TECHNOLOGICAL SOLUTIONS TO BIODIVERSITY MONITORING:
A DIGITAL BIODIVERSITY PLATFORM

AUTHORS & CONTRIBUTORS

Angela Brennan (Lead Scientist, Conservation Science Partners), Aoife Toomey (Digital Science Lead, bp), Maarten Kuijper (Biodiversity Subject Matter Expert, bp), Matthias Wagner (Remote Sensing Expert, bp), Kais Maayah (Senior Data & Applied Scientist, Microsoft), Marek Ichas (Senior Technical Program Manager, Microsoft), Joanna Mainguy (Director EMEA, Energy & Resources Industry, Microsoft)

SUGGESTED CITATION

1   CONTENTS

2 EXECUTIVE SUMMARY

In response to the global decline in biodiversity, bp, Microsoft and Conservation Science Partners (CSP) have partnered to develop tools to help address the challenge of monitoring biodiversity and efforts to restore it. Guided by the adage "you cannot manage what you don't measure," our collaboration aims to develop innovative solutions to better measure, monitor, and manage biodiversity.

Monitoring biodiversity is critical to understanding impacts, informing conservation actions, and tracking progress towards conservation goals. Recently, guidelines have been provided by the Task Force for Nature-based Financial Disclosures (TNFD), International Union for Conservation of Nature (IUCN), and others for assessing impacts on biodiversity and the risks from biodiversity loss. However, there is limited specificity on what and how to measure and monitor biodiversity and thus a clear need for scientifically informed and technology-enabled solutions. Therefore, we formed a partnership to do just that: to develop a biodiversity monitoring solution that integrates ecological models and theory with data science.

Our solution aimed to combine advanced machine learning methods with Microsoft's Planetary Computer and publicly available species observation data (from the Global Biodiversity Information Facility [GBIF]) to develop an important conservation tool – called a habitat suitability model (HSM) – frequently used by ecologists and conservation practitioners to map species distributions and track key biodiversity metrics. The HSM framework was developed within a digital pipeline for continuous biodiversity data integration and adaptive model development, making the HSM a rapid, scalable, and automated tool.

The tool and technologies were piloted at bp's Cherry Point Refinery in Washington State, because it is an active site with ongoing wetland restoration and forest management. HSMs were developed for 52 plant and animal species for each year from 2014 through 2022. Preliminary findings suggest increasing species richness in restored sites and other natural areas, and little to no change in species richness in the more industrialized areas. While these findings may indicate improvements in habitat, further study is required for validation and ongoing assessment of restoration impacts.

HSMs have become an increasingly important tool for biodiversity monitoring, but they have some known limitations mainly related to the inherent biases associated with opportunistically collected data like the GBIF data that we used. Integrating systematically collected site-level field data will be an important way to account for such biases in the future and is being explored as a next step. Recent advances in technology also give us a unique capability to record and track species and environmental conditions at temporal and spatial scales not seen before, and as the cost of these technologies decrease, there is an opportunity to deploy them at scale. Integration of these data with HSMs can then generate more accurate inference, at finer resolutions and broader extents, moving us towards temporally and spatially continuous monitoring of biodiversity.

This project brought our companies together to develop innovative solutions to a globally important sustainability problem. The HSMs and digital biodiversity platform developed here provide a foundation for moving forward. Combining this modeling tool with field data from sites could provide an opportunity to spot problems before they arise and monitor progress towards biodiversity restoration targets.

3   INTRODUCTION

3.1   THE BIODIVERSITY CRISIS

Our world is facing a biodiversity crisis brought on by multiple human drivers of environmental change. Recent analyses show that observed species' populations have declined on average by 69% since 1970 [1] and suggest that a million plant and animal species will face extinction in the coming decades [2]. This represents an unprecedented rate of loss – tens to hundreds of times higher than the average over the last 10 million years [2] – and it affects all areas of the globe, particularly areas of Latin America and Africa and our freshwater, grassland, and forest ecosystems [1,2].

The primary driver of these losses is rapid land and sea use change [2]. More than 70% of the world's land area has been significantly altered for the purposes of agriculture, development, and resource extraction, with 85% of wetlands and roughly 32% of forests having been destroyed; and 66% of the world's oceans have been experiencing negative anthropogenic impacts [2]. While habitat destruction is globally widespread, many of its effects often start locally leading to population declines and extirpations that cumulatively can trigger broader scale extinctions [3]. These declines, extirpations, and extinctions can then affect whole ecosystems and the natural processes they provide and that humans depend on.

The inextricable links between biodiversity and the natural processes that underpin human well-being means that biodiversity loss is a threat not only to precious species and genetic diversity, but to humanity's food supply, health, and security [4]. A recent World Economic Forum survey identified biodiversity loss as "one of the fastest deteriorating global risks over the next decade" [5], ranking it among the top global risks to human society next to climate action failure and extreme weather [6]. Among the most important reasons biodiversity loss is a threat to human society is via its effects on climate change. The destruction of biodiversity in the form of key carbon-storing ecosystems, for example, like peatlands, mangrove, and tropical forests, have been shown to contribute roughly 20% of the total human CO_2 emissions [7]. Moreover, the world's land and ocean ecosystems are key to absorbing about 56% per year of the CO_2 emitted by humans [7].

While the full extent of the risks of biodiversity loss are uncertain, the ensuing environmental consequences may be disproportionately larger than the loss of a single species or population. Ecosystem complexities and non-linear responses of biodiversity to environmental change correspond to potential tipping points, where ecosystems may not be capable of maintaining equilibrium beyond a certain impact-threshold [8]. When ecosystems are pushed past these thresholds, there is a risk of large, abrupt, and potentially irreversible ecosystem collapse [9]. Therefore, conserving or restoring biodiversity is critical to reducing global risks to human society and ensuring the resiliency of Earth's life support systems.

3.2   THE NEED FOR TRANSFORMATIVE CHANGE

The major human drivers of biodiversity loss stem from globally outpaced production and consumption patterns [2,10]. Given the severity of the risks of continuing with business as usual, it is clear that transformative change is needed to end the crisis. [2,4,11,12] Indeed, a "nature positive" movement has emerged that aims for a net positive effect on nature by 2030 and a resilient planet by 2050 [1,13]. This

movement goes well beyond previous goals of limiting or halting biodiversity loss to focus on restoring and enhancing biodiversity and ecosystems for the benefit of people and nature.

G7 leaders have called for global system-wide change in order to ensure a nature positive world [14]. The Taskforce on Nature-related Financial Disclosures (TNFD) is supporting and recommending shifts in global financial flows toward nature-positive outcomes [15]. And, as the driving force in global conservation policy, the new Kunming-Montreal Global Biodiversity Framework (GBF) outlines nature positive global goals that aim to "catalyze, enable and galvanize urgent and transformative action by Governments, subnational and local governments, and with the involvement of all of society to halt and reverse biodiversity loss" [16]. However, while the 196 signatory nations to the GBF are now working to implement national strategies for achieving these goals, collective action is needed across governments, the private and public sectors, and academic and civil society to truly bend the curve on biodiversity.

The world now faces the challenge of achieving this collective biodiversity ambition, and key to this challenge is the lack of accessible tools for measuring and monitoring biodiversity, and the data and assessment pipelines needed for efficient decision making. We see three critical constraints affecting efficient and effective tracking of progress towards conservation targets, including: (1) limited data availability on the current state of biodiversity; (2) limited understanding of what biodiversity benefits can arise from certain operations and conservation interventions; and (3) limited processes for measuring and monitoring biodiversity benefits at scale.

3.3   THE PARTNERSHIP AND GOAL

bp recognizes the importance of taking action on biodiversity, and thus sought out a partnership with Microsoft and Conservation Science Partners (CSP) that would enable the development of ecologically informed, technological solutions for tracking biodiversity. Addressing this challenge together will not only help bp with site-level data on biodiversity and conservation impact assessment, but also help guide the broader regulatory and reporting landscape towards nature positive outcomes.

bp also recognizes that addressing the challenge of global biodiversity decline requires transformative change. In 2020 bp updated its biodiversity position, setting out aims to have a net positive impact on biodiversity in new projects and to enhance biodiversity around existing major operating sites. To achieve this, the aim is to restore, maintain and enhance biodiversity, with greater effort on quantifying any change and progress. Because this aim requires bp to collect more data than ever before, it will require technological solutions that can handle the processing and analysis of large volumes of data to extract actionable information and enable strategic decision making.

Microsoft was the logical company to partner with because of their own biodiversity goals. Microsoft aims to leverage technological advancements to reduce biodiversity loss and, by working with customers and clients, unlock new scientific and commercial opportunities in ecosystem monitoring. The bp-Microsoft partnership ultimately aims to combine bp's energy and geospatial capabilities with Microsoft's data and digital technologies to address biodiversity challenges, and, importantly, to accelerate the development and scaling of these solutions.

To fully round out the team on this effort, Conservation Science Partners (CSP) joined as the third member, bringing scientific expertise in deploying ecological models at scale and in using rigorous science to inform conservation actions. CSP works across sectors to provide research and science

capacity, focusing on efforts that can inform biodiversity conservation and conservation policy. CSP's Analytics Lab logically fit in with bp and Microsoft's goals as they aim for projects that have a potential for impact and/or innovation at the intersection of ecology and data science.

Collectively, our goal was to integrate scientifically supported ecological models and theory with advances in data science to develop technological biodiversity monitoring solutions. To do this, we leveraged advanced machine learning methods with Microsoft's Planetary Computer – a cloud platform of global environmental data – and publicly available species observation data from the Global Biodiversity Information Facility (GBIF) to develop habitat suitability models (HSMs) for a range of plant and animal species. HSMs, otherwise referred to as species distribution models, are scientifically supported, quantitative approaches to mapping potential species distributions [17–24] and understanding what factors affect the probability of species occurrence [25]. They can be readily refined or updated with new data sources and used to evaluate and track biodiversity over space and time [17].

This project has two main objectives: (1) develop HSMs as the basis for monitoring changes to habitat suitability and biodiversity, evaluating the effects of conservation and management interventions, and testing practical and ecological hypotheses that can be used to inform the broader application of these tools; and (2) develop a digital pipeline for continuous biodiversity data integration and adaptive HSM development at scale, enabling rapid and automated biodiversity assessments.

As an initial step toward deploying HSMs at scale, a 'feasibility study' was piloted at bp's Cherry Point Refinery, located in USA's Pacific Northwest (Fig. 1), where many restoration and management interventions have been and are being implemented to enhance biodiversity.
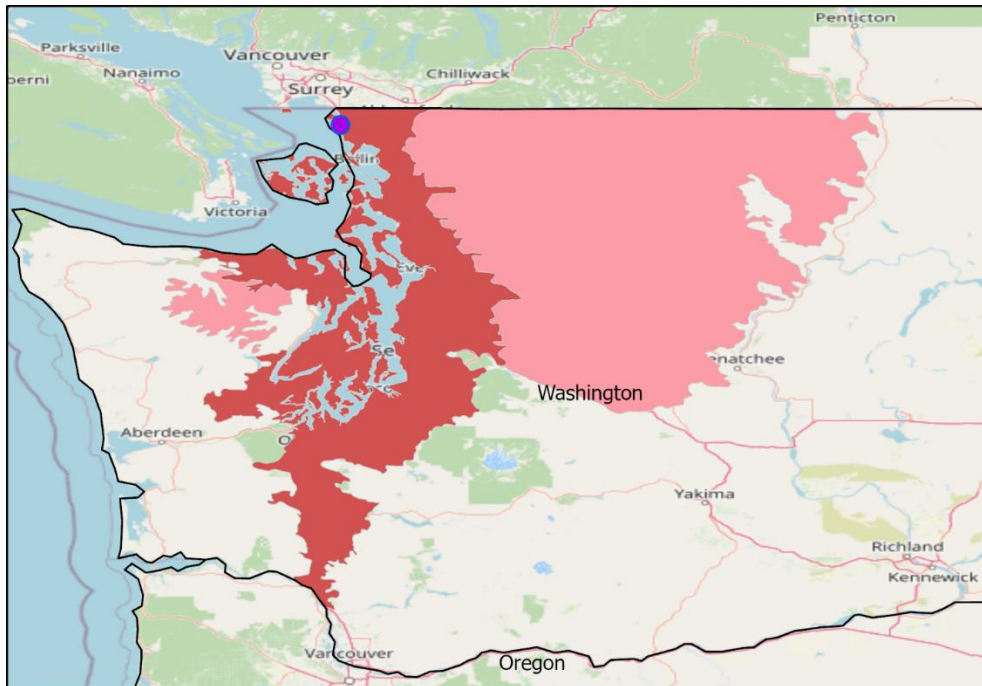
Figure 1. Feasibility study focusing on the Cherry Point Refinery (purple circle) in Washington, USA. Species occurrence and environmental data within the surrounding Puget Lowlands (dark pink) and North Cascades (light pink) ecoregions were used to train the habitat suitability models.

4 HABITAT SUITABILITY MODELS

Habitat suitability models (HSMs) have become an increasingly important tool for evaluating a variety of applied and fundamental questions in ecology, conservation biology, natural resource management, and climate change impact research [17,25–31]. These models rely on empirical relationships between species' occurrence data and environmental variables to predict probabilities of occurrence and ultimately infer their broader distribution. However, environmental conditions are one of several factors affecting a species' true distribution (otherwise referred to as its realized environmental niche) across space and time, which can also include the dispersal ability of a species and complex biotic interactions (e.g., competition and predation) [31]. Consequently, it is critical to evaluate HSM predictions against independent species occurrence data to understand where models can accurately approximate a species' true distribution [17,26,27]. Therefore, we sought to generate HSMs for multiple species of interest, initiate a process for evaluating model accuracy, and develop a pipeline for future, rigorous evaluation via model training and testing with ongoing field data collection.

The output of an HSM is a map with values ranging from 0 to 1, depicting the probability of species occurrence (or, depending on the method, relative likelihood of species occurrence [26]). When HSMs are developed for many species, the spatial predictions of suitable habitat can be aggregated into indices of biodiversity that can be used for evaluating the benefits or impacts of management actions for biodiversity enhancement [32]. Two of these metrics are described in *Measuring Biodiversity* below.

We developed HSMs described in the next sections to evaluate the feasibility of a digital platform for tracking changes in biodiversity (see Fig. 2 for HSM workflow).
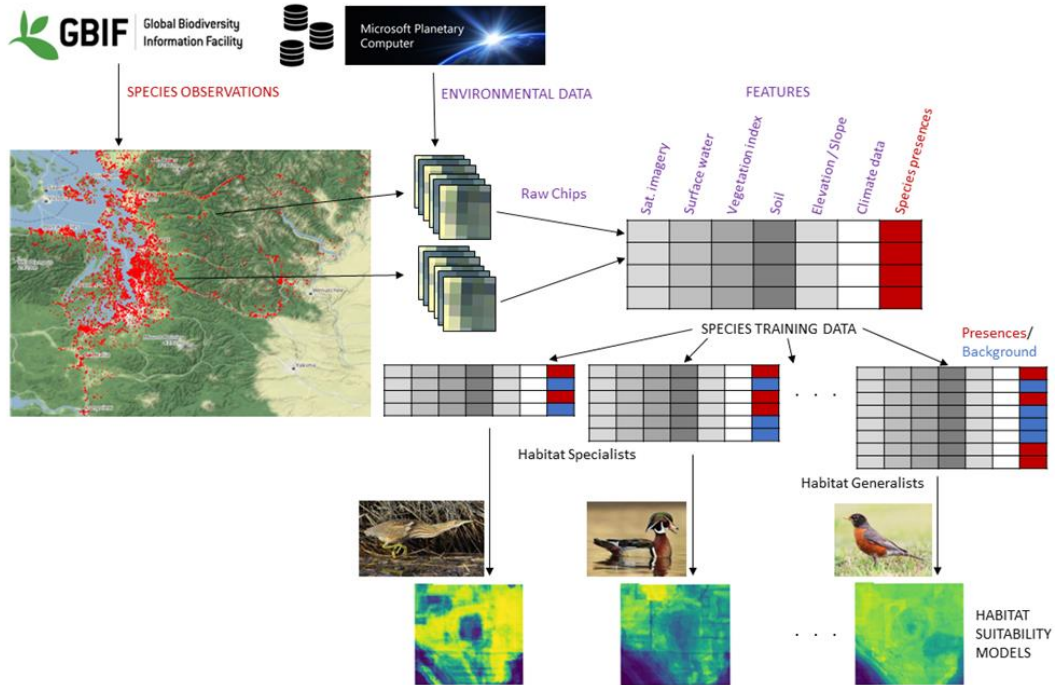

Figure 2. Habitat suitability modeling workflow, with the sequence of steps following the arrows from top left to top right, to bottom right. The amount of species training data varies in this figure, as it depends on the number of presences recorded in the Global Biodiversity Information Facility (GBIF). For example, the American bittern (*Botaurus lentiginosus*; picture on left) had fewer observations than the wood duck (*Aix sponsa*; picture in center) and the American robin (*Turdus migratorius*; picture on right). The American bittern and wood duck are considered habitat specialists (i.e., species that thrive in a narrow set of environmental conditions) and the American Robin is considered a generalist (i.e., species that can occur in a range of environments). Background samples (blue rows) represent the locations, and associated features, where species were not recorded. Background sampling methodology is described below.

4.1   Pilot Site: Cherry Point Refinery

The area of focus of the pilot study is located within the Terrell Creek watershed in the State of Washington, USA. Terrell Creek is bordered by emergent, scrub-shrub and forested wetland habitats. Land use in the wider area includes industrial (e.g., bp Cherry Point Refinery), agricultural, and forested areas. In addition to impacts from the refinery itself, the area owned and managed by bp adjacent to Terrell Creek has been impacted by historical and ongoing agricultural use (currently hay production). Over the past 20 years, bp has embarked on several different wetland mitigation projects in the form of wetland creation, wetland rehabilitation, wetland enhancement, and upland enhancement projects, with the latest project constructed in 2022 measuring 102 acres. The total area of wetland restoration area measures approximately 479 acres. Immediately south of the wetland restoration areas lies the refinery complex.

bp is interested in monitoring the progress of wetland restoration and benefits to biodiversity at these sites over time and in comparing biodiversity metrics here with that of other wetlands in the area.

4.2   Species Occurrence Data

We used species occurrence data from the Global Biodiversity Information Facility (GBIF) [33,34], as this is an international network of publicly available biodiversity data (e.g., iNaturalist, eBird) with millions of recorded species occurrences attributed with a data source, location and time recorded, and taxonomic classification. We compiled all GBIF observations that occurred from 2014-2022 within the Puget Lowlands and North Cascades ecoregions surrounding the Cherry Point Refinery (Fig. 1). We then subset these data to include only those observations identified to species and only those species with at least 500 observations to ensure there was sufficient data for training and testing. From this list we then identified which species were habitat generalists (i.e., species that can live in many different environments) and habitat specialists (i.e., species that thrive only in a narrow range of environmental conditions). Given the focus on wetland restoration at the Cherry Point Refinery, we sought to include species with a preference for wetlands at any point in their life cycle (e.g., American bittern); however, we also included several forest specialists (e.g., ruffed grouse) given recent forest management also occurring within and around the study area. Our goal with generating HSMs for a wide range of species was to measure biodiversity and better understand how taxonomic group and habitat specialization relates to model performance.

4.3   Environmental Variables

We used publicly available environmental datasets with global coverage to allow tracking of changes in habitat conditions over time and deployment of our pipeline across other bp sites. We leveraged the large data catalog available on Microsoft's Planetary Computer to make use of five different types of input datasets that are described below. These types, their corresponding layers, and how these layers were aggregated into model training features is outlined in Table A1 of Appendix A.

Landsat multispectral satellite imagery: We used 30-m resolution Landsat-8 Level-2 Surface Reflectance multispectral satellite imagery as this enables frequent revisiting of sites under consistent observation conditions. Bands in the visible and infrared portions of the electromagnetic spectrum capture abundant information on environmental conditions, including vegetation and soil, as well as urban structures and

agricultural activities. Although focusing on Landsat-8, the long historical catalog of the Landsat missions allows for a relatively easy extension to older records.

TerraClimate weather data: To capture climatic conditions, we used monthly aggregated TerraClimate weather records. This dataset enables us to do historical analysis potentially extending back several decades. The global coverage and gridded maps further allow for a more granular differentiation of habitats compared to spatially limited single-station measurements.

NASA elevation data: Altitude, terrain roughness, and aspect are critical drivers of species distributions. The global, high spatial resolution NASA digital elevation model (DEM) provides granularity to distinguish terrain attributes of habitats at 30-m resolution.

Surface water data: The presence of surface water in the form of rivers and lakes, as well as oceans, in the vicinity of a site is one of the most important factors in determining suitability of a habitat for many plant and animal species. While large water bodies are usually persistent over the course of multiple years, smaller, ephemeral water sources can disappear from one season or year to the next. To capture this, we opted for dynamically generated binary maps of surface water based on Landsat-8 multispectral satellite imagery (using the automated water extraction index [AWEIsh] thresholded at zero) instead of a static land cover map [35].

Multispectral indices: To further highlight certain aspects of environmental conditions, we made use of a selection of indices derived from Landsat-8 multispectral imagery, including the normalized difference vegetation index (NDVI), normalized difference water index (NDWI), and continuous AWEIsh as these are sensitive to vegetation health, plant water, and surface water.

4.4 MODELING APPROACH

We used a supervised binary classification model for each focal species. We first experimented with several types of regression and machine learning models on a subset of our focal species to examine modeling speed and accuracy before running models for all species. Based on these experiments, we landed on Microsoft's machine learning Light Gradient Boosting Model library (LightGBM) because it performed best and is known to be robust and well-suited for classification tasks that rely on input variables with vastly different scales and distributions. After our initial experimentation phase, we applied this gradient boosting algorithm to the remaining focal species.

The gold standard for HSMs is to train models on species presence and absence data collected following a scientifically guided, stratified random sampling design, as this greatly improves the discrimination between suitable (i.e., where a species is likely to be present) and unsuitable habitats (i.e., where a species is likely to be absent) and our ability to draw broader conclusions about a species distribution [17]. However, "true" data on species absences are often logistically and financially difficult to obtain across large study areas. In these cases, models can be trained with presence-only data augmented with background samples, which are in principle equivalent to "pseudo-absences" and thus meant to approximate environmental conditions where the species of interest was not present [17,36]. Then, similar to the presence-absence gold standard, environmental conditions at presences can be statistically compared to those at background sampling locations, to generate inference on the relative likelihood of

species occurrence (as opposed to actual probabilities of occurrence generated when using presence-absence data) [26]. Since GBIF species occurrence data is presence-only [37], we augment these observations with background samples using three approaches briefly explained below that differ in how they attempt to account for the bias in opportunistically collected data.

4.4.1 Background Sampling Methods

Bias layer: This approach builds off the "Factor Bias Out" method used in Maxent HSM modeling, which uses focal species presences to inform where background samples (i.e., pseudo-absence locations) will be drawn [38,39]. Here, each focal species' presences are viewed as being drawn from an unknown probability distribution over the geographic region of interest. We used Gaussian kernel density estimation to obtain the probability density distribution of focal species' GBIF observations. Background samples were then drawn from this estimated distribution such that they exhibit the same geographic bias as the species observations themselves. Key to this approach, is the ability to tune the estimated probability density distribution such that the background points are suitable for model training. For example, a loose fit to the focal species observations would result in background samples that are, on average, far from the species observations and may not enable model training that is sufficiently discriminative. On the other hand, background samples that are too close to the species observations are likely to falsely represent a pseudo-absence (i.e., when presences and pseudo-absence occur at the same location). Therefore, we optimized this geographic bias by tuning the bandwidth parameter of a Gaussian kernel.

Target-group: Following this method, background samples are selected at random from GBIF observations of similar species (i.e., the target group) to represent the same specimen collection or observation bias as the focal species [40,41]. This method also aims to select background points that are most likely to be absences, given collection/observation methods are generally similar for similar species. For example, birders are likely to record all bird species seen or heard (except perhaps for the very common birds) and therefore a bird species not recorded is likely to be absent. In our study, we considered the target group to be species that belong to the same taxonomic class as the focal species. We applied this method only to a subset of our focal species because initial tests suggested it was less accurate compared to the other two background sampling approaches.

Environmental clustering: For this final background sampling approach, we use K-means clustering to cluster all GBIF observations for focal species based on the environmental features. The background samples were then randomly drawn, in equal numbers across all clusters. This allows us to compare the focal species observations to background samples across the full range of environmental conditions in the region of interest.

4.4.2 Model Training and Evaluation

For each focal species, we randomly split the available GBIF observations into 85 % training/validation and 15 % testing data. Background samples for the test set were randomly drawn from all GBIF observations, excluding those of the corresponding focal species. We selected the best-performing hyper-parameter set for each species model based on 5-fold cross-validation on the training/validation set.

We used several machine learning evaluation metrics, including precision and recall (see description in Fig. 3), and F1 score to evaluate overall model performance. Precision measures how often our model

classifications of habitat were true habitat, whereas recall measures how often our models classified true habitat as suitable habitat. F1 score (scaled between 0 and 1) is defined as the harmonic mean of precision and recall, thus, combining the two into a single metric.
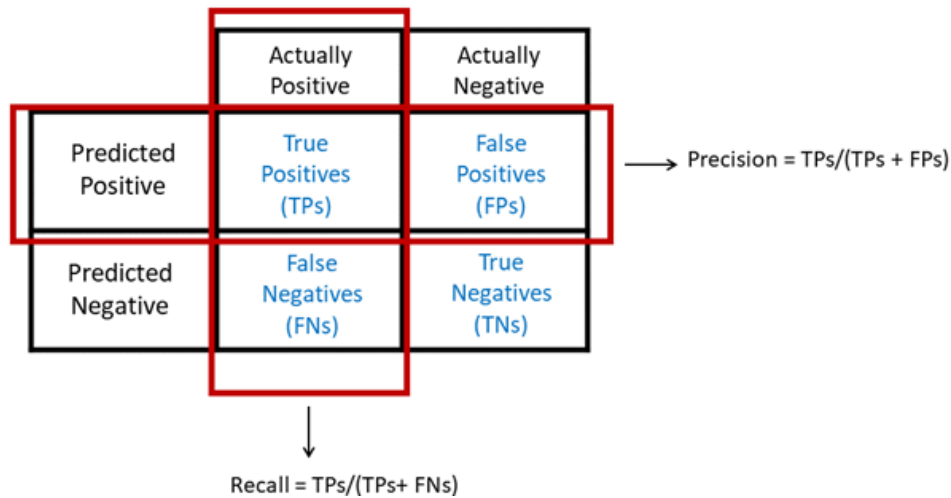

Figure 3. Confusion matrix, defining precision and recall. Precision can answer how often our classification of habitat were correct, and recall can answer how often we classified true habitat as habitat. The columns describe the true conditions (i.e., species habitat or not), and the rows describe the HSM-predicted conditions (i.e., suitable versus unsuitable habitat).

4.5 MEASURING BIODIVERSITY

We selected two metrics of biodiversity in this pilot study – estimated species richness and habitat intactness – because both can be obtained from HSMs and provide information about different aspects of biodiversity (described below). Both are also key metrics recommended to be used, either by themselves (species richness) or incorporated into other metrics (habitat intactness is a component of the Ecosystem Integrity Index [42]), by the International Union for Conservation of Nature (IUCN) [43], United Nations Environment Programme (UNEP), and the TNFD [44].

Relative species richness: Species richness measures the number of different species present in a given area and can be estimated by stacking and summing individual HSMs. Using this method, richness is reliably estimated (i.e., estimated richness = true richness) only when HSMs are generated with presence-absence data and represent probability of species occurrence [26,45]. When HSMs are generated with presence-background data representing relative likelihood of species occurrence, richness is not expected to be reliably estimated, but has been shown to be correlated with true richness (i.e., estimated richness = index of true richness) [26]. Because our HSMs were developed with presence-background data rather than presence-absence data, we were able to estimate an index of richness, hereafter referred to as "relative species richness".

Habitat intactness: Habitat intactness is an index of habitat condition based on habitat quality, quantity, and connectivity. This is a valuable index because habitat impacts are the primary cause of biodiversity loss across the globe, and these impacts to habitats can occur via the loss of total area, loss of quality (i.e., degradation), and/or loss of connectivity (i.e., fragmentation). The loss of habitat area affects the number of species and size of populations that can depend on that area. The loss of quality affects the

ability to acquire nutritional and reproductive requirements, which then affects survival and reproduction, and the loss of connectivity can limit and even prevent movement and access to those nutritional and reproductive resources. To evaluate habitat intactness, we used the following habitat intactness index created by Beyer et al. (2020) [46],

$$Q = \frac{\sum_{i=1}^{N} \sum_{j=i}^{N} w_i w_j{}^z \exp{(-\beta d_{ij})}}{\sum_{i=1}^{N} \sum_{j=i}^{N} \exp{(-\beta d_{ij})}}$$

where d_{ij} is the distance between grid cells i and j, w is a measure of the quality of the grid cell in the range $0 - 1$, and N is the number of grid cells within a spatial unit (i.e., study area of interest). z is a parameter that scales the product of the two cell qualities and β is a parameter that scales the effect of distance between the grid cells. Therefore, this index uses gridded continuous representations of habitat quality (such as HSMs where raster grid cell values equate to habitat suitability) and is designed to be proportional to habitat area and quality and to decline monotonically as fragmentation increases.

5 RESULTS AND DISCUSSION

5.1 MEASURING HABITAT SUITABILITY

Using the GBIF platform we were able to obtain data for 52 focal species of plants and animals across the study area that met our inclusion criteria of occurring within the two ecoregions of interest in Washington State, having more than 500 observations in GBIF, and being recorded to species level. In total, our final dataset included four amphibian species, 34 birds, 1 mammal, and 13 plants (see full list in Table 2A, Appendix A). Fifteen of these species were considered to have a preference for wetlands based on their known life histories. For example, we included the American bittern (*Botaurus lentiginosus*), which is a species of wading bird in the heron family. This bird prefers bogs, marshes, and vegetated areas around lakes and ponds. Our list also included bird species like the ruffed grouse (*Bonasa umbellus*), which is an early successional forest specialist.

Our 52 species-specific HSMs indicated that suitable habitat in the vicinity of the Cherry Point Refinery varies within each individual HSM and between each species' HSMs; though, as expected, suitable habitat frequently overlapped with the more natural areas and unsuitable habitat overlapped with more industrialized spaces. For example, for one of our wetland species, the American bittern, we found high habitat suitability values in the wetlands north of the refinery where restoration has been ongoing for many years (Fig. 4). In the same area, we also found some evidence of higher habitat suitability for one or our habitat generalist species, the American robin (Fig. 4). Overall, however, the American robin, who is a common habitat generalist, was found to have lower habitat suitability across the study area compared to the American bittern. This may be a result of observers not recording or unevenly recording common species across all the locations that they are seen. We explored some of the differences in habitat suitability between habitat specialists and generalists below but believe that integrating site-level field data will be an important way to account for these types of biases in the future.

In addition to differences among habitat specialization, we also found some unanticipated anomalies in where habitat was predicted to be suitable. For example, we found some instances of high suitability

predicted in the industrialized portions of the study area that may be due to water vapor or high reflectance from the impervious surfaces but require further investigation.
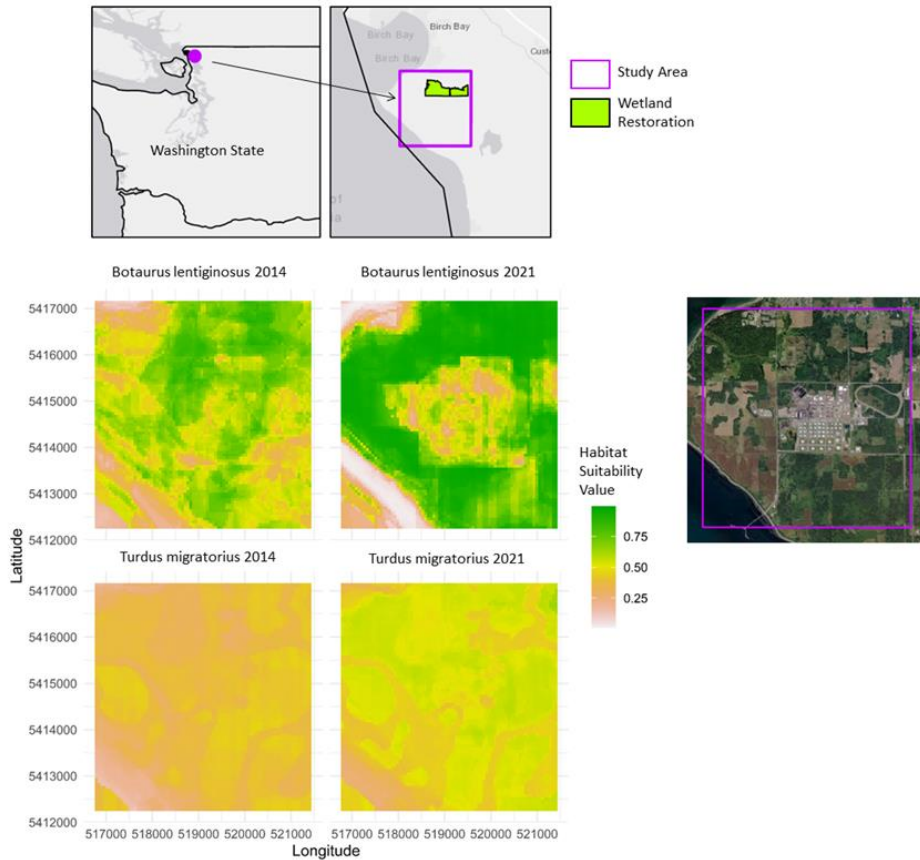

Figure 4. Habitat suitability models (HSMs) for two species and two years (2014 and 2021). The top row indicates the study area that bounds the HSMs depicted in the center and bottom rows. The center row depicts the HSM results for the American bittern (*Botaurus lentiginosus*), with the far-right image representing the aerial image of the study area bounded by the purple box. The bottom row depicts the HSM results for the American robin (*Turdus migratorius*). Habitat suitability values reflect the estimated relative likelihood of species occurrence within a grid cell.

For this pilot project, we engaged in a significant effort to account for biases in the GBIF data via the testing and evaluation of three methods of background sampling. We found that the HSMs developed using the bias layer method of background sampling had the highest recall but the lowest precision (see Fig. 3 for a description of these metrics), compared to other background sampling methods (Fig. 5). Finding low precision is surprising given the use of this method in the scientific literature and its recommendation for reducing biases associated with opportunistic data (see section *Challenges and lessons learned* below). The environmental clustering method on the other hand had lower recall than the bias method, but much higher precision, whereas the target group method, which was applied to only a subset of species from our initial model experiments, appears to have the lowest recall and

lowest average precision of the background sampling methods. We believe that combining methods such as the bias layer (highest recall) and environmental clustering (highest precision on average) could be a path towards creating even better performing models that account for multiple types of bias.
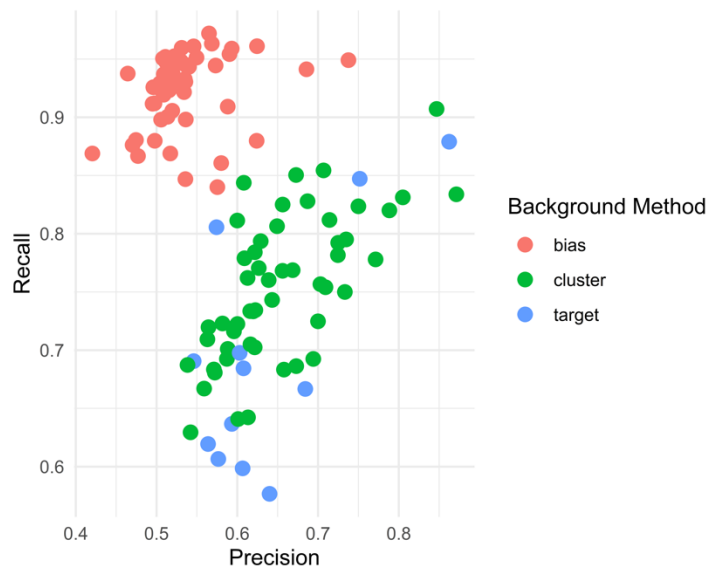

Figure 5. Comparison of recall and precision of HSMs developed from three different background sampling methods. The bias layer (bias) and environmental clustering (cluster) methods were applied to all 52 species. The target group (target) method was applied only to 12 species in an initial examination of methods.

By focusing on the F1 score, which aims to balance recall and precision, and evaluating how this metric varies by taxonomic group and habitat specialization, we were able to better understand some of the factors affecting model performance. We found that on average the environmental clustering method of background sampling resulted in the best performing HSMs for plant species (Fig. 6, top left panel). HSM performance for animals, on the other hand, was similar across background sampling methods. We found that HSMs with the highest F1 score were those created for habitat specialists (Fig. 6, top right panel) over those created for generalist species. We also observed a higher HSM performance for species with a preference for wetland habitats (Fig 6, bottom left panel). In other words, species having a strong preference for wetlands (e.g., the American bittern) resulted in models that were more accurate than models for non-wetland species (e.g., the American robin or ruffed grouse). We plan to continue integrating new data into the future and further evaluating how species life history may affect models. This is a key interest, as there may be other factors not associated with environmental conditions that affect where species are recorded, such as dispersal ability and biotic interactions. Incorporating local field survey data with GBIF data and using biotic interaction networks [47] or integrated species distribution model (iSDM; e.g., [48]) could help to disentangle some of these effects.
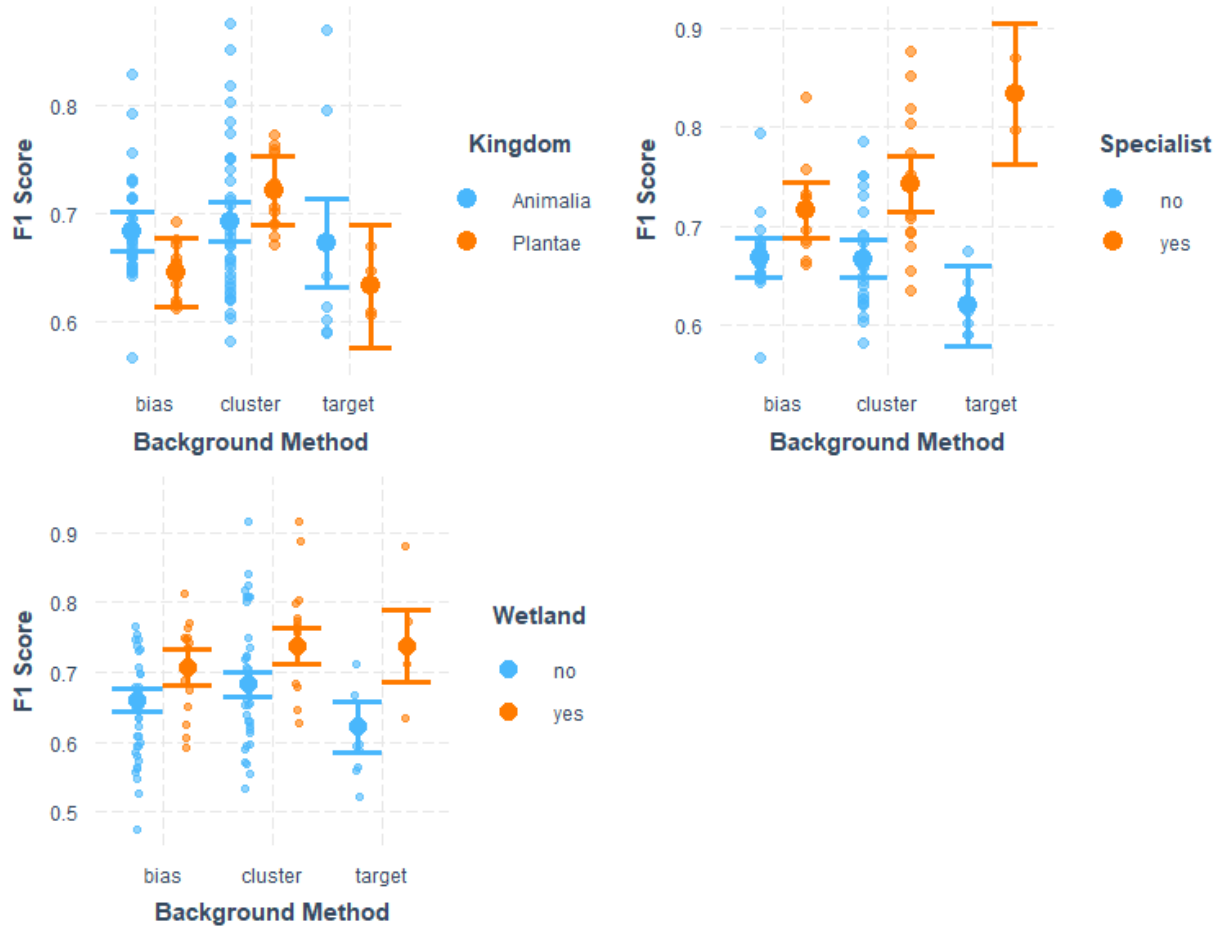
Figure 6. F1 scores for HSMs separated by the background sampling method used and species' taxonomic kingdom (top left panel), whether the species were habitat specialists or not (top right panel), or whether the species are known to prefer wetlands at any point in their life cycle (bottom left panel). Depending on the panel, yes represents specialist species or species with a wetland preference.

5.2 MEASURING BIODIVERSITY

Our preliminary, continuous index of relative species richness indicated little to no change in richness over the main industrialized portions of our study area (center pixels of Fig. 7), while across the surrounding property there were areas of increasing richness (green pixels in Fig. 7), including in areas where wetland restoration has been ongoing (locations indicated in Fig. 4). Because this index was generated from a range of species, it is a start to examining species richness and can be useful for examining spatial and temporal trends. However, as it is an index of richness, the actual values may be less meaningful until integrated with local field survey data. We also aim to add in more recent GBIF data as it is recorded, and further tune the background sampling approaches, which are all avenues for improving model performance and bolstering our understanding of how biodiversity is changing over space and time.
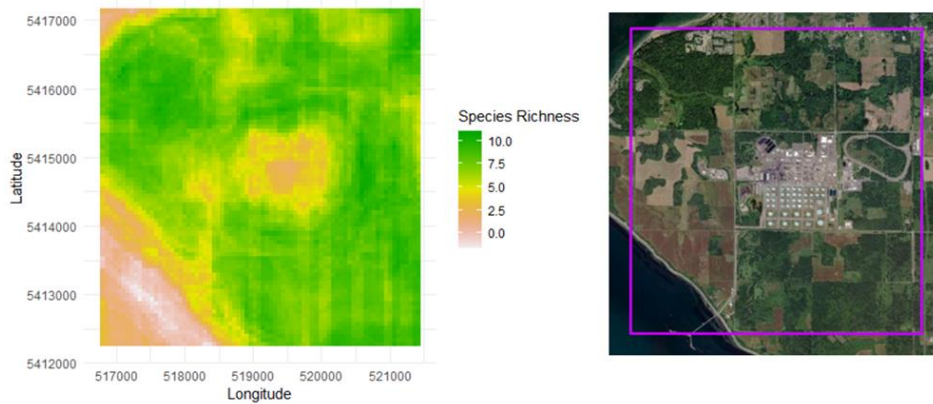
Figure 7. The left panel depicts the estimated change in relative species richness from 2014 to 2022 over the Cherry Point Refinery (i.e., a value of 10 indicates that relative richness increased by 10 species). Because we focused on terrestrial species and not marine species, we caution any interpretation of the marine environments along the western edge. The right panel depicts the aerial image of the study area bounded by the purple box.

Within the wetland restoration areas (identified in Fig. 4), relative species richness tended to increase slightly over time (Fig. 8, left panel). These are preliminary findings that may indicate true improvements in habitat and subsequent biodiversity but should be validated with further study. For example, examining the contribution of each species' HSM to this trend could help us understand which species and/or species groups (e.g., specialists and generalists) were most influential.

Looking across the entire study area, habitat intactness also tended to increase slightly on average (Fig. 8, right panel). This suggests that habitat intactness – which accounts for habitat quality, area, and connectivity – has been increasing from a multi-species perspective. However, there was substantial variability in habitat intactness across species. Therefore, these results need further validation and evaluation to understand for what species and species groups habitat intactness is increasing, decreasing, or not changing.
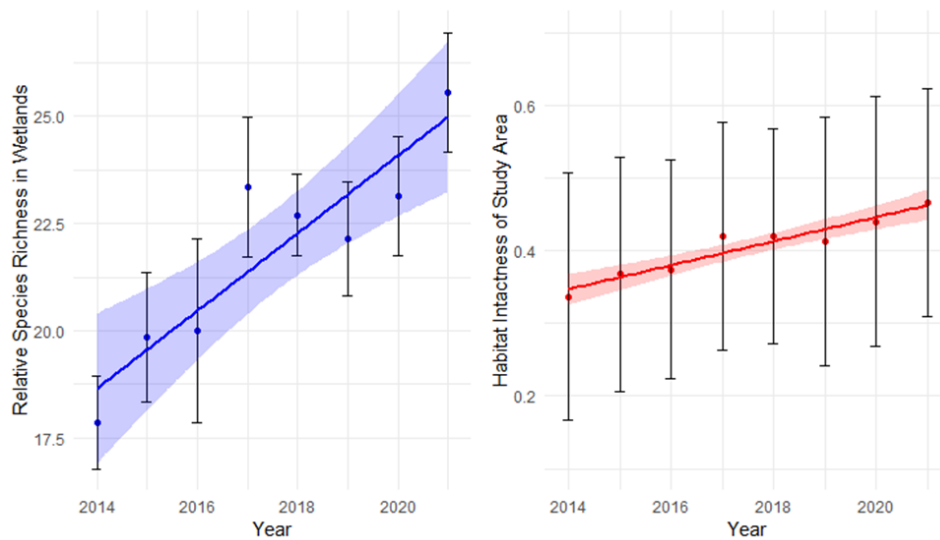
Figure 8. Estimated trends and 95% confidence intervals in relative species richness within the wetland restoration areas (left panel) and habitat intactness estimated across the entire study area (right panel). Error bars in left panel represent the standard deviation in relative species richness within the wetlands (i.e., variation in grid cell values). Error bars in right panel represent the standard deviation in habitat intactness across species. Habitat intactness (Q) is calculated using the equation shown in section *4.5 Measuring Biodiversity*.

5.3 CHALLENGES AND LESSONS LEARNED

In this application, the HSMs and our subsequent measures of relative species richness and habitat intactness are a function of the species selected, which is based on species with greater than 500 observations in GBIF. Consequently, very rare species or vagrant species that have few records were excluded, following the assumption that a representative geographic distribution cannot be reliably inferred from the few records. In addition to this bias against rare species, there is a bias against relatively abundant species that, from an observer point of view, do not warrant a recording in GBIF because of how common they are. This also applies to species and species groups that are either difficult to identify to species level or are typically underreported (e.g., individual grass species).

These issues largely stem from the inherent biases associated with GBIF data, which while containing millions of records and thus a wealth of information about biodiversity, are opportunistically collected. Because they are opportunistically collected, and not collected following a statistically rigorous sampling design (e.g., stratified random), species presences are more likely to be recorded near roads and human activities, and charismatic or interesting species are more likely to be recorded than common species.

Moreover, given the wealth of observations in GBIF and easy access, it may also be easy to overlook the importance of thinking about the relevancy of certain species to an HSM. For example, if selecting forest specialist species when the study area largely covers wetlands, your habitat suitability score will be lower. Therefore, if one wants to measure improvements in wetland habitat across spatial or temporal gradients, one should choose species or a subset of species that are more closely associated with the wetlands of the region of interest. The beauty of the present approach is that you can choose from a

range of species, to qualify a specific habitat suitability, but also choose a single species to infer their likely distribution across the landscape.

It is important to recognize and understand how opportunistically collected data can lead to model uncertainty (e.g., false predictions of species distribution). The following are other factors that are also likely to affect interpretation of HSMs.

Assumption of equilibrium: Underlying HSMs is the assumption that species habitat preferences are constant over space and time, and that all suitable habitats are occupied and all unsuitable habitats are unoccupied [17,49]. This may be unrealistic as species distributions are likely not static, but instead changing/evolving over space and time [50]. Invasive species, for example, may have only begun invading a new region and not yet occupy all suitable habitats by the time species observations are recorded. Species habitat preferences may also be changing with climate change. To address this limitation, researchers are increasingly incorporating dynamic approaches to estimate temporal changes in species distributions [50].

Lack of incorporation of biotic interactions: HSMs often do not account for biotic interactions, such as competition and predation, which can affect the distribution and abundance of species. These interactions are difficult to account for in typical HSMs.

6 DIGITAL BIODIVERSITY PLATFORM

Implementation of these HSMs formed the backbone of a digital biodiversity platform that we developed within bp's Azure environment, thereby creating one place for storing biodiversity data from different sources and for handling AI machine learning analyses, evaluating model inference, and creating data visualizations. The digital biodiversity platform significantly accelerates creation of new models and makes it easy to manage them through the whole life cycle. Via this platform, everything is automated and orchestrated using Microsoft's Planetary Computer and Azure's newest solutions.

Our development of the platform within Azure enables integration of biodiversity modeling with the following advanced data science functionalities:

Automated model training and deployment: Azure Machine Learning (ML) offers features like automated machine learning, hyperparameter tuning, and model deployment pipelines, which help accelerate model productization. We used these capabilities to build a platform to automate the entire process of data ingestion, processing, model training, deployment and monitoring.

Collaboration and version control: The platform enables team collaboration and version control, allowing team members to work on the same codebase and model versioning. Azure ML provides support for Git integration (software used for version control), allowing the team to manage and track code changes more effectively.

Scalability and performance: The platform provides access to scalable resources for training and deploying models, such as high-performance computing (HPC) clusters and GPUs. Azure ML offers a range of compute options, including Azure Virtual Machines, Azure Batch, and Azure Kubernetes Service (AKS), which can help scale up or down model implementation based on the team's needs.

Monitoring and logging: The platform provides real-time monitoring and logging of model performance and usage, helping the team to identify and resolve issues quickly. Azure ML provides Azure Monitor, which helps tracking performance and health of deployed models.

Integration with other tools and services: The platform can be integrated with other tools and services, such as Jupyter Notebooks. Azure ML also provides integrations with Azure services like Azure Data Factory, Azure DevOps, and Azure Blob Storage.

Given the presence of these functionalities, the platform naturally serves as a framework for future development aimed at expanding the range of analyses, applying new models, and extending visualization capabilities. Moreover, future implementation timelines are expected to be much faster than the initial development, as the whole design and its application and guidelines are now firmly in place.

7 WHERE DO WE GO FROM HERE?

The science is clear: protecting and restoring nature is essential to achieving the world's biodiversity, climate, and sustainability goals, and past conservation efforts have not solved the problem. The recent Kunming-Montreal Global Biodiversity Framework represents an inflection point for biodiversity, calling for the transformative changes needed to bend the curve on biodiversity loss and achieve a nature positive world.

Bending the curve on biodiversity loss requires a better understanding of the status and trends of ecosystems and species. Monitoring and evaluation are critical to advancing this understanding, and to identifying areas of high conservation value, such as areas with high species richness or unique ecosystems that may be at risk from habitat loss, climate change, or other threats. Better monitoring data is also necessary to help prioritize conservation interventions, allocate resources more effectively, and understand the benefits of conservation interventions, such as the ecosystem services provided by intact ecosystems.

Advancing progress towards a nature positive world requires more accessible technologies for monitoring and evaluating the state and changes in biodiversity. Recent advances in technology, described below, now give us a unique capability to record and track species and environmental conditions in new ways and at temporal and spatial scales not seen before. Finding ways to collect and integrate these data into our HSM pipeline is key to improving our modeling approach and ability to accurately track biodiversity.

eDNA: Advances in next-generation sequencing technologies have unlocked the use of environmental DNA (i.e., DNA that is shed by organisms in the environment) as a tool for monitoring biodiversity. Water, soil, and even air samples can now be analysed to give a snapshot of the biodiversity present in the area and soon it will be possible to use these tools to identify unique individuals for estimating species' densities.

Bioacoustics: Bioacoustics are emerging as an important remote-sensing tool for conservation due to the development of cheap recording devices (<$100 per unit) with broad bandwidth recording

capabilities and advances in deep learning algorithms that enable automated identification of different species by comparing the spectral shape of the sound recorded against a library of sounds.

Drones: High resolution drone surveys are also being used to collect highly accurate and detailed data about species and their habitats. Drones equipped with high-resolution cameras can be flown over large and difficult-to-reach areas, providing a more comprehensive view of the biodiversity present in a particular region. This data can be used to monitor changes in biodiversity over time, identify areas of high conservation value, and inform conservation management strategies. Drones can also be equipped with LiDAR and other sensors to help researchers gather information on the structure and composition of ecosystems, including vegetation cover, topography, and soil characteristics.

Hyperspectral sensors: Hyperspectral sensors have the ability to capture data at higher spectral resolution than multispectral sensors. This enables researchers to detect subtle differences in vegetation and land cover, such as variations in leaf pigments, that can indicate changes in ecosystem health and biodiversity.

Synthetic Aperture Radar: Synthetic Aperture Radar (SAR) can penetrate clouds and vegetation cover to provide data on topography, soil moisture, and other environmental variables. SAR can also detect changes in surface structures over time, such as the expansion of human settlements or changes in the distribution of water bodies, which can affect biodiversity.

Machine learning and computer vision: AI technologies are rapidly advancing in their ability to monitor biodiversity, by providing new ways to analyze and interpret large volumes of data. By training computer algorithms to recognize patterns and features in images, researchers can automate the identification and classification of species and their habitats. For example, computer vision algorithms can be trained to recognize individual species from photographs or drone footage, allowing researchers to collect data on species distributions and population sizes. Similarly, machine learning can be used to analyze sound recordings and identify species based on their vocalizations. These techniques can also be used to monitor changes in biodiversity over time, such as shifts in species distributions or changes in habitat quality.

As the cost of these technologies decrease, there is an opportunity to deploy them at scale in ways that overcome some of the limitations and biases currently associated with opportunistically collected citizen science data like GBIF. Integration with HSMs can then generate more accurate inference, at finer resolutions and broader extents, moving us towards temporally and spatially continuous monitoring of biodiversity. Our digital biodiversity platform is a tool that can help take us in that direction.

We know there is significant work to do to get our planet on the right track, but through partnerships like these, we have a chance to make a lasting difference.

8 REFERENCES

1. WWF. *Living Planet Report 2022 - Building a nature-positive society.* https://www.worldwildlife.org/pages/living-planet-report-2022 (2022).
2. IPBES. Summary for policymakers of the global assessment report on biodiversity and ecosystem services of the Intergovernmental Science-Policy Platform on Biodiversity and Ecosystem Services. https://ipbes.net/system/tdf/ipbes_global_assessment_report_summary_for_policymakers.pdf?file=1&type=node&id=35329 (2019).
3. Dirzo, R. *et al.* Defaunation in the Anthropocene. *Science* **345**, 401–406 (2014).
4. Secretariat of the Convention on Biological Diversity. *Global Biodiversity Outlook 5.* https://www.cbd.int/gbo5 (2020).
5. WEF. The Global Risks Report 2023 18th Edition. www.weforum.org (2023).
6. WEF. Nature Risk Rising: Why the Crisis Engulfing Nature Matters for Business and the Economy. www.weforum.org (2020).
7. IPCC. *Land–climate interactions.* *Climate Change and Land* (Cambridge University Press, 2022). doi:10.1017/9781009157988.004.
8. Scheffer, M. *et al.* Anticipating Critical Transitions. *Science* **338**, (2012).
9. Barnosky, A. D. *et al.* Approaching a state shift in Earth's biosphere. *Nature* **486**, 52–58 (2012).
10. UN DESA. *The Sustainable Development Goals Report.* https://unstats.un.org/sdgs/report/2022/ (2022).
11. Díaz, S. *et al.* Pervasive human-driven decline of life on Earth points to the need for transformative change. *Science* **366**, (2019).
12. Dasgupta, H. The Economics of Biodiversity: The Dasgupta Review. (2021).
13. Locke, H. et al. A Nature-Positive World: The Global Goal for Nature. (2021).
14. G7. 2030 Nature Compact. (2021).
15. TNFD. The TNFD Nature-Related Risk and Opportunity Management and Disclosure Framework - Beta v0.2. (2022).
16. CBD. *Kunming-Montreal Global Biodiversity Framework.* https://www.cbd.int/article/cop15-final-text-kunming-montreal-gbf-221222 (2022).
17. Guisan, A., Thuiller, W. & Zimmerman, N. E. *Habitat Suitability and Distribution Models, with Applications in R.* (Cambridge University Press, 2017).
18. Hirzel, A. H., Le Lay, G., Helfer, V., Randin, C. & Guisan, A. Evaluating the ability of habitat suitability models to predict species presences. *Ecol Modell* **199**, 142–152 (2006).
19. Elith, J. *et al.* Presence-only and presence-absence data for comparing species distribution modeling methods. *Biodiversity Informatics* **15**, 69–80 (2020).
20. Elith, J. *et al.* Novel methods improve prediction of species' distributions from occurrence data. *Ecography* **29**, 129–151 (2006).
21. Valavi, R., Guillera-Arroita, G., Lahoz-Monfort, J. J. & Elith, J. Predictive performance of presence-only species distribution models: a benchmark study with reproducible code. *Ecol Monogr* **92**, (2022).
22. Valavi, R., Elith, J., Lahoz-Monfort, J. J. & Guillera-Arroita, G. Modelling species presence-only data with random forests. *Ecography* **44**, 1731–1742 (2021).

23. Elith, J. & Leathwick, J. R. Species distribution models: Ecological explanation and prediction across space and time. *Annu Rev Ecol Evol Syst* **40**, 677–697 (2009).

24. Fithian, W., Elith, J., Hastie, T. & Keith, D. A. Bias correction in species distribution models: Pooling survey and collection data for multiple species. *Methods Ecol Evol* **6**, 424–438 (2015).

25. Smith, A. B. & Santos, M. J. Testing the ability of species distribution models to infer variable importance. *Ecography* **43**, 1801–1813 (2020).

26. Guillera-Arroita, G. *et al.* Is my species distribution model fit for purpose? Matching data and models to applications. *Global Ecology and Biogeography* **24**, 276–292 (2015).

27. Santini, L., Benítez-López, A., Maiorano, L., Čengić, M. & Huijbregts, M. A. J. Assessing the reliability of species distribution projections in climate change research. *Divers Distrib* **27**, 1035–1050 (2021).

28. Ranc, N. *et al.* Performance tradeoffs in target-group bias correction for species distribution models. *Ecography* **40**, 1076–1087 (2017).

29. Case, M. J. & Lawler, J. J. Integrating mechanistic and empirical model projections to assess climate impacts on tree species distributions in northwestern North America. *Glob Chang Biol* **23**, 2005–2015 (2017).

30. Bellard, C., Bertelsmeier, C., Leadley, P., Thuiller, W. & Courchamp, F. Impacts of climate change on the future of biodiversity. *Ecol Lett* **15**, 365–377 (2012).

31. Guisan, A. & Thuiller, W. Predicting species distribution: Offering more than simple habitat models. *Ecol Lett* **8**, 993–1009 (2005).

32. Strassburg, N. *et al.* Strategic approaches to restoring ecosystems can triple conservation gains and halve costs. *Nat Ecol Evol* **3**, 62–70 (2018).

33. Tewksbury, J. J. *et al.* Natural history's place in science and society. *Bioscience* **64**, 300–310 (2014).

34. Cretois, B. *et al.* Identifying and correcting spatial bias in opportunistic citizen science data for wild ungulates in Norway. *Ecol Evol* **11**, 15191–15204 (2021).

35. Feyisa, G. L., Meilby, H., Fensholt, R. & Proud, S. R. Automated Water Extraction Index: A new technique for surface water mapping using Landsat imagery. *Remote Sens Environ* **140**, 23–35 (2014).

36. Phillips, S. J. *et al.* Sample selection bias and presence-only distribution models: implications for background and pseudo-absence data. *Ecological Applications* **19**, 181–197 (2009).

37. Bird, T. J. *et al.* Statistical solutions for error and bias in global citizen science datasets. *Biol Conserv* **173**, 144–154 (2014).

38. Phillips, S. J., Dudík, M. & Phillips, S. J. Modeling of species distributions with Maxent: new extensions and a comprehensive evaluation. *Ecography* **31**, 161–175 (2008).

39. Dudík, M., Schapire, R. E. & Phillips, S. J. Correcting sample selection bias in maximum entropy density estimation.

40. Barber, R. A., Ball, S. G., Morris, R. K. A. & Gilbert, F. Target-group backgrounds prove effective at correcting sampling bias in Maxent models. *Divers Distrib* **28**, 128–141 (2022).

41. Botella, C., Joly, A., Monestiez, P., Bonnet, P. & Munoz, F. Bias in presence-only niche models related to sampling effort and species niches: Lessons for background point selection. *PLoS One* **15**, (2020).

42. Hill, S. L. L. *et al.* The Ecosystem Integrity Index: a novel measure of terrestrial ecosystem integrity with global coverage. *Biorxiv* (2022) doi:10.1101/2022.08.21.504707.

43. Stephenson, P. J. & Carbone, G. *Guidelines for planning and monitoring corporate biodiversity performance*. (IUCN, International Union for Conservation of Nature, 2021). doi:10.2305/iucn.ch.2021.05.en.

44. UNEP. Nature Risk Profile: A methodology for profiling nature related dependencies and impacts. (2023).

45. Calabrese, J. M., Certain, G., Kraan, C. & Dormann, C. F. Stacking species distribution models and adjusting bias by linking them to macroecological models. *Global Ecology and Biogeography* **23**, 99–112 (2014).

46. Beyer, H. L., Venter, O., Grantham, H. S. & Watson, J. E. M. Substantial losses in ecoregion intactness highlight urgency of globally coordinated action. *Conserv Lett* **13**, 1–9 (2020).

47. Staniczenko, P. P. A., Sivasubramaniam, P., Suttle, K. B. & Pearson, R. G. Linking macroecology and community ecology: refining predictions of species distributions using biotic interaction networks. *Ecol Lett* **20**, 693–707 (2017).

48. Landau, V. A., Noon, B. R., Theobald, D. M., Hobbs, N. T. & Nielsen, C. K. Integrating presence-only and occupancy data to model habitat use for the northernmost population of jaguars. *Ecological Applications* 1–15 (2022) doi:10.1002/eap.2619.

49. Pearman, P. B., Guisan, A., Broennimann, O. & Randin, C. F. Niche dynamics in space and time. *Trends in Ecology and Evolution* vol. 23 149–158 Preprint at https://doi.org/10.1016/j.tree.2007.11.005 (2008).

50. Milanesi, P., Della Rocca, F. & Robinson, R. A. Integrating dynamic environmental predictors and species occurrences: Toward true dynamic species distribution models. *Ecol Evol* **10**, 1087–1092 (2020).

9 APPENDIX A

Table 1A. List of environmental variable types (input variables), the type-specific layers, and how the data were aggregated into features for model training and implementation.

ID	input variables	layer	description	full temporal range	aggregation			# features
					temporal	temporal function	spatial function	
8	Multispectral Bands (L-8)	COASTAL	reflectance image (DN * 0.0000275 - 0.2)	full previous calendar year	seasonal	median	mean	4
9					seasonal	median	standard deviation	4
12		BLUE	reflectance image (DN * 0.0000275 - 0.2)		seasonal	median	mean	4
13					seasonal	median	standard deviation	4
16		GREEN	reflectance image (DN * 0.0000275 - 0.2)		seasonal	median	mean	4
17					seasonal	median	standard deviation	4
20		RED	reflectance image (DN * 0.0000275 - 0.2)		seasonal	median	mean	4
21					seasonal	median	standard deviation	4
24		NIR	reflectance image (DN * 0.0000275 - 0.2)		seasonal	median	mean	4
25					seasonal	median	standard deviation	4
28		SWIR1	reflectance image (DN * 0.0000275 - 0.2)		seasonal	median	mean	4
29					seasonal	median	standard deviation	4
32		SWIR2	reflectance image (DN * 0.0000275 - 0.2)		seasonal	median	mean	4
33					seasonal	median	standard deviation	4
							SUBTOTAL	**56**
36	Multispectral Indices (L-8)	NDVI	calculated on L-8 reflectance: (NIR - RED) / (NIR + RED)	full previous calendar year	seasonal	median	mean	4
37					seasonal	median	standard deviation	4
44		NDWI	calculated on L-8 reflectance: (NIR - SWIR1) / (NIR + SWIR1)		seasonal	median	mean	4
45					seasonal	median	standard deviation	4
48		AWEI_sh	calculated on L-8 reflectance: BLUE + 2.5*GREEN - 1.5*(NIR+SWIR1) - 0.25*SWIR2		seasonal	median	mean	4
49					seasonal	median	standard deviation	4
							SUBTOTAL	**24**

Table 1A continued.

ID	input variables	layer	description	full temporal range	aggregation temporal	aggregation temporal function	aggregation spatial function	# features
56	**NASA DEM**	elevation	elevation above sea level	single observation (2000)	none	none	none	1
57		slope	slope of terrain		none	none	none	1
58		aspect	aspect (direction) of terrain		none	none	none	1
							SUBTOTAL	**3**
59	**TerraClimate**	Ws	monthly average wind speed (m/s)	10 full previous calendar years; values for each season in each year summed/averaged (depending on variable) before further aggregation	seasonal	mean	nearest	4
60					seasonal	standard deviation	nearest	4
61		Ppt	monthly accumulated precipitation (mm)		seasonal	mean	nearest	4
62					seasonal	standard deviation	nearest	4
63		Swe	modeled(?) snow water equivalent at end of month (mm)		seasonal	mean	nearest	4
64					seasonal	standard deviation	nearest	4
65		Tmax	monthly maximum air temperature (°C)		seasonal	mean	nearest	4
66					seasonal	standard deviation	nearest	4
67		Tmin	monthly minimum air temperaturs (°C)		seasonal	mean	nearest	4
68					seasonal	standard deviation	nearest	4
							SUBTOTAL	**40**
69	**Water**	surface water (binary)	surface water binary map derived from Landsat-8 AWEI_sh; thresholded at 0	full previous calendar year	seasonal	median	% water/no water	4
70					seasonal	median	dist. to nearest pixel	4
							SUBTOTAL	**8**

Table 2A. List of 52 focal species for which we developed habitat suitability models.

Species	Common Name	Number of GBIF Observations
Aegolius acadicus	Northern saw-whet owl	1231
Aix sponsa	Wood duck	13821
Anas platyrhynchos	Mallard duck	81533
Ardea herodias	Great Blue Heron	63304
Bombycilla cedrorum	Cedar waxwing	33327
Bonasa umbellus	Ruffed grouse	2171
Botaurus lentiginosus	American bittern	1441
Branta canadensis	Canada goose	67812
Bucephala albeola	Bufflehead	45796
Buteo jamaicensis	Red-tailed hawk	53972
Cardellina pusilla	Wilson's warbler	19722
Catharus ustulatus	Swainson's thrush	24629
Charadrius vociferus	Killdeer	30539
Chordeiles minor	Common nighthawk	3080
Cornus sericea	Red osier dogwood	779
Dryobates pubescens	Downy woodpecker	41326
Dryocopus pileatus	Pileated woodpecker	27478
Gallinago delicata	Wilson's Snipe	5381
Haliaeetus leucocephalus	Bald eagle	79663
Hirundo rustica	barn swallow	35496
Holodiscus discolor	Oceanspray	2265
Ixoreus naevius	Varied thrush	29574
Lithobates catesbeianus	American bullfrog	522
Lonicera involucrata	Black twinberry	604
Melospiza lincolnii	Lincoln sparrow	8693
Odocoileus hemionus	Black-tailed deer	3376
Oemleria cerasiformis	Indian plum	2462
Passerculus sandwichensis	Savannah sparrow	20588
Poecile atricapillus	Black-capped chickadee	99852
Porzana carolina	Sora	1425
Pseudacris regilla	Pacific tree frog	1703
Pseudotsuga menziesii	Douglas-fir	2943
Rallus limicola	Virginia rail	7242
Rana aurora	Northern red-legged frog	509
Rosa nutkana	Nootka rose	785
Rubus parviflorus	thimbleberry	2197
Rubus spectabilis	Salmonberry	3179
Sambucus racemosa	Red elderberry	1279
Setophaga coronata	Yellow-rumped warbler	34660

Table 2A continued.

Species	Common Name	Number of GBIF Observations
Setophaga petechia	Yellow warbler	14621
Sphyrapicus ruber	Red-breasted sapsucker	21765
Spiraea douglasii	Rose spirea	946
Strix varia	Barred owl	10721
Sturnus vulgaris	Starling	80621
Symphoricarpos albus	Common snowberry	2366
Tachycineta bicolor	Tree swallow	22905
Tachycineta thalassina	Violet-green swallow	41403
Taricha granulosa	Rough-skinned newt	751
Thuja plicata	Western redcedar	3085
Tsuga heterophylla	Western hemlock	1220
Turdus migratorius	American robin	139168
Vireo gilvus	Warbling vireo	14853