

Phylogenetic diversity and EDGE approach in conservation of birds of prey in Europe

Dragos Mihail STEFĂNESCU^{1,*}, Emil MARINESCU²

- ¹ Faculty of Horticulture, Department of Biology and Environmental Engineering, University of Craiova, 13, Al. I. Cuza Str. 200585, Craiova, Romania
- ² Faculty of Sciences, Department of Geography, University of Craiova, 13, Al. I. Cuza Str., 200585, Craiova, Romania * Corresponding author. mihailstefanescu@yahoo.com

Received on 21-04-2021, reviewed on 20-08-2021, accepted on 01-09-2021

Abstract

Biodiversity of our planet is rapidly eliminated, at rates much higher than ever observed in human history. The birds of prey, among others few groups of bird species in Europe, have the highest proportion of threatened and near threatened species per taxonomic group and also, 25% of birds of prey species are experiencing population decline. Today, more than never in our modern life, we have to fight for nature conservation. Our understanding of biological diversity has broadened due to the fact that the use of phylogenies in ecology is increasingly common. If our conservation efforts are directed to maximize the preservation of biodiversity in a broad sense, we have to think beyond species. If we treat the species as evolutionary units, and not like types, our conservation efforts will preserve not only the organism, but the organism capacity to responde to environmental changes. In this paper I aimed to highlight the importance of phylogenetic information in conservation of birds of prey species in Europe through the EDGE approach. This metric has been implemented to prioritise species, beeing the only global initiative to focus on conservation of threatened species with significant amount of unique evolutionary history. Using this approach in conservation, we can be more confident that we will have the potential to preserve more functional trait diversity than expected. The top five birds of prey EDGE species in Europe are: osprey (Pandion haliaetus), the black-winged kite (Elanus caeruleus), the egyptian vulture (Neophron percnopterus), the european honey-buzzard (Pernis apivorus) and the bearded vulture (Gypaetus barbatus), according their EDGE scores.

Keywords: birds of prey, phylogenetic diversity, evolutionary distinctiveness, EDGE, conservation

Rezumat. Diversitatea filogenetică și abordarea EDGE pentru conservarea speciilor de păsări de pradă în Europa

Biodiversitatea planetei noastre este eliminată rapid, cu rate mult mai mari decât cele observate vreodată în istoria omenirii. Păsările de pradă, printre altele câteva grupuri de specii de păsări din Europa, au cea mai mare proporție de specii amenințate și aproape amenințate per grup taxonomic și, de asemenea, 25% dintre speciile de păsări de pradă se confruntă cu declinul populației. Astăzi, mai mult ca niciodată în viața noastră modernă, trebuie să luptăm pentru conservarea naturii. Înțelegerea noastră asupra diversității biologice s-a extins datorită faptului că utilizarea filogeniilor în ecologie este din ce în ce mai comună. Dacă eforturile noastre de conservare sunt îndreptate spre maximizarea conservării biodiversității într-un sens larg, trebuie să gândim dincolo de specii. Dacă tratăm speciile ca unități evolutive și nu ca tipuri, eforturile noastre de conservare vor păstra nu numai organismul, ci și capacițatea organismului de a răspunde la schimbările de mediu. În această lucrare mi-am propus să evidențiez importanța informațiilor filogenetice în conservarea speciilor de păsări de pradă din Europa prin abordarea EDGE. Aceast indicator a fost implementat pentru a prioritiza speciile, fiind singura inițiativă globală care se concentrează pe conservarea speciilor amenințate care posedă o cantitate semnificativă de istorie evolutivă unică. Folosind această abordare în conservare, putem fi mai încrezători că vom păstra o mai mare diversitate de trăsături funcționale. Primele cinci specii de păsări răpitoare EDGE din Europa sunt: uliganul pesacr (Pandion haliaetus), gaie cu aripi negre (Elanus caeruleus), vulturul egiptean (Neophron percnopterus), viesparul (Pernis apivorus) și vulturul barbos (Gypaetus barbatus), conform scorurilor lor EDGE.

Cuvinte-cheie: păsări de pradă, diversitate filogenetică, distinctivitate evolutivă, EDGE, conservare

Introduction

Biodiversity of our planet is rapidly eliminated, at rates much higher than ever observed in human history. Whether we are talking about habitat destruction and fragmentattion, pollution, overexploitation of forestry and fishery resources, invasive species, and to the effect of climate changes, a high number of species were already extinct and others have suffered several population declines, situation recognized today as the "sixth mass extinction" (Pellens& Grandcollas, 2016).

Today, more than never in our modern life, we have to fight for nature conservation. Most often,

biodiversity conservation was based on traditionally measures like species richness, number of endemics and threatened species at different sites, considering all species as equals, regardless to their evolutionary history (Pellens& Grandcollas, 2016). At the same time, species richness (number of species) recorded in a local community is the simplest concept of diversity (Mittelbach & McGill, 2019).

Species play a fundamental role in the functioning of ecosystems, two mechanisms being involved: niche complementarity and species selection (Mittelbach & McGill, 2019). It is known that systems with many species produce more biomass and capture more resources than those with only a few species, at

different trophic levels and habitats (Van Dyke & Lamb, 2020).

Our understanding of biological diversity has broadened due to the fact that the use of phylogenies in ecology is increasingly common (Tucker et al., 2016). If our conservation efforts are directed to maximize the preservation of biodiversity in a broad sense, we have to think beyond species (Cadotte & Davies, 2016). If we treat the species as evolutionary units, and not like types, our conservation efforts will preserve not only the organism, but the organism capacity to respond to environmental changes (Van Dyke & Lamb, 2020). Grouping closely related species into evolutionary clade that share much of their evolutionary history, we will get groups of species by more similarities regarding their life histories and ecology (Cadotte & Davies, 2016). In order to maximize biodiversity rather than just species richness in our conservation efforts, one way will be to measure all traits for each species, by selecting those species that maximize trait diversity. Using phylogeny as a simple proxy, we can assume that phylogenetic relatedness should be correlated with species morphology and ecology, and, by maximizing the preservation of phylogenetic diversity we will enhance the preservation of phenotypic and ecological diversity (Cadotte & Davies, 2016).

Unfortunately, the resources currently available for conservation are insufficient, and for this reason, conservation planners have been forced to prioritise which species should receive the most protection (Isaac et al., 2007). So, any conservation plan focuses on the key concept of prioritization (Bromham, 2016). Starting from the idea that some species are closer to extinction than others, one way is to rank species according to their risk of extinction, categorization provided by **IUCN** (International Union Conservation of Nature) Red List (Bromham, 2016). Another, complementary way is to rank species independently of haw rare or threatened they are, considering the evolutionary distinctiveness of a species, or its relative uniqueness within a phylogeny (Bromham, 2016; Cadotte & Davies, 2016).

Conservation priority setting must have as its key component the maximizing of phylogenetic diversity (Faith, 1992; Witting & Loeschcke, 1995; Isaac et al., 2007), a biodiversity measure based on phylogenetic branch lengths, calculated as the sum branch lengths connecting all species involved (Bromham, 2016). By measuring phylogenetic diversity, we are able to weight the number of species in a sample by their shared evolutionary history (Swenson, 2020). However, the use of phylogenetic diversity in conservation has been limited so far, for multiple reasons, but the most obvious is that it can be difficult to evaluate the connection between phylogeny and

values of biodiversity that most people are familiar with (Bromham, 2016).

In response to the phylogenetic diversity limitation, a program named EDGE (Evolutionarily Distinct and Globally Endangered) has been developed, to prioritize species for conservation, based on a combination of their phylogenetic position and their IUCN Red List category (Bromham, 2016). In this way, we will finally get a list of species that are both evolutionarily distinct and globally endangered, so called EDGE species (Isaac et al., 2007).

Conservation prioritisation approaches that do not take phylogenetic relationships between species into consideration will fail to prevent the loss of large amounts of phylogenetic and functional trait diversity (Gumbs et al., 2018). A metric widespread to integrate phylogeny into the prioritisation of species is evolutionary distinctiveness (Gumbs et al., 2018).

In this paper we aimed at highlighting the importance of phylogenetic information for the conservation of birds of prey species in Europe through the EDGE approach. The birds of prey, among other few groups of bird species in Europe, have the highest proportion of threatened and near threatened species per taxonomic group and also, 25% of birds of prey species are experiencing population decline (BirdLife International, 2015; BirdLife International, 2021). Bevond the ecosystem services provided by scavengers and predators, birds of prey species are indicators of biodiversity and environmental health, and can structure biological communities, being at the same time particularly sensitive to anthropogenic threats (McClure et al., 2018).

In Europe there are nesting some 40 birds of prey species (Keller et al., 2020). In this paper we have included a number of 39 species, excluding shikra (Accipiter badius), which nests only in a confined area, Armenia and Azerbaijan (Keller et al., 2020), with unclear status in Eastern Europe.

Methods

We can explore and describe large scale-patterns of biodiversity and analyse how these patterns emerged over evolutionary time, starting from digital data that describe species distributions, which have recently seen a very rapid growth (Fjeldså et al., 2020).

Species data acquisition

Data for birds of prey were obtained from BirdLife (http://datazone.birdlife.org) in a shapefile format, for all 39 species. Subsequent processing operations were made in ArcMap 10.2 (https://www.esri.com).

Convert raw input distribution data to community

Raw species distribution data available were converted as polygons to a community composition data frame (grid), at spatial grains of 0.5 decimal degrees and to extent of Europe, for downstream analyses. For this purpose, we utilized phyloregion R library (Daru et al., 2020).

Birds of prey phylogeny

To get an information regarding phylogenetic relationships between the 39 birds of prey species from Europe, a distribution of 3000 full molecular trees was downloaded from BirdTree.org (https://birdtree.org), a globally birds phylogeny database (Jetz et al., 2012). We obtained the Maximum Clade Credibility tree (best suported tree) using mean node heights (20% of trees were used as burnin) and the TreeAnnotator software, version 2.6.6 (Drummond & Rambaut, 2007). From this tree, we extracted node ages and 95% HPD (Height Posterior Density) and also the posterior probability for each node. HPD usually represents the uncertainty of inferred divergence times. Plotting the tree was made with RevGadgets library from R (Tribble et al., 2021).

Phylogenetic diversity (PD)

According to Faith (1992), phylogenetic diversity (PD) is a biodiversity measure based on phylogenetic branch lengths connecting all the species in a set, with higher biodiversity score for a set of species representing distantly related lineages than the same number of species that are each other's close relatives (Bromham, 2016). We calculated PD for our group of 39 birds of prey species of Europe, for each grid cells, by summing all the edge lengths from the vector of edge lengths (Cadotte & Davies, 2016), measured in millions of years (Myr), based on phylogeny.

Evolutionary distinctiveness (ED)

Based on Isaac et. al. (2007), evolutionary distinctiveness (ED) was calculated by dividing the total phylogenetic diversity of a clade amongst its members, by applying a value to each branch of the phylogenetic tree equal to its length divided by the number of species substending the branch. Thus, for a species, ED is the sum of these values for all branches from which the species is descended, to the root of the phylogeny (Isaac et al. 2007), measured in millions of years (Myr). Species with many splits from root to tip have many close relatives and are less evolutionary distinct (Cadotte & Davies, 2016).

EDGE (Evolutionarily Distinct and Globally Endangered) calculation

To obtain EDGE score for each bird of prey species, we combined ED with threat status, using the relation (Isaac et. al. 2007; Cadotte & Davies, 2016, Bromham, 2016):

 $EDGE = \ln(1 + ED) + GE * \ln(2)$

where GE (Global Endangerment) is the IUCN Red List category weight (Least Concern = 0, Near Threatened and Conservation Dependent = 1, Vulnerable = 2, Endangered = 3, Critically Endangered = 4). Finally, EDGE species scores are interpreted as the log-transformed expected loss of evolutionary diversity, in which each increment in threat status ranking corresponds to a doubling of extinction probability (Isaac et. al. 2007; Cadotte & Davies, 2016).

This metric has been implemented by the EDGE of Existence programme at the Zoological Society of London to prioritise species in several taxonomic groups, beeing the only global initiative to focus on conservation of threatened species with significant amount of unique evolutionary history (Gumbs et al., 2018). Using this approach in conservation we can be more confident that we will have the potential to preserve more functional trait diversity than expected (Redding et al., 2009; Gumbs et al., 2018).

EDGE species are species that have an above median ED score and are also threatened with extinction (Critically Endangered, Endangered or Vulnerable on the IUCN Red List).

Species richness and pylogenetic diversity maps for the European birds of prey nesting species were made with the help of *phyloregion* R library (Daru et al., 2020). Also, ED and EDGE scores for each species were obtained with the same R library, using *evol_distint* and *EDGE* functions. We also conducted a linear regression with species richness as independent variable and phylogenetic diversity as dependent variable (Rueda-M butterflies) to find the magnitude of this relationship and to plot residuals to highlight the areas where these variables are different.

Information regarding species risk of extinction categorization were obtained from IUCN website (https://www.iucnredlist.org) and European Red List of birds (BirdLife International, 2015; BirdLife International, 2021).

We performed an one-way ANOVA to test if ED is distributed evenly between Least Concern species and the other categories of species grouped together (Near Threatened, Vulnerable, Endangered and Critically Endangered).

Results

The 39 birds of prey species that nest in Europe belong to two orders: *Accipitriformes* (family *Pandionidae* - 1 species; family *Accipitridae* - 28 species) and *Falconiformes* (family *Falconidae* - 10 species),

according to Del Hoyo, 2020 and Keller et al., 2020. The complete list of species is presented in Table 1.

Table 1: Evolutionary distinctiveness and EDGE scores for birds of prey in Europe with IUCN Red List assessments (in bold, the first five species with the largest magnitude for each metrics)

Species	Estimated ED in Myr	Red List category (for Europe only)*	EDGE score
Order Accipitriformes			
Family Accipitridae			
Aegypius monachus	26.542	LC	3.316
Gyps fulvus	26.542	LC	3.316
Gypaetus barbatus	34.667	VU	3.643
Neophron percnopterus	34.667	EN	4.038
Circus aeruginosus	17.066	LC	2.894
Circus macrourus	17.066	NT	2.900
Circus pygargus	18.089	LC	2.949
Circus cyaneus	18.694	NT	2.987
Elanus caeruleus	57.459	LC	4.069
Pernis apivorus	40.279	LC	3.721
Milvus milvus	15.312	NT	2.798
Milvus migrans	15.312	LC	2.792
Circaetus gallicus	34.215	LC	3.562
Haliaeetus albicilla	24.628	LC	3.244
Clanga pomarina	11.269	LC	2.507
Clanga clanga	11.269	EN	2.971
Aquila nipalensis	10.757	CR	3.156
Aquila adalberti	9.623	VU	2.432
Aquila heliaca	9.623	LC	2.363
Aguila chrysaetos	13.460	LC	2.672
Aquila fasciata	13.460	NT	2.678
Hieraaetus pennatus	14.737	LC	2.756
Accipiter brevipes	28.408	LC	3.381
Accipiter nisus	26.795	LC	3.325
Accipiter gentilis	25.182	LC	3.265
Buteo buteo	11.878	LC	2.556
Buteo lagopus	12.757	LC	2.622
Buteo rufinus	11.878	LC	2.556
Family Pandionidae			
Pandion haliaetus	62.309	LC	4.148
Order Falconiformes Family Falconidae			
Falco cherrug	11.698	VU	2.610
Falco rusticolus	11.698	LC	2.542
Falco peregrinus	13.350	LC	2.664
Falco vespertinus	18.580	NT	2.981
Falco eleonorae	14.415	LC	2.736
Falco subbuteo	14.415	LC	2.736
Falco biarmicus	11.852	EN	3.017
Falco naumanni	17.780	LC	2.933
Falco tinnunculus	17.780	LC	2.933
Falco columbarius	20.825	LC	3.083

*after European Red List of birds (BirdLife 2015; BirdLife International, 2021)

The dated phylogenetic tree showing relationships between birds of prey species are indicated in Figure 1, allowed to notice that ancestors of *Falconiformes* order species have diverged from the rest of the birds of prey species around 83.375

Myr (95% HPD:75.270 – 91.389), and osprey (*Pandion haliaetus*), the only species of family *Pandionidae*, has split from the rest of the group species of *Accipitriformes* order around 61.557 Myr (95% HPD:49.734 – 73.325). Also, the black-winged

kite (*Elanus caeruleus*) has a distinct evolutionary path over *Accipitriformes* order since around 56.527 Myr (95% HPD:45.063 – 67.578).

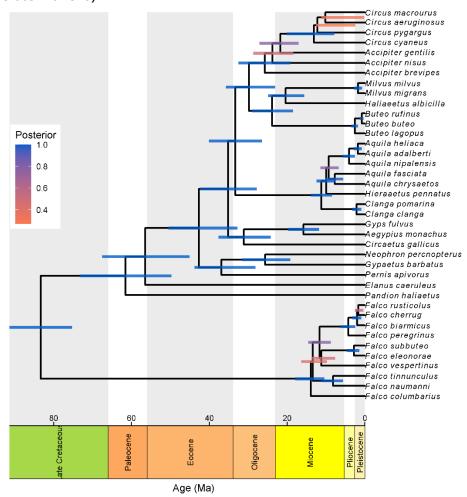


Fig. 1: The maximum-clade credibility phylogeny of birds of prey of Europe (see methodology for more informations). Bars correspond to the 95% credible interval of node ages, and are colored by the posterior probability of the clade

The spatial distribution of PD and species richness of birds of prey in Europe is quite uneven (Fig. 2, A and B), higher values of species richness and PD being concentrated within the eastern and southern part of Europe. Although species richness has a strong and significant effect on PD (adjusted R2 = 0.927, p \leq 0.0001), the map of residuals (Fig. 2, C) indicate that PD is underestimated in Eastern Europe (blues zones in Fig. 2, C) and overestimated in Western and Northern Europe (red zones in Fig. 2, C).

The values of ED (in Myr) and EDGE scores for each of 39 birds of prey species of Europe are indicated in Table 1. Most taxa are relatively young, with little evolutionary distinctiveness, ED scores distribution being slightly skewed to the right (Fig. 3). All the birds of prey from Europe, present in this

study, have a median ED equal with 17.066 Myr (Fig. 3). The highest value for this diversity metric (62.309 Myr) has been found for osprey (*Pandion haliaetus*), while the lowest value (9.623 Myr) is shared between the Spanish imperial eagle (*Aquila adalberti*) and the eastern imperial eagle (*Aquila heliaca*). Thus, osprey (*Pandion haliaetus*) is the most evolutionary distinct birds of prey species in Europe. The median EDGE score for species is 2.933, with 19 birds of prey species having an EDGE score greater than median value (Table 1; Fig. 3). At the top of the EDGE scores list we found the osprey (*Pandion haliaetus*), with 4.148, while at the opposite pole, with the lowest value – the eastern imperial eagle (*Aquila heliaca*), with 2.363 (Table 1).

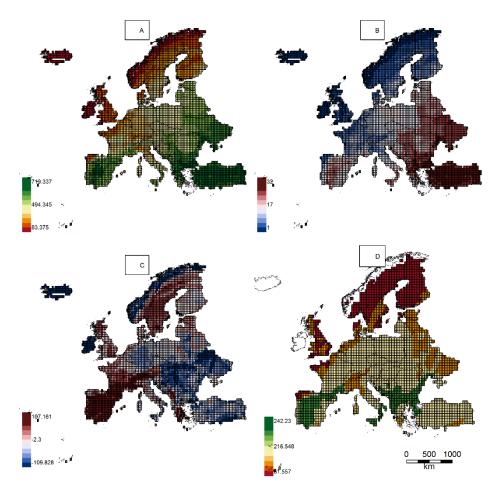


Fig. 2: Maps of diversity metrics. (A) Birds of prey phylogenetic diversity, (B) birds of prey species richness, (C) residuals of birds of prey phylogenetic diversity regressed on birds of prey species richness, and (D) phylogenetic diversity for the top five birds of prey EDGE species. All maps were plotted in grid cells of 0.5° x 0.5°

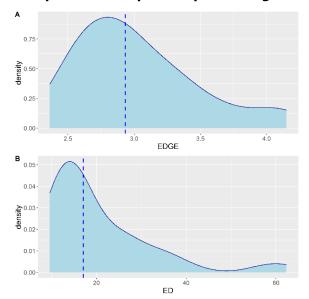


Fig. 3: Density distribution for (top) EDGE and (down) ED scores for birds of prey species of Europe. The dashed line represents the median value

Moreover, out of the 39 birds of prey species of Europe, 12 (30,77%) were considered at high risk for extinction (Table 1), according to IUCN (Near Threatened, Vulnerable, Endangered or Critically Endangered). The remaining 27 birds of prey species are in the Least Concern category, having a slightly higher mean of ED scores (2.968, using log transformed scores) than mean of ED scores (2.758) for those species with high risk of extinction, but the relationship is not significant ($F_{1,37} = 1.634$; p = 0.209; using log transformed ED scores), thus ED being distributed almost evenly between this two category of species.

Discussion

Birds of prey species, as top predators, are critical for maintaining ecosystem structure, function and services. They link ecosystem processes and energy fluxes by their effect on trophic webs, extended to the lower levels (Cruz et al., 2021). During the last few decades, populations of some birds of prey species has decline

dramatically, so they face extinction unless effective conservation measures are taken (Cruz et al., 2021).

The top five birds of prey EDGE species in Europe are: osprey (Pandion haliaetus), the black-winged kite (Elanus caeruleus), the Egyptian vulture (Neophron percnopterus), the European honey-buzzard (Pernis apivorus) and the bearded vulture (Gypaetus barbatus), according to their EDGE scores (Table 1). Data in Table 1 related to these five species indicate that the IUCN status of species (Critically Endangered, Endangered or Vulnerable) alone does not guarantee a high priority for conservation, the European honey-buzzard (*Pernis* apivorus), the black-winged kite (Elanus caeruleus), and osprey (Pandion haliaetus) being least exposed to extinction, categorized as Least Concern, their distinctive evolutionary paths causing them to be placed in the first EDGE positions. Thus, the only "true" EDGE birds of prey species are the Egyptian vulture (Neophron percnopterus) and the bearded vulture (Gypaetus barbatus), with both an above median ED score and highly threatened status. Geographically, this top five birds of prey EDGE species are mostly spread in the Mediterranean region (Fig. 2, D).

Statistically, this analysis identified 19 birds of prey within Europe (with EDGE score higher than median EDGE value) as EDGE species (Table 1), thus, species with high priority attention for conservation. Among them, one is considered as Critically Endangered (Aquila nipalensis) and three are grouped in the Endangered IUCN category (Neophron percnopterus, Clanga clanga and Falco biarmicus). The most endangered birds of prey species in Europe is the steppe eagle (Aquila nipalensis), according to European Red List of birds (BirdLife International, 2015; BirdLife International, 2021), considered as Critically Endangered, with only an estimated population of 1000 pairs in Europe (Keller et al., 2020). Its ED score (10.757 Myr) is below the median value (17.066 Myr), a reason why its EDGE score (3.156) is not the highest, but bigger than median EDGE value (2.933).

The three birds of prey species categorized as Endangered in Europe by IUCN are: the Egyptian vulture (Neophron percnopterus), the greater spotted eagle (Clanga clanga) and the lanner falcon (Falco biarmicus). The Egyptian vulture (Neophron percnopterus) has disappeared from the northern part of its range (Ukraine), with populations becoming more fragmented (Keller et al., 2020). About 50% of the European breeding population is restricted to Iberian Peninsula (Keller et al., 2020). Its ED score (34.667 Myr) is above median value, leading this species to be on the third position on the EDGE species list (Table 1). The breeding range of the greater spotted eagle (Clanga clanga) in Europe is limited by 62°N and 52-53°S (Keller et al., 2020). This species has disappeared from the southern part of Eastern Europe: Romania, Bulgaria, Moldova and southern Ukraine (Keller et al., 2020). Its EDGE score (2.971) is slightly above median

EDGE score (2.933), given that its evolutionary isolation is relative short, the greater spotted eagle (Clanga clanga) and the lesser spotted eagle (Clanga pomarina) being two sister species (which have an exclusive common ancestor), which started on distinct evolutionary paths around 2.122 Myr (95% HPD:0.885 according to inferred phylogenetic 3.244), relationships from the best supported tree. The lanner falcon (Falco biarmicus) is present in Europe from Italy across the Balkan Peninsula to Anatolia, south of 45 oN, but this species has registered a continuous decline, with massive losses in Italy, western Balkans and Turkey (Keller et al., 2020). Despite his low ED score (11.852 Myr), this species "pass" the EDGE test, requiring increased attention for conservation.

Among the 39 bird of prey species in Europe, three of them are considered by IUCN as Vulnerable: the bearded vulture (*Gypaetus barbatus*), the Spanish imperial eagle (*Aquila adalberti*) and the saker falcon (*Falco cherrug*). The bearded vulture (*Gypaetus barbatus*) is an EDGE species, with an EDGE score of 3.643 (Table 1), while the other two species are not, despite their vulnerability to extinction. This contradiction arises from the fact that the Spanish imperial eagle (*Aquila adalberti*) and the saker falcon (*Falco cherrug*) have low values for ED (see Table 1).

Thirteen birds of prey species of those 19 species with EDGE score higher than median EDGE value are considered Least Concern by IUCN in Europe, these species being important in terms of originality, or irreplaceability. On the other hand, among the species that are not included in the first 19 positions of the EDGE ranking list, there are species listed as Near Threatened or Vulnerable (see Table 1), but with a relative lower uniqueness compared to other species.

According to Isaac et al. (2007), the EDGE approach can be used for conservation in a number of ways, prioritizing the most evolutionary distinct species when all factors were equal and resources are limited, generating easily a list of high-priority species that required urgent conservation or to use EDGE scores to weight species' importance in selecting reserve networks.

Conclusions

Birds of prey species, as top predators, are critical for maintaining ecosystem structure, function and services, most of them being in a great risk of extinction.

Based on the information related to the evolutionary history of the species and their probability of extinction, we can find an efficient way to prioritize species for conservation. For this purpose, EDGE program is a global initiative to focus on conservation of threatened species with significant amount of unique evolutionary history. Using this approach in conservation, we can be more confident that we will

have the potential to preserve more functional trait diversity than expected.

The top five birds of prey EDGE species in Europe are: osprey (*Pandion haliaetus*), the black-winged kite (*Elanus caeruleus*), the egyptian vulture (*Neophron percnopterus*), the european honey-buzzard (*Pernis apivorus*) and the bearded vulture (*Gypaetus barbatus*), according their EDGE scores.

References

- BirdLife International (2015). European Red List of Birds. BirdLife Europe
- BirdLife International (2021). European Red List of Birds. BirdLife Europe
- Bromham, L. (2016). An Introduction to Molecular Evolution and phylogenetics. Oxford University Press
- Cadotte, M.W., & Davies, T.J. (2016). Phylogenies in Ecology: a guide to concepts and methods. Princeton University Press
- Cruz, C., Santulli-Sanzo, G., Ceballos, G. (2021). Global patterns of raptor distribution and protected areas optimal selection to reduce the extinction crises. *PNAS*, 118 (37) .e2018203118
- Daru, B.H., Karunarathne, P., Schliep, K. (2020). phyloregion: R package for biogeographic regionalization and macroecology. *Methods in Ecology and Evolution*, 11, 1483–1491. doi:10.1111/2041-210X.13478
- Del Hoyo, J. (2020). All the Birds of the World. Lynx Edicions
- Drummond, A.J., & Rambaut, A. (2007). BEAST: Bayesian evolutionary analysis by sampling trees. *BMC Evolutionary Biology*, 7:214.doi: 10.1186/1471-2148-7-214
- Faith, D.P .(1992). Conservation evaluation and phylogenetic diversity. *Biological Conservation*, 61: 1–10
- Fjeldså, J., Les Christidis & Ericson G:P. (2020). The Largest Avian Radiation. The Evolution of Perching Birds, or the Order Passeriformes. Lynx Edicions
- Gumbs, R., Gray, C.L., Wearn, O.R., Owen, N.R. (2018). Tetrapods on the EDGE: Overcoming data limitations to identify phylogenetic conservation priorities. *PLoS ONE* 13(4): e0194680 https://doi.org/10.1371/journal.pone.0194680.
- Isaac, N.J.B., Turvey, S.T., Collen, B., Waterman, C., Baillie, J.E.M. (2007). Mammals on the EDGE: Conservation priorities based on threat and phylogeny. *Plos ONE* 2(3): e296. doi:10.1371/journal.pone.0000296
- Jetz, W., Thomas, G.H., Joy, J.B., Hartmann, K., Mooers, A.O. (2012). *Nature*, 491: 444-448. doi:10.1038/nature11631

- Keller, V., Herrando, S., Voříšek, P., Franch, M., Kipson, M., Milanesi, P., Martí, D., Anton, M., Klvaňová, A., Kalyakin, M.K., Bauer, H-G., Foppen, R.P.B (2020).
 European Breeding Bird Atlas 2: Distribution, Abundance and Change. European Bird Census Council (EBCC) and Lynx Edicions
- McClure, C.J.W., Westrip, J.R.S., Johnson, J.A., Schulwitz, S.E., Virani, M.Z., Davies, R., Symes, A., Wheatley, H., Thorstrom, R., Amar, A., Buij, R., Jonse, V.R., Williams, N.P., Buechley, E.R., Butchart, S.H.M. (2018). State of the world's raptors: Distributions, threats, and conservation recommendations. *Biological Conservation*, 227: 390–402
- Mittelbach, G.G., & McGill, B.J. (2019). Community ecology. Oxford University Press
- Pellens, R., & Grandcollas, P. (2016). Phylogenetics and conservation biology: Drawing a path into the diversity of life. pp. 1-18 in Pellens, R., & Grandcollas (ed.) Biodiversity Conservation and Phylogenetic Systematics, Preserving our evolutionary heritage in an extinction crisis. Springer, Switzerland
- Redding, D.W., DeWolff, C.V., Mooers, A. Ø. (2009). Evolutionary distinctiveness, threat status, and ecological oddity in Primates. *Conservation Biology*, 24(4): 1052-1058. DOI: 10.1111/j.1523-1739.2010.01532.x
- Rueda-M, N, Salgado-Roa, F.C., Gantiva-Q, C.H., Pardo-Diaz, C., Salazar, C. (2021). Environmental drivers of diversification and hybridization in Neotropical butterflies. *Frontiers in Ecology and Evolution*, 9:750703. doi: 10.3389/fevo.2021.750703
- Swenson, N.G. (2020). Phylogenetic Ecology: A History, Critique, and Remodeling. The University of Chicago Press
- Tribble, C.M., Freyman, W.A., Landis, M.J., Lim, J.Y, Barido-Sottani, J., Kopperud, B.T., Hohna, S., May, M.R. (2021). RevGadgets: an R Package for visualizing Bayesian phylogenetic analyses from RevBayes. *bioRxiv*, doi: https://doi.org/10.1101/2021.05.10.443470
- Tucker, C:M., Cadotte, M.W., Carvalho, S.B., Davies, T.J., Ferrier, S., Fritz, S.A., Grenyer, R., Helmus, M.R., Jin, L.S., Mooers, A.O., Pavoine, S., Purschke, O., Redding, D.W., Rosauer, D.F., Winter, M., Mazel, F. (2016). A guide to phylogenetic metrics for conservation, community ecology and macroecology. *Biological Reviews*, 92(2): 698-715
- Van Dyke, F., & Lamb, R.L. (2020). Conservation Biolog: Fundations, Concepts, Applications. Springer, Switzerland
- Witting, L., & Loeschcke, V. (1995). The optimization of biodiversity conservation. *Biological Conservation*, 71: 205–207.