

Random-split validation overstates the skill of machine-learning models of global coral bleaching severity

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Abstract

Global compilations of coral bleaching surveys are increasingly used to train machine-learning models of bleaching severity, but such models are often evaluated with random train–test splits that ignore duplicated records, spatial dependence and differences among contributing survey programmes. We re-examined an earlier analysis of the Global Coral Bleaching Database (BCO-DMO dataset 773466) that reported a random-split random forest R^2 of 0.688. The result was reproducible, but it was obtained on 32,716 records, 34.5% of which duplicated another record exactly because Reef Check surveys are stored once per substrate category. After collapsing records to 21,527 sampling events, we compared random, site-grouped, spatial-block ($1-10^\circ$), leave-one-realm-out and forward temporal validation for models using coordinates, thermal-stress metrics, other environmental variables, or indicators of the contributing data source. Random-forest R^2 fell from 0.60 (random) to 0.53 (new sites), 0.18 (1° blocks) and 0.02 (10° blocks), and was at most 0.06 in held-out realms. Coordinates alone predicted worse than the mean under all block designs. Indicators of the contributing source alone explained 0.35–0.37 of the variance under every cross-validation design, more than any environmental model under spatial validation. Within the single-protocol Reef Check subset, no predictor set achieved positive R^2 under spatial blocks. The all-predictor model retained moderate ability to rank events with at least 50% bleaching (AUC 0.73 under 5° blocks). These results indicate that the apparent skill of pooled bleaching-severity models largely reflects record duplication, interpolation between nearby surveys, and heterogeneity in how bleaching was measured, rather than transferable environment–bleaching relationships.

Keywords: coral bleaching; spatial cross-validation; data leakage; machine learning; thermal stress; data heterogeneity

1 Introduction

Mass coral bleaching, the loss of symbiotic algae from coral tissue under stress, has become one of the most widespread ecological consequences of ocean warming (Hughes et al., 2017, 2018). Satellite-derived thermal-stress indices, most prominently Degree Heating Weeks (DHW), are the operational basis for bleaching alerts (Liu et al., 2014), and global compilations of field observations now make it possible to relate observed bleaching severity to such indices across thousands of reefs (Donner et al., 2017; Sully et al., 2019; van Woesik and Kratochwill, 2022).

The availability of these compilations, together with accessible machine-learning libraries, invites a simple workflow: merge bleaching observations with environmental covariates, split the records at random into training and test sets, fit a flexible regressor, and report the test-set coefficient of determination. Such numbers are easy to obtain and easy to misread. Records collected at the same site, during the same event, or by the same monitoring programme are not independent, and a random split places close relatives of each test record in the training set. Under these conditions a flexible model can score well

by recognising where, when, or by whom a record was collected rather than by learning a transferable relationship between environment and response (Roberts et al., 2017; Ploton et al., 2020; Kapoor and Narayanan, 2023). Whether spatially structured validation is always the correct remedy is itself debated, because the appropriate test depends on the prediction task (Wadoux et al., 2021; Meyer and Pebesma, 2021); what is not debated is that the validation design must match the claim being made.

This study began as a re-examination of an earlier technical report by the author, which fitted linear regression, random forest and gradient boosting models to the Global Coral Bleaching Database (van Woesik and Kratochwill, 2022) and reported a random-split random-forest R^2 of 0.688. Here we ask how much of that apparent skill survives (i) removal of duplicated records, (ii) validation designs that withhold whole sites, spatial blocks of increasing size, entire biogeographic realms, or later years, and (iii) restriction of the predictor set to coordinates, thermal-stress metrics, or non-geographic environmental variables. We also test a source of structure that has received less attention in this setting: the database merges seven programmes with different survey methods and outcome scales, and we quantify how much of the predictable variation is attributable to the identity of the contributing programme. Our aim is diagnostic rather than to propose a new bleaching model.

2 Materials and methods

2.1 Data

We used the Global Coral Bleaching Database export distributed by the Biological and Chemical Oceanography Data Management Office as dataset 773466, version 2 (van Woesik and Burkepile, 2022), described by van Woesik and Kratochwill (2022) and released under a CC BY 4.0 licence. The database compiles bleaching surveys from seven sources (Reef Check, the database of Donner et al., 2017, AGRRA, FRRP, and three smaller published compilations) and attaches site descriptors and thermal metrics from the Coral Reef Temperature Anomaly Database (CoRTAD) version 6 to each sampling event (van Woesik and Kratochwill, 2022). The file analysed here (41,361 rows, 62 columns) was taken from the author's public code repository and has the column structure documented by BCO-DMO; it was not byte-compared against a fresh BCO-DMO download (Section 5).

The response was `Percent_Bleaching`, described by van Woesik and Kratochwill (2022) as a site-level estimate of bleached relative to unbleached coral colonies, expressed as a percentage. The twelve predictors of the original analysis were retained for comparability: latitude and longitude; survey depth; seven CoRTAD thermal metrics (`SSTA`, `SSTA_Mean`, `SSTA_Maximum`, `SSTA_DHW`, `SSTA_DHWMean`, `TSA`, `TSA_Mean`); mean turbidity; and cyclone frequency. In CoRTAD, `SSTA_DHW` accumulates weekly anomalies of at least 1 °C relative to the weekly climatology over the preceding 12 weeks, and `TSA` is the weekly temperature minus the maximum weekly climatological temperature (van Woesik and Kratochwill, 2022). `SSTA_DHW` is therefore related to, but not identical with, the NOAA Coral Reef Watch DHW product used for operational alerts (Liu et al., 2014).

2.2 Preprocessing

Records were converted to numeric values, the database's no-data code was treated as missing, and records with any missing model variable were removed, exactly as in the original analysis. This left 32,716 complete records rather than the 41,361 reported in the original report, which had quoted the raw row count. `SSTA_Mean` equals zero in every complete record and was dropped from all new analyses (11 predictors).

Inspection showed that Reef Check surveys appear once per substrate category (hard coral, nutrient-indicator algae and, occasionally, fleshy seaweed). These rows share the sample identifier, site, date, depth, all predictors and the bleaching value, and differ only in substrate cover. As a result, 11,300 of the complete records (34.5%) duplicate another record exactly in all model variables. We collapsed records to one per sampling event (`Sample_ID`), giving 21,527 events at 9,568 sites from 1983 to 2019. Predictors were constant within every event; for the 8 events with differing bleaching values, the mean was used.

The response distribution differs sharply among sources (Fig. 2). Overall, 42.5% of events report no bleaching and 7.5% report at least 50%. Reef Check events ($n = 11,242$) have mean bleaching of 2.5% and 66% zeros. Events from the Donner et al. (2017) compilation ($n = 4,118$) have mean bleaching of 32.8% and no zeros in this export, consistent with the removal of no-bleaching reports during its compilation (Donner et al., 2017). In addition, 26% of Donner events and 50% of events from the Kumagai compilation take the values 5.5, 30.5 or 75, which are consistent with midpoints of the severity classes 1–10%, 11–50% and >50% used by Donner et al. (2017). The response is therefore a mixture of continuous survey percentages and coded categories, measured under different sampling designs.

2.3 Replication of the original analysis

The original script was run with only its input path corrected. It fits ordinary least-squares linear regression, a random forest (Breiman, 2001) with 200 trees, and gradient boosting (Friedman, 2001) with 200 trees, learning rate 0.05 and depth 3, on a single random 80/20 split (seed 42) of the complete records. We repeated the identical procedure on the deduplicated events, and, for the original split, counted test records that have an identical copy (all predictors and response) in the training set.

2.4 Validation designs

All new analyses used the 21,527 sampling events and compared the following designs, chosen to represent increasingly demanding prediction tasks (Roberts et al., 2017):

1. **Random 5-fold** cross-validation over events, which tests interpolation among events.
2. **Site-grouped 5-fold**, in which all events from a site are held out together, which tests prediction at unsampled sites.
3. **Spatial block 5-fold** with blocks of 1° , 5° and 10° of latitude and longitude (521, 174 and 87 occupied blocks), which tests prediction progressively further from training data. Blocks were assigned to folds at random with group-aware splitting.
4. **Leave-one-realm-out**, holding out each of the four realms with at least 800 events (Tropical Atlantic, Central, Western and Eastern Indo-Pacific); the four small realms were always kept in training.
5. **Temporal**: training on events up to 2010 and testing on events from 2011 to 2019, both for all test events and for test events at sites absent from training.

Fold sizes are listed in Supplementary Table S1. Grouped folds are unequal in size because sampling is concentrated in a few regions, for example the 10° test folds range from 1,686 to 9,881 events.

2.5 Predictor groups and models

For each design we fitted models with five predictor sets: (i) coordinates only; (ii) the six remaining thermal metrics; (iii) thermal metrics plus depth, turbidity and cyclone frequency (environment without

coordinates); (iv) all 11 predictors; and (v) indicator variables for the seven contributing sources. Set (v) is not a usable predictor of bleaching in practice. It is included as a diagnostic that measures how much variance is explained by which programme produced a record.

We used three learners with hyperparameters fixed in advance: the random forest settings of the original analysis (200 trees, scikit-learn defaults otherwise), histogram-based gradient boosting with default settings, and linear regression with predictors standardised inside each training fold. No hyperparameters were tuned, so no test fold informed model choice. Analyses used scikit-learn (Pedregosa et al., 2011); software versions are given in Section 5.

2.6 Performance measures

For the k -fold designs, out-of-fold predictions were pooled across folds and we report the coefficient of determination (R^2), mean absolute error (MAE, percentage points), root-mean-square error, Spearman rank correlation, and the area under the ROC curve (AUC) obtained when predicted values are used to rank events with at least 50% bleaching. Each is compared with a baseline that predicts the training-fold mean. For realm and temporal holdouts we report the same metrics for each test set. R^2 values below zero indicate predictions worse than the test-set mean. Ranges across folds are shown as an indication of variability; we do not attach confidence intervals because folds share training data and are not independent replicates.

2.7 Sensitivity analyses and diagnostics

To separate spatial transfer from outcome heterogeneity, we repeated the k -fold, realm and temporal designs using (a) Reef Check events only ($n = 11,242$), a single programme with a common protocol, and (b) events from the four sources that report continuous percentages ($n = 16,673$), excluding Donner, Kumagai and Safaie. We also computed held-out permutation importance for the all-predictor random forest under random and 5° block validation, permuting individual predictors and whole predictor groups (five repeats per fold, reported as the percentage increase in mean squared error). Because impurity-based importance is biased towards continuous, high-cardinality and correlated predictors (Strobl et al., 2007), it is reported only for comparison with the original analysis. We tested whether each predictor group could identify the contributing source (random forest classifiers, site-grouped cross-validation, AUC), refitted the source-indicator model with thermal and all predictors added, and checked the stability of pooled skill over three further fold assignments.

These analyses are predictive and descriptive. They evaluate how well associations learned from the database transfer to new events, sites, regions and years; they do not estimate causal effects of any predictor.

3 Results

3.1 Replication and the effect of duplicated records

The original script reproduced the reported random-split results to within 0.001 in R^2 (Table 1; random forest $R^2 = 0.687$ versus 0.688 reported), on 32,716 rather than 41,361 records. Of the 6,544 test records, 3,650 (56%) had an exact copy in the training set. On these records the random forest achieved $R^2 = 0.89$ with MAE = 1.37 percentage points; on the remaining 2,894 test records, R^2 was 0.60 and MAE 8.16 percentage points. Repeating the same 80/20 procedure on deduplicated events reduced the random forest R^2 to 0.611, while linear regression and gradient boosting changed little (Table 1). The original script

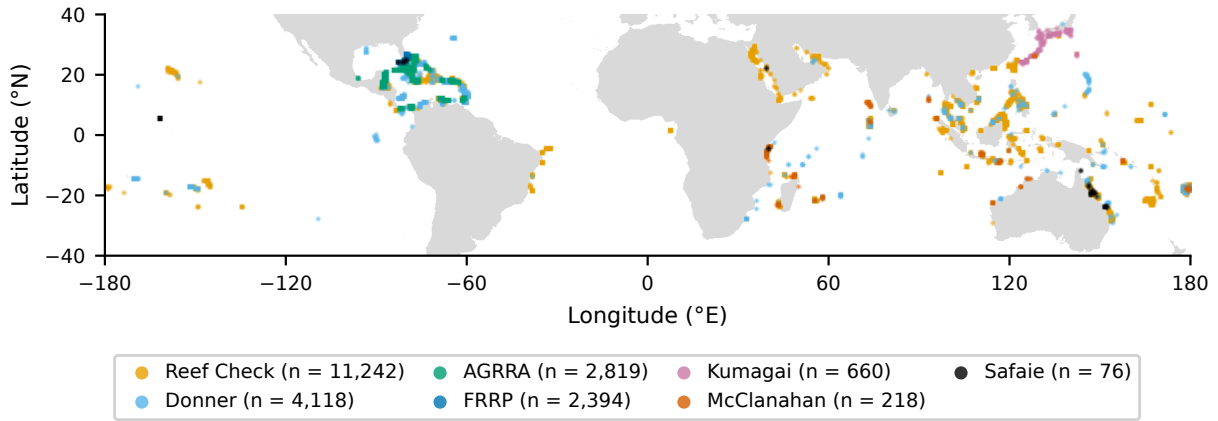


Figure 1: Locations of the 21,527 sampling events in the analysis, coloured by contributing data source. Grey shading shows land.

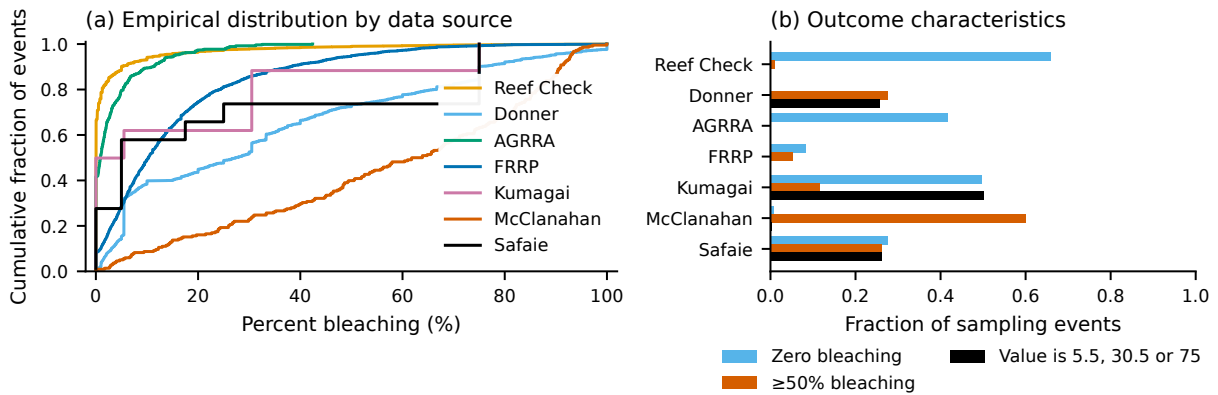


Figure 2: Bleaching severity differs among contributing sources. (a) Empirical cumulative distribution of percent bleaching. (b) Fractions of events with zero bleaching, with at least 50% bleaching, and with values of exactly 5.5, 30.5 or 75 (consistent with midpoints of categorical severity classes).

also computed, but did not report, an unshuffled 5-fold cross-validation with mean $R^2 = -31.2$. Because the file is ordered such that two of these contiguous folds contain only zero-bleaching records, that result reflects row order rather than a meaningful validation design, and we do not interpret it further.

3.2 Skill declines as validation moves away from training data

Under random 5-fold validation of deduplicated events, the all-predictor random forest explained 0.60 of the variance (Table 2, Fig. 3). Holding out whole sites reduced this to 0.53. With spatial blocks, R^2 fell to 0.18 (1°), 0.08 (5°) and 0.02 (10°). MAE rose from 6.9 to 13.9 percentage points, close to the 14.1 percentage points of a model that predicts the training mean.

The predictor groups degraded differently. Coordinates alone gave $R^2 = 0.44$ under random validation, and negative values under all three block designs (-0.25 to -0.16), so their apparent contribution depends on interpolating between nearby records. Thermal metrics alone gave 0.54 under random validation, 0.43 at new sites, and 0.12, 0.05 and 0.00 under the three block designs. Adding depth, turbidity and cyclone frequency to the thermal metrics changed these values by 0.06 or less. Gradient boosting followed the same pattern (0.52 to 0.05). Linear regression was weak throughout but almost insensitive to the design (0.16 to 0.12), and under 5° and 10° blocks it outperformed the random forest and was close to gradient boosting. The advantage of the flexible models over a linear fit therefore appears only when test records have close neighbours in the training data.

Table 1: Replication of the original random 80/20 analysis. “Reported” values are from the original report; “Reproduced” re-runs the original code on the 32,716 complete records (6,544 test records); “Deduplicated” applies the identical procedure to the 21,527 sampling events (4,306 test events). MAE and RMSE in percentage points.

Model	Reported		Reproduced			Deduplicated		
	R^2	MAE	R^2	MAE	RMSE	R^2	MAE	RMSE
Linear Regression	0.139	10.12	0.139	10.12	16.49	0.155	12.65	19.10
Random Forest	0.688	4.36	0.687	4.37	9.94	0.611	6.94	12.96
Gradient Boosting	0.373	7.88	0.373	7.88	14.07	0.391	9.93	16.21

Table 2: Pooled out-of-fold performance on 21,527 sampling events under five validation designs. Values are computed on the concatenated out-of-fold predictions. The data-source model uses only indicators for the contributing programme and serves as a diagnostic, not a usable predictor. MAE in percentage points (pp).

	Random	Site-grouped	Block 1°	Block 5°	Block 10°
<i>Random forest, out-of-fold R^2</i>					
Coordinates only	0.44	0.17	−0.25	−0.27	−0.16
Thermal only	0.54	0.43	0.12	0.05	0.00
Environment (no coordinates)	0.58	0.49	0.12	0.04	0.00
All predictors	0.60	0.53	0.18	0.08	0.02
Data source only	0.37	0.37	0.36	0.35	0.35
<i>Other learners, all predictors, R^2</i>					
Gradient boosting (HGB)	0.52	0.48	0.21	0.12	0.05
Linear regression	0.16	0.16	0.11	0.11	0.12
<i>Random forest, all predictors, other metrics</i>					
MAE (pp)	6.9	8.2	12.0	13.2	13.9
MAE of training-mean baseline (pp)	14.3	14.3	14.3	14.3	14.1
Spearman ρ	0.74	0.68	0.43	0.34	0.27
AUC, events $\geq 50\%$	0.94	0.93	0.77	0.73	0.71

Ranking skill decayed less than R^2 . Predicted values ranked events with at least 50% bleaching with AUC = 0.94 under random validation and 0.73 under 5° blocks, and Spearman correlation fell from 0.74 to 0.34. Some transferable ordinal information thus remains even where absolute predictions are poor. Results were stable across three further fold assignments (Supplementary Table S8).

3.3 The identity of the data source explains more transferable variance than the environment

Indicators for the seven contributing sources explained 0.37 of the variance under random validation and 0.35 under 10° blocks (Table 2). Under every spatial block design, this source-only model outperformed every environmental and geographic model, with lower MAE (9.8 versus 13.2 percentage points at 5°). When the source indicators were combined with the other predictors (Supplementary Table S4), the environmental and geographic variables added substantially to the source-only model under random and site-grouped validation ($R^2 = 0.65$ and 0.62), but little or nothing under spatial blocks (0.40, 0.34 and 0.30 for 1°, 5° and 10°, against 0.36, 0.35 and 0.35 for source alone). Adding thermal metrics alone to the source indicators lowered block-design R^2 (0.28 at 5°).

The predictors themselves carry much of the source information. Under site-grouped cross-validation, random forest classifiers using thermal metrics alone distinguished Donner records from all other sources with AUC = 0.94 and Reef Check records with AUC = 0.97; coordinates alone gave 0.87 and 0.96 (Supplementary Table S5). This is expected, because the Donner compilation contains records collected during recognised bleaching events, while Reef Check surveys are routine and concentrated in particular

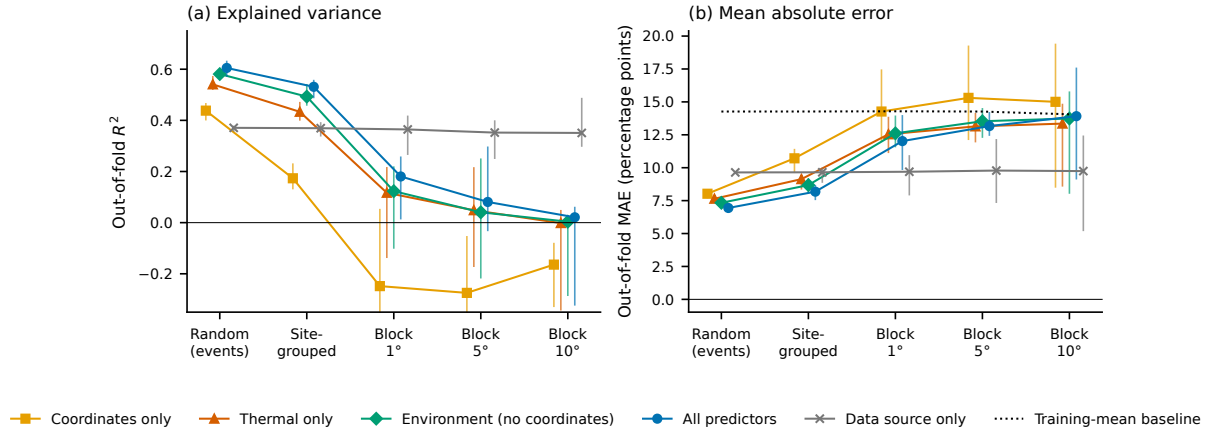


Figure 3: Random forest skill by validation design and predictor set. Points are pooled out-of-fold values; vertical lines span the five individual folds. (a) Coefficient of determination. (b) Mean absolute error, with the dotted line showing a baseline that predicts the training-fold mean.

Table 3: Random forest performance in held-out realms and later years. R^2 by predictor set; MAE (pp) for the all-predictor model and for the training-mean baseline. Temporal models were trained on events up to 2010.

Test set	<i>n</i>	Coord.	Thermal	Env.	All	MAE	Baseline MAE
<i>All sources</i>							
Tropical Atlantic	10,993	−0.07	−0.09	−0.06	0.01	15.9	14.5
Central Indo-Pacific	7,316	−0.44	−0.45	−0.25	−0.57	13.6	14.7
Western Indo-Pacific	1,687	−0.08	−0.09	−0.07	0.06	15.9	16.1
Eastern Indo-Pacific	868	−0.12	−0.09	−0.18	−0.20	14.0	13.1
Temporal: test 2011–2019	7,409	−0.51	0.06	0.09	0.11	9.6	13.9
Temporal: test 2011–2019, new sites	5,725	−0.57	0.11	0.13	0.14	10.5	14.4
<i>Reef Check only</i>							
Tropical Atlantic	2,101	−0.05	−0.06	−0.04	−0.02	7.0	5.3
Central Indo-Pacific	6,503	−0.19	−0.24	−0.67	−0.20	4.5	4.1
Western Indo-Pacific	1,455	−5.67	−1.10	−1.39	−4.04	11.0	3.3
Eastern Indo-Pacific	752	−0.30	−0.51	−0.51	−1.12	8.2	3.4
Temporal: test 2011–2019	5,642	−0.34	−0.20	−0.20	−0.22	3.9	3.9
Temporal: test 2011–2019, new sites	3,992	−0.34	−0.17	−0.17	−0.17	3.8	3.8

regions and years. A model of severity can therefore partly predict the source, and with it the source-specific outcome scale.

3.4 Transfer between realms and to later years

No environmental or geographic model transferred to a held-out realm (Table 3, Fig. 4). The all-predictor random forest had R^2 between -0.57 (Central Indo-Pacific) and 0.06 (Western Indo-Pacific), and in the Tropical Atlantic and Eastern Indo-Pacific its MAE exceeded that of the training-mean baseline. Thermal-only models had negative R^2 in all four realms. Thermal and environmental models nevertheless ranked severe events in the Central Indo-Pacific with AUC between 0.77 and 0.80. In the forward temporal test, the all-predictor model explained 0.11 of the variance in 2011–2019 (0.14 at sites not sampled before 2011), with MAE of 9.6 percentage points against 13.9 for the baseline.

3.5 Single-protocol and continuous-score subsets

Within Reef Check events alone, which share a single protocol, random validation gave $R^2 = 0.30$ for all predictors and 0.27 for thermal metrics, and every spatial block design gave negative R^2 (Supplementary

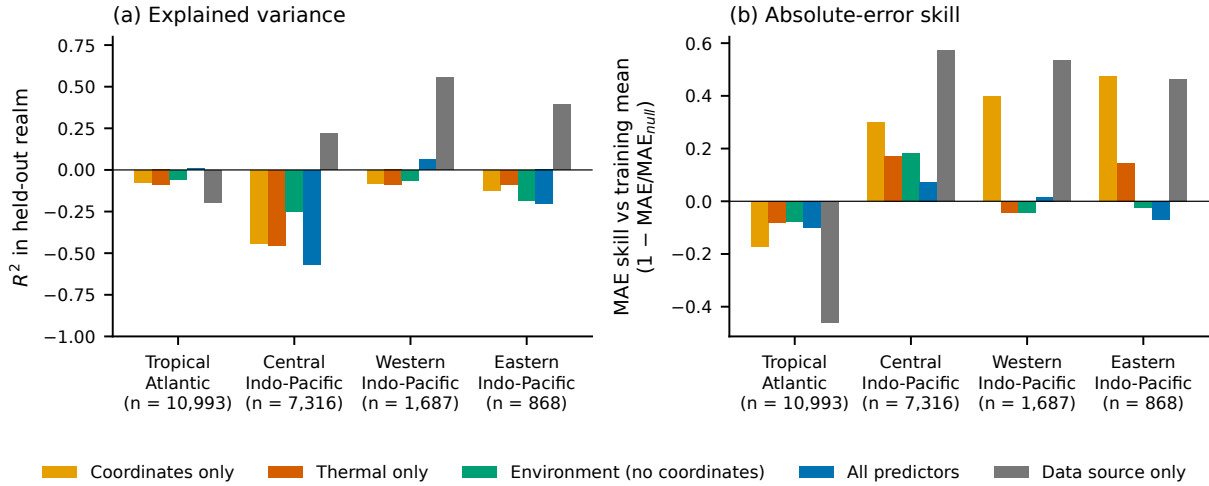


Figure 4: Random forest performance when each major realm is withheld from training. (a) R^2 in the held-out realm. (b) Absolute-error skill relative to predicting the training mean; values below zero are worse than that baseline. Sample sizes refer to the held-out realm.

Table S2, Fig. S1). Reef Check realm and temporal holdouts were also negative. Restricting to the four continuous-score sources gave intermediate results: $R^2 = 0.57$ under random validation, 0.16 under 1° blocks and -0.03 under 10° blocks.

3.6 Predictor importance depends on the validation design

Held-out permutation importance changed with the validation design (Fig. 5, Supplementary Table S6). Under random validation, jointly permuting the two coordinates increased test MSE by 130.2%, nearly as much as permuting all six thermal metrics (146.7%), and longitude was the most important single predictor (101.6%). Under 5° blocks, all importances were much smaller because the unpermuted error was already high, but the thermal group (30.6%) mattered more than the coordinates (12.5%), and SSTA_DHW became the most important single predictor (21.1% versus 14.4% for longitude). The prominence of longitude in the original analysis therefore reflects interpolation within densely sampled regions rather than a transferable relationship. Impurity-based importance on the complete records reproduced the original ranking (Supplementary Table S7).

Errors were strongly severity-dependent under both designs (Fig. 6). Predictions were biased upwards for events with no bleaching (mean error 2.8 percentage points under random and 9.0 under 5° block validation) and strongly downwards for severe events. For the 538 events with more than 75% bleaching, the mean error was -29.3 percentage points under random validation and -62.2 under 5° blocks. The models are thus least reliable for the events of greatest ecological concern.

4 Discussion

4.1 What the original performance measured

The random-split R^2 of 0.69 reported for this dataset is reproducible, but it does not measure the ability to predict bleaching severity at reefs or times outside the training data. Part of it arose from duplicated records, and deduplication alone lowered the same 80/20 estimate to 0.611: Reef Check surveys are stored once per substrate category in the flattened export, so a random split places identical copies of most Reef Check test records in the training set. This is a property of how the relational database was flattened, not

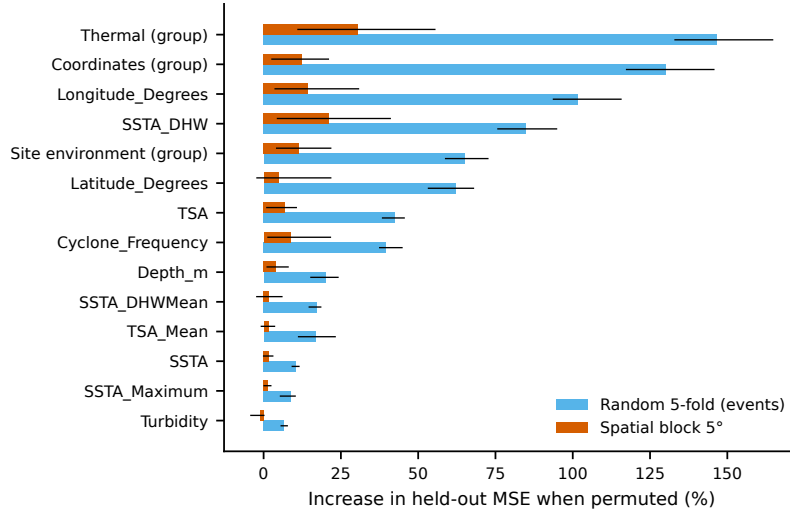


Figure 5: Held-out permutation importance for the all-predictor random forest under random and 5° spatial block validation. Bars show the mean percentage increase in test mean squared error over five folds (five permutations per fold); whiskers span the fold range. Group entries permute all members of the group jointly.

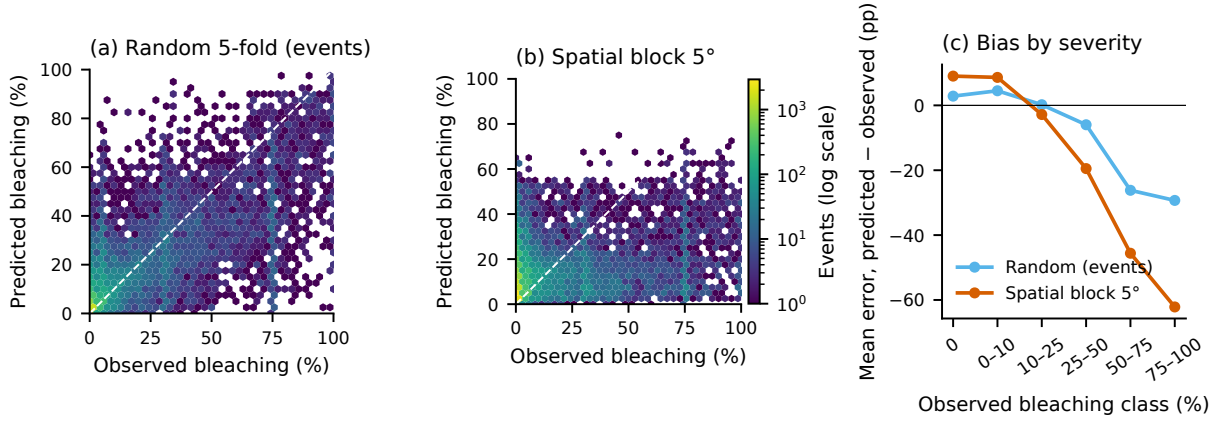


Figure 6: Observed versus predicted bleaching for the all-predictor random forest under (a) random and (b) 5° spatial block validation, and (c) mean prediction error by observed severity class.

an error in the database, which was checked for duplicate sampling events across sources (van Woesik and Kratochwill, 2022). It is, however, a direct route to the kind of train–test leakage described by Kapoor and Narayanan (2023), and an instance of pseudoreplication in Hurlbert’s sense (Hurlbert, 1984): substrate rows are not independent observations of bleaching. Any analysis of this file that treats rows as units should first collapse them to sampling events.

The remaining random-split skill largely reflects interpolation among nearby, similar events. Coordinates were the most important predictor in the original impurity ranking, yet coordinates alone predicted worse than the mean as soon as test records were separated from training records by even 1°. The tree ensembles outperformed linear regression only when close neighbours were available, and their advantage disappeared under 5° and 10° blocks. These patterns match those reported for large-scale ecological mapping (Ploton et al., 2020) and the general warnings of Roberts et al. (2017).

4.2 Which validation design is appropriate?

Spatial cross-validation is not automatically correct. Wadoux et al. (2021) showed that it can be pessimistic when the goal is to estimate accuracy within a well-sampled region, and Meyer and Pebesma (2021)

argued that the relevant question is whether new predictions fall inside the predictor space covered by the training data. The appropriate design depends on the intended use. If the goal is to estimate bleaching at unsurveyed sites inside the regions already covered by surveys, the site-grouped estimate ($R^2 \approx 0.53$) is the most relevant of our designs. If the goal is to transfer a model to poorly surveyed regions, the block and realm results apply, and they indicate essentially no skill in predicting severity magnitude. Neither design supports the claim, implicit in a random-split R^2 , that environmental conditions explain about two-thirds of global variation in bleaching severity.

4.3 Data-source heterogeneity

The most consequential structure we found was not spatial but methodological. The database combines programmes that measure different things: Reef Check reports continuous population-level percentages and contains many zero observations, whereas the Donner et al. (2017) compilation records only bleaching events, often as coded severity classes. A model that knows only the source explains about a third of the variance under every cross-validation design, and it outperforms all environmental models under spatial blocks. Because source is strongly structured in space and time, environmental and geographic predictors can partly act as proxies for it, and that proxy relationship does not carry over to new regions with a different mix of sources. Thermal metrics alone identified Donner records with $AUC = 0.94$ at unseen sites, so part of what random-split models learn from thermal stress is which programme, and which kind of record, produced each observation.

This has consequences beyond prediction. Associations estimated from the pooled response, including feature importance rankings, mix ecological signal with differences in sampling design and outcome coding. Within the single-protocol Reef Check subset, thermal metrics explained only about a quarter of the variance even under random validation, and nothing under spatial validation.

4.4 Ecological interpretation

These results should not be read as evidence against the role of thermal stress in bleaching, which is supported by extensive observational and experimental work (Hughes et al., 2017, 2018). Several features of this analysis limit what it can detect. The CoRTAD metrics are 4 km satellite products matched to survey dates, so they omit fine-scale temperature variation, local acclimatisation history and the lag between heat stress and the timing of a survey. Sully et al. (2019) found that the relationship between thermal stress and bleaching probability varies with latitude, which implies that a single global mapping from thermal metrics to severity should transfer poorly between regions. The response is also zero-inflated and heavily skewed, which is poorly suited to squared-error regression; models predicted too much bleaching where none occurred and too little where it was severe (Fig. 6). The persistence of moderate ranking skill under spatial validation ($AUC \approx 0.7$ for severe events) is consistent with the predictors carrying some transferable information about where severe bleaching is more likely, even though they predict its magnitude poorly; given the source identifiability results, part of this ranking skill may also reflect recognition of event-based records.

4.5 Limitations

Several choices limit the generality of these results. (1) Hyperparameters were fixed at the original values and not tuned; tuning might change random-split results slightly, but it is unlikely to turn negative block-design R^2 positive, given that a linear model and a differently regularised boosting model behaved similarly. (2) Spatial blocks were defined on a regular latitude–longitude grid, so block area varies with

latitude, and grouped folds differ in size. (3) Realm and temporal holdouts confound transfer with changes in source composition. The Tropical Atlantic is the only realm with substantial AGRRA, FRRP and Donner contributions, the three Indo-Pacific realms are 86–89% Reef Check, and Donner records end before 2011, so withholding the Atlantic or later years also changes the measurement mix. (4) The temporal test used a single cut-off year. (5) Only the predictors of the original analysis were used; other variables in the database, such as TSA_DHW, distance to shore and exposure, were not evaluated. (6) The analysis plan was developed during this re-analysis after the original results were known and was not preregistered; the source-conditioned model and sensitivity subsets were added after the main results were inspected and should be regarded as exploratory. (7) The input file was taken from the author’s repository and checked against the documented structure, but not against a fresh download from BCO-DMO.

4.6 Recommendations

For analyses of this database, and of similar multi-source ecological compilations, we suggest: collapsing records to sampling events before modelling; choosing a validation design that matches the intended prediction task and reporting more than one design where the task is ambiguous; reporting results stratified by contributing source, or modelling source explicitly, for example with hierarchical or measurement-error models; and treating random-split feature importance as a description of the fitted model rather than as evidence about ecological drivers.

5 Conclusions

Random-split validation substantially overstated the skill of machine-learning models of global coral bleaching severity built from the Global Coral Bleaching Database. Removing duplicated records lowered the random forest R^2 from 0.687 to 0.60; withholding whole sites lowered it to 0.53; and spatial blocks of 1–10°, held-out realms and later years reduced it to 0.18 or lower. Indicators of the contributing data source explained more transferable variance than any combination of thermal, environmental and geographic predictors. Global bleaching compilations are valuable, but models fitted to them should be validated against the prediction task they are meant to serve, and pooled severity values from different survey programmes should not be treated as a single, homogeneous response.

Data availability

The bleaching and environmental data are the BCO-DMO dataset 773466, version 2 (van Woesik and Burkepile, 2022), distributed under a CC BY 4.0 licence at <https://www.bco-dmo.org/dataset/773466>. The copy analysed here (SHA-256: 78cc014b...bfacb, 41,361 rows) was obtained from the author’s repository, <https://github.com/aravmestry/coral-bleaching-prediction-dashboard> (commit 33c9380); it has the documented 62-column structure but was not byte-compared with a fresh download from BCO-DMO. This copy is redistributed, with attribution and under its original CC BY 4.0 licence, in the archived reproducibility package (<https://doi.org/10.5281/zenodo.23511976>).

Code availability

The original analysis code, dashboard and data file are publicly available at <https://github.com/aravmestry/coral-bleaching-prediction-dashboard>. The corrected reproducibility package for this preprint is distinct from that repository. It contains all revised analysis scripts, the exact package

versions (Python 3.13, NumPy 2.5.3, pandas 3.0.5, SciPy 1.18.1, scikit-learn 1.9.1, Matplotlib 3.11.2), numerical results, run logs, and figure- and table-generation code. It is archived on Zenodo as version 1.0 at <https://doi.org/10.5281/zenodo.23511976>. The code is released under the MIT License and the other author-created material under CC BY 4.0.

Author contributions

A.M. conceived the original project, compiled the original analysis and dashboard, and is responsible for this manuscript.

Use of AI tools

AI-assisted tools, including Claude (Anthropic), were used to support code development, statistical analysis, literature verification, and manuscript preparation. The author directed the research, evaluated the methods and findings, and assumes full responsibility for the scientific content and conclusions.

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Competing interests

The author declares no competing interests.

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Supplementary material

The supplementary material is included in this PDF as an appendix. It is also provided as a separate file in the reproducibility package.

S1. Data audit

The raw file contains 41,361 rows and 62 columns. Complete-case filtering on the twelve original predictors and Percent_Bleaching retains 32,716 rows. The main sources of missingness are Percent_Bleaching (no-data code in about 17% of raw rows) and Depth_m (about 4%); thermal metrics are missing in fewer than 0.5% of rows (file `results/missingness.csv`). Two small sources present in the raw file (9 rows) have no complete records. Among complete records, 11,300 rows duplicate another row in all model variables; nearly all belong to Reef Check sampling events recorded once per substrate category (hard coral, nutrient-indicator algae, fleshy seaweed; file `results/duplicates_by_source.csv`). The analysis table has one record per Sample_ID (21,527 events).

S2. Validation partitions

Table S1: Training and test sizes for every partition (all sources). “Groups” is the number of sites or spatial blocks in the test fold.

Design	Fold	n_{train}	n_{test}	Groups
Random 5-fold	0	17,221	4,306	–
Random 5-fold	1	17,221	4,306	–
Random 5-fold	2	17,222	4,305	–
Random 5-fold	3	17,222	4,305	–
Random 5-fold	4	17,222	4,305	–
Site-grouped 5-fold	0	17,087	4,440	1,914
Site-grouped 5-fold	1	17,304	4,223	1,914
Site-grouped 5-fold	2	17,273	4,254	1,914
Site-grouped 5-fold	3	17,199	4,328	1,913
Site-grouped 5-fold	4	17,245	4,282	1,913
Spatial block 1°	0	17,179	4,348	105
Spatial block 1°	1	17,236	4,291	104
Spatial block 1°	2	17,723	3,804	104
Spatial block 1°	3	17,740	3,787	104
Spatial block 1°	4	16,230	5,297	104
Spatial block 5°	0	17,694	3,833	35
Spatial block 5°	1	16,546	4,981	35
Spatial block 5°	2	17,765	3,762	35
Spatial block 5°	3	19,204	2,323	35
Spatial block 5°	4	14,899	6,628	34
Spatial block 10°	0	19,602	1,925	18
Spatial block 10°	1	17,986	3,541	18
Spatial block 10°	2	17,033	4,494	17
Spatial block 10°	3	19,841	1,686	17
Spatial block 10°	4	11,646	9,881	17
Leave-one-realm-out	Tropical Atlantic	10,534	10,993	1
Leave-one-realm-out	Central Indo-Pacific	14,211	7,316	1
Leave-one-realm-out	Western Indo-Pacific	19,840	1,687	1
Leave-one-realm-out	Eastern Indo-Pacific	20,659	868	1
Temporal (train ≤ 2010)	0	14,118	7,409	–
Temporal, unseen sites	0	14,118	5,725	–

S3. Sensitivity analyses

Table S2: Pooled out-of-fold performance using Reef Check events only ($n = 11,242$).

	Random	Site-grouped	Block 1°	Block 5°	Block 10°
<i>Random forest, R^2</i>					
Coordinates only	0.05	−0.07	−0.10	−0.33	−0.43
Thermal only	0.27	0.15	−0.12	−0.15	−0.18
Environment (no coordinates)	0.27	0.16	−0.15	−0.19	−0.23
All predictors	0.30	0.21	−0.10	−0.20	−0.40
<i>Gradient boosting (HGB), R^2</i>					
Coordinates only	0.10	0.07	−0.03	−0.10	−0.12
Thermal only	0.23	0.14	−0.09	−0.10	−0.11
Environment (no coordinates)	0.24	0.16	−0.05	−0.12	−0.13
All predictors	0.27	0.19	0.00	−0.10	−0.16
<i>Random forest, all predictors</i>					
MAE (pp)	3.1	3.4	4.8	5.2	6.1
Training-mean MAE (pp)	3.9	3.9	4.0	4.0	3.9
AUC, events $\geq 50\%$	0.93	0.92	0.72	0.65	0.60

Table S3: Pooled out-of-fold performance using the four continuous-score sources (Reef Check, AGRRA, FRRP, McClanahan; $n = 16,673$).

	Random	Site-grouped	Block 1°	Block 5°	Block 10°
<i>Random forest, R^2</i>					
Coordinates only	0.34	0.21	−0.10	−0.24	−0.72
Thermal only	0.51	0.36	−0.04	−0.09	−0.15
Environment (no coordinates)	0.54	0.44	−0.02	−0.10	−0.11
All predictors	0.57	0.49	0.16	0.02	−0.03
<i>Random forest, all predictors</i>					
MAE (pp)	3.8	4.6	6.5	7.1	7.5
Training-mean MAE (pp)	7.2	7.2	7.3	7.2	7.2
AUC, events $\geq 50\%$	0.95	0.94	0.82	0.78	0.77

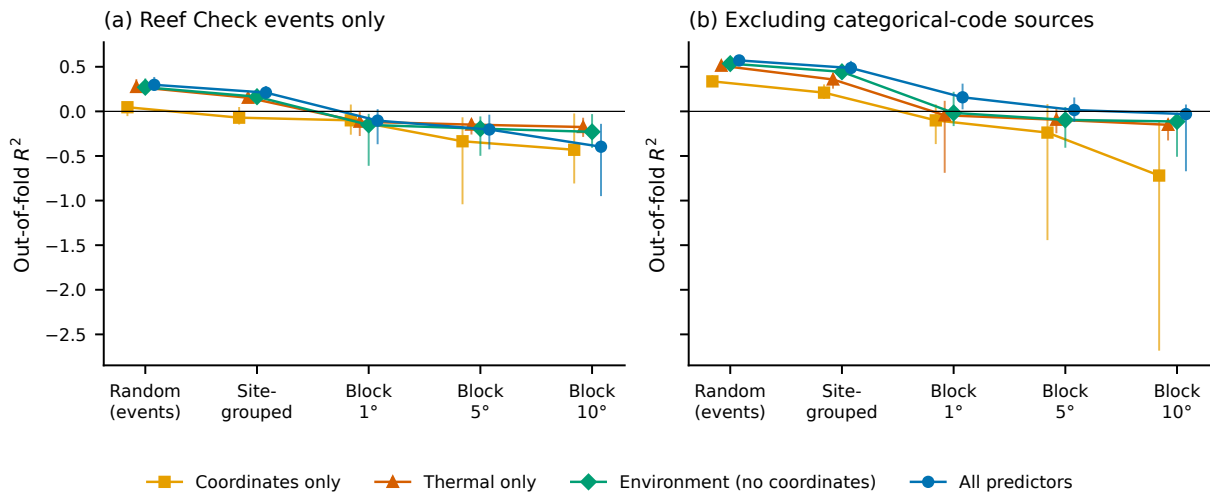


Figure S1: Random forest R^2 by validation design for (a) Reef Check events only and (b) the four continuous-score sources. Points are pooled out-of-fold values; vertical lines span individual folds.

S4. Source-conditioned models

Table S4: Random forest R^2 (pooled out-of-fold) for models using data-source indicators alone or combined with thermal or all predictors. Fold assignments are identical to Table 2.

Predictors	Random	Site-grouped	Block 1°	Block 5°	Block 10°
Data source only	0.37	0.37	0.36	0.35	0.35
Data source + thermal	0.61	0.53	0.34	0.28	0.27
Data source + all predictors	0.65	0.62	0.40	0.34	0.30

Table S5: How well each predictor group identifies the contributing source. AUC of random forest classifiers under site-grouped 5-fold cross-validation (0.5 = no discrimination).

Task	Predictors	AUC
Donner vs all other sources	Coordinates only	0.87
Donner vs all other sources	Thermal only	0.94
Donner vs all other sources	Environment (no coordinates)	0.94
Donner vs all other sources	All predictors	0.95
Reef Check vs all other sources	Coordinates only	0.96
Reef Check vs all other sources	Thermal only	0.97
Reef Check vs all other sources	Environment (no coordinates)	0.98
Reef Check vs all other sources	All predictors	0.99

S5. Predictor importance and correlation

Table S6: Held-out permutation importance for the all-predictor random forest: mean percentage increase in test MSE (five folds, five permutations each).

Predictor	Random 5-fold	Spatial block 5°
Thermal (group)	146.7	30.6
Coordinates (group)	130.2	12.5
Longitude_Degrees	101.6	14.4
SSTA_DHW	84.9	21.1
Site environment (group)	65.0	11.6
Latitude_Degrees	62.0	4.8
TSA	42.6	6.9
Cyclone_Frequency	39.7	8.7
Depth_m	20.0	3.9
SSTA_DHWMean	17.2	1.8
TSA_Mean	16.8	1.6
SSTA	10.5	1.8
SSTA_Maximum	8.9	1.4
Turbidity	6.6	-1.2

Table S7: Impurity-based importance of random forests fitted to all complete records (original analysis) and to deduplicated sampling events. Shown for comparison only; impurity importance is biased towards continuous and correlated predictors (Strobl et al., 2007).

Predictor	Complete rows	Sampling events
Longitude_Degrees	0.250	0.169
SSTA_DHW	0.135	0.135
Latitude_Degrees	0.102	0.153
TSA	0.097	0.102
Depth_m	0.096	0.101
Cyclone_Frequency	0.088	0.087
SSTA	0.064	0.062
TSA_Mean	0.053	0.046
Turbidity	0.040	0.043
SSTA_Maximum	0.037	0.039
SSTA_DHWMean	0.037	0.063
SSTA_Mean	0.000	—

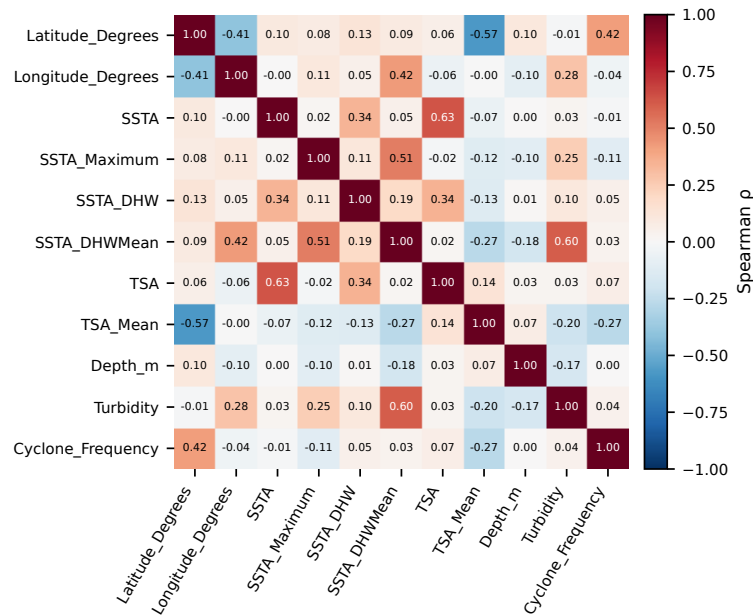


Figure S2: Spearman correlations among the 11 predictors across sampling events.

S6. Stability across fold assignments

Table S8: Range of pooled random forest R^2 across three additional fold assignments (seeds 1–3).

Design	Predictors	Min R^2	Max R^2
Random 5-fold	Thermal only	0.545	0.548
Random 5-fold	Environment (no coordinates)	0.583	0.584
Random 5-fold	All predictors	0.603	0.608
Site-grouped 5-fold	Thermal only	0.420	0.444
Site-grouped 5-fold	Environment (no coordinates)	0.476	0.497
Site-grouped 5-fold	All predictors	0.519	0.539
Spatial block 5°	Thermal only	−0.006	0.037
Spatial block 5°	Environment (no coordinates)	−0.005	0.058
Spatial block 5°	All predictors	0.080	0.118