TOWARDS SCALABLE DEEP SPECIES DISTRIBUTION MODELLING USING GLOBAL REMOTE SENSING

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ABSTRACT

Destruction of natural habitats and anthropogenic climate change are threatening biodiversity globally. Addressing this loss necessitates enhanced monitoring techniques to assess the impact of environmental shifts and to guide policy-making efforts. Species distribution models are crucial tools that predict species locations by interpolating observed field data with environmental information. We develop an improved, scalable method for species distribution modelling by proposing a dataset pipeline that incorporates global remote sensing imagery, land use classification data, environmental variables, and observation data, and utilising this with convolutional neural network (CNN) models to predict species presence at higher spatial and temporal resolutions than well-established species distribution modelling methods. We apply our approach to modelling Protea species distributions in the Cape Floristic Region of South Africa, demonstrating its performance in a region of high biodiversity. We train two CNN models and compare their performance to Maxent, a popular conventional species distribution modelling method. We find that the CNN models trained with remote sensing data outperform Maxent, underscoring the potential of our method as an effective and scalable solution for modelling species distribution.

1 INTRODUCTION

Species distribution models (SDMs) are an essential tool for biodiversity conservation due to their linkage of science to decision-making (McShea, 2014), with two prevalent approaches to constructing them. The first uses expert knowledge of a species’ range and its habitat preferences within that range (Luedtke et al., 2023). The second fits SDMs using machine learning approaches that model field observations of species occurrences as non-linear functions of bioclimatic and environmental spatial layers. Maxent (Phillips et al., 2006) is the most widely adopted approach (Elith et al., 2011); a recent dataset on the global distribution of utilised plants fitted Maxent models to predict distributions of 28,235 plant species (Pironon et al., 2024). SDMs have traditionally used spatial layers with course-grained spatiotemporal resolution, making it hard to produce local fine-grained predictions for species occurrence. Furthermore, SDMs generally only use the data at a single observation point and do not leverage information about the surrounding area, which can provide valuable insights into a species’ habitat such as proximity to water and neighbouring vegetation type.

We aim to provide a globally applicable method for creating SDMs, with the broader goal of providing an accurate view of where wild plant and animal species live across the planet for decision-makers to balance biodiversity preservation with human needs. Mapping at high resolution is becoming increasingly important for policymaking as climate and anthropogenic changes have local effects that are not captured by coarse environmental variables. Our approach combines convolutional neural network (CNN) models (LeCun et al., 2015) that exploit spatial information with high-resolution satellite data to produce accurate SDMs that also track local habitat changes. Using remote sensing data as predictive features for SDMs also makes the models more applicable to regions where ground-based features are unavailable due to funding constraints, political instability or lack of capacity (Cavender-Bares et al., 2022).

Previous work has created datasets to train SDMs (Joly et al., 2014; Gillespie et al., 2021) along with approaches (Botella et al., 2018; Deneu et al., 2019, 2021), but they focus on data-rich areas...
such as Europe and the USA. We extend these processes to globally available data and investigate how they perform in regions of high biodiversity, specifically via a case study of modelling species under the Protea genus in the Cape Floristic Region in South Africa, one of the global biodiversity hotspots (Myers et al., 2000). We present a dataset pipeline that combines remote sensing imagery data, land use land classification data and environmental variables with species observations to create a species distribution modelling dataset, which we then use to train two different versions of a CNN architecture to perform species distribution modelling. We compare the performance of these approaches to Maxent, which we train using only environmental variables.

2 DATASET, MODEL AND METHODS

2.1 DATA SOURCES

A key aspect of species distribution modelling is the collection of ground truth observation data which provides information on species’ locations. Most models are created using historical datasets from herbariums or smaller-scale, local datasets collected by ecologists. Historical datasets are difficult to utilise with more temporally high-resolution remote sensing data. Given the rapid rate of climate change and anthropogenic habitat changes over recent years, there is no guarantee that natural habitats are still found at the site of these observations (Bracken et al., 2022). We use iNaturalist (Van Horn et al., 2018) as a crowd-sourced reference dataset for our pipeline, as it provides both recent and global species presence observation data.

We use Sentinel 2 (S2) cloudless satellite basemaps (EOX) in the RGB 10m resolution bands along with land-use land classification (LULC) data (see Figure 1), combined with traditional low-resolution 1km bioclimatic environmental variables from WorldClim V2 based on temperature and precipitation. The S2 data provides a visual representation of the environment from which key habitat features can be extracted. Recent work by Diaz et al. (2019) highlighted that anthropogenic land use changes, such as land clearing for agriculture or settlement expansion, have been the primary drivers of biodiversity loss over the last 50 years, making it an important variable to include in SDMs. We use “Dynamic World”, a near real-time map (Brown et al., 2022) to leverage fine-grained 10m resolution LULC classifications for SDMs.

2.2 DATASET PIPELINE

The dataset creation pipeline in Figure 1(right) extends that proposed by Gillespie et al. (2021), incorporating additional filtering, data sources and methods for creating dataset splits. The following sections briefly detail the key elements of filtering observations and creating the training splits.

2.2.1 FILTER REFERENCE DATA

We use the Global Biodiversity Information Facility, an online network that combines biodiversity data from a variety of sources, to download and preliminarily filter the iNaturalist observation data based on parameters such as location, recording date, and location uncertainty distance. Once these observations are downloaded we then further filter them via a shapefile for the region of interest – in our case, the Cape Floristic Region (Hoffman et al., 2016). To address the uncertainty in the location of the data points, as well as address any potential changes that may have occurred to vegetation coverage over time, we extract the Dynamic World land classification for each observation location and remove observations classified as “water” or “built”.

Figure 1: Sample S2-Cloudless and LULC classifications data (left) and the data pipeline (right)
The co-occurrence of species has an important impact on the existence of many species (Wisz et al., 2013). We leverage species co-occurrence information by training a model to simultaneously predict the occurrence of all species at a given location, not just the species of interest. Furthermore, including other species should have a regularising effect on the model and stop it from overfitting when training, as well as providing “pseudo-absences” (Barbet-Massin et al., 2012) that allow the model to learn where the species do not occur. Thus although we aim to only perform species distribution modelling for Proteas, we include all species in the Tracheophyta phylum in our dataset. To include co-species information in our data points, we use a per-observation method (Gillespie et al., 2021). This method creates patches centered on an observation that represents a single iNaturalist entry. Each patch is a geographic area and is labelled with all species in observations intersecting with it. This means a single observation may occur in multiple neighbouring patches.

2.2.2 CREATE TRAINING SPLITS

When performing data analysis with geospatial data, a commonly encountered phenomenon is spatial autocorrelation (Getis, 2008). Spatial autocorrelation between the training and evaluation sets can cause an overly optimistic view of model performance (Karasiak et al., 2022; Ploton et al., 2020; Kattenborn et al., 2022). Including points in the test set that are spatially close to points in the train set could mean these points share very similar features. One solution to this is to split out data into test and train sets using some form of spatial clustering, to ensure spatial separation between training and evaluation splits.

To create a test set free from spatial autocorrelation, we use the method by Gillespie et al. (2021) with a different method for creating the validation set that is more representative of the statistics of the test set. We focus our evaluation on the six Protea species (Table 2) which had more than 100 test occurrences, more than 10 test observations and more training occurrences than test occurrences. To create the validation set, we first spatially cluster the data using K-means clustering (Arthur & Vassilvitskii, 2007) to ensure that the validation set provides good spatial coverage across the whole region of interest. We use 10 clusters in this work. For each cluster, we order the observations by the number of overlapping points and use the lowest 8% of each species of interest for the validation set. This reduces the number of observations that need to be removed from the training set due to their overlap with validation samples. To increase the number of occurrences for the species we then also include all neighbouring observations in the validation set. To account for spatial autocorrelation, we remove all the observations that overlap with any observations in the validation set from the train set.

However, constructing the split in this manner means that all samples in the validation set contained at least one Protea. This is not representative of the test set, where only about a quarter of the samples contain Protea species. Thus, we use the same method previously described to add samples that do not overlap with any Protea species to replicate the Protea presence/absence ratio. We sample \( x \times 3 \times \text{num protea examples} \) observations from each cluster, where \( x \) is determined by the proportion of the total number of samples that do not contain Proteas in that cluster. General statistics about the data split can be found in Table 1 and species splits can be found in Table 2.
Table 2: Number of observations and occurrences for the six Protea species of interest across the test, train, and validation sets.

<table>
<thead>
<tr>
<th>Species</th>
<th>Observations per Set</th>
<th>Occurrences per Set</th>
</tr>
</thead>
<tbody>
<tr>
<td></td>
<td>Test</td>
<td>Train</td>
</tr>
<tr>
<td><em>Protea repens</em> (PR)</td>
<td>28</td>
<td>662</td>
</tr>
<tr>
<td><em>Protea laurifolia</em> (PLA)</td>
<td>20</td>
<td>400</td>
</tr>
<tr>
<td><em>Protea nitida</em> (PNI)</td>
<td>18</td>
<td>500</td>
</tr>
<tr>
<td><em>Protea cynaroides</em> (PC)</td>
<td>13</td>
<td>634</td>
</tr>
<tr>
<td><em>Protea neriifolia</em> (PNE)</td>
<td>13</td>
<td>354</td>
</tr>
<tr>
<td><em>Protea lorifolia</em> (PLO)</td>
<td>11</td>
<td>108</td>
</tr>
</tbody>
</table>

2.3 MODELS AND EXPERIMENTATION

2.3.1 MAXENT

We use the Google Earth Engine (Crego et al., 2022) implementation of Maxent (Phillips et al.) with default settings to mirror the lack of fine-tuning in the deep learning model using only the bioclim variables. To create Maxent models for our species of interest, we use the same observations from the dataset described in the previous section. While some presence points in this dataset have been removed through the pipeline filtering, these points were spatially close enough that they would have very similar if not duplicate environmental variable values, given the resolution of the WorldClim V2 rasters. Thus it should not affect predictive performance.

2.3.2 DEEP LEARNING MODEL

We use the Deepbiosphere model (Gillespie et al., 2021) to perform our experimentation with our remote sensing dataset. Given an input data sample, including image data and environmental variable values, the model can be configured to predict either the families, genera, and species that occur or just the species that occur. We choose the former option, as this gives us the ability to predict where the Protea genus occurs, as well as each of our species of interest. Gillespie also presents a novel loss function, frequency-scaled binary cross-entropy loss, which proportionally weights absence and presence predictions equally. Since samples mostly consist of absence predictions, this prevents the model from learning to always predict species as absent.

For data preprocessing, we follow the TResNet (Ridnik et al., 2021) image preprocessing procedure. We do not use any augmentation strategies while training. We train two models, one using satellite images and environmental variables, which we shall refer to as Deepbiosphere$_{Image}$, and the other using satellite images, Dynamic World LULC images and environmental variables, which we shall refer to as Deepbiosphere$_{Image+DW}$. For the latter approach, we stack the satellite images and Dynamic World LULC images and pass the six-channel input to the CNN. To train the models we use the Adam optimizer with a learning rate of $1 \times 10^{-4}$, and a batch size of 165 and train for 100 epochs. Using our validation metrics, we choose the best-performing model checkpoint, and evaluate these models on the test set.

3 RESULTS

**Comparative Efficacy.** Area Under the Curve Receiver Operating Characteristics ($AUC_{ROC}$) is one of the most common metrics used to measure species distribution model performance. We report this metric to compare our models across the selected Protea species (see Table 2). Both Deepbiosphere$_{Image}$ and Deepbiosphere$_{Image+DW}$ on average outperform Maxent with respect to $AUC_{ROC}$ by 2.99 and 2.72 percent respectively. The results also suggest that this method for species distribution modelling performs well in areas of high biodiversity, which is crucial to scaling SDMs globally to include the tropical belt where an estimated two-thirds of the world’s terrestrial biodiversity lives. Despite our dataset containing about double the number of total species as the
Table 3: \(AUC_{ROC}\) results for the Maxent model, Deepbiosphere\(_{Image}\) model, and Deepbiosphere\(_{Image+DW}\) model for the Protea repens (PR), Protea laurifolia (PLA), Protea nitida (PNI), Protea cynaroides (PC), Protea neriifolia (PNE), and Protea loriifolia (PLO) species.

<table>
<thead>
<tr>
<th></th>
<th>PR</th>
<th>PLA</th>
<th>PNI</th>
<th>PC</th>
<th>PNE</th>
<th>PLO</th>
</tr>
</thead>
<tbody>
<tr>
<td>Maxent</td>
<td>0.7524</td>
<td>0.9282</td>
<td>0.8165</td>
<td>0.9166</td>
<td>0.8453</td>
<td>0.8709</td>
</tr>
<tr>
<td>Deepbiosphere(_{Image})</td>
<td>0.8159</td>
<td>0.9392</td>
<td>0.8280</td>
<td>0.9143</td>
<td>0.9040</td>
<td>0.9082</td>
</tr>
<tr>
<td>Deepbiosphere(_{Image+DW})</td>
<td>0.8292</td>
<td>0.9192</td>
<td>0.8036</td>
<td>0.9324</td>
<td>0.9031</td>
<td>0.9059</td>
</tr>
</tbody>
</table>

dataset created by [Gillespie et al.] (2021), we achieve similar performance albeit on different remote sensing data.

**Presence vs Absence.** The crowd-sourced dataset (iNaturalist) used for our observations does not contain true absence points which makes it difficult to compare and interpret the negative predictions of the models [Lobo et al.] (2010). Thus to fully evaluate the models, a dataset comprised of true absence and presence data collected in a structured field campaign is required. Such a dataset would also allow for analysis of biases in the citizen science dataset and understanding how these affect model performance.

**Land Use Datasets.** While there is a difference in performance between the Deepbiosphere models and Maxent, there is no substantial difference between the performance of the two Deepbiosphere models. The Deepbiosphere\(_{Image}\) model mostly outperforms the Deepbiosphere\(_{Image+DW}\) model in the per-species metrics. Our hypothesis here is that the land use land cover classification (LULC) classes are too course-grained in Dynamic World and, being derived from the same Sentinel-2 imagery used as input to our model, the network may be extracting relevant information directly from the images during training. The decrease in performance of the Deepbiosphere\(_{Image+DW}\) model versus Maxent for the Protea Nitida reveals the brittleness caused by this duplication, as the Deepbiosphere\(_{Image}\) model remains an improvement over Maxent.

## 4 CONCLUSIONS AND FUTURE WORK

In this work, we investigated the use of remote sensing data and CNN models to provide an improved method for performing scalable species distribution modelling. We found that using a deep learning approach has provided us with an exciting alternative that is at least as accurate as the prevalent Maxent method, and also one that naturally scales up with more data availability. While we used a case study of Protea species in the Cape Floristic Region in South Africa to illustrate the technique, our ambition is to extend this analysis to the full spectrum of plant and animal species worldwide to facilitate more accurate policymaking for environmental preservation. However, a major barrier is the sparseness of occurrence datasets for many species; incredibly, 30% of utilised plant species have fewer than 10 records in digital databases, which is too few to fit simple SDMs. Thus there are huge discrepancies in the amount of data available across geographies, with the tropics most poorly represented [Chapman et al.] (2024). While the collection and digitalisation of large field datasets is the long-term solution, the approach presented here of combining LULC and habitat classification with sparse observation data could also work for data-deficient species if we combine expert ecological knowledge [Merow et al.] (2022) in the training process.

Another advantage of Maxent which needs to be incorporated into deep learning SDMs is that approaches for addressing sample biases and other problems are well developed [Elith et al.] (2010), although there is evidence that non-parametric models (especially ensembles thereof) can outperform this approach [Valavi et al.] (2021). Future work should properly investigate the effect of and methods for addressing sample bias in deep learning SDMs.

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