Actual and future predicted occupancy of the Black Kite in Spain

- Case study of the course Monitoring and occupancy modelling -

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ABSTRACT

Climate change affects and will affect all levels of biodiversity. The Black Kite, as an abundant top predator, plays an important ecological role in Spain. The main goal is to assess the current occupancy of the Black Kite in Spain an make predictions for the change of occupancy due to climate change in the future. Furthermore, it is analysed which site covariates are important for the occurrence of the Black Kite. For accounting the climate change it is assumed that the annual mean temperature will increase and the total precipitation will decrease in Spain in the next 80 years. The main method is a static occupancy model with a spatial scale of 21 km^2 (grid cells). The eBird data set from 2019 is filtered for repeated surveys and used as the data source for fitting the occupancy model. The selection of site covariates is based on ecological knowledge of the focal species and an exploratory analysis with a Random Forests model. As detection covariates the duration of the observation and number of observers are selected. Used site covariates are the tree cover, grass cover, bare soil cover, annual mean temperature, isothermality, annual precipitation, distance to closest landfill and distance to closest river or lake. For the area of the mainland of Spain, the model predicts a mean occupancy probability under actual climate conditions of 52.6 %, in contrast of only 37.8 % under future climate conditions. The main driver is that the occupancy decreases with high annual mean temperature values. The uncertainties of the model are discussed and the transferability of the results to conservation planing is evaluated.

1 Introduction

Climate change affects all levels of biodiversity (Bellard et al. 2012; Garcia et al. 2014). A main task in ecological research is to build accurate models to predict the biological response to climate change (Urban et al. 2016; Araújo and Rahbek 2006).

One of the affected groups by the climate change are birds of prey. Birds of prey play a crucial role in ecosystems. Very often they are top predators. They can be regarded as flagship species, because they are very vulnerable to human activity, because of their role as top predator in food chains and because of the attractiveness of their behavior to humans. Furthermore, they provide regulating, supporting and cultural ecosystem services (Donázar et al. 2016).

A raptor species with a very wide distribution is the Black Kite, *Milvus migrans* (Boddaert, 1783). The distribution of this species ranges from Western Europe to East Asia and Australia (BirdLife International 2021). The species is mainly migratory and the European population stays in the winter in sub-Saharan Africa. The individuals leave the breeding area between July and October and come back back between February and May (Panuccio et al. 2014; BirdLife International 2021). In this case study the focus lies on the Black Kite population in Spain.

Citizen science data are often used in species distribution modelling, because of the high data availability. However there are some challenges in using these data sets, for example

the spatio-temporal bias of the of the observations. For instance people tend to watch for birds more in the breeding season and around their own home (Robinson et al. 2018; Reich et al. 2018). Two techniques are available to overcome this difficulties. First, it is possible to filter out low quality observations. Second, it is possible to apply statistical techniques to address sampling bias and observational heterogeneity (Steen et al. 2019). In this study the second option is used. Observational heterogeneity and imperfect detection is tackled with an extension of species distribution model, the so-called occupancy model (MacKenzie et al. 2002).

The model is used to learn more about the ecology of the focal species. This knowledge can be used in conservation planning.

The main questions are (1) which site covariates are most important for the occurrence of the Black Kite and (2) what happens to the Black Kite population in Spain under future climate conditions.

2 Methods

Data of the species occurrences are from eBird data (Sullivan et al. 2009; Cornell Lab of Ornithology 2021). The dataset is filtered for repeated surveys, that were done three to ten times in the same area between April and June of 2019. Only standing or travelling surveys with a total distance up to 5 km with one to five observers were used. To get an overview a map with all observations was produced using QGIS Development Team (2021).

Data preparation, selection of covariates, model selection, model evaluation and prediction were done with R Core Team (2021). Exploratory analysis of the covariates were done in Van Rossum and Drake (2009). An ODMAP-Protocol (Zurell et al. 2020) describing typical steps in species distribution modelling can be found in the electronic appendix (here).

Spatial resolution of the model

The home range size differs between younger not breeding individuals, that are one to seven years old, so-called floaters, (Blas et al. 2009) and the breeding individuals. Floaters had in south Spain an home range size over 300 km², breeding females 43 km² and breeding males 80 km² (Tanferna et al. 2013). However, these home range values were observed with radio-tracking of individuals and later on the calculation of the minimum convex polygon. The main activity is probably more restricted to centre of the area.

A resolution of 2.5 minutes (roughly 21.5 km²) was chosen. It is possible to argue that the size is too small for the large home range sizes of the Black Kite. However through spatial subsampling the data loss is higher with a coarser resolution and the connection between the observations and the site variables becomes less strong.

Selection of detection covariates

Detection covariates that are present in the eBird data are used. These are the day of the year, time when observation started, duration of observation, walking distance and protocol type (standing or travelling). The two most important covariates from the Random Forests model (see section on exploratory analysis of covariates) were used in the final model.

Selection of site covariates

First a preliminary selection of site covariates was compiled. These set include all bioclimatic variables (Fick and Hijmans 2017), land cover fractions, as the tree cover, the grass cover and the bare soil cover (Buchhorn et al. 2020b), and the distance between the centre of the raster cells to the closest landfill and the closest river or lake.

In the next step ecological hypotheses were formulated based on existing ecological knowledge from the literature. Some of the covariates were selected based on these hypotheses. As an additionally step, all preliminary covariates were used to fit a Random Forests model and to get the importance of all the covariates for predicting the detection probability of the Black Kite. The most important covariates from these analysis were added to the list of covariates.

The covariates from the ecological hypotheses and from the Random Forests model were tested for collinearity with the Variance Inflation Factor (as implemented in Heiberger 2020). Highly collinear covariates were removed. Maps of the final site covariates can be found in the appendix (see Figure 7). The complete selection process is shown in Figure
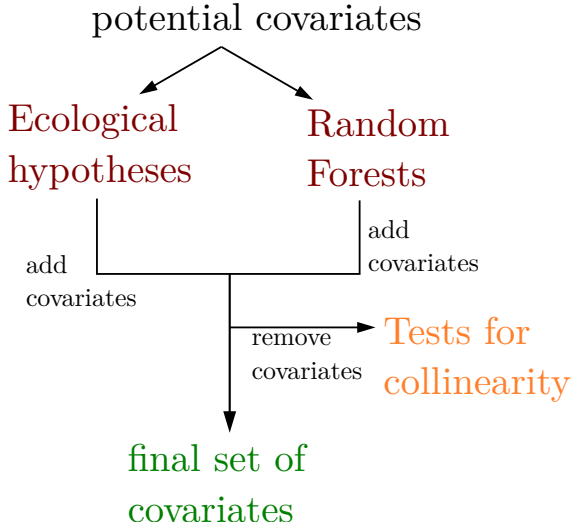
1 and further explained in the next sections.

potential covariates

Figure 1: Procedure of selecting site covariates for the occupancy model

Data preparation of site covariates

For all raster operations Hijmans (2021) was used. Bioclimatic variables were download from Fick and Hijmans (2017) in the target resolution. Tree cover, herbaceous vegetation cover and bare soil cover were downloaded (Buchhorn et al. 2020a; Buchhorn et al. 2020b). The raster images were merged to one file and then cropped to mainland of Spain. The resolution was resampled to the target resolution using a bilinear interpolation.

Land cover data was retrieved in vector format (Copernicus Land Monitoring Service 2018) and cropped to the mainland of Spain. The distance between each centre of the raster cell to all polygons of landfills and rivers or lakes was calculated with Bivand and Rundel (2020). Afterwards, the minimum distance was saved.

Ecological justification of site covariates

The selection of covariates is based on existing ecological knowledge about the focal species. A list of all site covariates and a corresponding simplified hypothesis can be found in Table 1.

Table 1: Site covariates and simplified hypothesized response of occupancy of the Black Kite, arrows symbolize the expected occupancy probability with higher values of the respective covariate

Site covariates
Annual Mean Temperature ↘
Annual precipitation ↗
Tree cover ↘
Grass cover ↗
Bare soil cover ↘
Distance to closest river or lake ↘
Distance to closest landfill ↘

The Black Kite uses a variety of feeding sources, for example birds, fish, crayfish, insects, carrion, vegetable matter and smaller mammals (Sergio and Boto 1999; Vinuela and Veiga 1992; BirdLife International 2021). Part of the prey is found in wetlands and marshes and it was proposed that the Black Kite has a habitat binding to wetlands and marshes (Veiga and Hiraldo 1990; Tanferna et al. 2013). Accordingly, the distance to the closest lake or river was calculated and used as a site covariate. The distance to the closed lake or river was used, because it is more important that lakes or rivers are nearby than that the Black

Kite was actually observed in a cell with a lake or a river.

It has been shown that Black Kites visit landfills for feeding (De Giacomo and Guerrieri 2008; Blanco 1994). Therefore the distance to the closest landfill were analysed. The landfill cover was not used, because in most of the raster cells landfills are not present and therefore the model fitting will not be optimal.

Black Kites breed in branches of trees. However, closed woodlands are avoided (Tanferna et al. 2013). Therefore the hypothesis is that the occupancy of the Black Kite follows a unimodal distribution with regard to the tree cover, where the occupancy is high at low to intermediate tree cover. In contrast, there should be a positive relationship with the grass cover, because the Black Kite is searching for prey in open landscapes. The bare soil cover is especially high in the mountains, the hypothesis is that the Black Kites is more a lowland species in Spain and avoids areas with high bare soil cover.

The annual mean temperature is added, because it is hypothesized that the Black Kite is negatively affected by too high annual mean temperatures. Additionally, a high annual precipitation may lead to more vegetation and more prey for the Black Kite. Both covariates are especially important for predicting the change of occupancy due to climate change.

Exploratory analysis of site and detection covariates

An exploratory analysis of the importance of the site and detection covariates was done using the machine learning method Random Forests (Ho 1995). All covariates as described before were used. These include all bioclim variables, land cover fractions, cover of water bodies, cover of landfills, distance to closest water body, distance to closest landfill and all detection covariates. From each grid cell one observation was selected and related to the site and detection covariates. Because of the higher number of non-detection an balanced Random Forest Classifier was used (Lemaître et al. 2017, with default parameters). Preparing the data, standardization of data and splitting in train and test data (80 % and 20 %) was done with Pedregosa et al. (2011), Harris et al. (2020), and McKinney (2010). 500 simulation were done to account variability in the model fit to the different data sets (each time one of the up to ten observations per grill cell was chosen). The mean and the standard error of the importance of all covariates was calculated. The effect of the most important covariates on the detection probability was tested. Therefore all other covariates were set to the mean and only the focal covariate was changed. The python script for conducting the analysis can be found in the appendix.

Selection of best model

A nullmodel, a model with only detection covariates, a model with only site covariates and a full model (site and detection covariates) were compared with the Akaike information criterion (AIC) and the Akaike information criterion corrected for small sample size
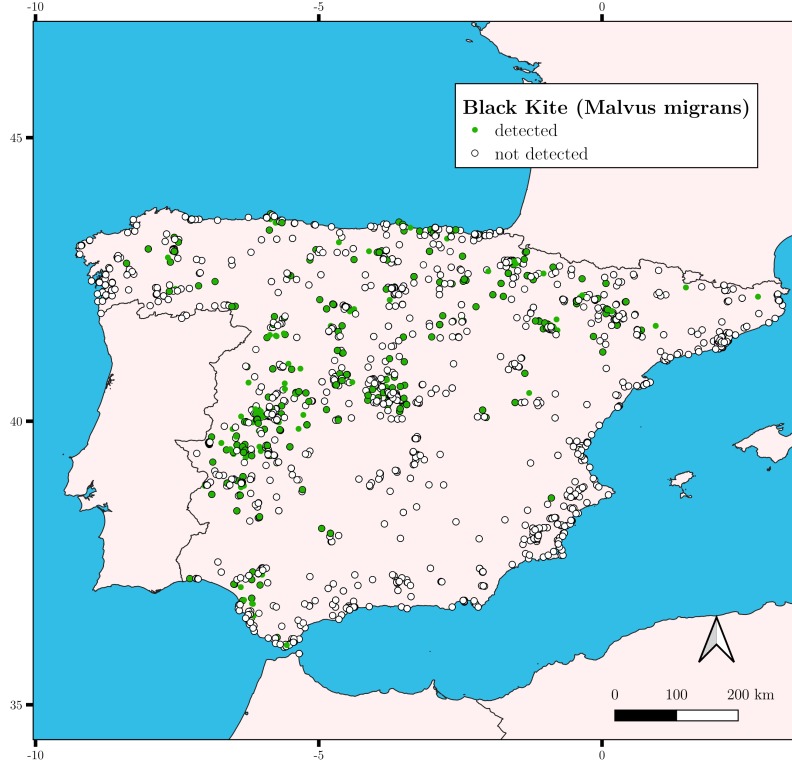
Figure 2: Detection of the Black Kite in the filtered eBird data set in Spain, each dot represents one observation within the repeated surveys, created with QGIS Development Team (2021)

(AICc) with Fiske and Chandler (2011). The model with the lowest AIC and AICc was chosen.

To compare the stability of the model an average model was build from the best model. Subsets of the best model were chosen with Bartoń (2020), all detection covariates were used as fixed terms (present in all subsetted models). Models were sorted according to the lowest AIC and selected with cumulative Akaike weight (Wagenmakers and Farrell 2004) larger than 95 %. The selected models are weighted with the AICs and averaged with Bartoń (2020).

Model evaluation

The predictive power of the best model is evaluated with the R^2-value (Nagelkerke 1991). A parametric bootstrapping approach is used to assess the goodness of fit ("parboot" function as implemented in Fiske and Chandler 2011). From the test results the $\hat{c}$-value was calculated. If this values is noticeably larger than one, it indicates overdispersion of the model. With this $\hat{c}$-value a quasi-Akaike information criterion corrected for small sample size (qAICc) was retrieved to see if there are big differences to the calculated AICc. Another goodness of fit as proposed by MacKenzie and Bailey (2004) was carried out (imple-
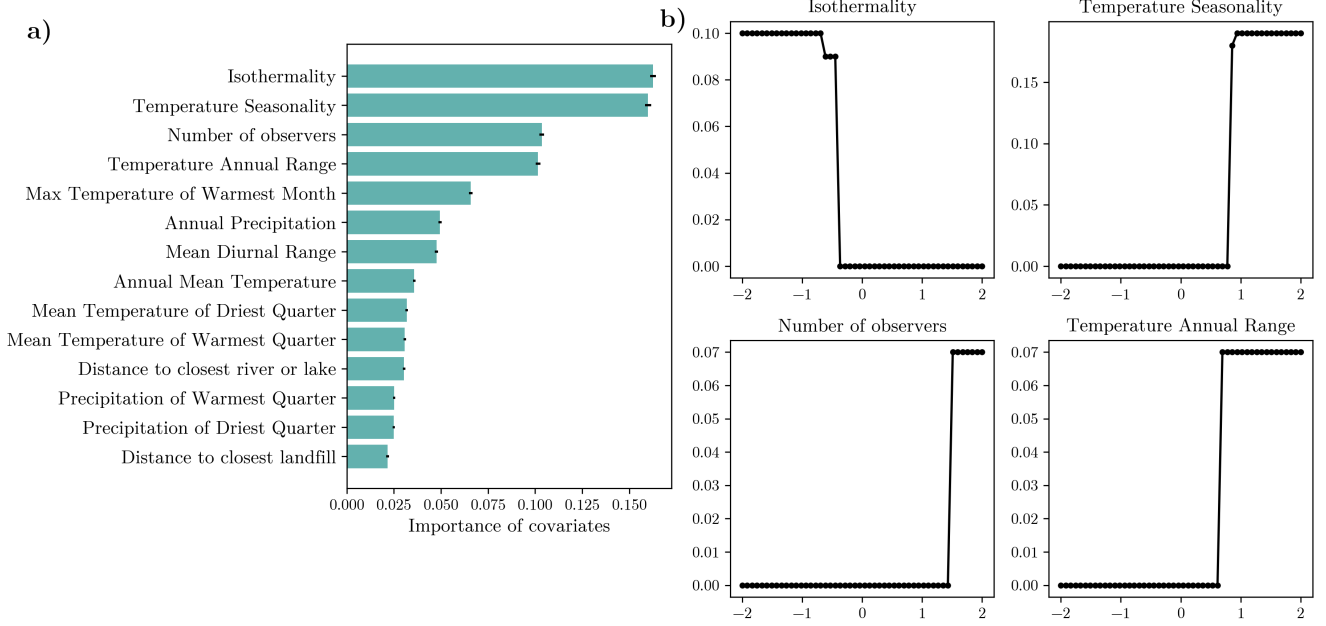
a)

b)

Figure 3: Relationship between covariates and detection probability, (a) importance of the covariates in the Random Forests model (only covariates with importance > 0.02 are included), mean importance values of 500 simulation are shown, black lines represent the standard error, and (b) influence of the four most important covariates on the detection probability of the Black Kite in Spain, the y-axis shows the probability, the x-axis the standardized value of the covariate, created with Hunter (2007)

mented in Mazerolle 2020).

Prediction

First, predictions were done first on the grid cells with observational data and secondly with the best model for the mainland of Spain. A map was produced with the predicted occupancy and the standard error of the prediction. The outcome of the best model were compared to the results from the average model.

Prediction of future climate conditions were done accordingly to existing knowledge about the climate change. The annual temperature will likely rise around 3 °C and the annual rainfall will decrease around 10 % from 2020 to 2100 (AEMET 2021). Iturbide et al. (2021)

show under the SSP2 4.5 scenario (Riahi et al. 2017) an increase between 2 and 3 °C and a decrease of total precipitation between 5 % and 20 % in different areas of Spain (mean values of 32 models, 2081-2100, relative to 1995-2014). The model agreement is high for the temperature increase, however the signal is not robust for the decrease in total precipitation. These data set is used to model the future occupancy of the Black Kite. The interactive atlas provides regional predictions on a spatial scale of 95 km edge length of a raster cell. GeoTIFFs were downloaded for the change in annual mean temperature and the annual total precipitation (change from 1995-2014 to 2081-2100). These raster files were cropped to the

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mainland of Spain and resampled to the target resolution (2.5 minutes of a degree). Maps of the changes in the target resolution can be seen in the appendix (see Figure 8). The change in temperature and precipitation were applied to the respective bioclimatic variables (Fick and Hijmans 2017).

We will only incorporate the habitat suitability in relation to climate factors and omit all biological mechanisms that are proposed to play a role for prediction by Urban et al. (2016) like demography or evolution of a population. It is therefore a simplistic model, but the goal is to catch the main trend.

The effect of the site and detection covariates were tested. Accordingly, all other covariate than the target covariate were set to the mean value and the predictions were done in the range of the target covariate that the model was fitted to. Occupancy probabilities were produced for this range the uncertainty was measured with the standard error.

3 Results

A map with all filtered observation from the eBird data set is shown in Figure 2. It can be observed that the main distribution is in central Spain. The Black Kite was detected from the coast of the Gulf of Cadiz northwards up to the western Pyrenees. However, in the southeastern part of Spain detections of the Black Kites are rare.

Exploratory analysis of covariates

The Random Forests model could explain close to 100 % of the detection of the Black Kite in the train and the test data set. An overview of the most important covariates can be found in Figure 3a.

Especially important are covariates that deal with temperature evenness over the year like isothermality, temperature seasonality and temperature annual range. The only detection covariate that really plays a role is the number of observers. More observers improve the chance to detect a Black Kite (see Figure 3b). Land cover fractions are not represented under the most important covariates. The annual precipitation is sixth influential covariate. The distance to the closest river or lake and the distance to the closest landfill play minor role.

The four most important factor, namely the isothermality, temperature seasonality, temperature annual range and maximal temperature of warmest month were added as preliminary covariates.

Occupancy model

Seven site covariates were analysed from the ecological hypotheses and four were added from the Random Forests model. Because of the high collinearity temperature seasonality, temperature annual range and maximal temperature of warmest month were excluded from the final list of covariates. After that the variance inflation factor was for all covariates below 1.9. The highest correlation exists
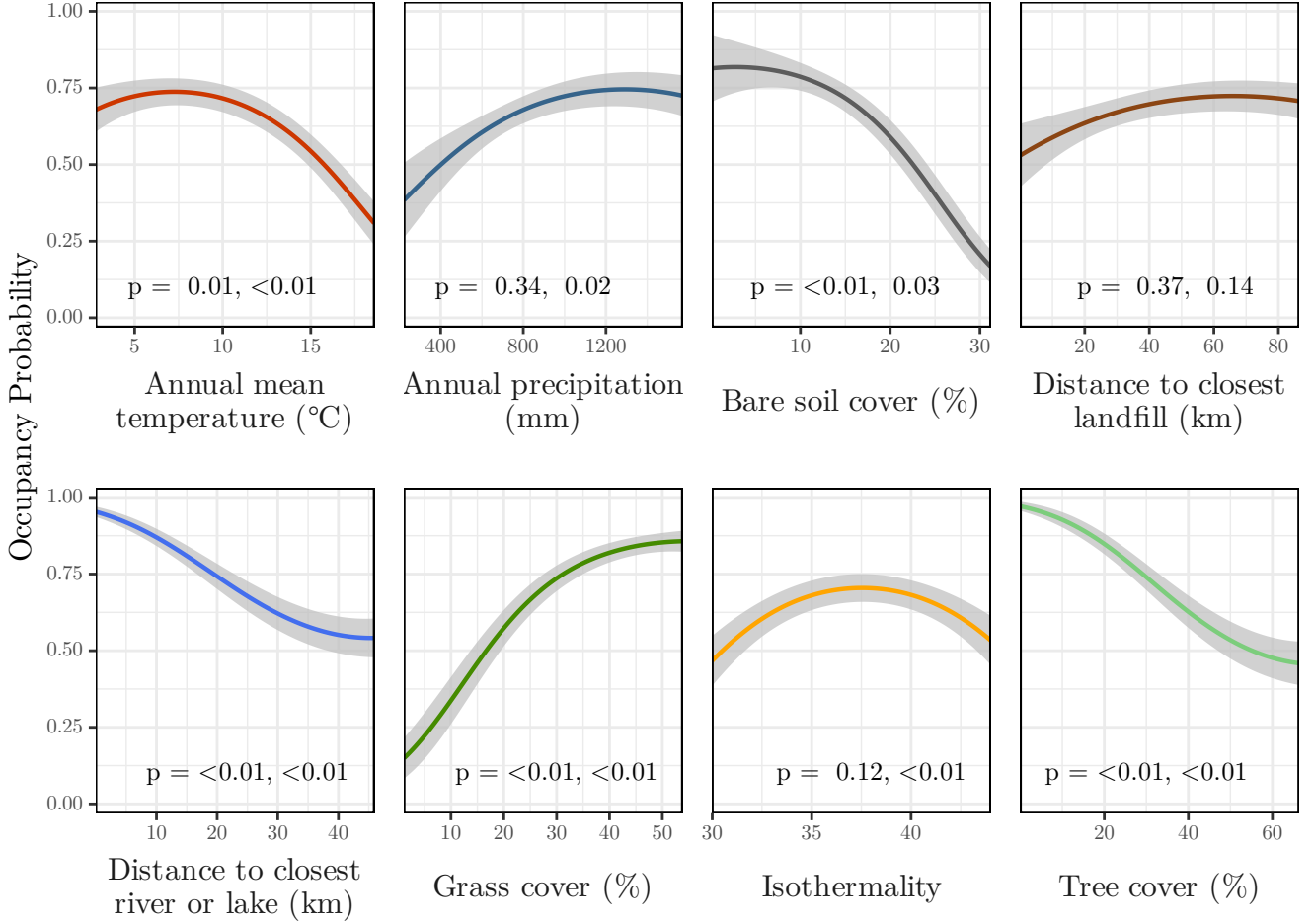
Figure 4: Predicted occupancy of the full model in response to site covariates, for each plot only the focal site covariate was varied, grey areas represent the standard error, the p values show the significance of the first and the second coefficient, created with Wickham (2016)

between the tree cover and the annual precipitation (Pearson $\rho = 0.62$).

The final best model is the full model and consists of 20 parameters and has an AIC of 4578. The second best model with only the site covariates has an AIC that is 143 higher (delta AIC). The AICc gives roughly the same result. In the full model there are two detection covariates, namely the number of observers and the duration of observation. The explained variance in the detection of the Black Kite is 35 % (R^2-value).

An average model was build from three single models. These are one model with all site covariates except the distance to closest landfill, the full model and a third model with all site covariates except the annual precipitation and the closest distance to landfills.

All site covariates are fitted as polynomials of two degrees. These are in the full model the annual mean temperature, the isothermality, the annual precipitation, the bare soil cover,
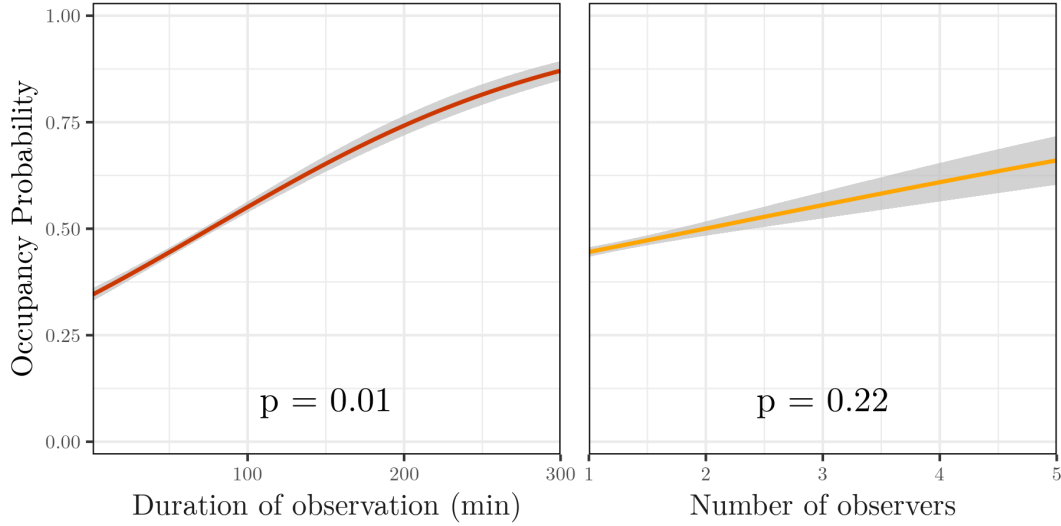
Figure 5: Predicted occupancy in response to detection covariates, for each plot only the focal detection covariate was varied, grey areas represent the standard error, the p values show the significance of the coefficient, created with Wickham (2016)

the grass cover, the tree cover, the distance to closest river or lake and the distance to closest landfill. All estimated values of the site covariates are significant different from zero, except the first coefficients of the isothermality and the annual precipitation and both coefficients of the distance to the closest landfill. The occupancy probability shows a positive relation with the grass cover and the annual precipitation. A unimodal relationship can be seen between the isothermality and the annual mean temperature and the occupancy probability of the Black Kite. Bare soil cover, distance to closest lake or river and a high tree cover have a negative influence on the occupancy probability (see Figure 4). These results go inline with the outcome of the average model. The uncertainty is high in the site covariates annual precipitation and the distance to closest landfill, the occupancy probability shows the same clear response to all other site covariates

as with the full model (see Figure 9 in the appendix).

The duration of the observation has a positive influence on the occupancy probability and the coefficient is significant different from zero. In contrast, the number of observers does not show a significant result (see Figure 5).

The full model predicts for the grid cell with observational data that 522 out of 1032 grid cells are occupied (51 %, median best unbiased predictor from occurrence state). In 503 grid cells was the Black Kite detected (49 %). The MacKenzie and Bailey (2004) goodness-of-fit test shows that the full model adequately fits the data ($\hat{c} = 0.83$, $p = 1$). Also the parametric bootstrap test does not indicate a lack of fit ($\hat{c} = 0.97$, $p = 0.86$). The $\hat{c}$-values are below zero, for this reason no QAIC and QAICc are calculated (they have the same values as the AIC and AICc when setting the $\hat{c}$-value to one).
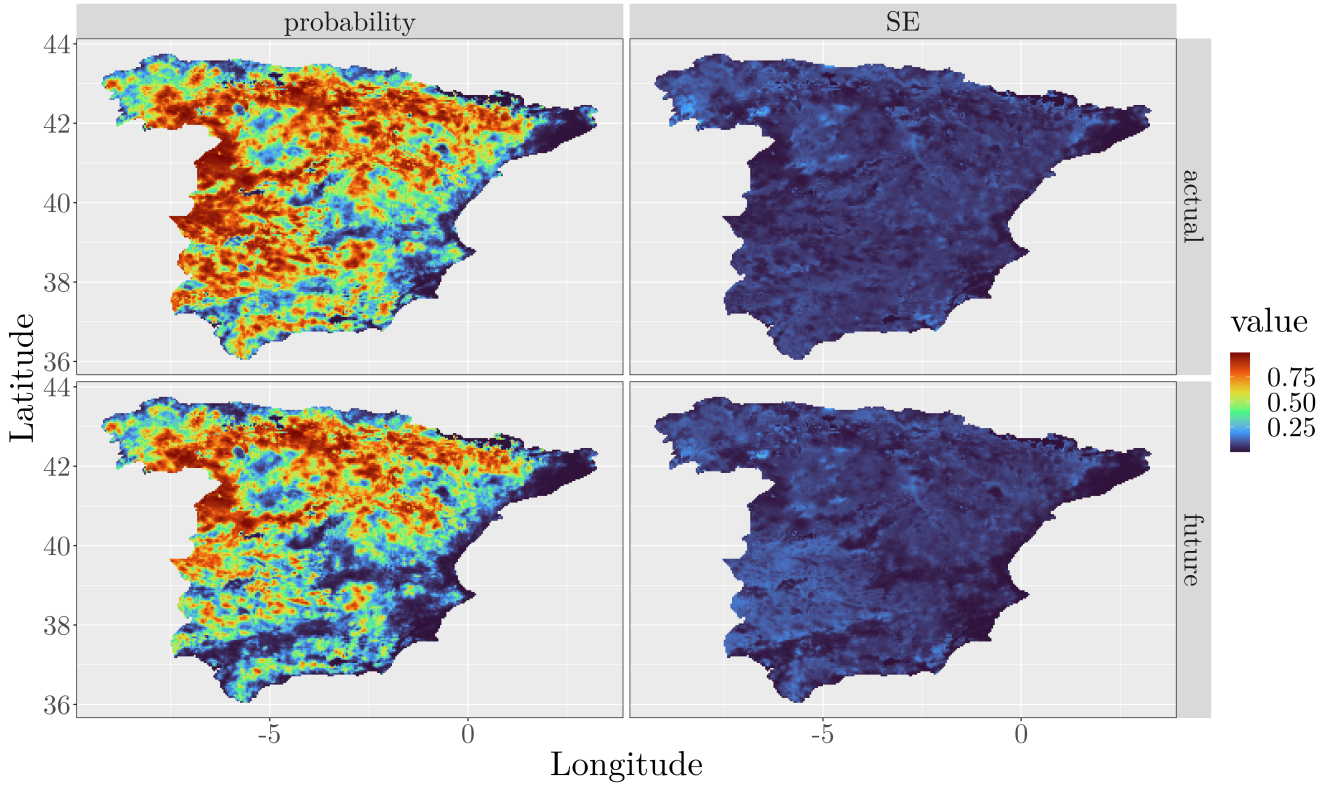
Figure 6: Occupancy map under actual and future climate conditions predicted with the full model, the occupancy probability is shown in the left maps, the corresponding standard error in the plots on the right side, created with Wickham (2016)

For the area of the mainland of Spain, the mean occupancy probability under actual climate conditions is 52.6 % (16748 grid cells with occupancy probability $>=$ 0.5). The mean occupancy probability decreases and is 37.8 % under future climate conditions (10290 grid cells with occupancy probability $>=$ 0.5). This decrease in occupancy is also visible in the map especially between Sevilla and Madrid (see Figure 6). In 92 % of all grid cells there is a lower occupancy probability under future climate conditions, in contrast in only 8 % of all grid cells the occupancy probability is higher under future climate conditions. The average model predicts very similar results (see Figure 10 in the appendix).

4 Discussion

My results imply that the climate change may negatively affect the occupancy of the Black Kite in Spain. However even if higher annual mean temperature has a clear negative effect on the occupancy of the Black Kite, the uncertainty for the annual precipitation is high. The climate predictions from the IPCC (Iturbide et al. 2021) had a very coarse scale in comparison with the scale of the occupancy model (95 km versus 4.6 km edge length) and the mod-

els had no robust signal about the decrease in annual precipitation in Spain. Furthermore, the annual mean temperature and the annual precipitation are not the only factors that influence the occupancy of the Black Kite. Also changes in the habitat will affect the occurrence of the Black Kite. Additionally, many biological mechanisms of the Black Kite are not covered in this simple model.

Tanferna et al. (2013) point out some challenges in the protection of birds of prey. These are the large home range sizes (especially for younger not breeding individuals), they uses different habitat types in different seasons of the year and they often need non-identical habitat characteristics on different spatial scales. That is why it is not so easy to derive conservation management measures from this study. Nevertheless, the grass cover and distance to closest river or lakes play an important role for the occupancy probability of the Black Kite in Spain as already mentioned in the literature (Tanferna et al. 2013; Veiga and Hiraldo 1990). It can be concluded that the Black Kite searches in open landscape and along rivers and lakes for prey. Conservation of the prey of these landscapes will probably also positively affect the population of the Black Kite.

However, no effect of the distance to closest landfill was detected here as proposed by Blanco (1997) and Blanco (1994). It is unlikely that landfills really do not play a role for searching for food. A possible explanations for this mismatch are that large landfills that are probably well visible in the Corine Land Cover data set (Copernicus Land Monitoring Service 2018) are often covered in reality and not accessible to the Black Kite. It is also possible that the citizen scientist did not look often around landfills and therefore the data fit is not good.

The duration of observation is the only significant detection covariate in this study. Maybe it would help to add other detection covariate to tackle the imperfect detection. An example would be the weather. The weather can influence the sight of the observers and the activity of the Black Kites. Beyond that study it would be possible to implement more detection covariates.

A possible extension of this static occupancy model would be a dynamic occupancy model. A dynamic occupancy model can give more insights on the population trends and can make more accurate predictions (Green et al. 2019). However, data from more than one year is needed to perform such an analysis.

A further addition would be to build a stochastic individual-based model that uses the occupancy map that is produced here as a habitat suitability map (see for example Zurell et al. 2012). Due to the relatively low population size of the Black Kite as a top predator stochastic processes may play a large role. Furthermore, colonization process of new areas can be explicitly modelled. However, it may be challenging to really implement the complete winter migration to Africa.

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Supplementary Information

The appendix consists of extra graphics and code for repeating the analysis.

Graphics
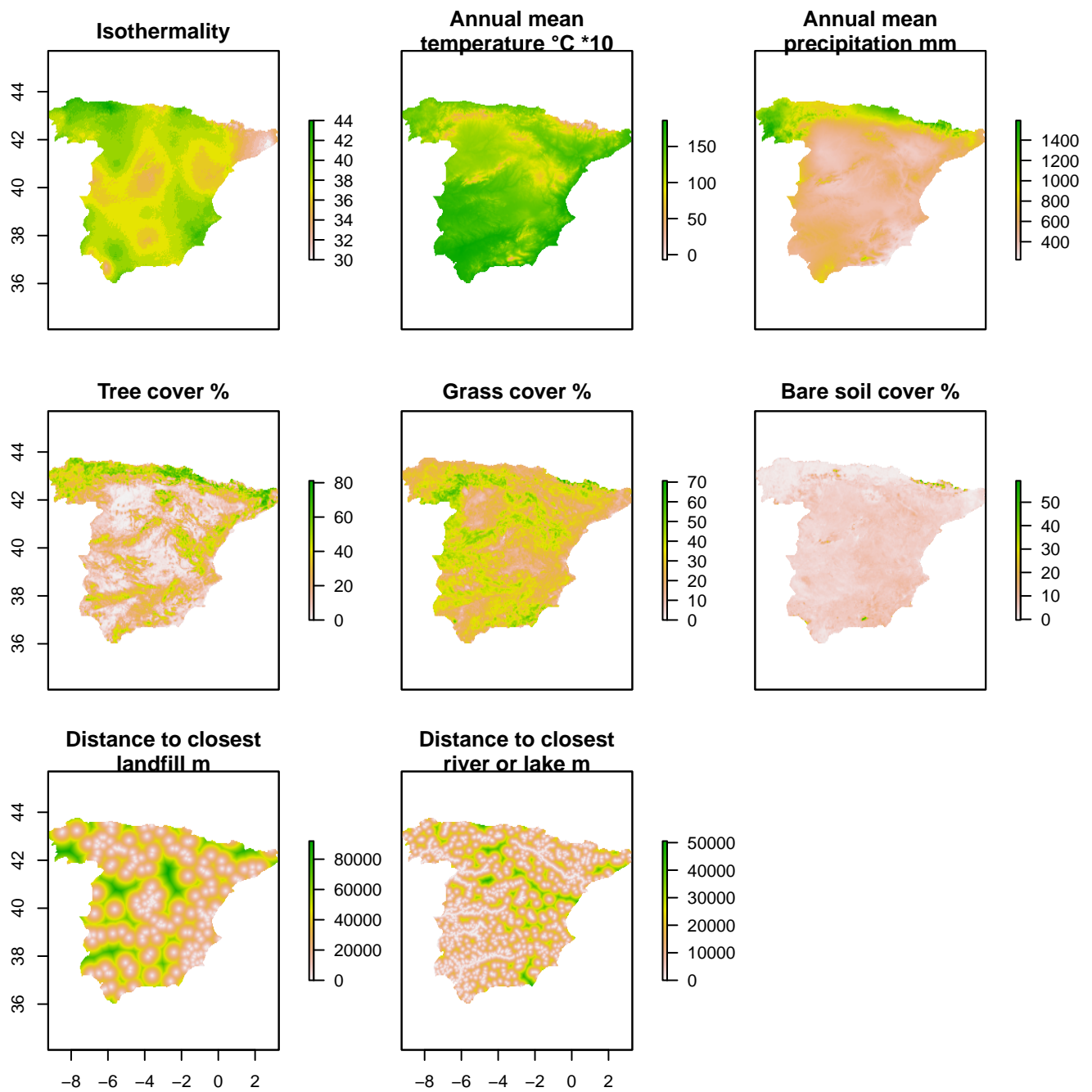
Figure 7: Maps of all site covariates, created with Hijmans (2021)
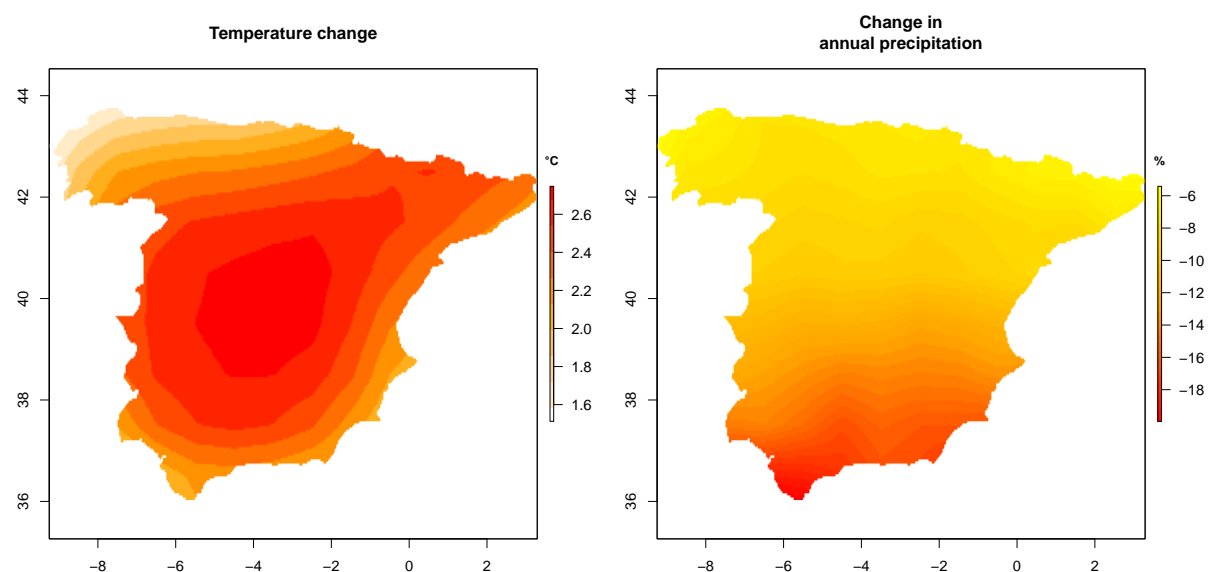
Figure 8: Change in the annual mean temperature and the annual precipitation between 1995-2014 and 2081-2100 with the SSP2 4.5 pathway, mean of 34 models (Iturbide et al. 2021), created with Hijmans (2021)
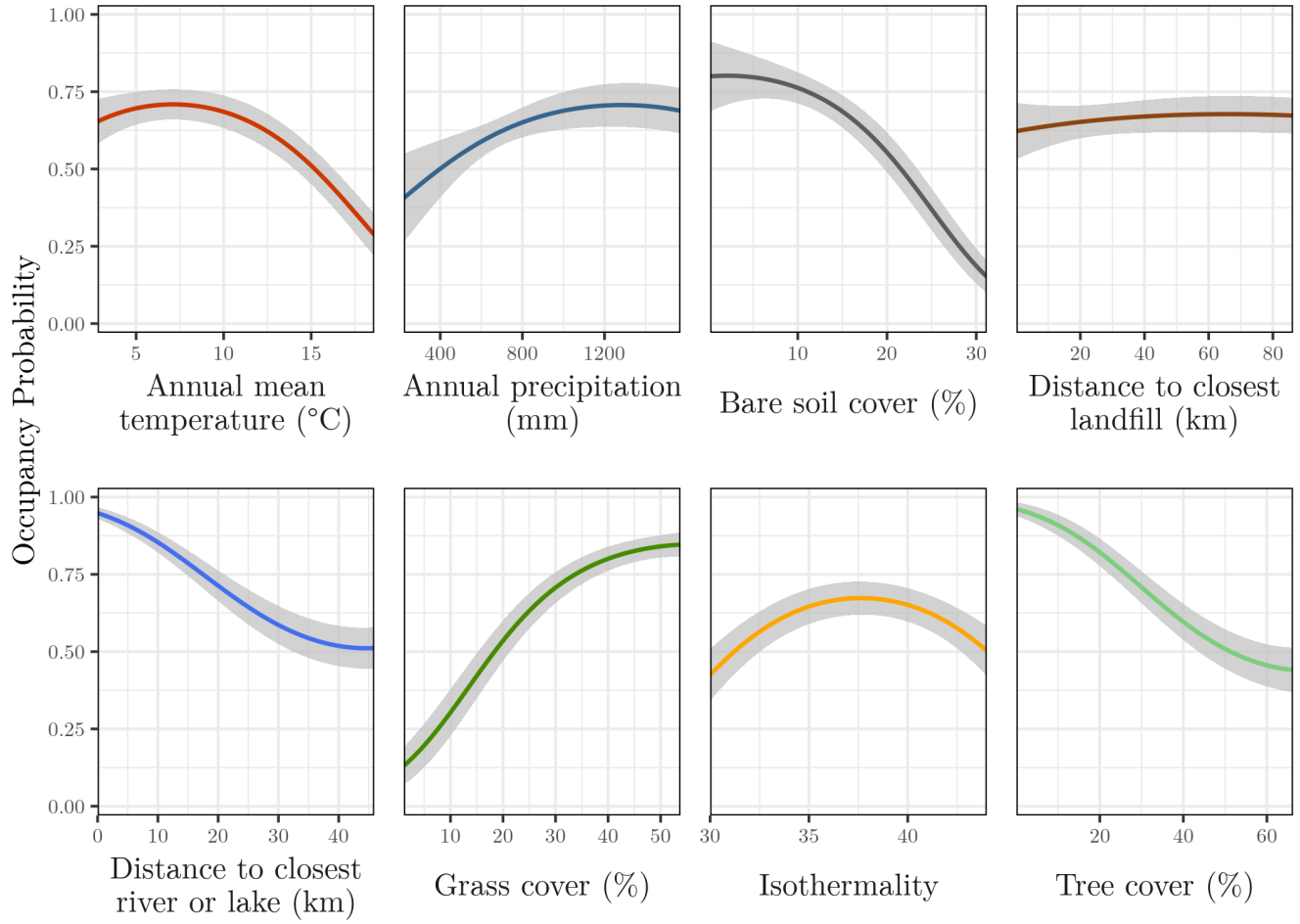
Figure 9: Predicted occupancy of the average model in response to site covariates, for each plot only the focal site covariate was varied, grey areas represent the standard error, created with Wickham (2016)
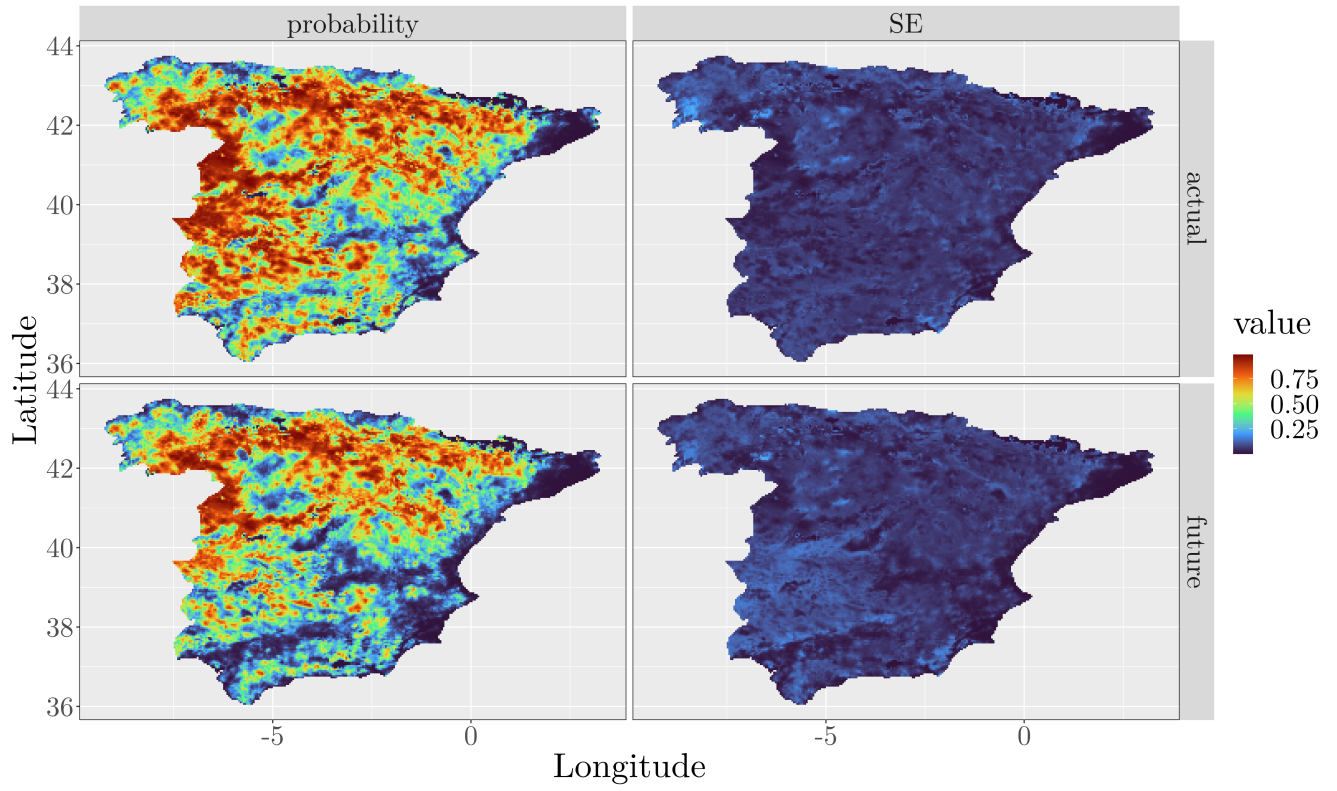
Figure 10: Occupancy map under actual and future climate conditions predicted with the average model, the occupancy probability is shown in the left maps, the corresponding standard error in the plots on the right side, created with Wickham (2016)

Code

The data and the R and Python Code can be found at
https://github.com/FelixNoessler/QCB_Black_Kite

The R-scripts for running the analysis are also embedded here (Python script is further down on page 54):

```r
############################################################
# First script
# Prepare the environmental data
#   - Land cover data
#   - Bioclimatic variables
#   - Distance to closest landfill and river or lake
#
# save everything as a raster stack in the target
# spatial resolution
#
# Prepare the change in annual temperature and
# in annual precipiytion for the prediction of
# of the futre climate condtions
#
############################################################



# Install required packages -------------------------------------------------
packages <- c("ggplot2", "gridExtra", "dplyr",
              "tidyr", "purrr", "HH", "psych", "MuMIn",
              "rnaturalearth", "rmapshaper",
              "auk", "unmarked", "AICcmodavg",
              "raster", "rgeos", "sp", "sf")

install.packages(setdiff(packages, rownames(installed.packages())))


# Loading packages -------------------------------------------------
library(ggplot2)
library(dplyr)
```

```r
32

33

34   # Loading geometries for the mainland of Spain ---------------------------
35   spain <- rnaturalearth::ne_countries(country = 'spain',
36                                        scale = 'medium',
37                                        returnclass = 'sf')
38   # spain %>%
39   #   ggplot()+
40   #   geom_sf(fill='black')
41

42

43   spain_crop <- rmapshaper::ms_filter_islands(spain,
44                                              min_area = 100000000000,
45                                              drop_null_geometries=T)
46   # plot(sf::st_geometry(spain_crop))
47

48

49   # Prepare climate data --------------------------------------------------
50   ### Climate data
51

52   if (!file.exists('data/environmental_data/clim.grd')) {
53     clim <- raster::getData('worldclim',
54                             var = 'bio',
55                             res = 2.5,
56                             download = F,
57                             path = 'data/environmental_data')
58
59     raster::xres(clim) * 111.19
60
61     clim <- raster::crop(clim, spain_crop)
62     clim <- raster::mask(clim, spain_crop)
63
64     raster::writeRaster(clim,
65                         'data/environmental_data/clim.grd',
66                         format = 'raster',
67                         options = 'INTERLEAVE=BAND',
68                         overwrite = TRUE)
69   } else {
70     clim <- raster::brick('data/environmental_data/clim.grd')
```

```r
71    }
72
73
74    # Prepare land cover data -------------------------------------------------
75
76    ### Tree cover
77
78    if (!file.exists('data/environmental_data/lc_tree.grd')) {
79      lc_tree1 <- raster::raster('data/environmental_data/tree_cover1.tif')
80      lc_tree1 <- raster::crop(lc_tree1, spain_crop)
81      lc_tree1 <- raster::mask(lc_tree1, spain_crop)
82
83      lc_tree2 <- raster::raster('data/environmental_data/tree_cover2.tif')
84      lc_tree2 <- raster::crop(lc_tree2, spain_crop)
85      lc_tree2 <- raster::mask(lc_tree2, spain_crop)
86
87      lc_tree3 <- raster::raster('data/environmental_data/tree_cover3.tif')
88      lc_tree3 <- raster::crop(lc_tree3, spain_crop)
89      lc_tree3 <- raster::mask(lc_tree3, spain_crop)
90
91      lc_tree4 <- raster::raster('data/environmental_data/tree_cover4.tif')
92      lc_tree4 <- raster::crop(lc_tree4, spain_crop)
93      lc_tree4 <- raster::mask(lc_tree4, spain_crop)
94
95      lc_tree <- raster::merge(lc_tree1, lc_tree2, lc_tree3, lc_tree4)
96      raster::plot(lc_tree)
97
98      lc_tree_cover <- raster::resample(lc_tree, clim, method = 'bilinear')
99      names(lc_tree_cover) <- 'tree_cover'
100
101     raster::writeRaster(lc_tree_cover,
102                         'data/environmental_data/lc_tree.grd',
103                         format = 'raster',
104                         options = 'INTERLEAVE=BAND',
105                         overwrite = TRUE)
106     rm(lc_tree1, lc_tree2, lc_tree3, lc_tree4, lc_tree)
107   } else {
108
109     lc_tree_cover <- raster::raster('data/environmental_data/lc_tree.grd')
```

```r
110  }
111
112
113  ### Herbaceous vegetation
114
115  if (!file.exists('data/environmental_data/lc_herbs.grd')) {
116
117    lc_herbs1 <- raster::raster(
118      'data/environmental_data/herbaceous_vegetation1.tif')
119    lc_herbs1 <- raster::crop(lc_herbs1, spain_crop)
120    lc_herbs1 <- raster::mask(lc_herbs1, spain_crop)
121
122    lc_herbs2 <- raster::raster(
123      'data/environmental_data/herbaceous_vegetation2.tif')
124    lc_herbs2 <- raster::crop(lc_herbs2, spain_crop)
125    lc_herbs2 <- raster::mask(lc_herbs2, spain_crop)
126
127    lc_herbs3 <- raster::raster(
128      'data/environmental_data/herbaceous_vegetation3.tif')
129    lc_herbs3 <- raster::crop(lc_herbs3, spain_crop)
130    lc_herbs3 <- raster::mask(lc_herbs3, spain_crop)
131
132    lc_herbs4 <- raster::raster(
133      'data/environmental_data/herbaceous_vegetation4.tif')
134    lc_herbs4 <- raster::crop(lc_herbs4, spain_crop)
135    lc_herbs4 <- raster::mask(lc_herbs4, spain_crop)
136
137    lc_herbs <- raster::merge(lc_herbs1, lc_herbs2,
138                              lc_herbs3, lc_herbs4)
139
140    # raster::plot(lc_herbs)
141
142    lc_herb_cover <- raster::resample(lc_herbs,
143                                      clim,
144                                      method = 'bilinear')
145    names(lc_herb_cover) <- 'grass_cover'
146
147    raster::writeRaster(lc_herb_cover,
148                'data/environmental_data/lc_herbs.grd',
```

```r
                  format = 'raster',
                  options = 'INTERLEAVE=BAND',
                  overwrite = TRUE)

  rm(lc_herbs1, lc_herbs2, lc_herbs3, lc_herbs4, lc_herbs)
} else {

  lc_herb_cover <- raster::raster('data/environmental_data/lc_herbs.grd')
}


### Bare soil

if (!file.exists('data/environmental_data/lc_bare_soil.grd')) {
  lc_bare1 <- raster::raster('data/environmental_data/bare_soil1.tif')
  lc_bare1 <- raster::crop(lc_bare1, spain_crop)
  lc_bare1 <- raster::mask(lc_bare1, spain_crop)

  lc_bare2 <- raster::raster('data/environmental_data/bare_soil2.tif')
  lc_bare2 <- raster::crop(lc_bare2, spain_crop)
  lc_bare2 <- raster::mask(lc_bare2, spain_crop)

  lc_bare3 <- raster::raster('data/environmental_data/bare_soil3.tif')
  lc_bare3 <- raster::crop(lc_bare3, spain_crop)
  lc_bare3 <- raster::mask(lc_bare3, spain_crop)

  lc_bare4 <- raster::raster('data/environmental_data/bare_soil4.tif')
  lc_bare4 <- raster::crop(lc_bare4, spain_crop)
  lc_bare4 <- raster::mask(lc_bare4, spain_crop)

  lc_bare <- raster::merge(lc_bare1, lc_bare2, lc_bare3, lc_bare4)

  # raster::plot(lc_bare)

  lc_bare_soil <- raster::resample(lc_bare, clim, method = 'bilinear')
  names(lc_bare_soil) <- 'bare_soil'

  raster::writeRaster(lc_bare_soil,
                      'data/environmental_data/lc_bare_soil.grd',
```

```r
                         format = 'raster',
                         options = 'INTERLEAVE=BAND',
                         overwrite = TRUE)

  rm(lc_bare1, lc_bare2, lc_bare3, lc_bare4, lc_bare)
}else{

  lc_bare_soil <- raster::raster('data/environmental_data/lc_bare_soil.grd')
}



# Calculate distance to closest river or lake -----------------------------


if (!file.exists('data/environmental_data/distance_to_water.grd')) {
  water <- sf::st_read('data/environmental_data/clc2018_vector/clc2018.gpkg',
                       query = "SELECT * FROM clc2018
                        WHERE Code_18 == 511
                        OR Code_18 == 512")

  plot(sf::st_geometry(water),  axes = TRUE)


  ## load only the first
  clim <- raster::raster('data/environmental_data/clim.grd')




  raster_points <-  as(clim,"SpatialPoints")
  water_poly <- as(water, "Spatial")

  water_poly@proj4string
  raster_points@proj4string



  crs1 <- sp::CRS('+proj=laea
```

```
227                 +lat_0=52
228                 +lon_0=10
229                 +x_0=4321000
230                 +y_0=3210000
231                 +ellps=GRS80
232                 +units=m
233                 +datum=WGS84 +no_defs')
234
235   raster_points_transformed <- sp::spTransform(raster_points, crs1)
236   plot(sf::st_as_sf(raster_points_transformed), cex=0.2, pch=15, axes=T)
237
238
239   water_poly_transformed <- sp::spTransform(water_poly, crs1)
240   plot(sf::st_as_sf(water_poly_transformed),  axes = TRUE)
241
242
243   dist1 <- rgeos::gDistance(raster_points_transformed[1:10000,],
244                             water_poly_transformed,
245                             byid=T)
246
247   dist2 <- rgeos::gDistance(raster_points_transformed[10001:20000,],
248                             water_poly_transformed,
249                             byid=T)
250
251   dist3 <- rgeos::gDistance(raster_points_transformed[20001:30220,],
252                             water_poly_transformed,
253                             byid=T)
254
255
256   min_distances <- c(apply(dist1,2,min),apply(dist2,2,min),apply(dist3,2,min))
257   data.frame(min_distances)
258
259   raster_points_df <- sp::SpatialPointsDataFrame(raster_points,
260                                                  data=data.frame(min_distances))
261
262
263   crs2 <- raster::projection(clim)
264   raster_points_df_backtransformed <- sp::spTransform(raster_points_df,
265                                                       crs2)
```

```r
266
267    dist_raster <- raster::rasterFromXYZ(raster_points_df_backtransformed)
268
269    #raster::projection(dist_raster)
270    #raster::projection(clim)
271    #raster::plot(dist_raster)
272    #raster::plot(clim)
273
274    names(dist_raster) <- 'distance_to_water'
275    raster::writeRaster(dist_raster,
276                        'data/environmental_data/distance_to_water.grd',
277                        format = 'raster',
278                        options = 'INTERLEAVE=BAND',
279                        overwrite = TRUE)
280
281    distance_to_water <- dist_raster
282  }else {
283    distance_to_water <- raster::raster(
284      'data/environmental_data/distance_to_water.grd')
285  }
286
287
288
289  # Calculate distance to closest landfill ---------------------------------
290
291  if (!file.exists('data/environmental_data/distance_to_landfill.grd')) {
292    landfills <- sf::st_read(
293      'data/environmental_data/clc2018_vector/clc2018.gpkg',
294      query = "SELECT * FROM clc2018
295      WHERE Code_18 == 132")
296
297    plot(sf::st_geometry(landfills),  axes = TRUE)
298    landfills
299
300    ## load only the first
301    clim <- raster::raster('data/environmental_data/clim.grd')
302
303
304
```

```r
raster_points <-  as(clim,"SpatialPoints")
landfills_poly <- as(landfills, "Spatial")

landfills_poly@proj4string
raster_points@proj4string



crs1 <- sp::CRS('+proj=laea
                 +lat_0=52
                 +lon_0=10
                 +x_0=4321000
                 +y_0=3210000
                 +ellps=GRS80
                 +units=m
                 +datum=WGS84 +no_defs')

raster_points_transformed <- sp::spTransform(raster_points, crs1)
plot(sf::st_as_sf(raster_points_transformed), cex=0.2, pch=15, axes=T)


landfills_poly_transformed <- sp::spTransform(landfills_poly, crs1)
plot(sf::st_as_sf(landfills_poly_transformed),  axes = TRUE)


dist1 <- rgeos::gDistance(raster_points_transformed[1:10000,],
                          landfills_poly_transformed,
                          byid=T)

dist2 <- rgeos::gDistance(raster_points_transformed[10001:20000,],
                          landfills_poly_transformed,
                          byid=T)

dist3 <- rgeos::gDistance(raster_points_transformed[20001:30220,],
                          landfills_poly_transformed,
                          byid=T)
```

```r
    min_distances <- c(apply(dist1,2,min),
                       apply(dist2,2,min),
                       apply(dist3,2,min))
    data.frame(min_distances)

    raster_points_df <- sp::SpatialPointsDataFrame(
      raster_points,
      data=data.frame(min_distances))


    crs2 <- raster::projection(clim)
    raster_points_df_backtransformed <- sp::spTransform(raster_points_df,
                                                        crs2)

    dist_raster <- raster::rasterFromXYZ(raster_points_df_backtransformed)


    #raster::projection(dist_raster)
    #raster::projection(clim)
    #raster::plot(log(dist_raster+1))
    #raster::plot(clim)

    names(dist_raster) <- 'distance_to_landfill'

    raster::writeRaster(dist_raster,
                        'data/environmental_data/distance_to_landfill.grd',
                        format = 'raster',
                        options = 'INTERLEAVE=BAND',
                        overwrite = TRUE)

    distance_to_landfill <- dist_raster
  } else {
    distance_to_landfill <- raster::raster(
      'data/environmental_data/distance_to_landfill.grd')
  }

```

```r
383
384   # Save all site covariates as one raster stack ----------------------------
385
386   variables <- raster::stack(clim,
387                              lc_tree_cover,
388                              lc_herb_cover,
389                              lc_bare_soil,
390                              distance_to_water,
391                              distance_to_landfill)
392
393
394
395   raster::writeRaster(variables,
396               'data/environmental_data/variables_spain.grd',
397               format = 'raster',
398               options = 'INTERLEAVE=BAND',
399               overwrite = TRUE)
400
401   # rm(clim, lc_tree_cover, lc_herb_cover, lc_bare_soil,
402   #    distance_to_landfill, distance_to_water,
403   #    spain, spain_crop, variables)
404
405
406
407
408   # Changes in temperature and precipitation --------------------------------
409   prec_change <- raster::raster(
410     'data/environmental_data/climate_change/precipitation.tiff')
411   temp_change <- raster::raster(
412     'data/environmental_data/climate_change/temperature.tiff')
413
414
415   ### Precipitation
416   prec_change <- raster::crop(prec_change, raster::extent(c(-12,5,30,50)))
417
418
419   #### edge length of one raster cell in km
420   prec_change_crs_m <- raster::projectRaster(
421     prec_change,
```

```r
422      crs = '+proj=laea +lat_0=52 +lon_0=10 +x_0=4321000
423      +y_0=3210000 +ellps=GRS80 +units=m +no_defs')
424  poly1 <- raster::rasterToPolygons(prec_change_crs_m)
425  sqrt(raster::area(poly1[1,])) / 1000
426
427  prec_change_rs <- raster::resample(prec_change, clim, method = 'bilinear')
428  prec_change_rs <- raster::crop(prec_change_rs, spain_crop)
429  prec_change_rs <- raster::mask(prec_change_rs, spain_crop)
430
431  ### Temperature
432  temp_change <- raster::crop(temp_change, raster::extent(c(-12,5,30,50)))
433
434  temp_change_rs <- raster::resample(temp_change, clim, method = 'bilinear')
435  temp_change_rs <- raster::crop(temp_change_rs, spain_crop)
436  temp_change_rs <- raster::mask(temp_change_rs, spain_crop)
437
438
439
440  # Plot the changes in a map ----------------------------------------------
441  pdf('results/climate_change.pdf', width=15, height=7)
442  par(mfrow=c(1,2),
443      oma = c(3, 4, 1, 2) + 0.1,
444      mar = c(0, 4, 4, 2) + 0.1)
445  pal1 = colorRampPalette(c('white', 'orange', 'red'))
446  raster::plot(temp_change_rs, main='Temperature change',
447               col = pal1(10),
448               legend.args = list(text = '°C', side = 3,
449                                   font = 2, line = 1, cex = 0.8))
450
451  pal2 = colorRampPalette(c('red', 'orange', 'yellow'))
452  raster::plot(prec_change_rs, main='Change in\nannual precipitation',
453               col = pal2(30),
454               legend.args = list(text = '%', side = 3,
455                                   font = 2, line = 1, cex = 0.8))
456
457  dev.off()
458  par(mfrow=c(1,1))
459
460
```

```r
461  # Save file as csv -----------------------------------------------------------
462  points <- raster::rasterToPoints(raster::brick(temp_change_rs,
463                                                   prec_change_rs))
464  change <- data.frame(points)
465
466  # avoid precision loss when saving the data frame
467  change$x <- sprintf("%.20f",change$x)
468  change$y <- sprintf("%.20f",change$y)
469
470  write.csv(change, "results/change_temp_prec.csv", row.names = FALSE)
471
472
473  # Clean up ------------------------------------------------------------------
474  rm(list = ls())
```

```r
############################################################
# Second script
#
#      1. Join the site covariates with the eBird data set
#      2. Standardize the site covariates
#      3. Do spatial subsampling
#      4. Store the data frame in the unmarked format
#
############################################################


# Loading packages -----------------------------------------------------
library(dplyr)



# Load data -------------------------------------------------------------

### Site covariates
variables <- raster::stack('data/environmental_data/variables_spain.grd')

### Bird data
milmig <- readr::read_csv('data/milmig.csv')

# filter for observations from the mainland of spain
# milmig <- milmig %>%
#   filter(!state_code=='ES-CN')



# Join eBird data and site covariates -----------------------------------
occ_var <- milmig %>%
  cbind(as.data.frame(
    raster::extract(variables,
                    milmig[,c('longitude', 'latitude')],
                    cellnumbers=T))) %>%
  tidyr::drop_na(bio1, tree_cover)

## save a data frame with not standardized covariates
write.csv(occ_var, "results/milmig_not_std.csv", row.names = FALSE)

```

```r
40
   # Standardize site covariates -------------------------------------------------
41
42
43 occ_var_std <- occ_var%>%
44   dplyr::mutate_at(c('bio1', 'bio2', 'bio3', 'bio4', 'bio5', 'bio6',
45                      'bio7', 'bio8', 'bio9', 'bio10', 'bio11', 'bio12',
46                      'bio13', 'bio14', 'bio15', 'bio16', 'bio17',
47                      'bio18', 'bio19',
48                      'tree_cover', 'grass_cover', 'bare_soil',
49                      'distance_to_water', 'distance_to_landfill'),
50                   ~(scale(.) %>% as.vector))
51
52
53 # Convert data frame to unmarked format ----------------------------------
54 occ_wide <- auk::format_unmarked_occu(
55   occ_var_std, site_id = 'site',
56   response = 'species_observed',
57   site_covs =c('cells', 'n_observations', 'latitude', 'longitude',
58               'bio1', 'bio2', 'bio3', 'bio4', 'bio5', 'bio6',
59               'bio7', 'bio8', 'bio9', 'bio10', 'bio11', 'bio12',
60               'bio13', 'bio14', 'bio15', 'bio16', 'bio17',
61               'bio18', 'bio19',
62               'tree_cover', 'grass_cover', 'bare_soil',
63               'distance_to_water', 'distance_to_landfill'),
64   obs_covs =c('time_observations_started','duration_minutes',
65               'effort_distance_km','number_observers', 'protocol_type',
66               'day_of_year'))
67
68
69 ### Convert the detection histories in 1=# presence/ 0= absence
70 # instead of TRUE/FALSE
71 cols <- sapply(occ_wide, is.logical)
72 occ_wide[, cols] <-lapply(occ_wide[, cols], as.numeric)
73
74
75 # Do spatial subsampling ----------------------------------------------------
76 # We can only have one (3 - 10 times repeated) observation per one grid cell!
77 occ_wide_clean <- occ_wide[!duplicated(occ_wide$cells),]
78
```

```r
# Part that is removed:
1- nrow(occ_wide_clean)/nrow(occ_wide)


# Save unmarked data as csv ------------------------------------------------
write.csv(occ_wide_clean, "results/milmig.csv", row.names = FALSE)


# Clean up -----------------------------------------------------------------
rm(list = ls())
```

```r
##########################################################
# Third script
#
#  Selection of covariates:
#      ... are based on ecological hypotheses and from
#          from the explanatory analysis with a Random
#          Forest model
#
#      --> here some covariates are excluded because of
#          collinerarity
#
##########################################################



# Load data ------------------------------------------------------------
occ_wide_clean <- read.csv("results/milmig.csv")



# Selected covariates --------------------------------------------------
random_forest_selection <- c('bio3', 'bio4', 'bio7', 'bio5')

ecological_selection <- c('bio1', 'bio12',
                          'tree_cover', 'grass_cover', 'bare_soil',
                          'distance_to_landfill',  'distance_to_water')

selected_covariates <- c(random_forest_selection, ecological_selection)
selection <- occ_wide_clean[, selected_covariates]



# Exclude some covariates ----------------------------------------------
selected_names <- names(selection)[! names(selection) %in% c('bio7', 'bio4', 'bio5')]



# Make a cluster dendrogram --------------------------------------------
## cluster with all selected covariates
cor1 <- abs(as.dist(cor(selection)))
clust1 <- hclust(1- cor1)
plot(clust1)

```

```r
40  ## cluster with some covariates removed
41  cor1 <- abs(as.dist(cor(selection[, selected_names])))
42  clust1 <- hclust(1- cor1)
43  plot(clust1)
44
45
46  # Correlation plots --------------------------------------------------------
47  ## Correlation plots with all covariates
48  psych::pairs.panels(selection)
49
50  ## Correlation plots with some covariates removed
51  psych::pairs.panels(selection[, selected_names])
52
53
54  # Test for collinearity ----------------------------------------------------
55  ## Test for collinearity with all covariates
56  HH::vif(selection)
57
58  ## Test for collinearity with some covariates removed
59  HH::vif(selection[, selected_names])
60
61
62  # Make maps of the final selected covariates -------------------------------
63  site_covariates <- raster::brick('data/environmental_data/variables_spain.grd')
64  site_covariates <- site_covariates[[selected_names]]
65
66  pdf('results/site_covs.pdf')
67  par(mfrow=c(1,1),
68      oma = c(0, 0, 0, 1) + 0.1,
69      mar = c(0, 4, 10, 2) + 0.1)
70  raster::plot(site_covariates, main=c('Isothermality',
71                                       'Annual mean\ntemperature °C *10',
72                                       'Annual mean\nprecipitation mm',
73                                       'Tree cover %',
74                                       'Grass cover %',
75                                       'Bare soil cover %',
76                                       'Distance to closest\nlandfill m',
77                                       'Distance to closest\nriver or lake m'))
78  dev.off()
```

```r
79
80
81
82  # Clean up ----------------------------------------------------------
83  rm(list = ls())
84  dev.off(dev.list()["RStudioGD"])
```

```r
############################################################
# Fourth script
#
# Build models with the unmarked package
#
# --> Compare different models with
#     information criterion
#
# --> evaluate the best model
#
# --> build an average model
#
############################################################

#
setwd("/home/felix/Dokumente/studium/Potsdam/Module/Biogeography/Black kite/R")

# Load packages --------------------------------------------------------
library(dplyr)
library(ggplot2)
library(unmarked)

# Load data ------------------------------------------------------------
occ_um <- formatWide(read.csv("results/milmig.csv"), type = "unmarkedFrameOccu")
summary(occ_um)


# Build models ---------------------------------------------------------
## Null model
occ_null <- occu(~ 1 ~ 1, occ_um)
summary(occ_null)
backTransform(occ_null, "state")

## Model only with detection covariates
detection_cov_model <- occu(~ duration_minutes
                                    + effort_distance_km
                                    ~ 1, data=occ_um)
summary(detection_cov_model)

```

```
40
41  ## Model only with site covariates
42  site_cov_model <-occu(~ 1
43                                       ~ poly(bio1, 2)
44                                       + poly(bio3, 2)
45                                       + poly(bio12, 2)
46                                       + poly(tree_cover, 2)
47                                       + poly(grass_cover, 2)
48                                       + poly(bare_soil, 2)
49                                       + poly(distance_to_water, 2)
50                                       + poly(distance_to_landfill, 2)
51                                       , data = occ_um)
52  summary(site_cov_model)
53
54
55
56
57  ## Full model with covariates
58  full_model <- occu(~ duration_minutes
59                                 + number_observers
60                                 ~ poly(bio1, 2)
61                                 + poly(bio3, 2)
62                                 + poly(bio12, 2)
63                                 + poly(tree_cover, 2)
64                                 + poly(grass_cover, 2)
65                                 + poly(bare_soil, 2)
66                                 + poly(distance_to_water, 2)
67                                 + poly(distance_to_landfill, 2), data = occ_um)
68  summary(full_model)
69
70  re <- ranef(full_model)
71  sum(bup(re, stat="mode"))
72  sum(bup(re, stat="mean"))
73
74
75  # Model selection ---------------------------------------------------------
76  ## Model selection with AIC
77  models_list <-list(Null = occ_null,
78                     detection = detection_cov_model,
```

```r
                   site = site_cov_model,
                   full_model = full_model)

un_models <- fitList(fits = models_list)
ModSelect <- modSel(un_models, nullmod = "Null")
ModSelect


## Model selection with AICc
AICcmodavg::aictab(models_list, second.ord = T)


best_model <- full_model



if (!file.exists('models.rda')) {

# Goodness of fit test of best model -------------------------------------
GOF <- parboot(best_model, nsim=500, ncores=8, report=T)
GOF

cHat <- GOF@t0 / mean(GOF@t.star)
cHat

### Another goodnes of fit test
AICcmodavg::mb.gof.test(best_model,
                        nsim=500,
                        plot.hist = F,
                        parallel=T,
                        ncores=8)



### QAICc
GOF1 <- AICcmodavg::aictab(models_list, c.hat = 1)
# --> it is the same as above, because the cHat value is below one


```

```r
118    # Build an average model --------------------------------------------------
119      ## Get the names of the detection covariates
120      det_terms <- MuMIn::getAllTerms(best_model) %>%
121        purrr::discard(stringr::str_detect, pattern = "psi")
122
123      ## Get combination of models, detection covariates are always present
124      occ_dredge <- MuMIn::dredge(best_model, fixed = det_terms)
125
126      ## Get the best models from the model list
127      occ_dredge_95 <- MuMIn::get.models(occ_dredge,
128                                         subset = cumsum(weight) < 0.95)
129
130      ## Get the average model based on model weights
131      #occ_avg <- MuMIn::model.avg(occ_dredge, fit = TRUE, revised.var = TRUE)
132      occ_avg <- MuMIn::model.avg(occ_dredge_95, fit=T)
133
134      ## Calculate the AICc for the average model
135      sum(occ_avg$msTable$AICc * occ_avg$msTable$weight)
136
137      ## Model coefficients of the average model
138      t(occ_avg$coefficients)
139
140      MuMIn::importance(occ_avg)
141
142      save(occ_avg, best_model, GOF, cHat, GOF1, file='models.rda')
143    }
144
145    # Clean up ----------------------------------------------------------------
146    rm(list = ls())
```

```
1   ########################################################
2   # Fifth script
3   #
4   #   Make all plots:
5   #        - Maps
6   #        - response of occupancy due to covariates
7   #
8   ########################################################
9
10  library(dplyr)
11  library(ggplot2)
12
13  # Load data ----------------------------------------------------------------
14  load('models.rda')
15  change <- read.csv('results/change_temp_prec.csv')
16  variables <- raster::brick("data/environmental_data/variables_spain.grd")
17
18
19  # Prepare data for predictions ---------------------------------------------
20  variables_selection <- c("bio1",
21                           "bio3",
22                           "bio12",
23                           "tree_cover",
24                           "grass_cover",
25                           "bare_soil",
26                           "distance_to_water",
27                           "distance_to_landfill")
28
29  variables.sel <- variables[[variables_selection]]
30
31  p_variables <- data.frame(raster::rasterToPoints(variables.sel) )
32  p_variables <- p_variables %>%
33    tidyr::drop_na(tree_cover, bio1)
34
35  change
36
37
38
39  change_joined <- p_variables %>%
```

```r
   left_join(change, by = c('x', 'y')) %>%
   select(x,y, temperature, precipitation) %>%
   mutate(temperature = temperature * 10,
          precipitation = 1 + precipitation/100)

mean(change_joined$temperature, na.rm=T)/10
mean(change_joined$precipitation, na.rm=T)



p_variables_std <- p_variables %>%
   mutate_at(variables_selection, ~(scale(.) %>% as.vector))

sd_bio1 <- sd(p_variables$bio1)
mean_bio1 <- mean(p_variables$bio1/ sd(p_variables$bio1))

sd_bio12 <- sd(p_variables$bio12)
mean_bio12 <- mean(p_variables$bio12/ sd(p_variables$bio12))

p_variables_std_future <- p_variables_std
p_variables_std_future$bio1 <-
   (p_variables$bio1 + change_joined$temperature) / sd_bio1 - mean_bio1
p_variables_std_future$bio12 <-
   (p_variables$bio12 * change_joined$precipitation) / sd_bio12 - mean_bio12

# Make predictions -------------------------------------------------------
# actual

# occ_avg, best_model
pred_actual <- unmarked::predict(occ_avg,
                                 newdata = select(p_variables_std,
                                                  -x, -y),
                                 type = "state")

# Predicted, fit
# SE, se.fit
actual_climate <- bind_cols(p_variables_std,
                            probability = pred_actual$fit,
                            SE = pred_actual$se.fit) %>%
```

```r
   select(x, y, probability, SE) %>%
   tidyr::pivot_longer(cols = c(probability, SE))


# future

# occ_avg, best_model
pred_future <- unmarked::predict(occ_avg,
                                 newdata = select(p_variables_std_future,
                                                  -x, -y),
                                 type = "state")

# Predicted, fit
v
future_climate <- bind_cols(p_variables_std_future,
                                    probability = pred_future$fit,
                                    SE = pred_future$se.fit) %>%
   select(x, y, probability, SE) %>%
   tidyr::pivot_longer(cols = c(probability, SE))

# join the data, preparation for plotting
data <- actual_climate %>%
   inner_join(future_climate, by = c("x", "y", "name")) %>%
   rename(actual = value.x,
          future = value.y,
          type = name)  %>%
   tidyr::pivot_longer(cols=c(actual, future))

# results/predictions_best_model.csv, or results/predictions_avg_model.csv
write.csv(data, 'results/predictions_avg_model.csv', row.names = F)

#### Plotting the map


# Plot the map -------------------------------------------------------------

# or load data:
# data <- read.csv('results/predictions_best_model.csv')
# data <- read.csv('results/predictions_avg_model.csv')
```

```r
data %>%
  ggplot(aes(x,y, fill=value))+
  geom_raster()+
  scale_fill_viridis_c(name="value", option="turbo")+
  theme(panel.border=element_rect(color="black",fill="transparent"),
        text = element_text(size=20))+
  labs(x="Longitude", y="Latitude")+
  coord_fixed()+
  facet_grid(~name ~ type)+
  theme(text = element_text(size=30, family = "LM Roman 10"))
# 'results/best_model_map.png' or 'results/avg_model_map.png'
ggsave('results/avg_model_map.png', width = 16, height=10)


# Mean probabilities
data %>%
  group_by(name) %>%
  filter(type == 'probability') %>%
  summarise(p = mean(value))

# sum of ells occupied
data %>%
  group_by(name) %>%
  filter(type == 'probability') %>%
  mutate(occ = value >= 0.5) %>%
  summarise(s = sum(occ))

data %>%
  tidyr::pivot_wider(names_from=name, values_from = value) %>%
  filter(type == 'probability') %>%
  mutate(lower = actual > future) %>%
  mutate(higher = actual < future) %>%
  summarise(lower = sum(lower), higher = sum(higher))

# total grid cells
nrow(data) / 4

# Prediction of covariates ----------------------------------------------
```

```
157
158  raw_data <- readr::read_csv('results/milmig_not_std.csv')
159  model_statistics <- readr::read_csv2('results/best_model.csv')
160
161  model_labels <- model_statistics %>%
162    rename(p = `P(>|z|)`) %>%
163    tidyr::pivot_wider(values_from=p, names_from = coef_no, id_cols=name) %>%
164    filter(name != '-') %>%
165    rename(first = `1`,
166           second = `2`) %>%
167    mutate(first = ifelse( round(first, 2) == 0,
168                           '<0.01',
169                           paste('', round(first, 2))),
170           second = ifelse(round(second, 2) ==0,
171                           '<0.01',
172                           paste('', round(second, 2))),
173           p =  paste('p = ',first, ', ', second, sep='')) %>%
174    select(name, p) %>%
175    mutate(name =
176             recode(name,
177                    bare_soil = "Bare soil cover (%)",
178                    tree_cover = "Tree cover (%)",
179                    grass_cover = "Grass cover (%)",
180                    bio1 = "Annual mean\ntemperature (°C)",
181                    bio3 = "Isothermality",
182                    bio12 = "Annual precipitation\n(mm)",
183                    distance_to_water = "Distance to closest\nriver or lake (km)",
184                    distance_to_landfill = "Distance to closest\nlandfill (km)"
185                    )) %>%
186    mutate(x = c(10, 38, 800, 30, 30, 15, 25, 45),
187           y = rep(0.1, 8))
188
189  variable_names <- c("bio1",
190                      "bio3",
191                      "bio12",
192                      "bare_soil",
193                      "tree_cover",
194                      "grass_cover",
195                      "distance_to_water",
```

48

```r
                      "distance_to_landfill")

rm(old_data)
for (i in seq_along(variable_names)) {
  variable_str <- variable_names[i]
  print(variable_str)


  newdata <- setNames(data.frame(
    matrix(ncol = length(variable_names),
           nrow = 1000)),
    variable_names)

  newdata[, i] <- seq(min(raw_data[, variable_str]),
                      max(raw_data[, variable_str]),
                      length.out = 100)

  newdata[is.na(newdata)] <- 0

  sd1 <- sd(newdata[, variable_str])
  mean1<- mean(newdata[, variable_str]/sd(newdata[, variable_str]))

  newdata[, variable_str] <- as.numeric(scale(newdata[, variable_str]) )

  # best_model, occ_avg
  predict_newdataset <- unmarked::predict(occ_avg,
                                          newdata = newdata,
                                          type = "state")
  # Predicted, fit
  # SE, se.fit
  plotting_data <- bind_cols(newdata,
                             occ_prob = predict_newdataset$fit,
                             occ_se = predict_newdataset$se.fit) %>%
    select(matches(variable_str), occ_prob, occ_se)

  plotting_data$x <- (plotting_data[, variable_str] + mean1)* sd1

  if (variable_str %in% c('bio1', 'bio2')) {
    plotting_data$x <- plotting_data$x / 10
```

```r
    } else if (variable_str == 'landfills'){
      plotting_data$x <- plotting_data$x * 100
    } else if (variable_str %in% c('distance_to_water',
                                   'distance_to_landfill')){
      plotting_data$x <- plotting_data$x /1000
    }

  new_data <- plotting_data %>%
    mutate(lower_se = occ_prob - occ_se,
           upper_se = occ_prob + occ_se) %>%
    select(x, occ_prob, lower_se, upper_se) %>%
    mutate(name = variable_str)

  if (i == 1){
    old_data <- new_data
  } else {
    old_data <- old_data %>%
      bind_rows(new_data)
  }
}



old_data %>%
  mutate(name = recode(name,
         bare_soil = "Bare soil cover (%)",
         tree_cover = "Tree cover (%)",
         grass_cover = "Grass cover (%)",
         bio1 = "Annual mean\ntemperature (°C)",
         bio3 = "Isothermality",
         bio12 = "Annual precipitation\n(mm)",
         distance_to_water = "Distance to closest\nriver or lake (km)",
         distance_to_landfill = "Distance to closest\nlandfill (km)")) %>%
  #filter(name != "Distance to closest\nlandfill (km)") %>%
  ggplot()+
  geom_text(data = model_labels,
            aes(x = x, y = y, label = p),
            family="LM Roman 10",
            size=3.5)+
```

```r
274    geom_ribbon(aes(ymin = lower_se,
275                    ymax = upper_se,
276                    x = x),
277              fill="gray", alpha=0.7) +
278    geom_line(aes(x=x, y=occ_prob, color=factor(name)),
279              size=0.8)+
280    scale_color_manual(values =
281                       c("Bare soil cover (%)" = "grey36",
282                         "Annual mean\ntemperature (°C)" = "orangered3",
283                         "Distance to closest\nriver or lake (km)" = "royalblue2",
284                         "Distance to closest\nlandfill (km)" = "chocolate4",
285                         "Tree cover (%)" = "palegreen3",
286                         "Grass cover (%)" = "chartreuse4",
287                         "Annual precipitation\n(mm)" = "steelblue4",
288                         "Isothermality" = "orange"))+
289    labs(x=NULL,
290         y="Occupancy Probability")+
291    theme_bw()+
292    theme(legend.position = "none",
293          panel.border = element_rect(color="black",fill="transparent"),
294          text = element_text(size=10, family="LM Roman 10"),
295          plot.margin=unit(c(2, 5, -5, 2), "points"),
296          panel.spacing = unit(0.8, "lines"),
297          strip.background = element_blank(),
298          strip.placement = "outside",
299          strip.text =  element_text(size=12, face='plain',
300                                     margin = margin(t = 0, r = 0, b = 10, l = 0)),
301          axis.title = element_text(size=12, face='plain'))+
302    scale_x_continuous(expand = expansion(mult = c(0, 0))) +
303    scale_y_continuous(limits = c(0,1),expand = expansion(mult = c(0.03, 0.03))) +
304    facet_wrap(. ~ name, scales="free_x", strip.position = 'bottom', ncol=4)
305 # 'results/avg_model_site_covariates.png', 'results/site_covariates.png'
306 ggsave('results/avg_model_site_covariates.png', width = 7, height = 5)
307
308
309 ######### detection covariates
310
311 summary(raw_data$duration_minutes)
312 summary(raw_data$number_observers)
```

```r
variable_names <- c('number_observers', 'duration_minutes')
newdata = setNames(data.frame(
  matrix(ncol = length(variable_names),
         nrow = 2000)),
  variable_names)
newdata[1:1000, variable_names[1]] <- seq(1, 5, length.out=1000)
newdata[1:1000, variable_names[2]] <- colMeans(raw_data[, variable_names[2]],
                                               na.rm=T)

newdata[1001:2000, variable_names[2]] <- seq(1, 300, length.out=1000)
newdata[1001:2000, variable_names[1]] <- colMeans(raw_data[, variable_names[1]],
                                                  na.rm=T)

best_model

predict_labels <- data.frame(
  name = c('Number of observers', 'Duration of observation (min)'),
  p = c('p = 0.22', 'p = 0.01'),
  x = c(3, 150),
  y = c(0.1, 0.1))


predict_newdataset <- unmarked::predict(best_model,
                                        newdata = newdata,
                                        type = "det")

plotting_data <- bind_cols(newdata,
                           occ_prob = predict_newdataset$Predicted,
                           occ_se = predict_newdataset$SE) %>%
  mutate(lower_se = occ_prob - occ_se,
         upper_se = occ_prob + occ_se,
         name = c(rep('Number of observers', 1000),
                  rep('Duration of observation (min)', 1000)))

plotting_data$x <- c(plotting_data[1:1000, 'number_observers'],
                     plotting_data[1001:2000, 'duration_minutes'])

plotting_data %>%
```

```r
352     ggplot()+
353     geom_text(data = predict_labels,
354               aes(x = x, y = y, label = p),
355               family="LM Roman 10", size=5)+
356     geom_ribbon(aes(ymin = lower_se,
357                     ymax = upper_se,
358                     x = x),
359               fill="gray", alpha=0.7) +
360     geom_line(aes(x=x, y=occ_prob, color=factor(name)),
361               size=0.8)+
362     scale_color_manual(values =
363                         c("Number of observers" = "orange",
364                           "Duration of observation (min)" = "orangered3"))+
365     labs(x=NULL,
366         y="Occupancy Probability")+
367     theme_bw()+
368     theme(legend.position = "none",
369           panel.border = element_rect(color="black",fill="transparent"),
370           text = element_text(size=10, family="LM Roman 10"),
371           plot.margin=unit(c(2, 5, -5, 2), "points"),
372           panel.spacing = unit(0.8, "lines"),
373           strip.background = element_blank(),
374           strip.placement = "outside",
375           strip.text =  element_text(size=12, face='plain',
376                                     margin = margin(t = 0, r = 0,
377                                                     b = 10, l = 0)),
378           axis.title = element_text(size=12, face='plain'))+
379     scale_x_continuous(expand = expansion(mult = c(0, 0))) +
380     scale_y_continuous(limits = c(0,1), expand =
381                         expansion(mult = c(0.03, 0.03))) +
382     facet_wrap(. ~ name, scales="free_x", strip.position = 'bottom', ncol=4)
383 ggsave('results/det_covariates.png', width = 6, height = 3)
```

Python script for running the Random Forest model:

```python
from sklearn import model_selection, preprocessing
from imblearn import ensemble
import pandas as pd
import numpy as np
import matplotlib.pyplot as plt

plt.rcParams.update({
    "font.family": "sans-serif",
    "font.sans-serif": ["Latin Modern Roman"]})

data = pd.read_csv('milmig.csv')

## observational covariates
observational_covariates = data.loc[:, 'time_observations_started.1':'day_of_year.10']
observational_covariates.loc[:,'site'] = data.site
stubnames = ['time_observations_started.', 'duration_minutes.', 'effort_distance_km.',
             'number_observers.','day_of_year.', 'protocol_type.']
obs_covariates_long = pd.wide_to_long(observational_covariates,
                                      stubnames,
                                      i='site',
                                      j='observation')
obs_covariates_long = obs_covariates_long.rename(
    columns={"time_observations_started.": "daytime",
             "duration_minutes.": "duration",
             "effort_distance_km.": "distance_km",
             "number_observers.": "n_observers",
             "day_of_year.": "day_of_year",
             "protocol_type.": "protocol_type"})
obs_covariates_long['protocol_type'] = preprocessing.LabelEncoder().fit_transform(
    obs_covariates_long['protocol_type'])
sc = preprocessing.StandardScaler(with_mean=False, with_std=False)
obs_covariates_transformed = sc.fit_transform(obs_covariates_long)


## site covariates
site_covariates = data.loc[:, 'bio1':'marshes']
site_covariates_long = site_covariates.loc[
```

```python
        np.tile(np.arange(0, len(site_covariates)), 10)]




## join covariates to one table
covs = np.concatenate((site_covariates_long.values,
                       obs_covariates_transformed),
                      axis=1)
column_names = np.append(site_covariates_long.columns,
                         obs_covariates_long.columns)



## detection
observed = pd.melt(data.loc[:, 'y.1':'y.10'])

## simulation
n_sim = 500

feature_imp = []
pred_data_all = []
for i in range(n_sim):

    random_numbers = np.random.randint(1, data.n_observations)

    y = observed.iloc[random_numbers, 1]
    x = covs[random_numbers, :]

    x_train, x_test, y_train, y_test = model_selection.train_test_split(
        x, y, test_size=0.0001)
    clf = ensemble.BalancedRandomForestClassifier()

    clf.fit(x_train, y_train)
    feature_imp.append(clf.feature_importances_)

    predict_data_list = []
    for name in column_names:
        mean_x = np.mean(x, axis=0)
        dummy_data = np.tile(mean_x[:, None], 50)
        covariate = np.linspace(-2, 2, 50)
```

```python
            dummy_data[column_names == name] = covariate
            pred = clf.predict_proba(dummy_data.T)
            predict_data_list.append(pred[:, 1])


    pred_data_all.append(predict_data_list)



feature_imp = np.array(feature_imp)
importance = np.mean(feature_imp.T, axis=1)
importance_sd = np.std(feature_imp.T, axis=1) / np.sqrt(n_sim)

proper_names ={"bio1": "Annual Mean Temperature",
              "bio2": "Mean Diurnal Range",
              "bio3": "Isothermality",
              "bio4": "Temperature Seasonality",
              "bio5": "Max Temperature of Warmest Month",
              "bio7": "Temperature Annual Range",
              "bio9": "Mean Temperature of Driest Quarter",
              "bio10": "Mean Temperature of Warmest Quarter",
              "bio12": "Annual Precipitation",
              "bio17": "Precipitation of Driest Quarter",
              "bio18": "Precipitation of Warmest Quarter",
              "distance_to_water": "Distance to closest river or lake",
              "distance_to_landfill": "Distance to closest landfill",
              "n_observers": "Number of observers",
              "duration": "Duration of observation"}

for key, val in zip(proper_names.keys(), proper_names.values()):
    column_names[key == column_names] = val


filter_index = importance > 0.02
selected_columns = column_names[filter_index]
selected_columns


plt.barh(np.arange(len(selected_columns)), np.sort(importance[filter_index]),
         xerr=importance_sd[filter_index][np.argsort(importance[filter_index])],
         align='center', color='#21918C', alpha=0.7)
plt.yticks(np.arange(len(importance[filter_index])),
           selected_columns[np.argsort(importance[filter_index])], size=12)
```

```python
116   plt.xlabel('Importance of covariates', size=12)
117   plt.tight_layout()
118
119   plt.savefig('importance_features.png', dpi=300)
120   plt.show()
121
122
123
124   #############
125   pred_data_all = np.array(pred_data_all)
126   plt.figure(figsize=(6, 6))
127
128   for i, name in enumerate(
129           selected_columns[np.argsort(importance[filter_index])][::-1]):
130       if i < 4:
131           plt.subplot(2,2, i+1)
132           data = pred_data_all[:, column_names == name, :]
133           y_pred = np.mean(data, axis=1)[1]
134
135           plt.plot(np.linspace(-2, 2, 50), y_pred, '.-k')
136           plt.title(name)
137   plt.tight_layout()
138   plt.savefig('response.png', dpi=300)
139   plt.show()
```