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SUPPORTING INFORMATION

Using species richness and functional traits predictions to constrain assemblage predictions from stacked species distribution models

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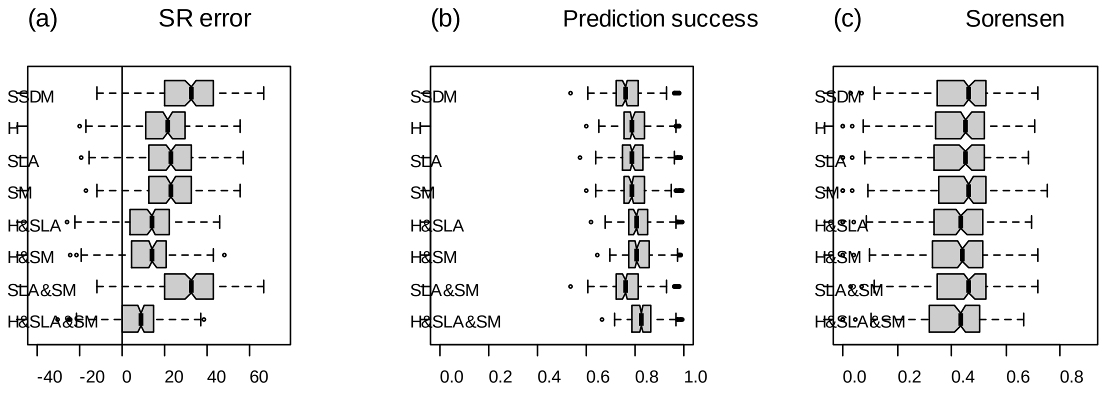
Appendix S1 Assemblage evaluation metrics and supplementary results.

Table S1 Confusion matrix used to compute the assemblage evaluation metrics.

		observed	
		0	**1**
predicted	**0**	*TN*	*FN*
	1	*FP*	*TP*

Figure S1 Results from true skill statistic (TSS) thresholding criterion: the boxplots compare results from the 'trait range' rule test for single traits and all their combinations when using TSS to binarize the SDM predictions. The metrics utilized in the comparison are: (a) species richness error, i.e. predicted SR – observed SR (first column), (b) prediction success, i.e. sum of correctly predicted presences and absences divided by the total species number (second column), and (c) Sørensen index, i.e. a statistic used to compare the similarity of two samples (third column). Abbreviations: H, height; SLA, specific leaf area of the community; SM, seed mass.



Appendix S2 Evaluation results for SDMs and MEMs.

Table S2 Summary of the SDMs evaluation results.

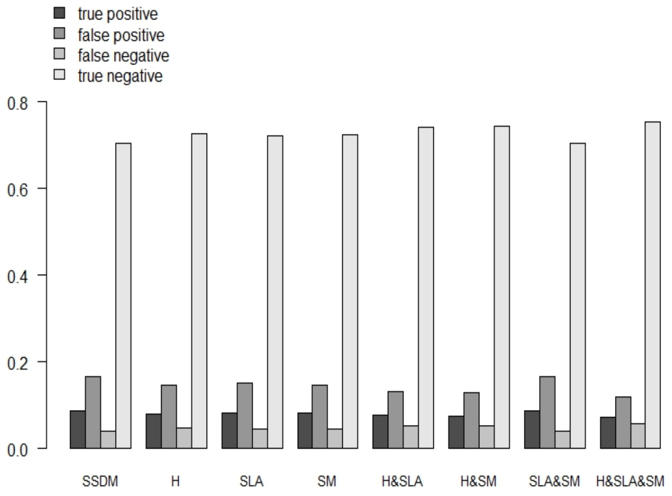
	GAM	**GBM**	**GLM**
AUC mean	0.803	0.783	0.799
AUC stdev	0.078	0.081	0.077
TSS mean	0.541	0.507	0.537
TSS stdev	0.142	0.137	0.142

Table S3 Values of Spearman correlation test between observed and predicted values of trait percentiles.

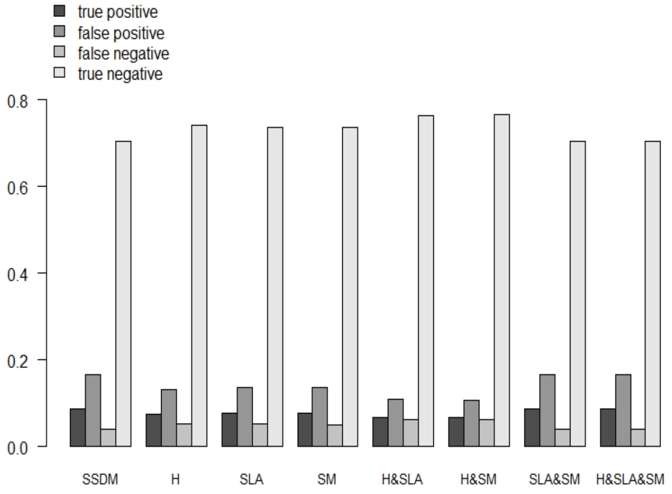
Percentile	**Trait**	**ρ**
1st	H	0.711
1st	SLA	0.759
1st	SM	0.152
99th	H	0.859
99th	SLA	0.584
99th	SM	0.514
5th	H	0.825
5th	SLA	0.803
5th	SM	0.350
95th	H	0.887
95th	SLA	0.652
95th	SM	0.528
10th	H	0.848
10th	SLA	0.814
10th	SM	0.550
90th	H	0.867
90th	SLA	0.677
90th	SM	0.645

Appendix S3 Comparison of the assemblage predictions coming from the application of the trait range rule with three pairs of percentiles. Abbreviations: SSDM, sum of binary SDMs; H, height; SLA, specific leaf area of the community; SM, seed mass.

1st–99th



5th–95th



10th–90th