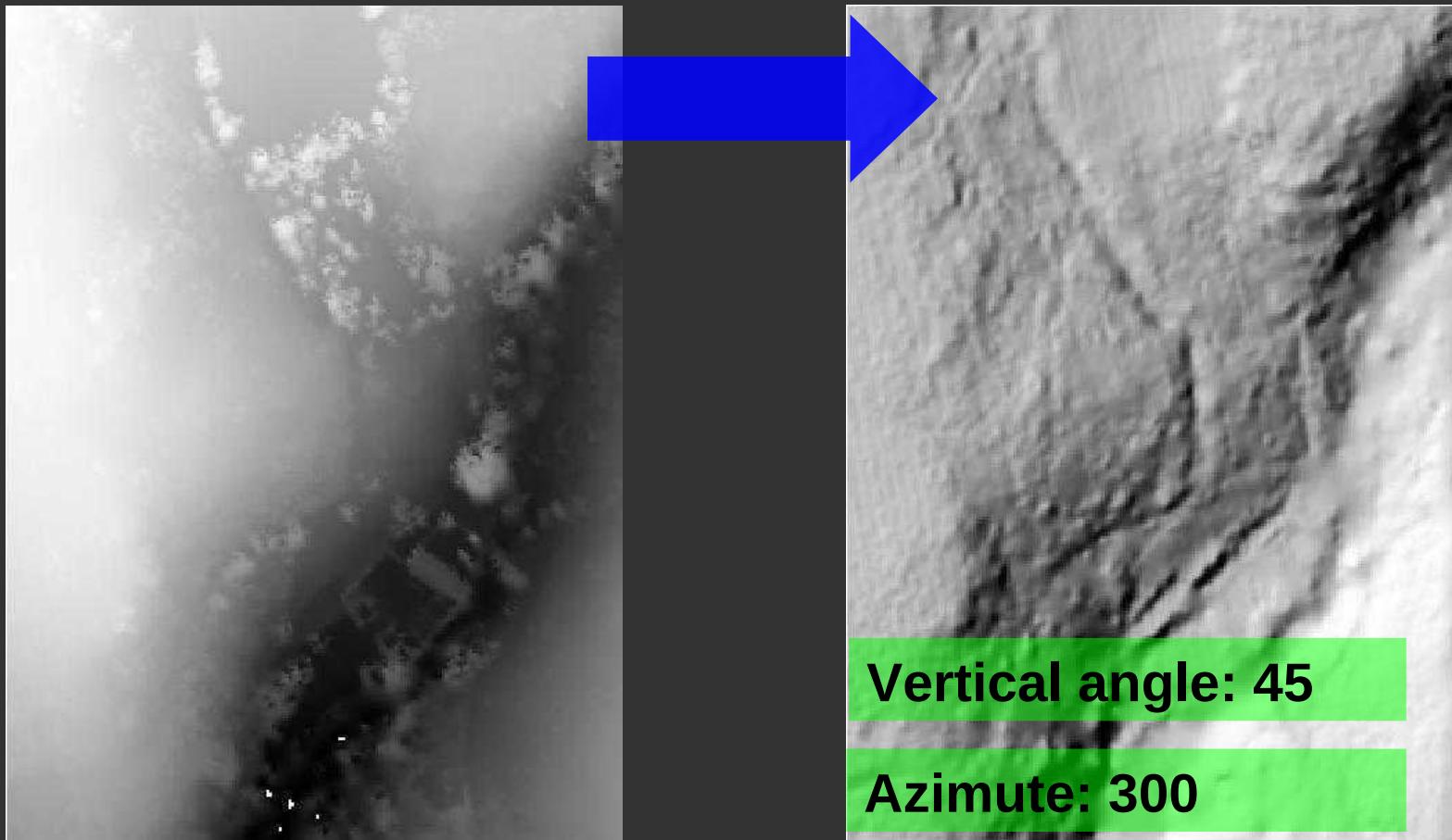


Relief



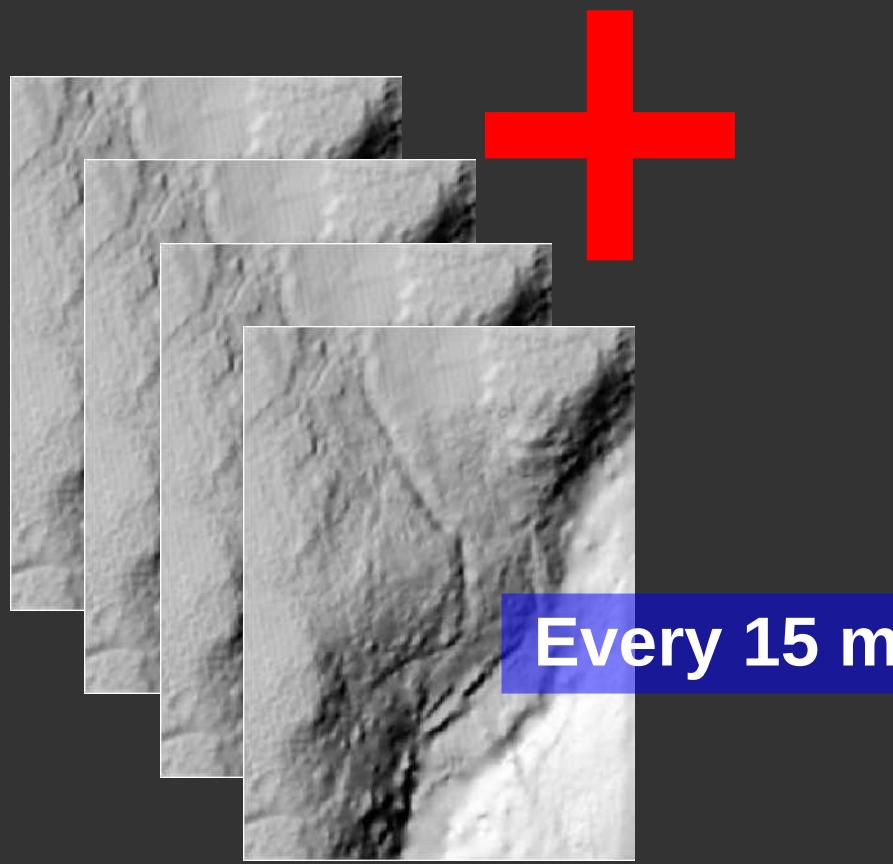
Ruggedness

# HIGH SPATIAL RESOLUTION MODELS



DSM

# HIGH SPATIAL RESOLUTION MODELS

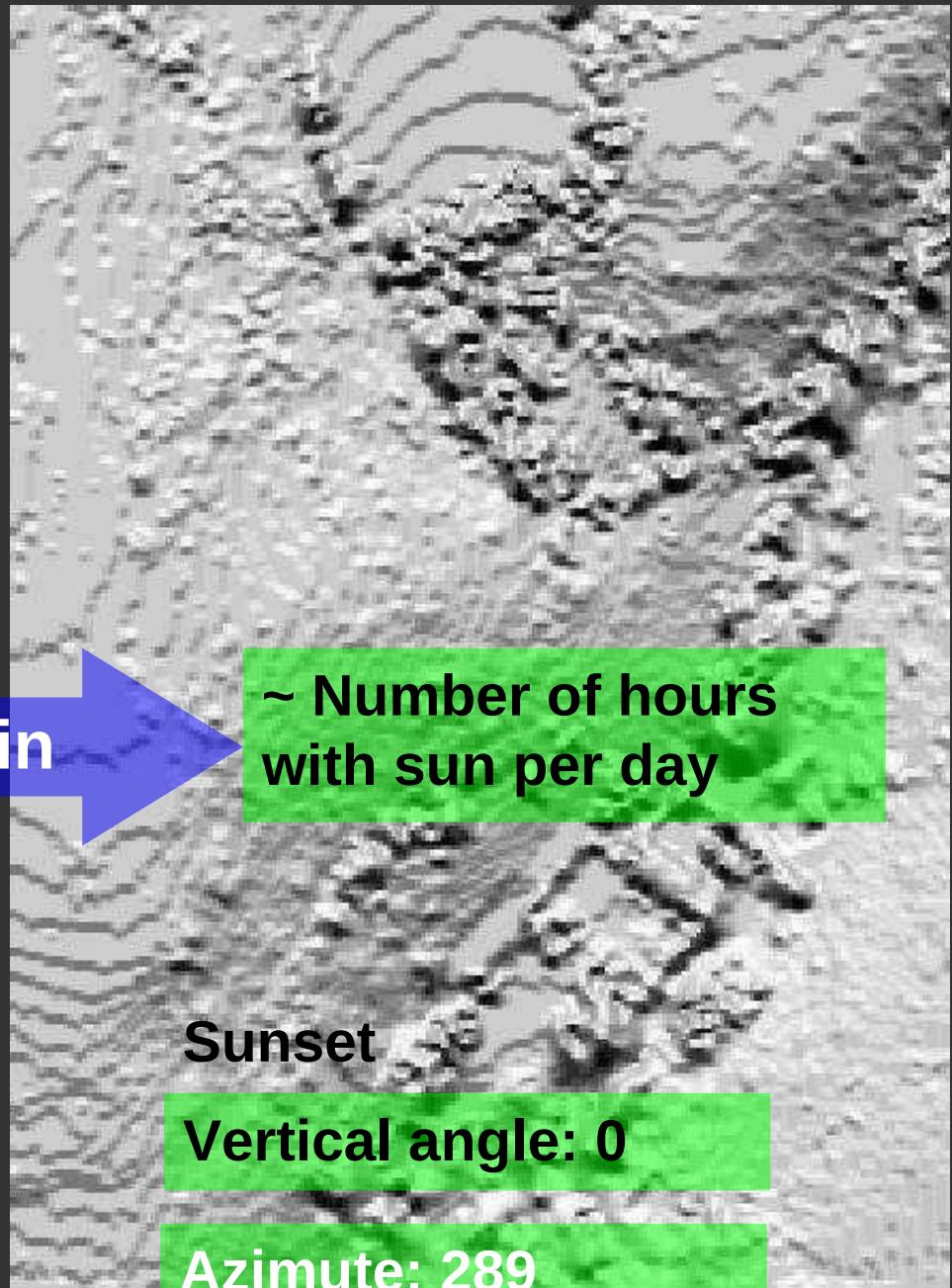


Sunrise

Vertical angle: 2

Azimute: 70

Every 15 min



Sunset

Vertical angle: 0

Azimute: 289

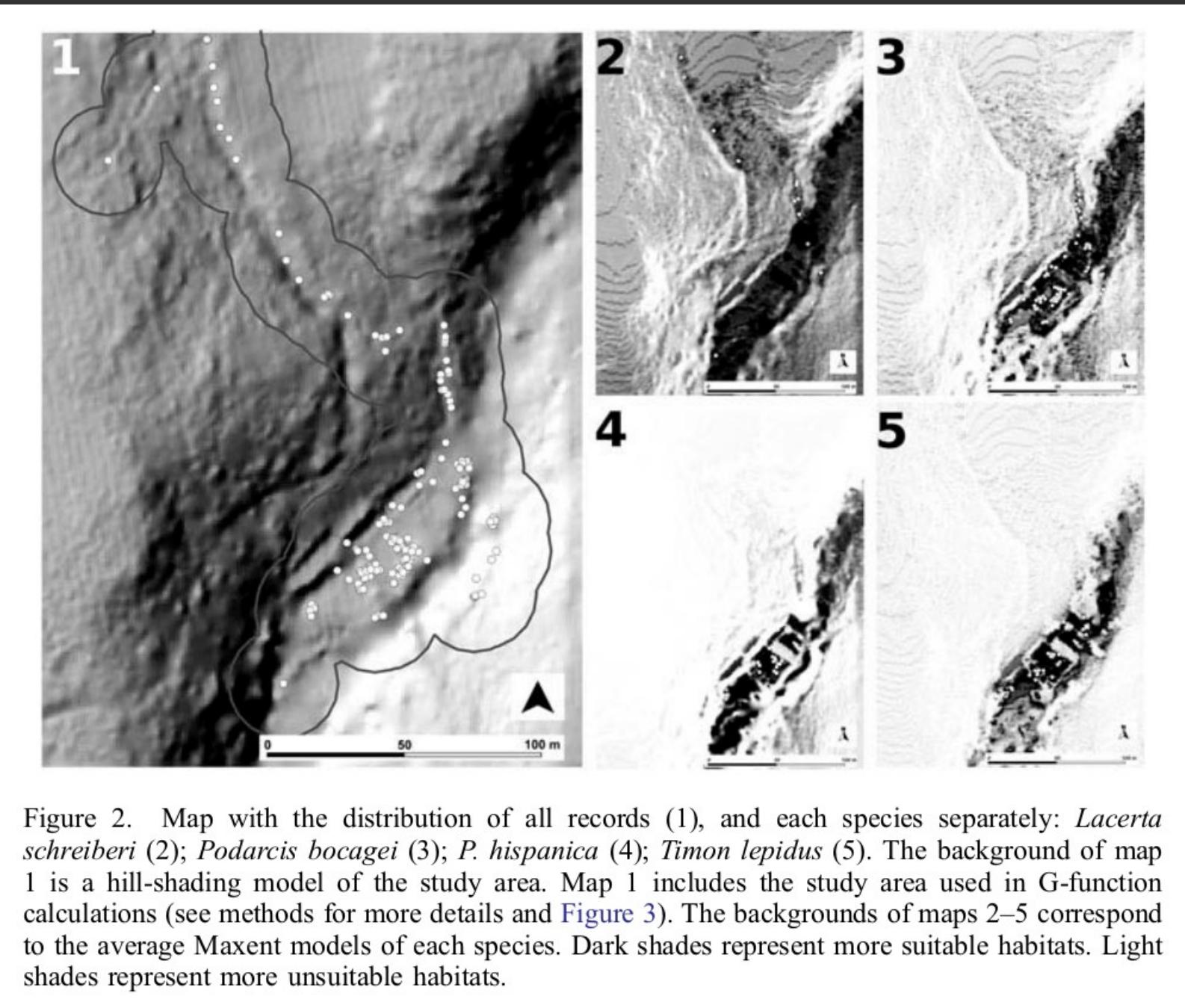


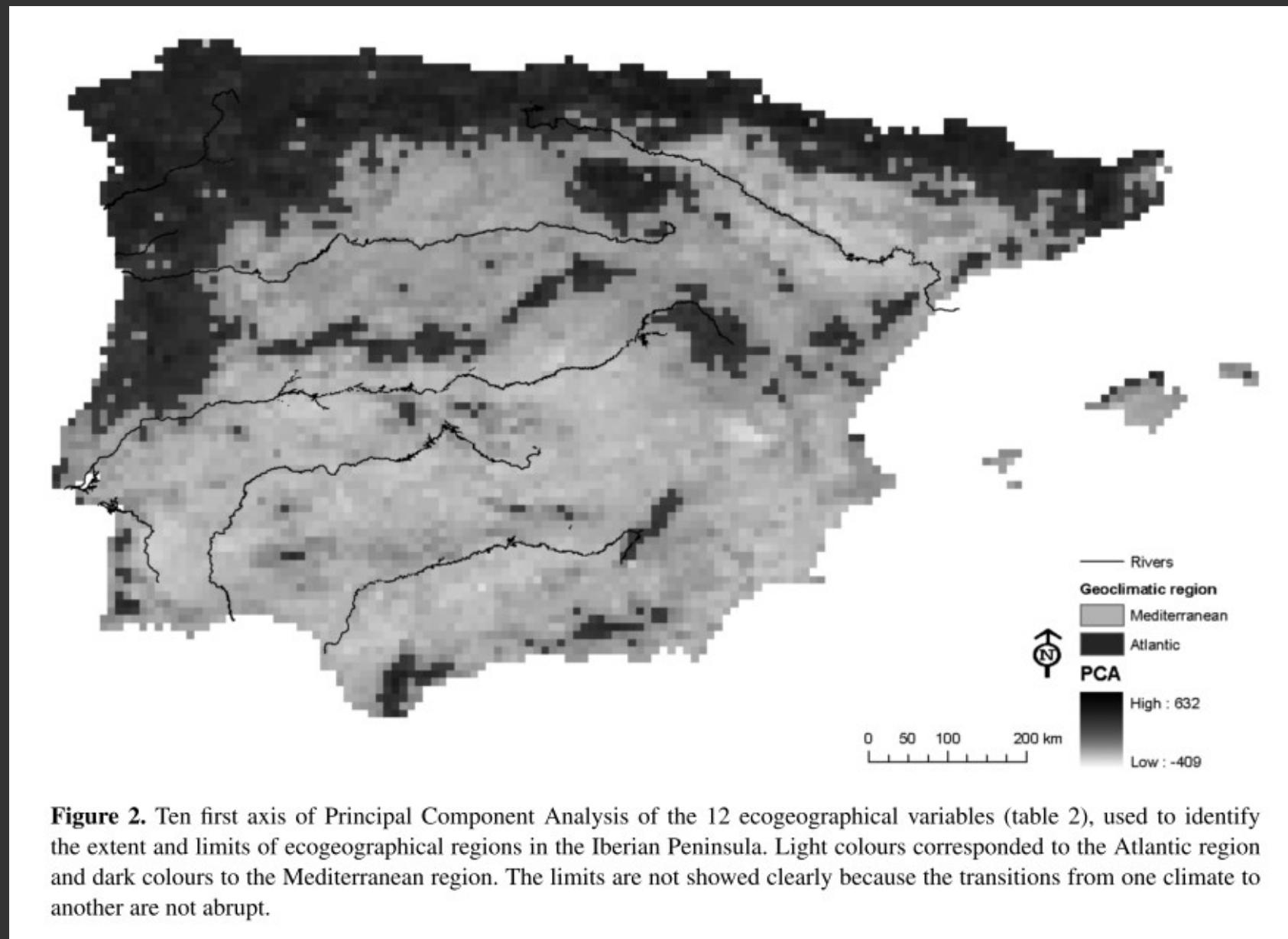
Figure 2. Map with the distribution of all records (1), and each species separately: *Lacerta schreiberi* (2); *Podarcis bocagei* (3); *P. hispanica* (4); *Timon lepidus* (5). The background of map 1 is a hill-shading model of the study area. Map 1 includes the study area used in G-function calculations (see methods for more details and Figure 3). The backgrounds of maps 2–5 correspond to the average Maxent models of each species. Dark shades represent more suitable habitats. Light shades represent more unsuitable habitats.

Amphibia-Reptilia 30 (2009): 185-206

## Biogeographical patterns derived from remote sensing variables: the amphibians and reptiles of the Iberian Peninsula

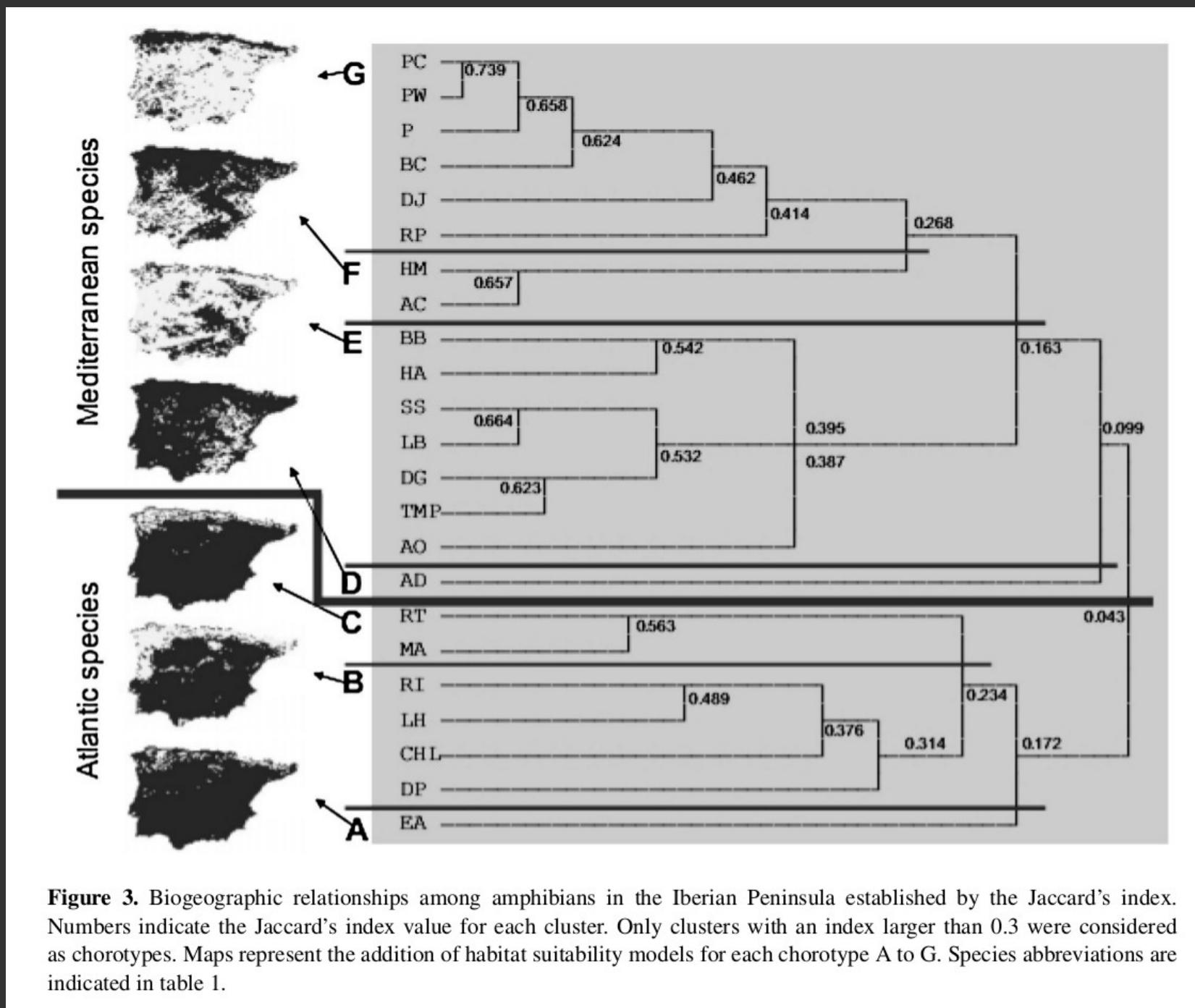
N. Sillero<sup>1,\*</sup>, J.C. Brito<sup>2</sup>, A.K. Skidmore<sup>3</sup>, A.G. Toxopeus<sup>3</sup>

- To determine the extent and limits of geoclimatic regions in the Iberian Peninsula.
- To establish species chorotypes within the selected taxonomic groups.
- To identify hotspots of species density within each geoclimatic region.
- To determine regions of low or lacking herpetological data.
- Ecological Niche Factor Analysis (ENFA).

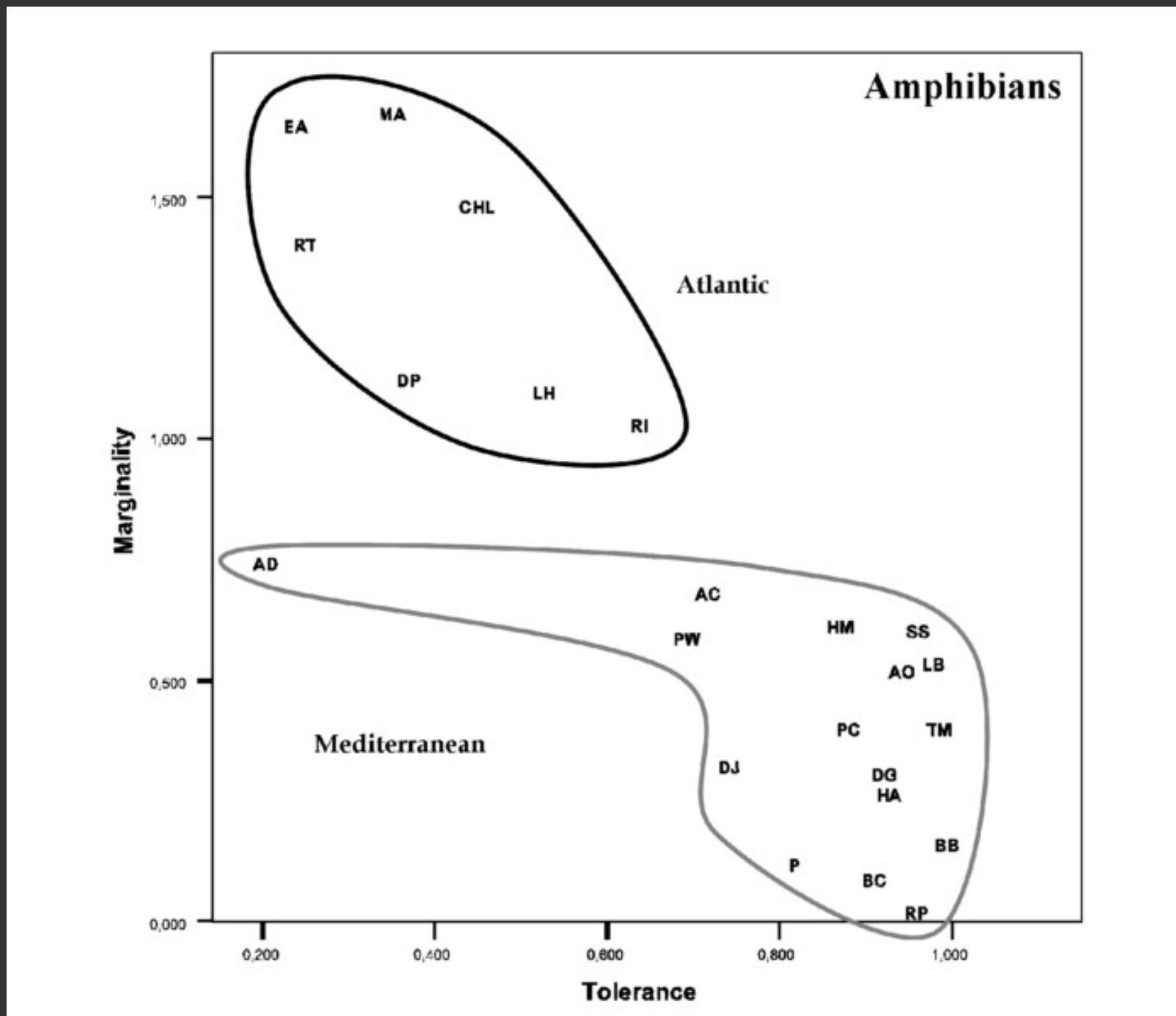


**Figure 2.** Ten first axis of Principal Component Analysis of the 12 ecogeographical variables (table 2), used to identify the extent and limits of ecogeographical regions in the Iberian Peninsula. Light colours corresponded to the Atlantic region and dark colours to the Mediterranean region. The limits are not showed clearly because the transitions from one climate to another are not abrupt.

# SPECIES RICHNESS AND CHOROTYPES



**Figure 3.** Biogeographic relationships among amphibians in the Iberian Peninsula established by the Jaccard's index. Numbers indicate the Jaccard's index value for each cluster. Only clusters with an index larger than 0.3 were considered as chorotypes. Maps represent the addition of habitat suitability models for each chorotype A to G. Species abbreviations are indicated in table 1.



# SPECIES RICHNESS

Observed

Predicted

Observed

Predicted

Atlantic

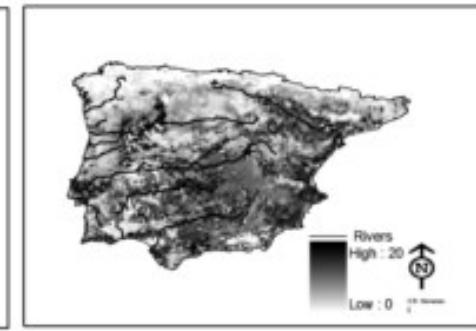
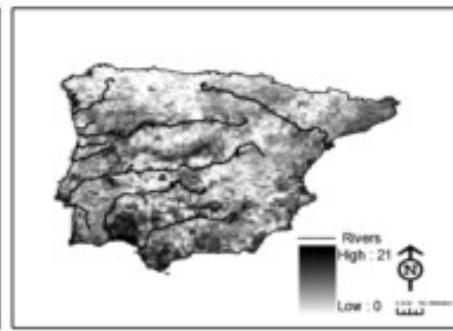
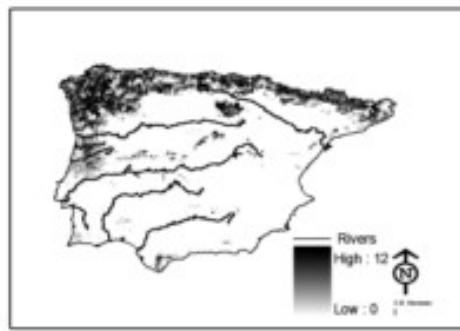
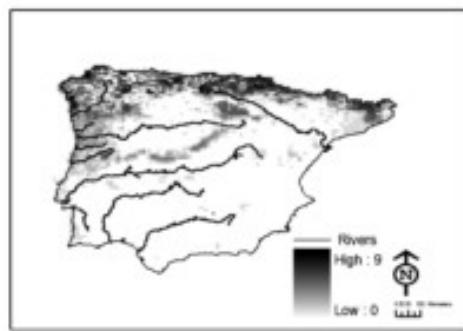
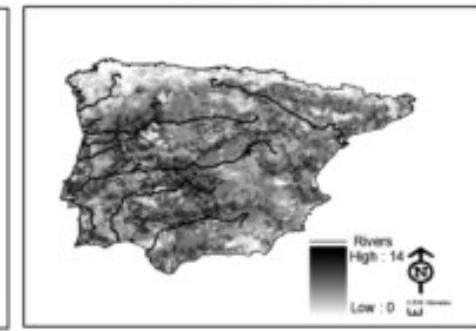
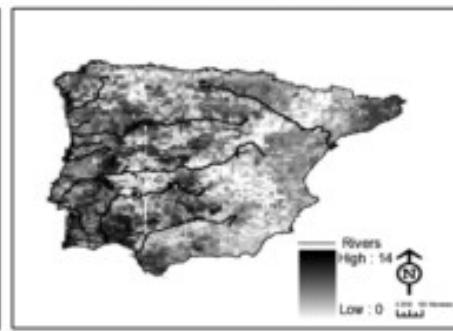
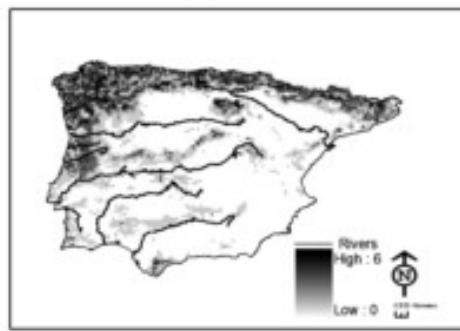
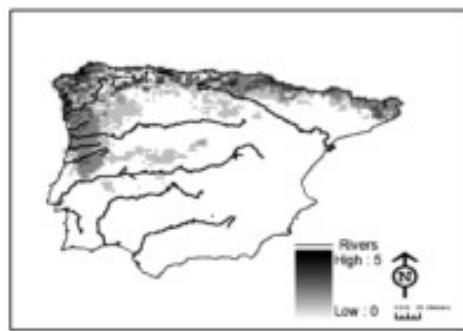
Atlantic

Mediterranean

Mediterranean

Amphibians

Reptiles



**Figure 6.** Observed and predicted species density of amphibians and reptiles in the Iberian Peninsula by biogeographic group. Light-dark colour scale represents number of species per  $10 \times 10$  km UTM squares.



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## Modelling of wildlife fatality hotspots along the Snowy Mountain Highway in New South Wales, Australia

Daniel Ramp <sup>a,\*</sup>, Joanne Caldwell <sup>b</sup>, Kathryn A. Edwards <sup>a</sup>,  
David Warton <sup>c</sup>, David B. Croft <sup>a</sup>

<sup>a</sup> *School of Biological, Earth and Environmental Sciences, University of New South Wales, Sydney, NSW 2052, Australia*

<sup>b</sup> *New South Wales Department of Environment and Conservation, Tumut, 2720, New South Wales, Australia*

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Received 9 February 2005

Available online 19 August 2005

- To develop a framework for recording fatality information, developing predictive models and identifying hotspot locations.
- Logistic regression.

Table 3

Deviance explained by the final model for each species using the complete data set with degrees of freedom in brackets along with the area under the curve (AUC)

Species	Predictors	Deviance		% Deviance Explained	AUC
		Null	Residual		
Eastern grey kangaroo	S + R6 + SOI6 + T + W + F	2961.1 (2135)	2261.5 (2129)	23.6	0.794
Wallabies	R3 + T + F	783.3 (2135)	606.32 (2132)	22.5	0.858
Common wombat	S + SIN250 + SOI6 + T + W + E	777.2 (2135)	691.9 (2129)	11.0	0.778
Feral animals	R1 + T + W	1455.2 (2135)	1038.5 (2132)	28.6	0.872
Birds	R1 + SOI1 + T + G + W	1314.3 (2135)	1243.5 (2130)	5.4	0.672

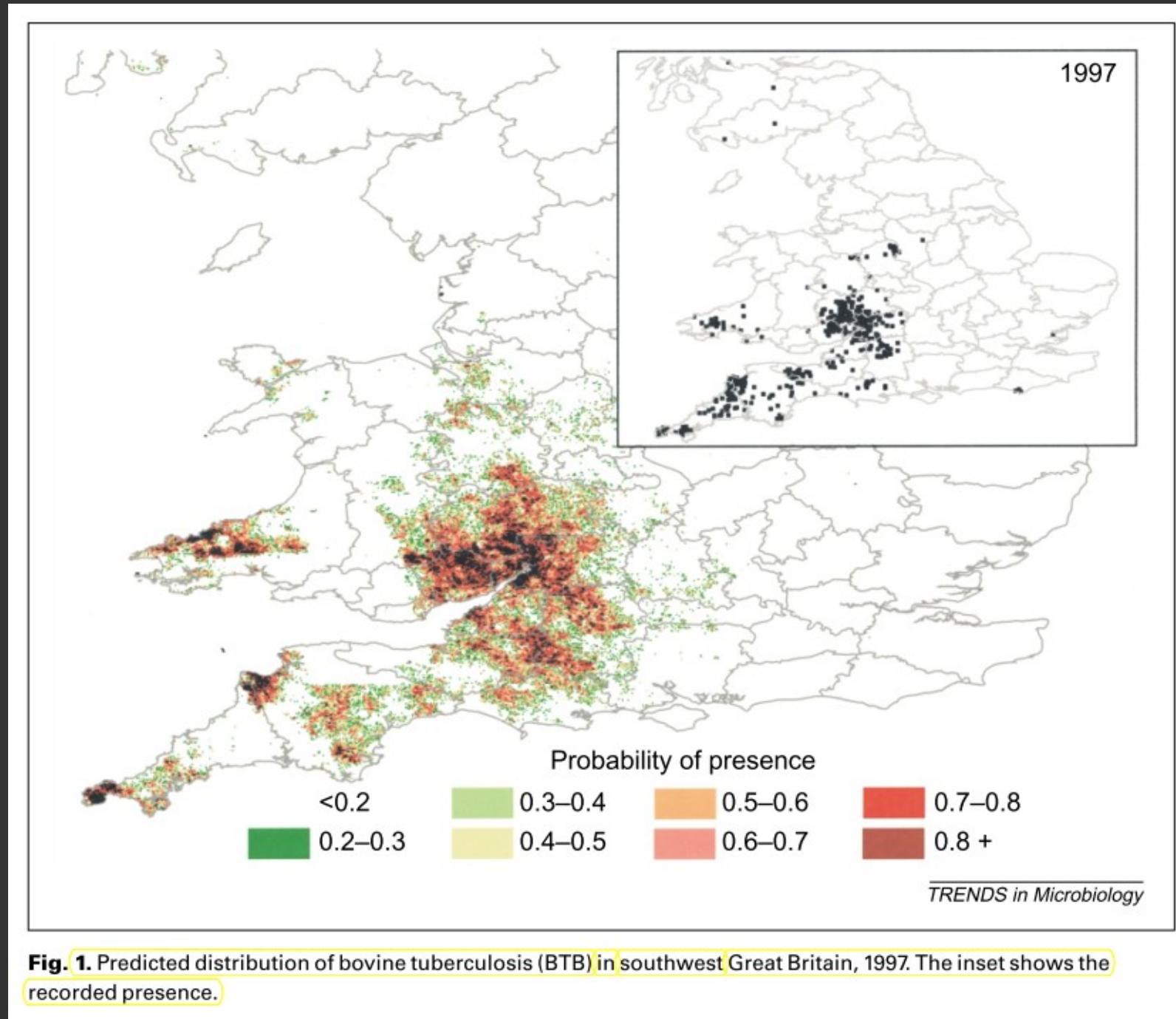
Symbols for predictor variables are slope (S), sinuosity (SIN\*), rainfall (R\*), southern oscillation index (SOI), distance to nearest town (T), distance to nearest gully (G), distance to water (W), elevation (E), forest (F) and SE/NW modified aspect (A). For rainfall and southern oscillation index, the numbers after the symbol indicate the number of months over which the values were calculated, while for sinuosity the value after the symbol indicates the distance (m) over which the value was calculated.

Research News

# Mapping bovine tuberculosis in Great Britain using environmental data

G.R. William Wint, Timothy P. Robinson, David M. Bourn, Peter A. Durr, Simon I. Hay,  
Sarah E. Randolph and David J. Rogers

- Modelling directly the presence of the disease.
- Remote sensing as environmental data source.
- Logistic regression.



*Ecology*, 83(1), 2002, pp. 255–268  
© 2002 by the Ecological Society of America

## COMPARING CLIMATE AND VEGETATION AS LIMITING FACTORS FOR SPECIES RANGES OF AFRICAN TICKS

G. S. CUMMING<sup>1</sup>

*Department of Zoology, Oxford University, South Parks Road, Oxford OX1 3PS, UK*

- Modelling the distribution of the disease's vector.
- Logistic regression.

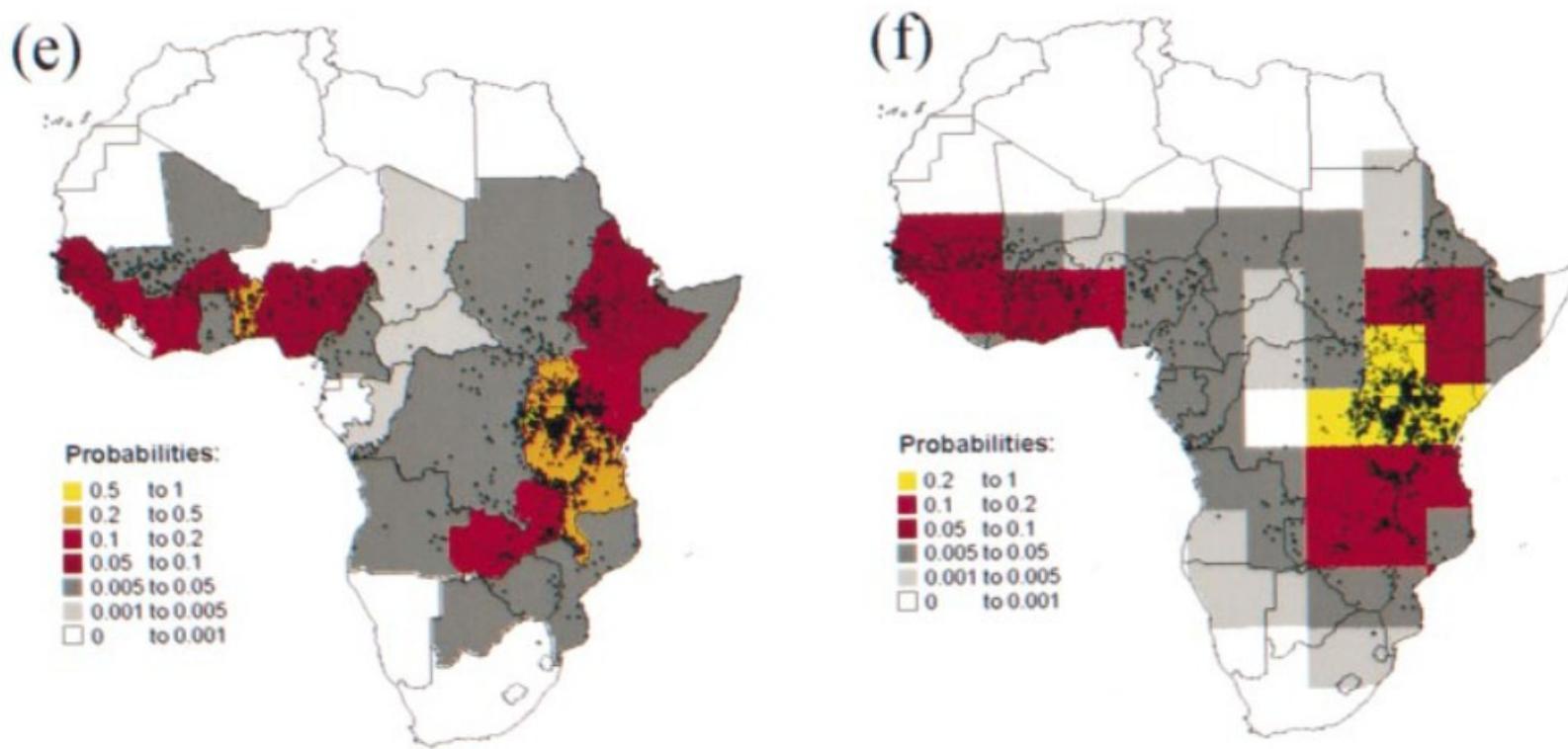


FIG. 4. Vegetation, climate, and an example of logistic regression model maps of Africa. (a) re-drawn map of Africa based on White (1983). Distinct polygons indicate different vegetation classes. In a few cases, different classes are shaded with the same color. (b) Map of 82 natural climatic categories derived from clustering rainfall, temperature, and elevation data. Note that no spatial information was included in the clustering procedure. (c–f) Examples of logistic regression models

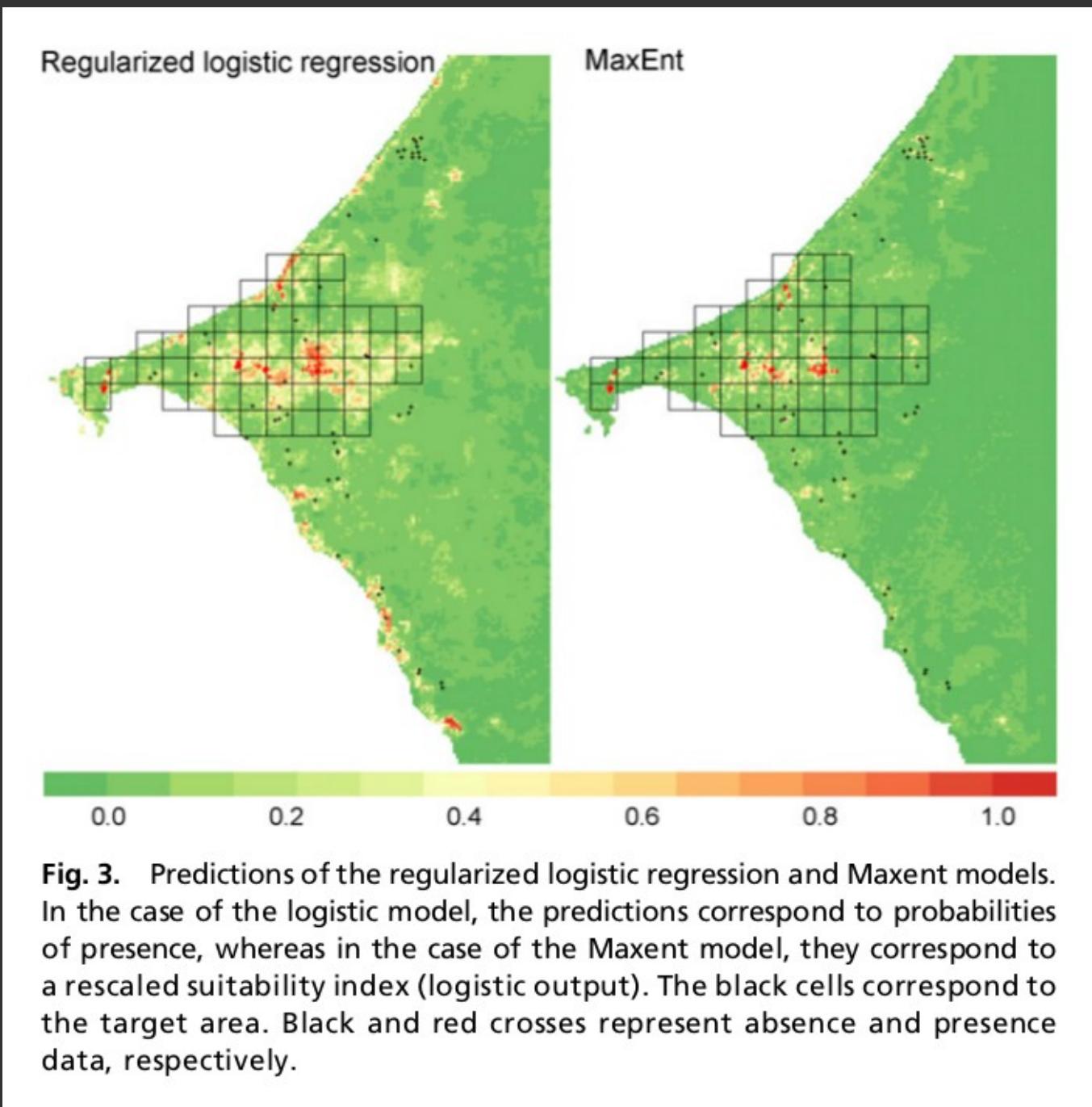


# Using species distribution models to optimize vector control in the framework of the tsetse eradication campaign in Senegal

Ahmadou H. Dicko<sup>a</sup>, Renaud Lancelot<sup>b,c</sup>, Momar T. Seck<sup>a</sup>, Laure Guerrini<sup>d,e</sup>, Baba Sall<sup>f</sup>, Mbargou Lo<sup>f</sup>, Marc J. B. Vreyen<sup>g</sup>, Thierry Lefrançois<sup>b,c</sup>, William M. Fonta<sup>h</sup>, Steven L. Peck<sup>i</sup>, and Jérémie Bouyer<sup>a,b,c,1</sup>

<sup>a</sup>Laboratoire National d'Elevage et de Recherches Vétérinaires, Institut Sénégalaïs de Recherches Agricoles, BP 2057, Hann, Dakar, Sénégal; <sup>b</sup>Unité Mixte de Recherche Contrôle des Maladies Animales Exotiques et Emergentes, Centre de Coopération Internationale en Recherche Agronomique pour le Développement, 34398 Montpellier, France; <sup>c</sup>Unité Mixte de Recherche 1309 Contrôle des Maladies Animales Exotiques et Emergentes, Institut National de la Recherche Agronomique, 34398 Montpellier, France; <sup>d</sup>Unité de Recherche Animal et Gestion Intégrée des Risques, Centre de Coopération Internationale en Recherche Agronomique pour le Développement, 34398 Montpellier, France; <sup>e</sup>Department Environment and Societies, University of Zimbabwe, Harare,

- Modelling the Tse-Tse fly.
- To help eradication programs.
- Logistic Regression and Maxent.
- Ecological Niche Factor Analysis (ENFA).



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Using species distribution modelling to predict bat fatality risk at wind farms

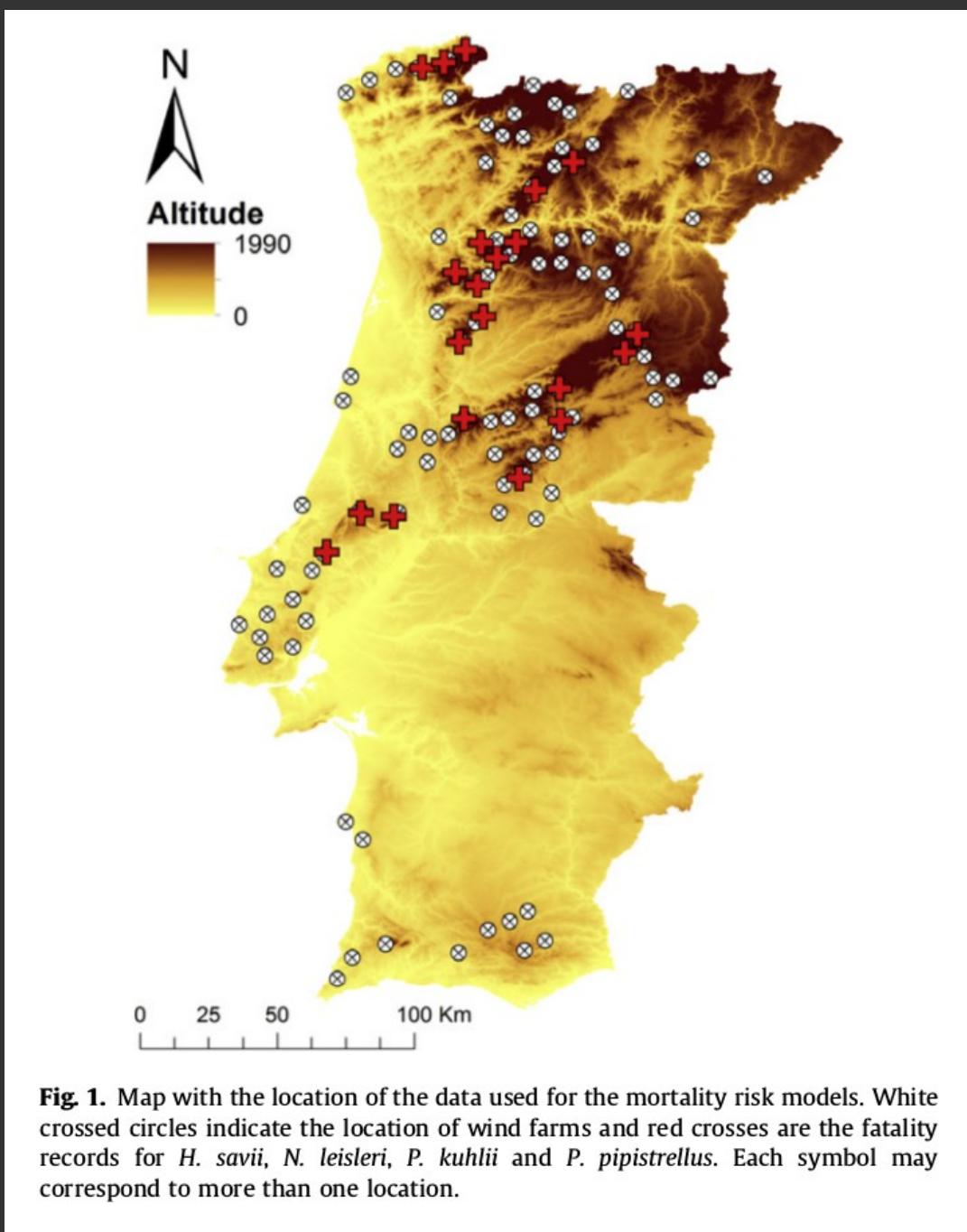
Helena Santos <sup>a,\*</sup>, Luísa Rodrigues <sup>b</sup>, Gareth Jones <sup>c</sup>, Hugo Rebelo <sup>a,c</sup>

<sup>a</sup> CIBIO, Centro de Investigação em Biodiversidade e Recursos Genéticos da Universidade do Porto, Instituto de Ciências Agrárias de Vairão,  
R. Padre Armando Quintas, 4485-661 Vairão, Portugal

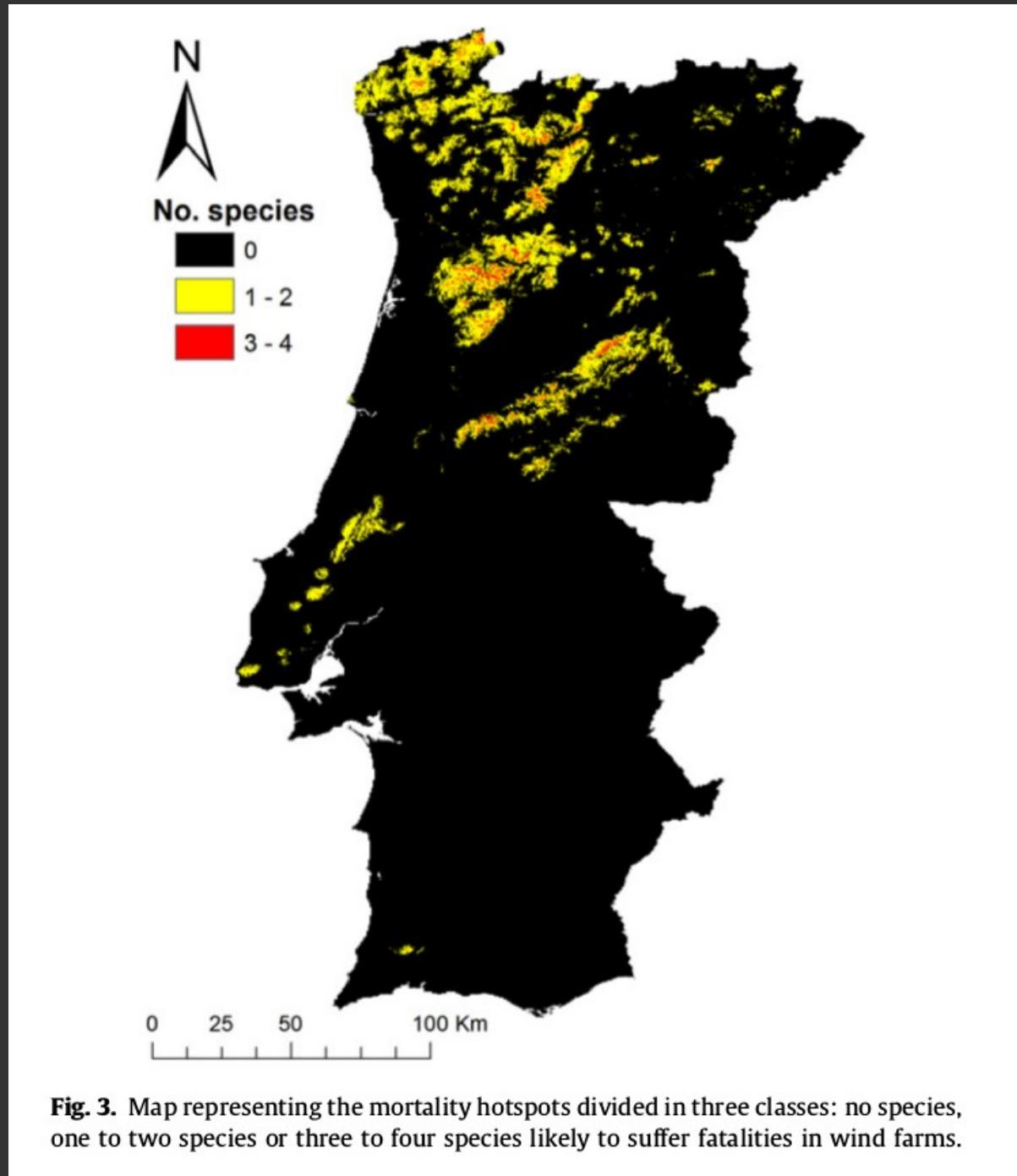
<sup>b</sup> ICNB, Instituto da Conservação da Natureza e da Biodiversidade, Rua de Santa Marta 55, 1169-230 Lisboa, Portugal

<sup>c</sup> School of Biological Sciences, University of Bristol, Woodland Road, Bristol BS8 1UG, United Kingdom

- Where are the areas of potentially high mortality risk for bats if wind farms are constructed?
- Which ecological variables promote bat mortality in wind farms?
- What is the range of values for these variables that increase mortality risk?
- How do mortality predictions relate to the species' predicted distributions and also to proposed areas for the construction of wind farms?
- Maxent.



**Fig. 1.** Map with the location of the data used for the mortality risk models. White crossed circles indicate the location of wind farms and red crosses are the fatality records for *H. savii*, *N. leisleri*, *P. kuhlii* and *P. pipistrellus*. Each symbol may correspond to more than one location.



*Diversity and Distributions*, (*Diversity Distrib.*) (2011) **17**, 408–421

BIODIVERSITY  
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## Incorporating evolutionary processes into conservation planning using species distribution data: a case study with the western Mediterranean herpetofauna

Sílvia B. Carvalho<sup>1,2,3,\*</sup>, José C. Brito<sup>1</sup>, Eduardo J. Crespo<sup>2,4</sup> and Hugh P. Possingham<sup>3,5</sup>

- Define conservation areas using species' chorotypes.
- ENMs are calculated with Maxent.

# LOCATION OF PROTECTED AREAS

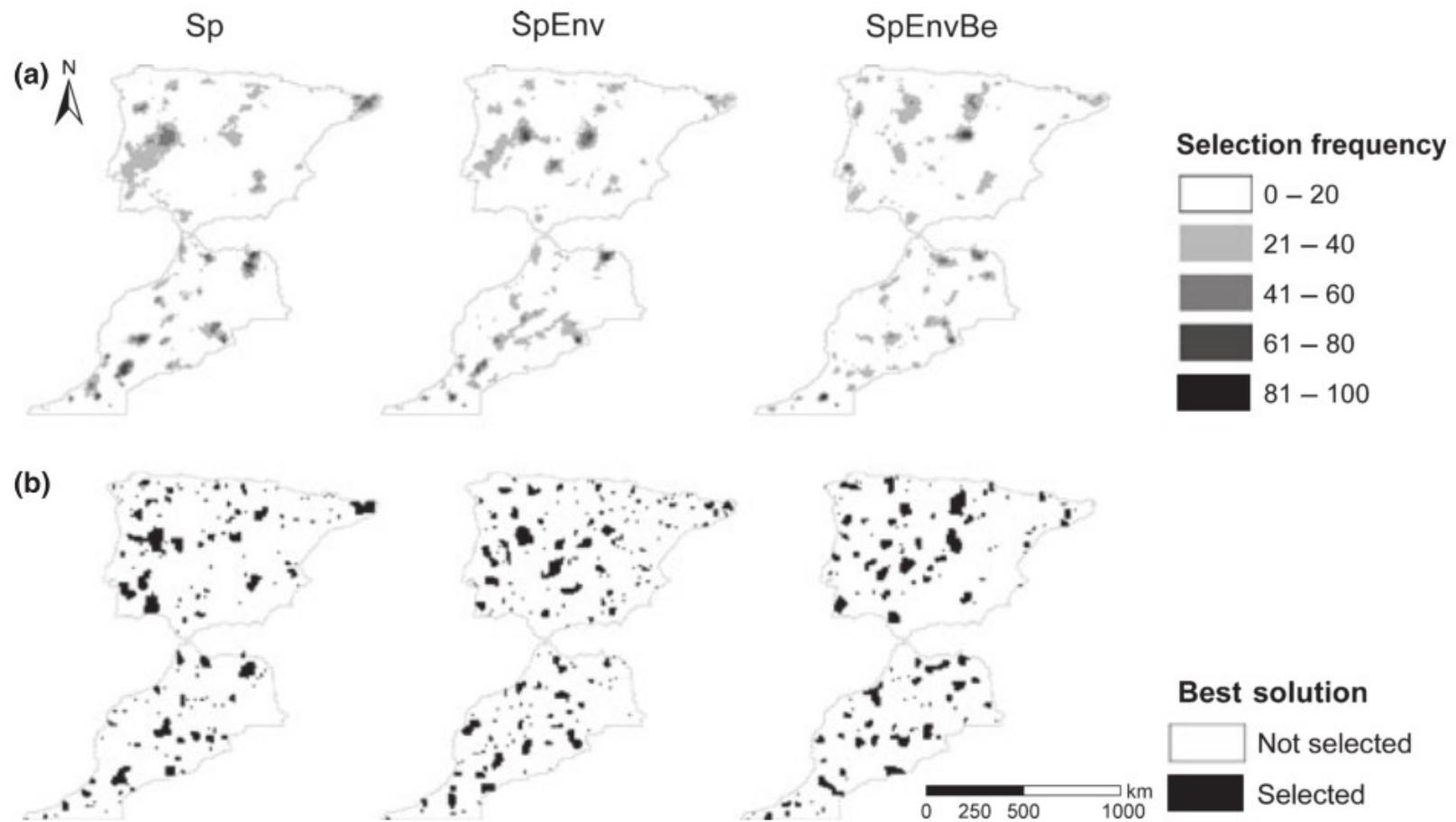


Figure 4 Spatial distribution of (a) Selection frequency values and (b) best solution, identified in each MARXAN scenarios: Sp, setting targets for species only; SpEnv, setting targets for species and for each environmental category of the overall area; SpEnvBE, setting targets for each species and for each environmental category identified within each biotic element. Maps shown in WGS 84 projection.

# The Use of Ecological Niche Modeling to Infer Potential Risk Areas of Snakebite in the Mexican State of Veracruz

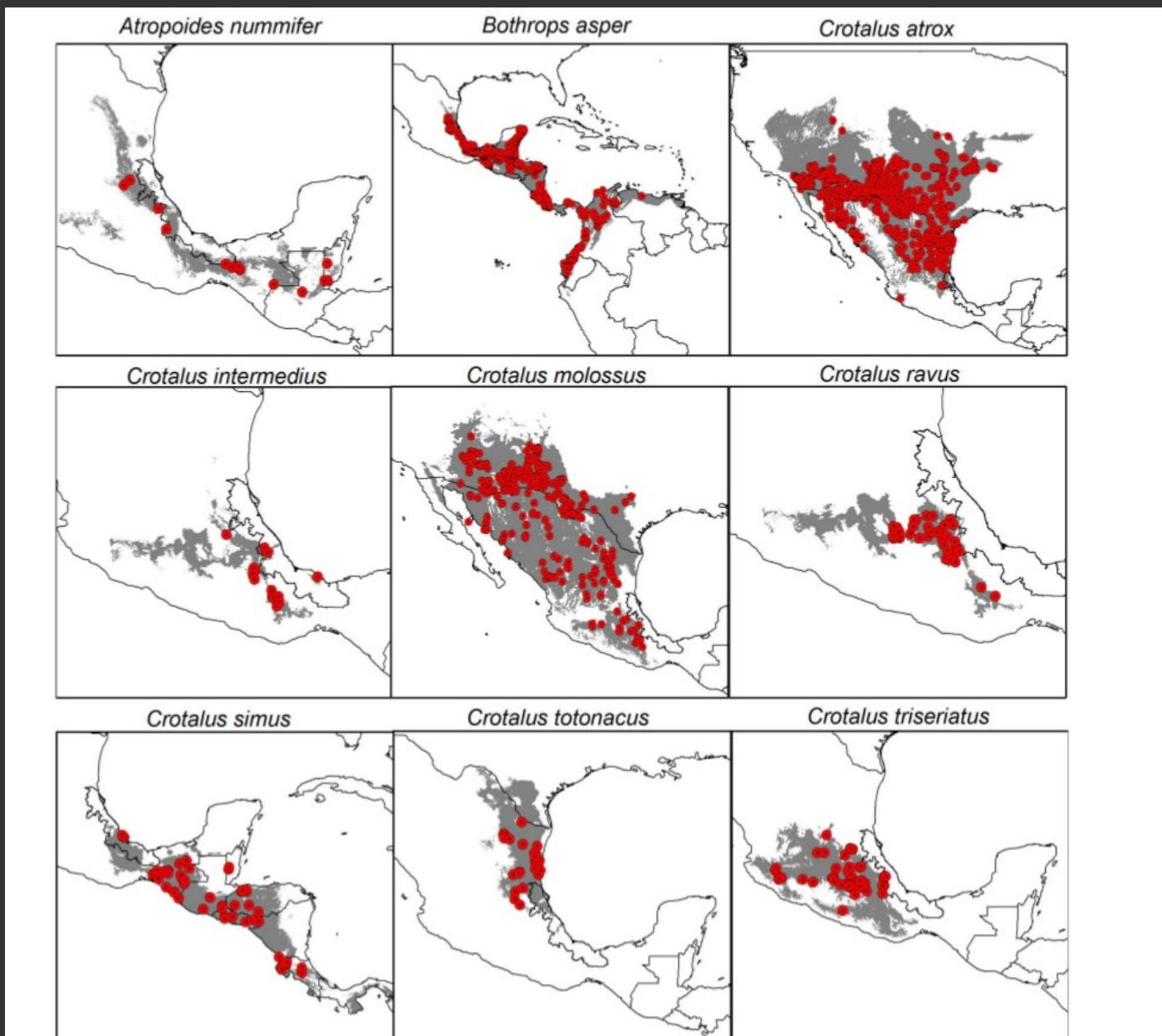
**Carlos Yañez-Arenas<sup>1\*</sup>, A. Townsend Peterson<sup>1</sup>, Pierre Mokondoko<sup>2</sup>, Octavio Rojas-Soto<sup>3</sup>,**

**Enrique Martínez-Meyer<sup>4</sup>**

**1** Biodiversity Institute, University of Kansas, Lawrence, Kansas, United States of America, **2** División de Posgrado, Instituto de Ecología A.C., Xalapa, Veracruz, México, **3** Red de Biología Evolutiva, Instituto de Ecología A.C., Xalapa, Veracruz, México, **4** Instituto de Biología. Universidad Nacional Autónoma de México, México City, México

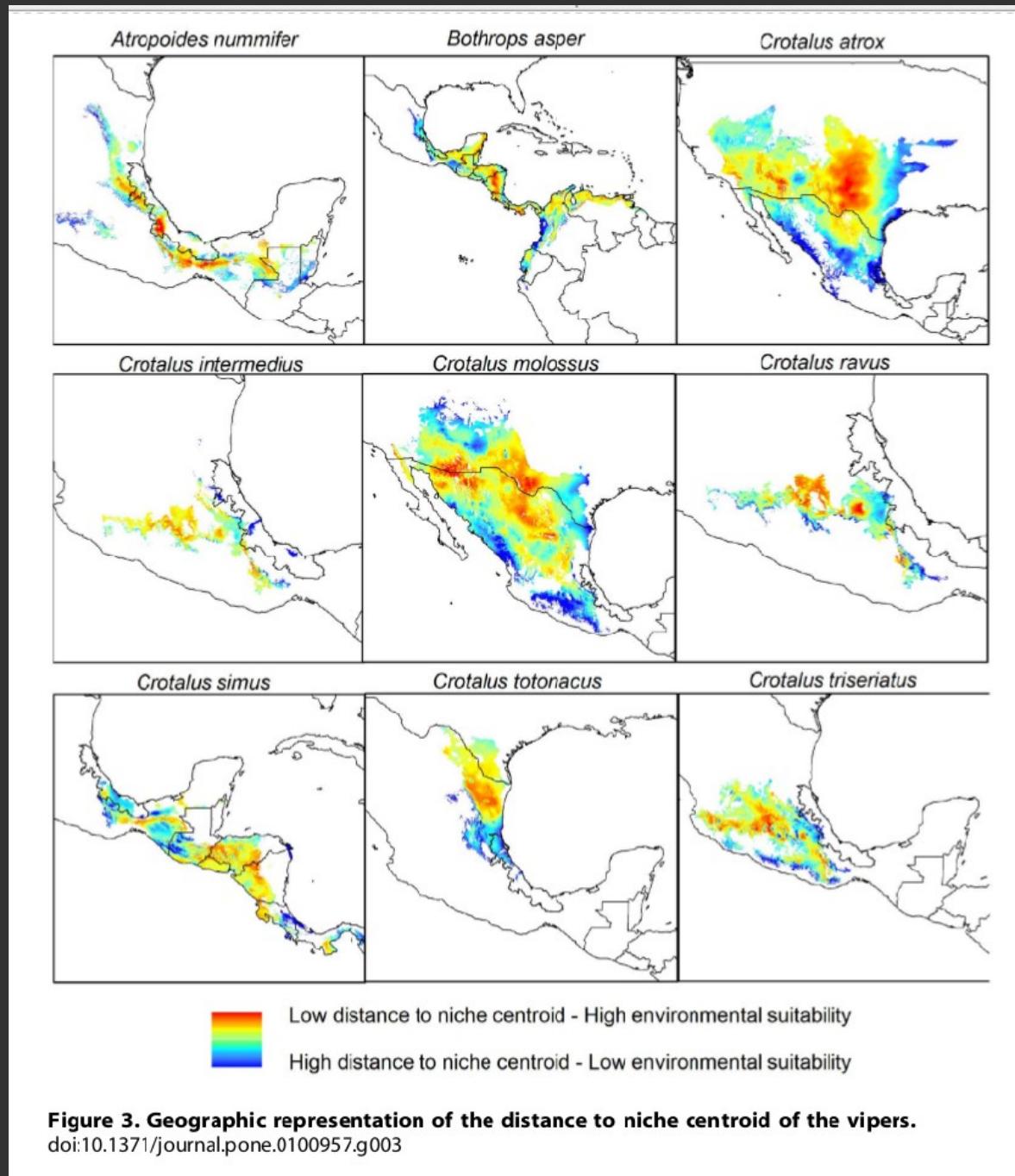
- Modelling risk areas of snake bites.
- Estimate potential geographic and ecological distributions of nine viper species.
- Distance to the species' niche centroid (DNC).
- Genetic Algorithm for Rule-set Production: GARP.

# MODELLING SNAKE BITES



**Figure 2. Occurrences and potential distributions of the vipers commonly distributed in Veracruz, Mexico.**  
doi:10.1371/journal.pone.0100957.g002

# MODELLING SNAKE BITES





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Journal of  
**Archaeological  
SCIENCE**

<http://www.elsevier.com/locate/jas>

## Human ecological niches and ranges during the LGM in Europe derived from an application of eco-cultural niche modeling

William E. Banks <sup>a,\*</sup>, Francesco d'Errico <sup>a,b</sup>, A. Townsend Peterson <sup>c</sup>, Marian Vanhaeren <sup>d</sup>, Masa Kageyama <sup>e</sup>, Pierre Sepulchre <sup>e</sup>, Gilles Ramstein <sup>e</sup>, Anne Jost <sup>f</sup>, Daniel Lunt <sup>g</sup>

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<sup>c</sup> Natural History Museum and Biodiversity Research Center, The University of Kansas, 1345 Jayhawk Boulevard, Lawrence, KS 66045-7561, USA

<sup>d</sup> Ethnologie préhistorique, UMR 7041-ArScAn, Université de Paris X, CNRS, 21 allée de l'Université, 92023 Nanterre Cedex, France

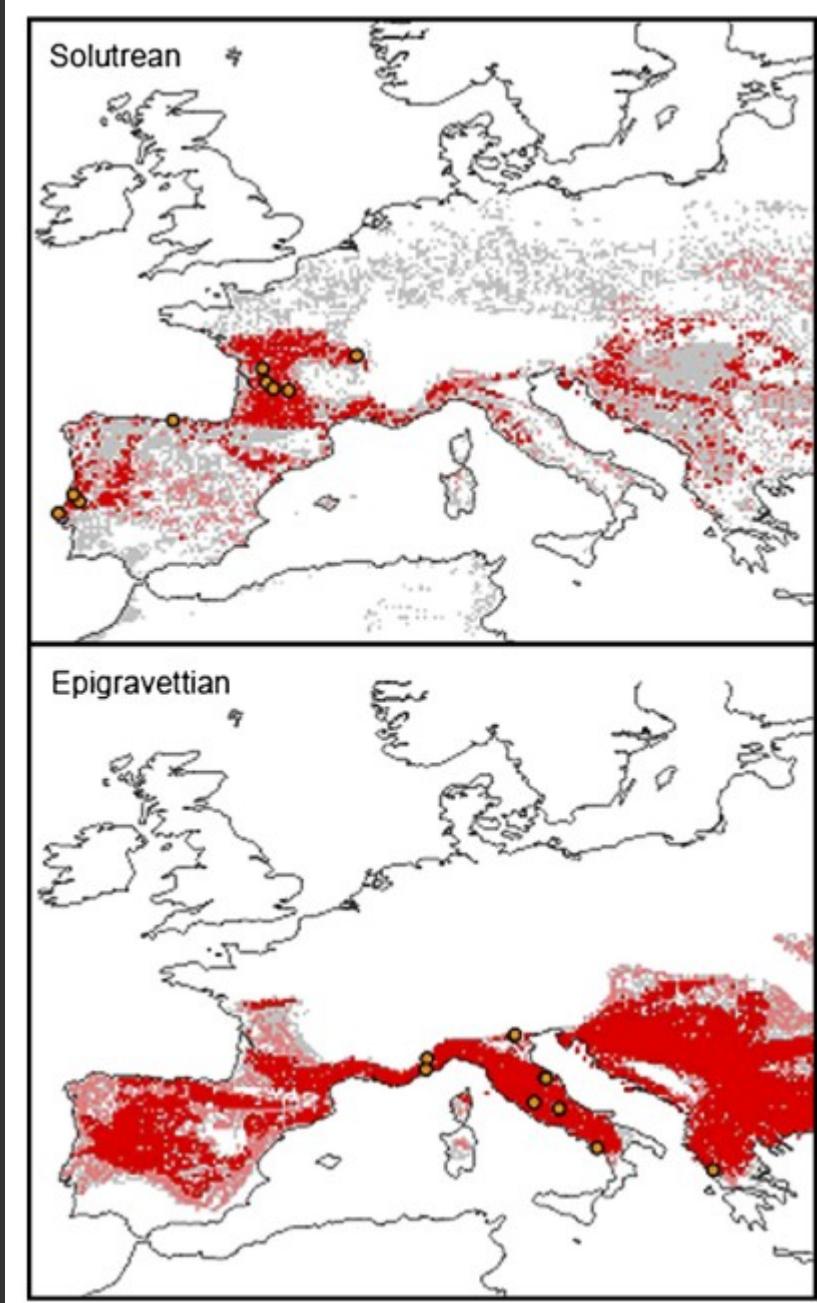
<sup>e</sup> Laboratoire des Sciences du Climat et de l'Environnement/IPSL, UMR 1572, CEA/CNRS/UVSQ, Saclay, L'Orme des Merisiers, Bâtiment 701, 91191 Gif-sur-Yvette Cedex, France

<sup>f</sup> UMR 7619 SISYPHE, Université Pierre-et-Marie Curie Paris VI, Boite 123, 4 Place Jussieu, 75252 Paris Cedex 05, France

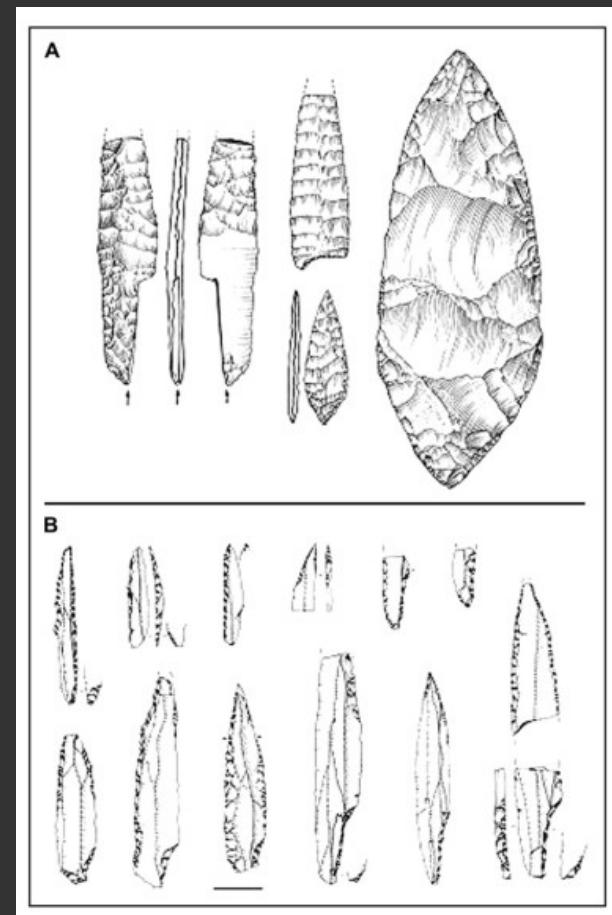
<sup>g</sup> School of Geographical Sciences, University Road, University of Bristol, Bristol BS8 1SS, United Kingdom

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# MODELLING HUMAN SETTLEMENTS



- Human cultures.
- Last Glaciar Maximum.
- Genetic Algorithm for Rule-set Production: GARP.



# QUESTIONS?