

# INTRODUCTION TO BIOMOD2

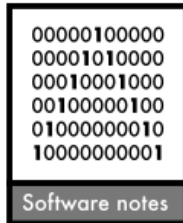
- Software for Ensemble modelling forecasting
- Written on R
- Cross-platform
- <http://www.will.chez-alice.fr/Software.html>
- Wilfried Thuiller

Global Change Biology (2003) 9, 1353–1362

## BIOMOD – optimizing predictions of species distributions and projecting potential future shifts under global change

WILFRIED THUILLER

*Centre d'Ecologie Fonctionnelle et Evolutive, Centre National de Recherche Scientifique, 1919 route de Mende,  
34293 Montpellier Cedex 5, France*



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# BIOMOD – a platform for ensemble forecasting of species distributions

**Wilfried Thuiller, Bruno Lafourcade, Robin Engler and Miguel B. Araújo**

*W. Thuiller (wilfried.thuiller@ujf-grenoble.fr) and B. Lafourcade, Laboratoire d'Ecologie Alpine, UMR CNRS 5553, Univ. Joseph Fourier, BP 53, FR-38041 Grenoble Cedex 9, France. – R. Engler, Dépt d'Ecologie et d'Evolution (DEE), Univ. de Lausanne, Bâtiment de Biologie, CH-1015 Lausanne, Switzerland. – M. B. Araújo, Dept of Biodiversity and Evolutionary Biology, National Museum of Natural Science, CSIC, C/Gutierrez Abascal, 2, ES-28006, Madrid, Spain and Rui Nabeiro Biodiversity Chair, Univ. of Évora, Colégio Luís António, Rua Romão Ramalho no. 59, PT-7000-671, Évora, Portugal.*

- **Generalised linear models (GLM)**
- **Generalised additive models (GAM)**
- **Multivariate adaptive regression splines (MARS)**
- **Classification tree analysis (CTA)**
- **Mixture discriminant analysis (MDA)**
- **Artificial neural networks (ANN)**
- **Generalised boosted models (GBM)**
- **Random forests**
- **Rectilinear envelope (similar to BIOCLIM)**
- **Maxent**

CRAN - Package biomod2 - Mozilla Firefox

https://cran.r-project.org/web/packages/biomod2/index.html

all × package bio... × CRAN - Pack... × +

## biomod2: Ensemble Platform for Species Distribution Modeling

Functions for species distribution modeling, calibration and evaluation, ensemble of models.

Version: 3.3-7

Depends: R (≥ 3.2.1), stats, utils, [sp](#), [raster](#), parallel, [reshape](#), [ggplot2](#)

Imports: [abind](#), [rasterVis](#), [pROC](#), [nnet](#), [gbm](#), [mda](#), [randomForest](#), [rpart](#), [MASS](#), methods, [PresenceAbsence](#), [dismo](#), [maxent](#), [earth](#)

Suggests: [ade4](#), [foreign](#), [Hmisc](#), [mgcv](#), [gam](#), [testthat](#), [ecospat](#), [caret](#)

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Author: Wilfried Thuiller [aut, cre], Damien Georges [aut, cre], Robin Engler [aut], Frank Breiner [aut]

Maintainer: Damien Georges <damien.georges2 at gmail.com>

Contact: Wilfried Thuiller <wilfried.thuiller@ujf-grenoble.fr>, Damien Georges <damien.georges2@gmail.com>

BugReports: <[https://r-forge.r-project.org/R/?group\\_id=302](https://r-forge.r-project.org/R/?group_id=302)>

License: [GPL-2](#)

URL: NA

NeedsCompilation: no

Materials: [NEWS](#)

CRAN checks: [biomod2 results](#)

Downloads:

Reference manual: [biomod2.pdf](#)

Package source: [biomod2\\_3.3-7.tar.gz](#)

Windows binaries: r-devel: [biomod2\\_3.3-7.zip](#), r-release: [biomod2\\_3.3-7.zip](#), r-oldrel: [biomod2\\_3.3-7.zip](#)

OS X Mavericks binaries: r-release: [biomod2\\_3.3-7.tgz](#), r-oldrel: [biomod2\\_3.3-7.tgz](#)

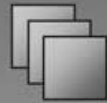
Old sources: [biomod2 archive](#)

Reverse dependencies:

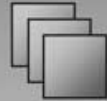
Reverse imports: [ecospat](#)

# Ensemble forecasting and uncertainty analysis in BIOMOD

Initial conditions  
State of the system



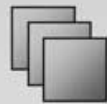
Model classes  
Different types of models



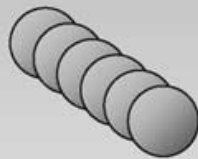
Model parameters  
Range of values for key parameters



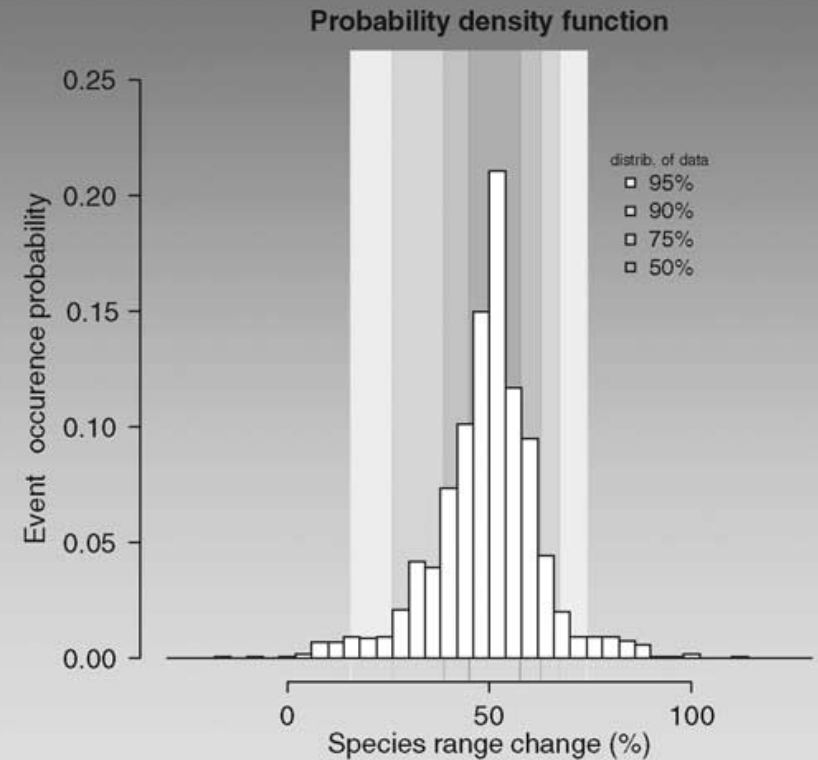
Climatic scenarios  
Ensemble of climatic projections

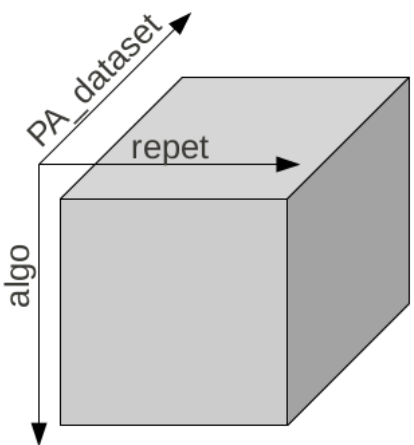
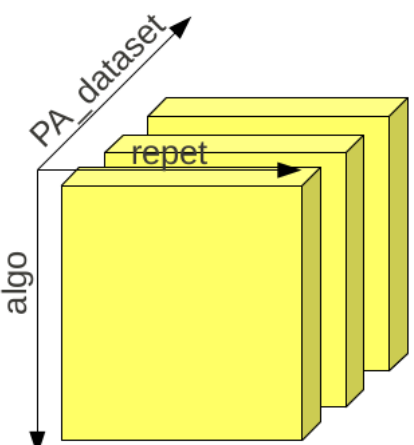


Ensemble of  
species/  
biodiversity  
projections

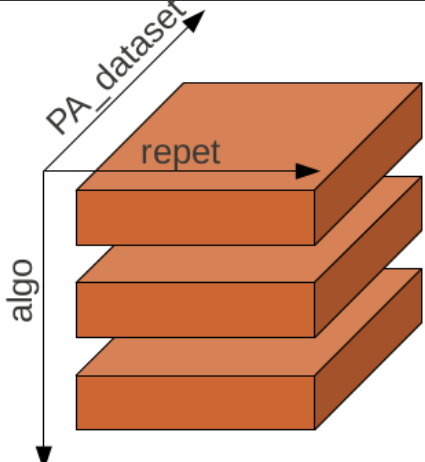
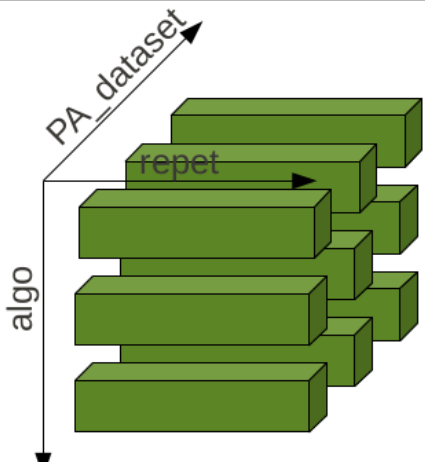


Probability  
density  
function

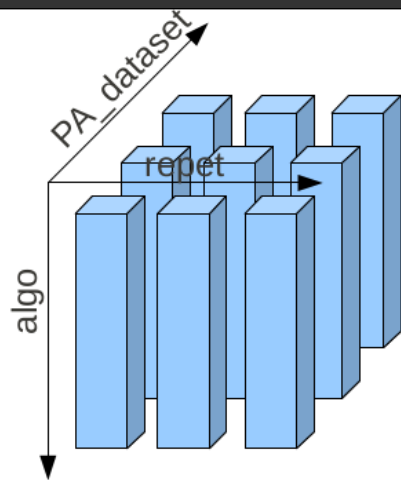


| Graphical representation  | 'em.by' value | Remarks   |
|---|---------------|---|
|   | 'all'         | <ul style="list-style-type: none"> <li>• Output: 1 ensemble model.</li> <li>• Evaluation: Ensemble models are evaluated on the evaluation data if some have been entered at BIOMOD_FormatingData(...) step. If not, the union of all PA_dataset points is used as reference. In the latter case, all 'NA' points (pseudo-absences) are considered as absences. This approach is not perfectly fair because some points used for individual models calibration are re-used for the ensemble models' evaluation.</li> </ul> |
|  | 'PA_dataset'  | <ul style="list-style-type: none"> <li>• Output: 1 ensemble model is built for each pseudo-absence dataset</li> <li>• Evaluation: Ensemble models are evaluated on the evaluation data if some have been entered at BIOMOD_FormatingData(...) step. If not the whole corresponding PA_dataset is taken as reference.</li> </ul>   |



|  |  |
|--|--|
|  <p>'algo'</p>             | <ul style="list-style-type: none"> <li>• Output: 1 ensemble model is built for each algorithm</li> <li>• Evaluation: Ensemble models are evaluated on the evaluation data if some have been entered at BIOMOD_FormatingData(...) step. If not, the union of all PA_dataset points is used as reference. In the latter case, all 'NA' points (pseudo-absences) are considered as absences. This approach is not perfectly fair because some points used for individual models calibration are re-used for ensemble models' evaluation.</li> </ul> |
|  <p>'PA_dataset+algo'</p> | <ul style="list-style-type: none"> <li>• Output: 1 ensemble model is built for each combination algorithm x pseudo absence selection (then the ensemble is made through the repetitions only).</li> <li>• Evaluation: Ensemble models are evaluated on the evaluation data if some have been entered at BIOMOD_FormatingData(...) step. If not the whole corresponding PA_dataset is taken as reference.</li> </ul>  |





**'PA\_dataset+repet'**

- Output: 1 ensemble model is built for each combination of pseudo absence selection x repetitions (then the ensemble is made through the algorithms only).
- Evaluation: Ensemble models are evaluated on the evaluation data if some have been entered at BIOMOD\_FormatingData(...) step. If not, the union of all PA\_dataset points is used as reference. In the latest case, all 'NA' points (pseudo-absences) are considered as absences. This approach is not perfectly fair because some points used for individual models calibration are re-used for ensemble models' evaluation.

- Load environmental data (as a stack of rasters)
- Load species data
- Format the data
- Define modelling options
- Compute the models
- Evaluate the models
- Spatialise the models (project them to current conditions)
- Ensemble the models
- Project the models in time and space

**.CSV FILE**

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X,X_WGS84,Y_WGS84,Rana
0,-6.2281289375,38.6478620677,0
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3,-4.9529660688,38.7295077502,0
4,2.6523583847,42.1759332625,1
5,-3.23978245,37.9883970183,1
7,-5.7353124897,37.7842523103,1
8,-7.5619772183,38.7224480643,1
9,-8.0325519941,37.3792082025,1
```

# QUESTIONS?