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Data driven fuzzy suitability modelling as a method for assessing habitat choice of migratory Red Kites (*Milvus, milvus*) across Spain

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Data driven fuzzy habitat suitability modelling as a preliminary method for assessing habitat choice of migratory Red Kites (*Milvus, milvus*) across Spain

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Master thesis, 30 credits, in *Physical Geography and Ecosystem Analysis*

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Abstract

As an increasing number of species drift onto the IUCN's list of endangered species, it has become increasingly important to understand the fundamental aspects that are essential in maintaining the fitness of these threatened species. One such species, *Milvus milvus* or commonly known as the Red Kite, has seen its populations and geographic extent reduced, primarily through human persecution, direct and indirect poisoning and habitat degradation. For this thesis, juvenile kites were tagged in Switzerland and then undertook a winter migration to Spain. During the months of December 2016 and January 2017 the data received was analysed and fuzzy membership functions were created based on 75% of the data, the training set, using different bioclimatic predictors that were deemed potentially important to species habitat choice. These functions were then combined using various weighted linear combinations (WLC), with both the combinations of predictors and their respective weights being altered in to best explain the habitat choice of the training set, the best result then being validated against the remaining 25% of the data, the validation set. Although the training set was well explained by the resulting WLC's, the model failed to explain the validation set's habitat choice with any statistical success. The model showed that no single predictor had the ability to explain the habitat choice and could be partially attributed to the absence of potentially significant predictors, such as a food source, which for the red kite, mostly consists of small mammals. This, along with the generally elevated species plasticity, could have been responsible for the shortcomings in the model's predictive abilities.

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List of abbreviations

BCMP – Bioclimatic predictors

CORINE - Coordination of information on the environment

DEM – Digital elevation model

EEA – European Environmental Agency

HSM – Habitat suitability model

KDE – Kernel density estimator

K-S – Kolmogorov Smirnov

NDVI - Normalised Difference Vegetation Index

RMSE – Root-mean-square error

RS – Relative spread

WLC – Weighted linear combination

Introduction

Due to the ever-increasing number of species that find themselves on the International Union for Conservation of Nature's red list of threatened species, isolating and understanding the bioclimatic limits that affect distribution is critical when undertaking and implementing meaningful conservation efforts. Both direct and indirect threats have resulted in heavy declines of the Red Kite (*Milvus. milvus*) populations across the extent of its fundamental niche and there is little understanding of the factors that explain its current distribution (Heuck et al., 2013).

Fuzzy models have been widely applied to create various environmental models and unlike previous models using crisp boolean values, the integration of varying degrees of membership has allowed for the inherent uncertainties to be taken into account as there is rarely a specific value which defines the bioclimatic limits of a species. This application makes different variables and predictors spatially inter-relatable, thus allowing for the construction of species habitat suitability or distribution models. One of the main constraints of applying fuzzy logic is the need for "expert knowledge", previous studies or input that defines the species-specific bioclimatic limits of said species in order to classify a predictor or variable into its subsequent fuzzy suitability value. This method is often subject contrasting values, specifically for species who exhibit a high level of plasticity or adaptability to biogeographic factors, such as the Red Kite (Vismara et al., 2001; Heuck et al., 2013). Being an allopatric species, its species-specific niche might vary across the extent of its fundamental niche and therefor adapted values for its bioclimatic limits might be necessary for different locations (Newton et al., 1994). To account for this, the use of data-driven fuzzy membership functions can potentially allow for the isolation of the local bioclimatic limits of a species in order to generate a more reliable suitability model and refine the understanding of the species needs to ultimately implement effective local conservation efforts.

1.1 Aims and Hypothesis

How a species prioritises habitat choices can be down to a variety of drivers, being a highly plastic species, Red Kites could display a strong preference for a specific underlying variable or parameter or a specific combination that might not be apparent at first glance could be the key to understanding habitat suitability. To test this the following hypothesis were formulated:

H1: The use of data driven fuzzy membership functions will allow the construction of a habitat suitability model that performs above the noise of species plasticity.

H2: The best performing model derived from the training data will best explain the distribution of the validation data.

H0: Species plasticity will not allow for the isolation of habitat preference and therefore little to no habitat preference will be found.

2.0 Background

2.1 *Milvus, milvus*

The Red kite (*Milvus, milvus*) and Black kites (*Milvus, migrans*) are the two main species of kites belonging to the genus, *Milvus*. Both species are opportunistic raptors who will usually favour open habitats for hunting purposes, but are usually located near fragmented forests or tree patches for roosting and breeding (Mougeot et al., 2011). The focus of this thesis will be on the former species, *Milvus milvus*, endemic to the western Palaearctic, which despite physical similarities, is currently much less successful than the more numerous and widely distributed sister species, *Milvus migrans* (Mougeot and Bretagnolle, 2006). The population is now at just a fragment of its former state as a result of human persecution and habitat degradation, mostly throughout the 19th century, where it was considered a pest species due to being mistakenly considered a threat to livestock and game species (Seoane et al., 2003; Smart et al., 2010; Pain et al., 2007) .

2.2 *Current population and distribution*

As previously noted, Black kites are currently widely distributed around the world and are regarded as one of the most abundant and successful birds of prey (Kumar et al., 2014). In contrast, the Red kite is currently listed as an endangered species worldwide under the Red List of the International Union for Conservation of Nature, Annex II of the Bern convention (Berny and Gaillet, 2008) and listed as a species of European conservation concern (BirdLife International, 2015). The Red Kite is a raptor species that is characterised by a largely European distribution (95% of population within European borders) extending only around 2 million km². Additionally, small populations are found dotted around the Mediterranean and sparse locations in Africa but their breeding status is uncertain (Seoane et al., 2003).

Germany, Spain and France currently host the majority of Red Kite populations, boasting around 75-85% of the current world population (Mougeot and Bretagnolle, 2006). Although the population stabilised in the 1970-1990, it has declined by almost 20% from 1990 to 2000 and up to 30% in the last 34.5 years (BirdLife International, accessed 2017), leading to the inclusion of the Red Kite on the previously stated European Red List. The population is currently deemed to be in decline as already decimated populations are shown to be dwindling across the majority of territories. In Spain the breeding population has been marked by a 46%

decline from 1994 to 2004 and surveys from 2004 estimate a reduction of the wintering population by 50% since 1994 and has continued to do so since (Mougeot et al., 2011; Mougeot and Bretagnolle, 2006).

Particularly heavy persecution led to the extinction of Red Kites within the UK and Scotland by the end of the 19th century (Pain et al., 2007). Only a small isolated remnant of the formally widespread population remained in Wales but due to genetic bottlenecks resulting from a restricted gene pool in conjunction with unfavourable climatic conditions and continued persecution, numbers struggled to increase (May et al., 1993; Smart et al., 2010). In addition to these issues, the Red Kite is a philopatric species therefore natural expansion of small populations is somewhat unlikely (Newton et al., 1994). In 1989 a re-introduction program using juveniles from other European countries was undertaken to try and reinstate a breeding population and through the controlled release of the juvenile kites and reduced persecution, a breeding population was able to take a foothold and now account for some 4-5% of the global population (Wotton et al., 2002). As a result of this program, the United Kingdom, along with Switzerland and Sweden, are the exception to the global declining trend and boast rising population numbers (Evans and Pienkowski, 1991; Schaub, 2012). Should the population trends in these countries be sustained, a reduction in the rate of decline and possibly outweigh the decline observed in Iberia and ultimately, a population increase could be observed (BirdLife International, 2015).

There are variations in the estimates for the current total number of breeding pairs, ranging from 10,800 upwards (Ferguson-Lees and Christie, 2001). A review of available data in 2009 concluded the population of Red kites to be around 21,000 to 25,500 breeding pairs, but more recently assessed by the European Red List of Birds to be closer to 25,200 to 33,400 breeding pairs (Birdlife International 2015). The variation in the estimations most likely stems from the difficulties in estimating raptor population sizes. Although there are several methods for estimating population sizes, these census techniques are somewhat inadequate for measuring groups of raptors. Many indirect estimation techniques are used for other groups of vertebrates, but few are developed for raptors and current methods such as direct counting, specifically the detection of nests or occupied territories are techniques that prove to be labour intensive, often inadequate and unsuitable for the red kite due to the wide distribution, high variety in habitats and low detectability of nests. This problem is seen to escalate during winter time as the raptors are not tied to a territory and may be categorised as mobile depending on meteorological and food-related factors (Viñuela, 1997).

2.3 Ecology

2.3.1 Habitat

Because of its generalist nature, specifying a general habitat template for the Red Kite is somewhat challenging. An agreed upon specification within literature is the presence of open areas within which to search for food (Seoane et al., 2003).

2.3.2 Diet

The Red kite exhibits perhaps the best example among raptors if a high level of dietary plasticity and is both predator and scavenger alike (Mougeot et al., 2011; Blanco et al., 1990; Hiraldo et al., 1993). Its diet has been documented to consist of small mammals, birds, reptiles, amphibians, insects and species of fish. Being a highly opportunistic species, the consumption of carrion can justify its frequent classification as a scavenger (Viñuela, 1997; García et al., 1998). Because of this documented plasticity within the species, there is no specific “dietary template” which can best describe the species. Dietary variations within same locations have been documented through pellet (regurgitated material) retrieved from nesting sites and evidence suggests that variations in diet are related to temporal and geographical differences in the availability of food sources (Mougeot et al., 2011). Additionally, it is suggested by Mougeot & Bretagnolle (2006) that the diet is related to specialisation and is shown to vary seasonally. This is supported Coeurdassier et al. (2012) who stipulate that kites show tendencies of local diet specialisation depending on food availability, particularly during outbreaks of certain prey species of small mammals. This occurrence was observed during outbreaks of the common vole in Spain where they accounted for 47% of the total biomass found in pellets (Sunyer and Viñuela, 1994). Similarly, Red Kites in Corsica showed an increase in breeding success when an abundant rabbit population was present (Mougeot and Bretagnolle, 2006).

Being highly opportunistic, the Red Kite is known for its exploitation of carrion found at livestock dumping sites at designated locations or simply close to livestock farms (Blanco, 2014; Viñuela, 1997; Mougeot et al., 2011). As previously noted, dietary composition seems a direct result of food availability. This is supported by Blanco (2014) who states that there are major dietary differences in Red Kites who are situated in wintering locations that do not have access to livestock carcasses. In these instances, there is evidence of the consumption of a large proportion of lagomorphs (European Rabbit) which supports findings of Mougeot et al. (2011).

2.4 Population Crash

2.4.1 Poisoning

Due to its highly opportunistic nature and dietary plasticity, the Red Kite is particularly susceptible to “accidental poisoning” (Berny and Gaillet, 2008). There is a significant amount of literature which deals with the poisoning of Kites from legal and illegal toxins used to target other species. The sources of the poisoning can be divided into two categories:

(i) Primary poisoning:

A study undertaken by Smart et al. (2010) found through post mortem examination that up to 55% of the illegally killed individuals in their sample died as a result of direct poisoning, most likely delivered in the form of carrion baits laced with poison. Direct poisoning is used to kill livestock and game predators, but the use of carrion baits will affect any species who happens across the bait.

(ii) Secondary poisoning.

The use of AKV treatments (anticoagulant rodenticides) are considered one of the most prominent threats and sources of secondary poisoning for Red Kites and other wildlife species (Coourdassier et al., 2012; Gómará et al., 2008). The use of the AKV treatments for controlling pest species population outbreaks proves particularly detrimental to Red Kites due to the fact, as previously stated, Red Kites can be prone to local prey specialisation based on prey availability which will lead to extended stays within areas subject to outbreaks (Ntampakis and Carter, 2005). None-lethal accumulation of these toxins by prey species inevitably results in a weakened state increasing the chance of being caught. This will inevitably lead to prolonged exposure of the Red Kite to rodenticides, which can lead to a trickle-down effect causing a build-up of toxins, thus resulting in internal haemorrhaging. Additionally, the accumulation of toxins as a result of the exposure to pesticides has also been observed to have adverse effects on predator species (Berny, 2007).

Another important source of secondary poisoning results from the consumption of un-retrieved game, leading to the ingestion of shot or lead (Pb) fragments. Pb dissolves at a rapid rate due to the high stomach acidity and a significant amount of Pb is dissolved between ingestion and regurgitation leading to high or lethal levels of Pb within the soft tissues (Mateo et al., 2007). Although statutory bans regarding the use of lead shot have been introduced in the United

Kingdom, the use lead ammunition remains an issue for a wide range of terrestrial birds (Pain et al., 2007).

2.4.2 Human Persecution

The European Rabbit (*Oryctolagus cuniculus*) has sharply declined over its historical range due to both myxomatosis in the 1950s and the haemorrhagic disease in 1988 (Villafuerte et al., 1998; Delibes-Mateos et al., 2007). Consequently, the red kite has experienced a decline in a major prey source. As previously stated, one of the main hypothesised reasons for the decline of the Red Kite has been the continued persecution by humans, specifically in the late 19th century under the pretext that the presence of the predator will have a negative impact on the local game species.

2.4.3 Habitat Degradation

As is quite common with many species occurring across agricultural lands, the Red Kite has been affected by the transformation of landscapes over time. Habitat fragmentation can both affect the kites but also the diversity and plenitude of prey sources (Roques and Negro, 2005).

There is a significant amount of literature that documents the importance of livestock carrion for Red Kites (Blanco, 2014; Blanco et al., 1990; García et al., 1998; Mougeot et al., 2011). Recent changes to the legislation involving the disposal of dead livestock have limited the use of ruminants as a source of food. Following the outbreak of the Bovine Spongiform Encephalopathy (colloquially known as mad cow disease) in 2001, strict sanitary legislation was implemented which heavily reduced the availability of livestock carrion. In 2011, the legislation was relaxed again but is now an unpredictable source of carrion due to the implementation and continued use of carrion destruction plants (Blanco, 2014).

2.4.4 Reduction of prey species

As previously stated, the distribution of the European Rabbit is of note as the decline in populations of the rabbit are of particular concern to raptor conservation efforts (Delibes-Mateos et al., 2007). It has been argued that the decline of the rabbit has played a role in the decline of predator species, including the Red Kite, both as a source of food and a point of intra and extra species conflict (Fernandez, 1993).

2.5 Habitat Suitability Modelling

Species are expected to be nonrandomly distributed as a result of their environmental preferences. A species with an optimal existential range for a certain variable (e.g. temperature for optimal photosynthesis) are expected to occur in areas that match or almost match this optimum (Hirzel et al., 2002).

Habitat suitability models (HSMs, also referred to as Habitat Suitability Index or Species Suitability Models) are a means of producing a continuous surface that relates the suitability of a certain area derived from the bioclimatic preferences, with the distribution of a species of interest. These relationships can be derived from expert knowledge or the statistical analysis of bioclimatic predictors or variables derived from the known distribution of said species. These models are used in the ecology field for land-management, decision making for habitat conservation and the identification of suitable reintroduction habitats (Lauver et al., 2002).

When the data regarding the species is limited due to a small sample set or the rarity of a species, a varied approach must be taken that contrasts from the standard comparison between observed presence data and absence data. This calls for the use of profile techniques that contrast with group discrimination approaches that require presence-absence or abundance data (Robertson et al., 2001).

Simple rendition of these models are made by using datasets containing the distributions of a certain species and deriving values for each bioclimatic predictor or variable relevant to suitability. These predictors are analysed to obtain the minimum and maximum values through cross referencing them with the known distribution records. These values are assumed to be the existential limits of the species (however these values are purely based of observed sample occurrences and can only represent the empirical limitations of the employed dataset). Each variable is then reclassified to produce a Boolean map, indicating areas where (1) values fit within max and min of species, therefore predicted presence or (0) value falls outside of max and min values, therefore predicted absence of said species. Following this, maps are then superimposed and multiplied using a Boolean AND function, producing an overlap of all the “survival ranges” of said species. In essence, any area of any variable which had a value of (0) will then produce a resulting value of (0) in the final overlay, stipulating that not all predictors were deemed satisfactory and will therefore indicate a lack of suitability for the species in question (Robertson et al., 2004).

Although this method provides a rough idea of a potential distribution of suitable areas, multiple issues can arise from the use of this simplistic binary classification technique. For the most part species bioclimatic thresholds are never crisp and absolute. When this assumption is made using Boolean logic, the loss of information and the propagation of error can occur.

A method used which serves to reduce the error generated by binary assumptions is the implementation of fuzzy classification. This technique is an extension of the simple Boolean logic in respect to the fact that it abides to the climactic limitations set by expert knowledge or data analysis but is characterised by continuous grades of suitability ranging from 0 to 1 (not suitable and most suitable respectively) allowing the quantification of suitability without being bound to the binary classification of defining a bioclimatic predictor or variable by suitable or not suitable (Store and Jokimäki, 2003; Robertson et al., 2004).

3.0 Methodology

3.1 Study site

The focus on this thesis will be limited to within the Spanish borders, which is home to the largest numbers of wintering birds in Europe and is the site of one of those rapid population declines in Europe (García et al., 1998). Spain occupies a majority share of the Iberian Peninsula with a total area of ~504,700 km². The majority of the region consists of highland plateaus, broken up by various mountain ranges situated across the country. The country is broken up into 17 regions (fig 1) and mainly has a semiarid climate.

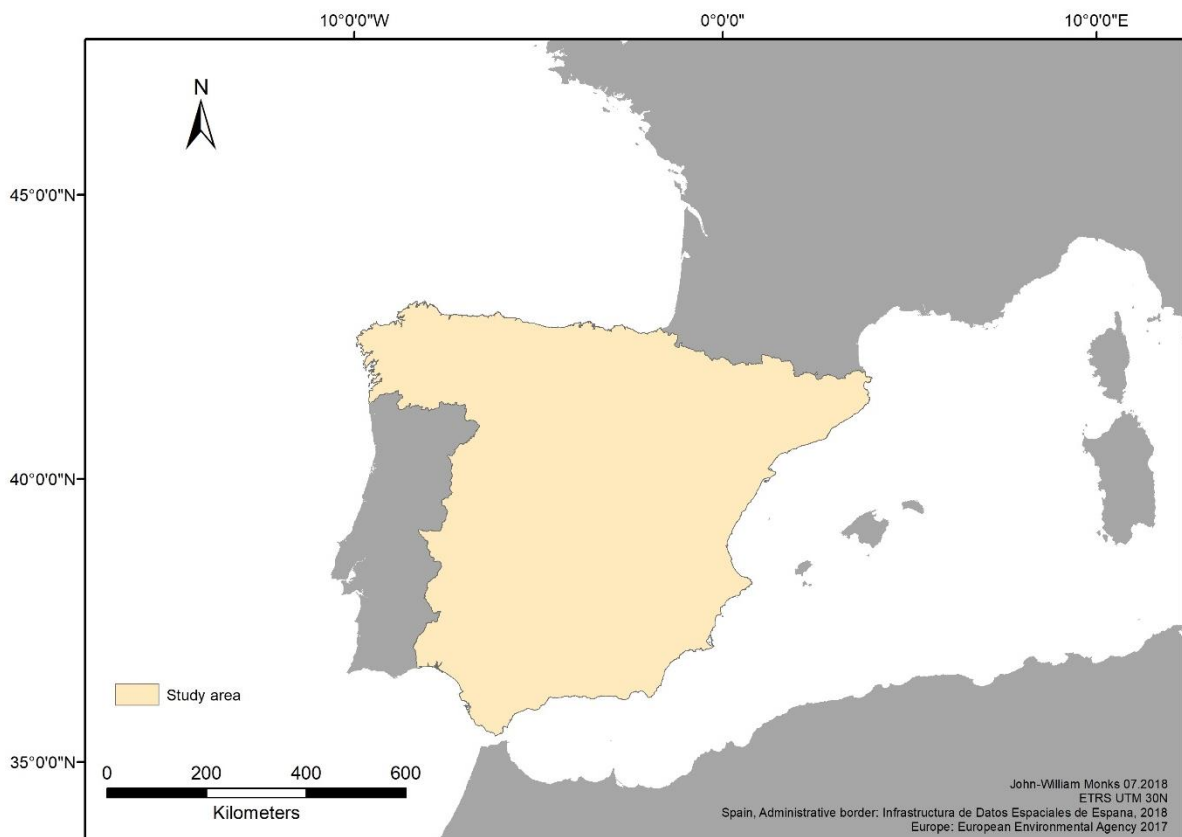


Figure 1 – The GPS data provided by the juvenile kites used for the study all occurred within the borders of Spain (yellow area), host to one of the largest breeding population of Red Kite

3.2 Experimental Design

As previously noted, simple Boolean models perhaps capture the bioclimatic limits of a species range but the simplicity in turn hinders the assessment of elements where the thresholds for suitability are not clearly defined. The fuzzy classification method not only allows the application of grades of suitability to areas that would be rejected using binary logic but also allows for the grades of suitability to highlight areas that are most suitable across the surface. This is specifically of interest to analysis that attempt to define a suitable range for an endangered species as it will allow the focus of funding and appropriate legislation to be directed to areas of maximal suitability thus maximising the conservation efforts chances of success.

Through the application of fuzzy logic, this paper aims to isolate the predictor(s) that best explain the distribution of the Red Kite (*Milvus milvus*) and to apply it across the extent of Spain to attempt to highlight areas that would be of consequence to the success of the species.

3.2.1 Bird position data

GPS Data was provided by the Swiss Ornithological Institute in Sepach, a non-profit foundation specialising in research and conservation efforts to support native species. The data provided was derived from the tagging of a total of 60 individuals (2 adults, 13 subadults born in 2015 and 45 juveniles born in 2016) tagged in Switzerland as fledglings which then migrated to Spain where the GPS data indicating their movements was logged from December 2016 to January 2017. These months were chosen as they can be considered “wintering months” where no migration from the Iberian Peninsula could be observed. Data on bird positions was logged up to every hour but a lot of variation was observed in the consistency of information received from the transponders due to unknown sources of interference. A total of 43,403 positions was logged over these two months. Data from 4 individuals was removed from the data set as they occurred within Portugal which was outside the area which was subject to analysis. In order to create training data from which the membership functions could be derived, 75% or 42 out of 56 individuals were selected at random to form the sample group, with the remaining 14 individuals left aside for model validation.

3.2.2 Home Range

In order to analyse what bioclimatic Predictors can be used to describe Red Kite distribution, an analysis of the operating area frequented by the training group was required. This area can be described as the home or wintering range and is defined as; area traversed by the individual in its normal activities of food gathering, mating and caring for young. An important element of the definition is the “occasional sallies outside of the areas should not be considered to be part of the home range” (i.e. outliers) (Seaman and Powell, 1996). For the purpose of conservation, it is imperative that the home range is not overestimated in order to provide a conservative estimate on the suitability of habitats. This allows the isolation of the areas that are indicative of the highest suitability and therefore provide the best grounds for successful species conservation efforts (Rayment et al., 2009). Previously, home ranges have been based on observations which proves problematic due to the fact that sequential observations of an individual prove challenging and repeated observations within an area are not indicative of the true utilization or home range and it becomes necessary to estimate where an individual has been found between observations. Multiple methods for the estimation of home ranges have been devised but one of the most successful is the kernel density estimator (KDE) (Worton, 1989; Silverman, 1986). This method was first introduced by Worton (1989) for the estimation of home ranges. Being nonparametric, KDE has the ability to estimate densities of any shape providing an adequate smoothing predictor is selected (Seaman and Powell, 1996). To apply KDE a univariate kernel is applied over each observation point in the sample. Within the scope of this paper, each recorded GPS point within an individual kite’s dataset had a circular kernel applied, with the surface value of the kernel highest above the point, diminishing with increased distance from the point.

As mentioned, KDE requires the integration of an appropriate smoothing predictor or “bandwidth”. Within GIS this element is referred to as the “search radius”. Having a narrower kernel applied to a point will allow proximal GPS points to have more influence than more distant points whilst a more broad kernel will allow for the encompassment of more distant values giving a more general image of the distribution (Silverman, 1986). Because of the movement variation within the data and the variation of GPS pings available from each individual, each kite needed a specific bandwidth to encompass the point density. Derived from Worton (1989) and adapted to GIS the formula for optimal bandwidth was selected according to equation 1.

$$h_{opt} = \left[\frac{2}{3n} \right]^{1/4} \sigma, \quad \text{Equation 1.}$$

where (n) is the sample size (i.e. number of GPS points) and (σ) is the standard distance within GIS. The Standard distance, similar to standard deviation, measures the degree to which features are concentrated or dispersed around the geometric mean of the GPS points.

h_{opt} was applied to each dataset as the “Search radius”. As described before, KDE applies a kernel to each GPS point. A raster layer is then produced (figure 2, left) whereby each cell is given a value derived by adding the values of all the kernel surfaces found at the specific point. Cells with a higher number of overlapping kernels will inevitably produce higher values and will be indicative of a higher density of GPS points.

By using this method, clusters of GPS points could be isolated. As can be noted from fig 2, not all GPS points should be taken into account as this will result in an overestimation (light blue) of the area where the individuals spent the majority of their time.

To remove data points that were considered to be “outliers” only the top 95% percentile of values were taken into account for further analysis. By removing the lowest 5% of values, GPS points with little to no overlap were isolated and could be excluded on with the assumption that these represent exploratory stints and not pertinent to habitat choice. The resulting areas and would henceforth representative of the “home range”.

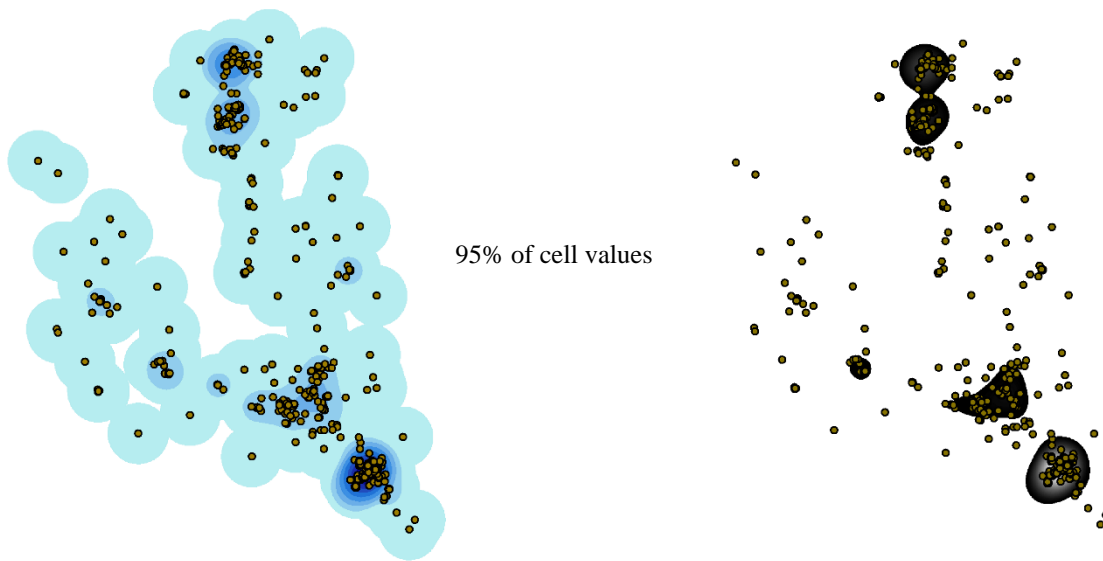


Figure 2 - Kernels are applied to each point. Points with overlapping kernels are a darker shade of blue and indicative of higher densities and therefore a higher cell value. By taking 95% of values the resulting black area is that of significant kernel overlap and therefore indicative of more time spent within that area allowing for the creation of the “home range”.

Employing h_{opt} to compute the area of each home range by using both standard distance and the number of observed GPS points meant that for several individuals, where the data was somewhat more sparse, a high spread in conjunction with a low number of data points meant that in some cases, the consideration of 95% of cell values vastly overestimated the home range of the Kite. The computed areas (fig 2) were analysed and based on a study by Hiraldo et al. (1991), any range that exceeded the maximum value of 100km^2 was re-considered. The overestimation of the kernel provided results of a home ranges running from 130km^2 up to 4900km^2 . Using visual guidance, cell values were taken into account based on a suitable standard deviation. This is a best-case approximation and as stipulated by Seaman and Powell (1996), “Since the true home range cannot be known for free-ranging animals, there is no way to determine the accuracy of these estimates”.

The result of these reclassified kernels was then assumed to be representative of the operating or home range of the individuals and would be the area (mask) within which the distribution, occurrence and percentage covers of different bioclimatic predictors would be derived.

3.2.3 Bioclimatic Predictors

In order to create training data which would best explain the distribution of the 25% remaining individuals, Bioclimatic predictors (BCMP) were selected based on previous studies and literature on the Red Kite.

Table 1 - A list of the bioclimatic predictor that were taken into consideration for the creation of the model. Each predictor was computed into a continuous raster of values covering the whole of the Iberian Peninsula.

<i>BCMP</i>	<i>Description</i>	<i>Source</i>
<i>NDVI</i>	Normalised difference vegetation index	MODIS satellite imagery ^a
<i>TEMP</i>	Interpolated temperature values (°C)	Meteorological Stations ^b
<i>WIND</i>	Interpolated wind values (m/s)	Meteorological Stations ^b
<i>FOR</i>	Percentage Forest cover	Modified from CORINE ^c
<i>OPEN</i>	Percentage Open Land cover	Modified from CORINE ^c
<i>CROP</i>	Percentage Crop cover	Modified from CORINE ^c
<i>GRA</i>	Percentage Grass cover	Modified from CORINE ^c
<i>SLO</i>	Slope (degrees)	Digital Elevation Model ^d
<i>ALT</i>	Altitude (m)	Digital Elevation Model ^d
<i>RAB</i>	Distribution of rabbit populations in boolean	Atlas of Spanish Mammals ^e

^a Raw data obtained from MODIS MOD13Q1 at a resolution of 250m on 17.08.2016

^b Raster interpolated using data provided by various stations distributed across Spain, obtained from the Spanish meteorological institute, Agencia Estatal de Meteorologica, averaged over December 2016 and January 2017 at a 250m resolution.

^c Four raster layers obtained by aggregating different land cover types (table 2) from CORINE land cover, obtained from the European Environmental Agency (2012) at a 250m resolution.

^d Predictors derived from a DEM of Spain, obtained from the European Environmental Agency at a 50m resolution.

^e Data recreated and based on a PDF from the Atlas of Spanish Mammals, Atlas de los Mamíferos Terrestres de España, Muñoz et al. (2002) using a 10km² grid system

Using various methods defined in each of their respective subsections, raster layers were obtained or created for each of the above BCMP. Areas within the home ranges had their values extracted and plotted. This allowed for the analysis of the values for each BCMP found within the home ranges in order to best assign linear functions and thus construct an appropriate fuzzy membership function representative of each specific BCMP.

NDVI

Normalised Difference Vegetation Index is increasingly used in ecological studies and has been highlighted as a useful tool thanks to links made between this index and animal performance, whereby it is theorised that a higher NDVI value will be indicative of a higher biological production of the area (Pettoirelli et al., 2005). The NDVI is derived from the red : near-infrared reflectance ratio (Eq 2) whereby the satellite sensor will capture the amounts of these wavelengths reflected by the surface.

$$\text{NDVI} = \frac{(\text{NIR} - \text{RED})}{(\text{NIR} + \text{RED})} \quad \text{Equation 2}$$

This theory is based upon the fact that for healthy plants, chlorophyll absorbs radiation in the red wavelengths (around 650nm) whilst the mesophyll will scatter radiation in the near infrared wavelengths (around 850nm). As can be seen in the figure below, NDVI has values that range from -1 to 1, where negative values are indicative of the absence of vegetation and positive values indicate vegetation, increasing up to a maximum value of 1.

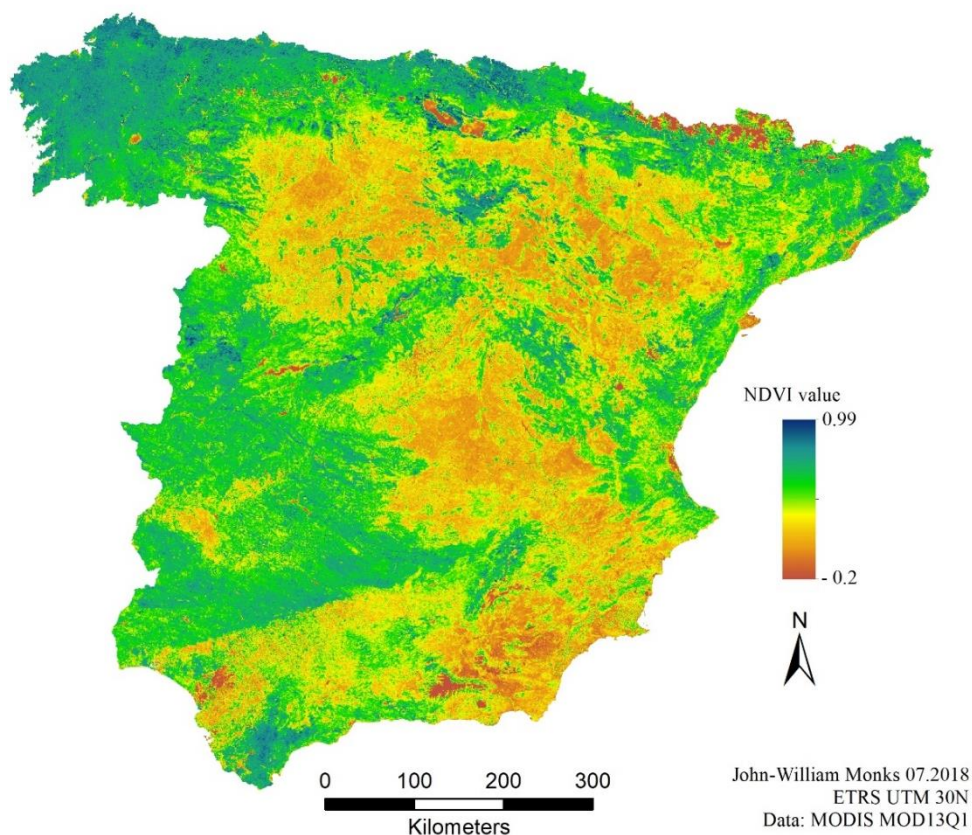
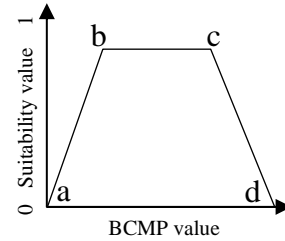


Figure 3 – NDVI across Spain from a clear day 01/2017. Higher values are indicative of higher levels of vegetative cover and negative values mark the absence of vegetation.

The NDVI values derived from the home range mask were then plotted in terms of frequency of occurrence at 0.01 intervals.

The data was separated up into three segments at points where the cell count increased, plateaued and decreased again in a significant manner. Linear trendlines were applied to each segment respectively and the x values for the intercepts were derived in order to create thresholds for the two-sided suitability function.

$$\mu x = \begin{cases} 0 & x < a \\ \frac{x - a}{b - a} & a < x < b \\ \frac{d - x}{d - c} & c < x < d \\ 1 & b < x < c \\ 0 & x > d \end{cases}$$



$$a = 0.13 \quad b = 0.32 \quad c = 0.6 \quad d = 0.9$$

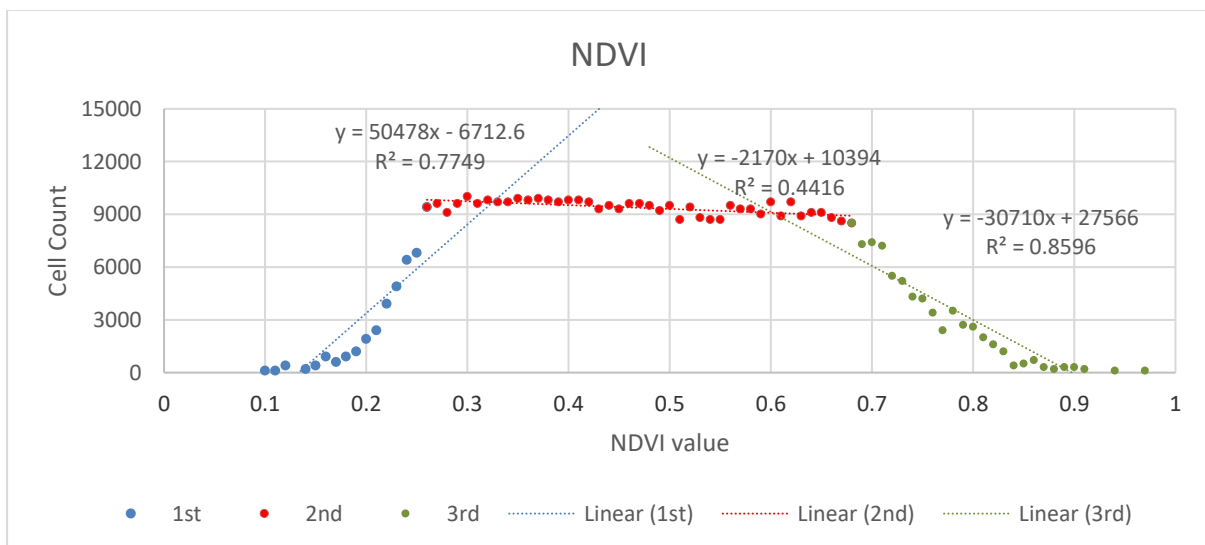


Figure 4 – Resulting fuzzy function for NDVI dataset. The data was divided into three sections based on thresholds where the data trend was seen to change. Trend line intercepts with each other and the x axis were then derived and x values were used to create the suitability function.

Wind and Temperature

In order to obtain continuous values for both wind speed and temperature, meteorological station measurements provided by the Spanish meteorological database had to be interpolated. As can be seen in figure four, values were obtained from 47 meteorological stations across Spain. Because data provided by meteorological stations is in the form of point locations, spatial interpolation is required to provide a surface of continuous values. Luo et al. (2008) concluded that ordinary kriging is one of best methods of interpolation for measuring windspeeds, only excelled by cokriging. Ordinary kriging was chosen due to restrictions imposed by the sparse nature of the meteorological sites.

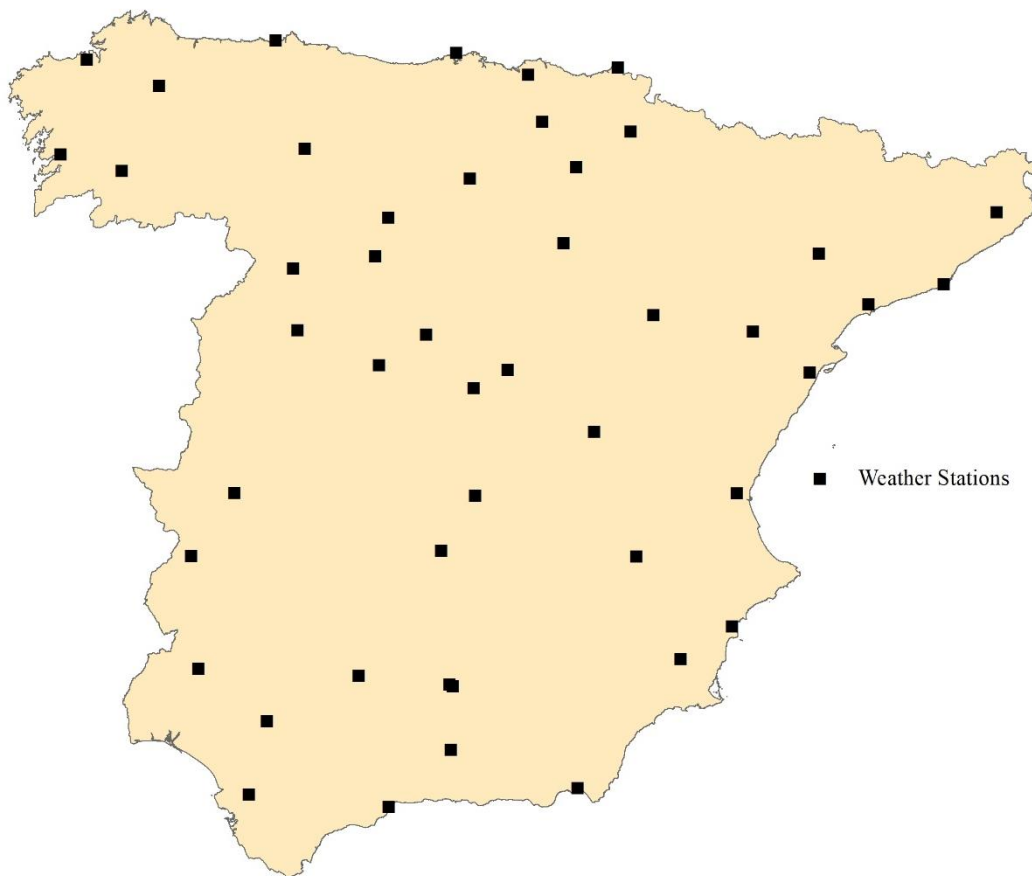


Figure 5 – Distribution of weather stations across Spain used for interpolating both wind and temperature values. A single weather station was selected from each province to ensure a wholesome distribution of points from which to interpolate temperature and windspeed.

Kriging is a method of spatially interpolating data between known points attributed weights based on spatial autocorrelation between these points in order to obtain unknown values (Krige, 1966).

The semi-variograms of wind speed and temperature was characterised by 12 lags with a size of 16.9kms and 27.9km respectively and created using a spherical models.

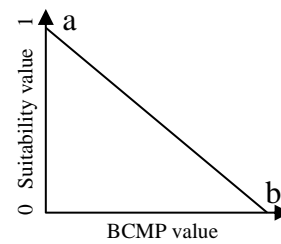
For both windspeed and temperature, a second order polynomial trend was detected and removed prior to interpolation and re-added to the result.

Visual inspection of wind speed data within the home ranges indicated no obvious pattern which was confirmed by a P-value of 0.76 and an R² value of 0.0019 and was therefore rejected as a relevant BCMP.

Regression analysis on temperature data resulted in a P-value of 0.0028 and was therefore accepted as BCMP of significance. A linear trend was fit to the data resulting in an R² value of 0.24 and was therefore used to create the function stipulating that lower temperatures yielded a higher suitability value.

$$\mu x = \begin{cases} 1 & x < a \\ \frac{b-x}{b-a} & a < x < b \\ 0 & x > b \end{cases}$$

$$a = 4.3 \quad b = 8.64$$



Altitude and Slope

These two topographical predictors were derived from a Digital elevation model (DEM) that was sourced from the European Environmental Agency (EEA) with a resolution of 50m. As with the other BCMP's, the area within the "home ranges" were extracted and subject to analysis.

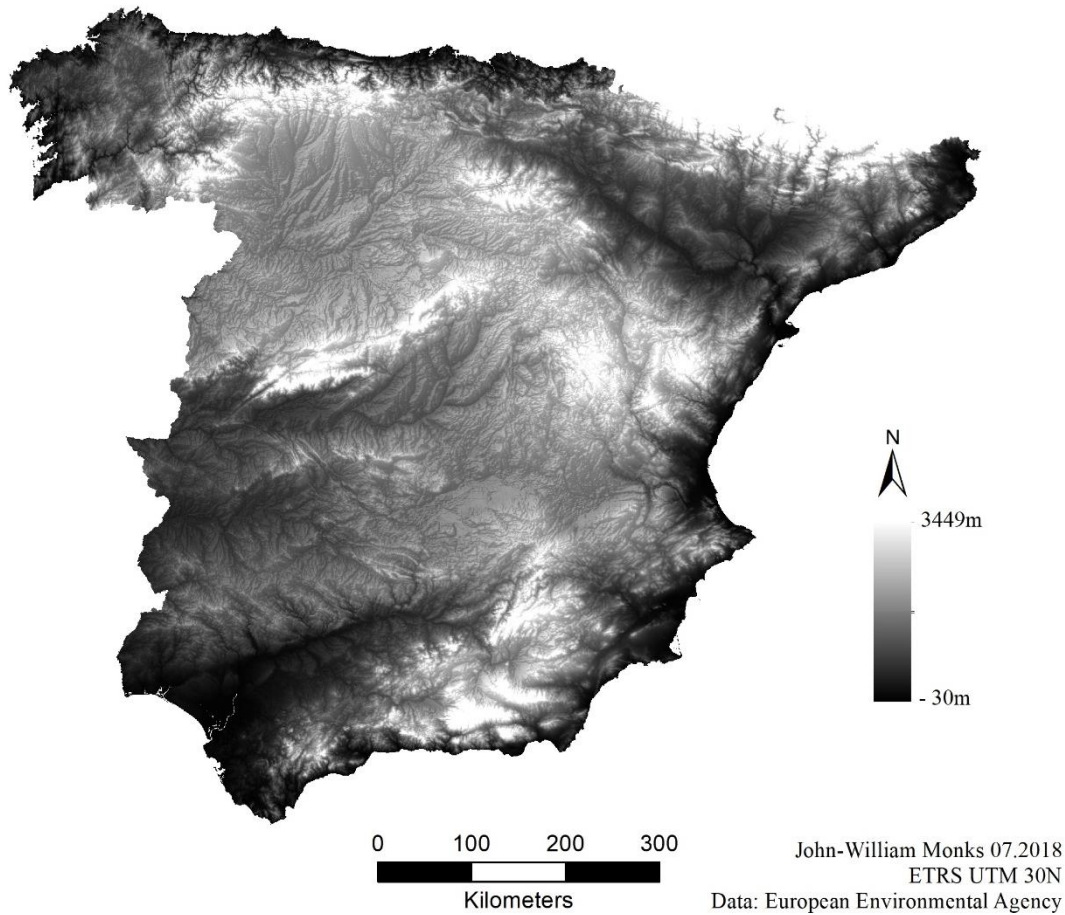
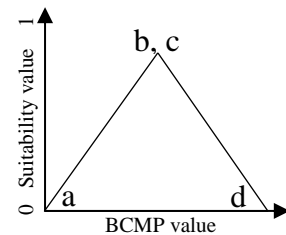


Figure 6 – DEM showing altitude variations across Spain. DEM obtained from the EEA provided attitude values across the extent of the study area. Lighter values are indicative of higher areas and darker lower.

Altitude was separated into 10m bins. The number of cells within the home range falling into each 10m bin was analysed. The plotted data (fig 5) indicated a peak at around 780m. This was used as the threshold value for to create a double-sided function using trend lines applied to each segment of the data. Here again, (b) and (c) were derived from the intersect of both trendlines ($x = 797$).

$$\mu(x) = \begin{cases} 0 & x < a \\ \frac{x-a}{b-a} & a < x < b \\ \frac{d-x}{d-c} & c < x < d \\ 1 & b < x < c \\ 0 & x > d \end{cases}$$



$$a = 86 \quad b = 796 \quad c = 798 \quad d = 1196$$

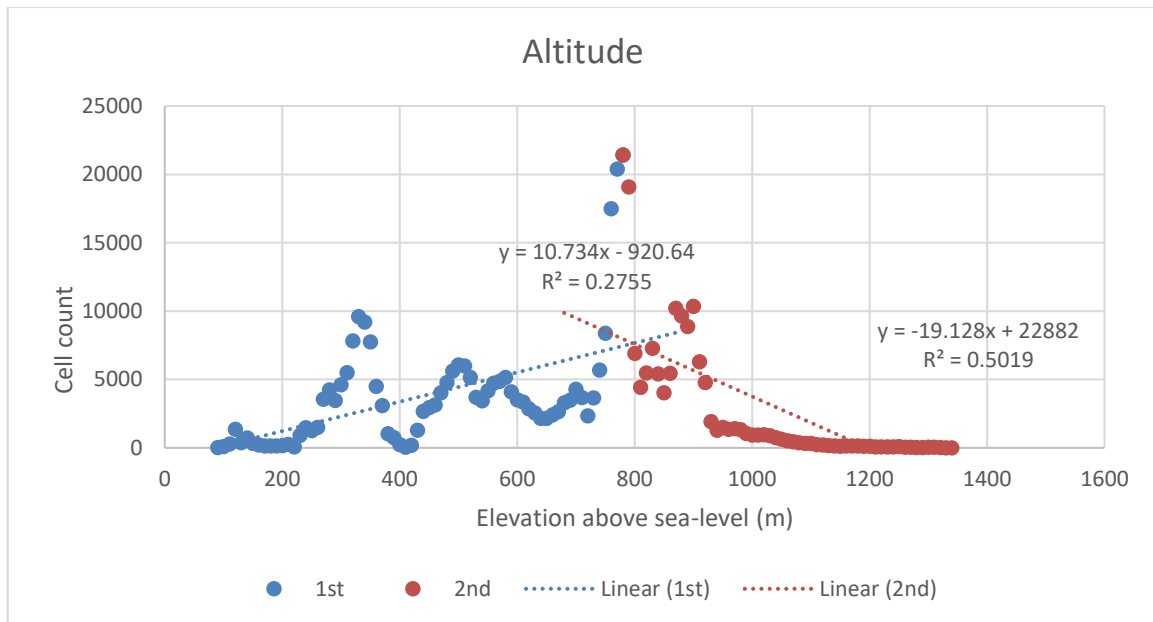


Figure 7 – Plotted values for cell count at each 10m interval within home ranges. Y=0 for trendline 1 and 2 represent (a) & (d) respectively and (b, c) was derived from linear (1st) = linear (2nd). The resulting R² Value for the trendlines 1 and 2 were 0.28 and 0.5 respectively.

In addition to elevation, the DEM also provided the data needed to derive the slope in degrees. The slope function within ArcGIS allows for the quantification of the topographical change from one cell to its neighbours. The resulting layer is a continuous surface of gradient values. Values within the “home ranges” were plotted. Due to the sheer number of values with low cell count a 1% exclusion treatment was applied to values whereby any value with a cell count below 1% of total count was excluded from the dataset. The resulting plot was fit with a linear trendline with a R² value of 0.68.

Corine Land Cover data:

Land cover data was obtained from CORINE (Coordination of Information on the Environment). CORINE was a project initiated in the 1980’s producing continuous land cover use for most of Europe. The layer used was the fourth instalment of the series, produced in 2012 with a resolution of 100m. Initially, Corine land cover is composed of 44 separate land cover categories. These were analysed and in accordance with literature by Seoane et al. (2003) and expert knowledge provided by the Swiss Ornithological Institute, the land covers were homogenised into 7 categories based on their characteristics and singular importance to Red Kites in the following fashion:

Table 2 – Categories by which land cover classes were homogenised based on their individual importance and characteristics

Settlement	Crops	Water	Grassland	Open Habitat	Wetlands	Forest
<ul style="list-style-type: none"> • Continous/dis-continous Urban fabric • Industrial or Commercial Units • Road and Rail Associated Land • Port Areas • Airpots • Mineral Extraction Sites • Dump Sites • Construction Sites • Green Urban Areas • Sport and Leisure Facilities 	<ul style="list-style-type: none"> • None-Irrigated Land • Permanently Irrigated Land • Rice Fields • Vineyards • Fruit Tree and Berry Plantations • Annual Crops Associated with Permanent Crops 	<ul style="list-style-type: none"> • Water Courses • Water Boadies • Coastal Lagoons • Estuaries • Sea and Ocean 	<ul style="list-style-type: none"> • Pastures • Complex Cultivation Patterns • Agricultural Land with High Areas of Natural Veg. • Natural Grasslands • Moors and Heathland 	<ul style="list-style-type: none"> • Sclerophyllous Vegetation • Transitional Woodland-Shrub • Beaches, Dunes. Sand • Bare Rocks • Sparsely Vegitated Areas • Burnt Areas 	<ul style="list-style-type: none"> • Glaciers and Perpetual Snow • Inland Marshes • Peat Bogs • Salt Marshes • Salines • Intertidal Flats 	<ul style="list-style-type: none"> • Olive Groves • Agro-Forestry • Broad-Leaved Forest • Coniferous Forest • Mixed Forest

The Home ranges were then used as masks to isolate the areas where the kites will have spent the majority of the two months and the cell values were then extracted and provided the information about what the specific land cover types that could be found within the homes ranges.

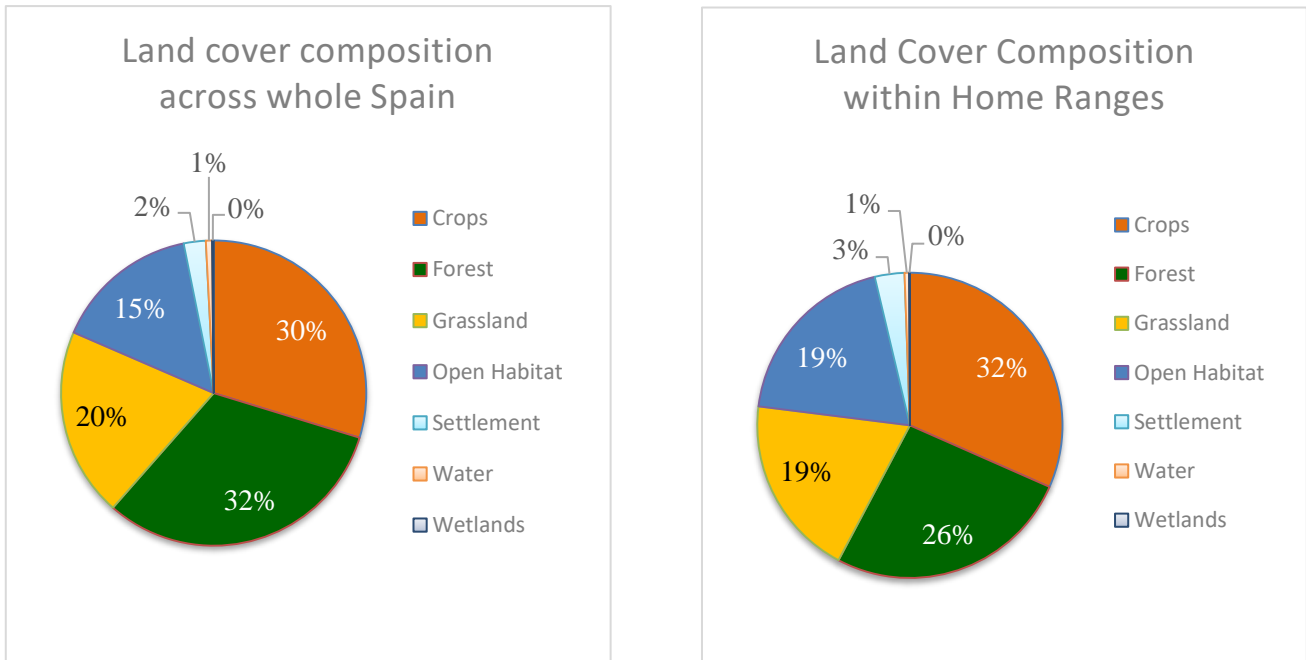


Figure 8 – Land cover across Spain, divided up into their respective type. Only a small amount of variation can be observed between the land cover composition for the whole of Spain (left) and that of the land cover within the home ranges (right).

From the homogenised land cover sets, four primary land cover types (Forest, Grassland, Crop and Open land) were identified (fig 8) and were extracted from the layer, the other land types were excluded from analysis due to their poor values and consistency. These layers were then isolated and extracted by attribute, resulting in four distinct Boolean layers pertaining to their respective types (fig 9)

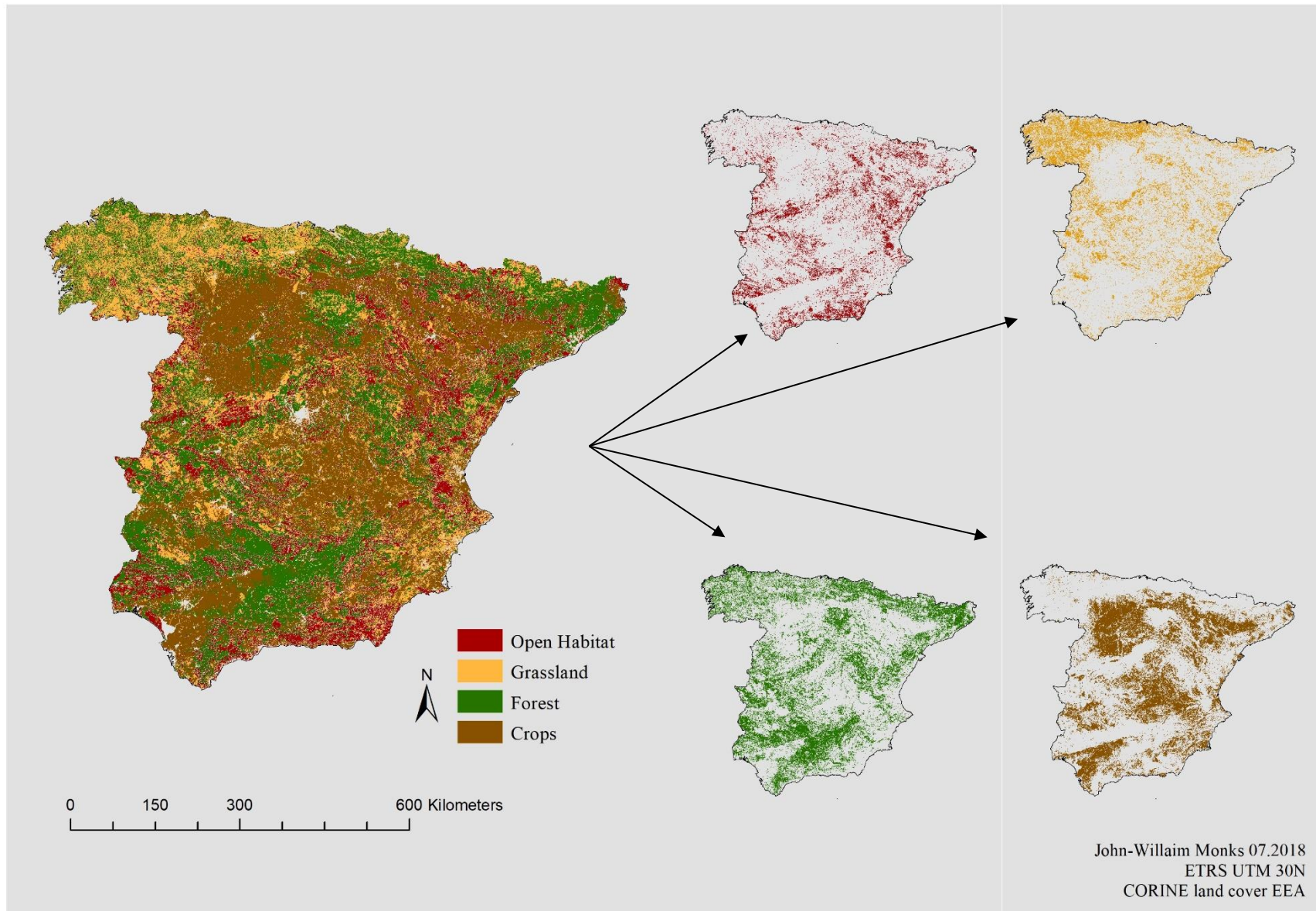
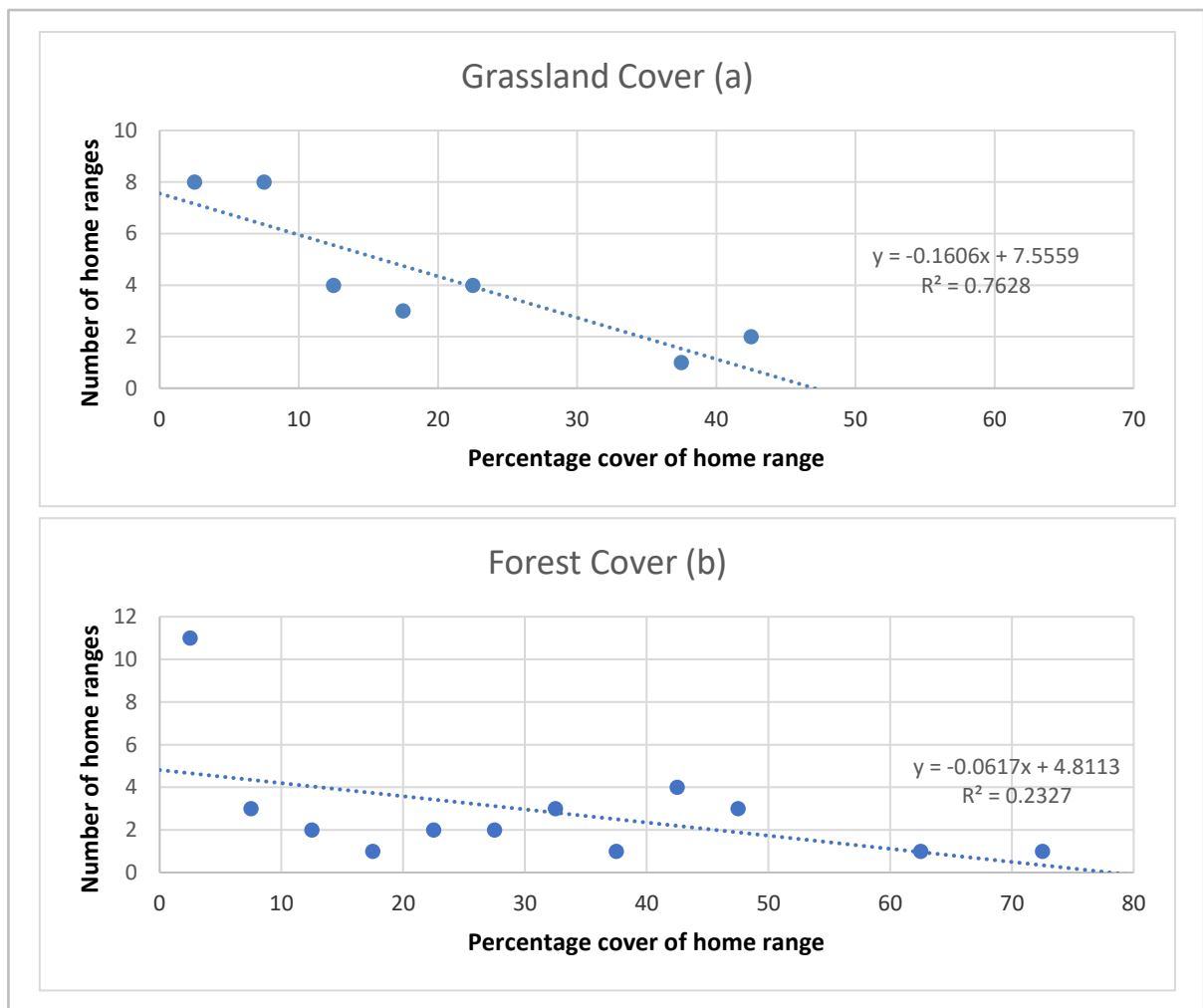


Figure 9 – The four primary land-cover types found within the home ranges, derived from CORINE 2014

Because there was no obvious specific land cover preference, analysis of the home range of each individual Kite of the training dataset was needed to isolate preferences and trends on which to base functions.

The composition of each individuals home range was broken down into a percentage value for the four major landcover types (open habitat, grassland, cropland and forest). The resulting land cover percentage values were then combined with those of the same class and categorised into 5% increments with the aim of isolating a notable general preference for land cover composition.



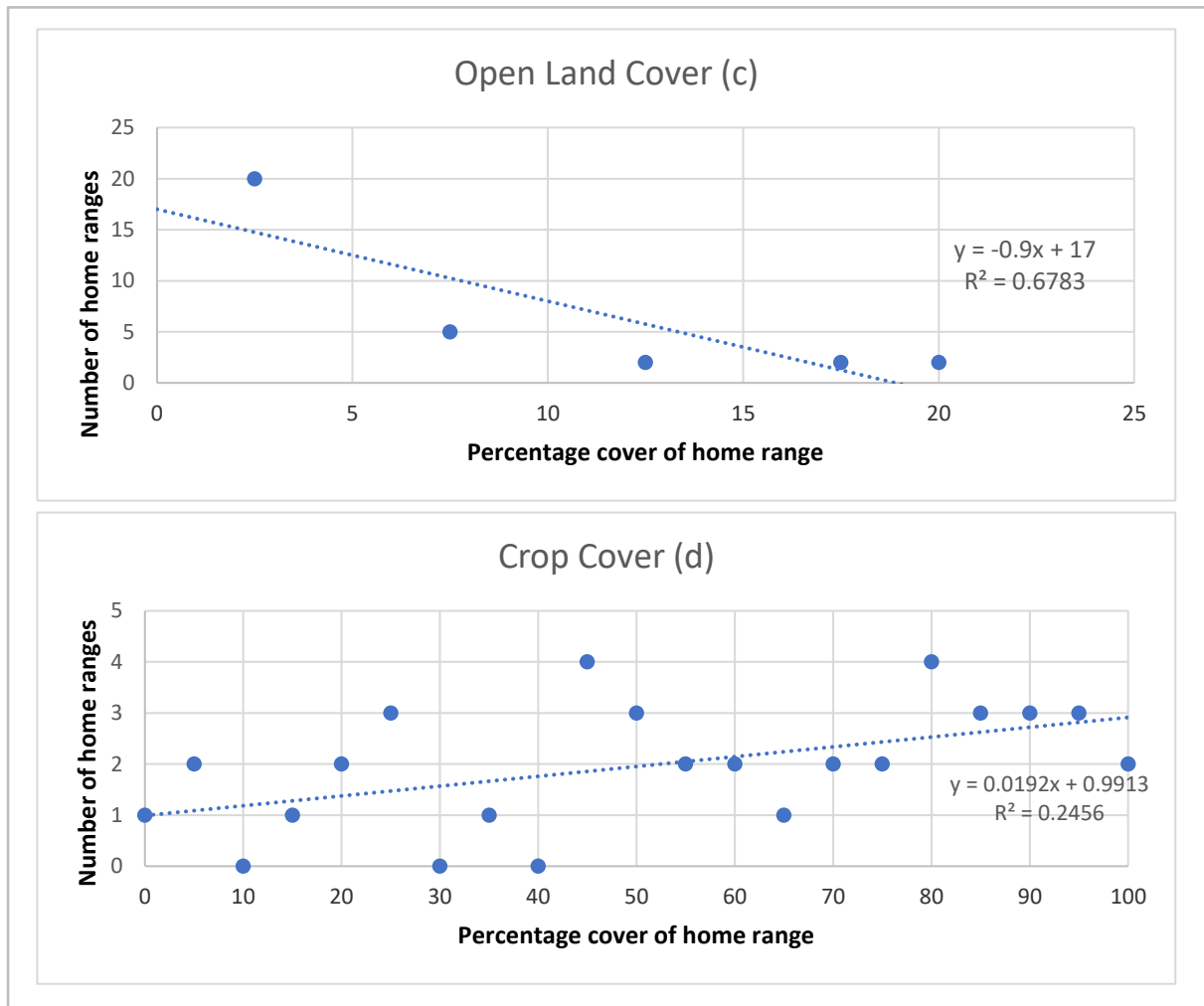


Figure 10 – Plotted values for land cover composition of each home range split into their respective categories and compressed into 5% increments to observe preference along with minimum and maximum values.

By isolating each individual land cover percentage value, patterns pertaining to preference emerged along with the maximum and minimum thresholds allowing for the implementation of fuzzy values based on the number of Kites within each 5% increment.

For the above plots, (a) to (c) exhibited similar trends whereby smaller percentages of the respective land cover results in a higher rate of choice, diminishing with an increase in the value. The figure relating to Crop cover (d) indicated a higher occupancy of areas with increased crop cover. Values were assumed to be indicative of species preference.

Table 3 – Thresholds for conditional statements stipulating maximum and minimum suitability as derived from the linear trends in fig 7.

(a) Grassland Cover		(b) Forest Cover	
Predictor	Percentage cover	Predictor	Percentage cover
a	0	a	0
b	47	b	78
(c) Open Cover		(d) Crop Cover	
Predictor	Percentage cover	Predictor	Percentage cover
a	0	a	0
b	19	b	100

In order to apply the functions to the landcover, each of the four land cover types were converted from simple Boolean to percentage-based values. This was achieved using the focal statistics tool within ArcGIS to assign each cell a percentage value. A 5x5km grid was used to assign the cell values based on the number of cells within that grid that were either of the specified land cover or not which were then divided by the total number of cells within the grid, resulting in a percentage value for each cell within the raster (fig 8).

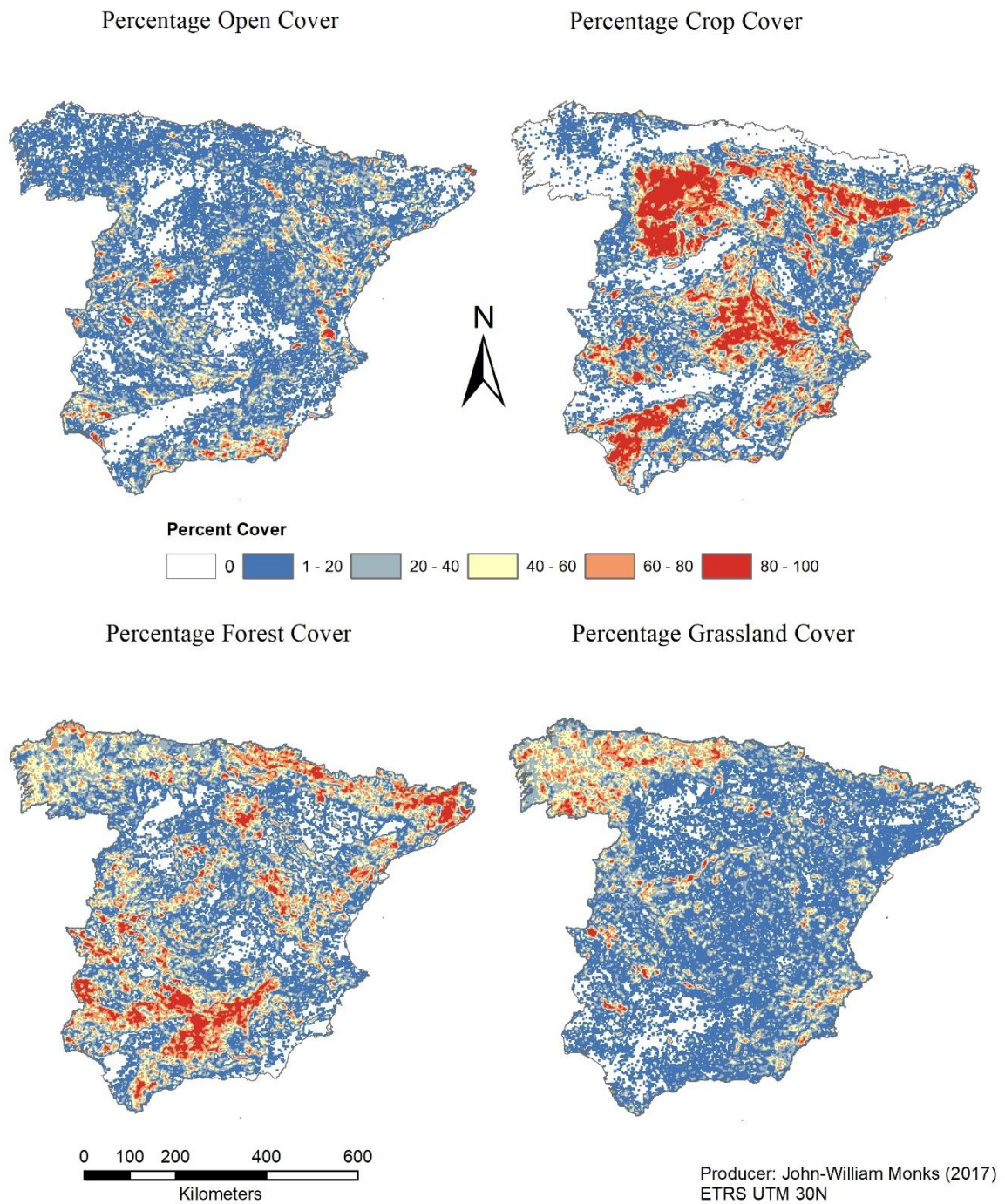


Figure 11 – The four relevant land cover types, with each cell value recalculated to create a percentage cover based on the number of surrounding cells of a that specific land cover type. Covers ranging from 0 percent, indicative of the absence of said cover to 100, indicative of complete cover.

Rabbit distribution data

Derived from the Spanish Mammals atlas, this data was digitised but unfortunately proved too coarse to derive any real distribution and was considered as detrimental to the model as too many areas would be taken into account and this was confirmed by extracting the Boolean values within the home ranges where no discernible pattern was present.

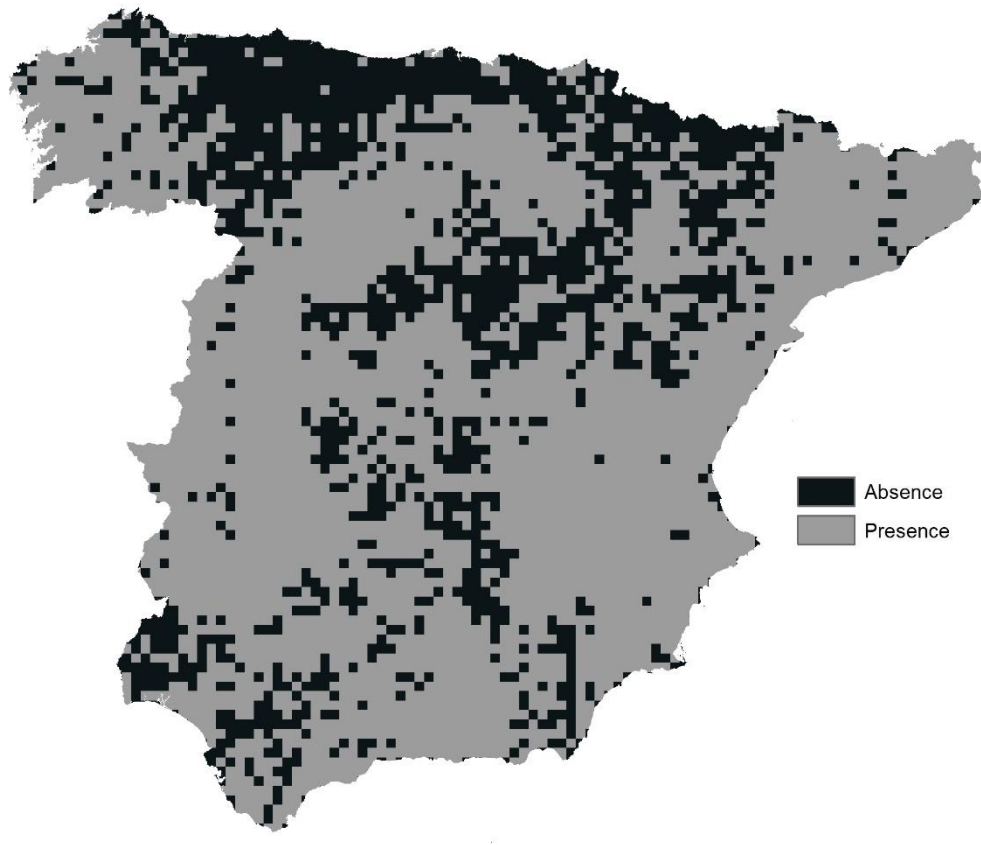


Figure 12 – Rabbit distribution across Spain recreated and based on a distribution map depicted in the Atlas de los Mamiferos. - Although a potentially viable BCMP given the importance of food sources, described to by literature found in section one, the coarse resolution meant no real results could be derived from using the rabbit distribution layer and had to be disregarded as a dataset.

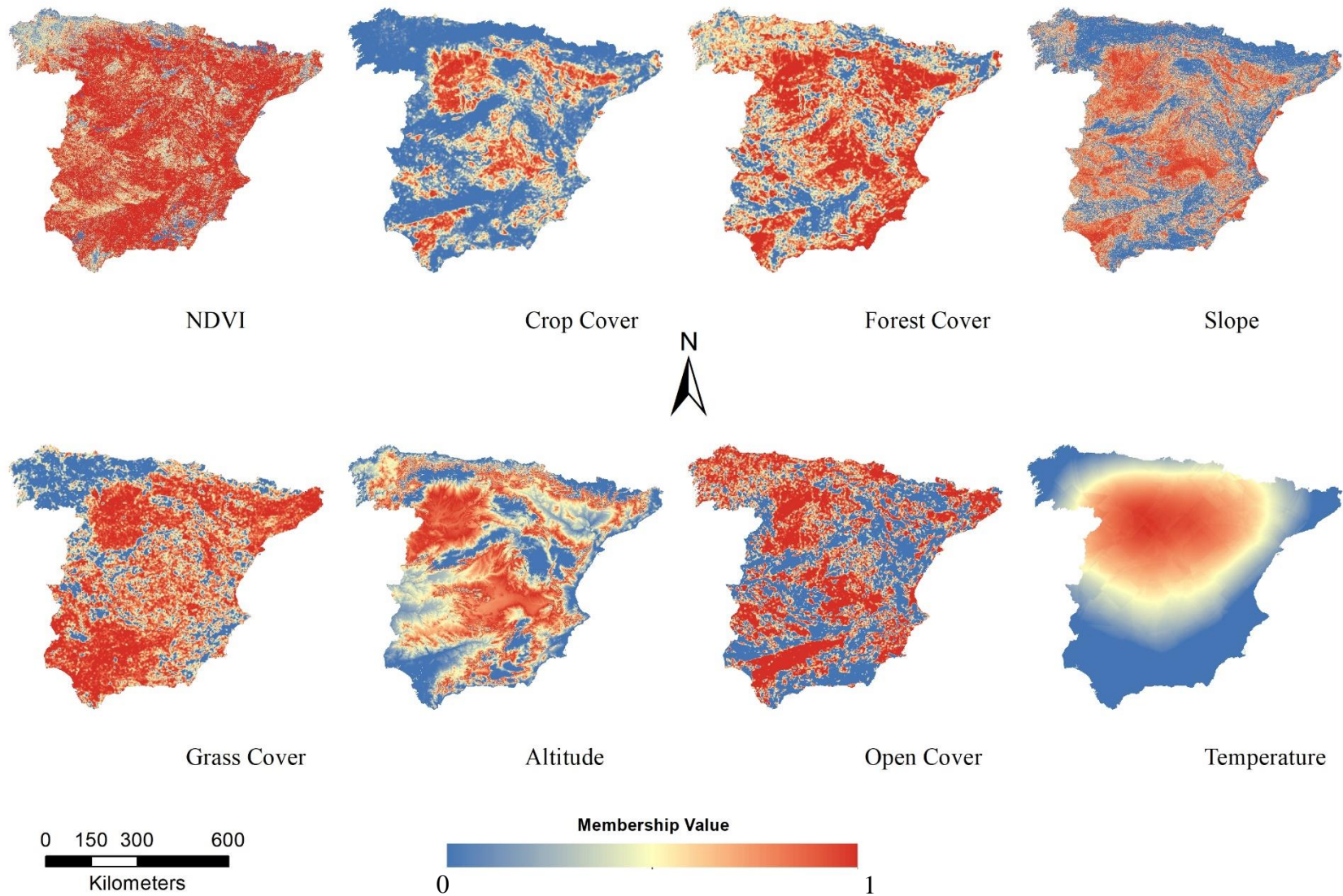


Figure 13 - The resulting fuzzy suitability raster layers produced by applying the fuzzy membership functions for each respective Bioclimatic Predictors. This data was henceforth used in the subsequent Weighted Linear Combinations

3.2.4 Weighted Linear Combination

As aforementioned, converting data into fuzzy values allows for data to be converted from a “crisp set” where values are, or are not, into varying values of membership. Once the distribution of the various bioclimatic predictors was established, the data was “fuzzified” in order to make the values inter-relatable allowing for multi-criteria/predictor evaluation. This was achieved by applying the functions from 3.2.3 to their respective data sets resulting in continuous values ranging from 0 to 1 corresponding with non-membership to complete membership, in this case corresponding to a complete suitability (Robertson et al., 2004), indicating the preferred values of the sample group within each respective BCMP (fig 9).

In multi-parameter analysis within GIS there are two methods which are commonly applied. The first uses a Boolean overlay, used for crisp values, where different parameters are combined with a selected logical operator such as (OR) or (AND) to yield a binary layer. The second and more applicable method uses Weighted Linear Combination (WLC), with which standardised or fuzzy values with varying degrees of membership can be combined or multiplied using pre-determined weights, yielding a continuous surface resulting from the weighted average of the combined parameters (Jiang and Eastman, 2000). This can be summed up as

$$S = \sum w_i \mu_i \quad \text{Equation 3}$$

where S is the suitability, w_i is the weight of parameter (or in this case predictor) i and μ_i is the criterion or fuzzy value of i (Drobne and Lisec, 2009). To apply WLC to establish the most suitable habitat based on the sample group, two elements had to be taken into consideration: What combination of BCMP's should be used and the importance or “weight” that each one will carry.

There are multiple techniques that can be used to predetermine weights ranging from arbitrarily attributing equal weights to all parameters, prior expert knowledge which utilises experience and observations or the Analytical Hierarchy Process which cross compares pairs of parameters within a square reciprocal matrix. In this thesis, the weights will be deduced by assessing the performance of several predictors in how well they manage to explain the training data and ultimately the validation data.

To quantify the result of each WLC, fuzzy values were extracted from the resulting combinations and masked off using the areas found within the kernels indicative of home range extent (fig 2). Following this, the fuzzy values were exported and tabulated into 0.05 increments as 0.1 bins were deemed too large and threatened to overly smooth out the data. The values were then made into a cumulative frequency distribution. Subsequently, the 25th percentile, median, 75th percentile and Interquartile range (IQR) were calculated. These statistics were combined to form the relative spread (RS) (IQR/median) of the fuzzy values in order to assign a single metric for the performance of each trial. This metric was used over other measures of spread as it is considered to be a method that is less sensitive to outliers. The overall aim of the exercise was to attempt to isolate the combination of weights and BCMPs within a WLC that would yield the lowest RS, signifying a high median and a little data spread.

Development Process

a) Single BCMP extract

To isolate the singular importance (if any) of the eight BCMPs, the fuzzy values within the home ranges were extracted from their respective layers to assess if and how well the fuzzy membership functions for each BCMP had captured the bioclimatic preferences of the kites. The inverse relative spread was then deduced and normalised to convert them into weights, ensuring that a lower RS will carry a higher weight.

b) Kolmogorov-Smirnov test

The K-S test was used to ensure that no single predictors performance was a mere reflection of the data as a whole. The K-S is a nonparametric test that allows the comparison of the probability distribution of two samples. In this specific case it was used to test the null-hypothesis that the fuzzy values within the home ranges match those from the distribution across the whole of Spain with a confidence of 95%. This can be surmised as $D > D\alpha$, where D is the biggest difference between both cumulative probability distributions and $D\alpha$ is the critical D value that must be exceeded in order to confirm that the two samples are from statistically different

distributions. The purpose of this was to identify BCMPs that appear to be good explanatory predictors when extracted from the home ranges but are also representative of the rest of Spain and consequently most likely a product of an abundance of high fuzzy values across the Spain in contrast to high fuzzy values as a result of habitat choice.

i) WLC – All BCMPs with equal weights (Benchmark WLC)

This is the first and most basic WLC in which all BCMPs are considered to be of equal importance in habitat choice resulting in eight BCMPs, each carrying a weight of $w_i = 0.125$. This would be used as a benchmark on which to base the performance of all subsequent WLCs.

ii) WLC – R² Weights

WLC using all of the BCMPs and the weights from the mean R² values derived from original fuzzy membership functions as normalised weights. The R² value is a direct measure of how well the function represents the data it is trying to explain. Therefore, it is assumed that the strength of how well the function fits the data will directly influence how well the WLC will capture species preference. Weights are as follows:

Table 4 – R² Vales derived from each of the respective membership functions from section 3.2 and normalised to represent relative weights.

FUNCTION	MEAN R²	NORMALISED w_i
NDVI	0.692	0.1761
TEMPERATURE	0.24	0.0610
FOREST	0.233	0.0593
OPEN	0.678	0.1726
CROP	0.246	0.0626
GRASS	0.763	0.1942
SLOPE	0.687	0.1748
ALTITUDE	0.389	0.099

iii) WLC – Minus one BCMP

A sensitivity test where eight separate WLCs were run, each time removing a BCMP from the combination resulting in a WLC with 7 BCMP's with equal of $w_i = 0.1429$. The relative spread of each product was then calculated to allow for the isolation of any BCMP which diminishes the performance of the habitat suitability model to be isolated. If the removal of a single BCMP significantly reduces the performance of the suitability model this is indicative of the importance of that predictor in explaining the overall suitability, and vice versa.

iv) WLC – K-S test $D > D_\alpha$ with equal weights

The predictors that rejected the K-S test's null hypothesis were compiled into a WLC with equal weights. Those that failed to reject the null-hypothesis that the BCMP values within the home ranges and that of those across the whole of Spain were from the same distribution were removed.

v) WLC- K-S test $D > D_\alpha$ using single predictor weights

The predictors that rejected the K-S test's null hypothesis were compiled into a WLC using the weights derived from the inverse RS for each value from the Single Predictor Extract as relative weights.

vi) WLC - K-S test

Following the K-S test, several WLC's were composed from the results. The first was using the D-values (Cumulative probability distribution whole of Spain – Cumulative probability distribution within home ranges) from all 8 predictors respectively to create weights relative to D. This was done to assess if the difference between the two distributions was indicative of the relative importance of the predictor. The resulting weights were as below, with temperature carrying the highest relative weight and NDVI and grass land cover carrying the lowest of the set.

Table 5 – Maximum Difference from Komogorov-Smirnov test from each bioclimatic parameter, normalised and used as relative weights for use as weights

BCMP	MAX D-VALUE	NORMALISED w_i
NDVI	0.1985	0.0803
TEMPERATURE	0.5205	0.2106
FOREST	0.3038	0.1229
OPEN	0.2676	0.1083
CROP	0.3318	0.1343
GRASS	0.1822	0.0738
SLOPE	0.3755	0.152
ALTITUDE	0.2909	0.2909

vii) WLC – Single predictor * Dvalue

A WLC using all eight BCMPs, where the inverse RS of the single predictor extract was calculated for each BCMP and normalised in order to be representative of their performance (lower RS=higher relative weight), defined as (sp_i) and multiplying them with the respective normalised D-value K-S test. The resulting suitability can be represented as follows:

$$S = \sum(sp_i * maxD_i)\mu_i \quad \text{Equation 4}$$

Table 6 – The respective resultant weights for each bioclimatic parameter when taking into consideration both Relative Spread and the Max Difference value from the Kolmogorov-Smirnov test

BCMP	($rs_i * maxD_i$)	NORMALISED w_i
NDVI	0.1985	0.0803
TEMPERATURE	0.5205	0.2106
FOREST	0.3038	0.1229
OPEN	0.2676	0.1083
CROP	0.3318	0.1343
GRASS	0.1822	0.0738
SLOPE	0.3755	0.152
ALTITUDE	0.2909	0.2909

viii) WLC – RS of Single Predictor

A WLC including all eight predictors with weights derived from the RS of fuzzy values from the initial single predictor extract (a)

ix) WLC – All equal - Minus one BCMP

A WLC using all predictors and taking the RS for each predictor during the sensitivity test, WLC (iii) and subtracting the RS of WLC (i), 0.3131 therefore resulting in a weight which is representative of the relative decrease in performance between the baseline WLC and that of removing a predictor from it.

3.2.5 Evaluation

The hypothesis **H1** “*The use of data driven fuzzy membership functions will allow the construction of a habitat suitability model that performs above the noise of species plasticity*” was evaluated by running each of the WLCs aforementioned and comparing the resulting RS of fuzzy values with that of the benchmark, WLC (i). The WLCs that produced layers whose RS of fuzzy values managed to outperform those of the benchmark WLC was then used to assess how well these managed to explain the distribution of the validation set. This was achieved by extracting the fuzzy values within the validation set’s home ranges, resulting in a RS which would be indicative of each of the WLCs performance. This in turn will allow for the hypothesis **H2** “*The best performing suitability model derived from the training data will best explain the distribution of the validation data*” to be accepted or rejected. For this hypothesis to be accepted, the WLC that best explained the distribution of the training set’s home range will subsequently also best explain the distribution of the validation set, producing the lowest RS of fuzzy values when extracted.

The WLC which produced the lowest RS of fuzzy values within the home ranges of the validation set then had its performance evaluated. This was done by creating 14 randomly distributed hypothetical or pseudo home ranges with an extent of 100km², corresponding to the number of individuals in the validation set. The extracted values were then tabulated and the cumulative probability of both the validation set and the pseudo homes ranges were assessed using the K-S test at 95% confidence, to verify how and if their distributions differed. This would allow for the acceptance or rejection of hypothesis **H1**

Lastly, the best performing habitat suitability model would be compared to the known distributions of *Milvus, milvus* from Birdlife international’s Red Kite distribution.

4.0 Results

4.1 Single BCMP extract

This was done as a preliminary evaluation to assess the performance of each BCMP. The cell count from the resulting fuzzy values allowed for an idea of how well the functions established in the methodology managed to capture the bioclimatic preferences of the training set itself by extracting the fuzzy values for each BCMP respectively. The extracted cell counts were plotted into cumulative probability functions with $\mu 0.05$ bins. A good explanatory BCMP should have a high median fuzzy value whilst having very little spread around this value. As aforementioned this would be represented by a low RS.

Table 7 – The resulting relative spread of fuzzy values from within the training set’s home ranges for each individual Bioclimatic predictor, again, the relative spread indicating how the severity of the data’s spread.

BCMP	IQR	MEDIAN μ_i	RS
NDVI	0.1357	0.9606	0.1412
TEMPERATURE	0.2117	0.7166	0.2954
FOREST	0.4966	0.8594	0.5778
OPEN	0.3954	0.8662	0.4055
CROP	0.6622	0.6164	1.0741
GRASS	0.2944	0.8726	0.3374
SLOPE	0.2811	0.8007	0.3510
ALTITUDE	0.3954	0.7297	0.5419

From this extract was very apparent that NDVI (in bold) was the strongest explanatory predictor on its own, having both high highest median and the smallest IQR. Crop cover however, performed relatively poorly, only scoring a median value of $\mu 0.61$.

Although NDVI scores well, it is to be expected due to the high amount of “very suitable” NDVI values that are present across Spain (fig 13, NDVI). 75% of the NDVI values across the whole of Spain yield a suitability value of $\mu 0.6$ or above and 50% of the exceed a suitability score of $\mu 0.95$.

4.2 Kolmogorov-Smirnov Test of the BCMPs

Only taking into account the RS of NDVI within the home ranges, it appears to be a good explanatory BCMP so it is therefore important to assess if this is the result of the Bioclimatic preferences and limits of the species being well explained by the fuzzy membership function from 3.2.3 or if the fuzzy values within the home ranges is representative of the distribution of those across the whole of Spain. The K-S test was used deduce if the BCMPS were from the same distribution as the general data with a 95% confidence using 20 increments of 0.05 for μ . In order to reject the null hypothesis that both datasets were from the same distribution, a critical value of $D\alpha = 0.294$ had to be exceeded. As can be deduced from table 8, NDVI, Altitude, Open cover and Grass land cover (in bold) all failed to reject the null hypothesis. Although these results suggest that the fuzzy values from these BCMPs are from the same distribution as the rest of Spain, they could still potentially be good explanatory variables and their influence would have to be deduced in subsequent WLC's.

Table 8 – Maximum Difference values representing the highest difference between the two cumulative frequency data sets. Four predictors yielded a Critical Difference value of < 0.294 and therefore had a 95% similar distribution.

PROBABILITY DENSITY FUNCTIONS								
BCMP	NDVI	Temp	Forest	Open	Crop	Grass	Slope	Alt
Max D-value	0.1985	0.5205	0.3038	0.2676	0.3318	0.1822	0.3755	0.2909

4.3 WLCs

The following WLCs were run each time using their respective predictors and the resulting fuzzy values were extracted from within the training set's home ranges in order to assess how well each WLC affected these values.

(i) All predictors with all weights equal

The resulting statistics (table 9) from the probability density function were considered the benchmark on which to base subsequent WLC performances.

Table 9 – Values derived by converting fuzzy values probability density table. Henceforth, values will be measured by their respective relative spread in order to assess their performance.

WLC i)					
STATISTIC	μ_i 25%	μ_i 50%	μ_i 75%	IQR	RS
μ_i	0.5904	0.7405	0.8223	0.2318	0.3131

(ii) WLC – R² Weights

The results from using the R² values to create the weights resulted in both the median and the IQR improving relative to WLC i) and therefore yielded a relative spread which was 6.31% lower than the benchmark.

Table 10 – Resulting values from using the respective R² values as relative weights from each bioclimatic predictor membership function.

STATISTIC	μ_i 25%	μ_i 50%	μ_i 75%	IQR	RS	$\Delta\%$
WLC ii)	0.6206	0.7703	0.8465	0.2258	0.2931	- 6.31

iii) WLC – Minus 1 predictor

Removing one predictor each time to see how this affected the model resulted in each predictor being confirmed as having a positive effect in explaining the distribution of the training dataset and by removing them, caused an overall decrease in the resulting performance. Although four predictors failed to reject the K-S null hypothesis, they are still shown to have a positive impact on the model performance and are therefore suggests that although the distributions are statistically similar at a 95% confidence level to the rest of Spain, they all play an integral part in explaining the overall distributions of the training data. Removing NDVI proved to have the most marked effect on the model performance, increasing the RS by 36% in relation to WLC (i). The least impactful BCMP but still beneficial to the model was crop cover, whose removal increased the RS by 11.46%.

Table 11 – Resulting relative spread value and subsequent percentage change based on WLC (i) as a result of sequentially removing one bioclimatic predictor.

BCMP REMOVED	μ_i 25%	μ_i 50%	μ_i 75%	IQR	RS	$\Delta\%$
NDVI	0.5542	0.7179	0.8602	0.3059	0.4261	+36.09

TEMP	0.5847	0.7440	0.8830	0.2983	0.4009	+28.03
FOREST COVER	0.6011	0.7387	0.8727	0.2716	0.3676	+17.41
OPEN COVER	0.5996	0.7366	0.8659	0.2663	0.3615	+15.45
CROP COVER	0.6182	0.7544	0.8815	0.2633	0.3490	+11.46
GRASS COVER	0.6016	0.7281	0.8663	0.2647	0.3636	+16.12
SLOPE	0.5876	0.7424	0.8738	0.2862	0.3855	+23.10
ALTITUDE	0.5573	0.7577	0.8558	0.2985	0.3940	+25.82

iv) WLC – Removing predictors where K-S test = $D < D\alpha$ with equal weights

In order to confirm the results of the previous WLC and confirm that although four home range BCMP distributions are from the same distribution as the rest of Spain, they still play an integral role in explaining the distribution of the training data, a WLC was run using only the predictors that successfully rejected the null hypothesis of the K-S test. The resulting change relative to the RS showed that removing the BCMPs degraded the model's performance by 49.93% relative to WLC (i).

Table 12 – Resulting percentage change in relation to WLC (i) where bioclimatic parameters that failed to reject null hypothesis were removed and the remaining few assigned equal weights

STATISTIC	$\mu_i25\%$	$\mu_i50\%$	$\mu_i75\%$	IQR	RS	$\Delta\%$
WLC vi)	0.4969	0.7116	0.831	0.3340	0.4694	+ 49.93

v) WLC – Removing predictors where K-S test = $D < D\alpha$ with using normalised respective RS from a) weights.

As previous examples have shown, each predictor has a different impact relative to its weight so the four BCMPs from the WLC (iv) were used with their weights derived from the RS of the single predictor extract of each respective BCMP. A significant increase in performance was noted although it still failed to out-perform the RS of WLC (i).

Table 13 – Resulting percentage change in the relative spread based on WLC (i) where bioclimatic predictors that failed to reject null hypothesis were removed and had their weights assigned based on their respective relative spread.

STATISTIC	$\mu_i25\%$	$\mu_i50\%$	$\mu_i75\%$	IQR	RS	$\Delta\%$
WLC v)	0.5723	0.7277	0.8206	0.2483	0.3412	+ 8.97

vi) WLC – All BCMPs with weights derived from the MaxD value from the K-S test

The weights derived from the MaxD value produced during the K-S test yielded a very slight increase in model explanatory performance, improving on WLC (i) by 0.29% due to a slightly lower IQR which outweighed its slightly lower median value.

Table 14 – Resulting percentage change of relative spread by using maximum difference value from Kolmogorov-Simonov test to assign weights.

STATISTIC	$\mu_i25\%$	$\mu_i50\%$	$\mu_i75\%$	IQR	RS	$\Delta\%$
WLC vi)	0.5863	0.7236	0.8122	0.2259	0.3121	- 0.29%

vii) WLC – Single predictor RS * Dvalue from K-S test

As a standalone statistic, the D-value from the K-S test did not significantly improve the models explanatory performance but in an attempt to acknowledge that some predictors did not vary from the distribution of the fuzzy values throughout the area outside of home ranges, the inverse relative spread each of the predictors was multiplied by the D-value from the K-S test in order to combine the performance of each predictor with how that performance varied from the general distribution of fuzzy values. The resulting RS value proved to be 16.19% more effective at explaining the distribution of the training set.

Table 15 – Resulting percentage change in relation for WLC (i) using the relative spread from the single predictor extract multiplied by the difference value derived from the Kolmogorov-Smirnov test.

STATISTIC	$\mu_i25\%$	$\mu_i50\%$	$\mu_i75\%$	IQR	RS	$\Delta\%$
WLC vii)	0.6396	0.76	0.8391	0.2483	0.2623	- 16.19%

viii) WLC – RS value of single predictor extract

Using the RS of the single predictor extract and converting them into normalised weights was modelled to see if the RS could be used as an indication of the weight that a BCMP might carry in explaining the distribution. A 21.53% increase in explanatory performance was noted.

Table 16 - Resulting percentage change when using the relative spread value of single predictor extract to assign weights.

STATISTIC	$\mu_i25\%$	$\mu_i50\%$	$\mu_i75\%$	IQR	RS	$\Delta\%$
WLC viii)	0.6644	0.7807	0.8562	0.1981	0.2456	- 21.53%

ix) WLC – RS of WLC All equal – RS of Minus one BCMP

Here the assumption was that the change between the two WLCs could represent the impact that each BCMP would have on explaining the distribution of the training set. The resulting change between the RS of both predictors was normalised and used as weights. This was the best performing WLC out of the set, yielding a 22.53% reduced RS of fuzzy values within the training set. Although the median value was slightly lower than that of WLC (viii), the improvement in the IQR produced an overall lower RS value.

Table 17 – Resulting percentage change of the relative spread when using the difference between the relative spread where all bioclimatic predictors carried equal weights and the respective relative spread where each bioclimatic predictor was sequentially removed

STATISTIC	$\mu_i25\%$	$\mu_i50\%$	$\mu_i75\%$	IQR	RS	$\Delta\%$
WLC ix)	0.6437	0.7490	0.8264	0.1827	0.2439	- 22.08%

4.4 Validation of WLC models

The benchmark WLC and all those that managed to outperform its explanatory result from the training dataset were then taken and evaluated by how well they managed to explain the validation set. WLC i), ii), v), vi), vii) and ix) were used and by extracting the fuzzy values found within the validation set's home range's, the following statistics were calculated.

Table 18 – Resulting percentage change of the relative spread when pitting each of the following weighted linear combinations against the result of the benchmark, WLC (i)

STATISTIC	$\mu_i25\%$	$\mu_i50\%$	$\mu_i75\%$	IQR	RS	$\Delta\%$
WLC i)	0.4217	0.5476	0.6625	0.2408	0.4397	-----
WLC ii)	0.4805	0.6125	0.7261	0.2457	0.4011	- 8.79
WLC vi)	0.3796	0.5163	0.6514	0.2717	0.5263	+ 19.68
WLC vii)	0.4604	0.5892	0.6888	0.2284	0.3876	- 11.86
WLC viii)	0.5121	0.6318	0.7152	0.2030	0.3214	- 26.91
WLC ix)	0.4622	0.5758	0.6963	0.2341	0.4066	- 7.53

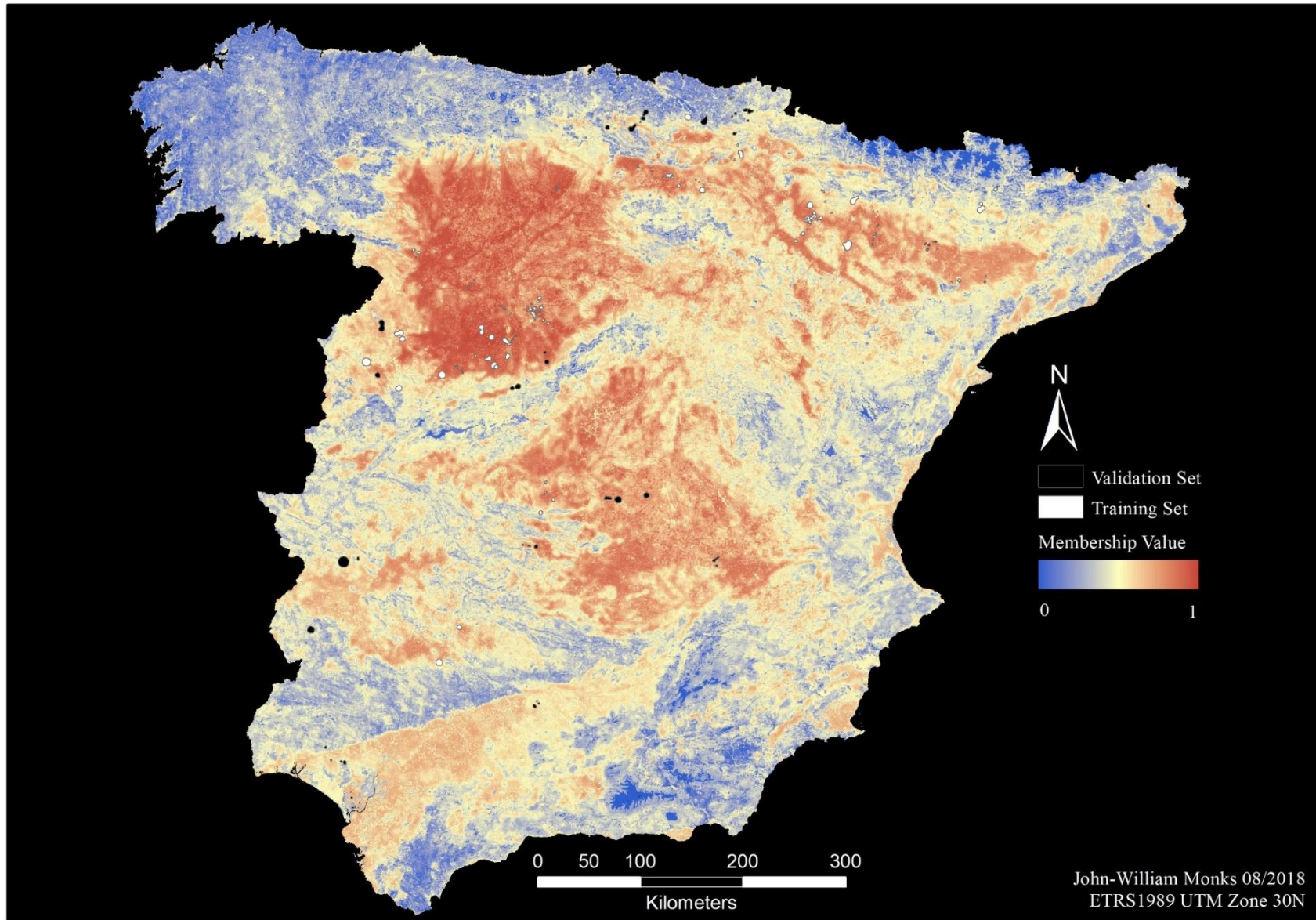


Figure 14 - The resulting suitability map produced by WLC (viii). The extracted values from the validation set (black) were tabulated in the above table. The distribution of the training set depicted for reference (white).

4.5 Validation home ranges vs Pseudo home ranges

As previously mentioned, 14 areas of 100km² were generated at random within Spain (fig 15) to see how well best performing WLC managed to explain the habitat choice of the validation set in comparison to how well it would explain randomly generated points.

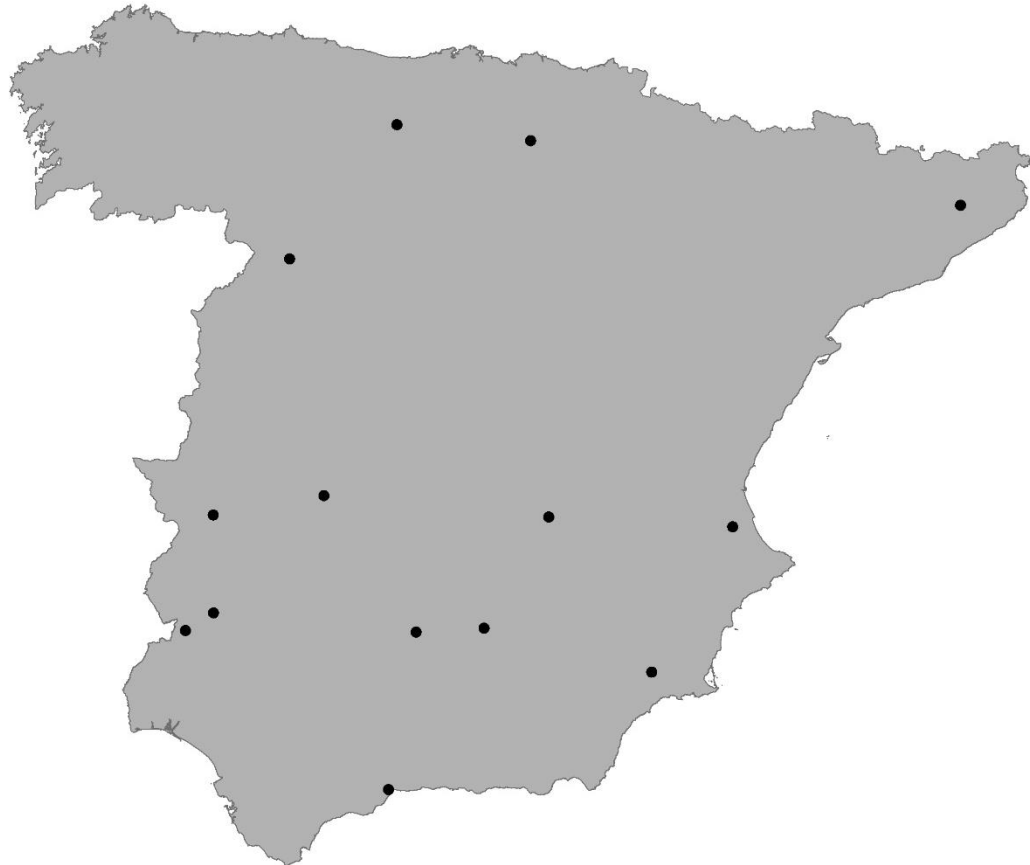


Figure 15 – Each point represents 1 of 14 randomly generated circular pseudo home ranges across the extent of Spain. Cell values were extracted from within these areas and calculated into a probability distribution table to compare with the probability distribution of WLC (viii)

Table 19 – Resulting relative spread of fuzzy values within pseudo home ranges (fig 15) and the resulting relative spread of fuzzy values using WLC (viii) within the validation set.

SET	$\mu_i25\%$	$\mu_i50\%$	$\mu_i75\%$	IQR	RS
RANDOM POINTS	0.447186	0.549792	0.669083	0.221897	0.403601
WLC (viii)	0.512105	0.631813	0.715155	0.20305	0.321377

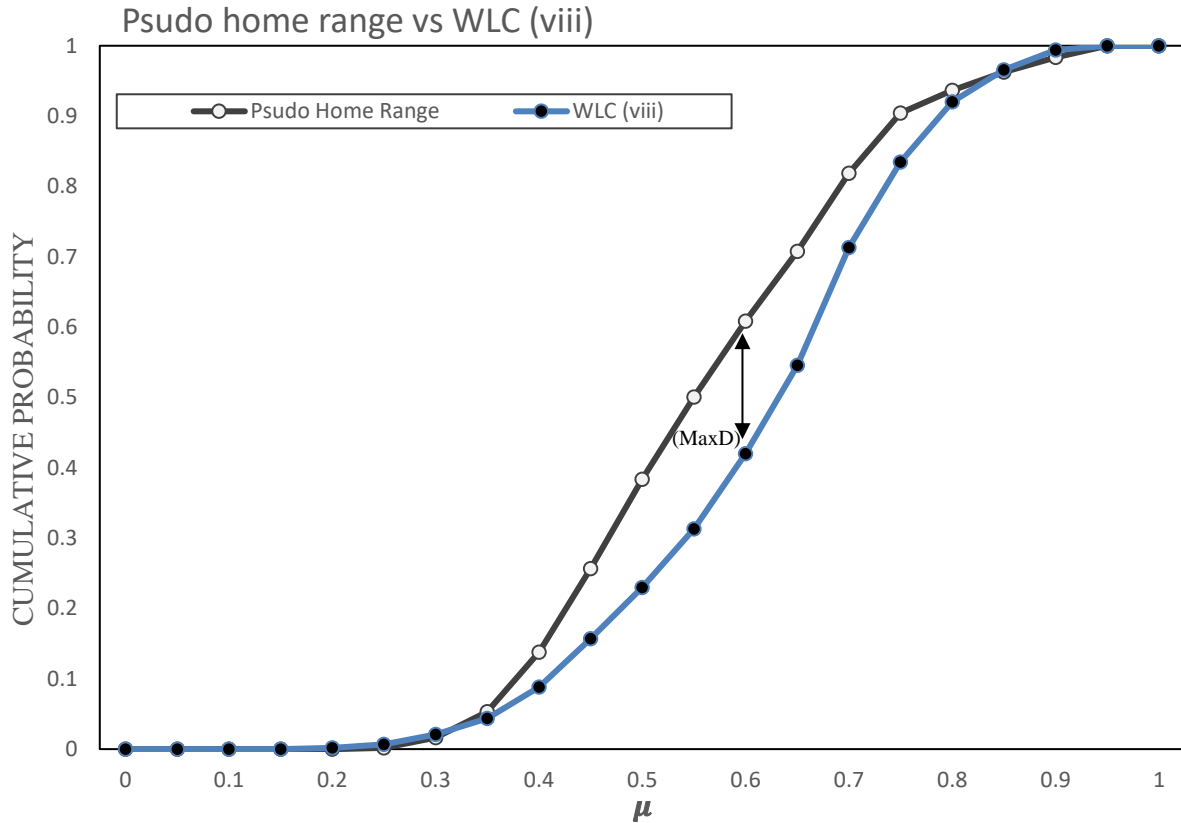


Figure 16 – Cumulative probability of WLC (viii) (weights derived from the relative spread of the single predictors compared to the cumulative probability of the pseudo home ranges. (MaxD) represents the maximum difference between the two data sets.

The maximum D-value was derived from comparing the two datasets in order to assess if $D < D\alpha$ to, in turn, reject or accept the null hypothesis. Resulting maximum D-value was at $\mu 0.6$, $D = 0.1882$ which failed to exceed the critical D value of 0.294 therefore confirming that the two datasets are not from statistically different distributions.

5.0 Discussion

This study showed that the use of simple linear functions to create BCMP degrees of membership does not allow for the construction of a habitat suitability model which statistically outperforms Red Kite species plasticity. The constructed functions are shown to explain the distribution of the training set relatively well but fall short when attempting to explain the home ranges of the validation set, confirmed by the KS test showing that the distribution of fuzzy values within the validation are not statistically different to those of a randomly generated set of hypothetical home ranges.

5.1 Model construction

The main objective of the study was to assess if it was possible to capture the species preference using the readily available data considered pertinent to habitat choice as dictated by the species literature. By isolating the fuzzy values for each single predictor, insight into their respective explanatory abilities was provided. NDVI proved to be good explanatory BCMP on its own but this was attributed to the fact that the majority of all NDVI values across Spain fall within the “highly suitable” category, confirmed through its failure to reject the K-S test null hypothesis, along with altitude, open land cover and grass land cover. Following these results, it was considered that these poor results might mean that these BCMPS were poor representations of species habitat choice and therefore a sensitivity test was constructed to analyse the impact that each BCMP had on the WLC. This was done by removing each predictor from the WLC to try and isolate BCMPS which potentially reduced the model’s explanatory success. Each iteration of the WLCs showed that by removing any one BCMP, the model’s explanatory power was weakened, ranging from 11.5% increased RS by removing crop cover to an increase of 36.1% when NDVI was removed, thus confirming that each BCMP played a relatively significant role in explaining the training sets extent.

This was also supported during WLC (iv) and (v) where predictors that failed to reject the null hypothesis for the KS test were removed. This was done in an attempt to remove the predictors that might be considered as noise as opposed to a BCMP that might have an impact on the habitat choice of Red Kites. Directly removing them and attributing equal weights the remaining predictors resulted in a significant degradation 49.9% in the model’s explanatory ability. To ensure a fair test, WLC (v) was also run to take into account that not all remaining BCMP’s would carry the same importance and thus adjusting the weights by using the

normalised RS values from the single predictor extract. Although this was shown to improve upon the result of WLC (iv), it also failed to exceed the baseline result, exhibiting a loss of 9% explanatory success.

Furthering this result the exercise was limited to “what importance or weight does each BCMP carry to best explain the distribution set and ultimately the validation set.

5.2 WLC weight combinations

In deriving what weight to assign each BCMP, the initial step in attempting to outperform the baseline WLC (i) for the training data, was to consider how well each membership function represented its respective data, represented here by the R^2 value. It was correctly assumed that the functions which were least representative of their respective cell counts would in turn have poor explanatory BCMP's. Adjusting the weights in proportion to this value allowed for a slight improvement of the model's explanatory success of 6.3% and in turn creating a new benchmark to improve upon.

WLC vi) was constructed on the basis that D-values for each predictor from the KS test might give some insight into the potential importance of each BCMP as one might assume that should this distribution have a strong variation then it could be the product of Kites actively seeking out or avoiding this BCMP. Although four predictors failed to exceed the critical D-value, differences were still notable between their distributions within the home ranges and that of those across Spain. The degree that the distribution of each BCMP within the home ranges varied from the overall distribution across Spain was used for the creation of normalised weights. This resulted in an unexpectedly low increase of 0.3% in relation to the baseline WLC's RS value. This could potentially be attributed to the fact that although some BCMP's distributions may vary significantly from those of the rest of Spain, they may still be a poor explanatory variable and this variation may be a bi-product of the relationship between BCMP's or an BCMP that has not been considered and is something that might be captured using multivariate linear regression within generalised additive models.

Although WLC (vi) proved only marginally more successful than the baseline, the fact that some BCMPs varied quite significantly suggests that some level of habitat selection is occurring. In an attempt to capture the importance of this without disregarding the fact that this high level of variation is due to the relationship with another factor or BCMP, WLC (vii) was undertaken, resulting in the 16.2% increase in explanatory ability. The improvement in the

explanatory ability compared to that of WLC (vi) can probably be attributed to factors like NDVI. Just taking into account the D-value results in NDVI carrying the lowest weight and temperature carrying significantly higher weight. As can be seen by analysing the extent and distribution of the high-end fuzzy values produced by temperature, one can deduce that this will result in the extremities of Spain being potentially underestimated and the upper central values overestimated. By combining the two results, both the success of single predictors habitat explaining potential and how much of this is due to a high or low spread of values across Spain can be taken into account.

A comparison was also made with the RS of the single predictor extract as a stand alone to see how including the D-value would change the explanatory power. The adverse effect occurred and WLC (vii) showed that taking into account the D-value actually decreased the model's ability to explain the training data. Taking the RS value of the single predictor extract alone as normalised weights proved to be the second most effective WLC, only outdone by the final WLC, WLC (ix). The final WLC was constructed to investigate if the difference between the performance of WLC (i), where all BCMPS were weighted equally and the relative difference of removing said BCMP from the model. This proved to be the most effective way of weighting the BCMP's and would be presumed to be the most effective at explaining the remaining 25% of kites, put aside for validation purposes.

5.3 Validation of resulting WLC's

In order to create a subsequent relative benchmark, the extracted values within the home ranges of the validation set using WLC (i) were again used as a basis to which all subsequent would be compared. As expected, nearly all WLC's managed to outperform the benchmark, producing varying results. WLC (viii) outperformed the benchmark by 26.9%. Falling short of its previous performance, WLC (ix) only managed a mere 7.5%. One of the most notable differences compared to the training set is that WLC (vi) proved to be less effective than the benchmark at explaining suitability, generating a higher RS of fuzzy values within the validation set. As with the cell extracts from the training sets, most of the derived WLC results from table 18 showed that there was an improvement of the explanatory ability when compared to their respective benchmark RS but when cross compared, the resulting RS values from the validation set extract, they proved to be all lower than the RS of the training sets benchmark WLC (RS 0.3131), suggesting that overall, results were comparatively worse and did not capture with any great success, the potential habitat choice of the juvenile Red Kites.

Although this was to be expected, to what degree the results captured or failed to capture habitat choice was to be determined by comparing how well they explained the validation set versus how well they could explain the pseudo home ranges in section 4.5. Once these 14 home ranges were generated the cell values were extracted and calculated in the same manner. The distributions of both the validation set from WLC (viii) and the pseudo home ranges (fig 15) were compared using the K-S test to assess if they were from the same distribution at a 95% confidence level. The resulting D-Value failed to exceed the critical D-value, confirming that the two datasets were from the same distribution. It can therefore be inferred that the model failed to explain the distribution of the validation set any more than the distribution of a random set suggesting that based on these results, the habitat suitability model derived from WLC (viii) was not a good representation of habitat choice within migrating juvenile Red Kites and therefore **H2**: *“The best performing suitability model derived from the training data will best explain the distribution of the validation data”*, can safely be rejected.

Based on this specific case, **H1**: *“The use of data driven fuzzy membership functions will allow the construction of a habitat suitability model that performs above the noise of species plasticity”* should also, be rejected. There are multiple potential explanations as to why the model failed to capture specific habitat choice but based on a comparison between WLC (viii) and the native extent of *Milvus milvus* in Spain (fig 17), it is discernible that multiple areas have been overestimated by the model. An observation that can be made is that the model successfully captured that the area that lies at the north-western tip of Spain, was unsuitable, confirmed by the lack of individuals from the juvenile group and by the known distribution, derived from Birdlife International (see appendix fig S1).

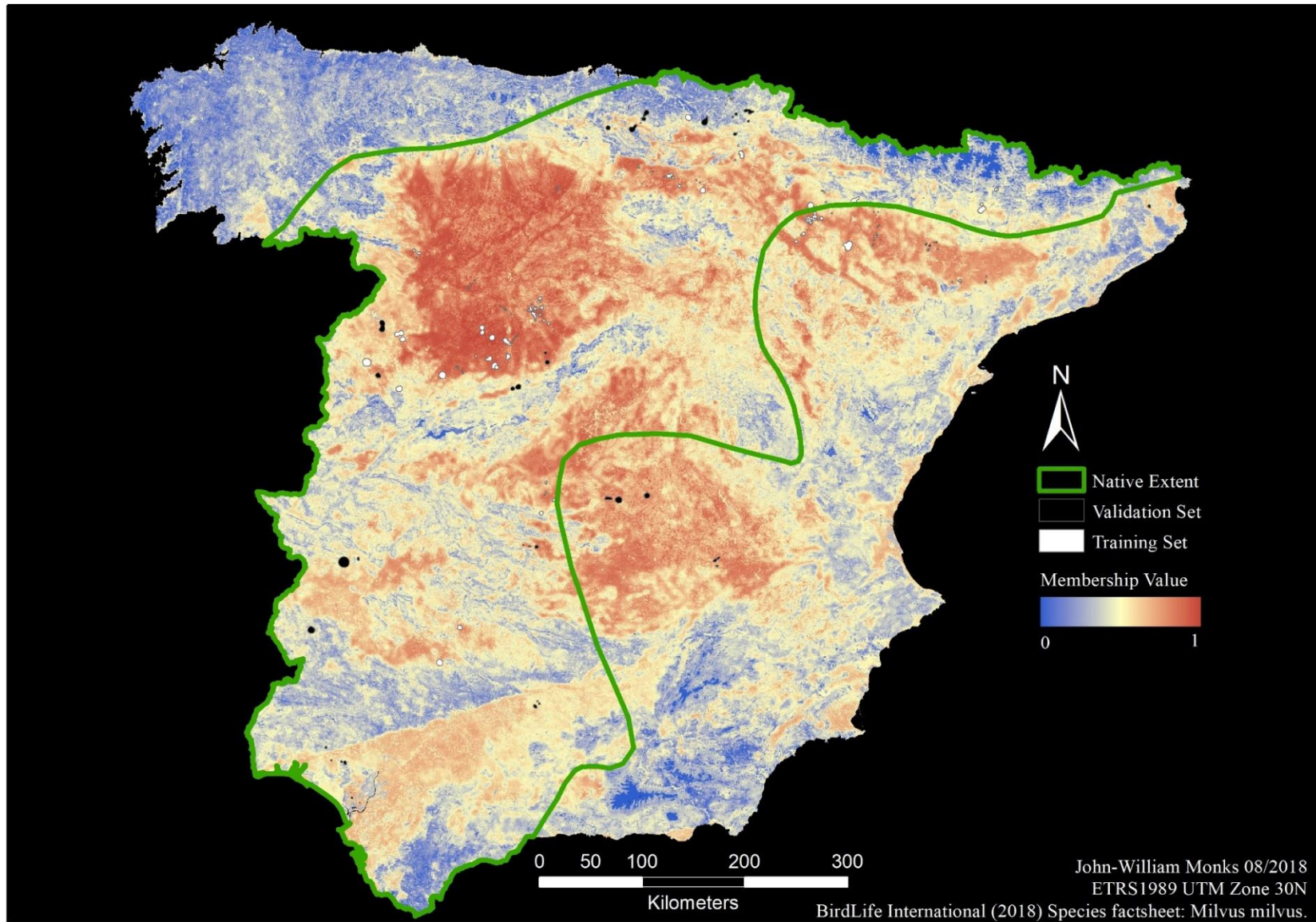


Figure 17 - The distribution of the native Red Kites is encompassed by the green line, visually recreated and based on figure S1 (appendix). Some of the data points from the juvenile kites occur well outside of the known distribution of native Red Kites

5.4 Limitations

The simplistic approach taken to attempt to capture species habitat preferences might potentially work, but on a less plastic and opportunistic species. There are multiple aspects of both the species and the data itself that are potential candidates that could explain the presence of high suitability or membership values.

From a purely visual perspective when comparing the distribution of the home ranges and the known distribution of native species there are several discrepancies between the two that could in part explain the differences between the two datasets. Within both the training data and the validation data 12 (28%) and 4 (28%) respectively were found outside of the “native extent” which can be a by-product of age, lack of experience, lack of local knowledge or simply trial and error on the bird’s behalf. Regardless of the reason, this will have contributed towards the inclusion of values within each BCMP which may have not been habitually picked by the native kites. A workaround that could be considered would be to use “leave one out cross validation” to eliminate any bias that the use of randomly chosen validation individuals might generate, specifically when using a smaller sample size where the model might be quite sensitive which individuals are used to validation.

Another limitation of this simplistic approach was the functions used to create the memberships on which the fuzzy values were derived from. The use of linear functions to capture species preference was potentially problematic in two ways. The first being that the low number of individuals used to create the functions will inevitably create gaps within the data whereby outliers will be taken into account or values which are suitable being disregarded due to there not being a sampled individual within that specified range. A good example for the shortcomings of this method would be the function that encompassed NDVI values.

Because of the high amount of suitable values generated by the NDVI membership function it proved to be a necessary but somewhat misleading BCMP. It was assumed that NDVI would be a good indicator of biological activity which would potentially compensate for the lack of “food source data”. A solution to this that could be applicable in subsequent studies would be to take into consideration rainfall. Negative correlations were observed between nestling growth rate and hatchling success and rainfall in spring. (Viñuela, 1997; Hiraldo et al., 1993), information that was originally disregarded when selecting pertinent BCMPs due to the sample kites being juveniles and the fact that the GPS points were recorded in winter. Although this

might not apply directly to their survival or habitat selection strategy, it cannot be disregarded that the avoidance of rainy areas could be attributed to an innate behaviour as a result of natural selection and breeding success. Coupled with a larger sample size it would be potentially possible to narrow down the window within which species preference occurs.

It is important to note that functions created out of data such as temperature are purely relevant to the dataset being used. In this case the function would only be applicable to temperatures within the timeframe of December of 2016 and January of 2017 and therefore most likely do not reflect a general preference for lower temperatures throughout the rest of the year.

Although the derivation of data from interpolated values from climate station data gives continuous surfaces this can induce a level of spatial uncertainties due to (i) interpolation errors (ii) lack of sufficient climate stations from which to derive data and (iii) these interpolations fail to encompass biologically relevant microclimates (Guisan and Zimmermann, 2000). This, along with the fact that too few points were included in order to do elevation-sensitive cokriging will have contributed towards a certain level of errors concerning both wind and temperature data.

The method by which the home range was devised was challenging in the fact that there is only so much one can do to try and isolate the true area of operation with limited samples. The overestimation produced using h_{opt} meant that the range of cells produced by the kernel density estimator that were taken into account were subjective. One individual “Wisk12” had a substantial spread of GPS points that an actual hub of operation, even using the density estimator, was hard to derive.

Even taking into account all the limitations related to data, the aspect that could have been the main source of error, will be the plasticity of the species in question. As mentioned, food proves to be one of the most significant factors when it comes to the habitat choice of Red Kites. Although a layer was created to try and capture this by considering the distribution of rabbits, a food source which is fairly consistently sought after by Red Kites (Mougeot and Bretagnolle, 2006; Fernandez, 1993), too little data was available regarding their specific distribution and therefore proved to be coarse to be useful. This could potentially be modelled in much the same way as was attempted within this study but with more individuals for a more solid base.

6.0 Conclusion

The aim of this thesis was to assess the effectiveness of using linear trends to create fuzzy membership functions to isolate potential BCMPs that might allow preliminary insight into habitat choice. In this specific case, a highly plastic species was selected, coupled with the individuals being migratory juveniles. Although the validation set proved to be relatively inconclusive and ultimately resulted in the rejection of **H1**, “The use of data driven fuzzy membership functions will allow the construction of a habitat suitability model that performs above the noise of species plasticity”, WLC viii explained the training data quite well showing that there are discernible patterns that this exercise could, with a larger sample size and a less opportunistic species, be a good preliminary method for assessing the importance of various habitats for the conservation of endangered species.

Considering its apparent importance throughout literature, the results also potentially support the importance of food sources as a variable and also suggest that to be able to highlight potentially suitable areas for a carnivorous species, one must initially work out the distributions of its sources of prey, which in many cases, poses quite a challenge. This specific method of attempting to isolate suitable habitats would be best tested with a species that exhibits more specific requirements along with a native population, as using juvenile migratory individuals will inevitably result in poor short term poor habitat choice without the input of experience.

Parameters such as NDVI are linked with biological production and therefore can be quite a good predictor, but the sheer amount of the suitable datapoints that exceed μ 0.75 highlight the importance of absence data that can help to define the bioclimatic limitations of a species allowing for a more narrow breadth of NDVI values to be taken into account. Coupled with the fact that in nature, things rarely occur in a linear trend, the fundamental key to improving the performance of this technique lies in managing to capture the behavioural response to BCMPs that deals with the overestimation that this model creates.

When attempting to isolate if one BCMP could be singled out as more important for habitat choice, the WLCs showed that removing any one BCMP degraded model performance, showing that each predictor chosen had a role to play. This helps to highlight the importance of understanding the complexity of habitat choice and individual species requirements. Models such as this show us that, although a species might have a forest to live in, a field to hunt it or a sea to swim in, these environments have complex interactions within them that may not be

apparent but can be critical when promoting the conservation of species and have an ever-increasing need for understanding.

7.0 References

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8.0 Appendix

8.1 Conditional Statements

- The following condition statements were using within ArcGis to apply the fuzzy membership functions created in the methodology.

NDVI :

```
Con((Float("spainndvi") < 0.13) | (Float("spainndvi") > 0.9), 0, Con((Float("spainndvi") >= 0.13) & (Float("spainndvi") <= 0.32), (Float("spainndvi") - 0.13) / (0.19), Con((Float("spainndvi") >= 0.6) & (Float("spainndvi") <= 0.9), (0.9 - (Float("spainndvi")))) / (0.3), 1)))
```

Crop Cover:

```
Con("cropoutput" <= 0, 0, Con(("cropoutput" > 0) & ("cropoutput" <= 100) , ("cropoutput" - 0) / (100 - 0), 1))
```

Forest Cover:

```
Con("forestfloat" > 78, 0, Con(("forestfloat" > 0) & ("forestfloat" <= 78), (78 - "forestfloat") / (78), 1))
```

Temperature:

```
Con(("tmp" > 8.64), 0, Con(("tmp" <= 8.64) & ("tmp" >= 4.31), (8.64 - "tmp") / (4.33), 1))
```

Altitude:

```
Con((Float("dem_int") < 86) | (Float("dem_int") > 1196), 0, Con((Float("dem_int") >= 86) & (Float("dem_int") <= 796), (Float("dem_int") - 86) / (796 - 86), Con((Float("dem_int") >= 798) & (Float("dem_int") <= 1196), (1196 - (Float("dem_int")))) / (1196 - 798), 1)))
```

8.2 Additional Maps



Figure S1 – Known native extent of *Milvus milvus* across Iberian Peninsula - BirdLife International (2018) Species factsheet: *Milvus milvus*.- BirdLife International (2018) IUCN Red List for birds. Downloaded from <http://www.birdlife.org> on 19/04/2018.