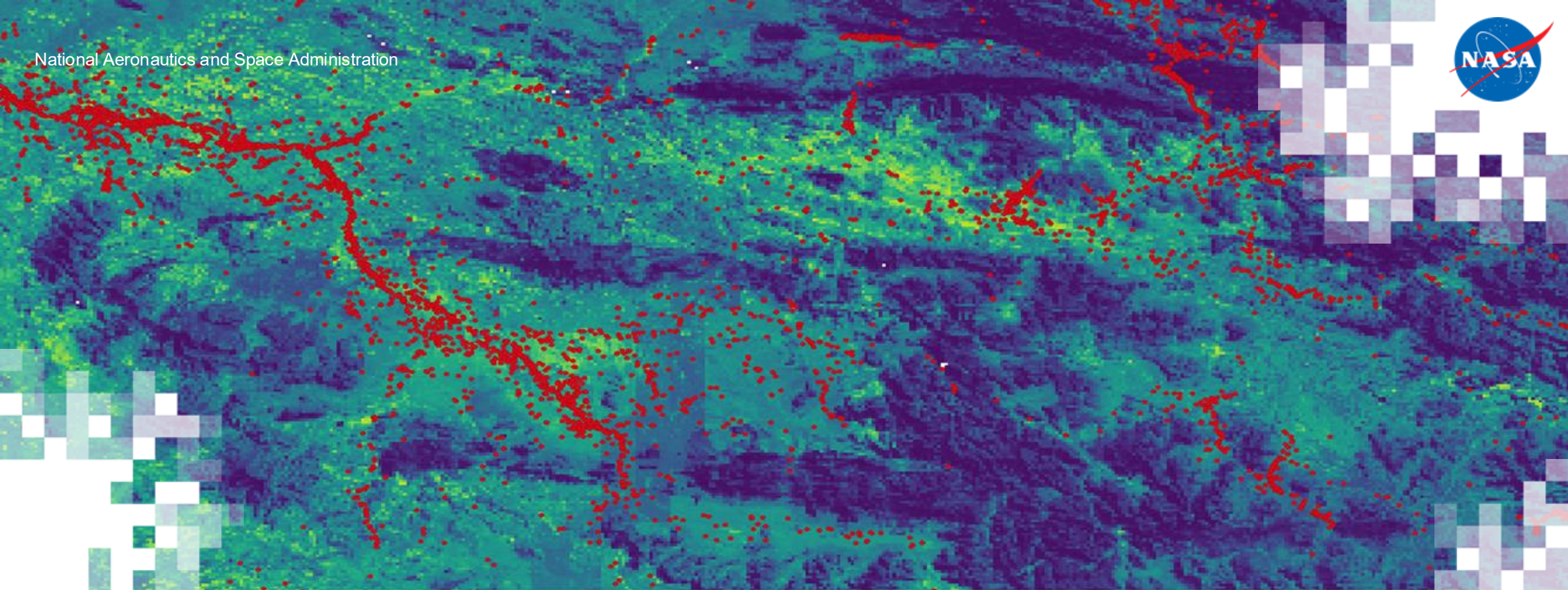




Species Distribution Modeling with Google Earth Engine

Part 2: Building, Evaluating, and Interpreting a SDM on GEE

ARSET Hosts: Justin Fain (NASA Ames/BAERI) & Sativa Cruz (NASA Ames/BAERI)

Guests: Ramiro Crego (University College Cork), Grant Connette (Smithsonian), & Jared Stabach (Smithsonian)

July 14, 2026



ARSET Eco Team

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Part 1 – Trainers



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Training Outline

Part 1

Foundations of
Species Distribution
Modeling with GEE

July 07, 2026

Session A: 9:00 a.m.
to 10:30 a.m. EDT
(UTC-4)

Session B: 4:00 p.m.
to 5:30 p.m. EDT
(UTC-4)

Part 2

Building,
Evaluating, and
Interpreting an
SDM on GEE

July 14, 2026

Session A: 9:00
a.m. to 10:30 a.m.
EDT (UTC-4)

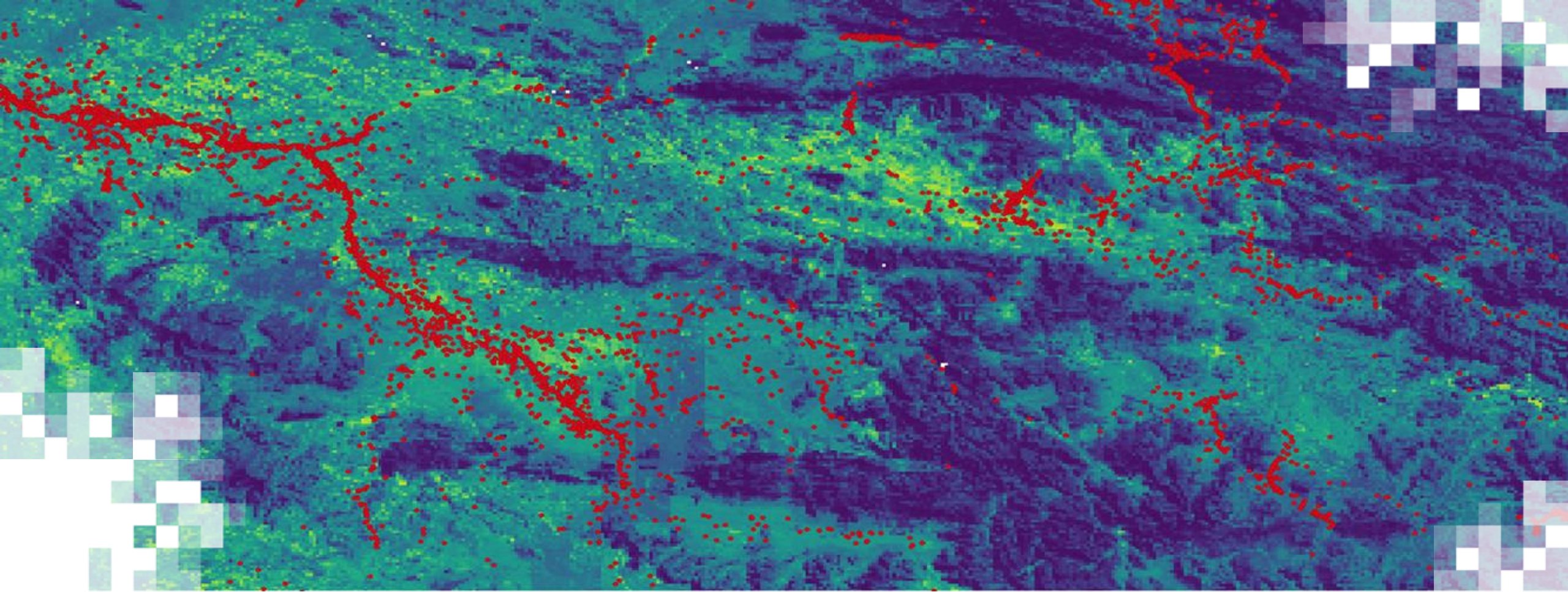
Session B: 4:00 p.m.
to 5:30 p.m. EDT
(UTC-4)

Homework

Opens July 14 – Due July 28– Posted on Training Webpage

A certificate of completion will be awarded to those who attend all live sessions and complete the homework assignment(s) before the given due date.





Species Distribution Modeling with Google Earth Engine

Part 2: Building, Evaluating, and Interpreting a SDM on GEE

Training Learning Objectives

By the end of this training, participants will be able to:

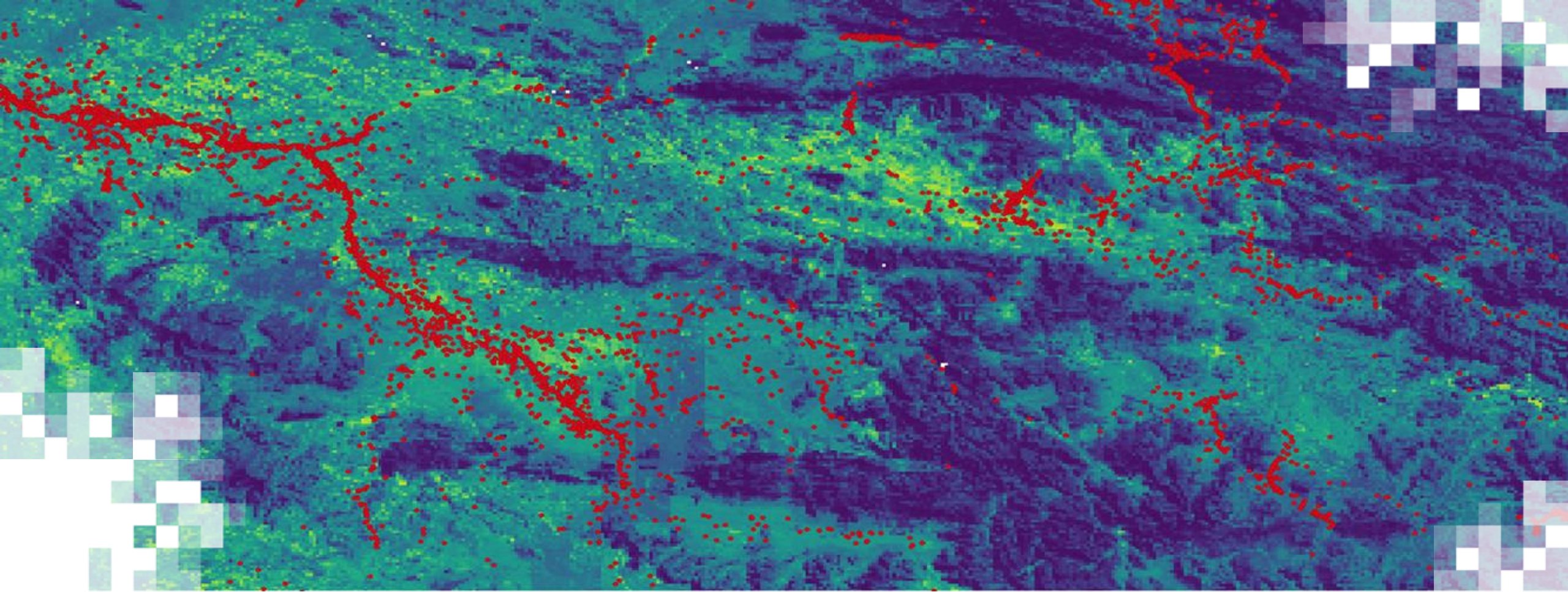
- Conduct basic operations and functions in the Google Earth Engine (GEE) web interface using JavaScript code.
- Identify core concepts and applications of species distribution modeling (SDM).
- Assess key SDM workflow decisions to ensure occurrence point independence, to select background points, and to choose ecologically relevant predictors.
- Access and manage analysis-ready spatial data from the GEE catalog as predictor variables.
- Fit species distribution models using machine learning models (e.g., Random Forest) in GEE using a reproducible code-based workflow.
- Critically evaluate the appropriateness of the model design and interpret predicted distribution and habitat suitability results.

Prerequisites

- [Part 2 of Visualizing Land Cover and Land Use Change with NASA Satellite Imagery](#)
- General knowledge of GIS
- Some coding experience

How to Ask Questions

- Please put your questions in the Questions box and we will address them at the end of the webinar.
- Feel free to enter your questions as we go. We will try to get to all of the questions during the Q&A session after the webinar.
- The remainder of the questions will be answered in the Q&A document, which will be posted to the training website about a week after the training.



Species Distribution Modeling with Google Earth Engine

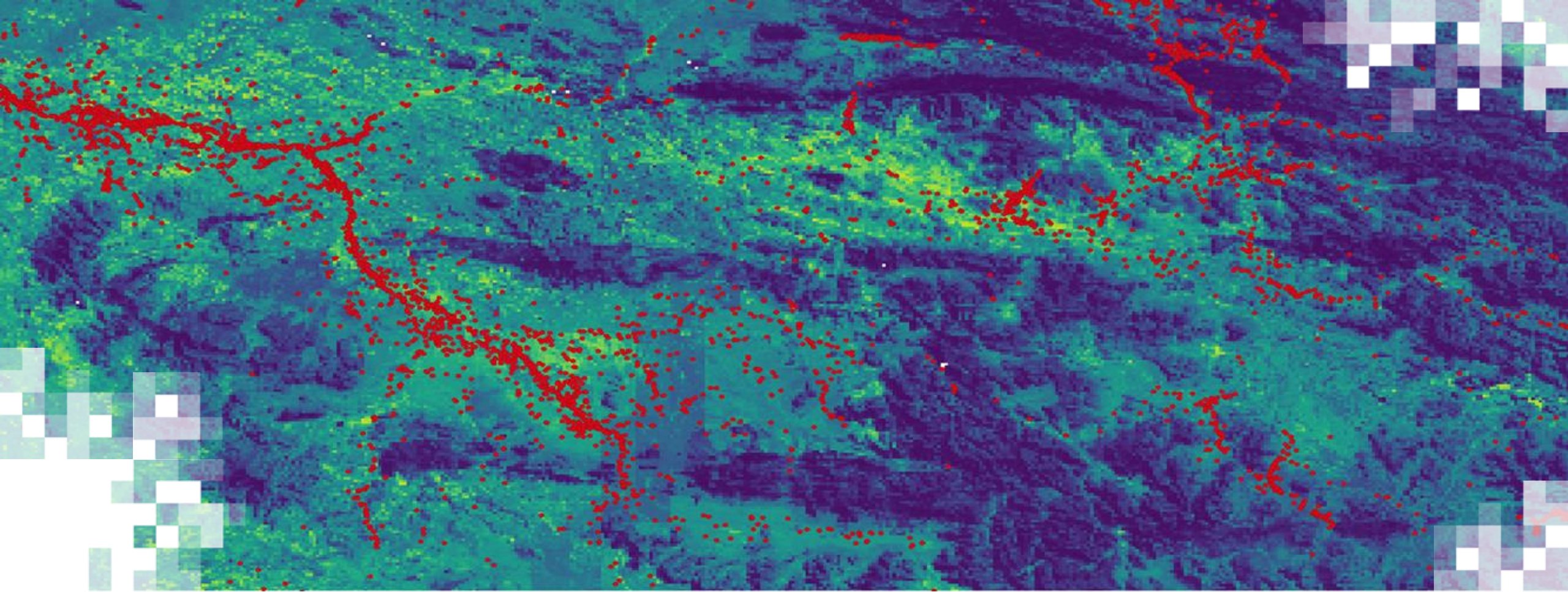
Ramiro Crego, Grant Connette, & Jared Stabach

July 14, 2026

Learning Objectives

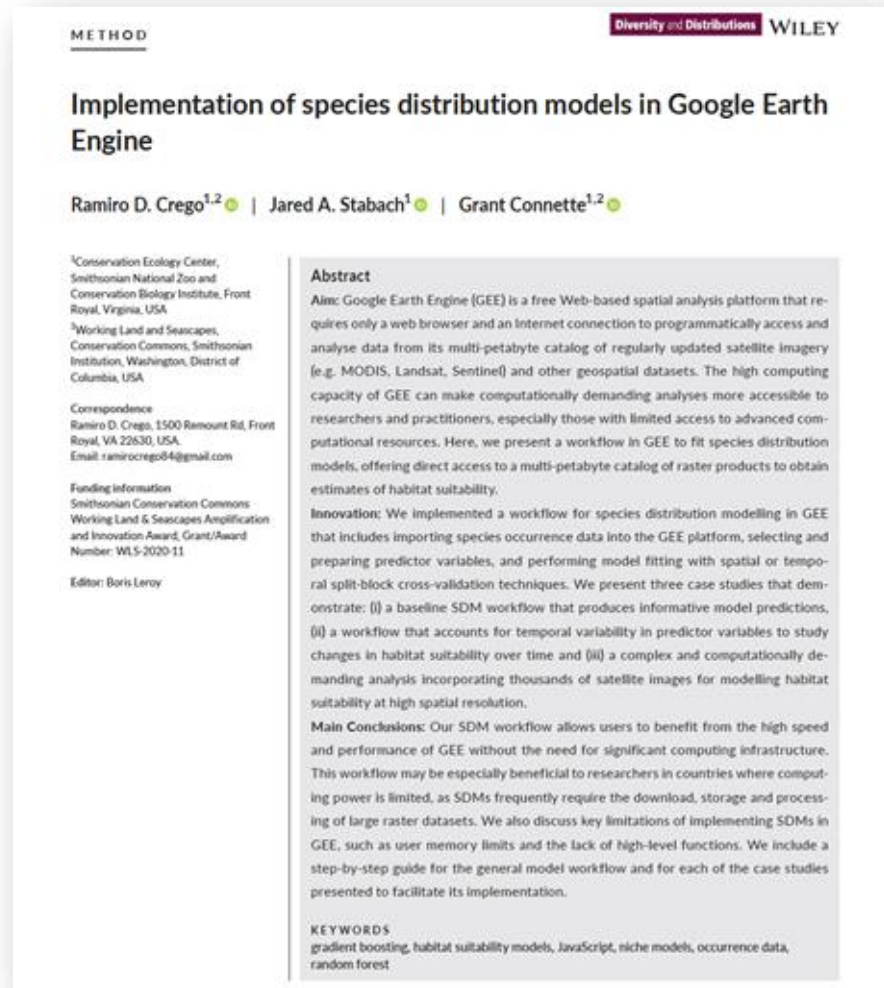
- Conduct basic operations and functions in Google Earth Engine (GEE) web interface using JavaScript code
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- Assess key SDM workflow decisions to ensure occurrence point independence, select background points, and choose ecologically relevant predictors.
- Access and manage analysis-ready spatial data from the GEE catalog as predictor variables
- Fit species distribution models using machine learning models (e.g., Random Forest) in GEE using a reproducible code-based workflow
- Critically evaluate the appropriateness of the model design and interpret predicted distribution and habitat suitability results





Building a Machine Learning Model

The Workflow



1. Species data upload
2. Preprocessing
3. Predictor variables
4. Presence and absence
 - a. Presence and absence
 - b. Presence and pseudoabsence
 - c. Presence and absence and pseudoabsence
5. Model fitting and model evaluation
6. Model predictions



Uploading Your Own Data as an Asset

1. In the Google Earth Engine interface, click on the 'Assets' tab and then the 'NEW' button. Under 'Table Upload', select 'CSV file (.csv)'.

2. In the 'Upload a new csv asset' dialog, click the 'SELECT' button to choose a file.

3. In the file selection dialog, select the 'Bradypus' CSV file.

4. In the 'Upload' dialog, set the 'Asset ID' to 'Bradypus'. Under 'Advanced options', set the 'X column' to 'lon' and the 'Y column' to 'lat'. Click the 'UPLOAD' button.

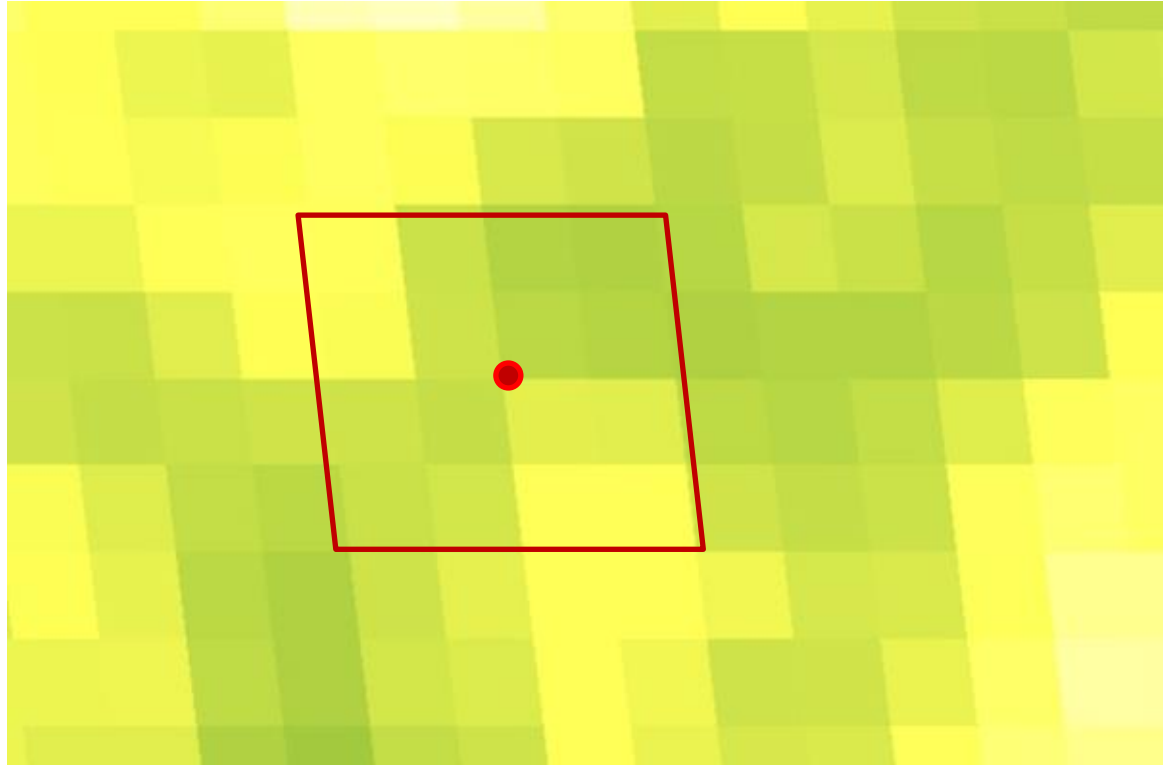
```
// Load presence data
var Data = ee.FeatureCollection('users/ramirocrego84/BradypusVariegatus');
print('Original data size:', Data.size());
```

```
// Visualize presence points on the map
Map.addLayer(Data, {color:'red'}, 'Presence', 1);
```



Define the Spatial Resolution of the Analysis

```
// Define spatial resolution to work with (m)  
var GrainSize = 1000;
```



Spatial Thinning of Presence Data

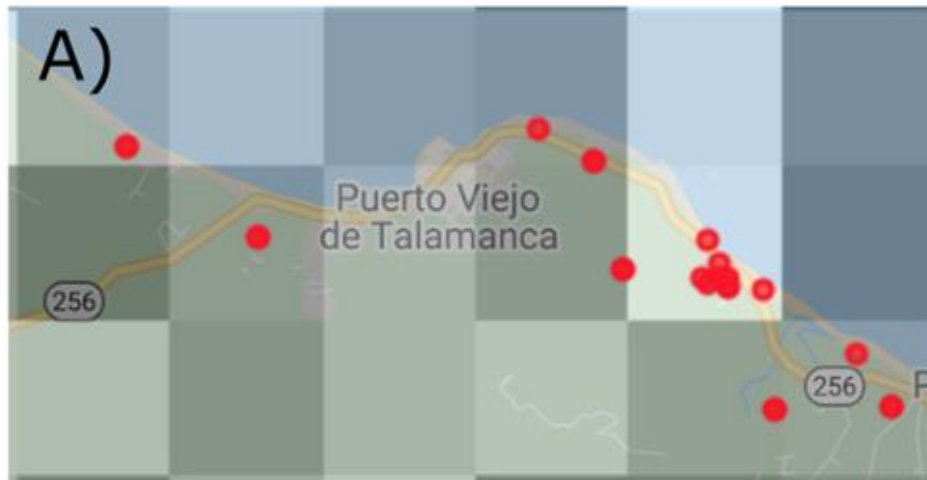
- People often record a species multiple times in the exact same location (e.g., near roads or in parks). We can thin presence data to mitigate effects of sampling bias on our model.
- We can thin our location data to one randomly selected occurrence record per pixel at the chosen spatial resolution (the raster pixel or grain size of the analysis).

```
function RemoveDuplicates(data){  
  var randomraster = ee.Image.random().reproject('EPSG:4326', null, GrainSize);  
  var randpointvals = randomraster.sampleRegions({collection:ee.FeatureCollection(data), scale: 10, geometries: true});  
  return randpointvals.distinct('random');  
}  
  
var Data = RemoveDuplicates(Data);  
print('Final data size:', Data.size());
```

Use print(...) to write to this console.

Original data size: JSON
571

Final data size: JSON
323



Define Your Area of Interest for Modelling

- The extent of the analysis should be carefully selected and constrained to a geographic region that is actually accessible to the species.
- Avoid massive analysis extents - comparing against distant absence points inflates accuracy metrics and focuses on obvious macro-scale patterns (e.g., forest vs. desert).

```
// Load region boundary from data catalog if working at a larger scale
var AOI = ee.FeatureCollection('USDOS/LSIB_SIMPLE/2017').filter(ee.Filter.eq('country_co', 'CO'));
Map.addLayer(AOI)

// Load country boundary from data catalog if working at a country scale
var AOI2 = ee.FeatureCollection('USDOS/LSIB_SIMPLE/2017').filter(ee.Filter.eq('wld_rgn', 'South America')).union().geometry();
Map.addLayer(AOI2)
```



Define Your Area of Interest for Modelling

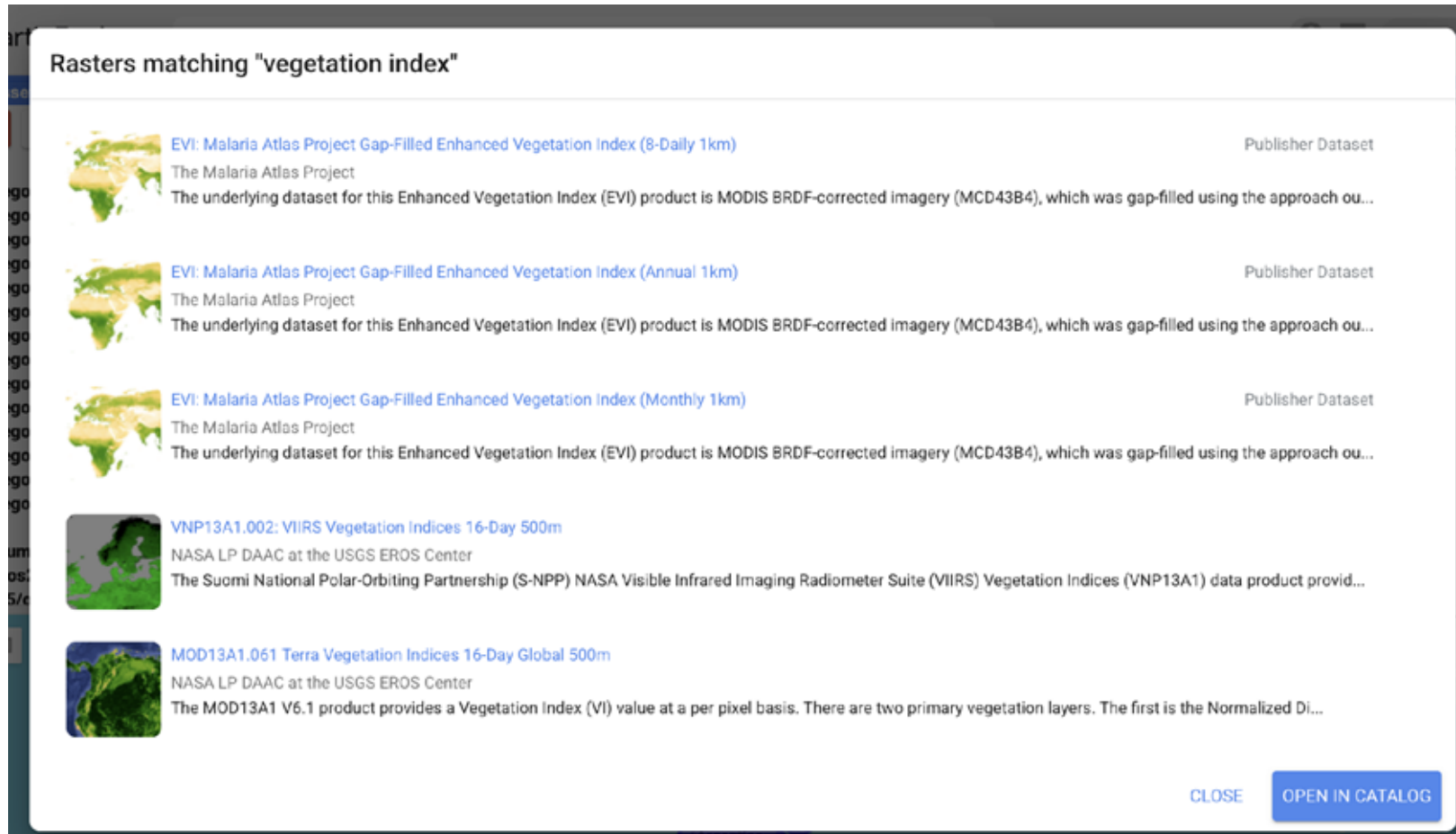
- The extent of the analysis should be carefully selected and constrained to a geographic region that is actually accessible to the species.
- Avoid massive analysis extents - comparing against distant absence points inflates accuracy metrics and focuses on obvious macro-scale patterns (e.g., forest vs. desert).

```
////////////////////////////////////  
// Section 2 - Define Area of Interest (Extent)  
////////////////////////////////////  
  
// Define the AOI  
var AOI = Data.geometry().bounds().buffer({distance:50000, maxError:1000});  
  
// Add border of study area to the map  
var outline = ee.Image().byte().paint({  
  featureCollection: AOI, color: 1, width: 3});  
right.addLayer(outline, {palette: 'FF0000'}, "Study Area");  
left.addLayer(outline, {palette: 'FF0000'}, "Study Area");  
  
// Center map to the area of interest  
right.centerObject(AOI, 4); //Number indicates the zoom level  
left.centerObject(AOI, 4); //Number indicates the zoom level
```



Selecting Predictor Variables

- A key advantage of implementing SDMs in Google Earth Engine is its cloud-hosted data catalog, allowing users to directly access many geospatial predictor variables via code.



Using Raw Satellite Data as Predictor Variables

Diversity and Distributions, (Diversity Distrib.) (2013) 19, 855–866

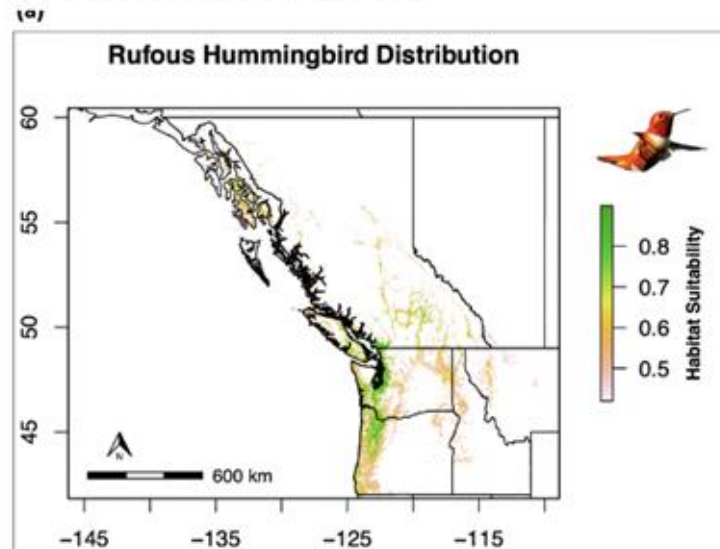


Species distribution modelling for the people: unclassified landsat TM imagery predicts bird occurrence at fine resolutions

S. M. Shirley^{1*}, Z. Yang¹, R. A. Hutchinson², J. D. Alexander³, K. McGarigal⁴ and M. G. Betts¹

Breeding habitat loss linked to declines in Rufous Hummingbirds

Kendall M. Jefferys¹, Matthew G. Betts², W. Douglas Robinson³, Jenna R. Curtis³, Tyler A. Hallman^{1,4}, Adam C. Smith⁵, Chloé Strevens⁴, Jesús Aguirre Gutiérrez^{1,6}



RESTORATION
ECOLOGY
The Journal of the Society for Ecological Restoration



RESEARCH ARTICLE

Validating habitat suitability assessments with post-translocation animal movement data

Ramiro D. Crego^{1,2,3,4}, Michael B. Brown^{3,5}, Jared A. Stabach⁷, Julian Fennessy^{5,6}, Stephanie Fennessy⁵, Pedro Monterroso⁷, Daniel van de Vyver⁷, Courtney Marnewick^{5,8}

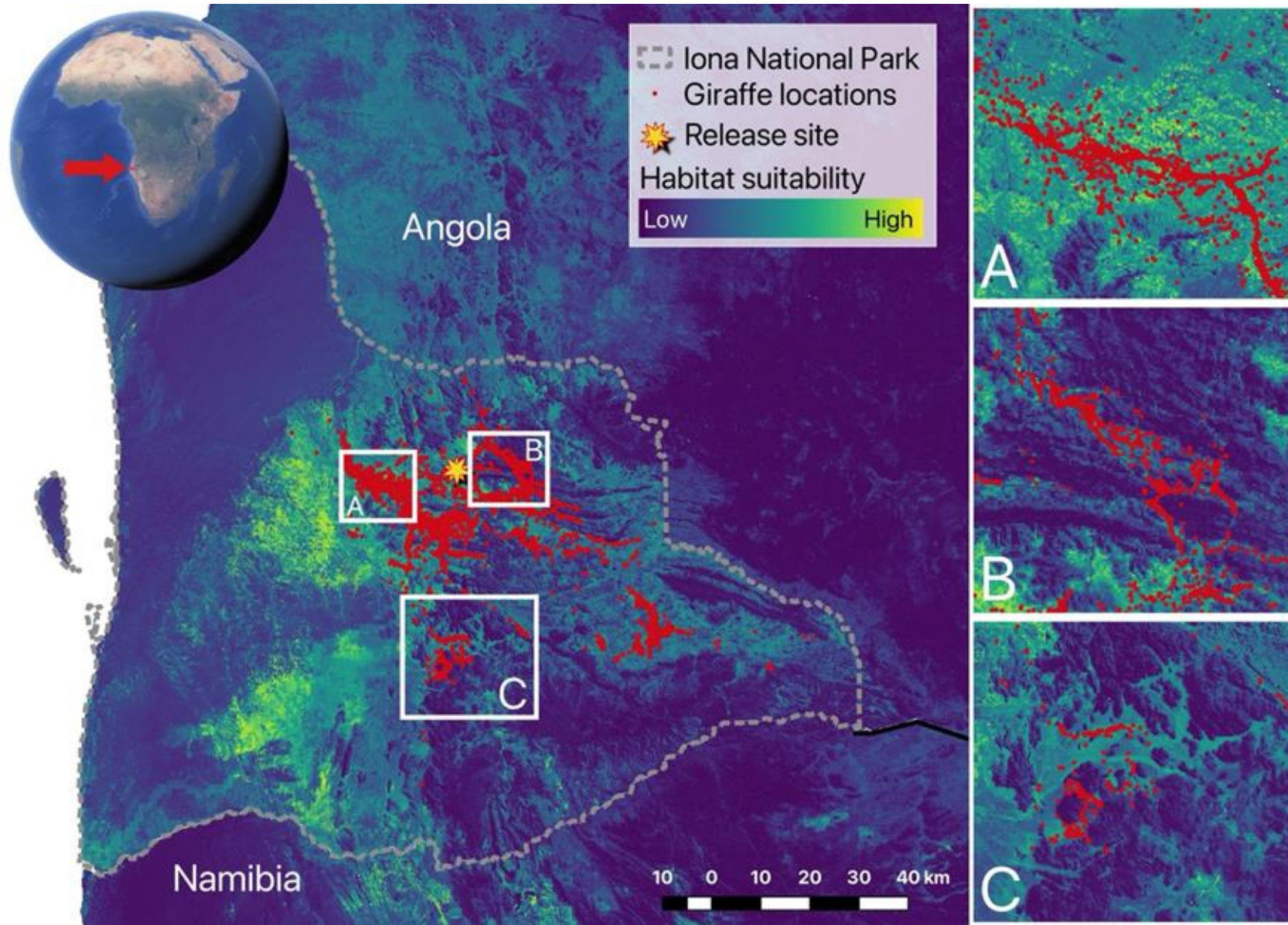
Wildlife translocations are essential for restoring species to their native habitats, and species distribution models (SDMs) have proven useful for identifying suitable habitats to guide this process. Validating model predictions with data from individual's post-translocation, however, is rare due to the frequent lack of monitoring data from translocated individuals. The translocation of 14 Angolan giraffe (*Giraffa giraffa angolensis*) in 2023 to Iona National Park (NP), Angola, to restore its devastated fauna provided an opportunity to test the ability of SDMs to inform suitable habitat for translocation programs. Here, we describe the SDM we developed and implemented using Google Earth Engine (GEE) to inform the translocation process, combining Angolan giraffe movement data from 45 individuals from a population in northern Namibia with moderate resolution satellite imagery to predict suitable habitat throughout Iona NP. We then used telemetry data from the 14 translocated individuals to validate the results from the model prediction and to summarize their movements post-translocation. The mean predicted habitat suitability of pixels used by Angolan giraffe was significantly higher than that of random locations across the landscape. Translocated giraffe movements and home ranges were comparable to those of giraffe from other populations. They displaced at least 21.6 km from the translocation release site and remained within the park limits. Our study represents a truly independent validation of a habitat suitability model prediction, demonstrating that SDMs combined with moderate-resolution satellite data can play a critical role in informing wildlife translocations.

Key words: Angola, *Giraffa giraffa angolensis*, giraffe, reintroduction, species distribution model

Suitable habitat maps are valuable to identify potential areas for animal translocations.

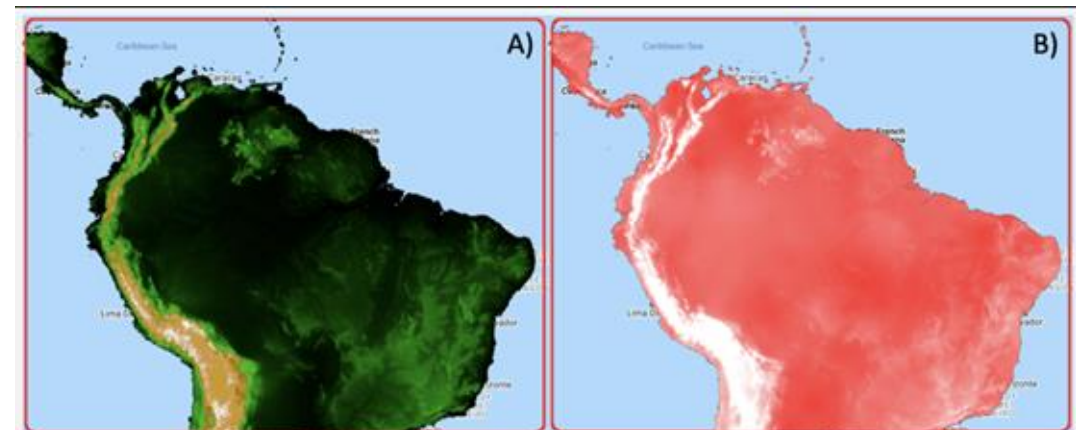


On 5 July 2023, 14 giraffe were translocated to Iona National Park



Selecting Predictor Variables

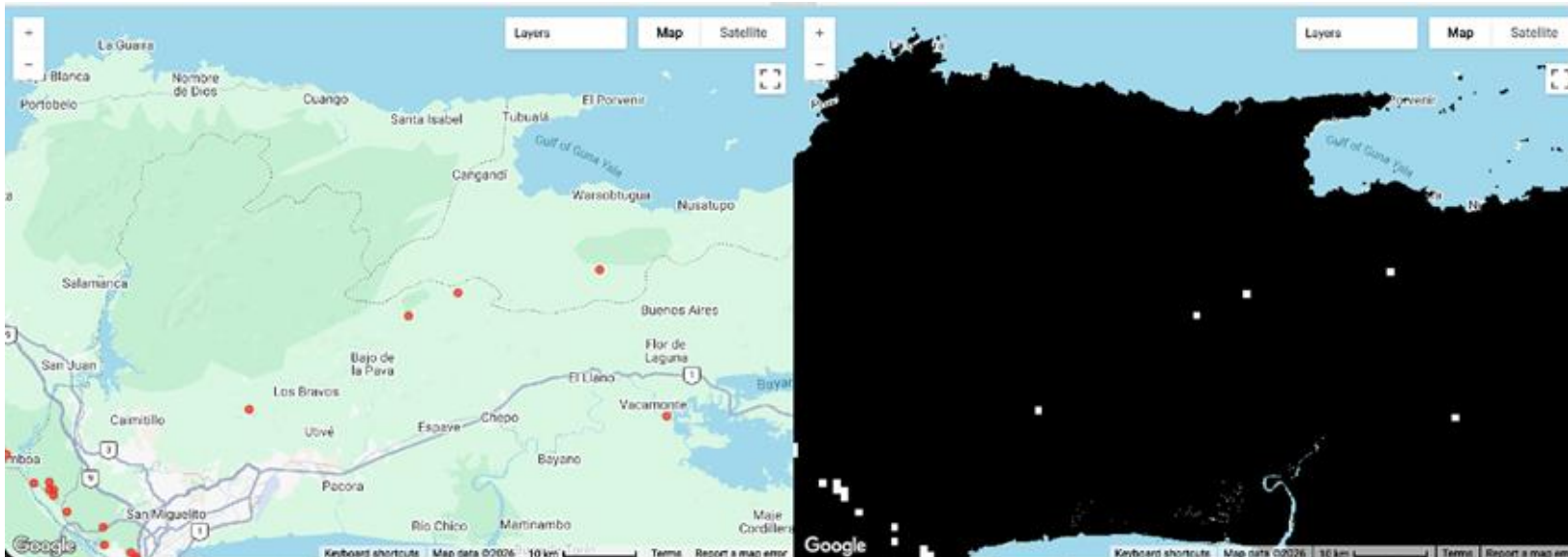
```
////////////////////////////////////  
// Section 3 – Selectiong Predictor Variables  
////////////////////////////////////  
  
// Load WorldClim BIO Variables (a multiband image) from the data catalog  
var BIO = ee.Image("WORLDCLIM/V1/BIO");  
  
// Load elevation data from the data catalog and calculate slope, aspect, and a simple hillshade from the terrain Digital Elevation Model.  
var Terrain = ee.Algorithms.Terrain(ee.Image("USGS/SRTMGL1_003"));  
  
// Load NDVI 250 m collection and estimate median annual tree cover value per pixel  
var MODIS = ee.ImageCollection('MODIS/061/MOD44B');  
var MedianPTC = MODIS.filterDate('2003-01-01', '2020-12-31').select(['Percent_Tree_Cover']).median();  
  
// Combine bands into a single multi-band image  
var predictors = BIO.addBands(Terrain).addBands(MedianPTC);  
print(predictors)  
  
// Mask out ocean pixels from the predictor variable image  
var watermask = Terrain.select('elevation').gt(0); //Create a water mask  
var predictors = predictors.updateMask(watermask).clip(AOI);  
  
// Display layers on the map  
right.addLayer(predictors, {bands:['elevation'], min: 0, max: 5000, palette: ['000000', '006600', '009900', '33CC00', '996600', 'CC9900', 'CC9966', 'FFFFFF', ]},  
'Elevation (m)', 0);  
right.addLayer(predictors, {bands:['bio05'], min: 190, max: 400, palette:'white,red'}, 'Temperature seasonality', 0);  
right.addLayer(predictors, {bands:['bio12'], min: 0, max: 4000, palette:'white,blue'}, 'Annual Mean Precipitation (mm)', 0);  
right.addLayer(predictors, {bands:['Percent_Tree_Cover'], min: 1, max: 100, palette:'white,yellow,green'}, 'Percent_Tree_Cover', 0);  
  
// Select subset of bands to keep for habitat suitability modeling  
var bands = ['bio04', 'bio05', 'bio06', 'bio12', 'elevation', 'Percent_Tree_Cover'];  
var predictors = predictors.select(bands);
```



Defining the Area to Create Pseudo-absences

- We first need to create a mask to avoid creating pseudo-absences in the same pixels where we have presence points.

```
////////////////////////////////////  
// Section 4 – Defining area for pseudo-absences and spatial blocks for model fitting and cross validation  
////////////////////////////////////  
  
// Make an image out of the presence locations. The pixels where we have presence locations will be removed from the area  
// to generate pseudo-absences.  
// This will prevent having presence and pseudo-absences in the same pixel.  
var mask = Data  
  .reduceToImage({  
    properties: ['random'],  
    reducer: ee.Reducer.first()  
  }).reproject('EPSG:4326', null, ee.Number(GrainSize));
```



Defining the Area to Create Pseudo-absences

Three main methods:

1. Generate random pseudo-absences across the entire study area (not recommended for pseudo-absence as it risks sampling suitable habitat; use only for creating background points).



Defining the Area to Create Pseudo-absences

Three main methods:

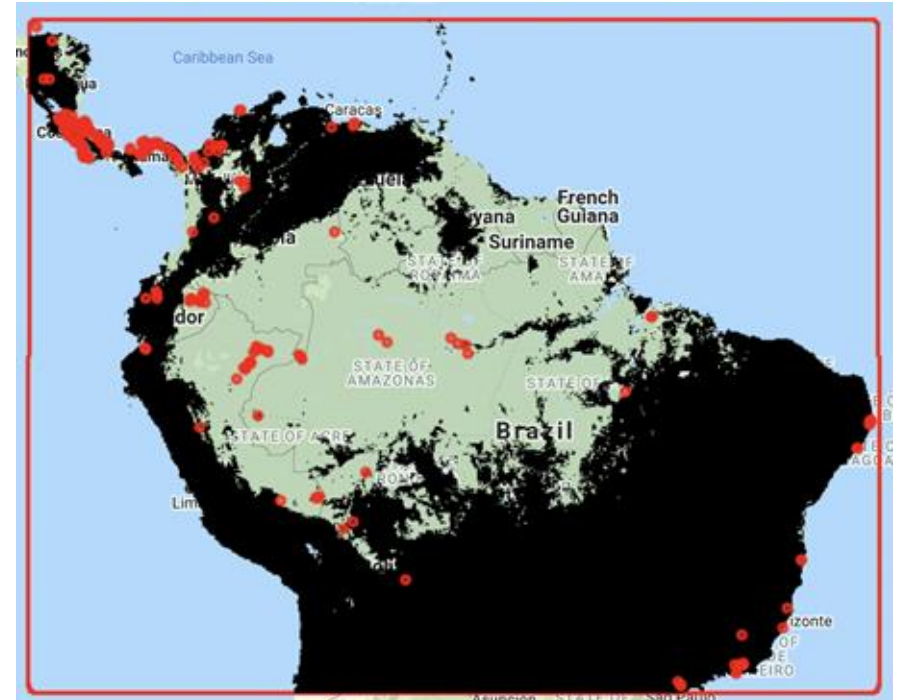
2. Generate pseudo-absences within a specified distance range from presence locations. This limits pseudo-absences to areas potentially accessible to the species (Araújo et al., 2019) and can be used to mirror potential spatial or environmental sampling bias present in the occurrence data (Phillips et al., 2009).



Defining the Area to Create Pseudo-absences

Three main methods:

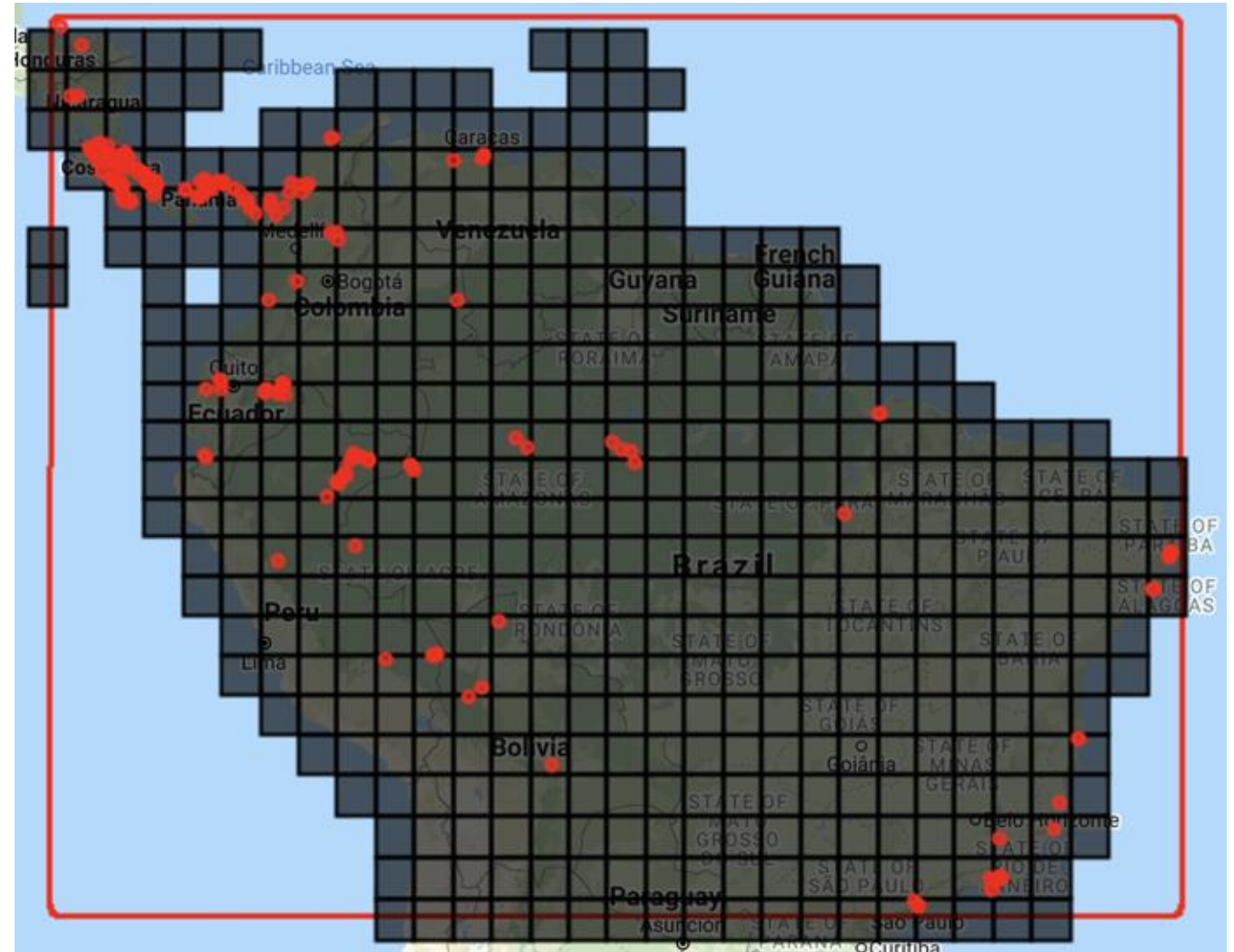
3. Constrain pseudo-absences by masking out suitable areas using an environmental profiling technique (Chefaoui & Lobo, 2008; Senay, Worner, & Ikeda, 2013). This ensures pseudo-absences are drawn from lower-suitability environments and minimizes false absences.



Spatial Block Cross-validation

Divide the study area into geographic blocks and randomly assign blocks into separate subsets for model training and validation (Roberts et al., 2017; Valavi, Elith, Lahoz-Monfort, & Guillerá-Arroita, 2019).

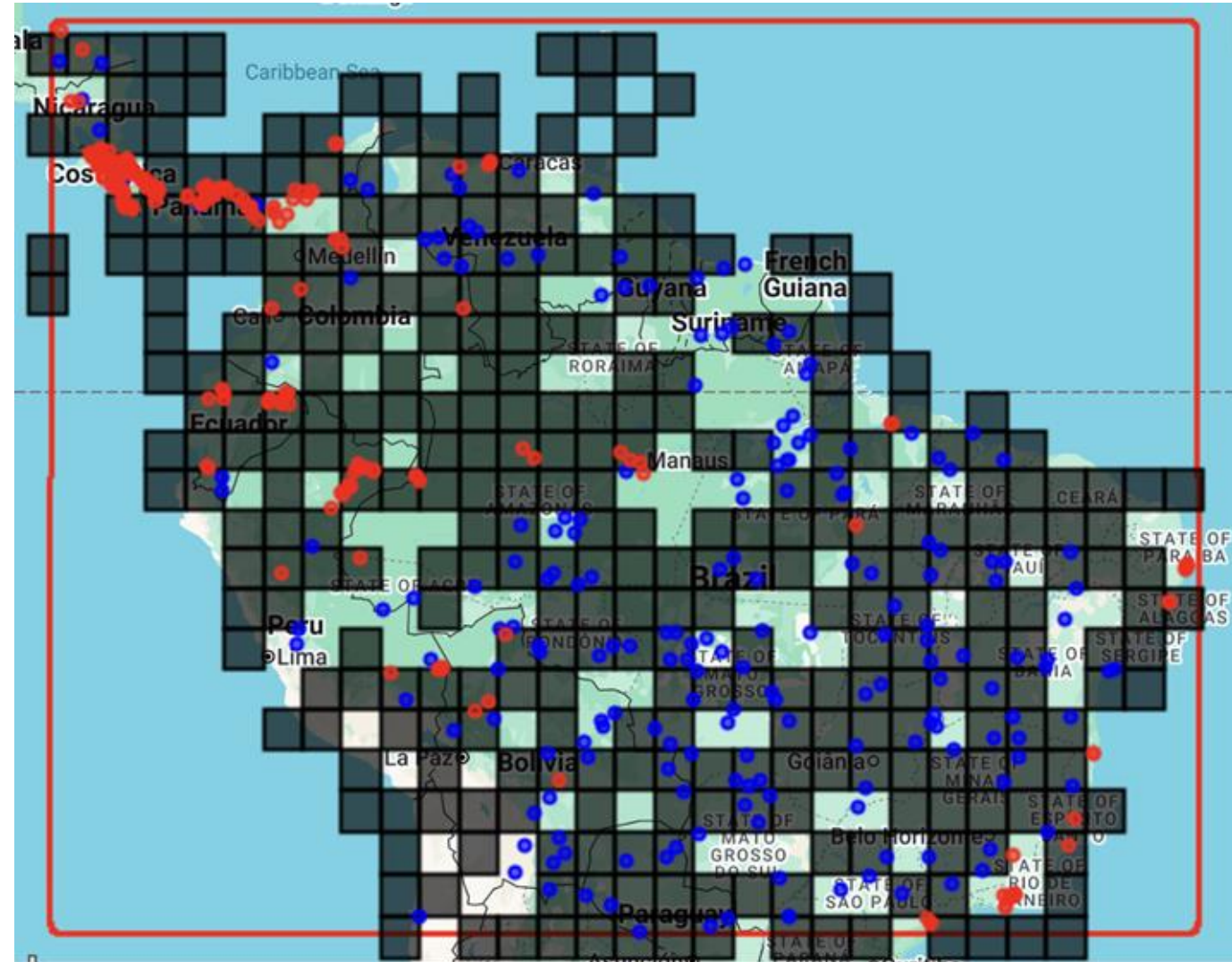
In our workflow, we run multiple model iterations with random block splits to create training and validation data sets.

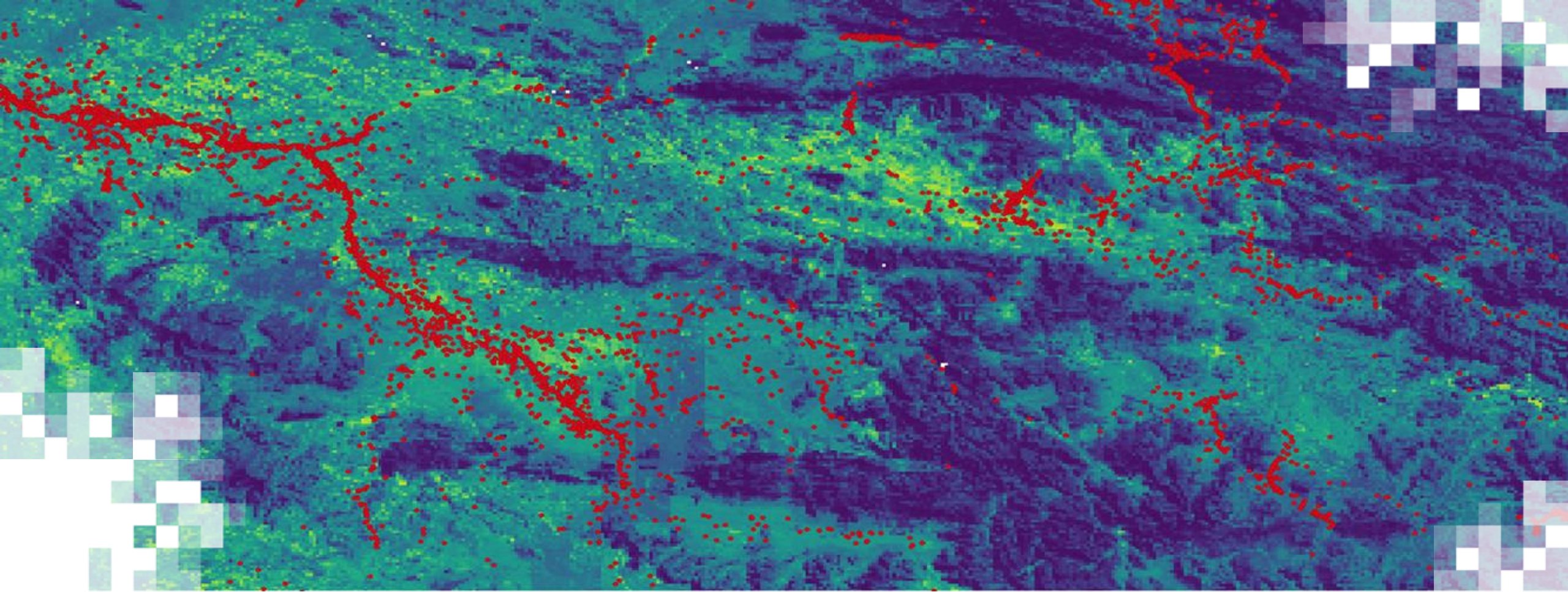


Spatial Block Cross-validation

We will select location data from 70% of the blocks for model training, including **presence** and **pseudo-absences**.

All points outside these blocks are going to be used for model testing.

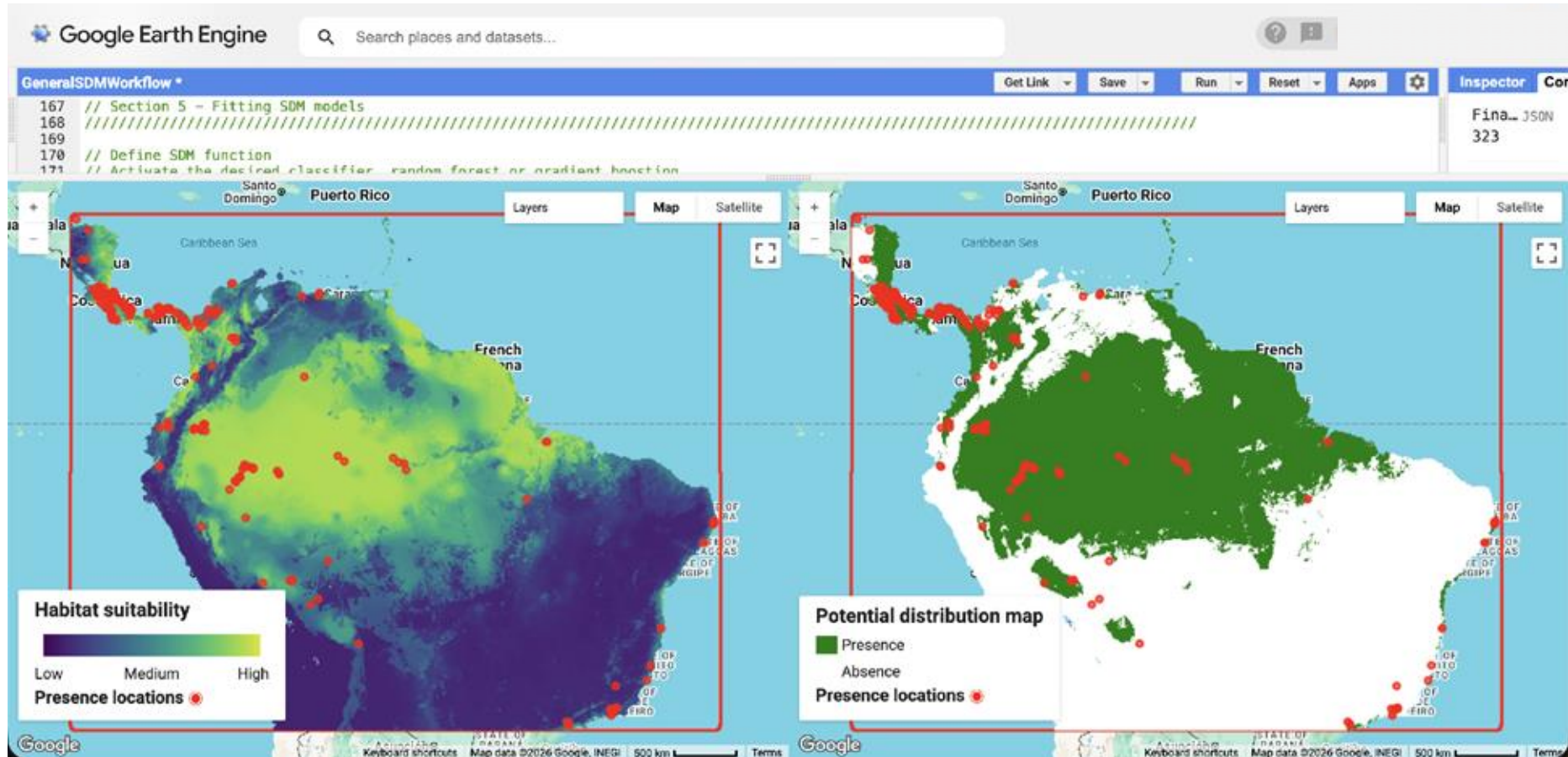




Model Fitting and Model Validation

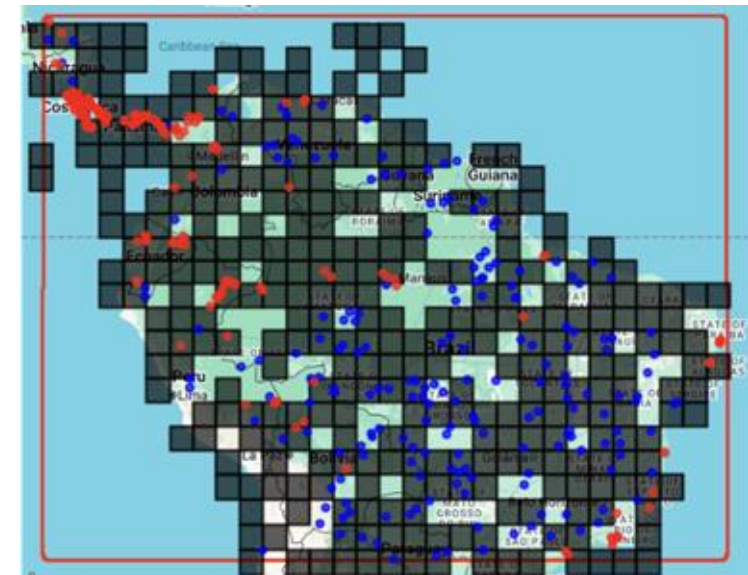
Fitting an SDM Model

- Next, we will define the SDM function.
- Let's go to the code editor.



Validating an SDM

- Ask basic questions:
 - Is this model meaningful?
 - Do the predictions make ecological sense?
- Derive evaluation metrics:
 - Deviance explained, residual patterns, goodness-of-fit test
- **Cross-validation:**
 - **Evaluation of model predictions with independent data**
 - **Partitioning data: training data vs. testing data**



Validating an SDM

- **Quantify model accuracy (Interpolation):** Test predictive performance of the model within the **same** region and timeframe as the training data (Araújo et al. [2019](#)).
- **Quantify model generality (Extrapolation):** Test predictive performance of the model in a **different** region and timeframe from the training data (Araújo et al. [2019](#)).



Methods for Model Validation

Threshold dependent metrics

- Requires presence/absence data (or pseudo-absences)
- Calculated from an error matrix (a.k.a. confusion matrix)
- Examples: Percent overall accuracy, Kappa, True Skill Statistic (TSS)
- Key challenge: selecting the optimal threshold for converting suitability to a binary 0/1 map

Threshold independent metrics

- Area under the Receiver Operating Characteristic Curve (AUC-ROC)
- Area under the Precision Recall Curve (AUC-PR)



The Error Matrix

		Predicted Class		
		Positive	Negative	
Actual Class	Positive	True Positive (TP)	False Negative (FN) Type II Error	Sensitivity $\frac{TP}{(TP + FN)}$
	Negative	False Positive (FP) Type I Error	True Negative (TN)	Specificity $\frac{TN}{(TN + FP)}$
		Precision $\frac{TP}{(TP + FP)}$	Negative Predictive Value $\frac{TN}{(TN + FN)}$	Accuracy $\frac{TP + TN}{(TP + TN + FP + FN)}$

Sensitivity (recall): the proportion of actual presence records the model correctly identifies out of all actual presences, emphasizing the prevention of false negatives

Specificity: the proportion of actual absence locations a model correctly identifies out of all actual absences, emphasizing the prevention of false positives

Precision: the proportion of predicted presence locations that are truly presences out of all total predicted presences, emphasizing the reliability of your suitability map



The Error Matrix: Example

Testing presence data

	x	
	x	x

Predicted probability

0	0.1	0.3
0.1	0.2	0.4
0.2	0.5	0.6

$$\text{Sensitivity} = \frac{\text{TP}}{\text{TP} + \text{FN}}$$

$$\text{Specificity} = \frac{\text{TN}}{\text{TN} + \text{FP}}$$

Threshold = 0

	x	
	x	x

0.1

	x	
	x	x

0.2

	x	
	x	x

Threshold = 0.3

	x	
	x	x

0.4

	x	
	x	x

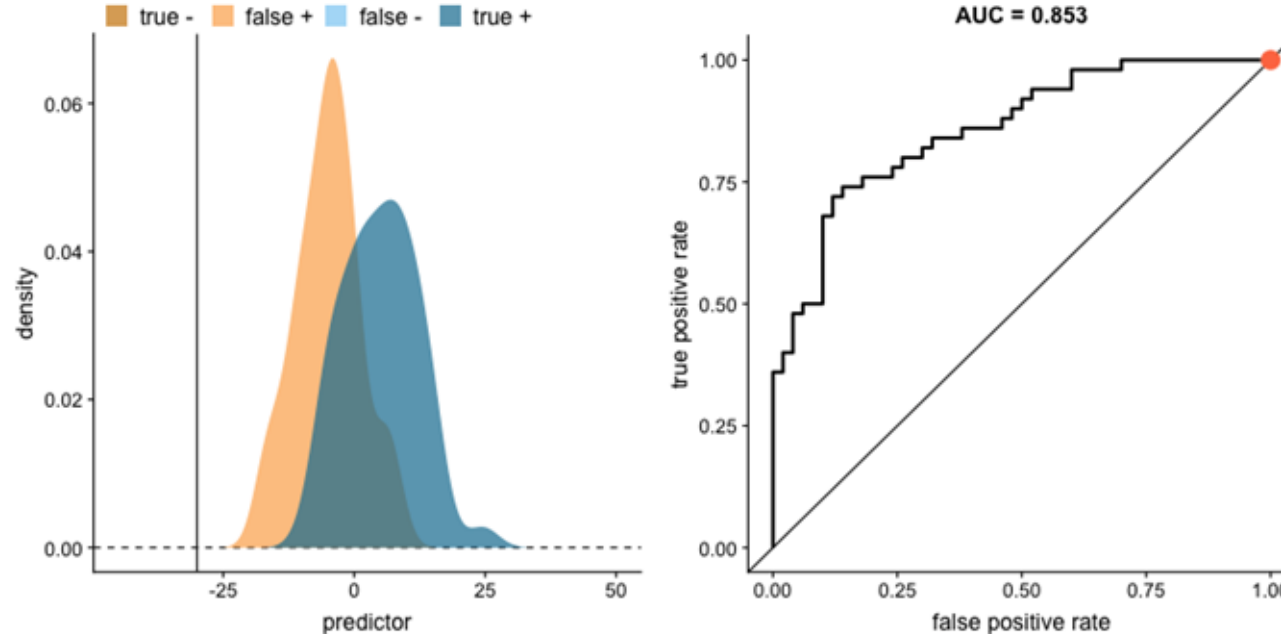
0.5

	x	
	x	x



Threshold Independent Validation: AUC-ROC

- Area under the ROC (AUC) provides a single measure of model performance
- Independent of any particular choice of threshold



[Image Source](#)



Threshold Independent Validation: AUC-ROC

- Area under the ROC (AUC) provides a single measure of model performance
- Independent of any particular choice of threshold
- The AUC ranges from 0 to 1

AUC = 1 indicates perfect discrimination between presence and absence/pseudo-absence locations

AUC = 0.5 discrimination is no better than random performance

AUC < 0.5 performance is worse than random

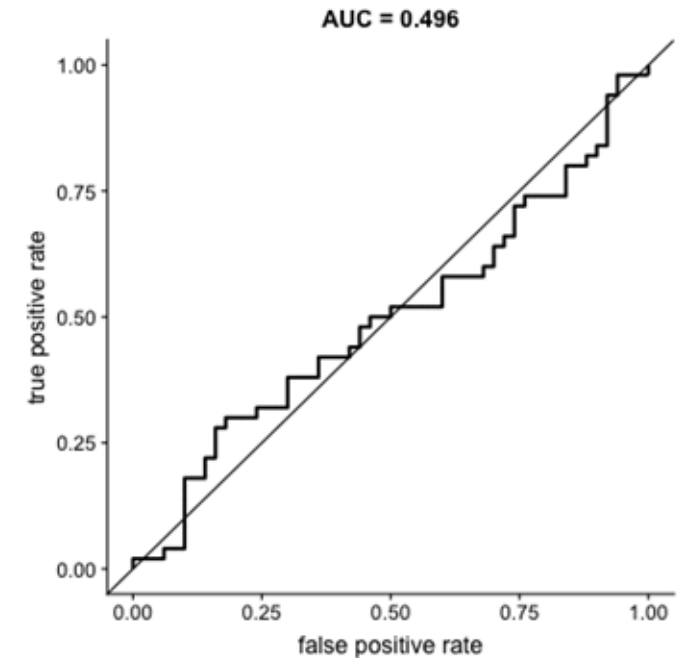
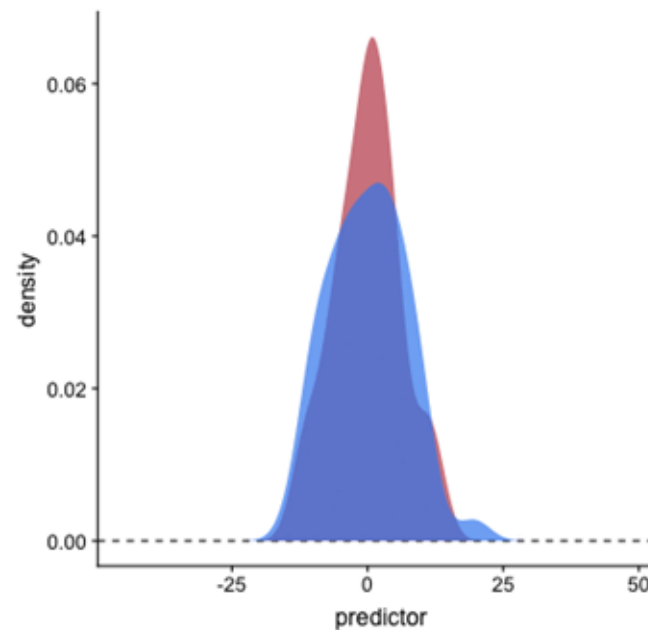
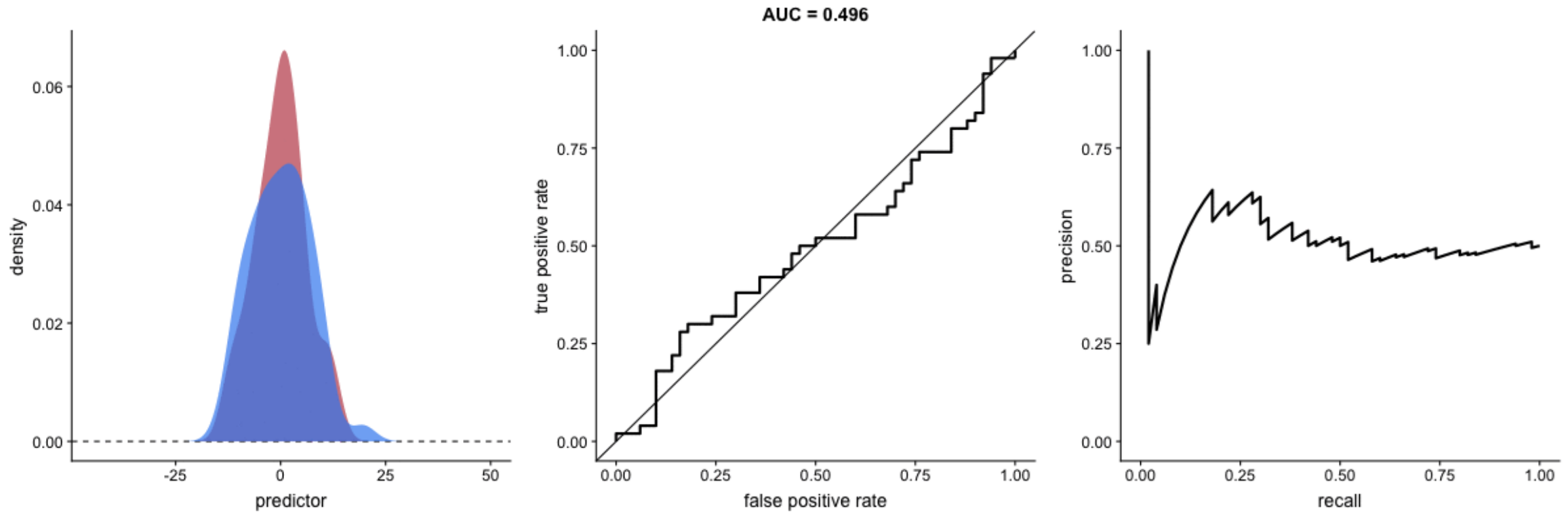


Image Source



Threshold Independent Validation: AUC-PR

- AUC-PR evaluates the model's ability to find true presences (Recall or Sensitivity) against the reliability of its suitability map (Precision) across all possible thresholds.

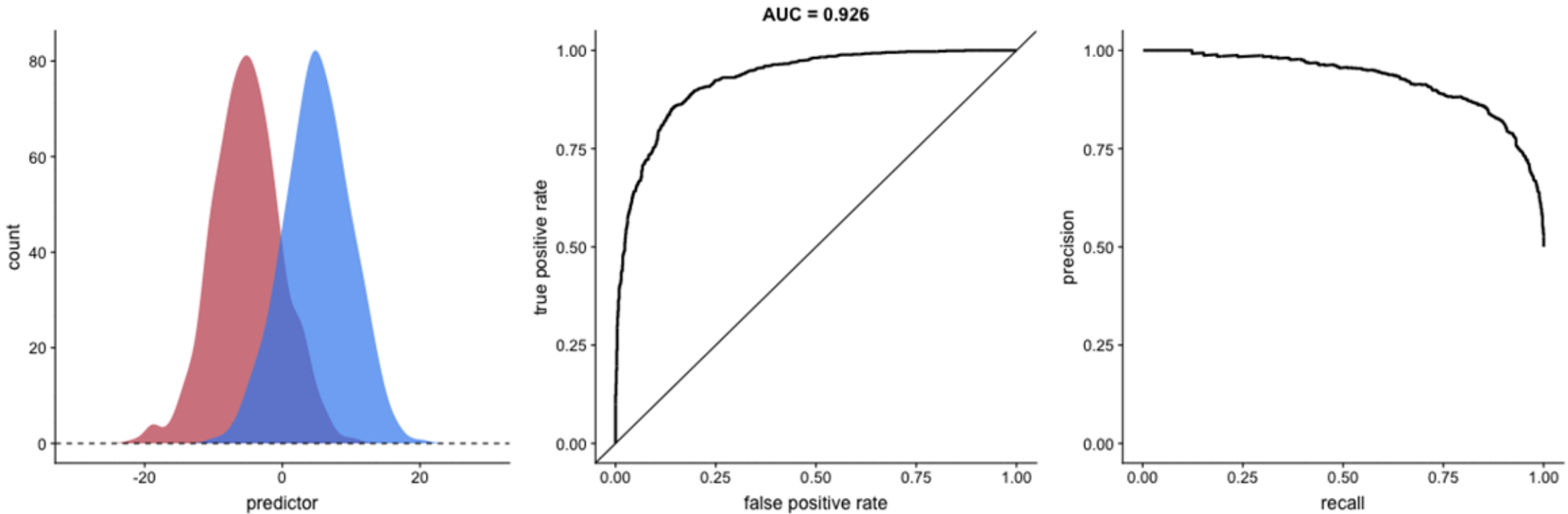


[Image Source](#)



The Problem of Class Imbalances

- AUC-ROC overestimates accuracy when the number of absences is much higher than the number of presences (e.g., rare species)
- Here we see 10,000 absences vs 50 presences



[Image Source](#)



Validating our Model

```
// Define partition for training and testing data
var split = 0.70; // The proportion of the blocks used to select training data
```

```
// Define number of repetitions
var numiter = 5;
```

```
// While the runif function can be used to generate random seeds, we map the SDM
// function over random created numbers for reproducibility of results
var results = ee.List([35,68,43,54,17]).map(SDM);
```

```
// Extract results from list
var results = results.flatten();
//print(results)
```

```
var AUCROCs = ee.List.sequence(0,ee.Number(numiter).subtract(1),1).map(AUCROCAccuracy);
print('AUC-ROC:', AUCROCs);
print('Mean AUC-ROC', AUCROCs.reduce(ee.Reducer.mean()));
```

```
var AUCPRs = ee.List.sequence(0,ee.Number(numiter).subtract(1),1).map(AUCPRAccuracy);
print('AUC-PR:', AUCPRs);
print('Mean AUC-PR', AUCPRs.reduce(ee.Reducer.mean()));
```

```
// Extract sensitivity, specificity and mean threshold values
var Metrics = ee.List.sequence(0,ee.Number(numiter).subtract(1),1).map(getMetrics);
print('Sensitivity:', ee.FeatureCollection(Metrics).aggregate_array("TPR"));
print('Specificity:', ee.FeatureCollection(Metrics).aggregate_array("TNR"));
```

```
var MeanThresh = ee.Number(ee.FeatureCollection(Metrics).aggregate_array("cutoff").reduce(ee.Reducer.mean()));
print('Mean threshold:', MeanThresh);
```

```
Number of presence and pseudo... JSON
▼ [[49,49],[75,73],[190,119],[... JSON
  ▶ 0: [49,49]
  ▶ 1: [75,73]
  ▶ 2: [190,119]
  ▶ 3: [182,139]
  ▶ 4: [69,69]
```

```
AUC-ROC: JSON
▼List (5 elements) JSON
  0: 0.9403508771929826
  1: 0.9640777495284178
  2: 0.929691368212576
  3: 0.8446691176470589
  4: 0.9077457345613772
```

```
Mean AUC-ROC JSON
0.9173069694284826
```

```
AUC-PR: JSON
▼List (5 elements) JSON
  0: 0.7904449098307224
  1: 0.8010769754187687
  2: 0.8324427108146504
  3: 0.8483621840917326
  4: 0.8416996331824128
```

```
Mean AUC-PR JSON
0.8228052826676573
```

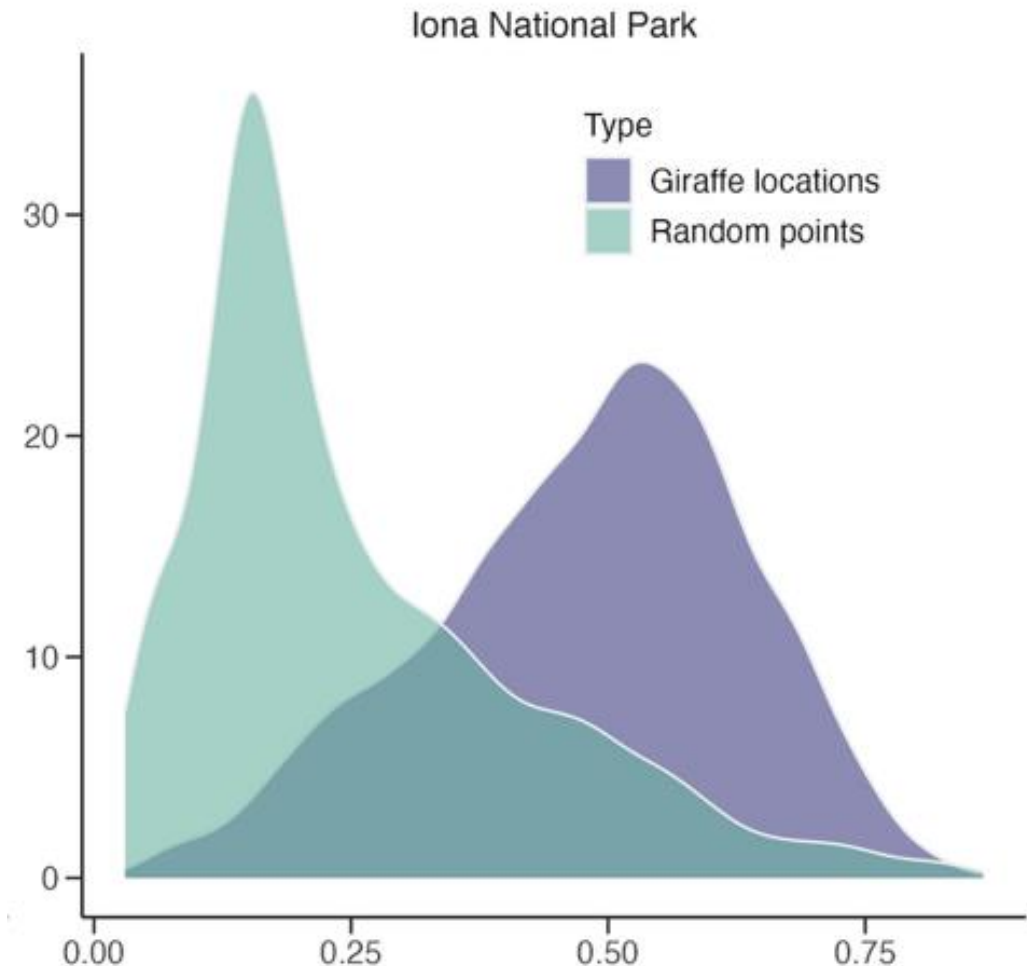
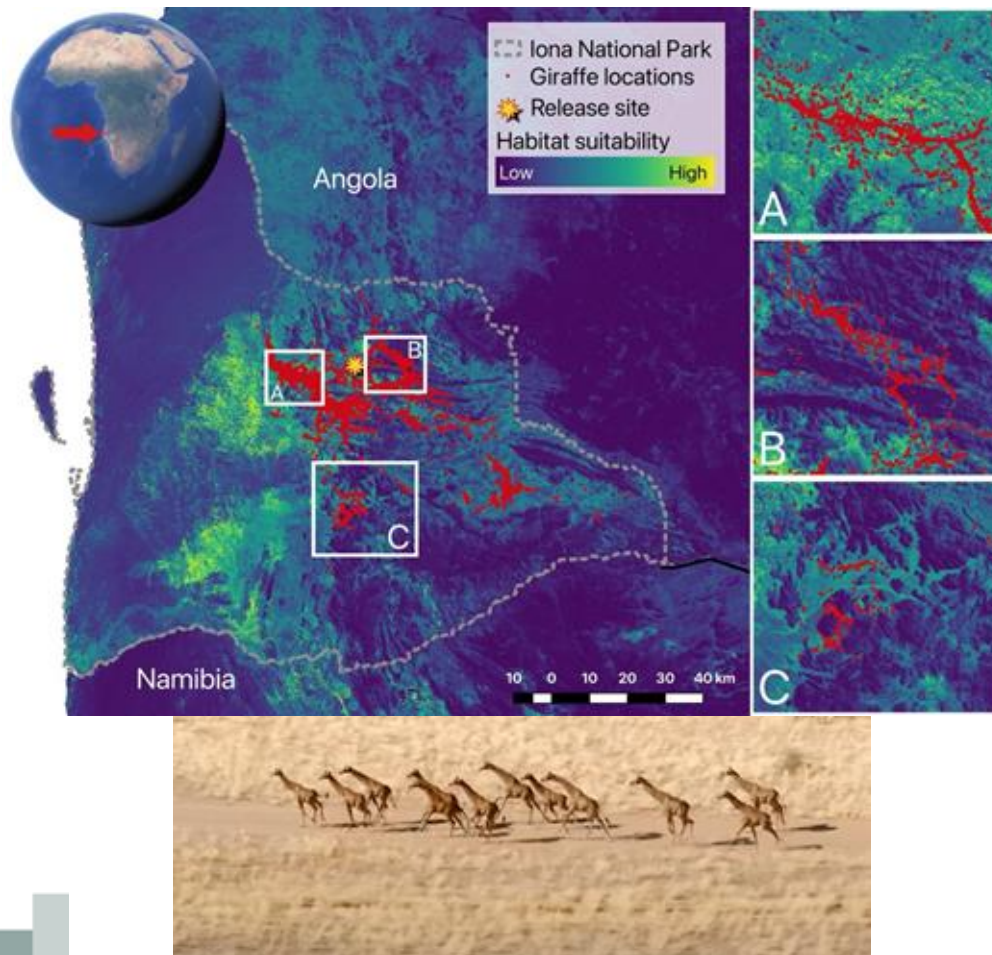
```
Sensitivity: JSON
▼List (5 elements) JSON
  0: 0.8043478260869565
  1: 0.7464788732394366
  2: 0.9320987654320988
  3: 0.9444444444444444
  4: 0.875
```

```
Specificity: JSON
▼List (5 elements) JSON
  0: 0.89
  1: 0.9343065693430657
  2: 0.7671232876712328
  3: 0.7058823529411765
  4: 0.8986486486486487
```

```
Mean threshold: JSON
0.4583333333333333
```


Importance of Independent Validation Data

It is often critical to quantify the generality of a model (i.e., capacity of the model to predict in a different region and/or timeframe from the training data).



Importance of Independent Validation Data

- **Prevent overfitting:** Ensure the model is not 'memorizing' the training data but failing to predict at new locations.
- **Ensure transferability:** Proves the reliability of your model to predict habitat suitability across different geographic areas and time periods.
- **Assess true accuracy:** Validating models with the same data used for training (even when using cross-validation) can give the false impression of high performance.

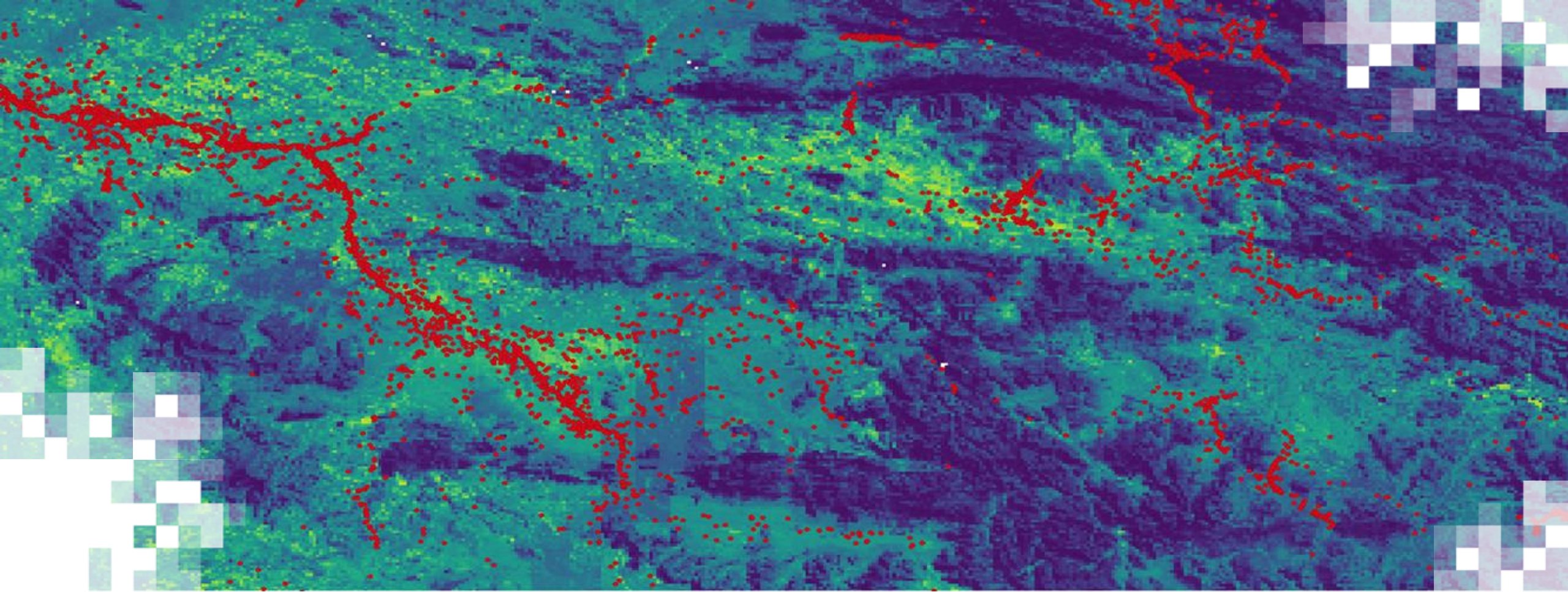


Exporting Model Outputs: “Batch Mode”

```
////////////////////////////////////  
// Section 9 – Export outputs  
////////////////////////////////////  
  
// Export final model predictions to drive  
  
// Averaged habitat suitability  
Export.image.toDrive({  
  image: ModelAverage, //Object to export  
  description: 'HSI', //Name of the file  
  scale: GrainSize, //Spatial resolution of the exported raster  
  maxPixels: 1e10,  
  region: AOI //Area of interest  
});  
  
// Export final binary model based on a majority vote  
Export.image.toDrive({  
  image: DistributionMap, //Object to export  
  description: 'PotentialDistribution', //Name of the file  
  scale: GrainSize, //Spatial resolution of the exported raster  
  maxPixels: 1e10,  
  region: AOI //Area of interest  
});  
  
// Export final binary model based on the threshold that maximises  
// the sum of specificity and sensitivity  
Export.image.toDrive({  
  image: DistributionMap2.unmask(-9999),  
  description: 'PotentialDistributionThreshold',  
  scale: GrainSize,  
  maxPixels: 1e10,  
  region: AOI  
});
```

```
// Export Accuracy Assessment Metrics  
  
Export.table.toDrive({  
  collection: ee.FeatureCollection(AUCROCs  
    .map(function(element){  
      return ee.Feature(null,{AUCROC:element}))),  
  description: 'AUCROC',  
  fileFormat: 'CSV',  
});  
  
Export.table.toDrive({  
  collection: ee.FeatureCollection(AUCPRs  
    .map(function(element){  
      return ee.Feature(null,{AUCPR:element}))),  
  description: 'AUCPR',  
  fileFormat: 'CSV',  
});  
  
Export.table.toDrive({  
  collection: ee.FeatureCollection(Metrics),  
  description: 'Metrics',  
  fileFormat: 'CSV',  
});
```





Modifying the Workflow to Get Variable Importance

Extracting Variable Importance

- Variable importance quantifies how effectively each environmental layer was able to sort presence points away from the absence points.
- These scores are a relative ranking meant to be compared against each other **within that specific model run** to see which predictors had the most influence.

```
// Variable importance
var variable_importance = ClassifierPr.explain().get('importance');
print("Importance Scores:", variable_importance);
```

Trained Classifier

Inspector Console Tasks

```
Importance Scores: JSON
▼ Object (8 properties) JSON
  NDVI: 18.94709770095551
  bio04: 3.4401175825680683
  bio05: 55.99599215661031
  bio06: 55.60322482033455
  bio12: 14.75910536688241
  elevation: 64.68974648600488
  gHM: 6.2875524769013325
  slope: 4.24039679675412
```



Extracting Variable Importance within a K-fold Loop

[Rest of SDM Function Above]

```
// Variable importance
var variable_importance = ee.Feature(null, ee.Dictionary(ClassifierPr.explain()).get('importance'));

return ee.List([ClassifiedImgPr, ClassifiedImgBin, trainingPartition, testingPartition, variable_importance]);
}

// While the runif function can be used to generate random seeds, we map the SDM function over fixed random numbers
var results = ee.List([618,143,421,554,213]).map(SDM);

// Extract results from list
var results = results.flatten();

//////////
// Variable importance

var VarImportance = ee.List.sequence(4,ee.Number(numiter).multiply(5).subtract(1),5).map(function(x){
  return results.get(x)});
var Var_Imp = ee.FeatureCollection(VarImportance);
print(Var_Imp);

var Variable_Imp = Var_Imp.reduceColumns({
  reducer: ee.Reducer.mean().repeat(ee.List(bands).length()),
  selectors: bands
});

print('Variable importance', Variable_Imp);
//[ 'bio04', 'bio05', 'bio06', 'bio12', 'elevation', 'slope', 'NDVI', 'gHM' ];
```



Variable Importance Interpretation

- **Methodological Decisions Affect the Ranking:** For example, if you expand your study area to a continental scale, regional climate variables will look massively important. If you clip that exact same model down to a single national park or watershed, climate becomes relatively uniform across the points, and localized variables (like slope, aspect, or canopy structure) will be at the top of the importance ranking.

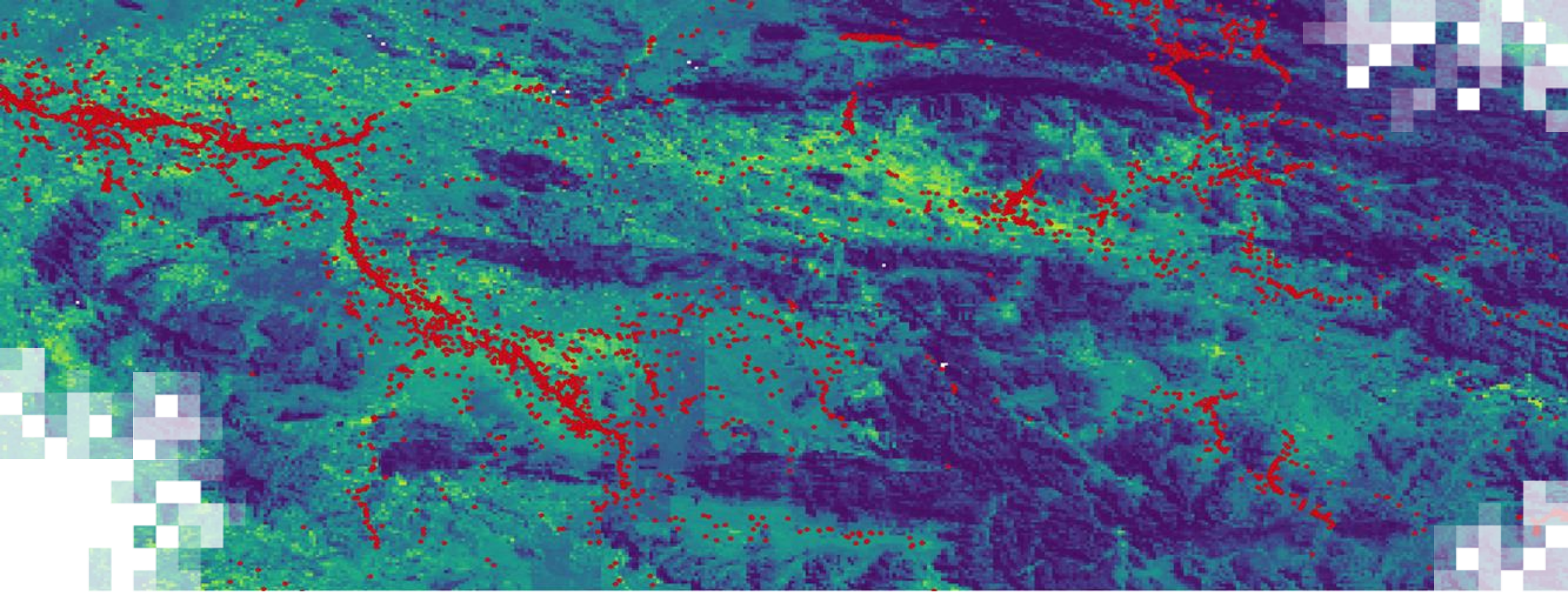


"Across this specific study area, and given our specific presence-absence dataset, precipitation was the most effective tool for distinguishing presence locations from absence locations."



"Precipitation is a more vital niche requirement for this species than soil type."





Additional Considerations

Model Evaluation Strategy

The Illusion of Predictive Power

Ploton et al. demonstrated that a standard random cross-validation showed an $R^2 > 0.50$, while spatial cross-validation revealed virtually null predictive power.

The Illusion of Failure

Wadoux et al., 2021 argued that spatial CV punishes the model for poor extrapolation rather than measuring how good the map is. It also results in information loss by fitting the model without fully representative data.

<https://doi.org/10.1038/s41467-020-18321-y>

OPEN

Spatial validation reveals poor predictive performance of large-scale ecological mapping models

Pierre Ploton¹, Frédéric Mortier^{2,3}, Maxime Réjou-Méchain¹, Nicolas Barbier¹, Nicolas Picard⁴, Vivien Rossi⁵, Carsten Dormann⁶, Guillaume Cornu^{2,3}, Gaëlle Viennois¹, Nicolas Bayol⁷, Alexei Lyapustin⁸, Sylvie Gourlet-Fleury^{2,3} & Raphaël Pélissier¹



Ecological Modelling

Volume 457, 1 October 2021, 109692



Short communication

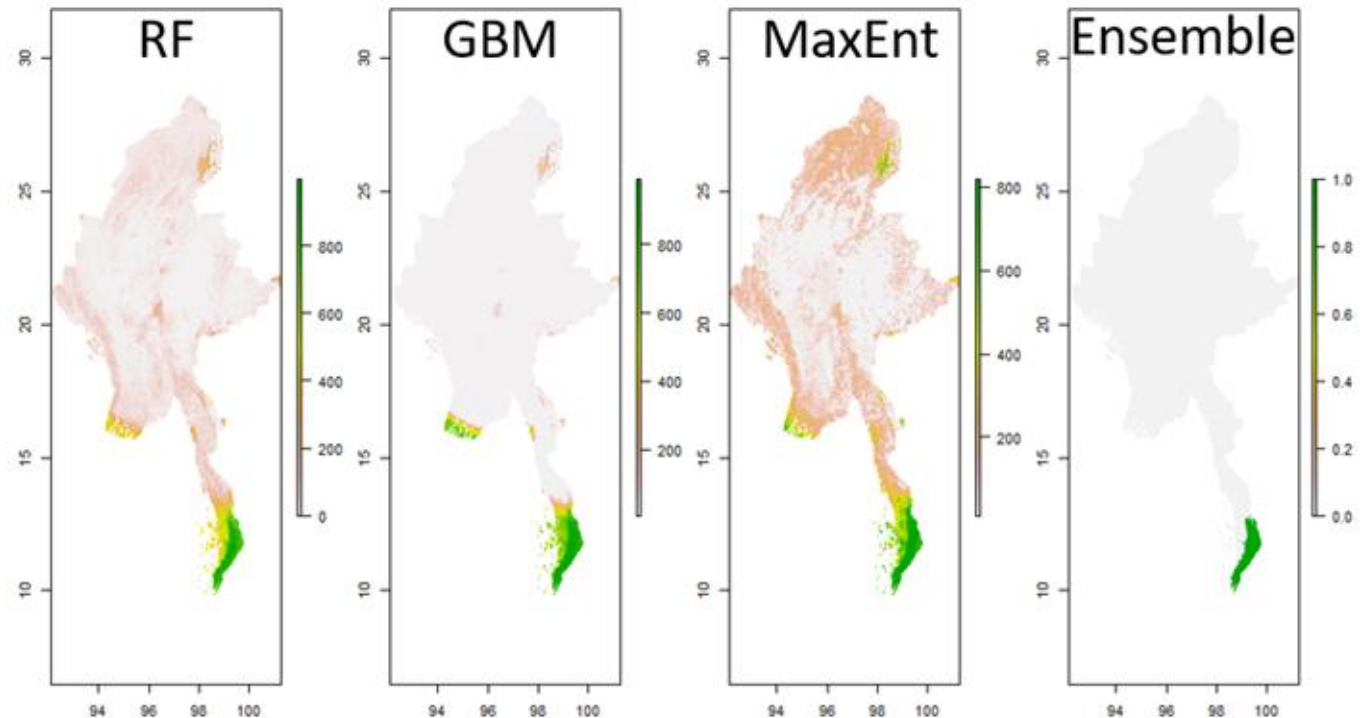
Spatial cross-validation is not the right way to evaluate map accuracy

Alexandre M.J.-C. Wadoux^a, Gerard B.M. Heuvelink^b, Sytze de Bruin^c, Dick J. Brus^d



Ensembling SDMs

- Can smooth over-prediction and under-prediction of individual models (e.g., Helmeted Hornbill example).
- However, it inherently averages out peak performance (best model averaged with worse models) and rarely beat the absolute "best" single model for a specific landscape.



Pitfalls & Best Practices: Part 1

Garbage In, Garbage Out: Avoid relying on unvetted, heavily clustered crowd-sourced presence data, or blindly throwing environmental layers into the model.

Ecological Predictor Curation: Select environmental layers based on known biological limiting factors rather than data convenience, and drop highly collinear variables.

Intentional Background Selection:

- If you have true absence data, use it!
- Absence $\neq$ Pseudo-absence $\neq$ Background
- Define your pseudo-absences strategically (e.g., using areas potentially reachable)

Objective-Driven Validation: Match your validation strategy to your goal; e.g., use random sampling to verify local map accuracy, but use spatial cross-validation if you are testing the model's regional transferability (e.g., the giraffe example).



Pitfalls & Best Practices: Part 2

Ensemble-Based Prediction: Avoid relying on a single "winning" cross-validation fold for your final outputs and average the continuous probability maps across all your folds to smooth out localized mathematical noise.

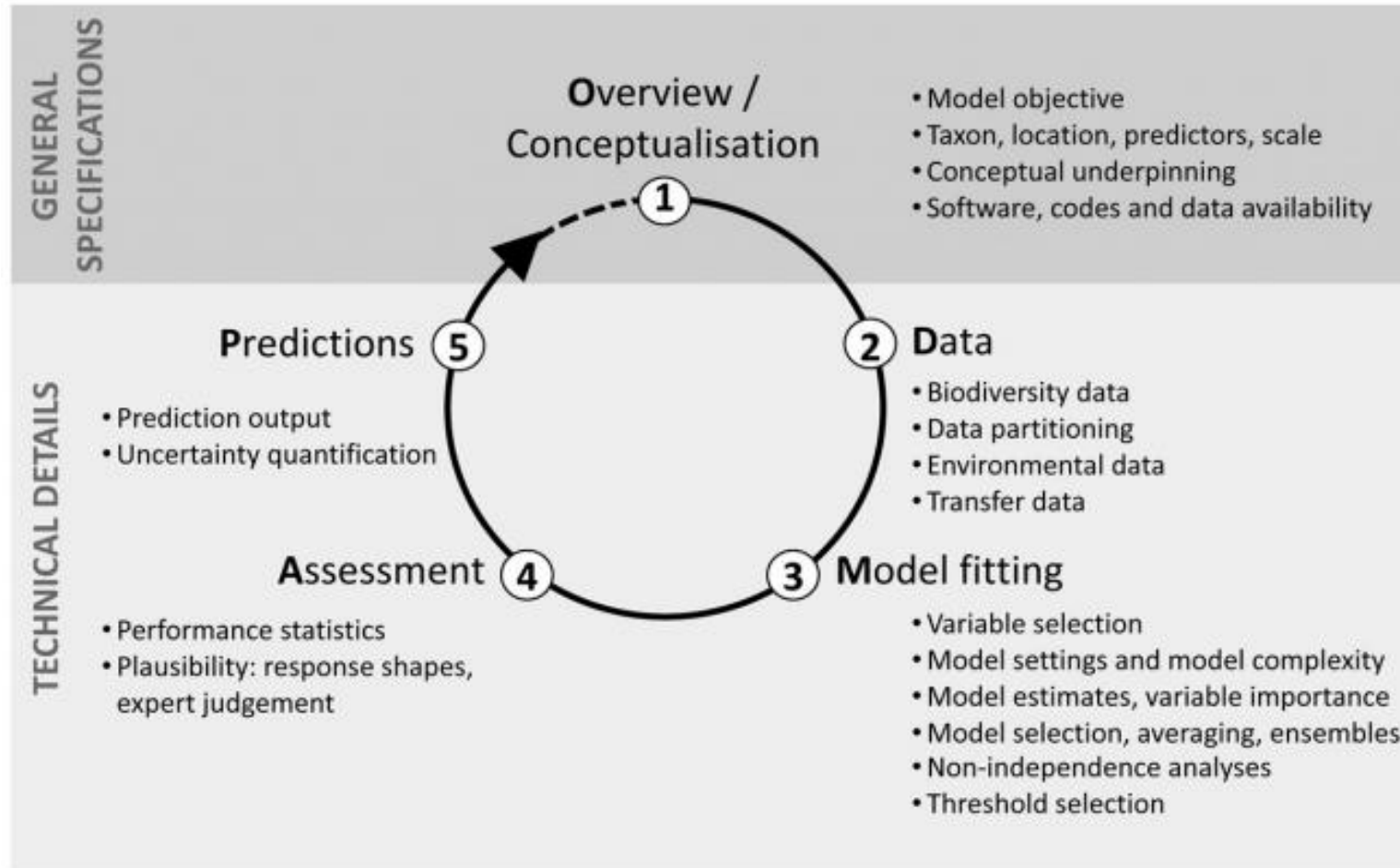
Model Extrapolation Risks: Many algorithms cannot extrapolate outside their training range. You can run a MESS (Multivariate Environmental Similarity Surfaces) analysis when projecting onto new geographic areas or future climates to flag where predictions may be unreliable.

Continuous Probability Over Binary Thresholds: Prioritize analyzing and reporting the raw, continuous habitat suitability gradients rather than over-relying on arbitrary binary presence/absence thresholds that discard meaningful ecological detail.

Suitability $\neq$ Presence



The ODMAP



ECOGRAPHY

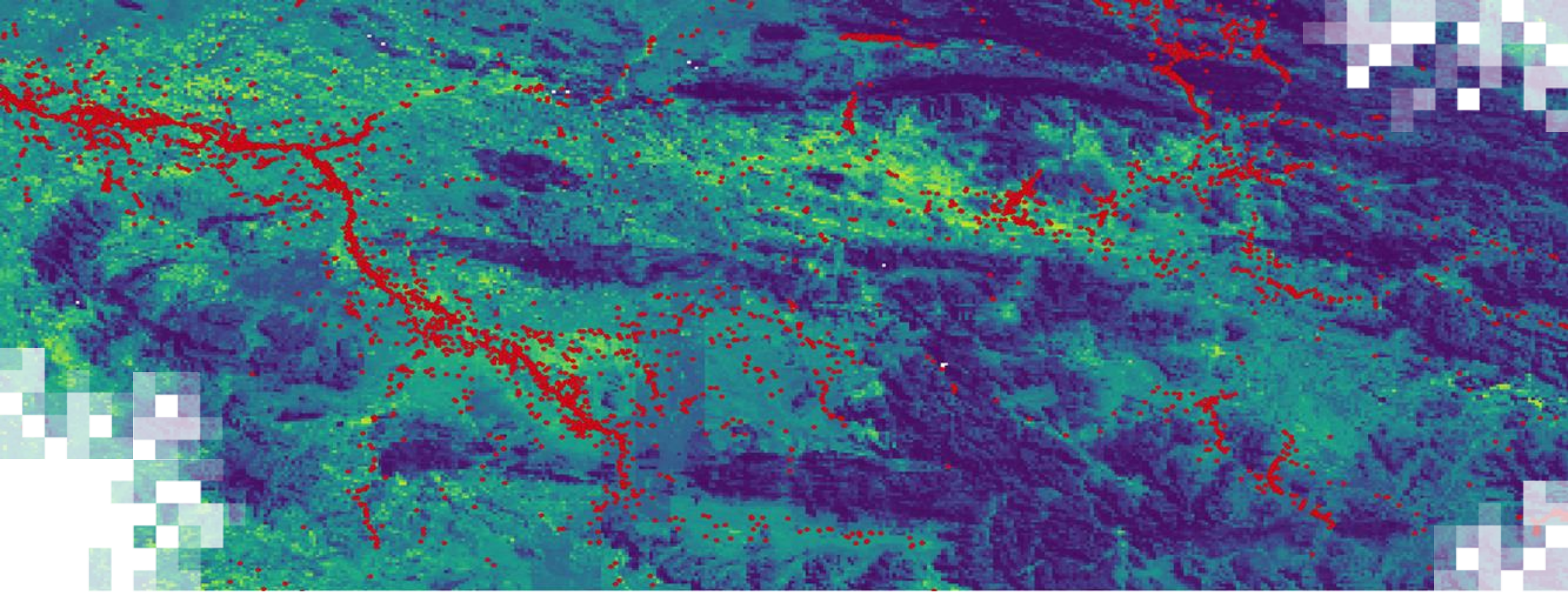
Review and synthesis

A standard protocol for reporting species distribution models

Damaris Zurell, Janet Franklin, Christian König, Phil J. Bouchet, Carsten F. Dormann, Jane Elith, Guillermo Fandos, Xiao Feng, Gurszteta Guillera-Arroita, Antoine Guisan, José J. Lahoz-Mondot, Pedro J. Leitão, Daniel S. Park, A. Townsend Peterson, Giovanni Rapacciuolo, Dirk R. Schmatz, Boris Schröder, Josep M. Serra-Díaz, Wilfried Thuiller, Katherine L. Yates, Niklaus E. Zimmermann and Cory Merow

EDITOR'S
CHOICE





Summary

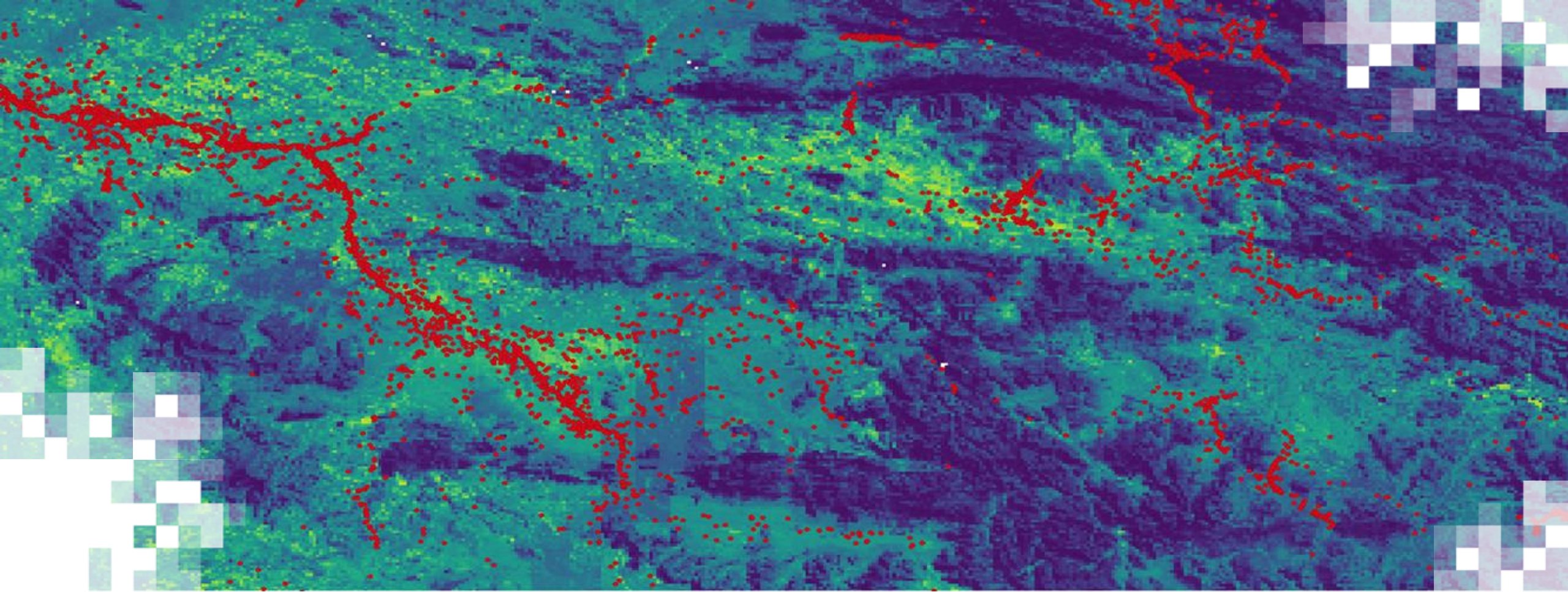
Resources

- Original [manuscript](#)



- The Google Earth Engine code and data used in this workshop and manuscripts are freely available at this [Google Earth Engine repository](#).





Species Distribution Modeling with Google Earth Engine

Part 2: Building, Evaluating, and Interpreting an SDM on GEE

Summary

Part 2 Training Summary

- Demonstrated end-to-end steps to build machine learning models within Google Earth Engine.
- Reviewed initial steps for uploading species data and essential preprocessing steps.
- Covered spatial thinning techniques for presence data and methods to define modeling Areas of Interest (AOIs).
- Evaluated criteria for choosing environmental predictors and accessed spatial data directly from the GEE catalog.
- Analyzed the concepts of true presence/absence data and techniques for generating pseudo-absence points.
- Contrasted methods for quantifying model accuracy (interpolation) versus model generality (extrapolation).
- Explored how to identify and rank the environmental layers most influential in predicting species distribution.
- Emphasized aligning model evaluation strategies directly with overarching project objectives.
- Pitfalls & Best Practices



Homework and Certificates

- **Homework:**
 - One homework assignment
 - Opens on 07/14/2026
 - Access from the [training webpage](#)
 - Answers must be submitted via Google Forms
 - **Due by 07/28/2026**
- **Certificate of Completion:**
 - Attend two live webinars (attendance is recorded automatically)
 - Complete the homework assignment by the deadline
 - You will receive a certificate via email approximately two months after completion of the course.



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 - sativa.cruz@nasa.gov

- [ARSET Website](#)
- [ARSET YouTube](#)

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- Participation is optional, and all responses are confidential.
- **Survey data are crucial to helping us understand how to better meet your needs. We want to help you use Earth observation data more effectively.**
- We read every survey comment – so please share your thoughts!

*The survey will come from noreply@alchemer.com. This is not spam.





Thank You!

