

## Appendix S2 - Methods and results from Biomod analyses

To make sure that our Maxent results were not biased because of the algorithm used, we modelled the potential distribution of each species using five different models implemented in the R package biomod2 (Thuiller et al. 2014). The five chosen models were: boosted regression trees (GBM, Ridgeway 1999), generalised additive models (GAM, Hastie & Tibshirani 1986), classification tree analysis (CTA, Breiman et al. 1984), multivariate adaptive regression splines (MARS, Friedman 1991), and random forests (RF, Breiman 2001). Since our data set includes only presence, we randomly extracted 2000 pseudo-absences from the “target-group” background (Phillips et al. 2009). The predictive power of the models was evaluated with a data-splitting procedure with each model trained on 80% of the data and evaluated on the remaining 20% using the true skill statistic (TSS, Allouche et al. 2006) as an accuracy measure.

The results of the five models were then averaged to create an Ensemble model. Only models with a TSS higher than 0.4 were included into the Ensemble model. In some cases, the TSS scores were lower than 0.4 for all models which impeded the creation of the Ensemble. In those cases, the models were rerun with a lowered number of pseudo-absences (1000 for 16 species and 500 for 6 species) to obtain TSS scores above 0.4. The number of pseudoabsences has been shown to have an effect on the accuracy of the model (Barbet-Massin et al. 2012) and a lower number of pseudo-absences might lead to over-estimation of the habitat suitability.

We compared two results of the biomod models with our main Maxent models: the importance of the environmental variables and the potential species richness (derived from the stacked SDM). The variables importance for each models have been standardise to fit to a 0-1 scale (Fig. S4). The variables importance is generally similar between models, with mean annual precipitation being the most important except in the RF model (where bio17 is most important). Bio17, second most important variable in our Maxent models, is secondly more important in three out of the five biomod models.

We calculated the correlation (Pearson's  $r$ ) between the Maxent S-SDM and the five biomod models, as well as the ensemble model to test if the patterns observed in the results of our Maxent models are supported by the other modelling methods (Fig. S5). The potential species richness derived from the Maxent model is highly correlated with the potential species richness derived from the GAM, GBM, and CTA models. The correlation is lower between Maxent and the MARS and Ensemble model, and negatively correlated with the RF model. The RF model is also negatively correlated with the other models, if not as strongly. SDM produced with the RF algorithm have been shown to perform better (obtain a higher TSS score) with a low number of pseudo-absences (equal to the number of presence). In our case, the RF models performed actually quite well and obtained a lower number of low TSS (under 0.4) than the other models (except GBM – Fig. S6). However, the high number of pseudoabsences, and the fact that they have been randomly selected, might have led to RF

models which highly underestimate individual potential species distribution (habitat suitability highly restricted around the presence points – results not shown).

Therefore, we argue that our Maxent models, although based on a single modelling algorithm, represent a good estimation of the potential grass species richness in West Africa.

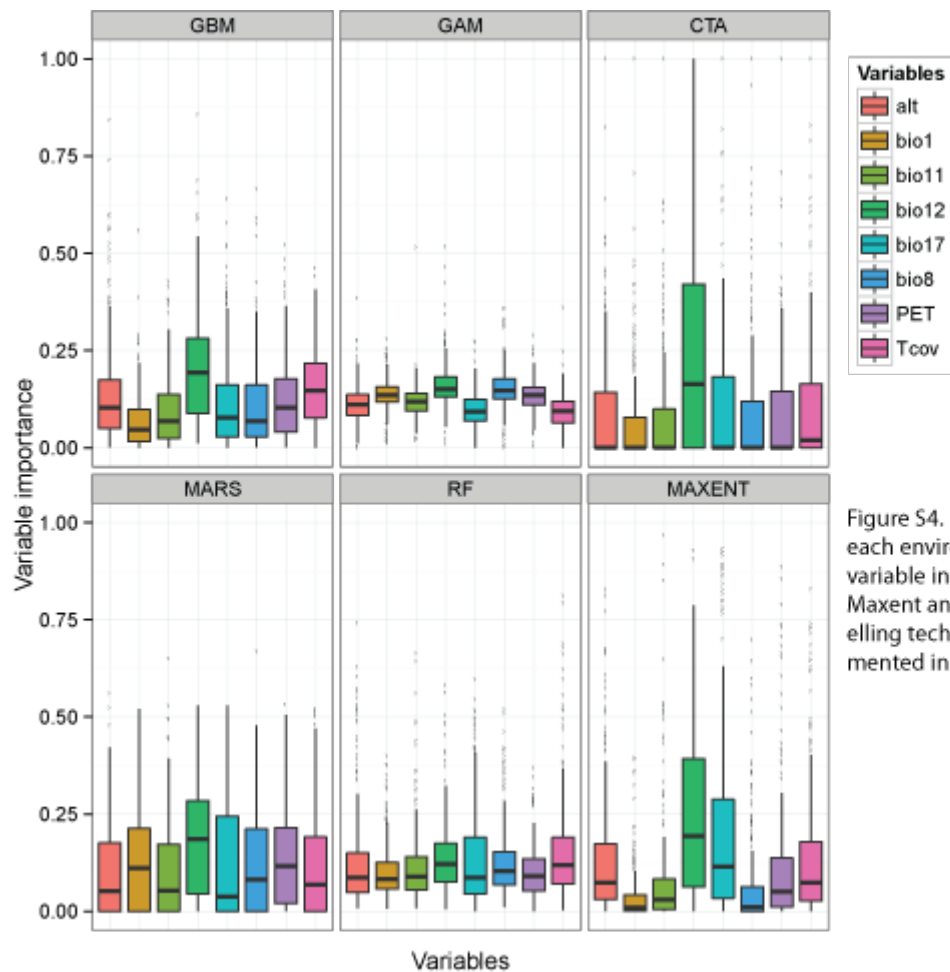


Figure S4. Importance of each environmental variable in the models. for Maxent and the five modelling techniques implemented in Biomod.

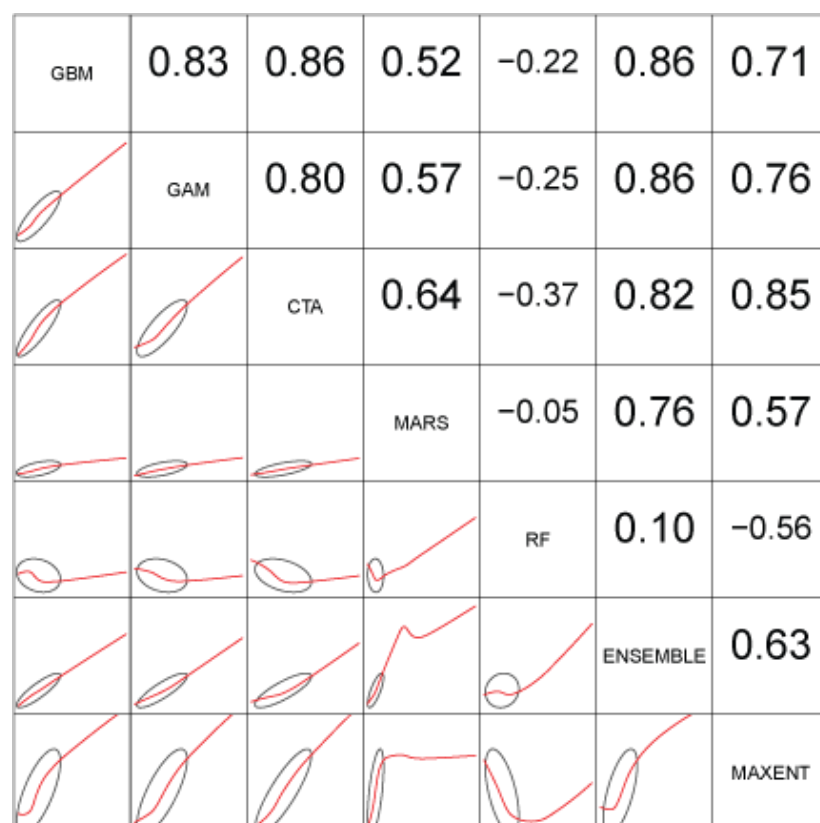


Figure S5. Correlation between the potential species richness derived from different models. Upper diagonal: Pearson's  $r$ . Lower diagonal: schematic scatterplot, each panel shows the bivariate (68%) concentration ellipse and a loess smoothed curve.

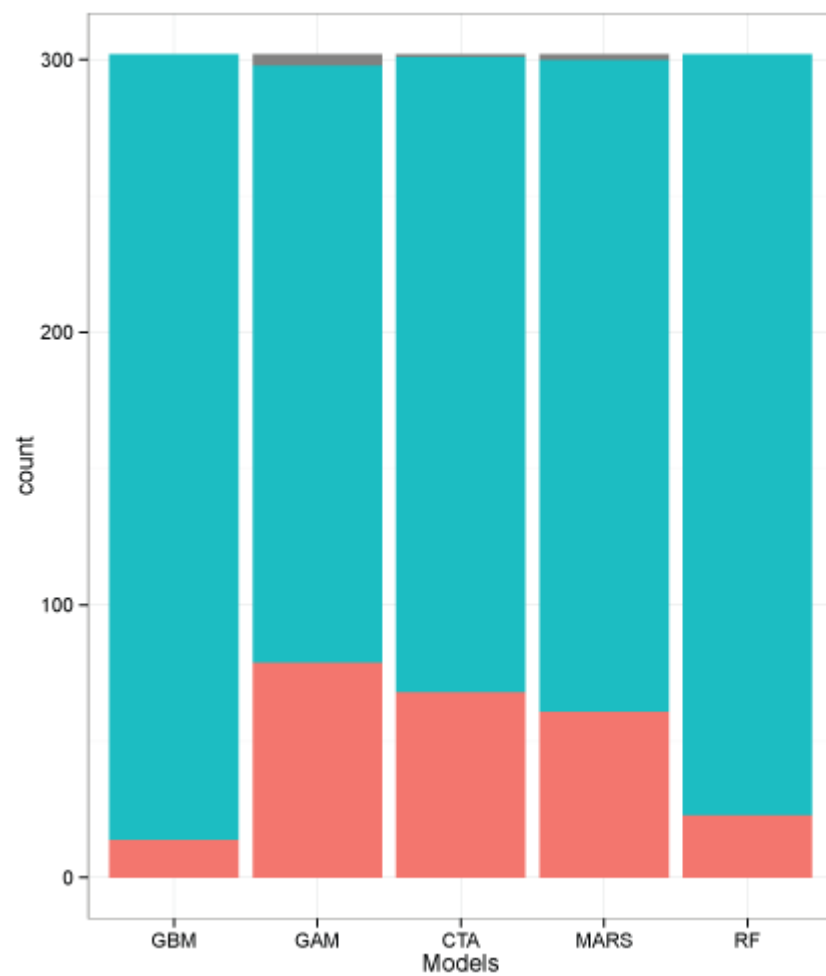


Figure S6. Counts of the TSS measures of all the individual species distribution models for the five different models. Blue indicates that the TSS measure was above 0.4, thus including the individual model in the Ensemble model.

- Allouche, O., Tsoar, A., & Kadmon, R. 2006. Assessing the Accuracy of Species Distribution Models: Prevalence, Kappa and the True Skill Statistic (TSS). *Journal of Applied Ecology* 43: 1223–1232.
- Barbet-Massin, M., Jiguet, F., Albert, C.H., & Thuiller, W. 2012. Selecting pseudo-absences for species distribution models: how, where and how many? *Methods in Ecology and Evolution* 3: 327–338.
- Breiman, L. 2001. Random Forests. *Machine Learning* 45: 5–32.
- Breiman, L., Friedman, J., Olshen, R., & Stone, C. 1984. *Classification and Regression Trees*. CRC Press Inc., Boca Raton.
- Friedman, J.H. 1991. Multivariate Adaptive Regression Splines. *The Annals of Statistics* 19: 1–67.
- Hastie, T., & Tibshirani, R. 1986. Generalized Additive Models. *Statistical Science* 1: 297–310.
- Phillips, S.J., Dudík, M., Elith, J., Graham, C.H., Lehmann, A., Leathwick, J.R., & Ferrier, S. 2009. Sample selection bias and presence-only distribution models: implications for background and pseudo-absence data. *Ecological Applications* 19: 181–197.
- Ridgeway, G. 1999. The state of boosting. *Computing Science and Statistics* 31: 172–181.
- Thuiller, W., Georges, D., & Engler, R. 2014. biomod2: Ensemble platform for species distribution modeling.