

Package **jSDM** functionalities

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1 Abstract

2 Results

2.1 Method validation and benchmark against state-of-the-art jSDMs

(HMSC, BayesComm, boral, s-jSDM)

2.1.1 Computational speed

2.1.2 Accuracy of the inference about species-environment and species-species associations

comparison of TSS and RMSE obtained with differents libraries

2.1.3 Predicting species occurrences

comparison of AUC obtained with differents libraries

2.2 Case study - Inference of biodiversity maps in Madagascar from forest inventories

2.2.1 Predictive performance of the model

compute AUC on inventory sites

2.2.2 Estimated species-species associations

sjSDM :plotAssociations()

2.2.3 Estimated species richness on inventory sites

2.2.4 Estimated species richness at Madagascar scale

2.2.5 Estimated species turn over at Madagascar scale

3 Methods

3.1 The structure of the jSDM problem

- Benefits of JSDBs over SDMs
- models definition (link function : probit, logit, log and data in long format)

3.2 Current approaches to fit the jSDM model structure

- $\Sigma = \Lambda\Lambda'$ Warton et al. (2015)
- inference method : Gibbs sampling using conjugate prior formula (probit link function) or Metropolis-Hastings algorithm (logit and log link function)

3.3 Methods and software to fit joint species distribution models

table to compare functionalities of HMSC, s-jSDM, boral (JAGS), greta, gjam, BayesComm, STAN and glvm

3.4 Benchmarking our method against state-of-the-art jSDM implementation

- datasets Wilkinson et al. (2019)
- n.mcmc
- compute AUC to assess the predictive performance of the models

3.5 Case study - Inference of biodiversity maps in Madagascar from forest inventories

3.5.1 Datasets

3.5.1.1 Forest inventory

3.5.1.2 Current environmental variables

3.5.2 Fitting joint species distribution model (JSDB)

3.5.2.1 Model definition

3.5.2.2 Parameters inference

3.5.2.3 Evaluation of MCMC convergence

3.5.3 Evaluation of predictive performance

compute AUC on inventory sites to assess the predictive performance of the model

3.5.4 Computation of species-species associations

3.5.5 Intrapolation of parameters between inventory sites

3.5.6 Species richness computation

3.5.7 Species turn over computation

4 Discussion

4.1 Computational performance

4.2 Inferential performance

4.3 Implications and outlook for ecological data analysis

5 Acknowledgments

6 Data Accessibility

References

Warton, David I., F. Guillaume Blanchet, Robert B. O'Hara, Otso Ovaskainen, Sara Taskinen, Steven C. Walker, and Francis K.C. Hui. 2015. "So Many Variables : Joint Modeling in Community Ecology." *Trends in Ecology & Evolution* 30 (12). Elsevier : 766–79. <https://doi.org/10.1016/j.tree.2015.09.007>.

Wilkinson, David P., Nick Golding, Gurutzeta Guillera-Arroita, Reid Tingley, and Michael A. McCarthy. 2019. "A Comparison of Joint Species Distribution Models for Presence-Absence Data." *Methods in Ecology and Evolution* 10 (2) : 198–211. <https://doi.org/10.1111/2041-210X.13106>.