

Preprint

This manuscript has been submitted to the *Journal of Quaternary Science*, special issue “Humans in the Earth System: Perspectives and Case-Studies on Population Dynamics and Cultural Evolution During the Pleistocene and Holocene”, and has not yet undergone peer review.

Spatially evaluated statistical reconstruction of Quaternary vegetation with PaleoVeg

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Article type: Research Paper

Special issue: Humans in the Earth System: Perspectives and Case-Studies on Population Dynamics and Cultural Evolution During the Pleistocene and Holocene

Running title: PaleoVeg palaeovegetation reconstruction

Abstract

Statistical vegetation–climate models translate palaeoclimate simulations into vegetation estimates for reconstructing Quaternary environments. We present PaleoVeg, which builds on the probabilistic approach of Shao et al. (2018) using a Random Forest and WorldClim 2.1 bioclimatic variables. It predicts probabilities for 11 vegetation and bare-ground classes and optionally applies class-specific CO₂ response factors. We compare configurations using annual mean temperature and precipitation alone or 17 bioclimatic predictors. Both use identical five-fold spatial cross-validation and a separate test comprising 132 withheld five-degree tiles. Expanding the predictor set increases mean cross-validation accuracy from 0.695 to 0.790 and macro F1 from 0.468 to 0.622. The full model achieves accuracy of 0.838 and macro F1 of 0.652 on the separate spatial test, although performance varies among classes and regions. In a matched Last Glacial Maximum experiment, PaleoVeg and archived Shao reconstructions show the same direction of CO₂-induced area change for all 11 classes. A complementary European application by Kern et al. (accepted for publication) finds similar broad temporal changes in PaleoVeg, pollen-based reconstructions, and JSBACH over 70–20 ka BP, alongside regional disagreements and differences in absolute forest estimates.

Keywords: palaeovegetation; machine learning; Random Forest; spatial cross-validation; Last Glacial Maximum

1 Introduction

Vegetation mediates exchanges of energy, water, carbon, and momentum between the land surface and atmosphere, processes represented explicitly in dynamic global vegetation models [Schaphoff et al., 2018]. Spatially explicit vegetation and land-cover boundary conditions are therefore important for palaeoclimate modelling,

dust-emission studies, and ecological interpretation of past environments [Harrison et al., 2020]. They can also provide ecological context for analyses of human responses to Quaternary environmental change. Timmermann et al. [2022] showed quantitatively that reconstructed climate and terrestrial net primary production affect inferred hominin habitat suitability and distributions. Archaeological evidence from the European Final Palaeolithic further associates spatially differentiated ecosystem change with regional demographic redistribution and changes in subsistence and mobility [Schmidt et al., 2025]. Shao et al. [2024] demonstrated how environmental suitability and resource availability can drive simulated population dynamics and dispersal.

Proxy syntheses provide evidence for past vegetation but remain spatially discontinuous, and pollen-derived vegetation estimates do not always map directly onto land-surface model classes [Prentice and Webb III, 1998, Dallmeyer et al., 2023]. Dynamic global vegetation models provide a mechanistic alternative by simulating plant functional types and associated biogeochemical processes, but this process representation also entails a more complex model and input-data system [Schaphoff et al., 2018]. A statistical model is useful when the immediate need is a reproducible vegetation estimate from gridded climate fields rather than a transient mechanistic simulation.

Shao et al. [2018] introduced a simple statistical solution. Modern Advanced Very High Resolution Radiometer (AVHRR) land-cover classes were related to modern rainfall and temperature, and the resulting class probabilities were transferred to Last Glacial Maximum climate. Nine pairs of annual mean, minimum, and maximum rainfall and temperature controls were tested. The best ensemble score was obtained using annual mean rainfall and annual mean temperature. The predicted probabilities were then modified by class-specific transition factors intended to represent the response to lower glacial atmospheric CO₂, derived from the modelling results of Woillez et al. [2011]. The study showed that probabilistic vegetation–climate relationships can produce global, interpretable palaeovegetation fields without a dynamic vegetation model.

PaleoVeg builds on this approach by extending the climate predictors and evaluating predictions in geographically withheld regions. Shao et al. [2018] assessed their model primarily through whole-grid agreement with the AVHRR classes used to construct the vegetation–climate relationships. Here, we use spatially separated training and test observations to assess geographic transfer, accounting for the spatial autocorrelation of environmental rasters [Roberts et al., 2017, Ploton et al., 2020].

PaleoVeg 1.0 builds on the probabilistic vegetation–climate formulation of Shao et al. [2018]: infer probabilistic modern vegetation–climate relationships from satellite land-cover classes, transfer those relationships to climate fields, and optionally apply the published low-CO₂ adjustment. It uses a Random Forest [Breiman, 2001], WorldClim BIOCLIM variables [Fick and Hijmans, 2017], and reusable training and inference software. Figure 1 relates the published formulation to the two PaleoVeg configurations.

We document the scientific lineage, data processing, model formulation, and software interfaces of PaleoVeg 1.0 and verify the implementation against the Shao goodness score and published CO₂ factors. We then compare the BIO1+BIO12 and 17-predictor configurations under identical spatial partitions and evaluate geographic transfer using separately withheld regions. The comparison isolates the effect of predictor-set expansion within the PaleoVeg framework.

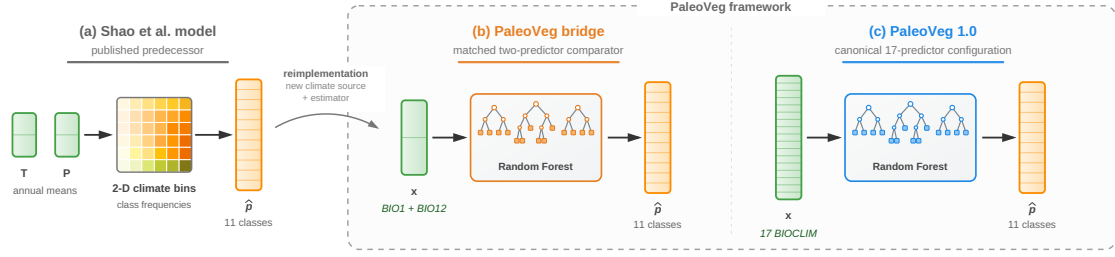


Figure 1: Schematic relationship between the Shao et al. (2018) model and the two PaleoVeg configurations. Shao model 5 estimates probabilities for 11 vegetation classes from a two-dimensional binned relationship between annual mean temperature (T) and precipitation (P). The BIO1+ BIO12 configuration (panel b) replaces the climate source and estimator with WorldClim BIO1 and BIO12 and a Random Forest, while PaleoVeg 1.0 retains the Random Forest framework and expands the input to 17 BIOCLIM predictors. The comparison between the two PaleoVeg configurations isolates the effect of predictor-set expansion within the Random Forest framework.

2 Scientific basis and relationship to Shao et al. (2018)

2.1 The published vegetation–climate model

For vegetation class i , Shao et al. [2018] denoted vegetation occurrence probability by P_i and represented it as a function of climate controls. For rainfall R and temperature T , observations were sorted into climate bins and the probability in bin (j, k) was estimated as

$$P_i(R_j, T_k) = \frac{N_i(R_j, T_k)}{\sum_m N_m(R_j, T_k)}, \quad (1)$$

where N_i is the number of AVHRR cells assigned to class i in that climate bin. Nine models combined annual mean, minimum, and maximum rainfall with the corresponding temperature summaries. Shao et al. identified model 5, using annual mean rainfall and annual mean temperature, as the best-performing configuration according to their goodness score, described in Section 5.3.

2.2 Development of the model formulation

PaleoVeg preserves the conceptual mapping

$$\begin{aligned} \text{modern climate and vegetation} &\rightarrow \text{probabilistic vegetation–climate model} \\ &\rightarrow \text{palaeoclimate vegetation probabilities,} \end{aligned} \quad (2)$$

PaleoVeg follows this formulation using WorldClim climate data and a Random Forest fitted directly to grid-cell observations. It retains the vegetation classes, probabilistic output, and CO₂ response factors of Shao et al. [2018]. Table 1 summarizes the shared components and the changes in climate data, estimation, and evaluation.

Table 1: Relationship between the published model and PaleoVeg 1.0.

Component	Shao et al. (2018)	PaleoVeg 1.0
Vegetation source	UMD 8 km classification derived from AVHRR	Same UMD 8 km classification
Climate source	ERA-Interim 1980–2009, 0.75°	WorldClim 2.1, 5 arc-minutes
Predictors	One rainfall and one temperature statistic per model	BIO1+BIO12 comparator or BIO1 and BIO4–BIO19
Estimator	Empirical two-dimensional bin frequencies	Random Forest classifier
Output	Class occurrence probabilities	Class probabilities
CO ₂ treatment	Published class transition factors	Same factors, normalized and parameterized by concentration
Evaluation	Whole-grid goodness relative to rearranged AVHRR	Blocked CV and external spatial tiles

2.3 Two-predictor comparator

The closest available WorldClim variables to annual mean temperature and annual rainfall are BIO1 and BIO12. We therefore define a two-predictor configuration that fits the PaleoVeg Random Forest using only

$$\mathbf{x}^{(2)} = (\text{BIO1}, \text{BIO12}). \quad (3)$$

The two-predictor configuration approximates the predictor information used by Shao model 5 while retaining PaleoVeg’s estimator and WorldClim source. Predictor choice can materially change the performance of ecosystem-level distribution models [Simensen et al., 2020]. Using the same rows and folds for both configurations isolates the predictor-set difference while holding the algorithm, target, and spatial samples fixed.

3 Data and preprocessing

3.1 Vegetation target

We use the University of Maryland (UMD) 8 km Global Land Cover Classification, version 1.0 [De Fries et al., 1998], retaining the vegetation dataset and class definitions used by Shao et al. [2018]. This preserves continuity with the predecessor model and compatibility with downstream workflows based on these classes. The classification was derived from the NASA/NOAA Pathfinder AVHRR Land (PAL) dataset [James and Kalluri, 1994], using selected annual metrics from 1984 observations and a decision-tree classifier trained with interpreted Landsat scenes [De Fries et al., 1998].

The classification follows the vegetation categories used by Shao et al. [2018]. Water, cultivated and managed land, permanent snow and ice, and documented anomalous values are omitted. The retained target contains 11 classes: evergreen needleleaf forest, evergreen broadleaf forest, deciduous needleleaf forest, deciduous

Table 2: WorldClim predictors used by PaleoVeg. BIO1 and BIO12 form the two-predictor model; all listed variables form the full model.

Variable	Description	Variable	Description
BIO1	Annual mean temperature	BIO11	Mean temperature of coldest quarter
BIO4	Temperature seasonality	BIO12	Annual precipitation
BIO5	Maximum temperature of warmest month	BIO13	Precipitation of wettest month
BIO6	Minimum temperature of coldest month	BIO14	Precipitation of driest month
BIO7	Annual temperature range	BIO15	Precipitation seasonality
BIO8	Mean temperature of wettest quarter	BIO16	Precipitation of wettest quarter
BIO9	Mean temperature of driest quarter	BIO17	Precipitation of driest quarter
BIO10	Mean temperature of warmest quarter	BIO18	Precipitation of warmest quarter
		BIO19	Precipitation of coldest quarter

broadleaf forest, mixed forest, woodland, wooded grassland, closed shrubland, open shrubland, grassland, and bare ground.

The AVHRR product supplies dominant class occurrence rather than sub-grid class fractions. For each grid cell g , the target is therefore a one-hot vector $\mathbf{y}_g \in \{0, 1\}^{11}$ with $\sum_i y_{gi} = 1$. The model output is a probability vector $\hat{\mathbf{p}}_g$ on the same simplex. These probabilities may be interpreted as the model-estimated occurrence probabilities of vegetation classes under the supplied climate, consistent with the probabilistic interpretation in [Shao et al. \[2018\]](#); they are not direct remotely sensed fractional cover observations.

3.2 Bioclimatic predictors

WorldClim 2.1 supplies global climate normals derived from weather-station observations and spatial interpolation [[Fick and Hijmans, 2017](#)]. PaleoVeg uses the 5 arc-minute rasters. The full predictor vector is

$$\mathbf{x}^{(17)} = (\text{BIO1}, \text{BIO4}, \text{BIO5}, \dots, \text{BIO19}), \quad (4)$$

excluding BIO2 and BIO3. Table 2 lists the variables. The predictor set represents mean climate, seasonality, temperature and precipitation extremes, and conditions during wet, dry, warm, and cold quarters. Random Forests do not require feature scaling, so predictor values retain their native WorldClim units.

3.3 Grid matching and complete-case filtering

The AVHRR vegetation and WorldClim climate rasters use slightly different grids. We use bilinear interpolation to obtain WorldClim predictor values at the sampling coordinates of each retained AVHRR pixel. The resulting training table contains the vegetation class, climate predictors, geographic coordinates, and five-degree tile identifier used for spatial evaluation.

Rows with any non-finite predictor are removed. The final data set contains 2,823,308 observations in 1314 occupied 5° tiles. Bare ground is the majority class (1,287,808 observations; 45.6%), whereas deciduous needleleaf forest is the least numerous retained class (60,588; 2.1%). We report macro-averaged and balanced metrics alongside overall accuracy because class frequencies are imbalanced.

4 PaleoVeg 1.0 model

4.1 Random Forest probability model

PaleoVeg uses the `RandomForestClassifier` implementation in scikit-learn. A Random Forest fits an ensemble of decision trees to bootstrap samples and averages their predictions [Breiman, 2001]. For tree $b \in \{1, \dots, B\}$, let $p_{bi}(\mathbf{x})$ be the fraction of training observations assigned to class i in the terminal leaf reached by $\mathbf{x}$. The forest probability is

$$\hat{p}_i(\mathbf{x}) = \frac{1}{B} \sum_{b=1}^B p_{bi}(\mathbf{x}). \quad (5)$$

The vector $\hat{\mathbf{p}}(\mathbf{x})$ is non-negative and sums to one.

Both model configurations use exactly the same hyperparameters: 100 trees, maximum depth 20, Gini splitting, square-root feature subsampling at each split, bootstrap sampling, minimum leaf size 1, no class weights, and random state 42. These values are fixed before the spatial comparison; no hyperparameter selection is performed on validation or external-test tiles. Parallel execution changes runtime but not model definition.

The full predictor model is designated PaleoVeg 1.0. The BIO1+BIO12 configuration is used for the predictor-set comparison. After validation, the distributed full model is refitted to all eligible observations using the locked configuration. Validation estimates always come from models that exclude the corresponding held-out regions.

4.2 Atmospheric CO₂ correction

The class factors reported by Shao et al. [2018] describe the ratio of vegetation cover under glacial and modern CO₂ in simulations analysed from Woillez et al. [2011]. PaleoVeg uses the published factors at 185 ppm listed in Table 5. Given uncorrected probabilities $\hat{p}_i$ and factors $f_i(c)$ at concentration c , corrected probabilities are

$$\hat{p}_i^{(c)} = \frac{f_i(c)\hat{p}_i}{\sum_j f_j(c)\hat{p}_j}. \quad (6)$$

At modern baseline concentration $c_0 = 310$ ppm, all factors equal one. PaleoVeg interpolates or extrapolates linearly from the published 185 ppm factors,

$$f_i(c) = 1 + \frac{310 - c}{310 - 185} [f_i(185) - 1]. \quad (7)$$

Concentrations producing a non-positive factor are rejected. Equation (7) reproduces the published factors at 185 ppm and permits evaluation at other concentrations. The optional correction represents CO₂ sensitivity through class-level post-processing factors; plant physiology is not modelled explicitly.

4.3 Software interfaces and portability

The Python interface accepts tabular pandas data or map-like NumPy arrays. Inputs are normalized to canonical BIOCLIM column names and checked for missing, non-numeric, non-finite, or out-of-training-range values. Outputs may contain class probabilities, dominant class, or both. Model loading is lazy and validates the SHA-256 digest of the serialized release artifact. A browser interface runs the same model

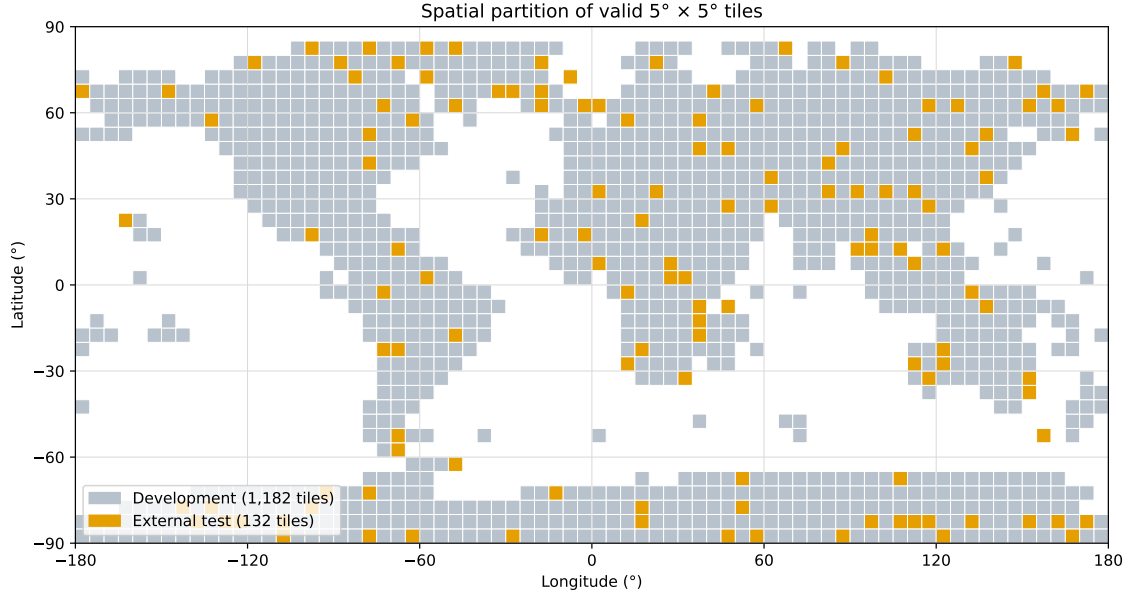


Figure 2: Global spatial partition. Grey $5^\circ \times 5^\circ$ tiles form the development region; orange tiles form the external test. Only tiles containing eligible complete-case observations are shown.

locally using Pyodide and provides tabular and NetCDF import/export. Unit tests cover predictor calculation, input normalization, model loading, CO_2 behaviour, browser parity utilities, spatial splitting, and the Shao goodness implementation. A user manual and executable examples are included with the source archive.

5 Verification and evaluation design

5.1 Spatial partitioning for training and evaluation

The global domain is divided into $5^\circ \times 5^\circ$ longitude–latitude tiles. After filtering, 1314 tiles contain at least one observation with a retained vegetation class and complete predictor values. We randomly select 132 of these tiles (10%, rounded upward; random seed 42) for the external spatial test and use the remaining 1182 tiles for model development (Fig. 2). All observations within a tile remain together in either the development or external-test set. The external region is not used for fitting, predictor choice, or interpretation until both configurations and metrics are fixed.

Within the development region, tiles are divided among five cross-validation folds using a deterministic algorithm that balances the number of observations per fold. All observations within each tile remain in the same fold. Each fold contains 236–237 tiles and 505,752–505,753 validation observations. For each fold, a fresh forest is fitted to the other four folds. The same manifest is used for both predictor configurations, giving a paired experimental design. Grouping observations in five-degree tiles keeps most local 8 km neighbourhoods in the same fold or external-test set, although observations on opposite sides of tile boundaries can remain close. The blocks also vary in physical area with latitude and cannot guarantee environmental independence [Roberts et al., 2017, Ploton et al., 2020].

After blocked cross-validation, each configuration is fitted to all 2,528,764 development observations and evaluated once on the 294,544 external observations.

Finally, production artifacts are fitted to all 2,823,308 observations. The production refit uses external observations and therefore has no associated external-test score; reported external metrics belong to the development-only fit.

5.2 Classification and probabilistic metrics

We measure dominant-class prediction performance using overall accuracy, balanced accuracy, macro F1, and weighted F1. We calculate overall accuracy as the proportion of correctly classified observations. Because bare ground accounts for nearly half the observations, we also report balanced accuracy, calculated as the mean recall across the 11 classes, and macro F1, calculated as the mean class-wise F1 score. These averages give each class equal weight. For comparison, we calculate weighted F1 by weighting each class-wise F1 score by its number of observations [Congalton, 1991, Sokolova and Lapalme, 2009, Brodersen et al., 2010].

We use multiclass log loss to evaluate the complete predicted probability vector, including the probability assigned to the observed class:

$$\mathcal{L}_{\log} = -\frac{1}{N} \sum_{g=1}^N \log(\hat{p}_{g,y_g} + \epsilon), \quad (8)$$

Here, y_g is the observed class, and we add ϵ to avoid taking the logarithm of zero. With log loss, confident incorrect predictions receive larger penalties. We use it as a proper scoring rule for assessing probabilistic predictions [Gneiting and Raftery, 2007].

5.3 Shao et al. goodness score

To retain a metric directly connected to the published predecessor, we implement Eq. 3 of Shao et al. [2018]. For class i ,

$$D_i = \frac{1}{N} \sum_{g=1}^N (\hat{p}_{gi} - y_{gi})^2. \quad (9)$$

A reference vegetation field is created by one deterministic random permutation of the categorical observed labels, preserving class prevalence and mutual exclusivity. Let y_{gi}^{rand} be its one-hot representation. Then

$$D_{i,\max} = \frac{1}{N} \sum_{g=1}^N (y_{gi}^{\text{rand}} - y_{gi})^2 \quad (10)$$

and

$$S_i = 1 - \frac{D_i}{D_{i,\max}}. \quad (11)$$

A perfect probability reconstruction has $S_i = 1$ and the rearranged reference has expectation near zero. The ensemble score is the unweighted mean of class scores. One permutation is used for exact reproducibility, with the same reference seed for both configurations in each evaluation set.

The printed Shao model-5 scores are included as historical context, but not treated as a controlled benchmark. They used ERA-Interim, climate-bin probabilities, and whole-grid self-consistency; PaleoVeg scores use WorldClim, Random Forests, and spatially held-out regions. The controlled test of predictor expansion is the paired comparison between the two PaleoVeg configurations.

5.4 Spatial correlation of prediction errors

Spatially separating training and test observations reduces the risk of evaluating the model on locations that closely resemble nearby training locations. However, prediction errors can remain similar across neighbouring tiles. We therefore estimate how far this similarity extends and compare that distance with the dimensions of the five-degree tiles used for evaluation [Legendre, 1993, Roberts et al., 2017].

For each vegetation class, we calculate the prediction error at each external-test location as the predicted probability minus the observed class indicator (one when the class is present and zero otherwise). We then examine whether these errors are correlated between locations at different distances from one another. All predictions used in this analysis come from the full model fitted only to development tiles. For class i at cell g , the signed probability residual is

$$r_{gi} = \hat{p}_{gi} - y_{gi}. \quad (12)$$

Up to 1000 cells were sampled without replacement from each external tile, yielding 105,102 cells across all 132 tiles. Equal maximum sampling per tile prevents the largest or most densely occupied tiles from dominating the spatial-scale estimate. We drew two million random pairs from this sample and calculated their haversine great-circle distances; 1,999,995 pairs fell within the analysed distance classes.

For residual variable r with sample mean $\bar{r}$ and variance s_r^2 , distance-class correlation was estimated as

$$\rho(h) = \frac{1}{|P_h|s_r^2} \sum_{(g,k) \in P_h} (r_g - \bar{r})(r_k - \bar{r}), \quad (13)$$

where P_h is the set of sampled pairs in distance class h . The distance-class residual correlation is a spatial correlogram [Sokal and Oden, 1978]. We estimate the distance beyond which prediction errors have little remaining spatial correlation. We identify the first distance interval where the absolute error correlation is at most 0.05 and remains at or below this threshold in every subsequent interval up to 1000 km. We report the upper boundary of that interval as the range of error correlation. Only intervals containing at least 100 pairs are used. Requiring the correlation to remain below the threshold prevents a single low estimate from determining the range.

5.5 Matched Last Glacial Maximum behavioural verification

We compared global vegetation-class areas in a Last Glacial Maximum experiment using the six CMIP5/PMIP3 simulations used by Shao et al. [2018]. For each model, we used monthly mean, minimum, and maximum temperature and precipitation from the `lgm` experiment and ensemble member `r1i1p1`. Table 3 lists the models and contributing modelling groups. The CMIP5 experimental framework and PMIP3 palaeoclimate experiments are described by Taylor et al. [2012] and Braconnot et al. [2012], respectively.

We interpolated the monthly fields to a common 1° grid and calculated the six-model ensemble mean. Monthly precipitation rates were converted to monthly totals using the month lengths specified by each source file’s CF calendar. As in Shao et al. [2018], we averaged the monthly climate fields before deriving the vegetation estimates. We calculated the 17 BIOCLIM predictors from this ensemble-mean climate, rather than averaging predictor values derived separately for each model. Climate-model uncertainty is not quantified in this experiment.

Table 3: PMIP3/CMIP5 Last Glacial Maximum simulations used in the matched behavioural-verification experiment and their contributing modelling groups.

Model	Contributing modelling group
CNRM-CM5	CNRM-CERFACS
FGOALS-g2	LASG-CESS
IPSL-CM5A-LR	IPSL
MIROC-ESM	MIROC consortium
MPI-ESM-P	MPI-M
MRI-CGCM3	MRI

We compare the PaleoVeg results with the 1° LGM vegetation reconstructions produced and archived as part of the original study by [Shao et al. \[2018\]](#). These reconstructions were generated using the original statistical vegetation model, driven by the six-model PMIP3 ensemble-mean climate, with and without the low-CO₂ correction. We compare global vegetation-class areas and their response to the CO₂ correction between the original model and PaleoVeg.

The full all-data PaleoVeg model was applied on terrestrial cells shared with the archived 1° Shao LGM reconstruction, once without and once with the published 185 ppm CO₂ correction. Area-weighted class fractions were calculated with weights proportional to $\cos(\text{latitude})$. We also calculate corresponding fractions from the archived Shao outputs and show the modern AVHRR training target as visual context. The comparison uses a common LGM land mask for the two reconstructions; the modern reference is calculated from the complete-case 8 km training grid and is not used for a formal LGM–modern change estimate.

We use this experiment to test behavioural correspondence between the two implementations. Both LGM reconstructions depend on the same climate-model ensemble and therefore do not provide independent validation. Numerical equality is not expected because PaleoVeg uses a different estimator and a 17-variable climate representation. We summarize correspondence by the Pearson correlation across the 11 area fractions and their mean absolute difference in percentage points. We separately compare the signed class-area response to the CO₂ correction. Predictor-range warnings are retained, because some glacial climates fall outside modern training support.

6 Results

6.1 Blocked spatial validation

The full model outperforms the BIO1+BIO12 model in every reported metric and every fold (Fig. 3; Table 4). Mean accuracy increases by 0.0949, balanced accuracy by 0.1464, macro F1 by 0.1542, weighted F1 by 0.0983, and the Shao goodness score by 0.0882. Mean log loss decreases from 0.869 to 0.563. The larger gains in balanced accuracy and macro F1 reflect improved performance across classes.

6.2 Class-wise comparison with the published score

The full model’s blocked-CV Shao score exceeds that of the BIO1+BIO12 model for every class (Fig. 4). The largest mean blocked-CV scores for the full model occur for

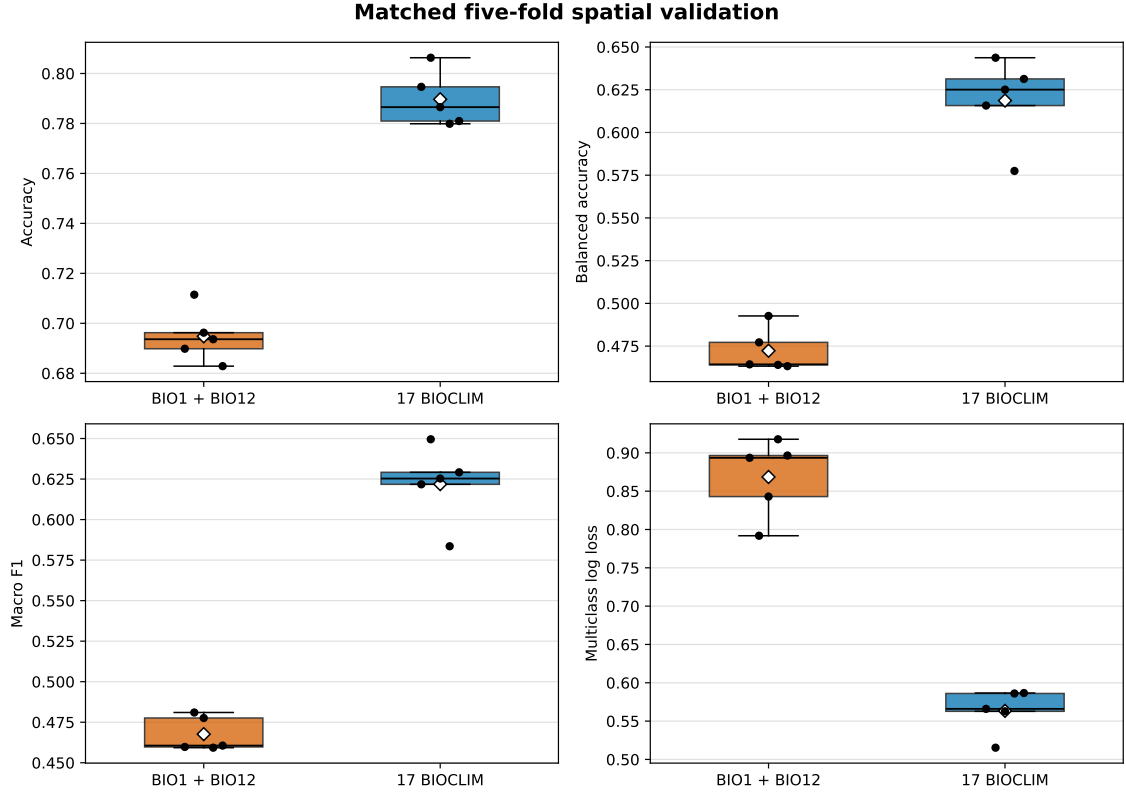


Figure 3: Matched five-fold spatial validation for the BIO1+BIO12 model (orange) and full 17-predictor PaleoVeg model (blue). Black circles are individual folds; coloured boxes show their distribution; horizontal black lines are medians; white diamonds denote arithmetic means across the five folds. Lower multiclass log loss is better; higher values are better for the other panels.

Table 4: Matched blocked-cross-validation and external-test performance. Cross-validation entries are fold mean $\pm$ sample standard deviation.

Evaluation	Predictors	Accuracy	Balanced acc.	Macro F1	Log loss	Shao score
Blocked CV	BIO1+BIO12	0.695 ± 0.011	0.472 ± 0.013	0.468 ± 0.011	0.869 ± 0.051	0.657 ± 0.008
Blocked CV	17 BIOCLIM	0.790 ± 0.011	0.619 ± 0.025	0.622 ± 0.024	0.563 ± 0.029	0.745 ± 0.011
External test	BIO1+BIO12	0.739	0.493	0.484	0.745	0.669
External test	17 BIOCLIM	0.838	0.652	0.652	0.449	0.766

bare ground (0.967) and evergreen broadleaf forest (0.870); the lowest occurs for deciduous broadleaf forest (0.595). The corresponding two-predictor values are 0.931, 0.809, and 0.527. The full model’s improvement is especially large for deciduous needleleaf forest, woodland, mixed forest, and evergreen needleleaf forest.

Shao model 5 reported an ensemble score of 0.51. The spatially held-out two-predictor and full PaleoVeg models obtain mean scores of 0.657 and 0.745, respectively. These values cannot be compared directly with the published score because their denominators and evaluation supports differ. The controlled comparison instead holds the target table, tile assignments, reference permutations, and Random Forest hyperparameters constant between the two PaleoVeg configurations.

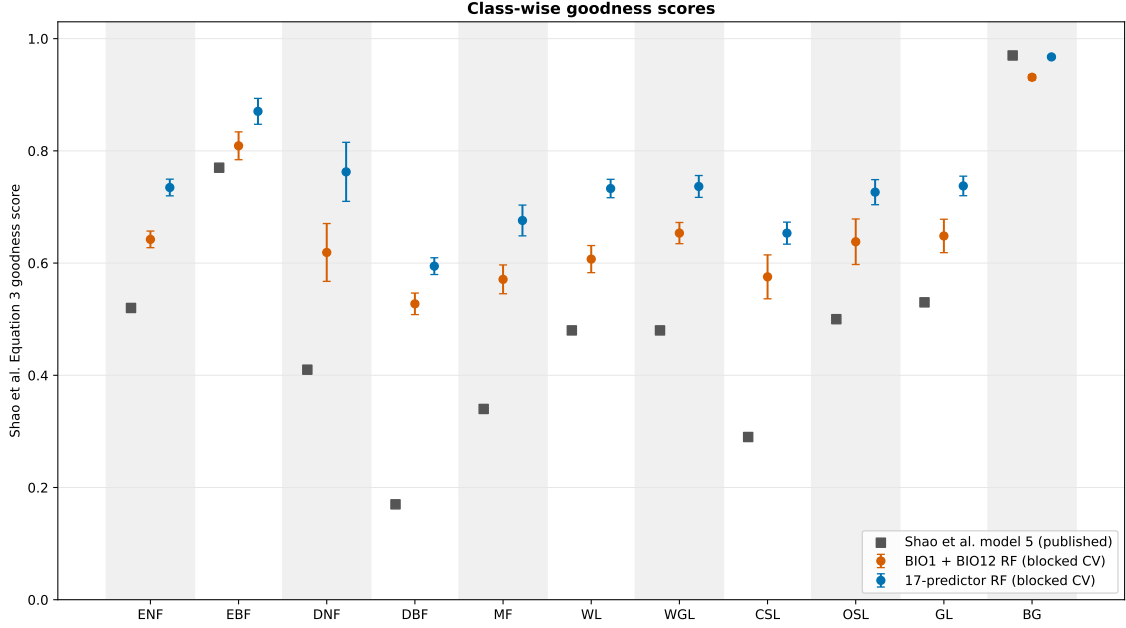


Figure 4: Class-wise Shao et al. Eq. 3 goodness scores. Grey squares reproduce the values printed for Shao model 5, which use ERA-Interim whole-grid self-consistency. Orange and blue points are mean PaleoVeg scores from five spatially blocked folds; error bars are fold standard deviations. Published and new scores use different climate products, estimators, and validation designs; the paired orange–blue contrast is the controlled predictor-set comparison. Class abbreviations are defined in Appendix A.

6.3 External spatial transfer and class errors

The external tiles happen to be easier than the average blocked fold for both configurations, but preserve the same model ordering. The full model reaches 0.838 accuracy, 0.652 balanced accuracy, 0.652 macro F1, and 0.449 log loss. Figure 5 shows that the full predictor set sharpens the diagonal of the normalized confusion matrix for most classes.

For the full model, external class F1 ranges from 0.085 for deciduous broadleaf forest to 0.983 for bare ground. Evergreen broadleaf forest (0.825), deciduous needle-leaf forest (0.791), and open shrubland (0.745) are comparatively well recovered. Deciduous broadleaf recall is only 0.049 despite 6024 external observations, indicating a structural overlap in BIOCLIM space rather than absence from the evaluation. Closed shrubland (F1 0.488) is the next weakest class. Global accuracy therefore does not represent performance uniformly across classes.

The full model improves accuracy in 99 of 132 external tiles (Fig. 6), with a median tile-wise improvement of 7.7 percentage points (IQR 0.0–21.8 percentage points). Thirty tiles have identical accuracies, and three have lower accuracy with the full predictor set. High accuracy in Antarctic and other bare-ground-dominated tiles partly reflects the easily separable majority class; balanced and class-wise metrics remain necessary.

6.4 Predictor contributions

Impurity-based importance in the all-data BIO1+BIO12 model is 0.566 for BIO1 and 0.434 for BIO12. In the full model, BIO5 (maximum temperature of the warmest

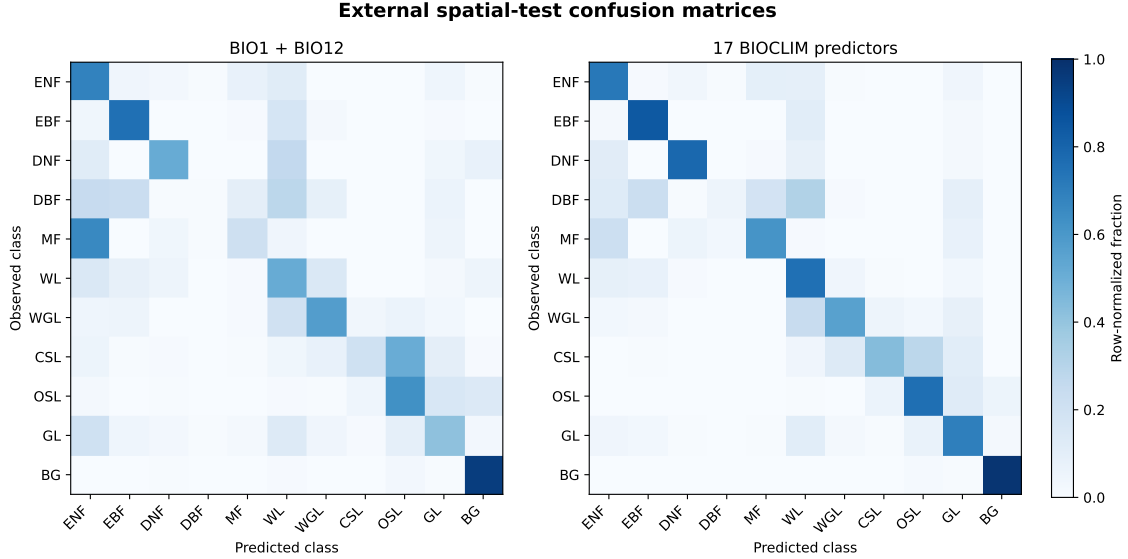


Figure 5: Row-normalized confusion matrices on the 132 external spatial tiles. Each row sums to one. The full predictor model improves discrimination across most vegetation classes, but deciduous broadleaf forest remains frequently confused with other forest and woodland classes.

month) is most important (0.145), followed by BIO1 (0.110), BIO10 (mean temperature of the warmest quarter; 0.093), BIO12 (0.080), and BIO18 (precipitation of the warmest quarter; 0.076; Fig. 7). Impurity importance is descriptive and can favour variables with more candidate split points or correlated alternatives [Strobl et al., 2007, 2008]; it is not a causal attribution.

6.5 Spatial scale of full-model residuals

All 11 signed class-probability residuals reached sustained $|\rho(h)| \leq 0.05$ within 100–500 km (median 300 km; Fig. 8). The shortest practical range was 100 km for deciduous needleleaf forest. Evergreen needleleaf forest, mixed forest, wooded grassland, and closed shrubland reached 300 km; evergreen broadleaf forest reached 400 km; and woodland, open shrubland, and bare ground had the largest estimated ranges of 500 km. At distances below 25 km, correlations ranged from -0.031 for deciduous broadleaf forest to 0.340 for bare ground, demonstrating why pixel-wise random partitioning would not remove local dependence.

A 5° tile spans approximately 555 km north–south and up to 555 km east–west at the equator. Its characteristic scale is therefore comparable to or larger than the complete 100–500 km signed-residual range.

6.6 Matched LGM global-area behaviour

In the matched LGM experiment, the low- CO_2 adjustment reduces total forest probability (the sum of the probabilities for evergreen needleleaf forest, evergreen broadleaf forest, deciduous needleleaf forest, deciduous broadleaf forest, and mixed forest) from 47.7% to 39.3% and increases woodland by 6.7 percentage points and grassland by 4.0 percentage points (Fig. 9). The archived Shao reconstruction has the same directions: forest decreases from 37.8% to 32.3%, woodland increases by 5.9 percentage points, and grassland increases by 4.1 percentage points. All 11

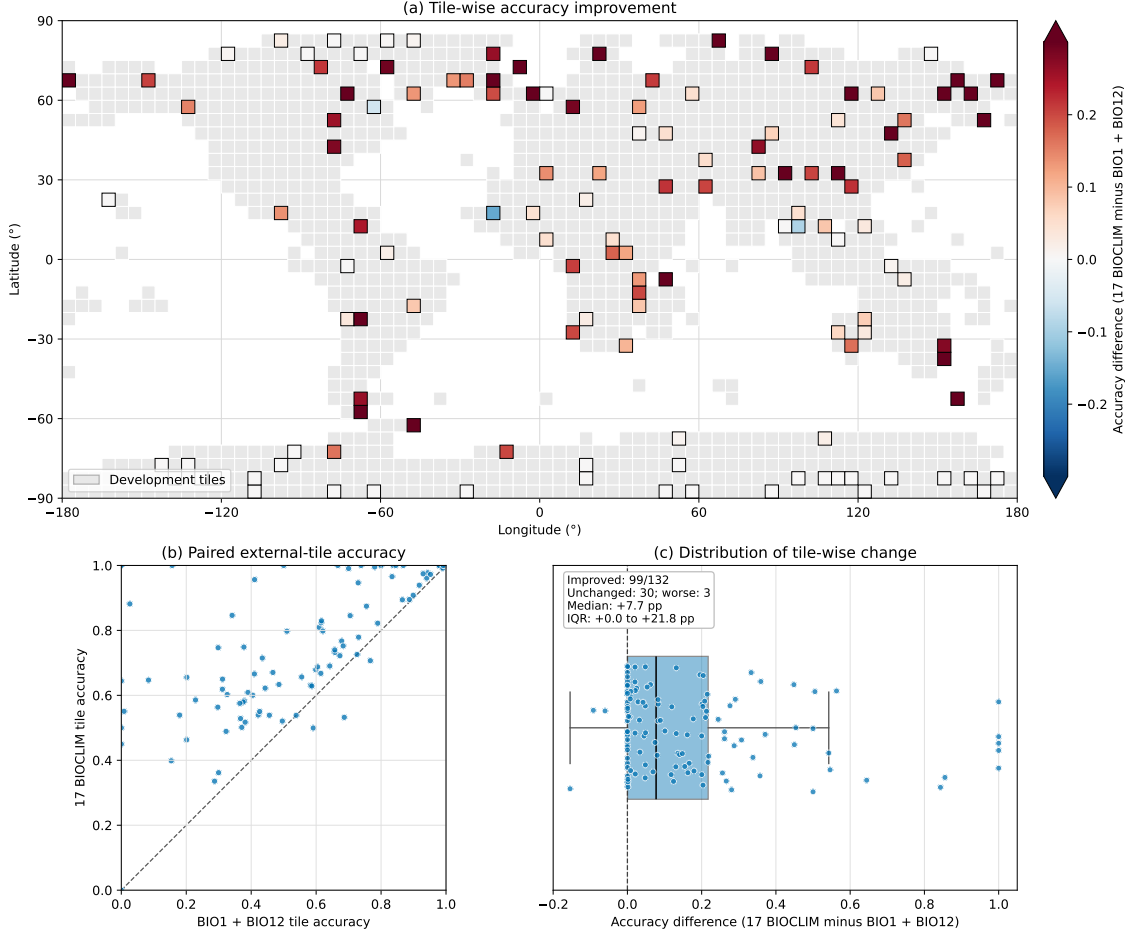


Figure 6: Tile-wise external-test comparison of the two predictor configurations. (a) Accuracy difference (17 BIOCLIM minus BIO1+BIO12) for the 132 withheld tiles. Light-grey cells are development tiles; white locations contain no eligible observations. Red indicates higher accuracy for the full model and blue lower accuracy. (b) Paired tile accuracies; the dashed line denotes equal performance. (c) Distribution of tile-wise accuracy differences; each point is one external tile, and the box shows the median and interquartile range.

class-area changes have the same sign in the two implementations.

The correlations between the PaleoVeg and archived Shao LGM class-area vectors are $r = 0.890$ without and $r = 0.947$ with the CO_2 correction. Their mean absolute differences are 3.06 and 2.60 percentage points, respectively. Substantial class-specific differences nevertheless remain, consistent with the changed estimator and climate representation. Figure 10 provides one spatially explicit example of the corrected PaleoVeg LGM output.

7 Discussion

7.1 Predictor choice and spatial evaluation

We compared the BIO1+BIO12 and 17-predictor configurations using the same Random Forest algorithm, vegetation observations, hyperparameters, spatial partitions, and random seeds. The configurations differ only in their climate predictors. Using all 17 predictors improves overall accuracy, macro F1, balanced accuracy, log loss,

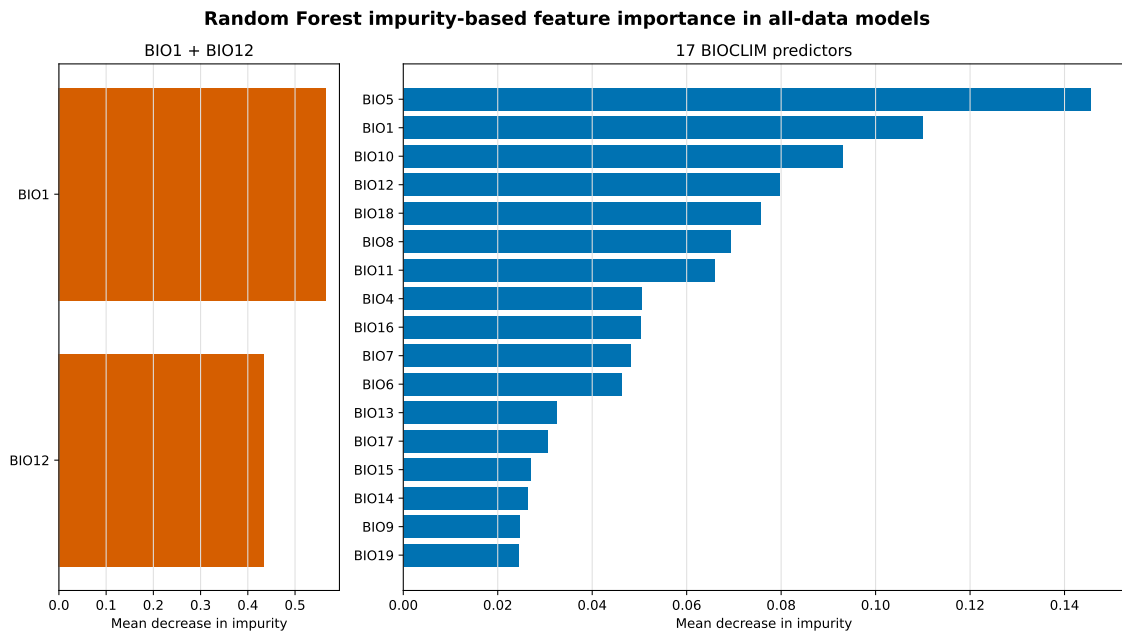


Figure 7: Random Forest mean-decrease-in-impurity importance for final all-data fits. The measure describes how frequently and effectively variables split the training data, but should not be interpreted causally.

and the Shao goodness score, with higher accuracy in 99 of the 132 external test tiles. These results indicate that the additional climate variables improve predictions in regions excluded from training.

The comparison with Shao model 5 involves differences in both the statistical model and the climate data. PaleoVeg uses a Random Forest and WorldClim predictors, while retaining the vegetation classes and CO₂ correction factors of the predecessor study. PaleoVeg achieves a higher Shao goodness score under spatially blocked cross-validation (0.745) than the published whole-grid score for Shao model 5 (0.51). Shao et al.’s published goodness score was calculated over the complete grid, whereas our spatial evaluation uses observations excluded from fitting. The higher score therefore accompanies a stricter separation of training and evaluation data.

Correlations between prediction errors fell to an absolute value of 0.05 or less at distances of 100–500 km, depending on vegetation class. For comparison, each five-degree tile extends approximately 556 km north–south. Keeping all observations within a tile together separates training and test observations over distances comparable to those measured error correlations. Separation remains incomplete at tile boundaries: neighbouring tiles can belong to different folds, and observations on either side of a shared boundary can be close together. Tiles also become narrower east–west towards the poles. Correlated errors may therefore remain between training and test locations.

The external test uses withheld locations from the same modern AVHRR product and period as the training data. It therefore measures geographic transfer within that dataset. Performance also varies among vegetation classes: deciduous broadleaf forest and closed shrubland remain poorly identified, despite the higher aggregate scores.

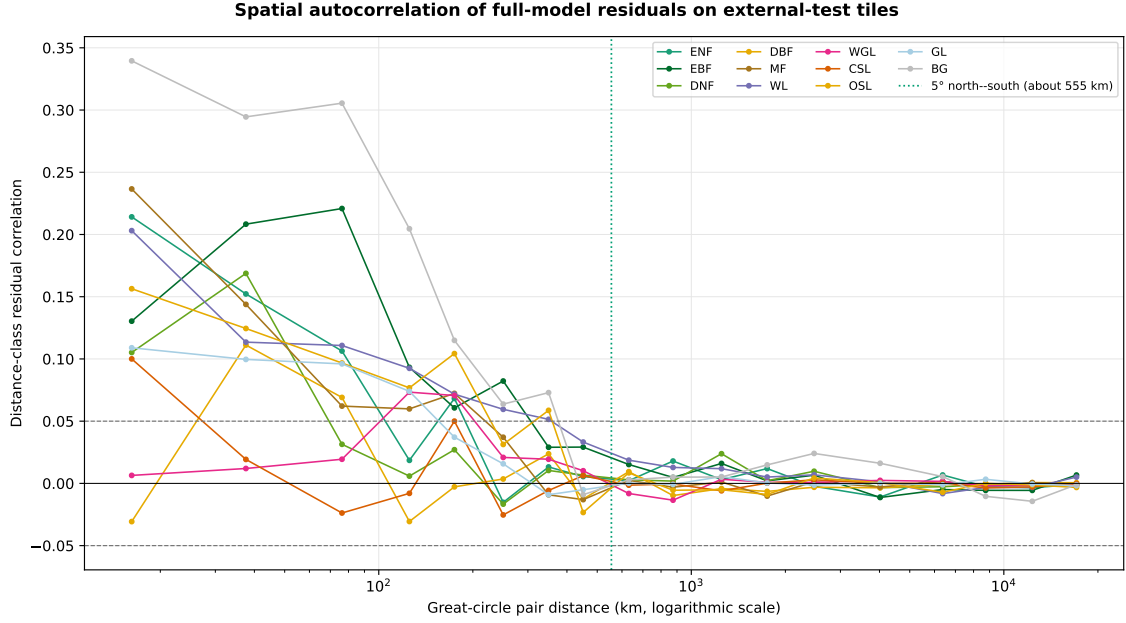


Figure 8: Distance-class autocorrelation of signed probability-minus-observation residuals on a geographically stratified sample from the untouched external spatial test. Dashed horizontal lines mark $|\rho| = 0.05$ and the dotted green line marks the approximate 555 km north–south extent of a 5° tile. Abbreviations follow Table 5.

7.2 Seasonal climate information and model structure

Annual mean temperature and annual precipitation do not distinguish climates with similar annual means but different frost exposure, warm-season temperature, precipitation concentration, or seasonality. The full predictor set includes variables describing these properties, including BIO5, BIO10, and BIO18. Their relatively high impurity importance and the higher held-out performance of the full model are consistent with additional information from seasonal conditions and climate extremes.

The Random Forest also replaces fixed climate bins with adaptive nonlinear partitions and interactions. Adaptive tree partitions do not require a predefined bin width and can use more than two predictors without an exponential empty-bin problem. The trade-off is reduced direct interpretability: a two-dimensional probability surface can be plotted completely, while a 17-dimensional forest requires partial summaries and diagnostic tools.

The AVHRR target records categorical dominant land cover. The predicted class probabilities describe uncertainty in those categories; they are not measurements of vegetation fractions within a grid cell. Random Forest probabilities can also be imperfectly calibrated [Niculescu-Mizil and Caruana, 2005]. We evaluated performance for individual vegetation classes using the Shao goodness score and confusion matrices, and assessed probabilistic predictions using log loss.

7.3 Comparison with other palaeovegetation reconstructions

In the matched LGM experiment, PaleoVeg and the archived Shao reconstructions produce similar global distributions of vegetation-class area, indicating that PaleoVeg retains the broad vegetation response of the Shao model despite changes in the statistical estimator and climate predictors. The shared direction of the CO_2 -

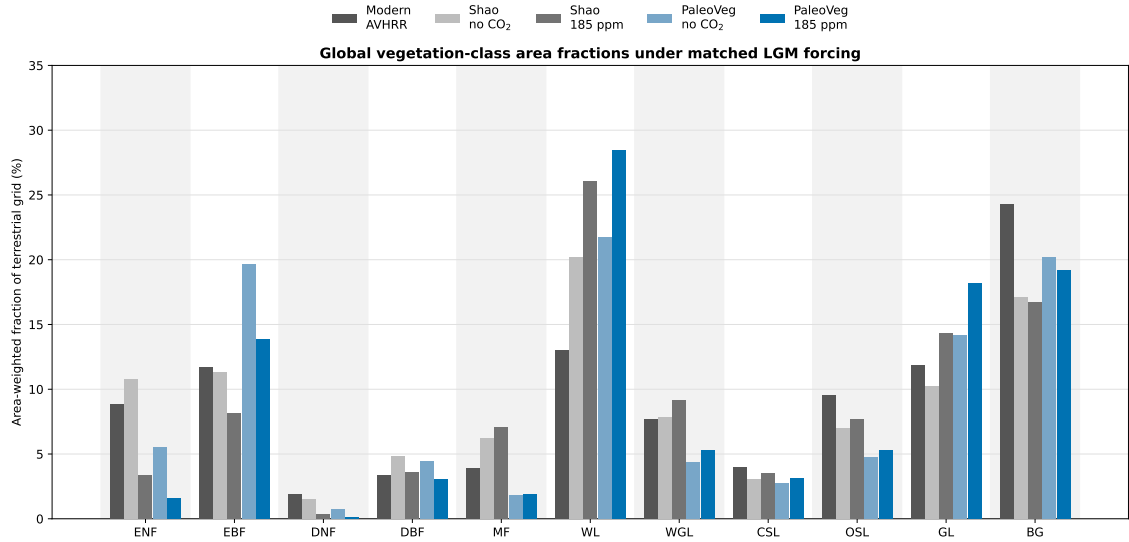


Figure 9: Area-weighted global vegetation-class fractions. The modern AVHRR target is shown for visual context. Shao et al. LGM fractions are calculated from their archived 1° outputs; PaleoVeg is driven by the matched ensemble mean of the six PMIP3 LGM climates and evaluated on the same terrestrial LGM grid. Both LGM reconstructions depend on the same climate-model ensemble, limiting the comparison to behavioural correspondence. Abbreviations are defined in Appendix A.

induced changes is partly expected because both implementations apply the same class-level response factors. Differences in absolute class areas show that these factors do not determine the reconstruction alone: the vegetation probabilities predicted before correction also matter. The comparison therefore identifies continuity in the models’ broad response alongside differences in their allocation of vegetation classes under the same LGM climate.

In a complementary study in this special issue, Kern et al. [accepted for publication] applied the Random Forest PaleoVeg implementation to Europe over 70–20 ka BP, using downscaled and bias-corrected HadCM3 climate and a concentration-dependent CO₂ correction. They compared the resulting forest probabilities with pollen-based Biomisation and REVEALS reconstructions and with the dynamic vegetation model JSBACH. For the continental time series, model estimates were sampled at grid cells with pollen observations in each 2,000-year interval. After standardization, the four methods showed similar broad temporal changes, including higher forest values during early MIS 3 and a subsequent decline towards the LGM.

Agreement was less consistent regionally. Kern et al. reported closer proxy–model agreement in Eastern Europe, the Iberian Peninsula, and the Middle East, while vegetation models indicated more forest than the pollen-based reconstructions in Western and Central Europe and the central Mediterranean. Absolute estimates also differed because the methods represent different quantities: forest probability in PaleoVeg, a forest index in Biomisation, land-cover estimates in REVEALS, and tree-cover fractions in JSBACH. Agreement in the broad temporal pattern therefore coexists with differences in regional vegetation and absolute forest estimates.

Applying modern vegetation–climate relationships to past conditions assumes that those relationships remain valid through time. Soils, disturbance, dispersal, and human influence also affect the modern vegetation used for training. Past climates can include predictor combinations and vegetation communities absent from

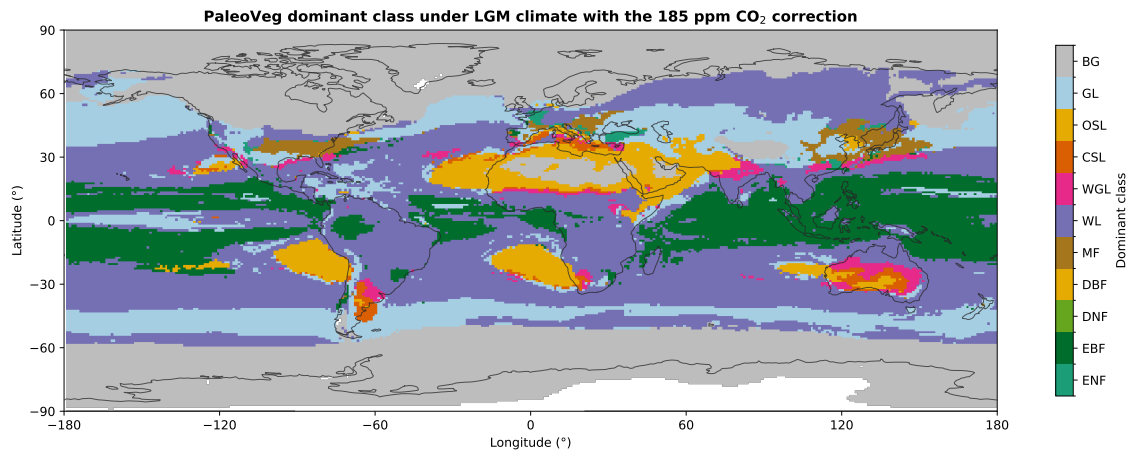


Figure 10: Dominant class in the PaleoVeg LGM application driven by the six-model PMIP3 ensemble mean and corrected to 185 ppm CO₂. Thin outlines show present-day coastlines as a geographic reference only; they are not LGM coastlines because sea level differed. White areas are outside the common terrestrial grid or lack complete predictors.

the training data; PaleoVeg checks individual predictor ranges but does not assess novel combinations of otherwise in-range values. The CO₂ adjustment likewise applies class-level response factors without representing local physiological acclimation, nutrient limitation, or changes in the relative abundance of C₃ and C₄ plants.

8 Conclusions

PaleoVeg 1.0 implements the statistical vegetation–climate reconstruction principle introduced by Shao et al. [2018], using a Random Forest and 17 BIOCLIM predictors while retaining the vegetation classes, probabilistic output, and optional published CO₂ response factors. In the matched predictor comparison, expanding from BIO1+BIO12 to 17 predictors increases spatially blocked cross-validation accuracy from 0.695 to 0.790, macro F1 from 0.468 to 0.622, and the Shao goodness score from 0.657 to 0.745. Accuracy improves in 99 of 132 separately withheld test tiles.

In the matched LGM experiment, PaleoVeg and the archived Shao reconstructions show the same directions of vegetation-class response to the low-CO₂ correction. The complementary study by Kern et al. [accepted for publication] compares PaleoVeg with pollen-based reconstructions and JSBACH across Europe over 70–20 ka BP. Their agreement in broad temporal changes, alongside regional differences and differing absolute forest estimates, extends the assessment of PaleoVeg from modern spatial prediction to its application under glacial conditions.

Data availability statement

The PaleoVeg source code is available at <https://github.com/roink/PaleoVeg> under the MIT License. The PaleoVeg 1.0.0 source code, spatial split manifest, aggregate validation results, figures, and analysis scripts are archived in Zenodo [Schlüter, 2026]. The trained model is available as an asset of the versioned release at <https://github.com/roink/PaleoVeg/releases/tag/v1.0.0>. The repository

contains a user manual, environment requirements, automated tests, model-training scripts, checksum checkers, and documented workflows for figure generation and residual spatial-autocorrelation analysis. WorldClim 2.1 is publicly available from <https://www.worldclim.org/data/worldclim21.html>. The published Shao 1° LGM comparison reconstructions are available under CC BY 4.0 from Shao [2018]; the repository provides a checksum-verified download workflow. The raw monthly PMIP3/CMIP5 LGM fields are available through the Earth System Grid Federation (ESGF; <https://wiki.lsce.ipsl.fr/pmip3/doku.php/pmip3%3Adatabase%3Aaccess>). The repository automates their direct retrieval, verifies the ESGF-advertised checksums, and reconstructs the 24 model-variable inputs used here. The archived workflow records the source filenames, ensemble-member identifiers, temporal coverage, download locations, checksums, and CDO processing steps. The repository does not redistribute raw or remapped PMIP3 fields because the CMIP5 terms place additional conditions on wider redistribution (<https://cds.climate.copernicus.eu/licences/esgf-cmip5>). The University of Maryland (UMD) 8 km Global Land Cover Classification, version 1.0 [De Fries et al., 1998], is preserved in GeoTIFF form at the author’s institute. The identity of this copy has been verified. The original GLCF distribution service is no longer available. Enquiries to UMD and the original researchers concerning licensing and redistribution received no response, and permission for public redistribution has not been established. Researchers seeking access to the preserved dataset for reproduction of the training can contact the corresponding author. The dataset’s provenance, metadata, and SHA-256 checksum are included in the archived source alongside the preprocessing code, environment requirements, and training configuration.

Author contributions

In accordance with the CRediT taxonomy, PS contributed conceptualization, data curation, formal analysis, investigation, methodology, software, validation, visualization, and writing (original draft, review, and editing).

Funding

This work was supported by the Ministerium für Kultur und Wissenschaft des Landes Nordrhein-Westfalen (grant HESCOR PB22-081).

Conflict of interest statement

The author declares no conflict of interest.

Acknowledgements

The author acknowledges Yaping Shao, Andreas Anhäuser, Patrick Ludwig, and Ehimen Williams for the scientific collaboration that led to the predecessor study, and Annika Vogel, Anne Dallmeyer, and Oliver Kern for scientific discussion. We acknowledge the World Climate Research Programme’s Working Group on Coupled Modelling, which is responsible for CMIP, and thank the climate-modelling groups listed in Table 3 for producing and making available their model output. For

CMIP, the U.S. Department of Energy’s Program for Climate Model Diagnosis and Intercomparison provides coordinating support and led development of software infrastructure in partnership with the Global Organization for Earth System Science Portals. OpenAI ChatGPT and Codex were used to assist with software development, figure generation, manuscript structuring, and language editing. The author reviewed and takes responsibility for all code, analyses, interpretations, and text.

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A Vegetation classes and CO₂ factors

Table 5: Retained PaleoVeg classes, abbreviations used in figures, stored AVHRR codes, and low-CO₂ factors at 185 ppm.

Code	Abbreviation	Vegetation class	Factor
1	ENF	Evergreen needleleaf forest	0.28
2	EBF	Evergreen broadleaf forest	0.73
3	DNF	Deciduous needleleaf forest	0.20
4	DBF	Deciduous broadleaf forest	0.76
5	MF	Mixed forest	1.00
6	WL	Woodland	1.62
7	WGL	Wooded grassland	1.62
8	CSL	Closed shrubland	1.66
9	OSL	Open shrubland	1.66
10	GL	Grassland	1.69
12	BG	Bare ground	1.15