METHODS ON ECOLOGICAL NICHE MODELLING

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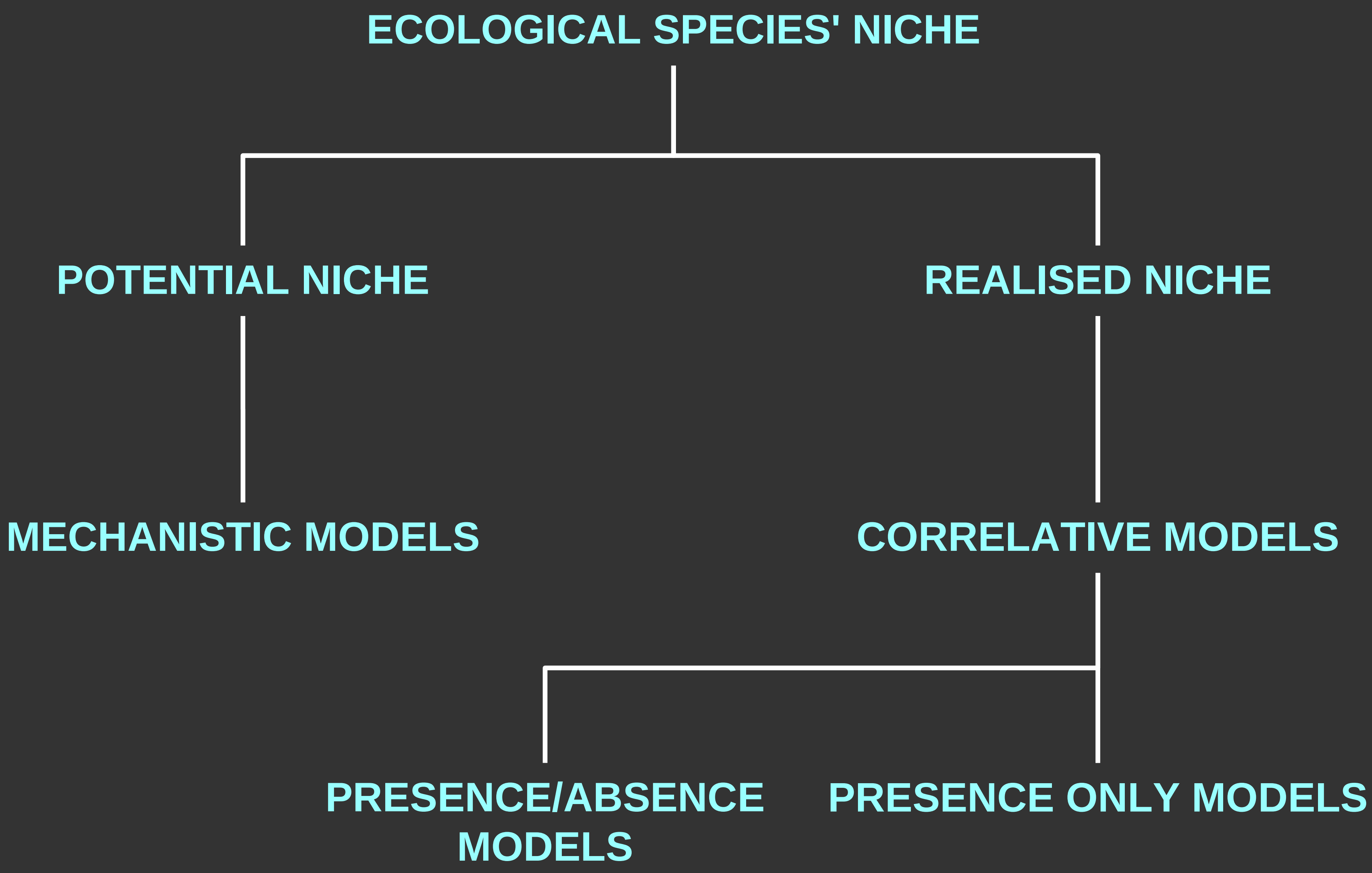
ECOLOGICAL NICHE MODELLING TECHNIQUES



ECOLOGICAL SPECIES' NICHE

POTENTIAL NICHE

REALISED NICHE

MECHANISTIC MODELS

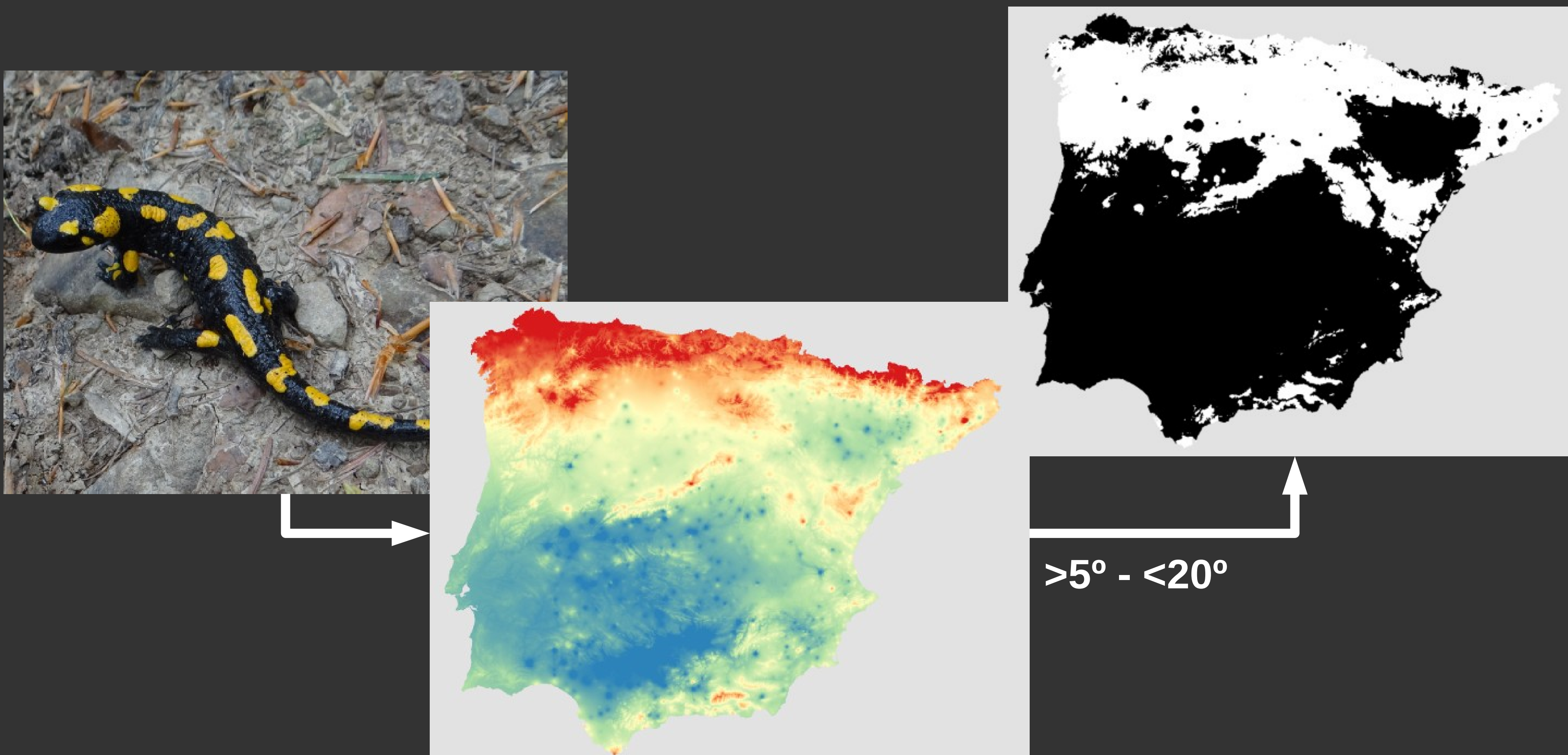
CORRELATIVE MODELS

PRESENCE/ABSENCE MODELS

PRESENCE ONLY MODELS

MECHANISTIC MODELS

- **Potential niche.**
- **There is no standard methodology.**
- **They use only physiological data.**
- **You must establish which is the mathematical relationship among physiological variables.**



- Realised niche.
- There are many standard methodologies.
- They use chorological data and environmental layers.
- Many different statistical ways to establish the relationship among species records' and environmental variables.
- Ensemble models (Araújo & New 2007).
- Each statistical methods is placed in a niche gradient (Jiménez-Valverde et al 2008)

MECHANISTIC MODELS

CORRELATIVE MODELS

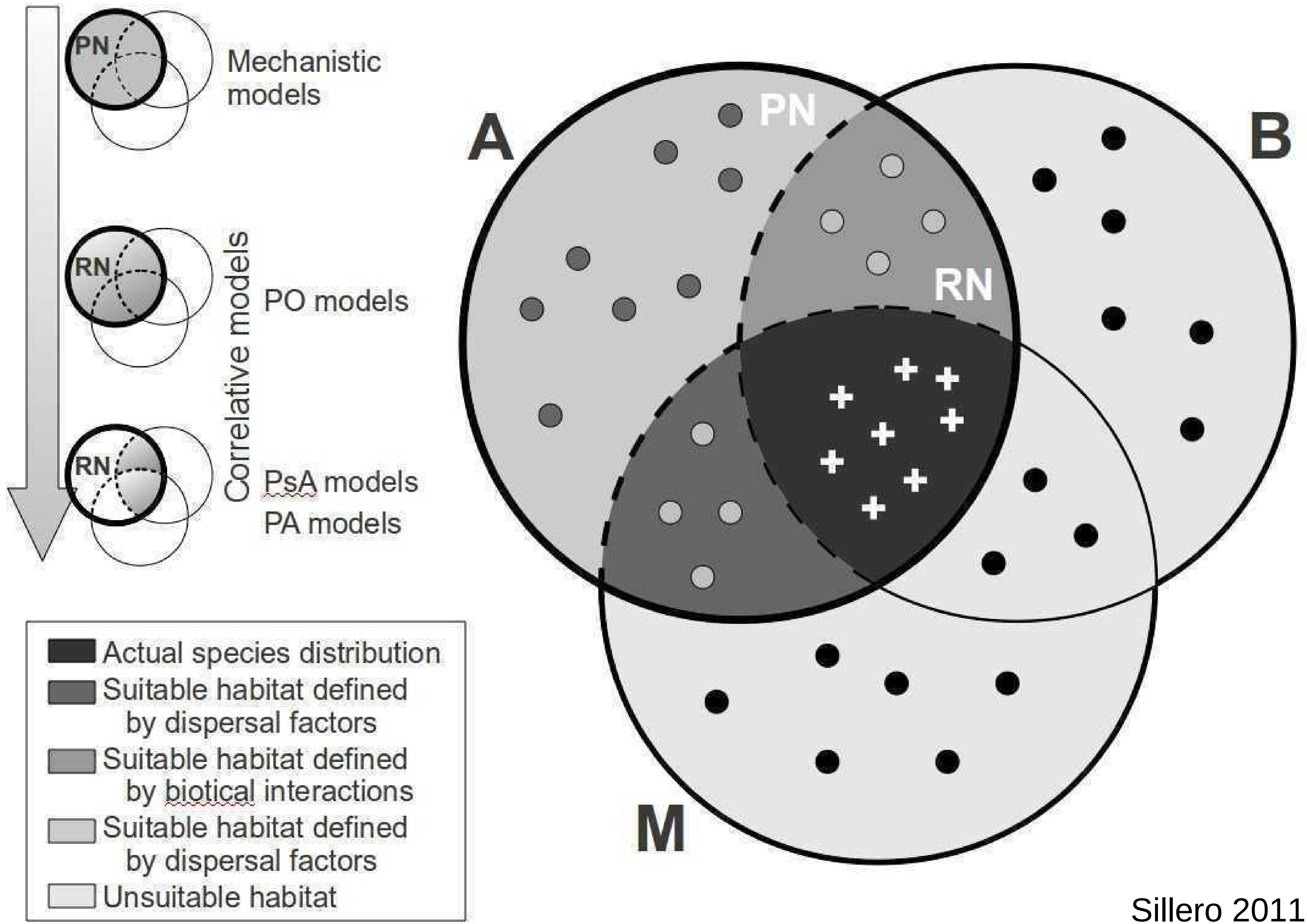
PRESENCE/ABSENCE MODELS

- Logistic regression
- Generalised Linear Models
- Generalised Additive Models
- Generalised Boosted Regression Models
- Random Forest
- Support Vector Machines
- Classification Tree Analysis
- Artificial Neural Network
- Flexible Discriminant Analysis
- Multiple Adaptive Regression Splines

PRESENCE ONLY MODELS

- Bioclim
- Domain
- ENFA
- GARP
- Maxent
- Mahalanobis distance

- **Presence/Absence data: to define the probability of finding a species in a particular place.**
- **Presence only data: to define the habitat suitability for a species in a particular place.**
- **The model output depends directly on the distribution of species' presences and absences.**
- **Presence records reflect the historical and dispersal factors.**



Sillero 2011

PRESENCE-ONLY MODELS

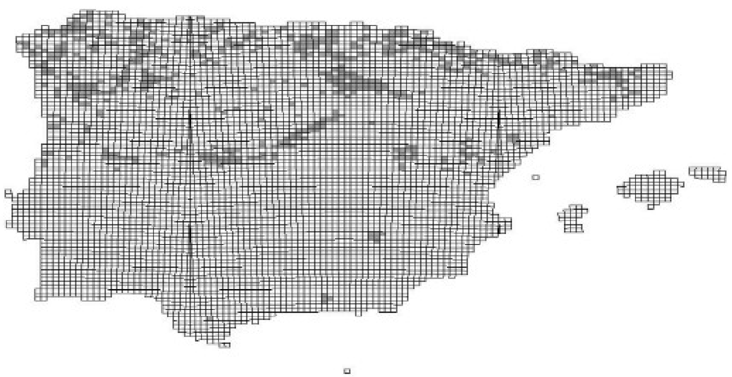
- Overlap Analysis
- Bioclim
- Domain
- Mahalanobis distance
- GARP

'True' presence-only models

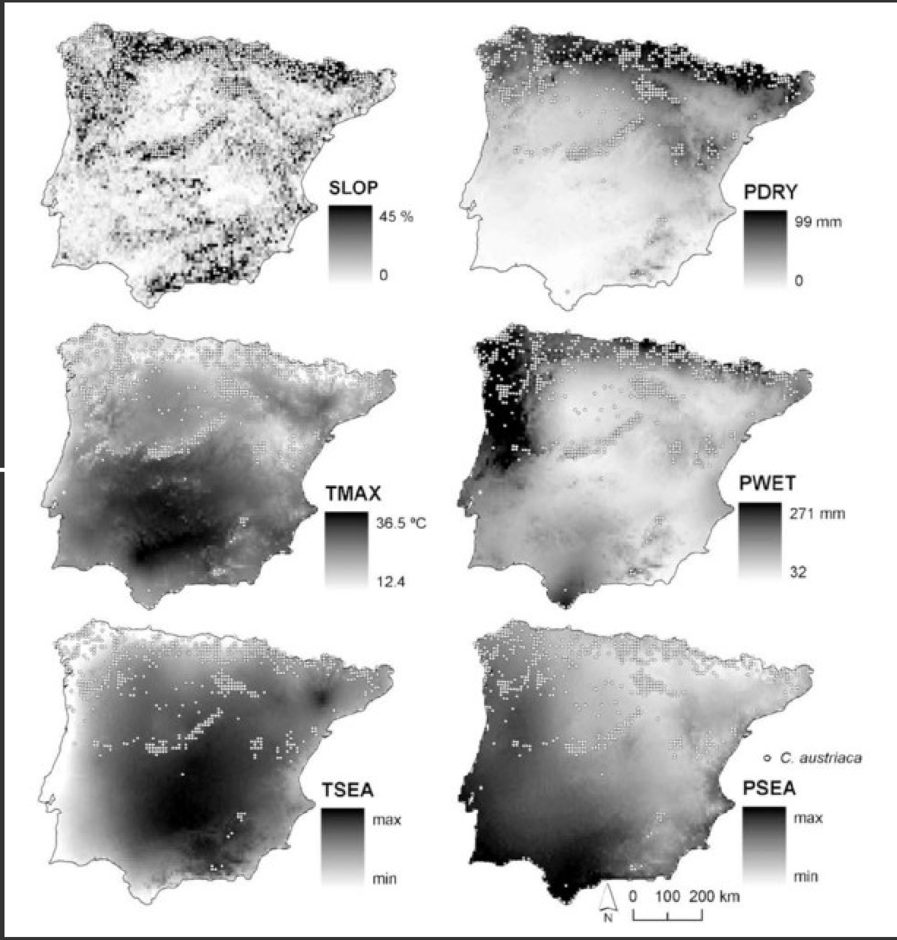
- ENFA
- Maxent

Background models

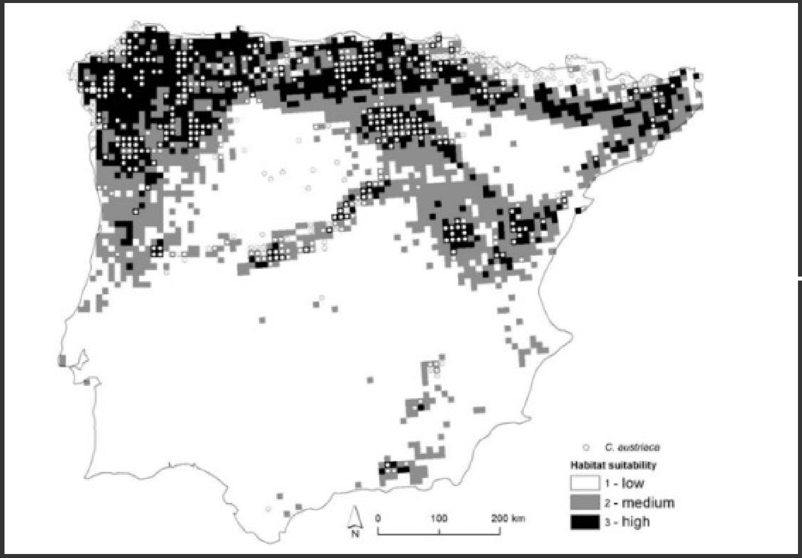
You only need environmental variables and species' records.



Species' records

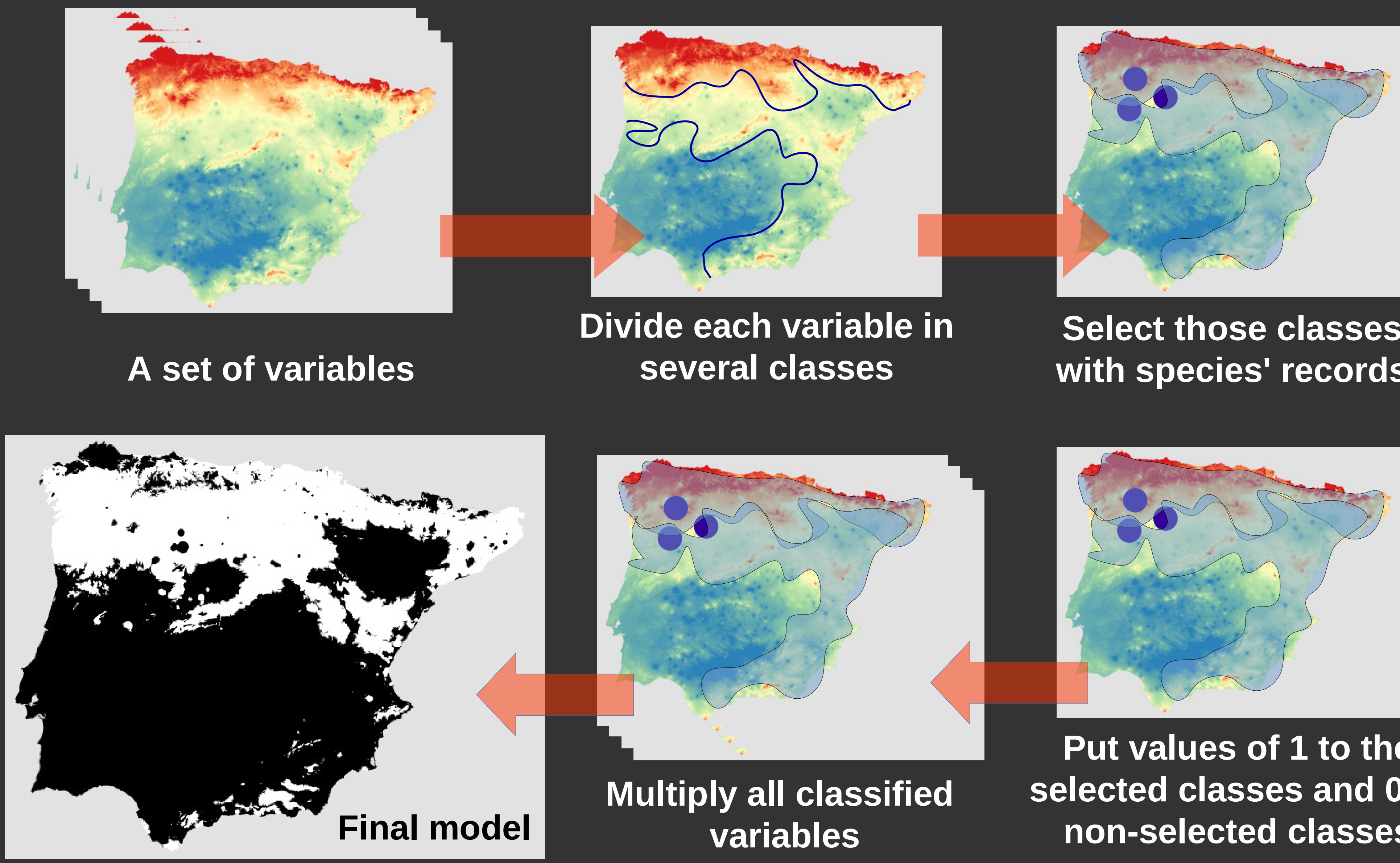


A set of variables



Final model

The most similar correlative method to mechanistic models.



- Most methods enclose the environmental space corresponding to species' records living in environmental extremes.
- Represent spatially in geographic space the surface occupied by these environmental extremes.

Carpenter et al 1993

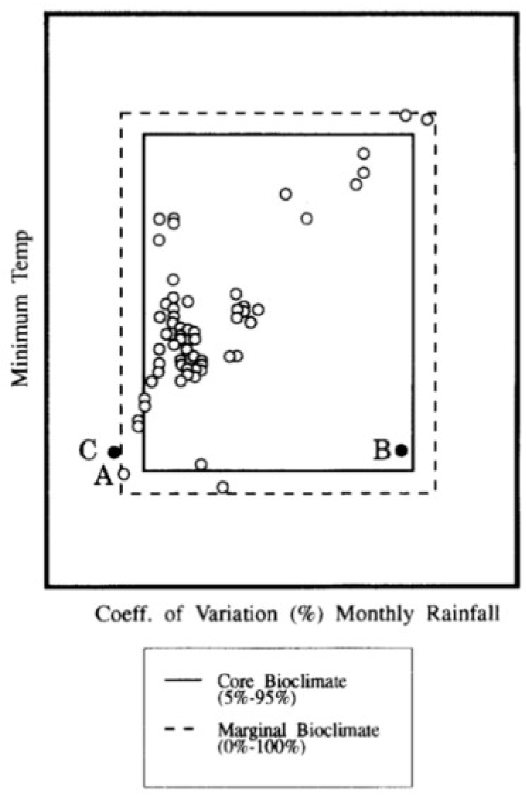


Figure 1. Boxcar environmental envelope.

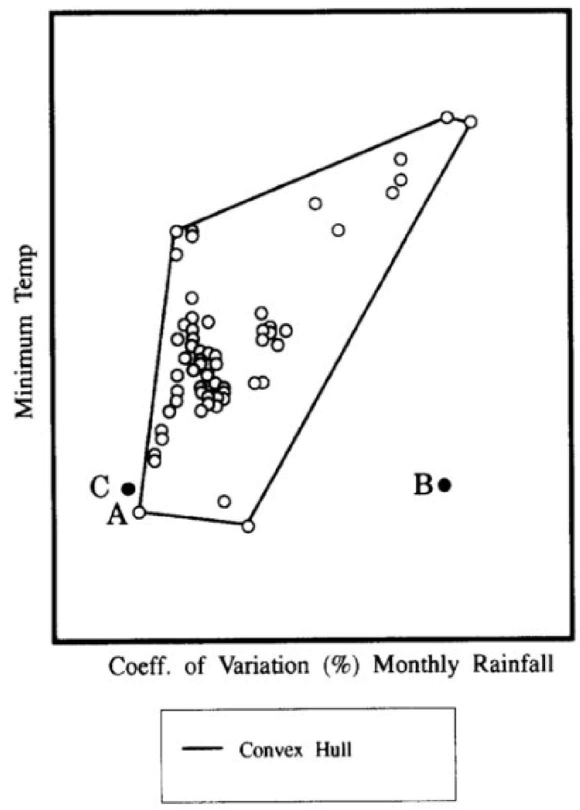


Figure 2. Convex hull environmental envelope.

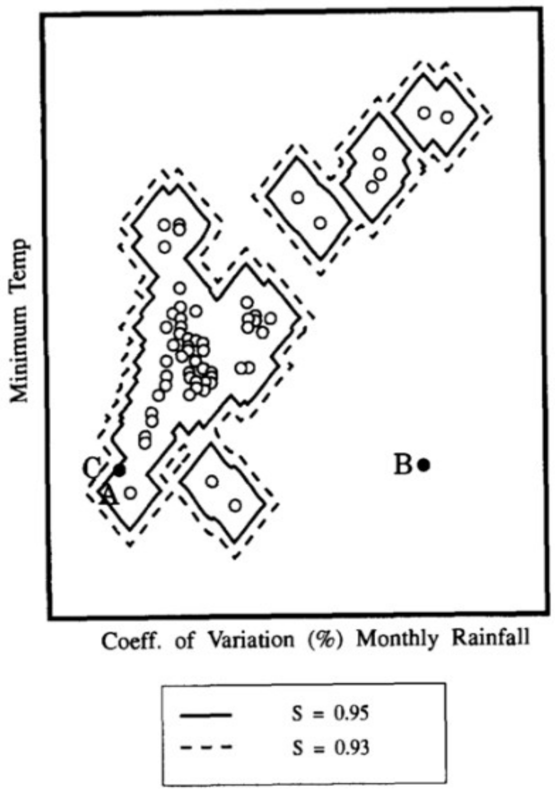


Figure 3. DOMAIN environmental envelope.

- **Climatic envelope model.**
- **Presence-only data.**
- **Similar to Overlap Analysis.**
- **Common Boxcar envelopes.**
- **Apply percentile limits.**

Beaumont et al 2005

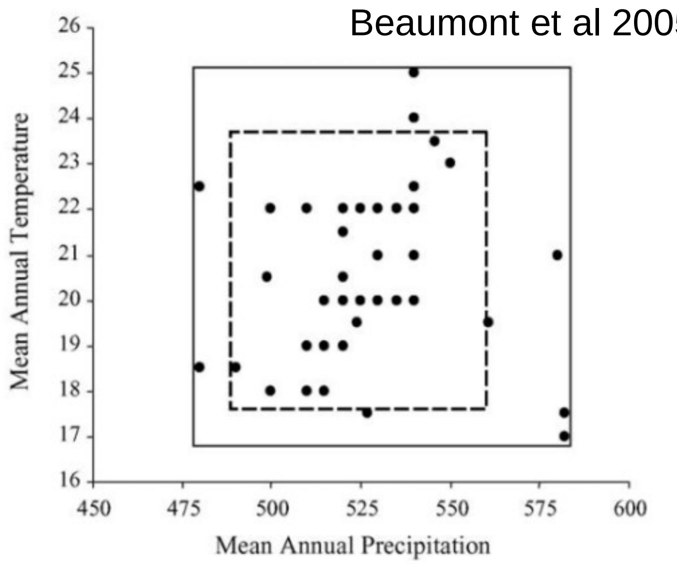


Fig. 1. Diagrammatic representation of a hypothetical two-dimensional bioclimatic envelope. Dots represent values of mean annual temperature and mean annual precipitation at each known location of a hypothetical species. In predicting a species' potential distribution, BIOCLIM would classify all locations with values within the extremes of the species envelope (unbroken line) as suitable. The dashed box represents those areas where climatic values outside of the 5–95th percentiles of the species envelope are excluded. This figure has been modified from Carpenter et al. (1993).

Carpenter et al 1993

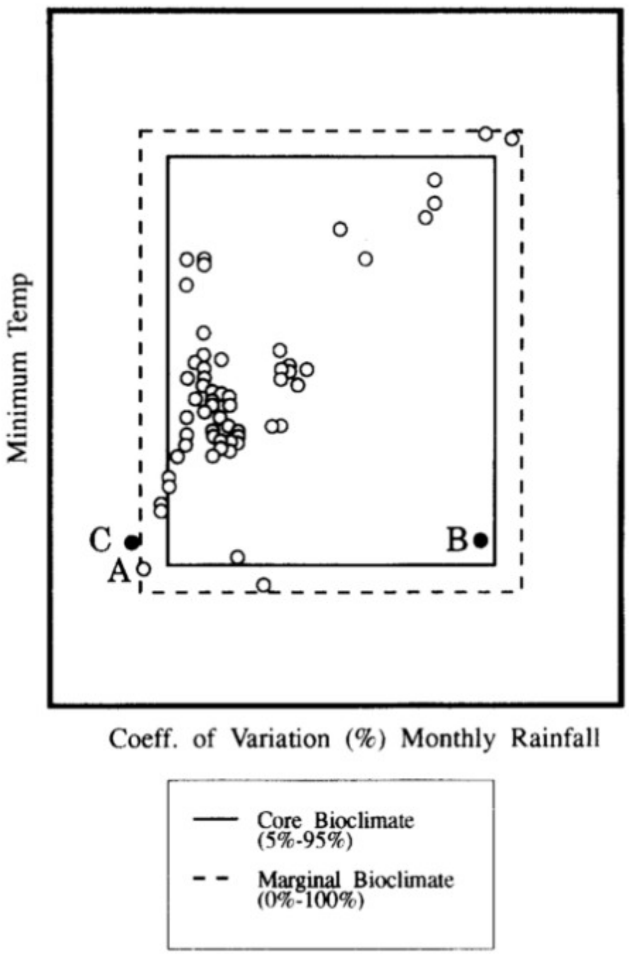


Figure 1. Boxcar environmental envelope.

- Climatic envelope model.
- Presence-only data.
- Convex Hull envelopes.
- CART algorithm.

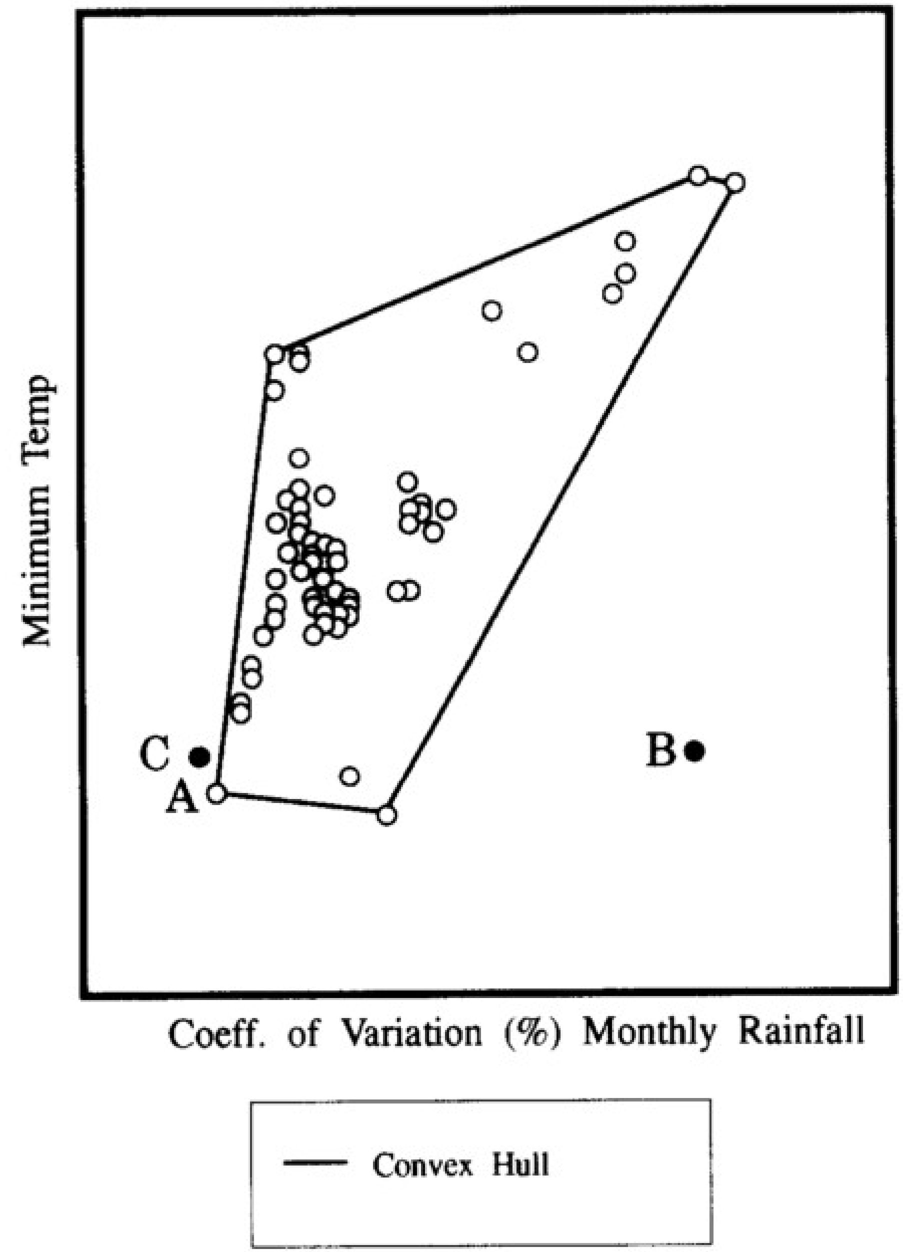


Figure 2. Convex hull environmental envelope.

Walker & Cocks 1991

- Climatic envelope model.
- Presence-only data.
- Parallelepiped envelopes.
- Gower metric.

$$d_{AB} = \frac{1}{p} \sum_{k=1}^{p} \left(\frac{|A_k - B_k|}{\text{range}k} \right)$$

Carpenter et al 1993

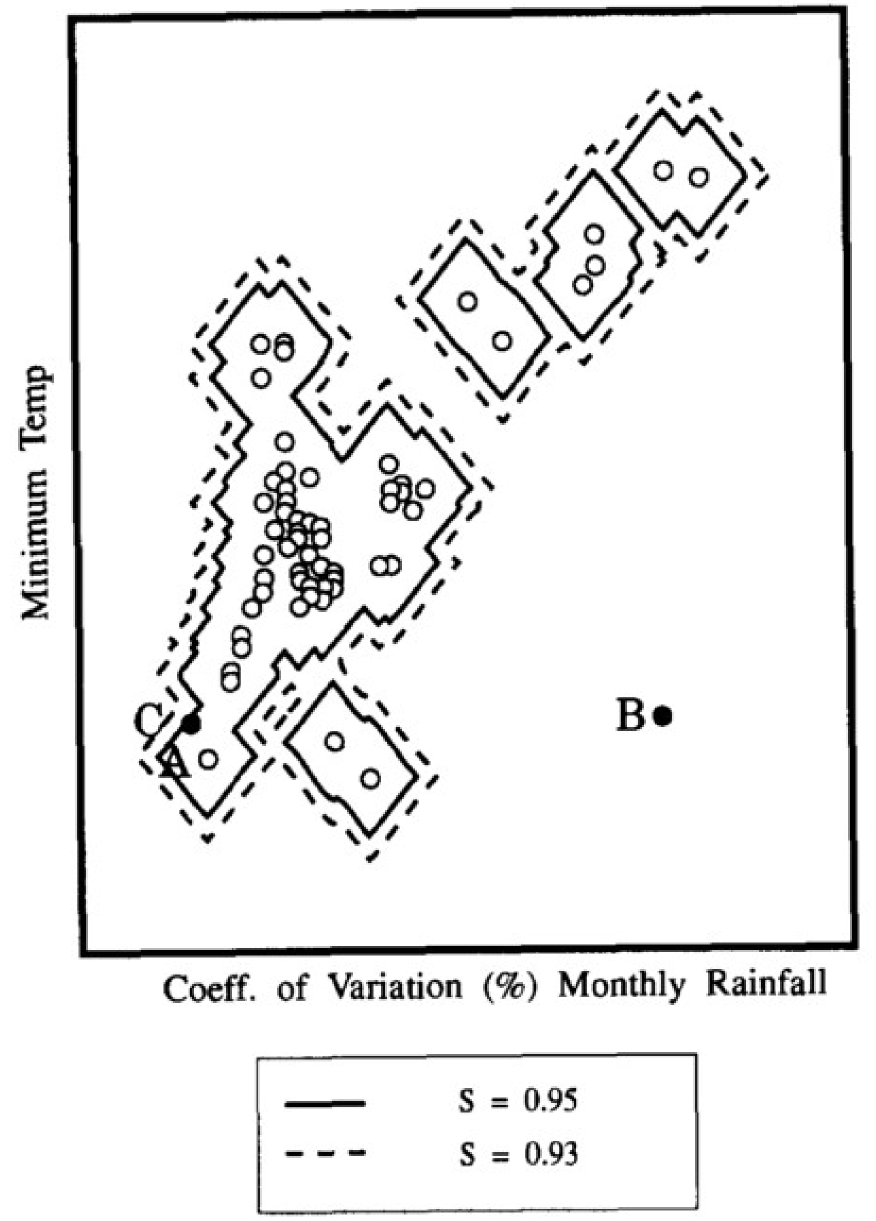


Figure 3. DOMAIN environmental envelope.

DOMAIN

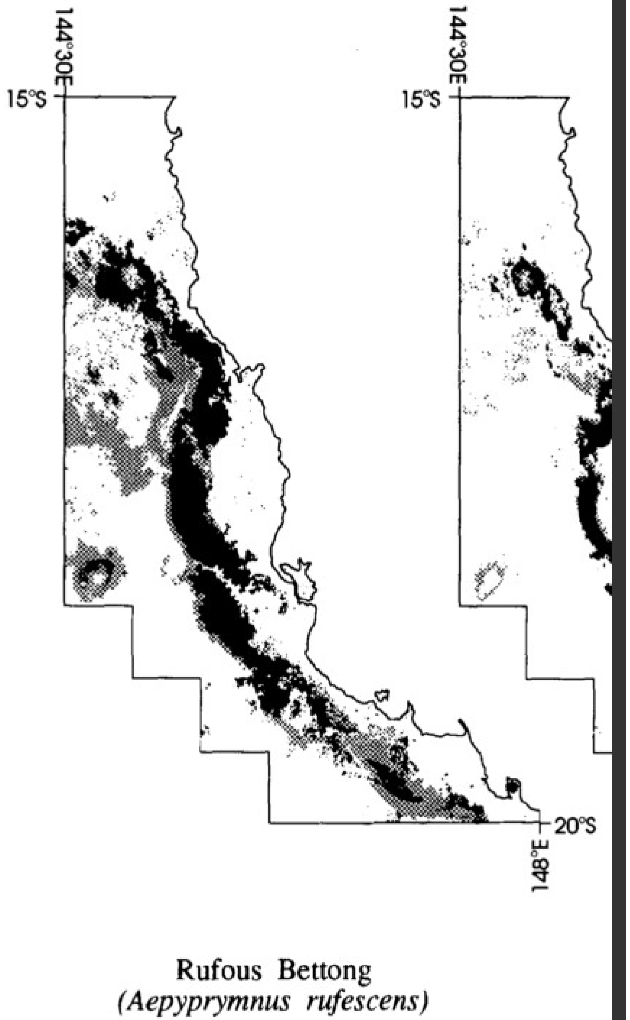


Figure 4. Boxcar projected distribution.

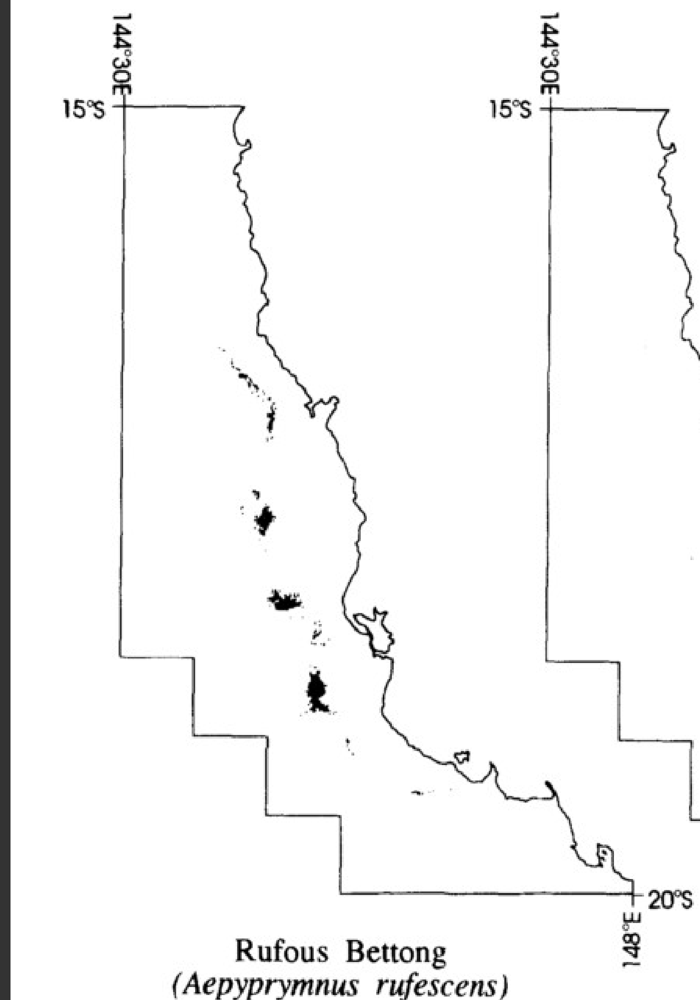


Figure 5. Convex hull projected distribution.

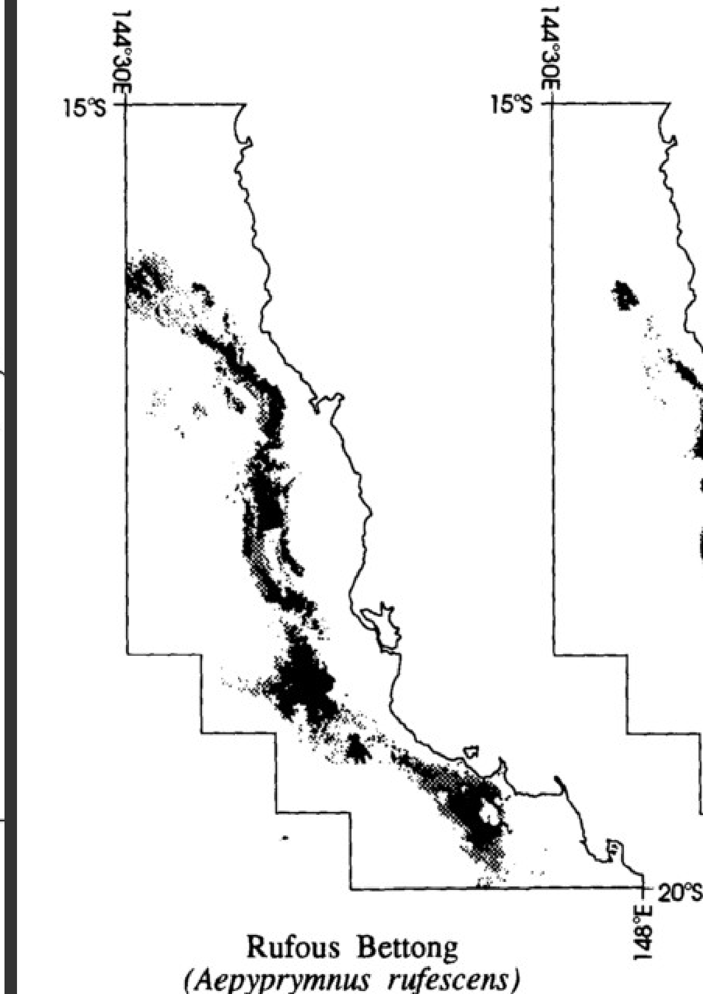
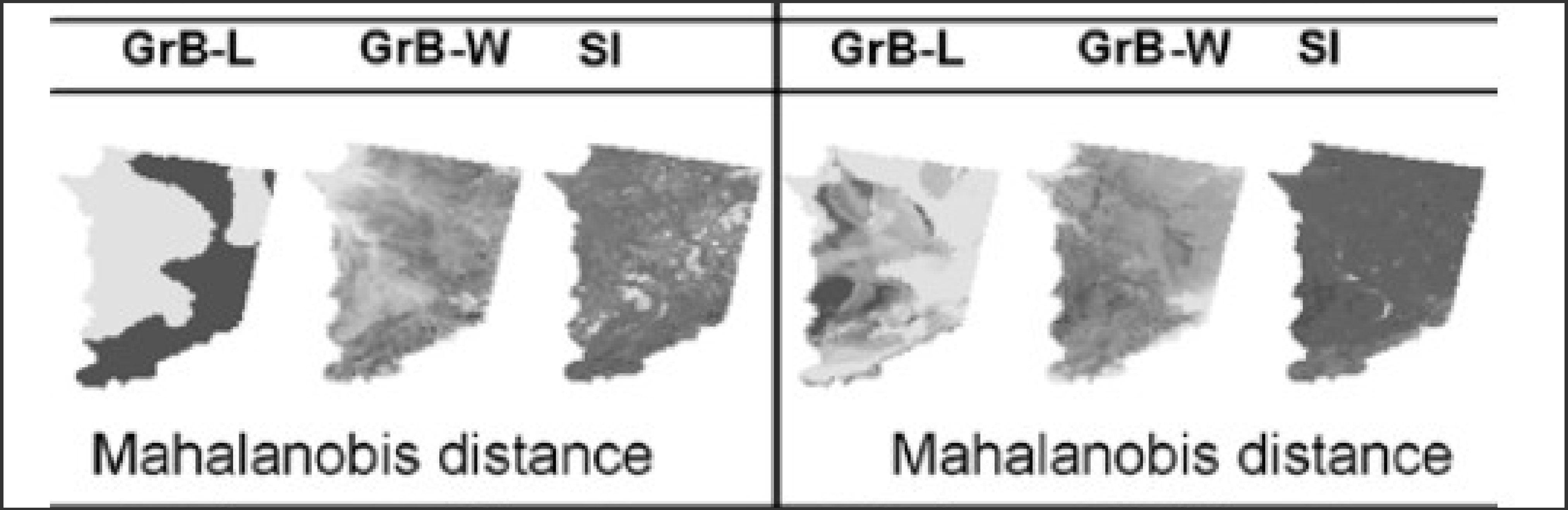


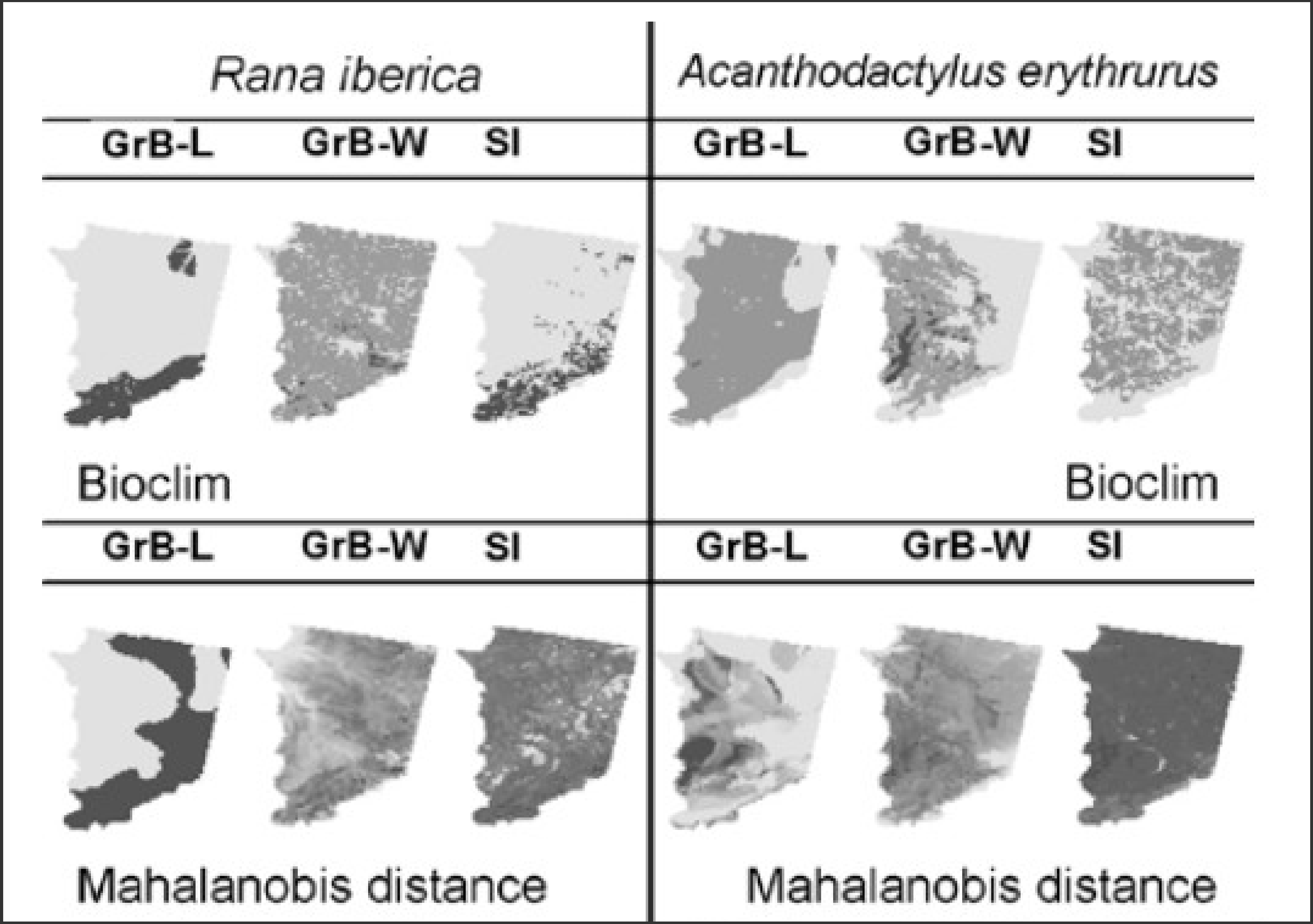
Figure 6. DOMAIN projected distribution.

Carpenter et al 1993

- Distance between a point P and a distribution D.
- It is a multi-dimensional generalisation of the idea of measuring how many standard deviations away P is from the mean of D.



Sillero et al 2012



Sillero et al 2012

- Many authors considered background data equal to pseudo-absences.
- Background data correspond to all the study area.
- Background data include the species' presences.
- Maxent extract 10000 points from all the background.
- ENFA calculates the mean and variance from background.
- Phillips et al 2009 proved that model performance increases using background data close to presence records.

Ecological Applications, 19(1), 2009, pp. 181–197

Sample selection bias and presence-only distribution models: implications for background and pseudo-absence data

Steven J. Phillips,[1,8] Miroslav Dudík,[2] Jane Elith,[3] Catherine H. Graham,[4] Anthony Lehmann,[5] John Leathwick,[6] and Simon Ferrier[7]

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Phillips et al 2009

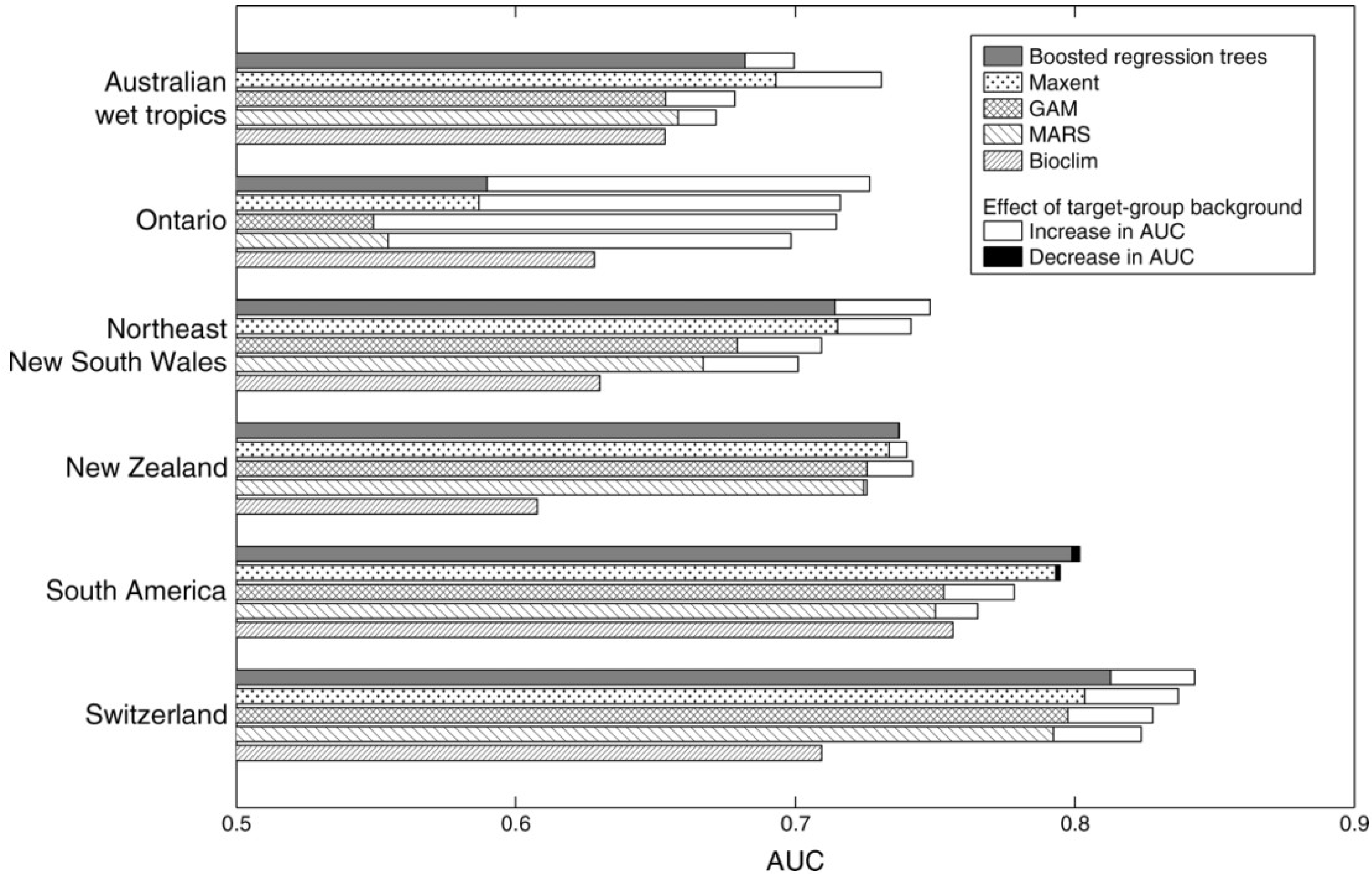


FIG. 4. Performance using target-group background of methods in each of the modeled regions, measured using area under the receiver operating characteristic curve (AUC) on independent presence–absence test data.

- Similar to a Principal Component Analysis but with ecological meaning.
- Presence-only data plus background data.
- Background data is the whole study area.
- It cannot produce ROC plots.
- Very difficult to compare with other methods.

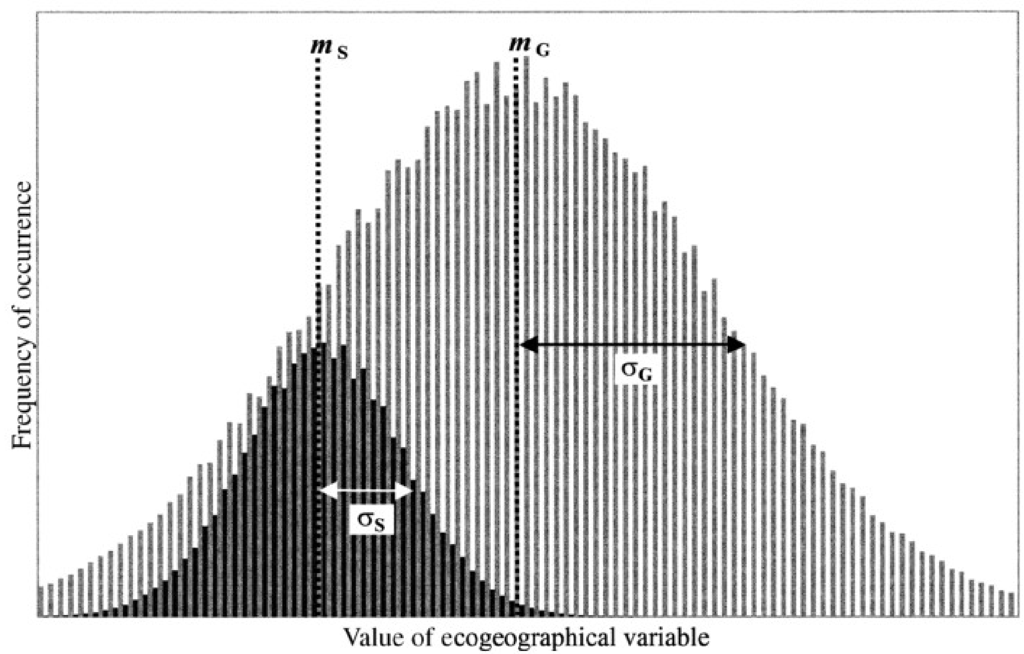


FIG. 1. The distribution of the focal species on any ecogeographical variable (black bars) may differ from that of the whole set of cells (gray bars) with respect to its mean ($m_S \neq m_G$), thus allowing marginality to be defined. It may also differ with respect to standard deviations ($\sigma_S \neq \sigma_G$), thus allowing specialization to be defined.

Hirzel et al 2002

- **Transform each variable in an uncorrelated factor.**

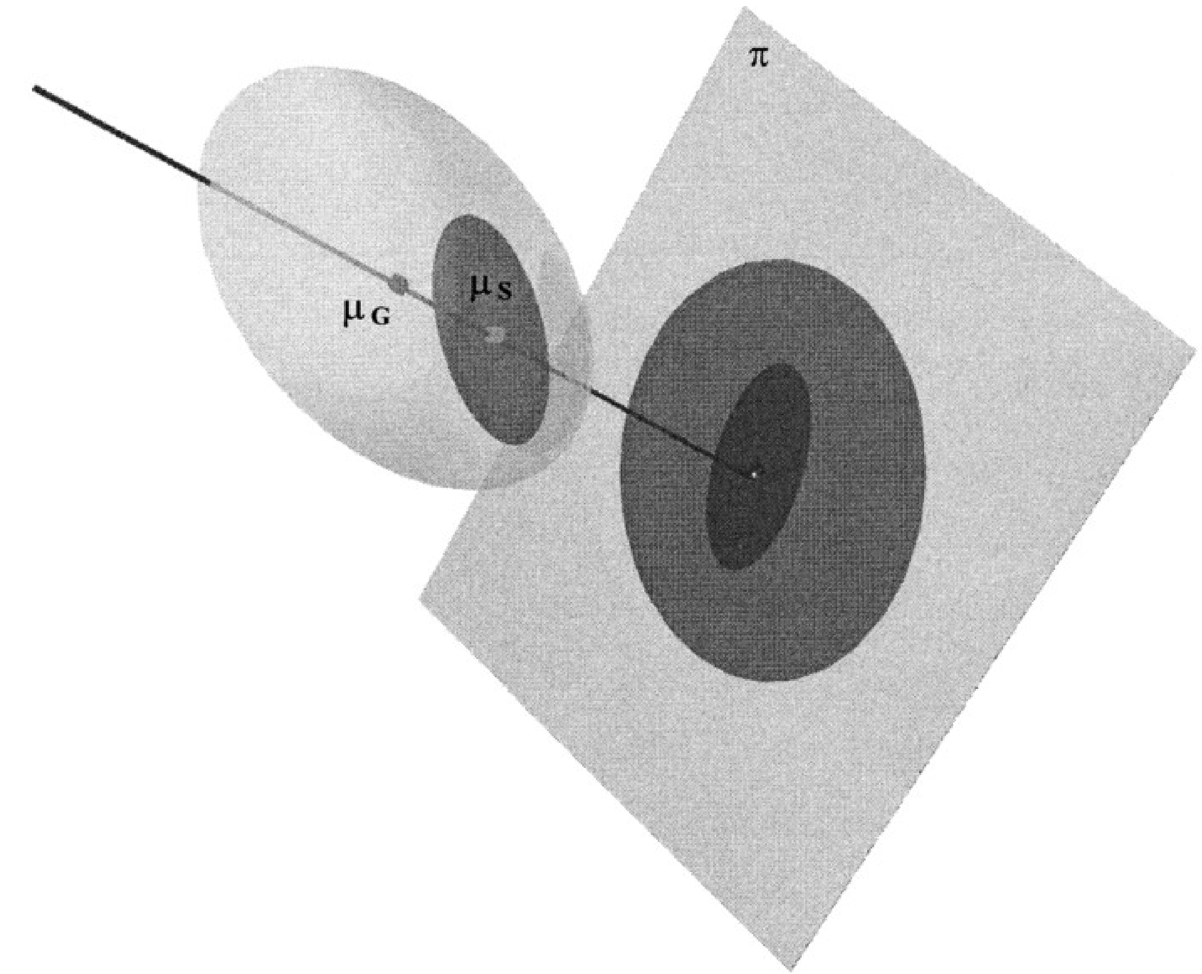


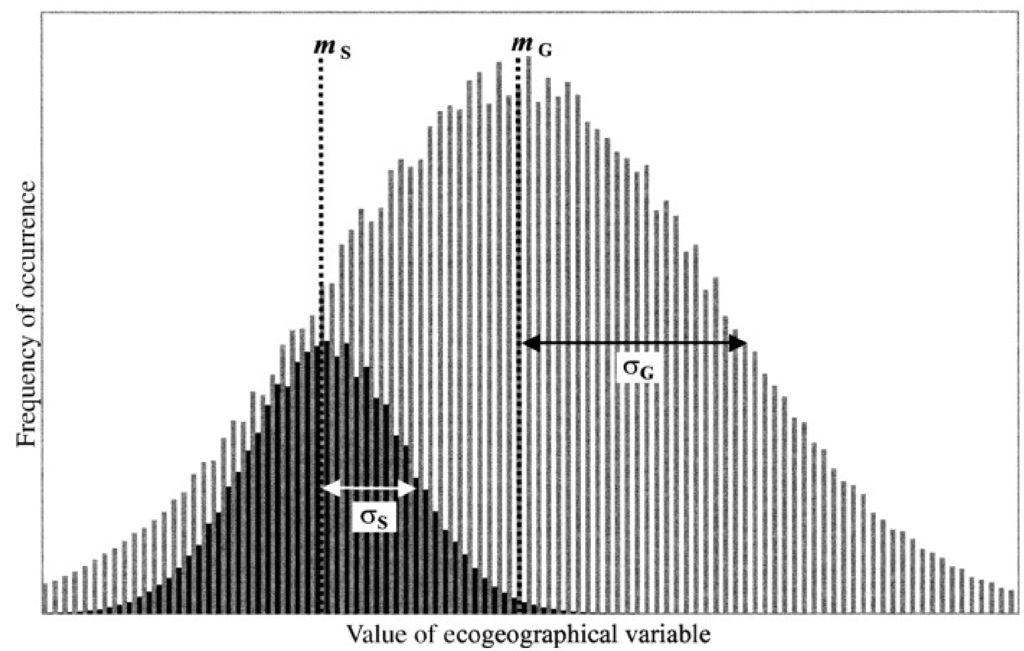
FIG. 2. Geometrical interpretation of the Ecological-Niche Factor Analysis. Square cells of the study area are represented in a three-EGV space. The larger, lighter balloon represents the global cloud of cells, while the smaller, darker balloon represents the subset of cells where the focal species was observed. The straight line passing through their centroids (μ_G and μ_S) is the marginality factor. In order to extract the variance associated with this factor, the cell coordinates are projected on a plane π perpendicular to it, thereby producing the two ellipses. In reality, those operations are typically conducted with 20–30 EGVs.

Hirzel et al 2002

- The first factor is called Marginality (M).
- The remaining factors are called Specialization (S).
- Tolerance is the inverse of the Specialization.

$$M = \frac{\sqrt{\sum_{i=1}^{V} m_i^2}}{1.96}$$

$$S = \frac{\sqrt{\sum_{i=1}^{V} \lambda_i}}{V}$$



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Hirzel et al 2002

- All factors are related by a **Geometric Mean**.

$$H_G(\mathbf{P}) = \sqrt[N]{\prod_{i=1}^{N} \delta(\mathbf{P},\mathbf{O}_i)}$$

Hirzel & Arlettaz 2003

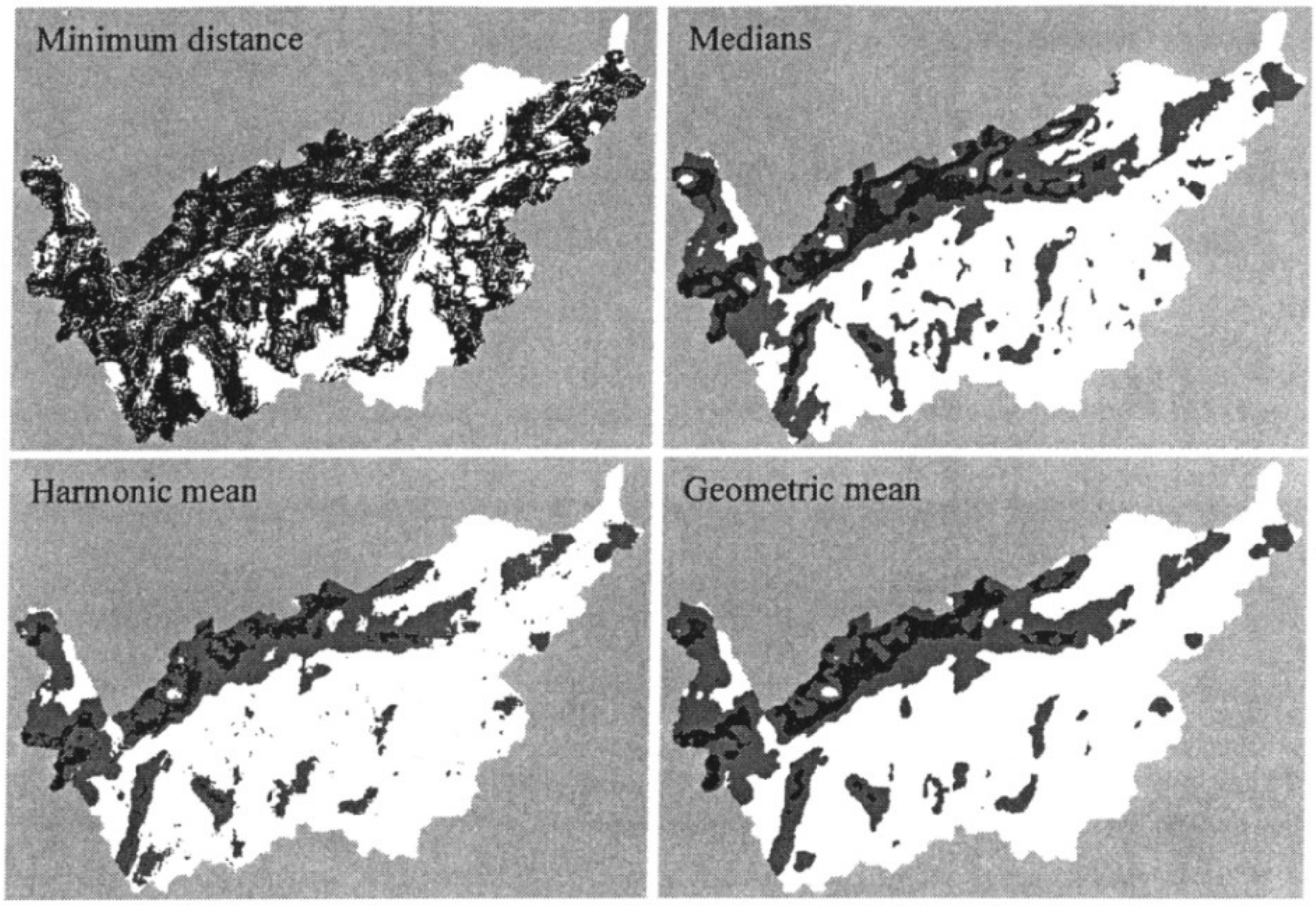
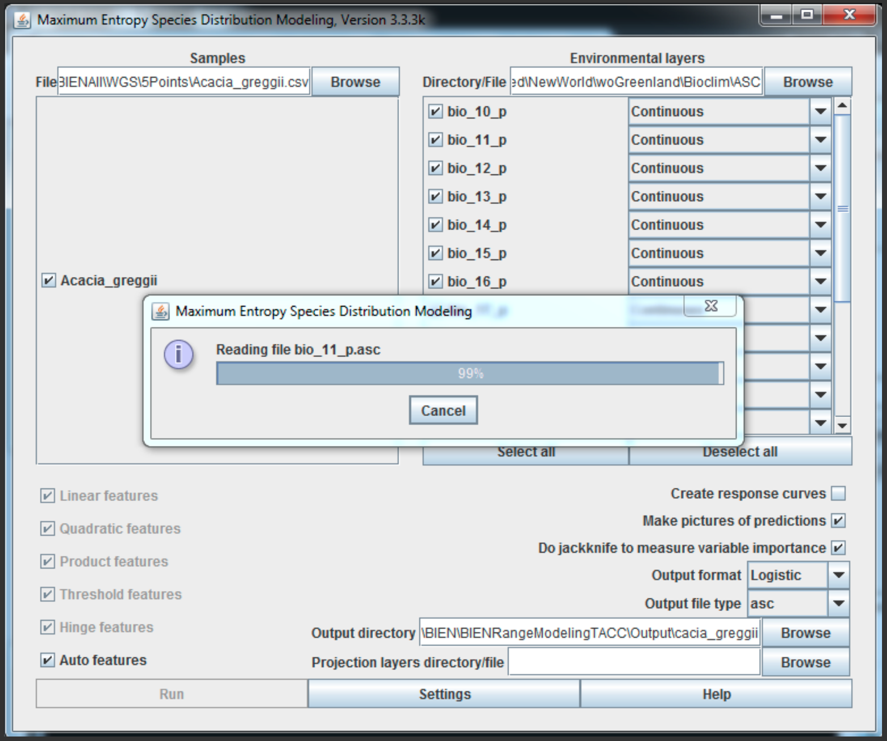


Figure 4. Habitat suitability maps resulting from the four tested algorithms, showing the spatial distribution of the core (black), marginal (dark grey) and unsuitable habitats (white).

- Calculates the distribution with the maximum entropy.
- Presence-only data plus background data.
- Background data is the whole study area and includes all presence data.
- Background data from areas close to presence records produce better models (Phillips et al 2009).



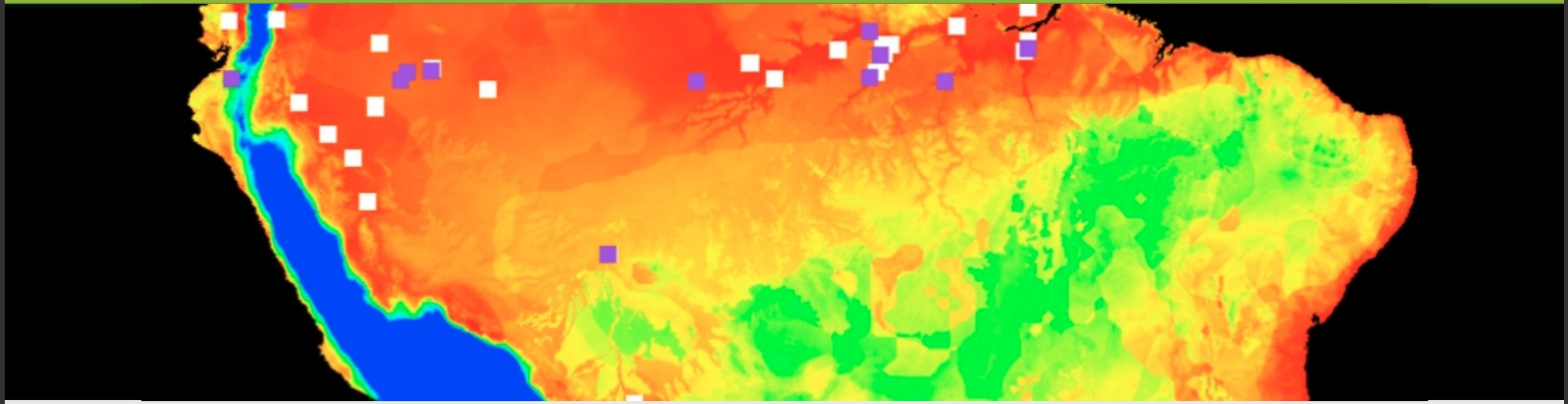
Phillips et al 2004, 2006, 2009, 2017

- **It is a machine learning method.**
- **Maxent uses the Gibbs algorithm.**
- **It can use continuous and categorical variables.**
- **Maxent is random method, so it is necessary to calculate the mean of several models.**
- **It can project several models to several scenarios at the same time.**
- **It is considered the most powerful presence-only method.**
- **Maxent calculates variable response curves and ROC plots.**
- **Jackknife for validation process.**

Phillips et al 2004, 2006, 2009, 2017

https://biodiversityinformatics.amnh.org/open_source/maxent/

Maxent software for modeling species niches and distributions



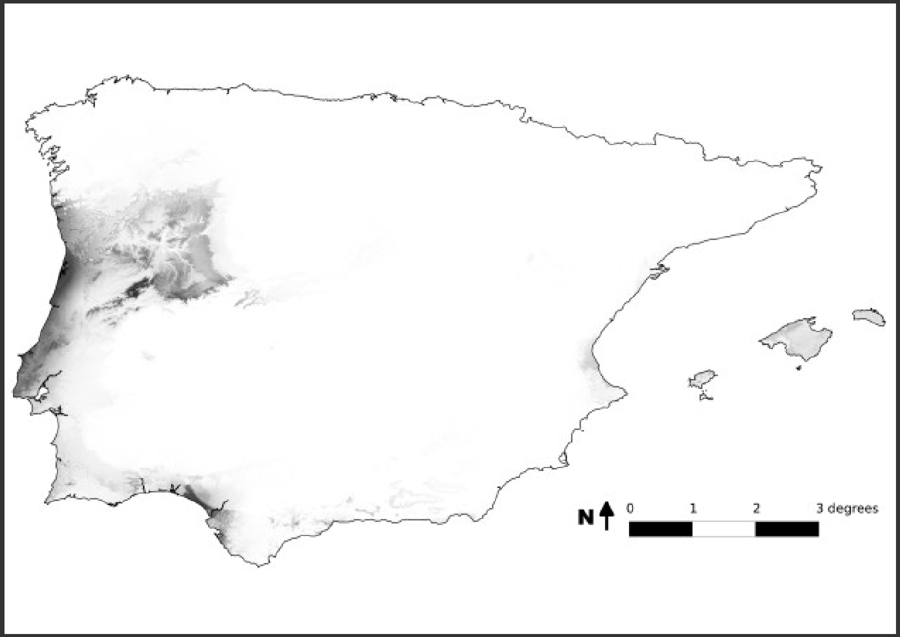
Maxent is now open source!

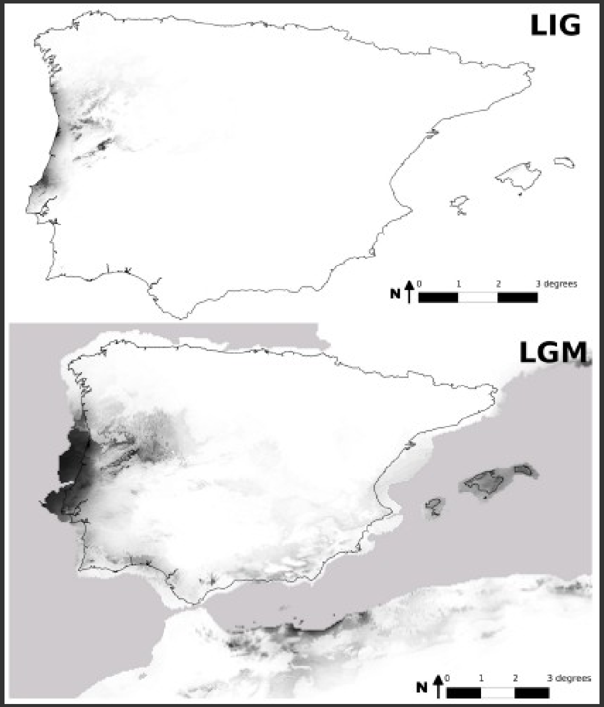
Use this site to download Maxent software for modeling species niches and distributions by applying a machine-learning technique called maximum entropy modeling. From a set of environmental (e.g., climatic) grids and georeferenced occurrence localities, the model expresses a probability distribution where each grid cell has a predicted suitability of conditions for the species. Under particular assumptions about the input data and biological sampling efforts that led to occurrence records, the output can be interpreted as predicted probability of presence (cloglog transform), or as predicted local abundance (raw exponential output).

Here you can download the open-source release of Maxent (under an MIT license; suggested citation below). See below for key changes in the current version.

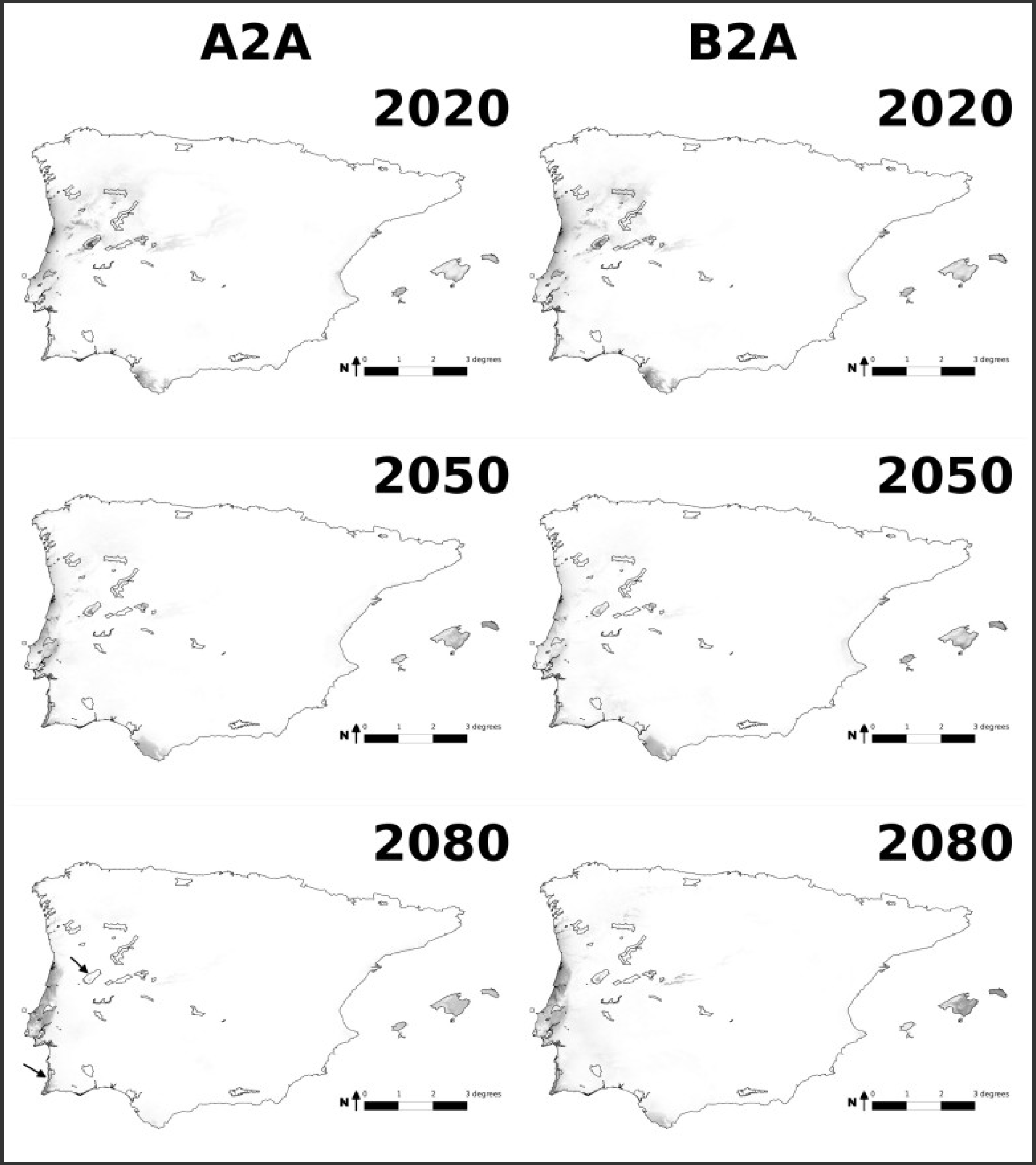
The idea for Maxent was first conceived of here at the Center for Biodiversity and Conservation at the American Museum of Natural History (AMNH) through a public-private partnership between the AMNH and AT&T-Research. Steven Phillips and the other developers of Maxent are still engaged in its development and maintenance, and the Google group will remain the main mechanism for user questions. Much additional information can be found in the Google group, software tutorials, and other resources listed below.

Main changes in Version 3.4.1



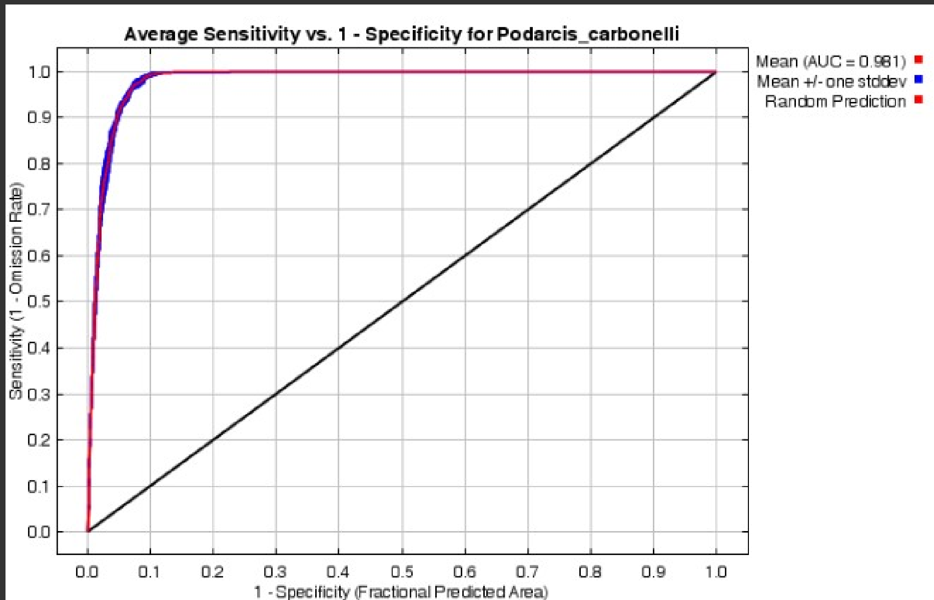


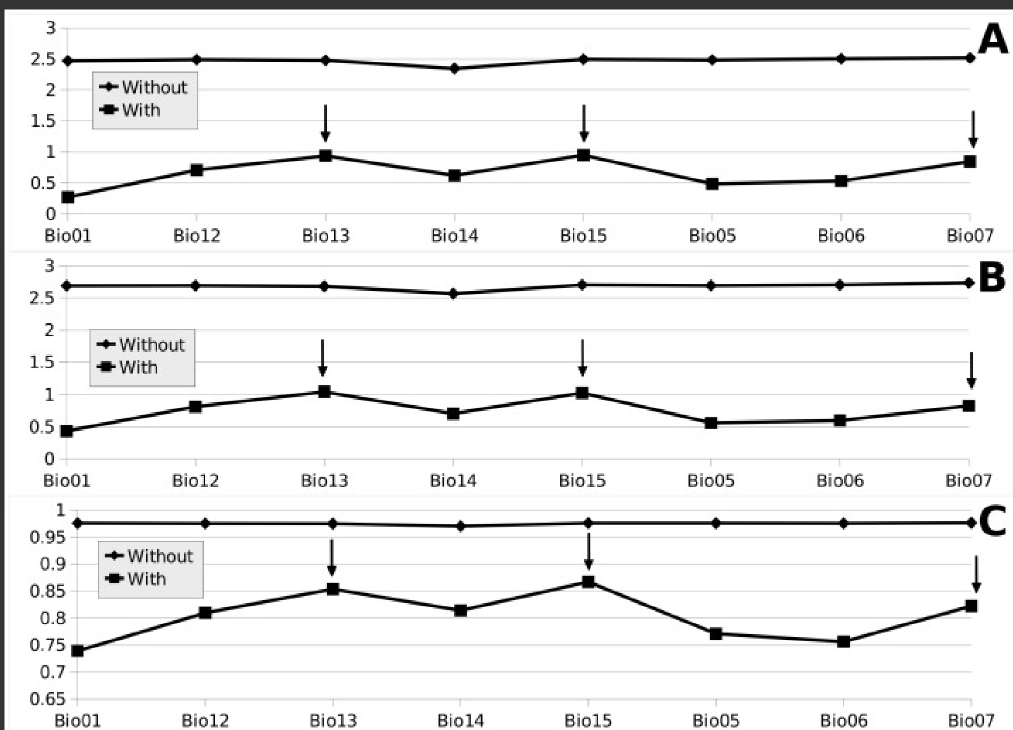
Sillero et al 2013

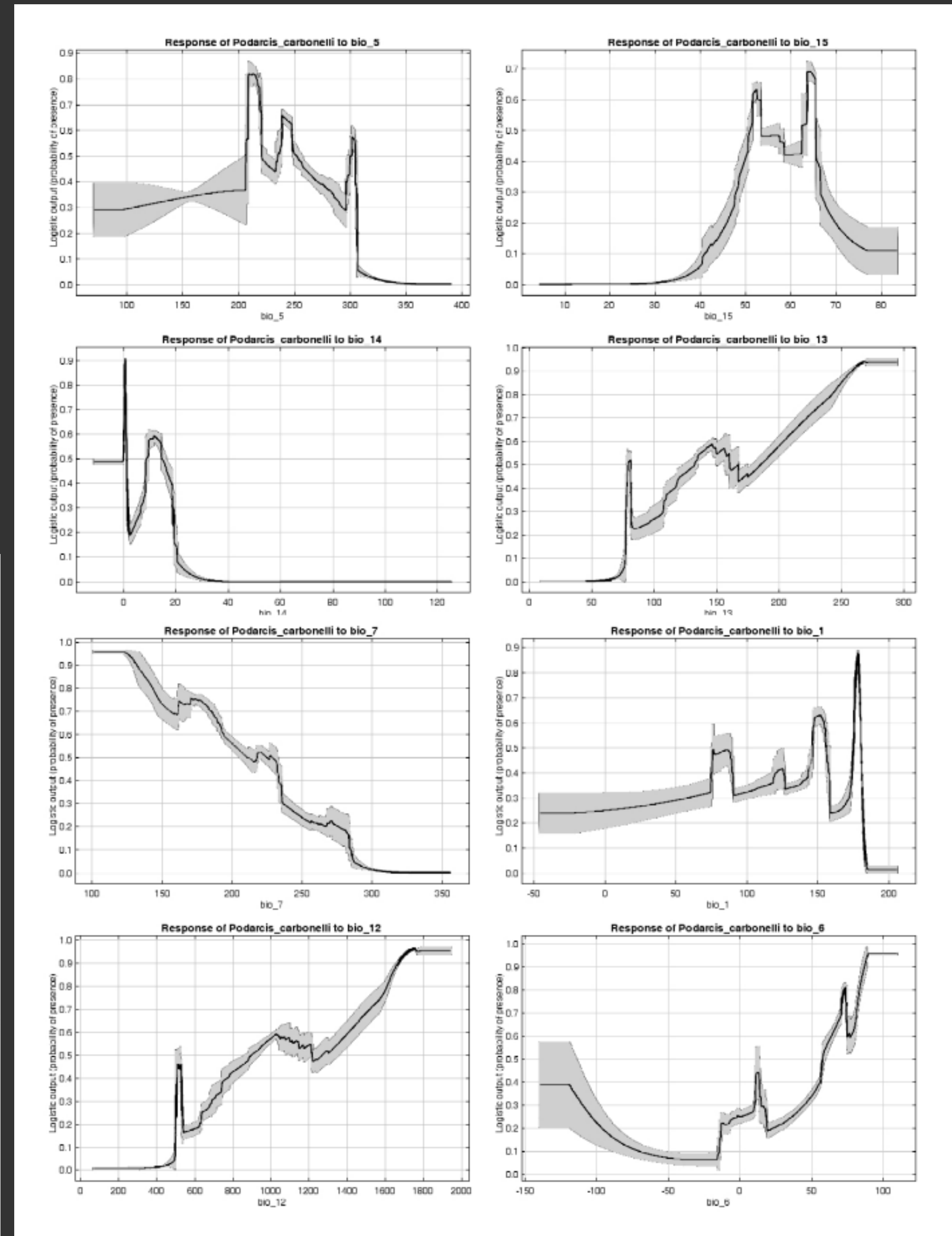


MAXENT: MAXIMUM ENTROPY

Sillero et al 2013







- Maxent, and methods in Dismo can be projected to other scenarios in time and space.
- Methods like Bioclim and Domain are considered the worst modelling methods because their calculated potential distribution are the largest.
- However, methods like Bioclim and Domain probably are the correlative methods representing the closest realised niche to the potential niche.

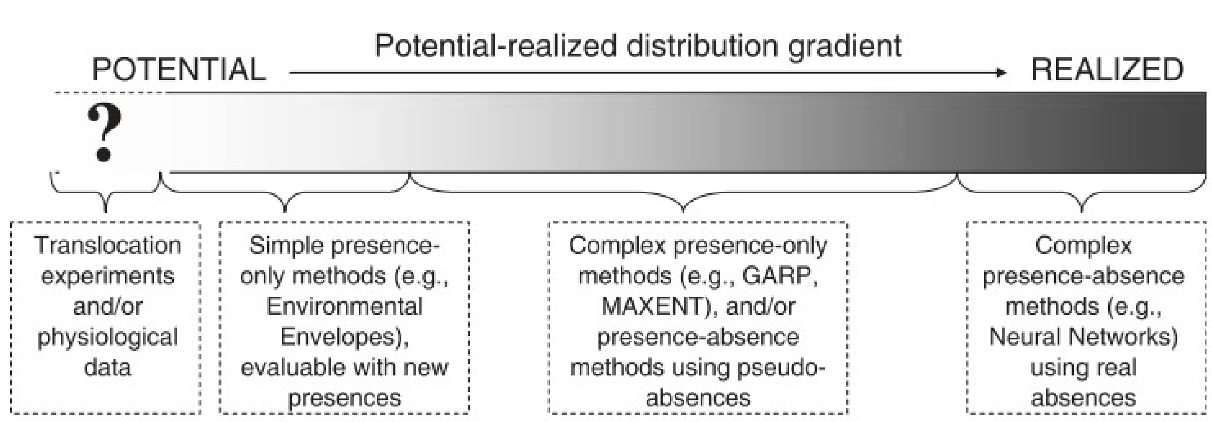
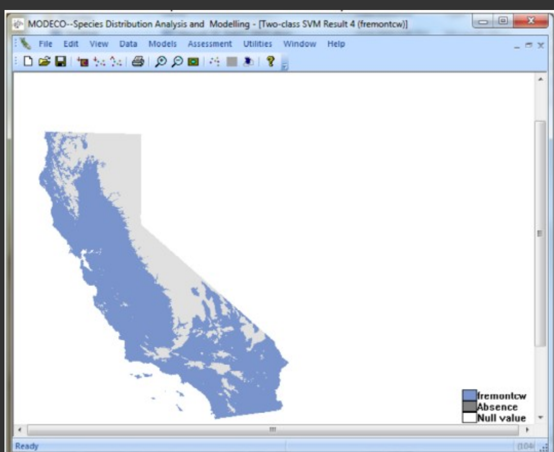
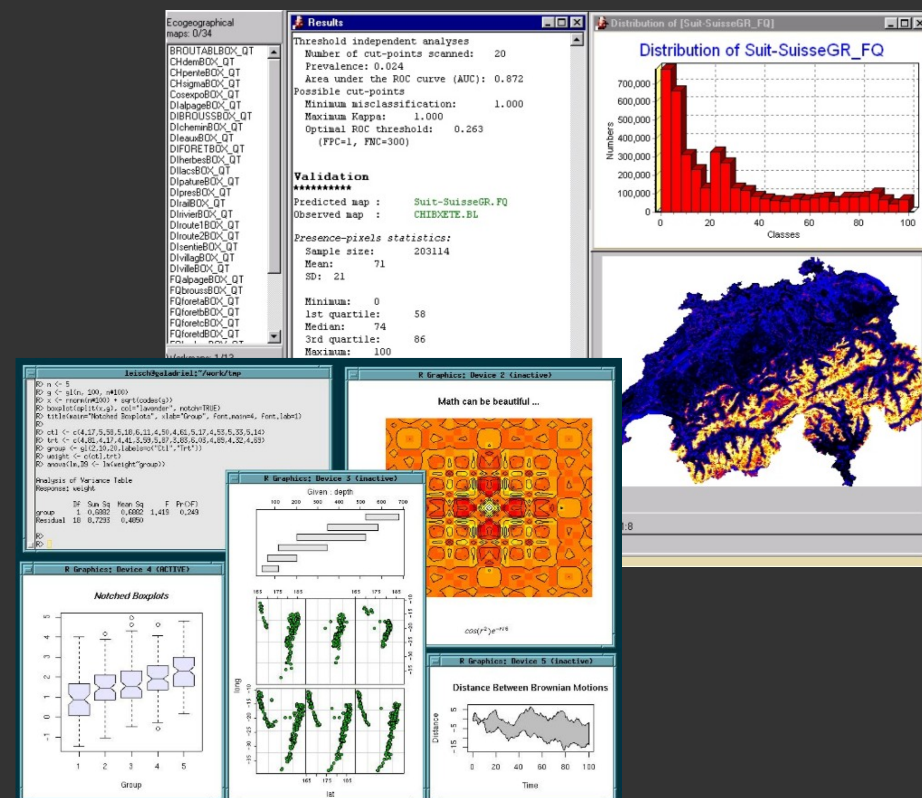


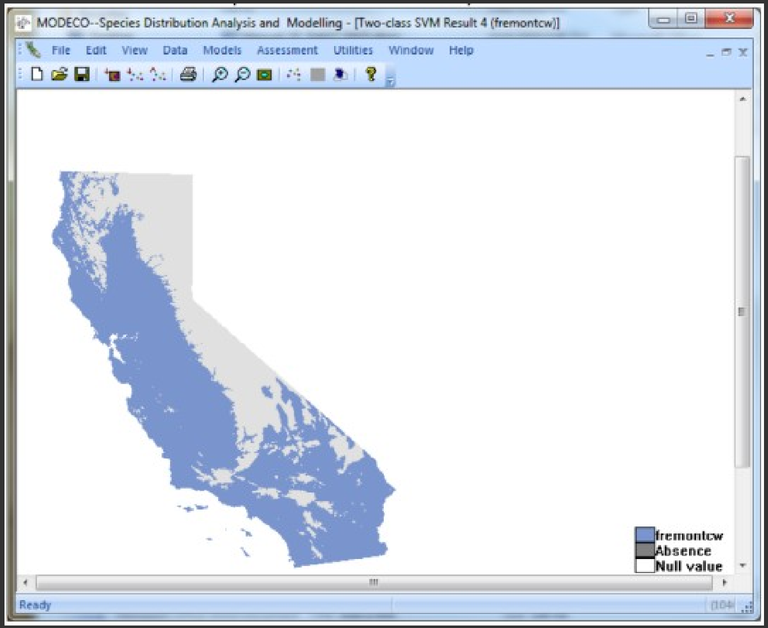
Figure 1 A conceptual potential-realized distribution gradient showing the modelling techniques and the characteristics of the training (and evaluation) data that are more adequate to describe each portion of this gradient. The discontinuous lines in the extreme left of the gradient mean that the potential distribution is a hypothetical concept that is hard to describe without a high amount of evidence from different sources.

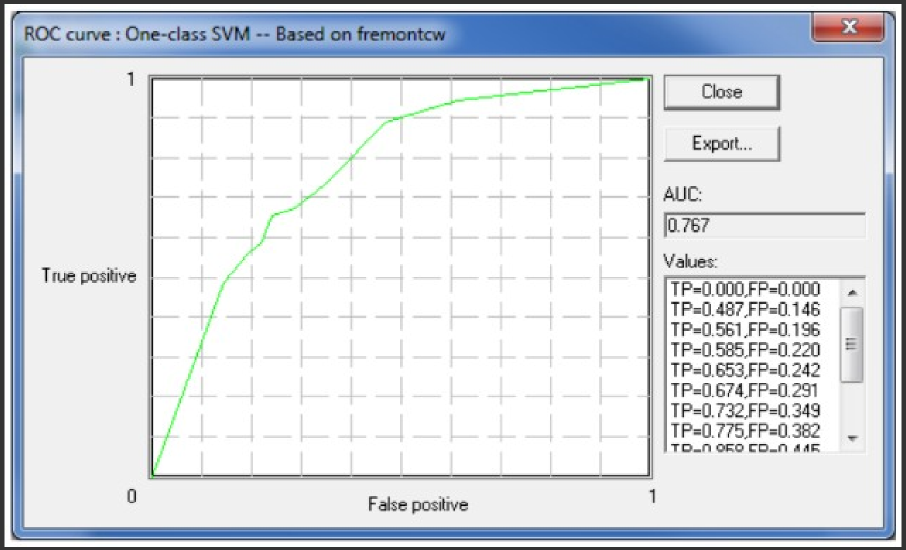
- **ModEco** → **Bioclim, Domain, Maxent, GLM**
- **openModeller** → **Bioclim, Domain, Mahalanobis Distance, GARP**
- **Biomapper** → **Ecological Niche Factor Analysis**
- **Maxent** → **Maximum Entropy**
- **R (dismo/Biomod2/sdm)** → **ENFA, Maxent**





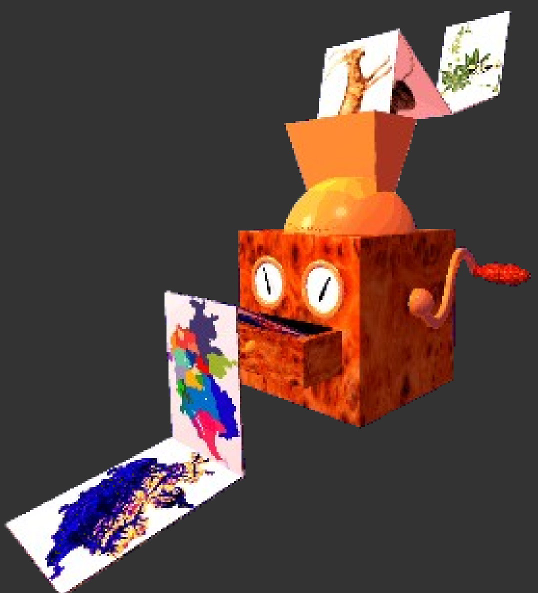
- Running only in Windows OS.
- ModEco implements multiple ENMs techniques.
- Support Vector Machines, BioClim, Domain, Generalized Linear Model, Maximum Likelihood Classification, Artificial Neural Network, Rough Set, Maxent, Classification Trees, Ensemble Model.
- It includes comprehensive tools for data visualisation, feature selection, and accuracy assessment.
- Ensemble modelling.
- http://gis.ucmerced.edu/ModEco/

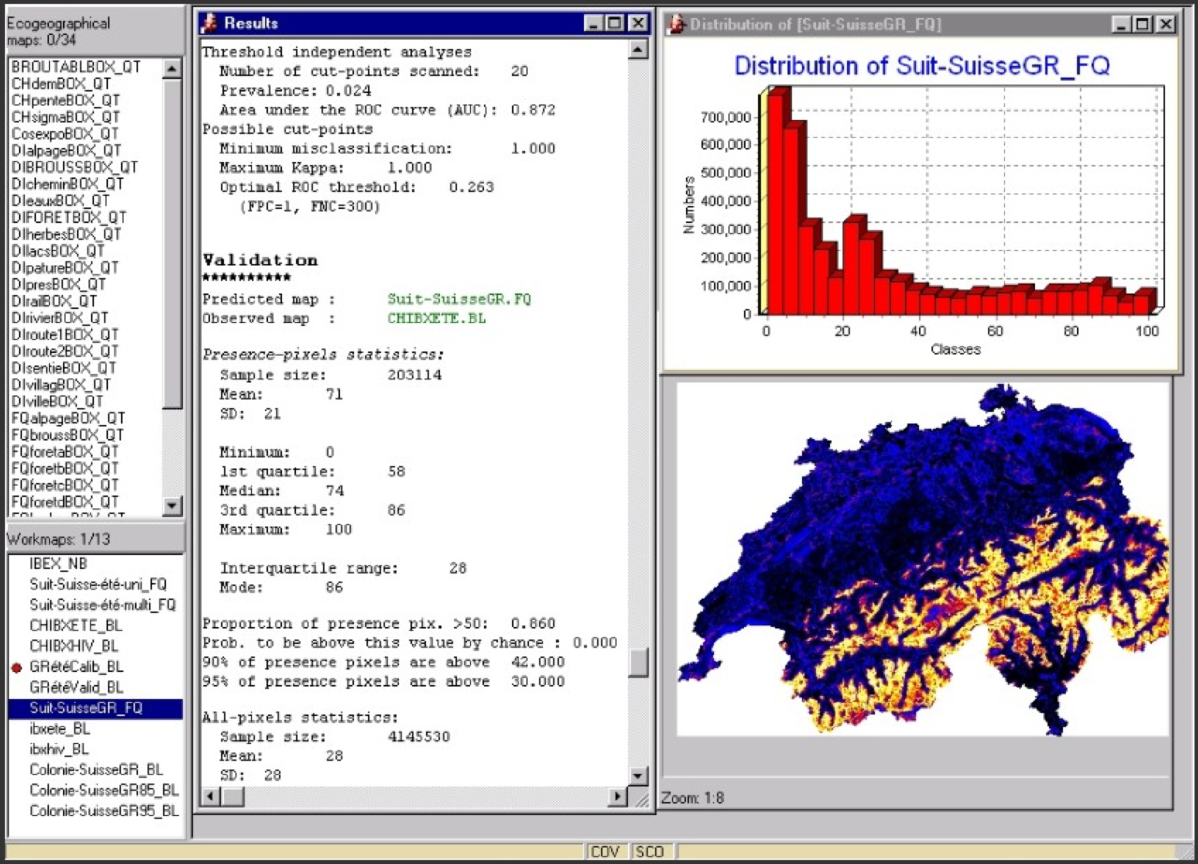




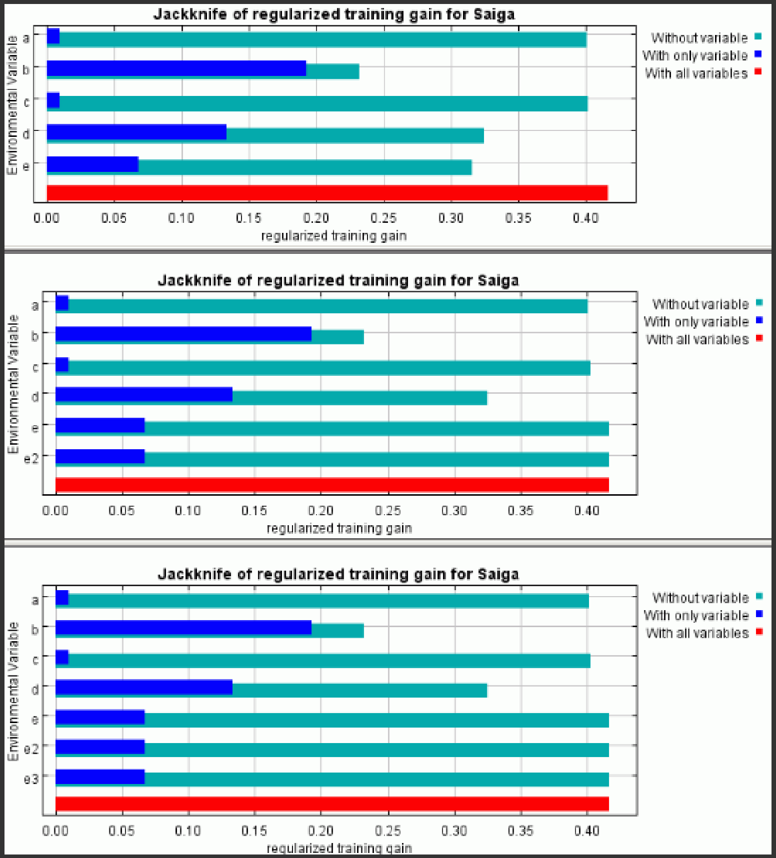
- **Software running several ENMs techniques.**
- **Bioclim, Domain, Mahalanobis Distance, GARP**
- **Written in C++.**
- **Running on Windows and Mac. Also in Ubuntu if compiled from source.**
- **Species coordinates as csv files.**
- **Environmental variables as ESRI ASCII files.**
- **Versions oM Desktop and oM Server.**
- **http://openmodeller.sourceforge.net/**

- Software for ENFA.
- Written in Delphi.
- Running only in Windows OS.
- Environmental variables and species coordinates as IDRISI rasters files.
- http://www2.unil.ch/biomapper/

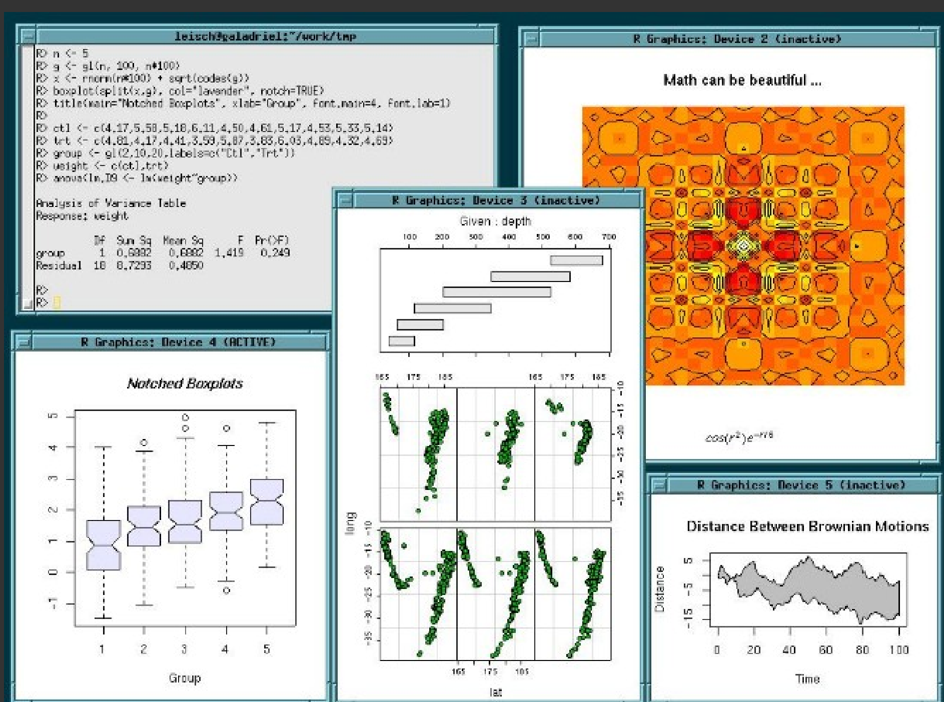


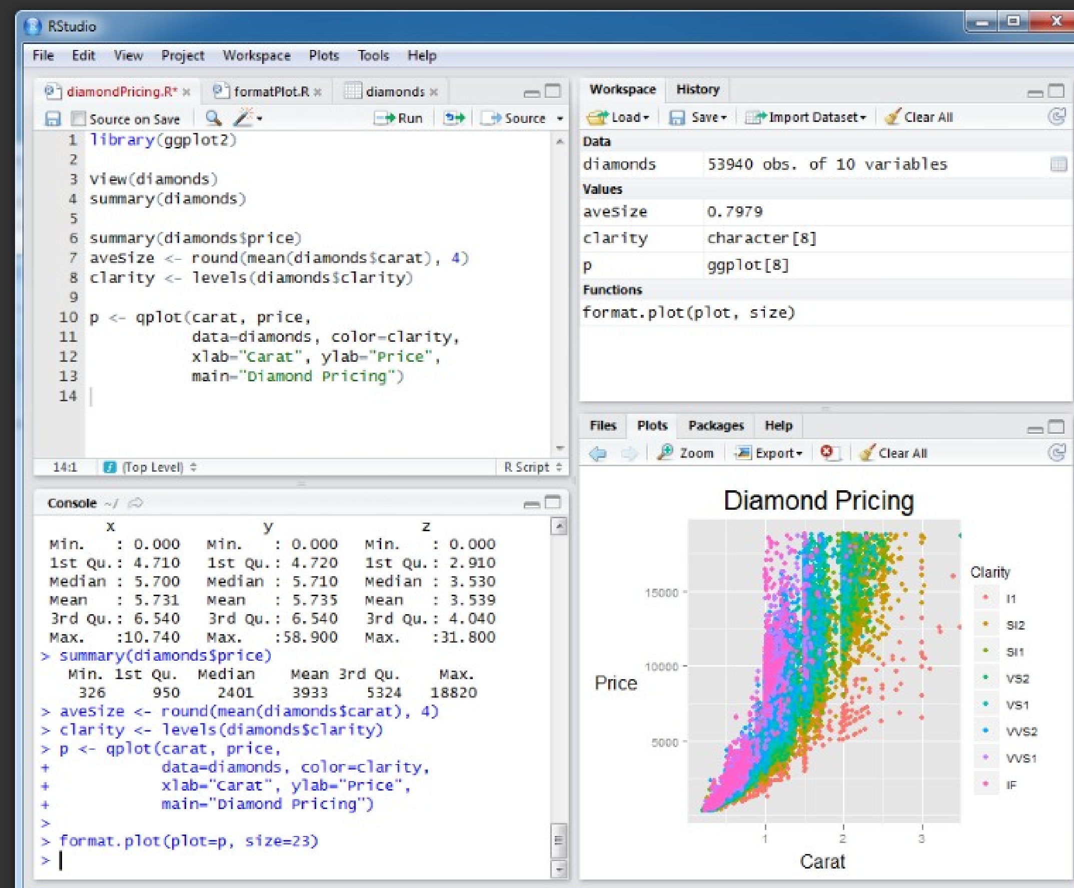


- Software for Maximum Entropy algorithm.
- Written on Java.
- Cross-platform.
- Species coordinates as csv files.
- Environmental variables as ESRI ASCII files.
- http://biodiversityinformatics.amnh.org/open_source/maxent/



- Software for statistical programming.
- R implements multiple ENMs techniques by installing different packages.
- Ade-habitat, Biomod2, SDMTools, dismo, sdm.
- GLM, GAM, ENFA, Maxent.
- Cross-platform.
- R-Studio.
- http://www.r-project.org/





Modelling:
- Dismo
- Biomod2
- Maxnet
- SDM
- rmaxent
- ENIRG: Ecological Niche in R-GRASS
- fuzzySim
- Maxlike
- NicheMapR
- enmSDM
- SDMPlay
- hSDM
- kuenm
- ssdm

Model comparison:
- ecospat
- ENMTools
- zoon

Model evaluation:
- ENMeval; evaluation of ENMs
- usdm: Uncertainty analysis for species distribution models
- modEvA: Model evaluation and analysis
- SDMTools
- blockCV

Virtual species:
- SDMvspecies
- virtualspecies

Model utilities:
-spThin: spatial thinning of species occurrence records
- MigClim: dispersal scenarios
- hypervolume: estimate volumes
- sdmpredictors
- eSDM: for creating and exploring ensembles of predictions from species distribution and abundance models
Climwin: evaluation of climate variables

CORRELATIVE MODELS

PRESENCE/ABSENCE MODELS

PRESENCE ONLY MODELS

- Logistic regression
- Generalised Linear Models
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- Random Forest
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- Flexible Discriminant Analysis
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- **Presence/absence data.**
- **Presence/pseudo-absence data.**
- **It is a particular case of Generalised Linear Models.**
- **The relationships among variables are linear.**
- **The most used method for ecological niche modelling.**

$$g(x)=\beta_0+\beta_1 x_1+\beta_2 x_2+\beta_3 x_3+\ldots+\beta_n x_n$$

Probability function of the logistic regression

$$\pi(x)=\frac{e^{g(x)}}{1+e^{g(x)}}$$

Brito et al 1996

- **Designed for dichotomous data.**
- **You can use continuous or categorical variables as environmental data.**
- **It is not a spatial method. You simply apply the resulting formula to a set of raster data.**
- **For this reason, you can project your formula to other sets of rasters (scenarios).**

$$g(x)=\beta_0+\beta_1 x_1+\beta_2 x_2+\beta_3 x_3+\ldots+\beta_n x_n$$

Probability function of the logistic regression

$$\pi(x)=\frac{e^{g(x)}}{1+e^{g(x)}}$$

Brito et al 1996

- The result is a continuous raster between 0 and 1.
- You can transform it into a habitat suitability map choosing a threshold.

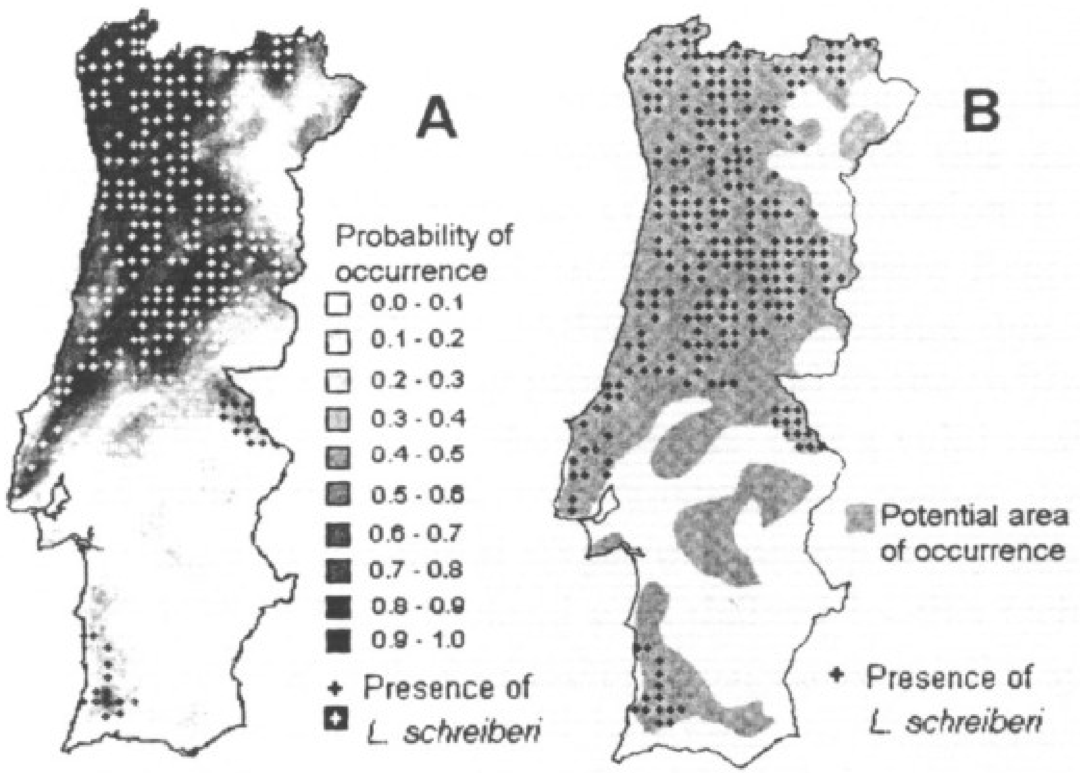


Fig. 5. Probability of occurrence of *L. schreiberi* according to the Logistic Regression equation of the final model (A) and potential area of occurrence of *L. schreiberi* according with the Overlap Analysis technique (B).

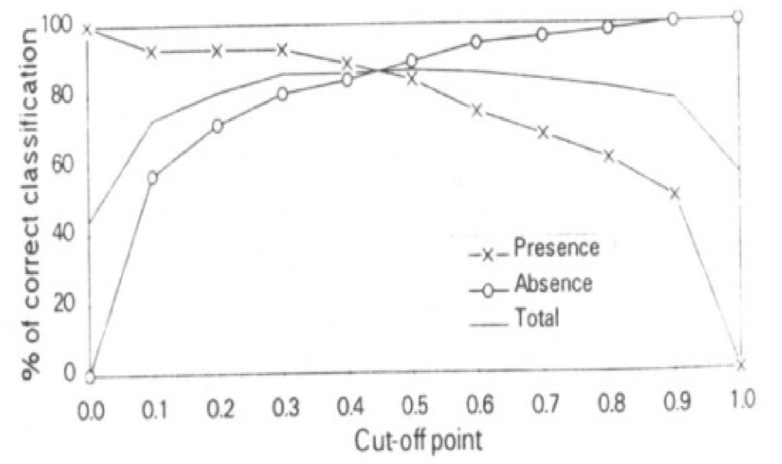


Fig. 3. Correct classification rates, for model 3, considering all possible cut-off points, at 0.1 intervals.

Brito et al 1999

- Presence/absence data.
- Non parametric solution to GLM.
- The relationships among variables are not linear.
- Smooth functions

$$g(\mathrm{E}(Y)) = \beta_0 + f_1(x_1) + f_2(x_2) + \cdots + f_m(x_m).$$

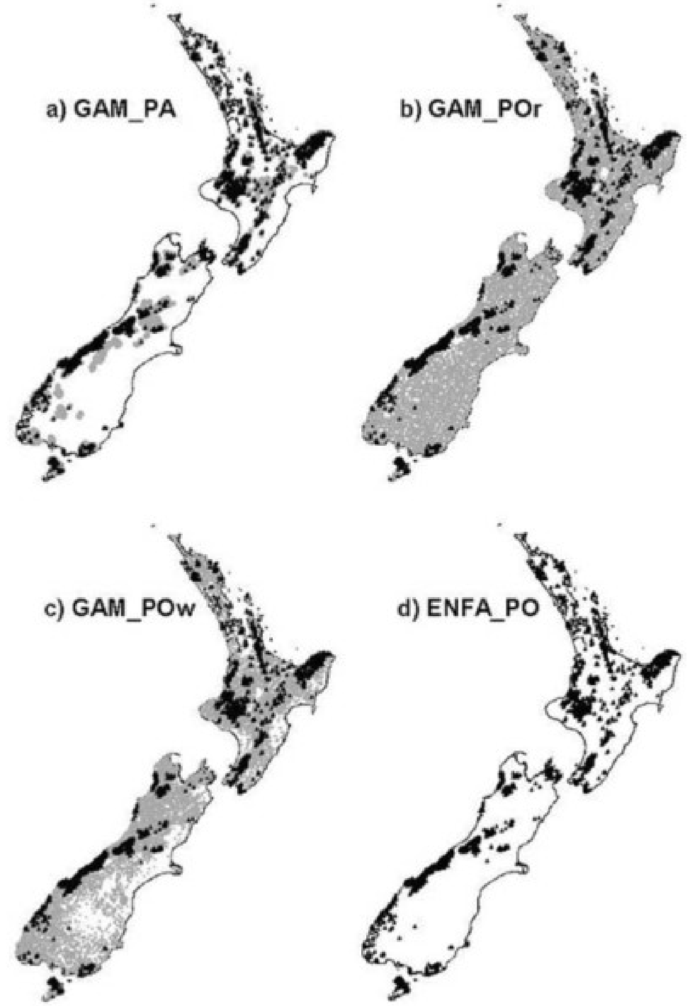
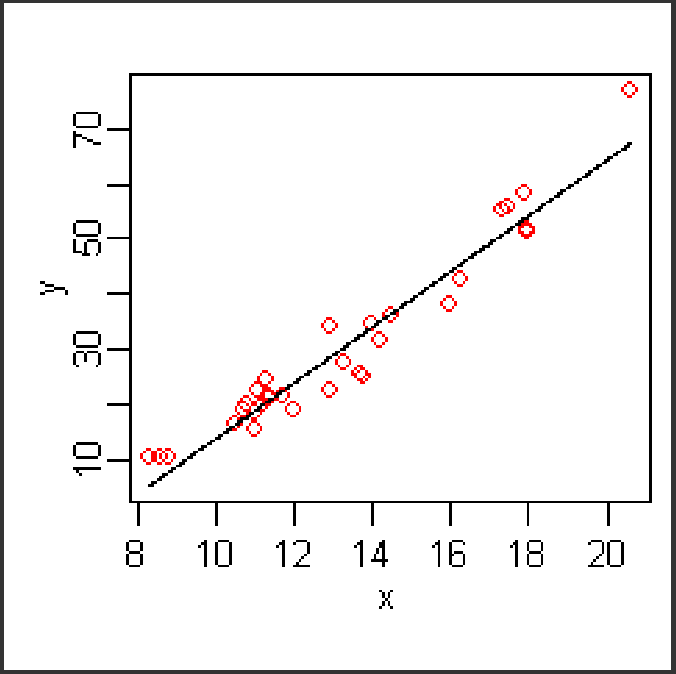


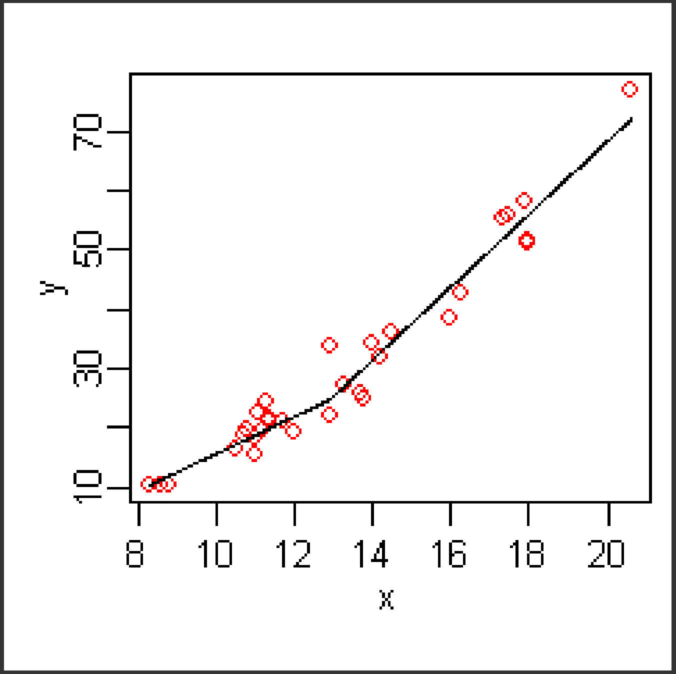
Fig. 3. Distribution of species data for ASPBUL (presence = 4367; absence = 15 508), derived from 19 875 selected RECCE plots of forested regions in New Zealand, in the four modeling methods: (a) GAM_PA: presence and absence data; (b) GAM_POr: presence data and random absences; (c) GAM_-POw: presence data and weighted random absences; (d) ENFA_PO: presence data only. Black = presences; gray = absences.

Zaniewski et al 2002

MULTIVARIATE ADAPTIVE REGRESSION SPLINES (MARS)

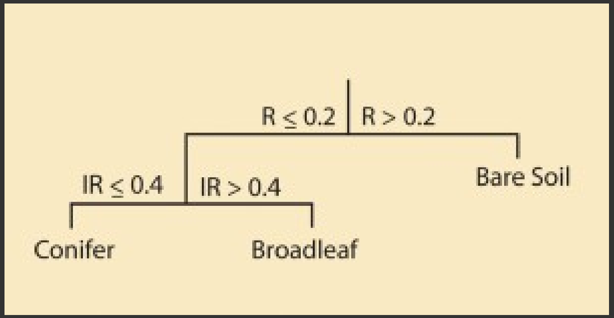
- Non-parametric regression analysis.
- MARS introduces non-linear features in a linear models.
- Piece-wise linear fits (a set of multiple sub-functions) rather than smooth functions.
- Similar to hinge features from Maxent.

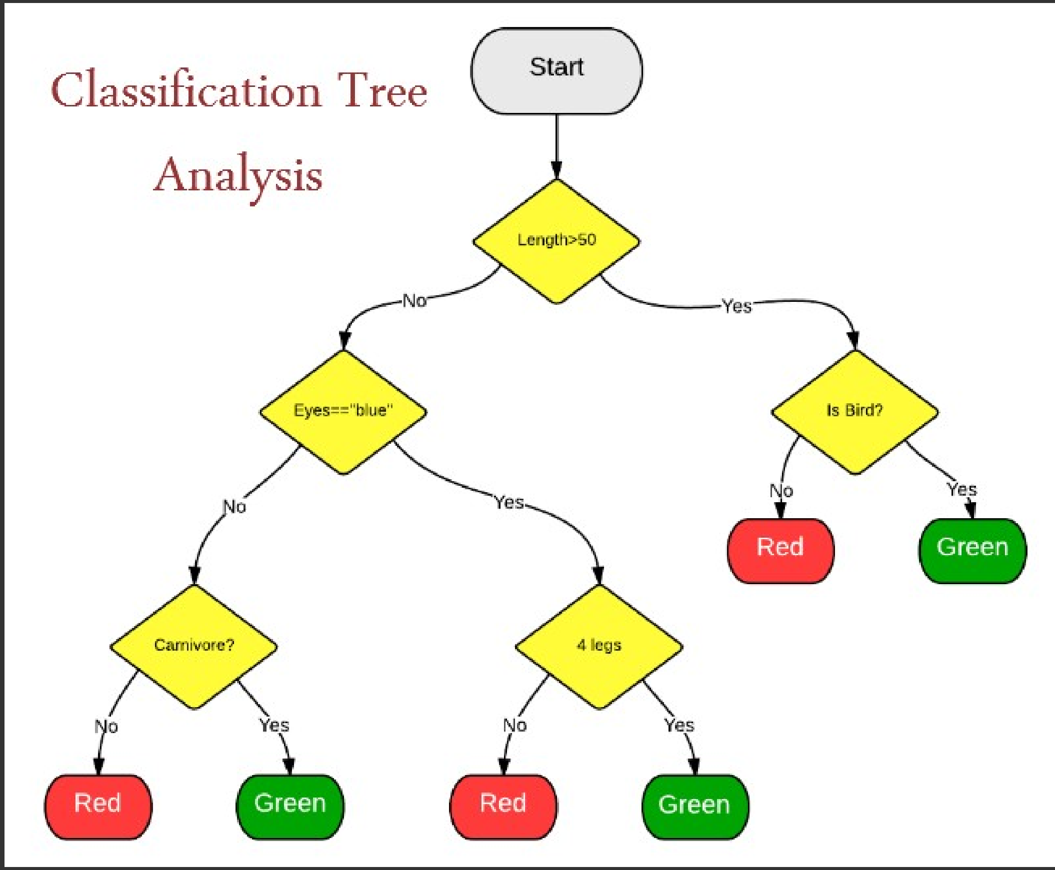




CLASSIFICATION TREE ANALYSIS (CTA)

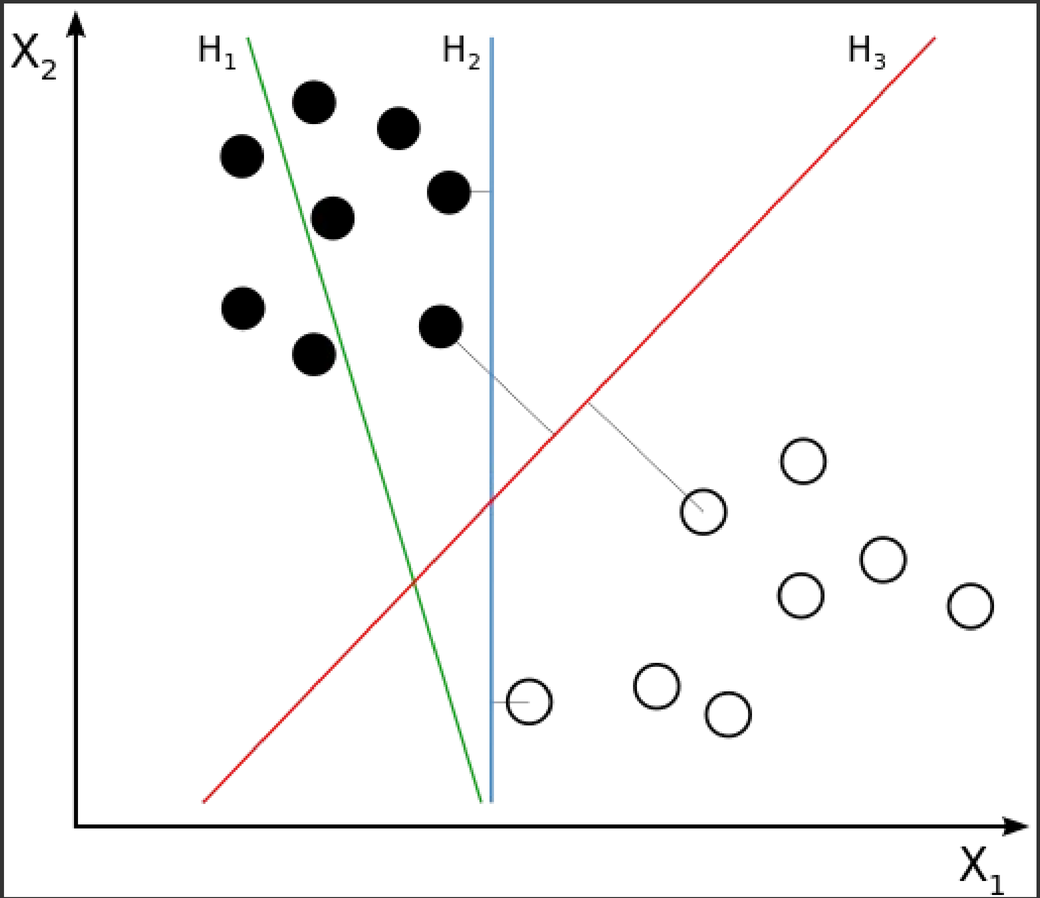
- **Machine learning algorithm for classification.**
- **Remote sensing**
- **Binary decision rules.**
- **Rules based on training data.**
- **The algorithm iteratively split a set of samples into two groups, minimising the variability within each subgroup while maximizing the contrast between the groups.**





- Supervised learning algorithms.
- They analyse data and recognise patterns, used for classification and regression analysis.
- Two training features.
- Two categories (present/absent).
- The SVM training algorithm assigns new features into each category
- Non-probabilistic binary linear classifier.
- Used very frequently in remote sensing.

- Categories are divided by a clear gap as wide as possible.
- New features are then mapped and predicted to belong to a category based on which side of the gap they fall.



- Categories are divided by a clear gap as wide as possible.
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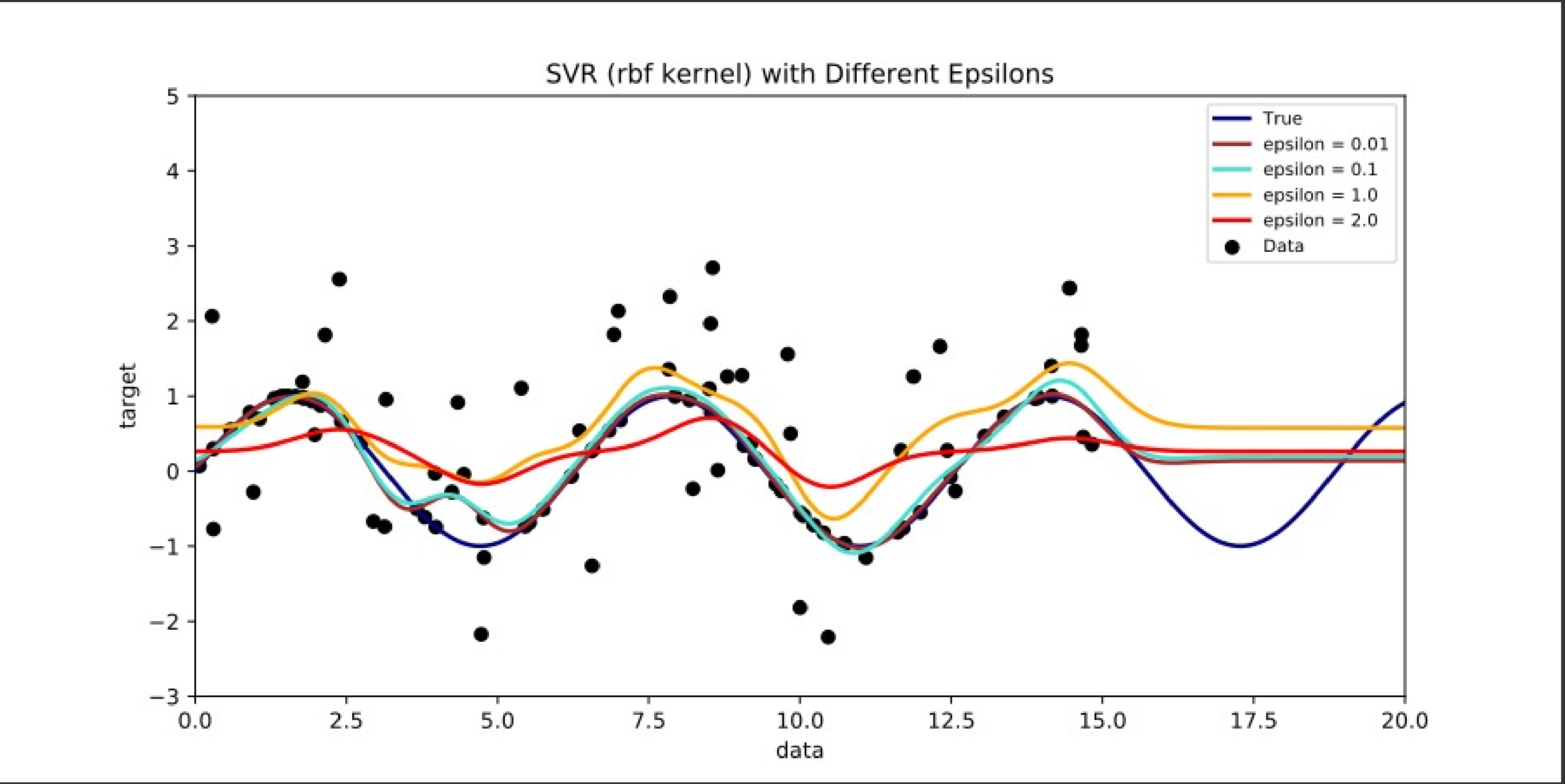


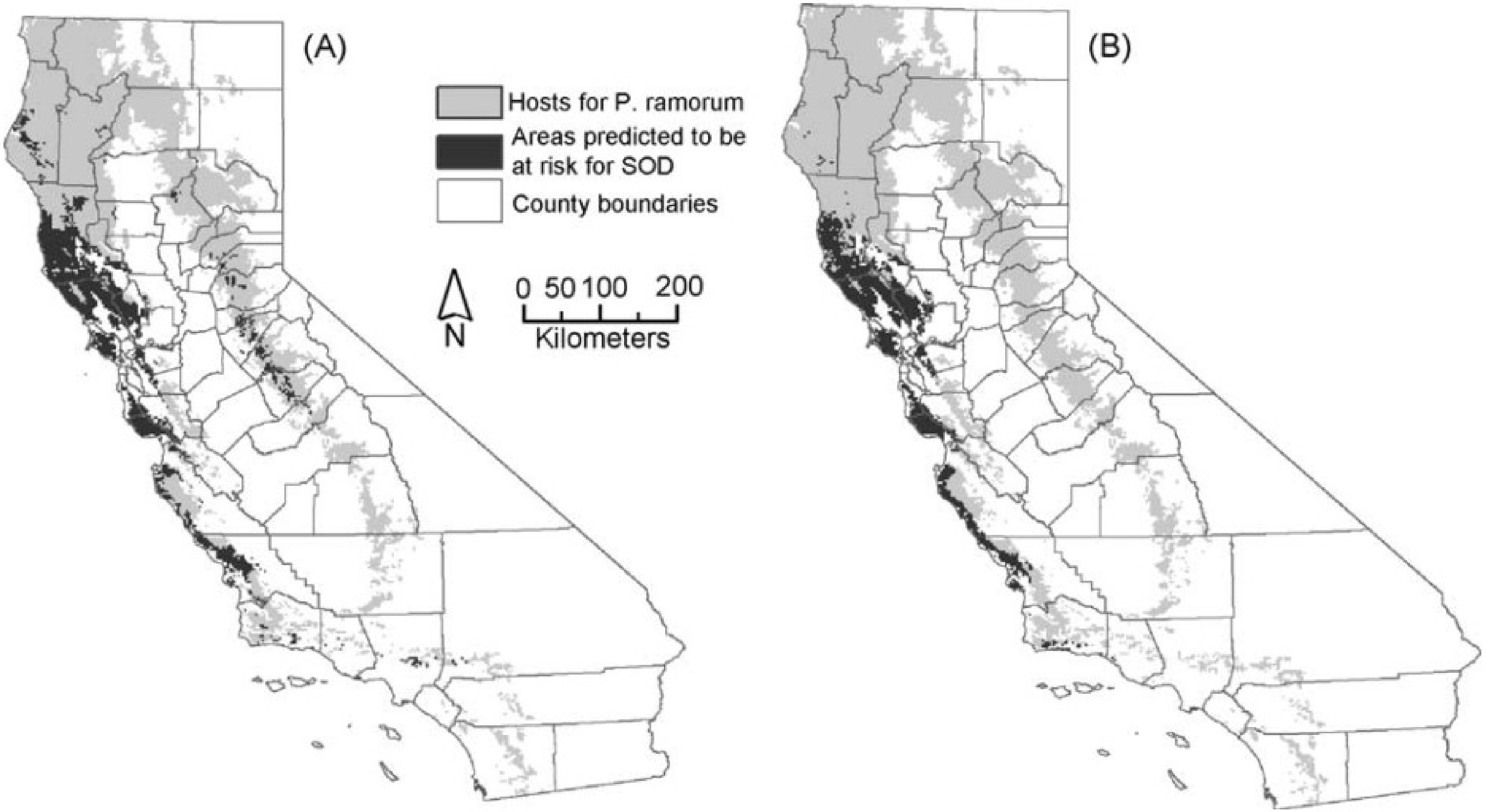
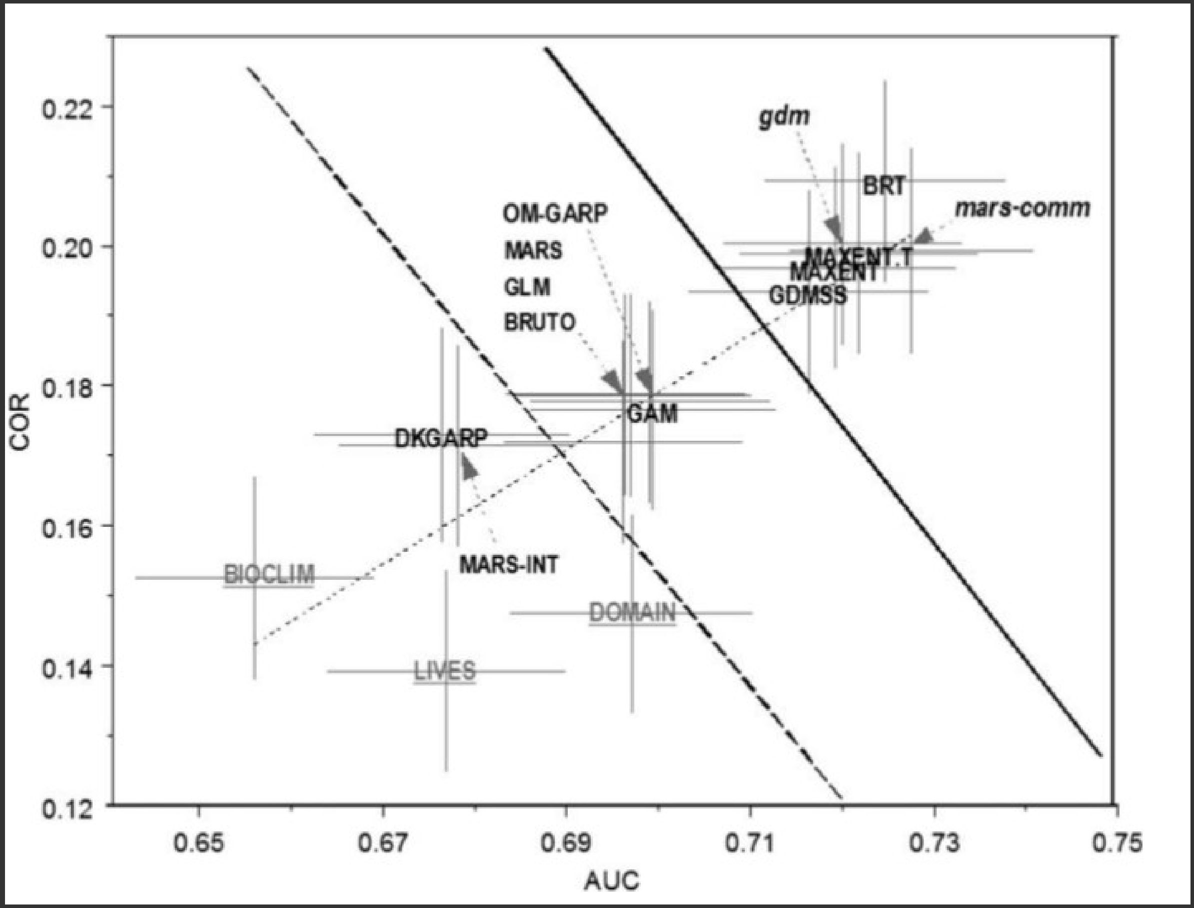


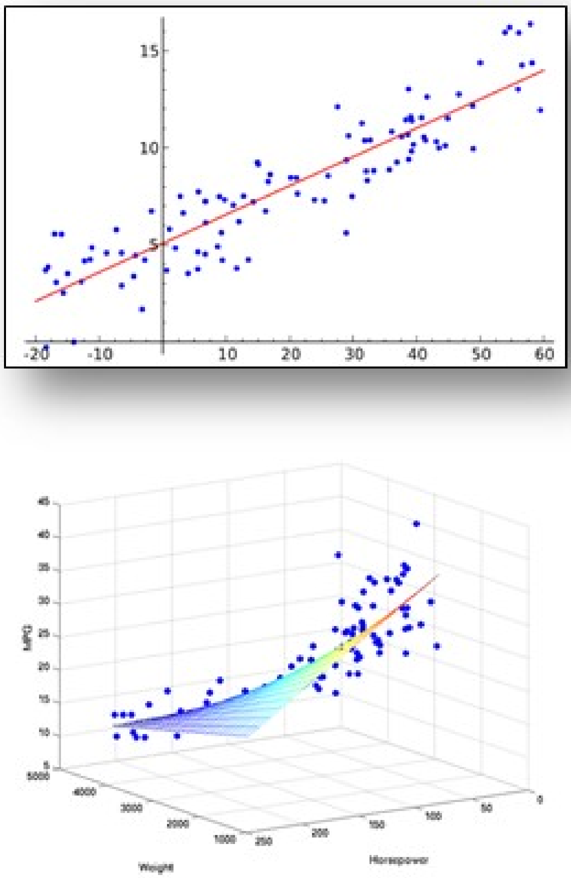
Fig. 3. Predicted area of SOD risk in California. Mapped results from: (A) one-class SVMs; and (B) two-class SVMs.

Guo et al 2005

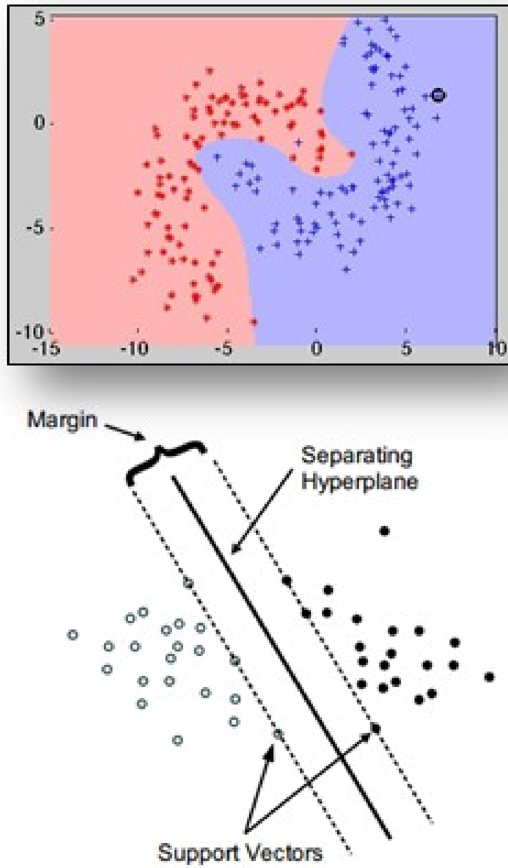
- Ensemble learning method for classification and regression.
- Prediction model by ensemble of weak prediction models.
- It learns iteratively from errors of previous models.
- The algorithm optimises a cost function by iteratively choosing a function that points in the negative gradient direction.



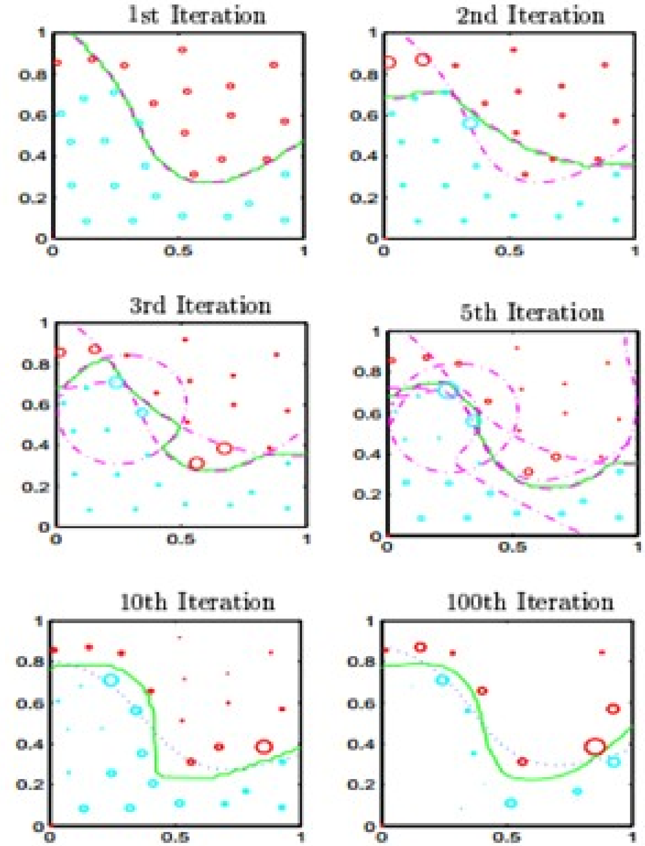
Elith et al 2006



Generalized Linear Models [8,9]



Support Vector Machines [1,7]



Adaptive Boosting [6]

- Computational models inspired by an animal's central nervous systems.
- This method is capable of machine learning as well as pattern recognition.
- ANNs are generally presented as systems of interconnected "neurons" which can compute values from inputs.
- They applied rules to each neuron to classify the data.

Tarroso et al 2012

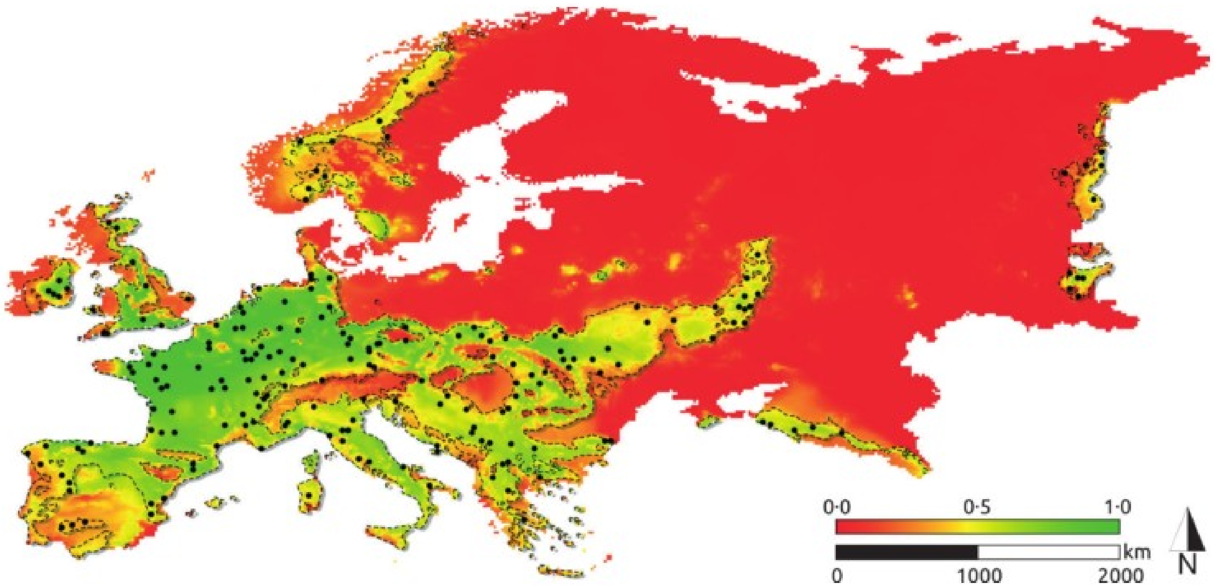
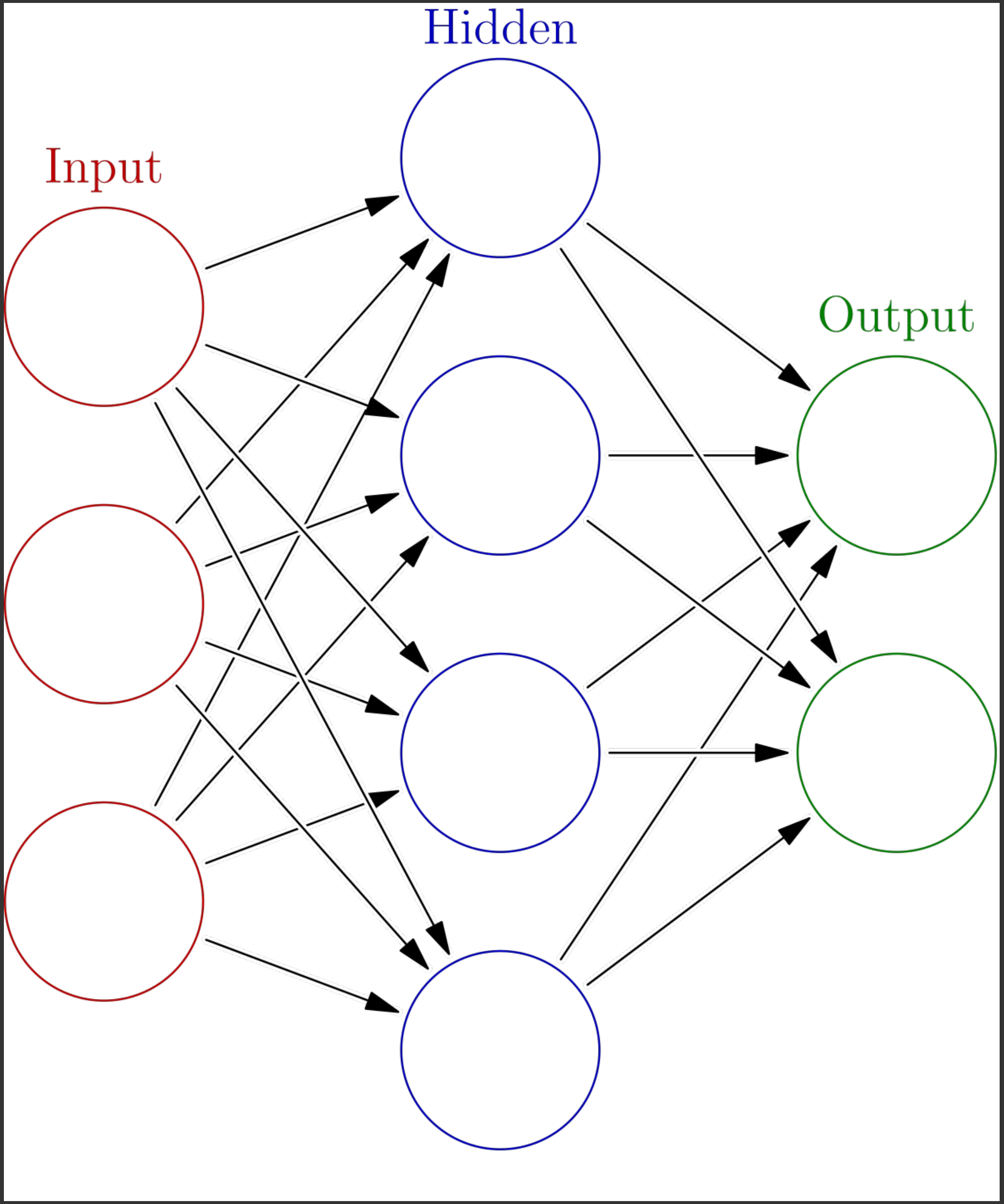


Fig. 2. Consensus model of the virtual species presence. The gradient describes the probability of presence. The black dots are the locations of the 100 presences used to model that were randomly selected from the distribution area of the virtual species delimited by the dashed line.



Each neuron holds a logistic regression with different parameters.

- Ensemble learning method for classification (and regression).
- The method applies the general technique of bootstrap aggregating.
- It operates by constructing a multitude of decision trees for each subsample.
- The final output is the mode classification or mean regression of the all individual trees.

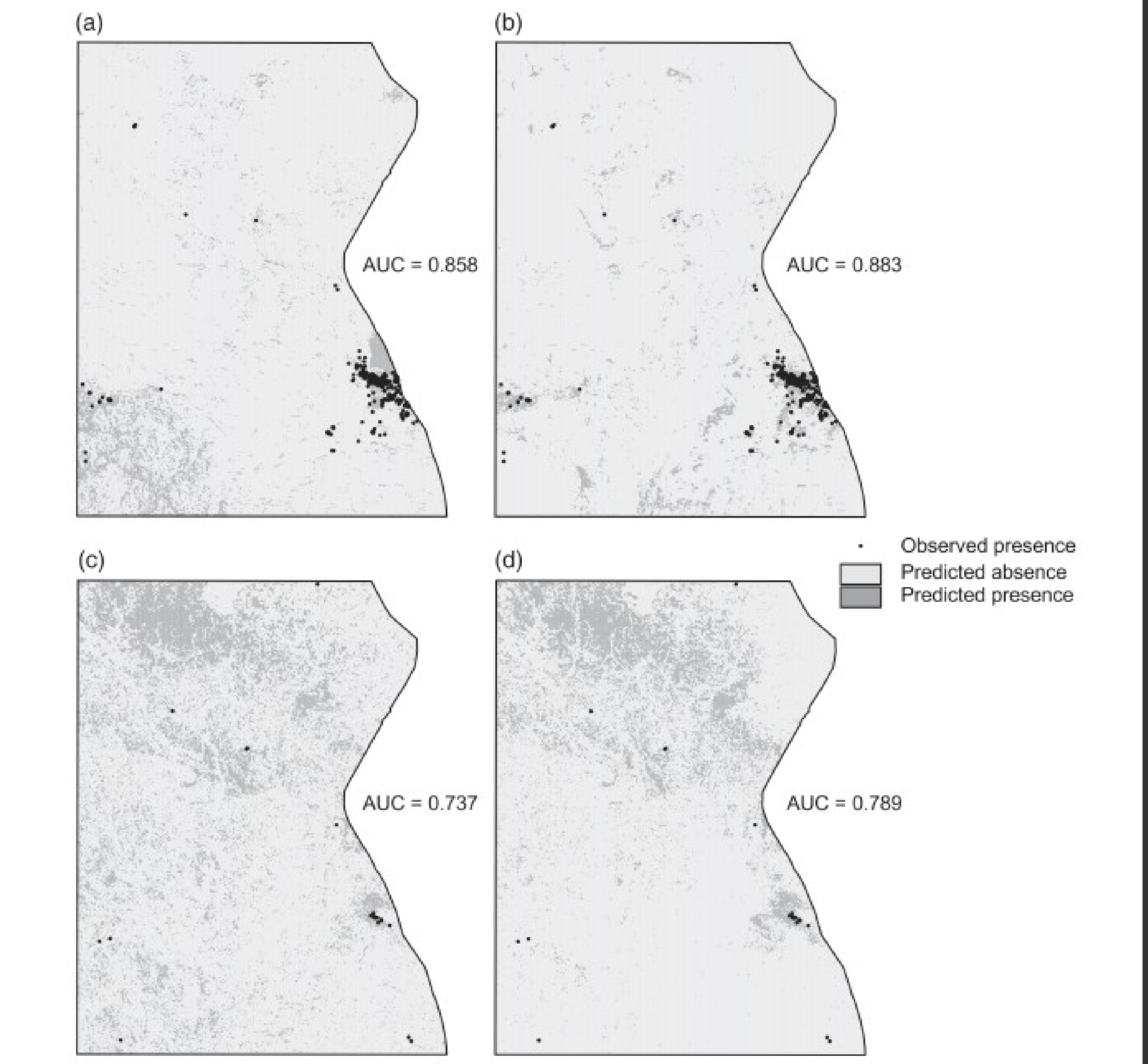
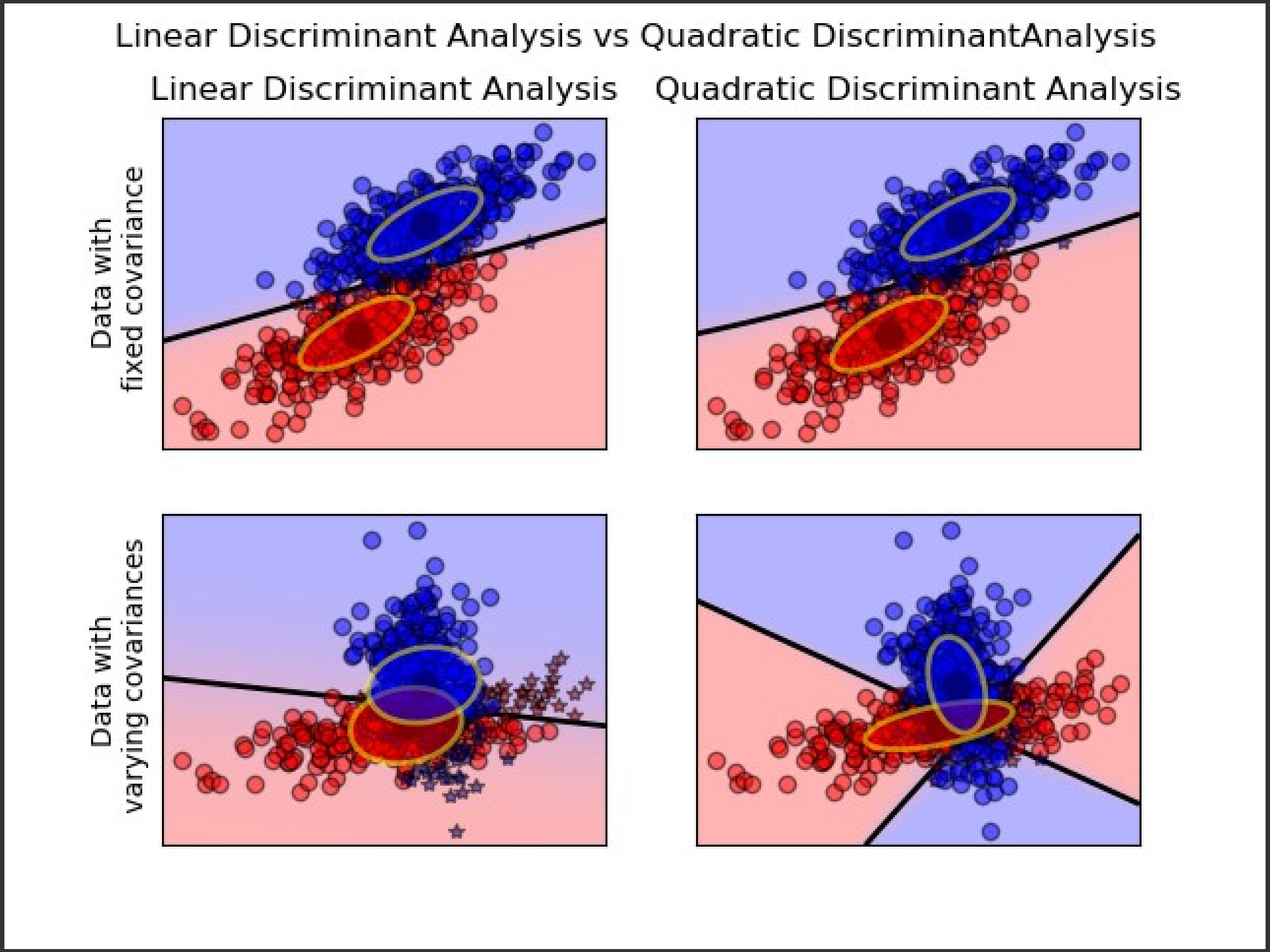


Figure 3 Predicted distribution of *Cypripedium calceolus* provided by multivariate adaptive regression splines (MARS) (a) and the weighted average (WA) consensus method (b), and of *Dactylorhiza incarnata* ssp. *cruenta* provided by random forest (RF) (c) and the WA consensus method (d). The black dots emphasize the observations of these threatened species in the study area. The area under the curve (AUC) values reflect the accuracy of the models based on the evaluation data set.

Marmion et al 2009

- Multi-group classification.
- Mixture of non-linear regression models.
- Replacing linear regression by any non-parametric regression method.



Marmion et al 2009

The different ecological niches are located on a gradient from the fundamental to the occupied niche.

The exact position where ENM lies on the niche gradient depends on:

- **species biology**
- **spatial resolution considered**
- **variables included in the model**
- **modelling method**

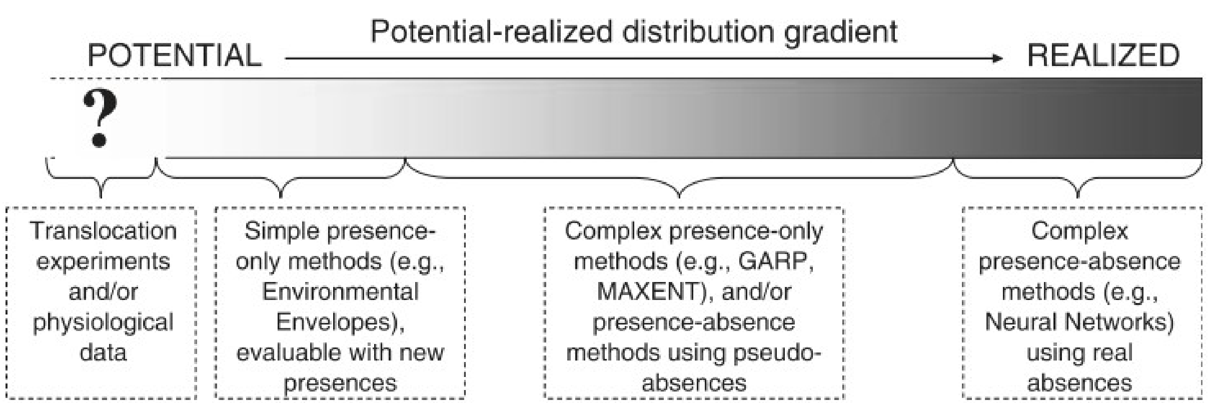


Figure 1 A conceptual potential-realized distribution gradient showing the modelling techniques and the characteristics of the training (and evaluation) data that are more adequate to describe each portion of this gradient. The discontinuous lines in the extreme left of the gradient mean that the potential distribution is a hypothetical concept that is hard to describe without a high amount of evidence from different sources.

- **Elith et al 2006 implemented 16 modelling methods.**

Table 4. Modelling methods implemented.

Method	Class of model, and explanation	Data[1]	Software	Std errors?[2]	Contact person
BIOCLIM	envelope model	p	DIVA-GIS	no	CG, RH
BRT	boosted decision trees	pa	R, gbm package	no	JE
BRUTO	regression, a fast implementation of a gam	pa	R and Splus, mda package	yes	JE
DK-GARP	rule sets from genetic algorithms; desktop version	pa	DesktopGarp	no	ATP
DOMAIN	multivariate distance	p	DIVA-GIS	no	CG, RH
GAM	regression: generalised additive model	pa	S-Plus, GRASP add-on	yes	AG,AL,JE
GDM	generalised dissimilarity modelling; uses community data	pacomm	Specialized program not general released; uses Arcview and Splus	no	SF
GDM-SS	generalised dissimilarity modelling; implementation for single species	pa	as for GDM	no	SF
GLM	regression; generalised linear model	pa	S-Plus, GRASP add-on	yes	AG,AL,JE
LIVES	multivariate distance	p	Specialized program not general released	no	JLi
MARS	regression; multivariate adaptive regression splines	pa	R, mda package plus new code to handle binomial responses	yes	JE, FH
MARS-COMM	as for MARS, but implemented with community data	pacomm	as for MARS	yes	JE
MARS-INT	as or MARS; interactions allowed	pa	as for MARS	yes	JE
MAXENT	maximum entropy	pa	Maxent	no	SP
MAXENT-T	maximum entropy with threshold features	pa	Maxent	no	SP
OM-GARP	rule sets derived with genetic algorithms; open modeller version	pa	new version of GARP not yet available	no	ATP

[1] p = only presence data used; pa = presence and some form of absence required – e.g. a background sample; comm = community data contribute to model fitting.
[2] any method can have an uncertainty estimate derived from bootstrapping the modelling; these data refer to estimates that are available as a statistical part of the method.

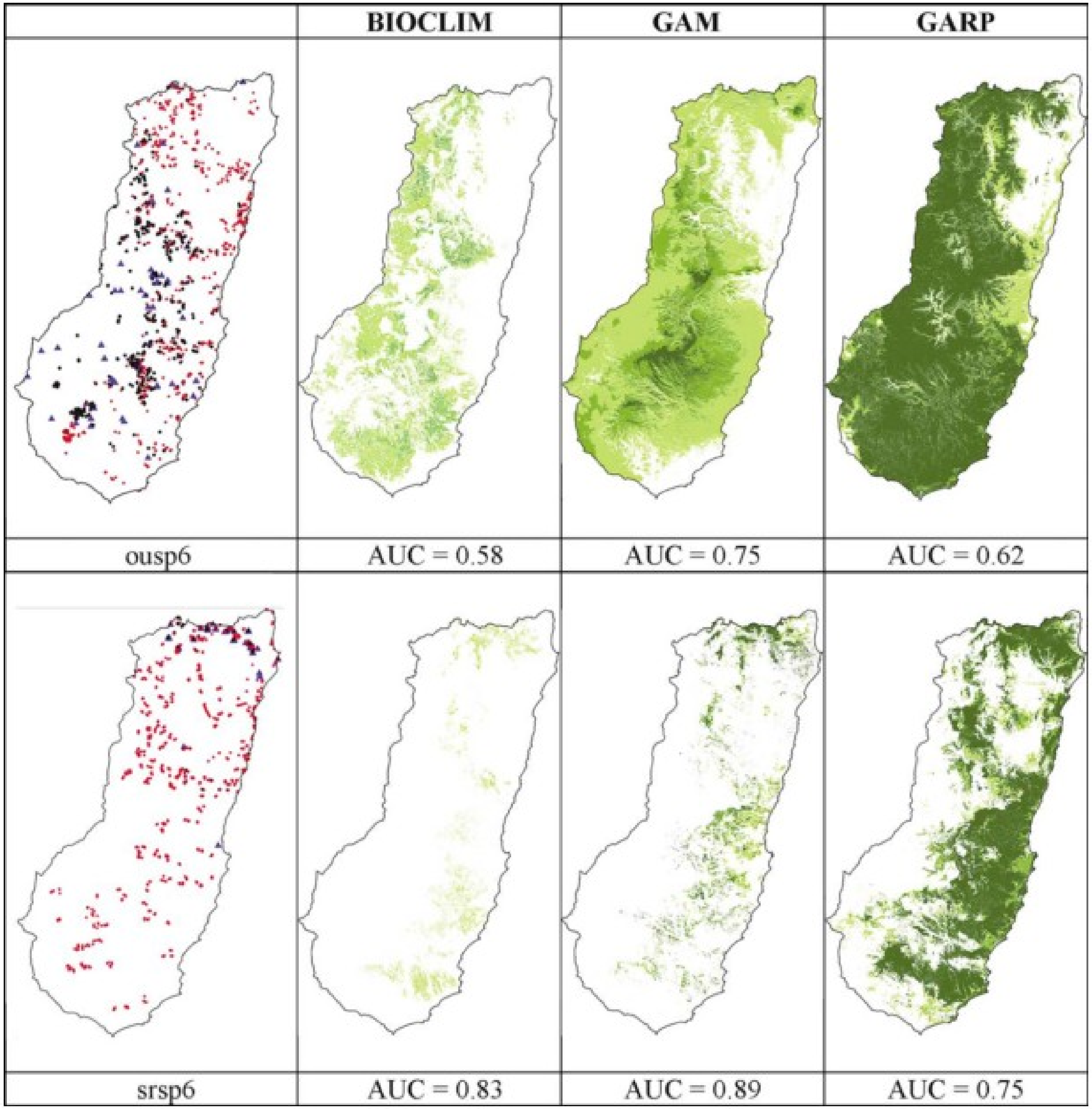


Fig. 1. Maps for two species from NSW for each of three selected techniques. Details: ousp6, *Poa sieberiana* (53 records for modelling and 512 presence/797 absence for evaluation); srsp6 *Ophioscincus truncatus* (79 model, 74/932 eval). The first column shows modelling sites (grey triangles) and evaluation sites: presence = black circle, absence = black cross.

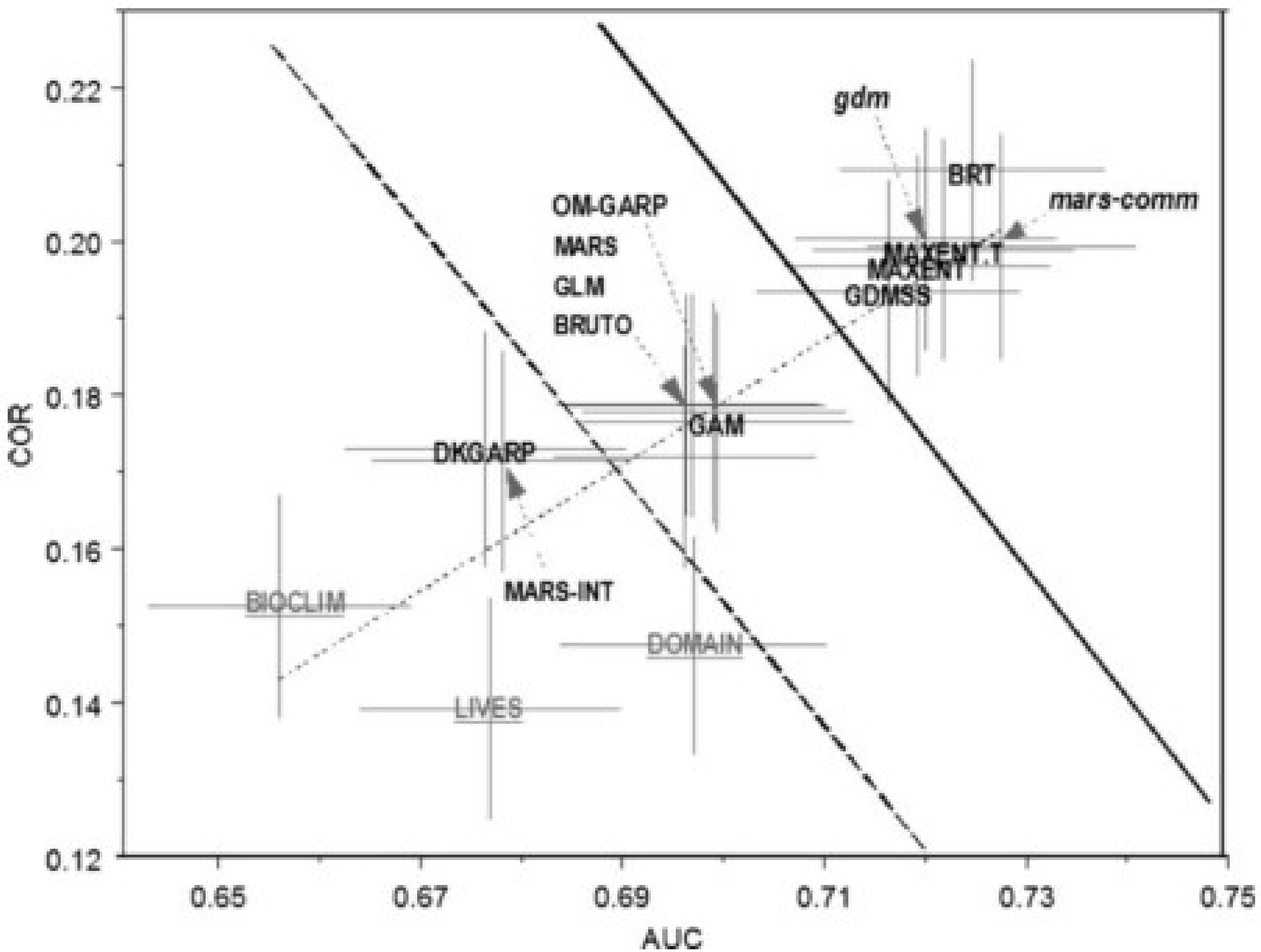


Fig. 3. Mean AUC vs mean correlation (COR) for modelling methods, summarised across all species. The grey bars are standard errors estimated in the GLMM (see Appendix), reflecting variation for an average species in an average region. The labels are broad classifications of the methods: grey underlined = only use presence data, black capitals = use presence and background samples, black lower case italics = community methods.

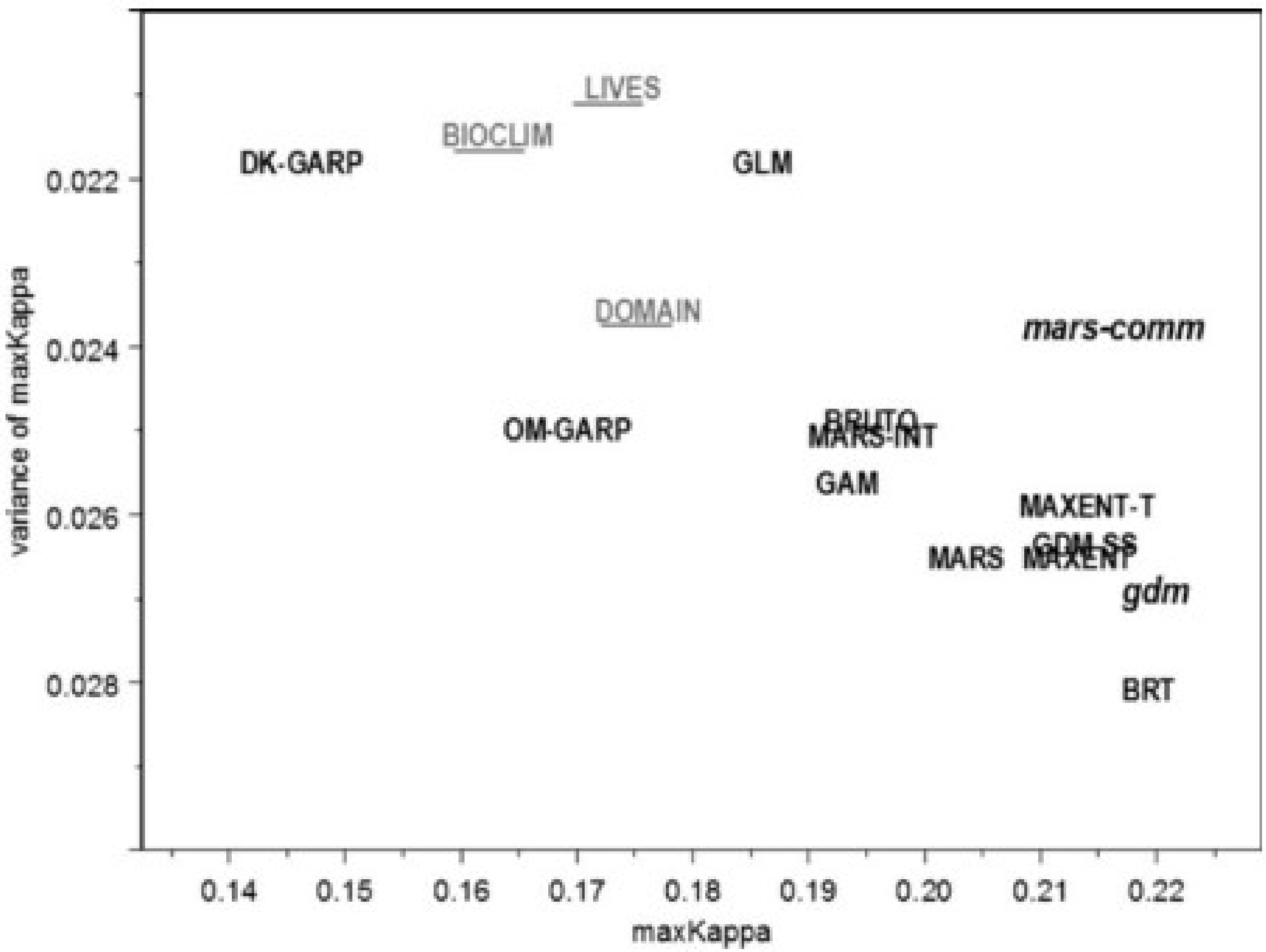
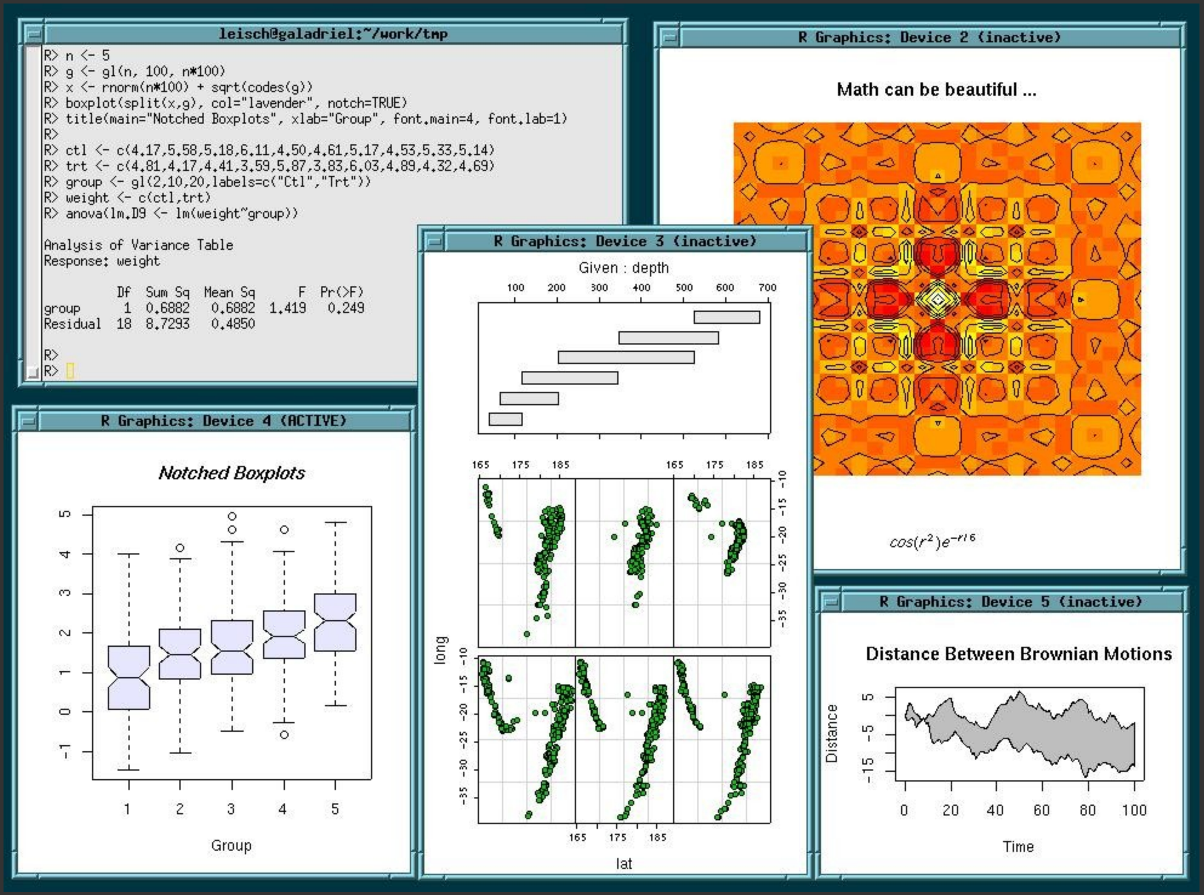


Fig. 4. Performance measured by maximum kappa and its variance across all species. Variance axis reversed so low is higher on plot; it is desirable to have high kappa and low variance (i.e. upper right in plot), for consistent and good performance. Labels as for Fig. 3.

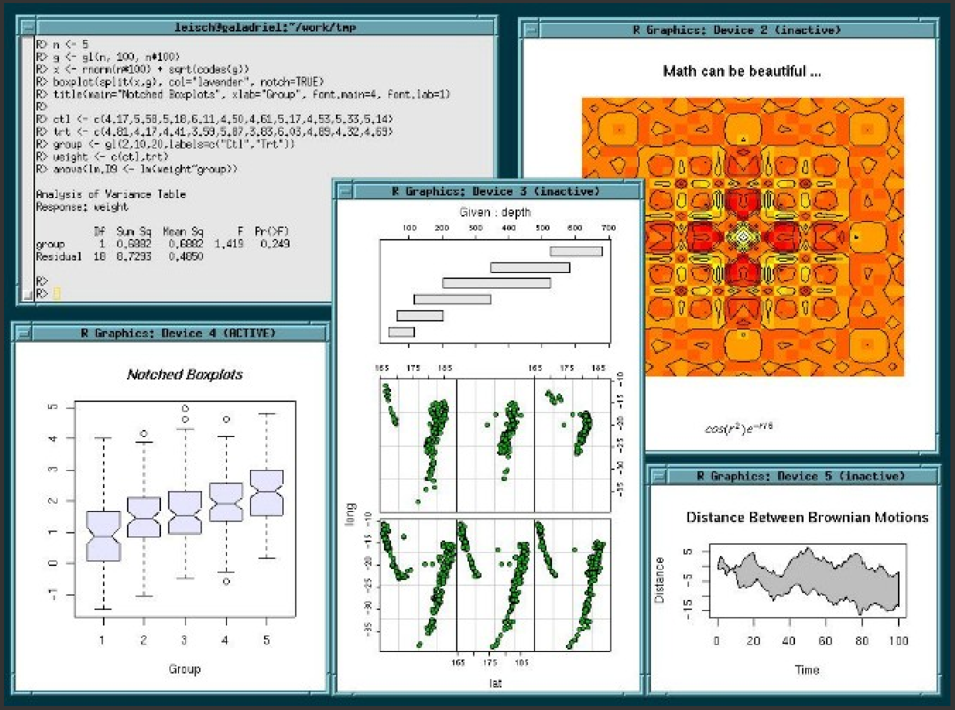
THERE IS NO BEST METHOD.

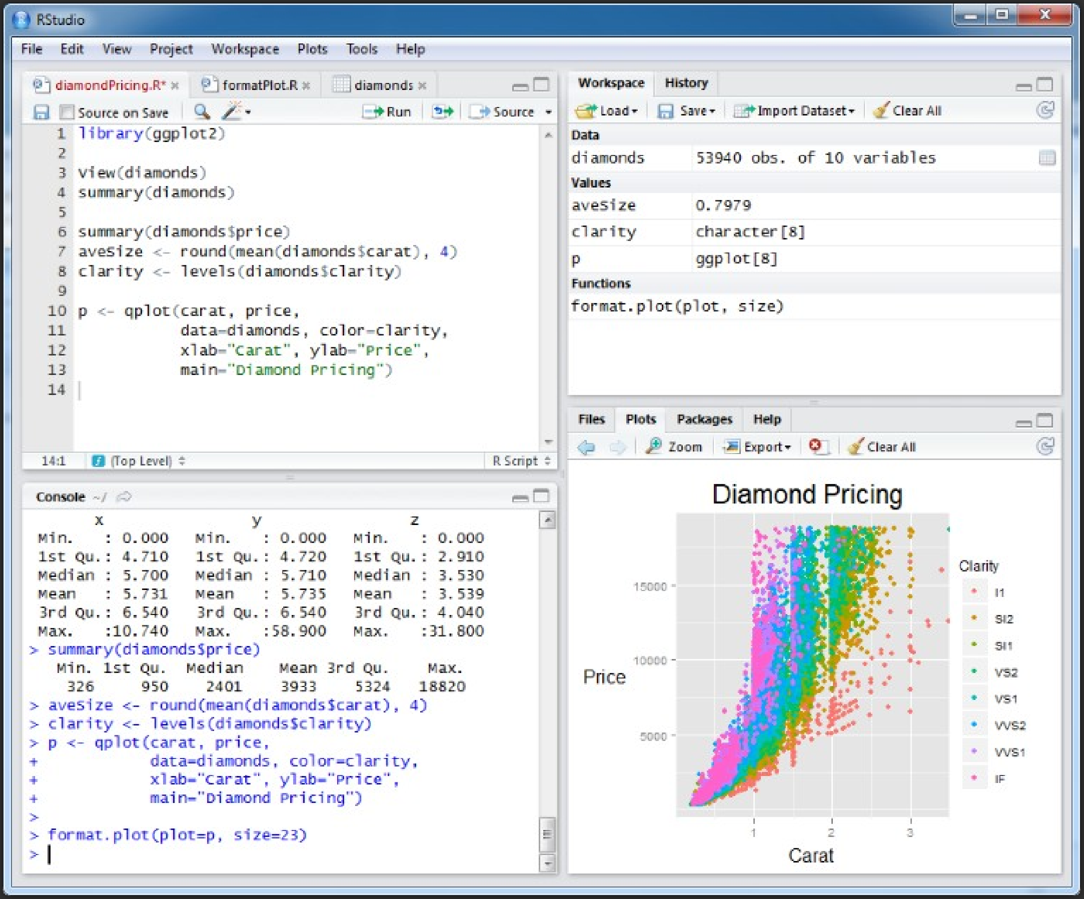
YOU MUST CHOOSE THE METHOD OR METHODS THAT FIT BETTER YOUR OBJECTIVES.

- **Any statistical software + GIS**
- **SPSS**
- **STATISTICA**
- **R (dismo/Biomod2/sdm) → Logistic Regression, GLM, GAM, Random Forest, etc**



- Software for statistical programming.
- R implements multiple ENMs techniques by installing different packages.
- Ade-habitat, Biomod2, SDMTools, dismo, sdm.
- GLM, GAM, ENFA, Maxent.
- Cross-platform.
- R-Studio.
- http://www.r-project.org/





Modelling:
- Dismo
- Biomod2
- Maxnet
- SDM
- rmaxent
- ENIRG: Ecological Niche in R-GRASS
- fuzzySim
- Maxlike
- NicheMapR
- enmSDM
- SDMPlay
- hSDM
- kuenm
- ssdm

Model comparison:
- ecospat
- ENMTools
- zoon

Model evaluation:
- ENMeval; evaluation of ENMs
- usdm: Uncertainty analysis for species distribution models
- modEvA: Model evaluation and analysis
- SDMTools
- blockCV

Virtual species:
- SDMvspecies
- virtualspecies

Model utilities:

-spThin: spatial thinning of species occurrence records
- MigClim: dispersal scenarios
- hypervolume: estimate volumes
- sdmpredictors
- eSDM: for creating and exploring ensembles of predictions from species distribution and abundance models

Climwin: evaluation of climate variables

QUESTIONS?