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Large scale breeding site selection and non-breeding individual movement patterns of Red-footed Falcons

PhD thesis

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General introduction

Birds are amongst the most widespread and mobile vertebrates of the world. Understanding the proximal and ultimate causes of avian distribution patterns has been in the center of ecological and biogeographical research. Birds are excellent model systems to study large scale distribution patterns as most species are highly mobile and their ability to travel large distances allows for less constrained spreading capabilities compared to any other taxa. More and more advanced tools exist in both spatial data handling and statistical methodology that enable researchers to infer on how the environment effects species. Not only did our methods to handle and analyse data evolve, but the boom in technology enabling tracking of birds now allows us to reveal individual decisions on a large spatial extent, such as long-range migration. Moreover, we are now able to link environmental factors to migratory trajectories and reveal astonishing athletic achievements of avian migrants.

In my thesis, I present a selection of studies that are connected through these methodological links. My model species is the Red-footed Falcon (*Falco vespertinus*). In the first chapter I focus on population level historic, current and potential future breeding site selection of this enigmatic raptor. In the second chapter I show how individuals fitted with state-of-the-art tracking devices cope with pre-migratory challenges and while en route.

Breeding distribution modelling of Red-footed Falcons in the Carpathian Basin

The Red-footed Falcon is a species of high international conservation concern ("near-threatened" in IUCN Red List, ANNEX I of European Commission’s Birds Directive 79/409/EEC) due to the
drastic breeding population decline of the past decades. Their breeding range extends from Central and Eastern Europe to northern Central Asia. The core of the EU population breeds in the Carpathian Basin. This small raptor is a facultative colonial breeder (i.e. breeding in colonies and in solitary pairs) that does not build a nest; falcons naturally breed in rookeries or in loose aggregations of magpie nests.

It is widely recognized that the loss of foraging habitats and/or breeding sites is predominantly responsible for the decrease in avian biodiversity. Red-footed Falcons have suffered from both during the past decades; their foraging habitats have been altered, while the drastic decrease in rookeries within the Carpathian Basin has had a serious impact on the available nesting sites.

Modelling habitat selection of the Red-footed Falcon: a possible explanation of recent changes in breeding range within Hungary

In this chapter I focused on understanding the reasons behind the documented shrinkage in breeding range of Red-footed Falcons within Hungary. The landscape scale distribution of rookeries remained stable while the density and size of rookeries decreased in the Carpathian Basin. The obvious consequences for Red-footed Falcons was that most of the potential breeding colonies disappeared, possibly causing the decline in the number of breeding pairs. However, the population decline also resulted in a shrinkage in breeding distribution of the falcons, yet the spatial pattern of still available rookeries does not necessarily cause such a phenomenon. In this study I analysed the presence probability of Red-footed Falcons at a colony in the current and historical breeding ranges using landscape scaled habitat variables. I used a potential
colony home-range size, estimated from observed home-range sizes in order to determine the scale of influential habitat variables. My results suggest that a probable cause of the observed range shrinkage is the urbanization of rooks in the historic breeding range of Red-footed Falcons. Within the current breeding range, the ratio of forests and open water surfaces had negative, while the ratio of grasslands had a positive effect on the probability of Red-footed Falcon presence. None of our models predicted presence at colonies outside the current breeding range.

Allocating active conservation measures using species distribution models: a case study of Red-footed Falcon breeding site management in the Carpathian Basin

One of the identified threatening factors of Red-footed Falcons possibly responsible for the worldwide population decline is the shortage of suitable colonial nesting sites. In theory, this problem can be resolved by establishing artificial colonies. However, the key to a successful large scale nest-box scheme is to provide these artificial colonies in habitats suitable for the species. A Hungarian-Serbian project aimed to establish such nesting facilities in northern Serbia; though, the lack of recent full scale habitat surveys hindered the designation of the locations of these artificial nesting sites. I used five different machine learning algorithms to model the distribution of nest-sites in Hungary, and in Romania. I then used the ensemble predictions of the best performing models to project the probability of Red-footed Falcon nest-site presence in Northern Serbia (predicted area). The models showed that three variables (the extent of grasslands, pastures and broad-leaved forests) had the highest importance in describing the spatial pattern of nest-sites in the mo-
delling area. The extent of grasslands and pastures had positive effects, while broad-leaved forests had negative impact on the probability of nest site presence. The predictions classified all the currently known colonies in the predicted area correctly. My results suggest that the potential breeding distribution in Serbia is similar to that of two decades ago, thus large scale land use changes are presumably not responsible for the reported population decline. The identified target areas constitute 11.5% of the original predicted area, thus largely reducing the extent of future monitoring areas. The target areas can also be used to pin-point locations for future nest-box colonies, and may provide aid in designating future Natura 2000 sites in Serbia.

Non-breeding individual movement patterns

Avian migrants have astonished laymen and scientists alike for centuries with their athletic achievements when it comes to travelling. Some of the most fascinating migratory routes discovered recently entail traversing thousands of kilometres in one flight crossing inhospitable areas like deserts or oceans.

The boom in technology enabling individual tracking of avian migrants now allows us to reveal such journeys, and has reformed research in migration ecology. The range of devices to deploy on birds is nowadays overwhelming, from Platform Transmitting Terminals (PTTs), GPS tags, GPS-GSM tags, light-level geolocators to GPS loggers, migratory species with as small as 10–12 gram average body weights can be individually tracked. However, a common trade-off of tracking, especially when remote signal sending devices are used, is that sample size is limited by the relative high costs of transmitters. Despite this, the individual migratory trajectories drawn by the tracked individuals help us better understand
how avian migrants cope with the challenges throughout their annual cycle.

In the following I present such case studies where I used the data of 8 satellite-tagged adult female Red-footed Falcons and analysed their individual movement patterns, focusing on two distinct time periods of their non-breeding movements.

Pre-migration roost site use and timing of post-nuptial migration of Red-footed Falcons as revealed by satellite tracking

Red-footed Falcons are gregarious trans-equatorial migrants, forming up to several thousand strong roost sites after the breeding season and before commencing migration. This pre-migration period is presumed to play a major role in defining the survival of long-range migrants. Here I investigate the autumn movements of 8 individuals caught and satellite-tagged within the Carpathian Basin. I found that birds may use multiple roost sites that can be separated by large distances. A single individual's home range was 88 km$^2$ and was near concentric to the roost site. Two individuals travelled to southern Ukraine soon after tag-deployment. The night localisation points of birds marked out 2 and 5 yet unknown potential roost sites in Hungary and in the Ukraine, respectively. Using the data of an international weekly roost-site survey (2006–2011) carried out in the Carpathian Basin, I cross-referenced the departure dates of tagged individuals with the 6 year means of counted individuals. The tagged birds commenced migration with the first 25% percent of the surveyed population. My results demonstrate that even a small number of satellite tagged birds show behavioural plasticity in terms of roost site selection indicating that post-breeding foraging habitat choice decisions may have substantial variability.
Falcons reduce risk by migrating through corridors of predictable rainfall in the African rainforest

Tropical rainforests act as ecological barriers to avian migrants, yet the reasons for this are unclear. I report evidence that dense and stochastic precipitation substantially explains the trajectories of falcons migrating within the African rainforest. I used 11 years of National Oceanic and Atmospheric Administration's highest resolution daily rainfall estimates to calculate the risk of migrants encountering dense rain. My analyses revealed the long-term existence of a north-south corridor in which the risk of precipitation was considerably lower than in surrounding areas. The migration routes of satellite-tracked Red-footed Falcons converged into this corridor, in which individuals avoided immediate concentrations of rain. My examination of published studies indicated that a second falcon species used the same corridor, while individuals of a third species migrated 1500 kilometres west through another lower risk corridor we had identified. These findings suggest the importance of rainfall in shaping the migration patterns of birds that pass through rainforests.
Summary of main scientific results

Here I briefly list the main results of my thesis:

1. I show that Red-footed Falcon breeding colony selection can be modelled effectively with landscape scale habitat variables, they prefer breeding sites where within the potential home-range grasslands have high, while urban areas, forests and open water surfaces have low percentages.

2. I identified a possible cause of reported breeding range shrinkage of Red-footed Falcons; Rooks, their nest-host species, have possibly altered their breeding site selection to urban areas in regions where the falcons have become extinct.

3. I show that species distribution modelling using landscape scale habitat variables, machine learning algorithms and their ensemble predictions are capable of identifying conservation target areas for Red-footed Falcons in areas where nature conservation resources are lacking.

4. I analysed the pre-migratory individual trajectories of satellite tracked Red-footed Falcons and the results indicate that tracked individuals show plastic behaviour on a continental scale when selecting pre-migratory roost sites.

5. I identified two and five yet unknown potential pre-migratory Red-footed Falcon roost sites in Hungary and in the Ukraine, respectively.

6. I present correlative evidence that migrant Red-footed Falcons traversing the African Congo Basin optimize their routes to avoid precipitation.
7. I demonstrate the existence of low rainfall risk corridors in the Congo Basin which Red-footed Falcons and tracked individuals of two sister species utilize when traversing the region.

8. For the first time I present correlative evidence that the African rainforest is potentially a meteorological barrier for avian migrants.
List of publications

Publications in peer-reviewed journals related to the thesis


Publications in peer-reviewed journals not related to the thesis


Kovács S., Fehérvári P., Nagy K., Harnos A., Csörgő T., Changes in migration phenology and biometrical traits of reed, marsh
and sedge warblers, Central European Journal of Biology, 7(1), 115–125, 2012. (IF: 0.818)


