PRIORITIZATION OF EVOLUTIONARILY DISTINCT

AND ENDANGERED SPECIES

IN CALIFORNIA

by

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ABSTRACT

Prioritization of Evolutionarily Distinct and Endangered Species in California

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There is neither enough time nor funding to save all species in need of conservation. We must therefore prioritize which species receive conservation attention. The focus of conservation efforts should be shifted toward maximizing the preservation of evolutionary history in order to conserve as many branches of the tree of life as possible. Studies on phylogenetically informed conservation prioritization are numerous on a global scale, but regional studies are few. The primary goal of this study was to demonstrate the use of the RED-E (Regional Evolutionary Distinctiveness and Endangerment) metric for conservation prioritization at the state level by creating a ranking of birds and mammals in the state of California. A further spatial analysis was conducted for birds using GIS to answer the following research questions: 1. Would prioritization by species richness alone be sufficient to protect evolutionarily distinct and endangered species? 2. To what degree are evolutionarily distinct and endangered species being protected by current government protected areas in California? The findings of this study indicate that the RED-E metric is compatible with conservation on a state scale and could easily be incorporated into California's current conservation prioritization system. Results of the spatial analysis showed that prioritization by species richness would not be sufficient to protect highly distinct and endangered species in California. Additionally, many highly distinct and endangered species exists within areas with minimal coverage of protected areas. The incorporation of phylogenetic information into conservation prioritization is just as relevant on a regional scale as a global one and more regional studies are needed.

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Chapter 1: Introduction and Literature Review

Introduction

Extinction rates have increased to up to 1000 times the background rate leading scientists to believe that we are currently in the middle of the sixth major extinction event in Earth's history (Isaac et al. 2007; Pimm and Brooks 2000; Purvis et al. 2000; Safi et al. 2013; Veron et al. 2015) As we continue to see the effects of climate change and habitat degradation, that rate will likely only increase. Barnosky et al. (2011) state that this mass extinction could progress to the point of losing 75% of all vertebrate life.

Unfortunately, even if we were to drastically increase conservation efforts, it would be impossible to help all species in need of conservation (Isaac et al. 2012). Furthermore, available conservation funding is nowhere near enough to keep up with the ever-increasing number of threatened species (Myers et al. 2000). It is clear that we must prioritize conservation attention to ensure the greatest return on investment for limited conservation dollars (Withey et al. 2012). The goal of conservation prioritization is to identify which species (or areas) represent the greatest conservation value. But when conservation value is subjective and driven by human needs and emotions (Arponen 2012), how do we choose?

Since the 1990s, it has been increasingly suggested that the focus of conservation efforts should be shifted toward maximizing the preservation of evolutionary history in order to conserve as many branches of the tree of life as possible (Hartmann and André 2013; Isaac et al. 2007; Veron et al. 2015; Faith 1992). Species belonging to old lineages with few members represent a greater amount of evolutionary history than more recently divergent species with many relatives (Isaac et al. 2007).

Faith's (1992) phylogenetic diversity (PD) is the most widely employed measure of evolutionary history. Preserving PD means preserving millions of years of evolutionary history and with that, the diversity of features evolved over that time and the "option values" that those features represent (Faith 1992). Veron et al. (2015) described Faith's option values as "biodiversity values that provide benefits and uses, often unanticipated, for future generations" (Veron et al. 2015). This includes benefits to humans as well as to ecosystems. These biodiversity values include what are usually referred to as "ecosystem services", natural processes which provide essential goods and services such as clean air and water, as well as food, medicines and resource materials. (Romanelli, Cooper, Campbell-Lendrum, et al. 2015). Preserving option values is beneficial to ecosystems because of the inherent importance of feature diversity to the healthy functioning of ecosystems, and also because preserving the diversity of features ensures a broad base of traits for future evolution (IUCN 2017a).

Current conservation strategies do a poor job of protecting PD (Brum et al. 2017). It has been demonstrated that PD is an important facet of biodiversity which captures evolutionary history (Faith 2015; Forest et al. 2007; Isaac et al. 2007; 2012) and that by conserving this evolutionary history, we may be protecting future ecosystem services (Erwin 2008; Forest et al. 2007; Veron, Pavoine, and Clergeau 2016). Unfortunately, despite the benefits, there seems to be little effort being made by agencies or NGOs to incorporate the measure (Safi et al. 2013). Faith's (1992) PD has since been expanded upon and has resulted in the creation of new methods of quantifying the evolutionary history held within a species or clade. Several of these measures also incorporate other metrics such as endemism and threat level (for review of extensions of PD see Faith (2013)). One such measure is EDGE (evolutionary distinctiveness and global endangerment) which combines threat level with evolutionary distinctiveness (ED), a measure of a single species' contribution to the phylogenetic diversity of its group (Isaac et al. 2007).

EDGE was designed to be implemented on a global scale, using the global threat rankings of the IUCN Red List (IUCN 2020). In a 2015 master's thesis, Emily Brantner adapted EDGE for use on a regional scale by developing RED-E (regional evolutionary distinctiveness and endangerment). Brantner demonstrated the concept by calculating RED-E scores for the birds and mammals of the United States. This study intends to further test this measure by producing RED-E scores for the birds and mammals of the state of California.

Literature Review

Searching for the most effective method of conserving our planet's biological diversity is not a new endeavor. Two of today's most well-known conservation organizations have been around for the better part of a century. The IUCN (International Union for the Conservation of Nature) was established in 1948 (IUCN 2017b), and BirdLife International traces its roots to the founding of the ICBP (International Committee for Bird Preservation) in 1922 (BirdLife International n.d.). Both organizations focus on evaluating extinction risk of individual species, one of the most common and powerful drivers of today's conservation efforts, and the primary focus of most governmental conservation action.

Almost all conservation prioritization can be broken into two categories: 1) unitbased approaches and 2) area-based approaches. Unit based approaches are those which focus on prioritizing individual units of biodiversity. Species are the most common unit used, but these can also be genera, features, genes, etc. Area based approaches are those which focus on prioritizing land for acquisition and protection. Conservation areas are prioritized based on a number of conservation goals such as to preserve a specific habitat type, set aside critical habitat for an endangered species, or to protect habitat for the highest possible number of biodiversity units within one area.

Area-based Conservation

Area based conservation is the one oldest forms of conservation, with some of the very first conservation efforts in the United States being the creation of reserves such as Yellowstone National Park, which was established in 1872 (U.S. National Park Service

2020a). Reserves are still widely used today, with 111 million acres of land in the U.S. being preserved as wilderness (U.S. National Park Service 2020b). Protecting lands from development in this way is vitally important to conservation as loss of habitat is currently one of the greatest threats to biodiversity (Brooks et al. 2002). There are many ways of prioritizing areas for conservation, an early example, and one that is still well known and widely used today, is the designation of biodiversity hotspots.

One of the seminal papers on hotspots, Myers' (2000) "Biodiversity Hotspots for Conservation Priorities" defined hotspots as areas with higher than ordinary numbers of endemic species that also are experiencing significant habitat loss. Myers used endemic plant species, and loss of primary vegetation as the qualifiers for selecting hotspots. Each hotspot was required to contain at least 0.5% of the world's plant species as endemics and have lost at least 70% of its primary vegetation. Numbers of endemic vertebrate species were included in the study as additional information but did not contribute to whether an area would be chosen as a hotspot. (Myers et al. 2000) Myers (2000) points out that there are other types of hotspots as well, for example those based on species richness, rarity, and taxonomic uniqueness.

Species-based Conservation

Threatened/Endangered Species

One of the most used, and probably most well-known, species-based measures for conservation prioritization is threat level or extinction risk. At the global level, the most widely regarded and comprehensive species level threat ranking is the IUCN Red List (IUCN 2020). IUCN (2020) assigns one of five ranks of threat level to species: least concern (LC), near threatened (NT), vulnerable (VU), endangered (EN), and critically

endangered (CR). NatureServe uses a similar five category ranking system from G5 (secure) to G1 (critically imperiled). NatureServe rankings and the determining data are also often used in evaluating species for listing under the Endangered Species Act (ESA) (Faber-Langendoen et al. 2012).

Prioritizing based on ecosystem value

Most prioritizations that are not based on ranking by threat level, are based on ranking by conservation value. In many cases this means the value that a species gives to its ecosystem. Some well-known methods have included keystone species (Paine 1969), umbrella species (Wilcox 1983), and indicator species (Noss 1990).

Paine's (1969) keystone species concept identified species which exert a disproportionate influence on the natural community in which they exist, often in such a way that their removal from the community would cause significant imbalance. One of Paine's (1969) initial examples of keystone species was the Triton's trumpet sea snail, a group of gastropods in the genus *Charonia*. *Charonia* were extirpated from some areas due to over-harvesting of the snails for their beautiful shells (Paine 1969). Paine (1969) identified them as keystone species after realizing that upon their extirpation, their primary food source, *Acanthaster planci*, the crown of thorns sea star, had dramatically increased in numbers, causing significant damage to reefs through over-predation of stony corals.

Conservation at Different Spatial Extents

Conservation prioritization efforts and conservation actions are undertaken at spatial extents from local to global. Each level of governing body must be responsible for the protection of the species with its borders regardless of the species' protection status elsewhere. It is far too risky to place the continued survival of shared species in the hands of others (Arponen 2012). Furthermore, each level of conservation has its own advantages. Large non-governmental organizations (NGOs) like IUCN have the ability to examine patterns of biodiversity and make prioritizations on a global scale. Such NGOs also have access to funding from donors around the world. This is particularly important because this funding can be directed toward protecting biodiversity in regions that would otherwise not have the financial resources necessary to make conservation a priority. Federal conservation has advantages over state level conservation when it comes to protecting wide ranging species. Federal protection is also important to ensure that a species receives protection from state to state regardless of the conservation budget or political ideology of individual states. State and local (county/city) conservation efforts benefit from having fewer species to conserve. The data used at this geographic extent is usually finer scale as well, so it is possible to turn the focus toward smaller biological units such as subspecies.

On a federal level in the United States, species are prioritized based on their threat level for potential protection under the Endangered Species Act (ESA). Responsibility for the evaluation of species and enforcement of the ESA is shared between the U.S. Fish and Wildlife Service (USFWS), which is primarily responsible for terrestrial and freshwater aquatic species, and National Oceanic and Atmospheric Administration (NOAA) Fisheries, also known as the National Marine Fisheries Service, which protects marine and anadromous species (National Oceanic and Atmospheric Administration 2019). Species are submitted as "candidates" and evaluated on a case by case basis. Once a candidate has been listed under one of the two ESA designations, "threatened" or

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"endangered", there will be a recovery plan drafted for that species, and a critical habitat designation made (U.S. Fish and Wildlife Service 2020).

This process has been heavily criticized, as the current political climate, and thus the federal conservation budget, has a dramatic effect on how many species might be listed or delisted during any four-year period (Puckett, Kesler, and Greenwald 2016). Additionally, although the timeline for completing a recovery plan once a species has been listed is two years, in practice this rarely happens (Puckett, Kesler, and Greenwald 2016). This slow response doesn't seem to be improving either. A 25 year old review by Tear et al. (1995) reported an average timeframe of at least five years from listing to recovery plan, and a recent review from Malcom and Li (2018) produced similar results showing that the five year average timeline still held true. However, despite complaints over its slow implementation, the ESA has also been shown to be highly effective. A report from the Center for Biological Diversity found that 85% of birds listed in the continental U.S. had shown population increase or stabilization since time of listing (Suckling et al. 2016). Another study examined data from the 1990s and found that having a critical habitat designation for two or more years more than doubled a species' likelihood of showing an upward population trend, and reduced their likelihood of being in decline by more than half (Taylor, Suckling, and Rachlinski 2005).

Phylogenetically Informed Conservation

Evolutionary History

There is a growing consensus in conservation biology that the focus of conservation should be to preserve as much evolutionary history (phylogeny) as possible by prioritizing conservation based on measures which take phylogeny into consideration such as phylogenetic diversity (PD) or evolutionary distinctiveness (ED) (Faith 1992; Forest et al. 2007; Isaac et al. 2007; 2012; Veron, Pavoine, and Clergeau 2016). Most conservation organizations prioritize species by threat level, often using rankings such as the IUCN Red List of Threatened Species (IUCN 2020) as a guide. This prioritization makes sense in that threat cannot be ignored lest conservation resources be wasted on species that could easily survive on their own. However, to consider threat alone is to consider all species as equally deserving of conservation, outside of their risk of extinction (Redding and Mooers 2006). But this is not the case, species are not equal in terms of the amount of evolutionary history they represent (Faith 1992).

Species are not distributed evenly on the tree of life (Isaac et al. 2007). Some branches are long and have few species at their tips, representing old lineages with millions of years of evolution since the last speciation. Other branches are shorter, having bifurcated many times due to more recent speciations, and contain numerous relatively young and closely related species. The extinction of an older species with few relatives results in a greater loss of evolutionary history (Isaac et al. 2007) (see Figure 1; (Erwin 2008).



Figure 1. Diagram of evolutionary history loss. This figure (Erwin 2008) demonstrates that taxonomic losses at different level result in the loss of different amounts of evolutionary history. Example A shows the extinction of seven taxa, with overall phylogenetic tree structure remaining intact. In example B, again seven taxa are lost, this time an entire clade, but the remaining tree structure remains intact. Example C shows the extinction of only six taxa but in this example the oldest clades are lost.

Phylogenetic Diversity

PD is measured for a subset of species, and is calculated by finding the minimum total length of all of the branches required to connect the species of that subset within a phylogenetic tree (Faith 1992; 2013; 2015; 2018). These branch lengths can be calculated based on evolutionary time, or morphological or molecular data may be used. What is important is that the data being used to determine branch length accurately represent the relative amounts of evolutionary change between taxa (Faith 2013).

PD is a valuable measure of biodiversity because it provides a way to quantify the relative feature diversity i.e. the number of unique features or traits within a group of taxa (Faith 2013). This is important because measuring feature diversity without a proxy such as PD would still be impossible today with our insufficient knowledge of the features of species (Faith 2013). Maintaining the highest possible number of unique features within a

subset of species helps ensure that the group has the most options for diversification and adaptation in the face of future stresses such as climate change (Faith 1992; Forest et al. 2007). This is one example of what Faith (1992) called "option value". The idea behind option value is that species possess features which have the potential to provide unforeseen benefits in the future (Faith 1992).

In a study regarding the preservation of evolutionary potential in plant species of the Cape of South Africa, Forest et al. (2007) illustrate the benefit of preserving option value by maximizing PD. The authors created a simulation to compare the amount of PD preserved when a protected area was chosen based on maximizing taxon complementarity (number of species not protected elsewhere) versus maximizing PD (Forest et al. 2007). Their results showed that more PD was in fact preserved when it was selected for directly. The authors demonstrated the significance of this by splitting the Cape plant species into three categories based on benefit to humans: food, medicine, and other (Forest et al. 2007). It was their finding that plants in each of the three categories were clustered on the phylogenetic tree and therefore maximizing the amount of PD preserved gave a much higher probability of conserving species from all three use categories (Forest et al. 2007). In other words, by prioritizing by PD, the authors were preserving the greatest number of unique traits, and therefore the highest option value.

Early criticisms of phylogeny-based conservation prioritization (Nee and May 1997) were based on two things: 1) concerns over the accuracy of information about phylogenetic relationships, and 2) claims that attempting to preserve evolutionary history was largely pointless due to the results of a model that showed that even in the event of the extinction of many random species, as much as 80% of the underlying evolutionary

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history would be preserved. The first criticism is no longer such a concern due to the creation of phylogenetic "supertrees" (Bininda-Emonds et al., 2007; Jetz, Thomas, Joy, Hartmann, & Mooers, 2012) which allow for more accurate quantification of the evolutionary history of entire classes (Isaac et al., 2007). The second criticism relies on the assumption that extinction occurs at random with respect to the position of species in the phylogenetic tree. This has been shown to be false and it has been demonstrated that extinction risk is phylogenetically clustered (Purvis et al. 2000). This means that loss of PD in the event of a mass extinction would be much higher than would be expected if species followed a pattern of random extinction.

Evolutionary Distinctiveness

Derived from Faith's (1992) PD (which is a summed measure of evolutionary history given for a group of species), ED divides PD between all members of the group and gives an individual ED value for each species. This has important implications for conservation because most conservation is species oriented. This means that conservation prioritization based on ED would give government agencies and conservation organizations a way to incorporate the protection of evolutionary history into current practices quite seamlessly.

Evolutionary distinctiveness (ED) measures how isolated a species is on the phylogenetic tree (Jetz et al. 2014). In the ED calculation developed by Isaac et al. (2007) (the method that this research follows), branch lengths are measured in millions of years (MY) and the phylogeny is ultrametric, meaning that all of the terminal branches end at the same point (Figure 2; (Isaac et al. 2007). Figure 2 (Isaac et al. 2007) demonstrates how ED is calculated. The value on the top of each branch represents the branch length,

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the value on the bottom of each branch is the number of species descending from that branch. The top and bottom numbers can be treated as a fraction and the sum of these values is then taken for all branches connecting a species to the root of the phylogeny (Isaac et al. 2007). For example, for species A, ED is calculated as 2/5+1/3+1/2+1/1=2.23 MY.



Figure 2. Hypothetical phylogeny from Isaac et al. (2007). A-G represent species. Numbers above and below the branches represent branch length and number of descendants, respectively. Branch lengths are represented as millions of years before the present (MYBP). ED scores for each species on the right.

How is ED different than PD

Both PD and ED are measures which quantify evolutionary history. However, PD measures the total evolutionary history of a clade, whereas ED measures each taxa's contribution to that total evolutionary history. If you were to take the sum of the ED

scores of all species within a group, the result would be equal to the PD of that group (Jetz et al. 2014). So why does ED matter? Why not just use PD? ED, in providing each species with an ED "score" allows for species to be ranked. Almost all conservation today, both governmental and non-governmental, is set up around prioritizing by ranking species. This means that ED fits in much more seamlessly with the way that most conservation prioritization typically occurs today.

EDGE

The most successful extension of ED today is EDGE, which combines a species' evolutionary distinctiveness (ED) with its global endangerment (GE), determined by the species' IUCN Red list ranking (Isaac et al. 2007). The EDGE metric is now the basis of a global conservation effort, the EDGE of Existence program, led by the Zoological Society of London (ZSL). The program is coordinating conservation action for 74 top EDGE species in 40 countries. The goal of the program is to bring attention to, and support the conservation of, evolutionarily distinct and globally endangered species that are otherwise being overlooked. The organization sends EDGE fellows into the field to perform surveys for poorly documented species, set up monitoring programs, educate the public about EDGE species, and work with local governments and conservation organizations to build their capacity to protect these unique taxa. ("EDGE of Existence : Evolutionarily Distinct & Globally Endangered" n.d.)

Studies have been conducted for many different taxa using EDGE. Full class rankings have been completed for mammals (Isaac et al. 2007), amphibians (Isaac et al. 2012), corals (Curnick et al. 2015; Huang, Davies, and Gittleman 2012), birds (Jetz et al. 2014), reptiles (Gumbs et al. 2018), and chondrichthyans (cartilaginous fishes) (Stein et al. 2018). The most recent of these studies, by Gumbs et al. (2018), is one of the broadest studies to date, providing EDGE scores for all tetrapods (a taxonomic designation that includes amphibians, birds, mammals, and reptiles), and is also the first study to include reptiles. This study is additionally significant because the authors were able to determine the best method of estimating ED scores for species with incomplete taxonomic information. This allowed them to estimate the ED of species missing from the phylogenetic tree with an average accuracy of within 1% (Gumbs et al. 2018). This example shows that the EDGE metric is continuing to be used and improved upon.

RED-E

Emily Brantner (2015) developed RED-E as an expansion upon the EDGE concept (Isaac et al. 2007; 2012) in order to adapt it for use on a regional scale i.e. not just using threatened status based on global endangerment. She demonstrated the use of the measure on a national scale creating a ranking of U.S. bird and mammal species. In calculating RED-E scores, Brantner followed the methodology from Isaac et al. (2007) for calculating ED. Brantner (2015) then adapted the formula for calculating EDGE (see page 23 of Methods), replacing the global endangerment (GE) score with a regional endangerment score (RE) created using the threatened and endangered listing statuses of the ESA.

Brantner (2015) compared each species' RED-E to their EDGE score and found that for mammals, RED-E scores were positively correlated with EDGE scores but that the differences between the scores produced changes in species' ranks by an average of 24 positions. Bird RED-E scores, however, were not positively correlated with EDGE scores, and changes to bird scores produced rank changes of an average of 13 positions.

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The study also included an examination of whether a species' RED-E ranking had any correlation with the amount of conservation funding that had been directed toward that species and found no such correlation (Brantner 2015). Finally, Brantner (2015) used the RED-E scores to create a ranked list of U.S. species which lack critical habitat designations as a demonstration of the practical applications of this method of prioritization.

Phylogenetically Informed Regional Conservation

The development of RED-E (Brantner 2015) serves to fill a gap in the literature where there are a lack of studies concerning phylogenetically informed regional conservation. RED-E is, to the best of my knowledge, the only regional adaptation of the EDGE concept, but is also one of few regional studies within the broader context of studies related to evolutionary distinctiveness and phylogenetic diversity.

In my review of the literature I came across two studies which involved phylogenetically informed conservation on a regional scale. The first study, by Veron, Pavoine, and Clergeau (2016) was focused on the preservation of evolutionary history in the Mediterranean Basin. This study used multiple metrics related to PD and ED to produce a recommendation for hotspots of evolutionary history. The authors then examined how well existing protected areas overlapped the proposed hotspots. Their findings indicated that ideal hotspot locations would vary greatly between taxonomic groups but that overall, evolutionary history clustered in certain areas of the region and those areas tended to be significantly under protected (Veron, Pavoine, and Clergeau 2016).

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In the second study, Forest et al. (2007) measured the PD of flora in the Cape of South Africa. The authors assert that although others have claimed taxon diversity to be a good surrogate for PD, they found the measures to be decoupled. Interestingly, their results showed that PD was not evenly distributed in the east and west portions of the Cape, with species in the west being phylogenetically clustered leading to a lower PD score relative to the east of the Cape. Forest et al. (2007) demonstrate that conservation based on taxon richness is not adequate to capture PD, especially when PD is heterogeneous across a region. The authors concluded that preserving PD would best preserve the evolutionary potential of flora in the Cape as well as provide the greatest option value by ensuring the preservation of edible, medicinal, and other economically important plants (Forest et al. 2007).

Both studies illustrate that even at a regional level, where conservation efforts should be more targeted due to the narrower area of focus and smaller number of species, current protections are inadequate to preserve evolutionary history. The incorporation of phylogenetic information into conservation prioritization is just as relevant on a regional scale as a global one and more regional studies are needed.

Chapter 2: Research Study

The primary goal of this study was to demonstrate the use of RED-E for conservation prioritization at the state level, by creating a ranking of birds and mammals in the state of California. A further spatial analysis was conducted for birds using GIS to answer the following research questions:

1. Would prioritization by species richness be sufficient to protect evolutionarily distinct and endangered species?

2. To what degree are evolutionarily distinct and endangered species being protected by current government protected areas in California?

Study Area

The State of California was chosen for this study because of its impressive biodiversity, both in terms of species richness and endemism. With 429 species of birds, 185 mammals, 85 reptiles, and 68 amphibians, California has the highest number of native vertebrate species of any U.S. state. California also has more endemic plant and animal species than any other state (California Department of Fish and Wildlife n.d.). California makes up the majority of the California Floristic Province (CFP), a biodiversity hotspot which covers most of California and spills over a bit into Oregon, Arizona, and the Baja region of Mexico. The CFP contains 6,143 species of vascular plants, a staggering 42% of which are endemic (Burge et al. 2016).

California is also unique to North America in its diversity of ecoregions and fascinating in its extremes. Death Valley, in the Mojave Desert, is famous for being the

hottest, driest place on Earth (Natural Features & Ecosystems—Death Valley National Park (U.S. National Park Service), n.d.). In contrast, California's mountain ranges, including the Sierra Nevada and southern Cascade ranges, are spotted with numerous glaciers and areas of permanent ice and snow. These two extremes, the desert and alpine climates, are just two of the five climates that exist in California. In the northwestern corner of the state, redwood trees dominate the southernmost extent of the Pacific temperate rainforest ecoregion. The state also has cool interior, steppe, and mediterranean climates, with the mediterranean climate being particularly rare, only existing in a handful of locations outside of the Mediterranean region (Kauffman 2003).

Methods

Calculating Evolutionary Distinctness

Choosing Phylogenetic Trees

I gathered published phylogenetic trees for mammals and birds from the literature, focusing on finding the newest phylogenetic tree for each class that was accepted in the scientific community and widely used. Following the methodology established by Isaac et al. (2007), and used by Brantner (2015), the tree used for mammals was a phylogenetic supertree published by Bininda-Emonds et al. (2007).

For birds I used a phylogenetic tree listed on birdtree.org (Jetz et al. 2012). There are several sets of trees on birdtree.org, some of which include only those species for which genetic confirmation of phylogenetic relationships exist. I chose to use the more inclusive trees because I was already intending to trim the trees to only those that exist within California and I wanted to ensure that as many species as possible from my relatively small subset would be present in the tree. Within the larger inclusive trees there were two sets, created using two different phylogenetic backbones based on Ericson et al. (2006), and Hackett et al. (2008) respectively. Following the methodology established by Emily Brantner (2015), I used a subset of 1,000 out of a total of 10,000 bird trees which Jetz et al. (2006).

Trimming the Trees

The chosen trees contain all known species on Earth for each class and so needed to be trimmed to only contain species found within the state of California. I created Excel spreadsheets of all bird species and all mammal species present in the trees and used a binary system to mark all species as California (1) or non-California (0) species. This allowed me to specify in RStudio which species should be trimmed. The *drop.tip* function was used to create a subset of only California species.

I chose to trim the trees down to California species before I calculated ED. This ensured that the ED of each species is only being calculated in relation to the other species in California, rather than all species globally. For guiding regional conservation efforts within California, it is more valuable to rank Californian species independently against themselves than against all species globally.

Calculating Regional Evolutionary Distinctiveness (RED)

Following the methodology provided by Brantner (2015), I calculated the RED scores within RStudio using the R packages Ape and Caper¹. For mammals, the tree used included three different date estimates: upper, lower, and best. RED was calculated separately for each of these and then the geometric mean was taken. For birds, the tree being used included 1,000 iterations of the tree, so I created a loop in R to calculate ED for all birds in each of the 1,000 trees and then took the mean of these calculations.

Calculating Regional Endangerment (RE)

Using the same methodology for birds and mammals, RE scores were calculated in Excel by converting the assigned state threat rank from California's Natural Diversity Database (California Department of Fish and Wildlife 2019) into a numerical value that could be combined with ED to calculate RED-E scores. The state of California uses the

¹ The full code used in RStudio is provided in Appendix A.

ranking system established by NatureServe (Faber-Langendoen et al. 2012) to create a state threat level system, which ranks species from S5 (secure) to S1 (critically imperiled). In order to use these rankings in my calculations, it was necessary for me to transform these rankings into integers, and to reverse the order so that as the threat level of the rank increased, the value increased numerically as well. (Table 1). In the database there are intermediate ranks such as S1S2 etc. which are used to express uncertainty (California Department of Fish and Wildlife 2019). These were transformed from a string to a numeric value by taking the average of the ranks. For example, an S1 would receive a rank of 4, and an S2 would receive a rank of 3 so the rank assigned for an S1S2 is 3.5, the mathematical average of the two ranks. Additionally, the database contains rankings which contain a question mark, such as S1S2, I therefore chose to ignore the question marks when assigning a RE score, for example S2? would be given a RE score of 3.

Threat Level	NatureServe Ranking	RE Score
Critically Imperiled	S1	4
	S1S2	3.5
Imperiled	S2	3
	S2S3	2.5
Vulnerable	S3	2
	\$3\$4	1.5
Apparently Secure	S4	1
	S4S5	0.5
Secure	S5	0

Table 1. Transformation of NatureServe Ranks into Regional Endangerment (RE) Scores. No species with a threat ranking below S4 existed in the dataset. Because species in the study were from the Special Animals List, it can be assumed that species presumed to be secure were not prioritized to receive a ranking.

Calculating RED-E Scores and Creating Rankings

Using the same methodology for birds and mammals, RED and RE were combined in Excel to create the final RED-E scores. The following equation from Emily Brantner (2015) was used for calculating RED-E. Brantner adapted this equation from the EDGE equation published by Isaac et al. (2007).

$$RED-E = \ln(1+ED) + RE * \ln(2)$$

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

Species were arranged by RED-E score in descending order and ranked from highest RED-E score to lowest with 1 being the highest rank. Any species having the same RED-E score were considered a tie and assigned the same rank.

Spatial Analysis of Avian RED-E Scores

Importing Bird Observation Data

All maps were created using ArcGIS Pro (hereafter Pro). In order to analyze bird RED-E spatially, I needed data on the location of birds in California. I obtained wildlife observation data from the California Natural Diversity Database (CNDDB) which contained spatial data for wildlife observations within California. The data divide the state of California into USGS 7.5-minute quadrangles (quads), each of which contains numerous attributes including my target attribute: the names of all species which have been observed in that quad. Exact observation location data is available through CNDDB, but its access and use are restricted in order to protect the exact locations of vulnerable

species. As I did not feel that this finer scale data was necessary for my analysis, I did not pursue it and decided to use the publicly available *tracked by quad* dataset.

Joining Bird Observations and RED-E Scores

I imported the file containing bird RED-E scores into Pro as a CSV file, first making sure that the column headings matched the attribute fields of the *tracked by quad* layer to which it would be joined. I created a join between the quad layer and the table of bird RED-E scores using species' scientific names as the join field.

Mapping RED-E Scores

Once species and RED-E scores were joined, it was possible to start mapping RED-E scores. However, since each 7.5-minute quad can contain multiple species, each with their own RED-E score, scores had to be aggregated. I used the *summarize attributes* geoprocessing tool to calculate the maximum, mean, and summed RED-E score for each quad. While trying to decide whether minimum, maximum, or mean would be the best way to visualize spatial patterns in RED-E scores, I realized that each aggregation method highlighted different aspects of the data and I decided to include them all (Figure 4).

Each of the three maps in were use ten quantiles so that each color on the map represents 10% of the data. The darkest color in each of the three maps represents the highest values and white represents the lowest values. I chose to symbolize them in this way because in further analyses I would be using quads with RED-E scores in the top 10% to narrow down a recommendation for prioritization.

Symbolizing RED-E Scores by Standard Deviation

Although I had already mapped mean RED-E scores (Figure 4), this map only displayed the mean of RED-E scores within each quad, which was not a good representation of the amount of variation in the data. I therefore decided to map the mean RED-E scores symbolized by standard deviations from the overall mean. In this way I would be able to visualize which quads had mean RED-E scores which were "typical" as well as which quads were outliers, with mean RED-E scores significantly higher or lower than the overall mean. I used Excel to calculate standard deviations and symbolized a map of bird RED-E scores by quad using the graduated colors symbology and setting manual intervals to define the classes which represent standard deviations.

Mapping Species Richness

To map species richness, I ran a definition query on a map displaying the *tracked by quad* dataset to narrow the dataset to birds only. I then used the *count* function of the *summarize attributes* tool to count the number of bird species within each quad.

Mapping Protected Areas in California

I imported spatial data from the California Protected Areas Database containing the boundaries of all national parks, wildlife refuges and other government protected areas in California and used the *merge features* tool to create one large outline of all protected areas. I then used the *summarize within* tool to calculate the area of overlap of protected land within each quad. This allowed me to then use the *summarize attributes* tool to calculate the percentage of overlap based on the new area field. This produced the map in Figure 9 which displays the percent of areal coverage of protected land within each quad.

Separating out quads with RED-E scores in the top 10%

For the purposes of this study, I decided to define "high" RED-E scores as those that fell in the top 10% of all scores. In order to easily see which quads contained top ranking RED-E species, I calculated the 90th percentile (upper 10%) in Excel using the nearest-rank method (top 10% = \geq 5.76.) In Pro, I then used a definition query on a map of all bird RED-E scores to display only quads containing species with RED-E scores greater than or equal to 5.76.

Making a Recommendation

I narrowed down the pool of recommended quads by identifying quads which contained birds with RED-E scores in the top 10%, which also had 10% or less coverage of government protected land, then selected the final quads based on complementarity in order to protect the greatest number of species in as few quads as possible. This resulted in the selection of 10 quads which would add protection for all 15 top RED-E species.

Results and Discussion

Rankings

Comparing Bird and Mammal RED-E

RED-E rankings were generated for 143 birds and, separately, for 119 mammals native to California. Avian RED-E scores ranged from 2.38 for the Caspian Tern (*Hydroprogne caspia*) to 6.82 for the Yellow-billed cuckoo (*Coccyzus americanus occidentalis*). The median RED-E score for birds was 4.42, the mean was 4.48, with a standard deviation of 0.85 (Appendix B). For mammals, scores ranged from 3.28 for the Yuma Myotis (*Myotis yumamensis*) to 6.84 for the Point Arena mountain beaver (*Aplodontia ruga nigra*). The median RED-E score for mammals was 4.98 and the mean was 5.04, with a standard deviation of 0.72 (Appendix C).

The maximum RED-E scores were similar for birds and mammals, differing by only 0.02. However, the mean and the minimum RED-E scores were lower for birds than for mammals. It appears that the mean skewed lower for birds due to a higher number of lower priority (S4 rank) species. There were 18 S4 rank birds and only two S4 rank mammals. Additionally, the minimum RED-E score was lower for birds because the two S4 ranked mammal species (which occupy the bottom two RED-E positions) have moderate ED scores compared to the very low ED scores of the bottom ranking birds. It is hard to say whether the low number of S4 (apparently secure) mammal species is a true reflection of higher average threat level, or a result of a lack of the comprehensive surveys needed to determine threat level.

Spatial Analysis of Avian RED-E



Figure 3. Topographic Map of the State of California. Included for reference.

Comparing Maximum, Mean, and Summed Bird RED-E Scores

The three maps in Figure 4 each display RED-E scores within 7.5-minute USGS quads in the state of California. Maps displaying RED-E scores by maximum, mean, and sum were all included because they each highlight different aspects of the data. The map displaying the maximum RED-E score Figure 4a) shows only the single highest RED-E score in each quad, making it easy to visualize where the highest-ranking species exist. However, this map does not allow for making a distinguishment between high scores which are typical and those which are outliers in their quads. The map of the mean (Figure 4b) highlights the "typical" RED-E score for each quad, allowing for identification of areas where the average RED-E score is higher. The drawback with this view is that it would be easy to overlook a high RED-E species if it existed in a quad with many low RED-E species. The map of summed RED-E scores (Figure 4c) is interesting because it incorporates species richness in each quad, which is particularly apparent when compared to Figure 7. This changes the way the data are displayed, as it becomes possible for a quad with multiple moderate RED-E scores or many low RED-E scores to "score higher" than a quad with one high RED-E score.

In both the maximum (Figure 4a) and summed (Figure 4c) bird RED-E score maps, the area along the southwestern coast between Los Angeles and San Diego had quads in the highest scoring categories. This same area did not have high mean RED-E scores (Figure 4b), probably because, as can be seen in Figure 7, this is an area of high species richness so the high number of species in this area lowered the mean RED-E scores. The inverse of this can also be seen. Along the Sierra Nevada Mountains just east of the San Joaquin Valley (see Figure 3 for reference) there is an area of high scores

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apparent on both the maximum and mean bird RED-E score maps. However, this area is not highlighted on the summed RED-E map, and it can be seen from Figure 7 that this is an area of low species richness, indicating that the high maximums increased the mean without the high species richness to dilute those scores.

One area of note that stands out with high scores on all three maps is the stretch that runs roughly north-south along the southeastern border with Arizona. The fact that this area is highlighted on all three maps is significant because not only were there high maximum RED-E scores, but there were multiple top scoring species, as indicated by the high mean. This area was apparent on the map of summed RED-E scores despite this not being an area of notably high species richness.







Figure 4. These maps display the a) maximum b) mean and c) sum of RED-E scores for birds observed within each USGS 7.5-minute quad in California. They are each symbolized by quantile with the darkest color representing the top 10% of values, and the white quads representing the lowest 10% of values. Areas of California withough quads represent areas where no birds were observed for which a RED-E score could be calculated.

a) Displays the RED-E score for only the single highest scoring bird species in each quad.

b) Displays the mean RED-E score of all bird species observed within each quad.

c) Displays the sum of the RED-E scores of all bird species observed within each quad.

Visualizing Bird RED-E Scores by Standard Deviations from the Mean

Individual variation of mean avian RED-E scores for each quad are displayed in Figure 5, by how many standard deviations the quad mean is from the overall mean. This allows for the recognition of any quads where the mean RED-E score is significantly higher or lower than the overall RED-E. One note of caution in interpreting this: quads with means ± 2 s.d. from the overall mean had low species richness, with none having more than three RED-E species in a quad. In contrast, quads in the ± 0.5 standard deviations category spanned the range of species richness values from 1 to the maximum of 56.



Figure 5. Mean Avian RED-E Scores within USGS 7.5-Minute Quads in California Symbolized by Standard Deviations from the Overall Mean. Standard deviations above the mean are shown in red, standard deviations below the mean, are shown in blue with darker colors representing greater distance from the mean in either direction.

Comparing Bird RED-E Scores and State Threat Rankings

A comparison between the map of maximum state threat ranking in Figure 6, and the RED-E score maps in Figure 4 shows that although there are areas of significant overlap between quads with high RED-E scores (especially maximum RED-E scores) and quads with highly threatened species, this overlap is not 100% and prioritization based on these maps would lead to different recommendations. Although threat level has been heavily used by decision-making bodies as a basis for conservation prioritization, prioritization based on RED-E scores is more useful than threat alone because RED-E not only takes threat level into account through RE but also ensures the protection of evolutionarily distinct species.



Figure 6: Maximum State Threat Ranking for Birds within USGS 7.5-Minute Quads in California. This map is displaying the maximum threat level of any bird within each quad. The state threat rankings are taken from the California Special Animals List (California Department of Fish and Wildlife 2019). California Department of Fish and Wildlife assigns the intermediate rankings (e.g. S1S2) to express uncertainty.

Comparing Avian RED-E Scores and Avian Species Richness

The map in Figure 7 displays avian species richness. It is notable that the greatest concentration of quads with high species richness occurs in the greater Los Angeles area (see Figure 3 for reference), an area that is one of the most populated in California. Additionally, quads within California's large protected areas generally showed low to moderate avian species richness.

The first of my research questions, 'would prioritization by species richness be sufficient to protect evolutionarily distinct and endangered species?' is answered by Figure 8. While high species richness and high RED-E scores do overlap somewhat, there are a significant number of quads where they do not. Therefore, it cannot be assumed that prioritization by species richness *alone* would sufficiently protect all highly evolutionarily distinct and endangered species in California.



Figure 7. Avian Species Richness within USGS 7.5-Minute Quads in California. They are each symbolized by quantile with the darkest color representing the top 10% of values, and the lighest quads representing the lowest 10% of values. Areas of CA withough quads represent areas where no birds were observed for which a RED-E score could be calculated.



Figure 8: Spatial Overlap of USGS 7.5-Minute Quads Containing Birds with RED-E Scores in the Top 10% and Quads with Bird Species Richness in the Top 10%. Yellow quads are those which contain birds with RED-E scores in the top 10%. Quads with a green stripe are those for which avian species richness was in the top 10%. Quads with a black outline are where top species richness and top RED-E scores overlap.

Percent Coverage of Protected Areas

To help understandwhere additional protection was needed in California, the maps shown in Figure 9 and Figure 10 were produced. Figure 9 shows all quads in California by the percentage of protected land within each quad. It is immediately apparent that California has an impressive network of protected areas. Especially of note is the extensive network of national forest and national park lands along the Sierra Nevada Mountains. However, when the data are focused to only show quads containing top RED-E bird species, as in Figure 10, it is easy to see that many high RED-E species exist outside of these highly protected quads. The data in Figure 10 were refined even further to only show quads with 10% or less protection which contained top 10% RED-E species and this served as the base for the final quad recommendation.



Figure 9: Government Protected Areas in California by Percent of Areal Coverage within USGS 7.5-Minute Quads. The darker the shade of green in this map, the higher percent coverage of protected land in that quad. Quads shown in red are those which had zero percent protection.



Figure 10: Percentage of Protection within USGS 7.5-Minute Quads in California Containing Birds with RED-E Scores in the Top 10%. The darker the shade of green in this map, the higher percent coverage of protected land in that quad. Quads shown in red are those which had zero percent protection. Quads have been removed from this map so that those shown are only those which contain birds with RED-E scores in the top 10%.

Making a Recommendation for Prioritizing RED-E Birds

Eliminating all quads except those containing high priority bird species (defined as birds with RED-E scores in the top 10%, observed in quads with 10% or less coverage of government protected land) resulted in 202 quads. To make a more meaningful recommendation, I mapped the resulting quads by number of species (Figure 11) in order to use complementarity to select the final quads.

Ultimately 10 quads were chosen (Figure 12) which would add protection for all 15 top RED-E species. The final recommendation included one quad in the north between Redding and Sacramento, one quad in the south which overlaps heavily into Arizona, and eight quads in the greater Los Angeles area. The clustering of high RED-E species near L.A. was particularly noteworthy. There are very high RED-E scores as well as very high species richness in this area. Examining the plausibility of protection within these quads was outside the scope of my research. However, I recognize that in an area such as this where competition for space between humans and animals is so fierce, this would be a significant challenge. The selected quad in the north is located between the Plumas National Forest and the Sacramento River Wildlife Refuge. It would seem that it may be particularly valuable to examine habitat connectivity within this quad, as it is bisected by highway 99 and surrounded by several large protected areas. The selected quad in Southern California overlaps heavily into Arizona and also closely borders the Fort Yuma Reservation. Additionally, the area within this quad appears primarily agricultural. It is likely that conservation within this quad would require not only cooperation between state and sovereign governments, but stakeholders in farming communities as well.



Figure 11. Count of High Priority Bird Species by Quad. Some quads have been removed to focus prioritization. Remaining quads are those which contain birds with RED-E scores in the top 10%, and for which the percent of areal coverage of protected land is less than 10%. Quads are symbolized by the number of high priority (top 10%) bird species they contain with white to black representing 1 to 5 species, respectively.



Figure 12. Quads in California Recommended for Prioritization. Quads outlined in red represent those which have been chosen as a recommendation for conservation prioritization.

How RED-E Performed at a State Level

In Brantner's 2015 thesis, she calculated RED-E scores using the EDGE formula from Isaac et al. (2007) (see page 23 of Methods) but replaced the global endangerment (GE) score with a regional endangerment (RE) score, created using the threatened and endangered listing statuses of the ESA. Although the metric worked well on a national level, Brantner (2015) had to try out several methods of weighting ESA threat ranks since there are only two designations and EDGE (Isaac et al. 2007) was designed to be used with the IUCN Red List's (IUCN 2020) five-category threat ranking system. Due to the fact that California uses the NatureServe threat ranking system which follows a fivecategory threat ranking, similar to IUCN, calculating RED-E scores for species in California was very straightforward and I think implementation would be seamless.

Conclusion

The goal of this thesis was to further research on the viability of the regional evolutionary distinctiveness and endangerment (RED-E) metric by examining its usefulness at the state level. Additionally, this research sought to examine spatial patterns of highly distinct and endangered species through GIS analysis of avian RED-E scores. It is demonstrated in the literature that although species richness and phylogenetic diversity sometimes show some correlation, the two metrics are just as often decoupled (Potter and Woodall 2012; Forest et al. 2007). This spatial analysis also demonstrated a similar decoupling of species richness and RED-E scores (Figure 8). Based on these results, this research concludes that it should not be expected that RED-E species will be sufficiently protected by the conservation of species richness alone. Furthermore, many top RED-E birds exist in quads in California which contain little to no government protected lands. In conclusion, the RED-E metric could be seamlessly incorporated into California's current system of conservation prioritization and it is my recommendation that it should be, and that further study should be done regarding the use of the RED-E metric to promote phylogenetically informed regional conservation in states beyond California.

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Appendices

Appendix A

Mammal R Code

Load R plugins

> library(ape)

> library(caper)

Load nexus file

> mammals<-read.nexus("Mammals.nex")

Create objects for different date estimates

> bestdates<-mammals\$mammalST_bestDates

> lowerdates<-mammals\$mammalST_lowerDates

> upperdates<-mammals\$mammalST_upperDates

Create a subset of non-California species

> AllMammalED<-read.csv("AllMammals.csv",as.is = TRUE)

> noncali<-subset(AllMammalED,California==0)

> drop<-noncali\$Species

Use the drop.tip function to remove non-California species

> CaliMammalEDbest<-drop.tip(bestdates,drop)

> CaliMammalEDlower<-drop.tip(lowerdates,drop)

> CaliMammalEDupper<-drop.tip(upperdates,drop)

Calculate ED for California species

> ed.calc(CaliMammalEDbest)

> ed.calc(CaliMammalEDlower)

> ed.calc(CaliMammalEDupper)

Load R plugins

```
> library(ape)
```

```
> library(caper)
```

Load tree file

> birds<-read.tree("AllBirdsEricson1.tre")</pre>

Load list of all bird species

> AllBirds<-read.csv("AllBirds.csv",as.is = TRUE)

Create subset of non-California species to be trimmed

> noncali<-subset(AllBirds,California==0)</pre>

> drop<-noncali\$Species

Trim the tree and change it back to multiphylo

> CaliBirds<-lapply(birds,drop.tip,drop)

> class(CaliBirds)<-"multiPhylo"

Create a loop for taking ED from 1000 different trees

> temp.list<-ed.calc(CaliBirds[[1]])</pre>

> names<-temp.list\$spp

> names<names\$species

> for(i in 1:1000){

temp.list<-ed.calc(CaliBirds[[i]])

spp.ed<-temp.list\$spp</pre>

temp.ed<-spp.ed\$ED

output.ed<-cbind(output.ed,temp.ed)</pre>

}

Average the ED outputs

```
> meanED<-rowMeans(output.ed)</pre>
```

> CaliBirds.name<-cbind(names,meanED)

Print to .csv file

> write.csv(meanED,file = "CaliBirdEDmean.csv")

Appendix B

California Bird Species Ranked by RED-E Score. Species names are from the California Special Animals List (California Department of Fish and Wildlife 2019). RED-E scores are rounded to two decimal places by differences in ranks represent actual differences in RED-E scores.

Rank	Species	Common Name	State Threat	ED	RED-E
1	Coccyzus americanus occidentalis	Yellow-billed cuckoo	S1	56.03	6.82
2	Strix nebulosa	Great gray owl	S 1	32.30	6.28
3	Melanerpes uropygialis	Gila woodpecker	S 1	30.11	6.21
4	Phoebastria albatrus	Short-tailed albatross	S 1	29.30	6.18
5	Parabuteo unicinctus	Harris' hawk	S 1	25.85	6.06
6	Gymnogyps californianus	California condor	S 1	24.94	6.03
7	Dendrocygna bicolor	Fulvous whistling-duck	S 1	24.60	6.02
8	Oceanodroma melania	Black storm-petrel	S 1	23.56	5.97
9	Rallus obsoletus levipes	Light-footed Ridgway's rail	S 1	23.36	5.97
9	Rallus obsoletus obsoletus	California Ridgway's rail	S 1	23.36	5.97
10	Oceanodroma furcata	Fork-tailed storm-petrel	S 1	22.98	5.95
11	Gavia immer	Common loon	S 1	22.48	5.93
12	Laterallus jamaicensis coturniculus	California black rail	S 1	20.10	5.82
13	Micrathene whitneyi	Elf owl	S 1	19.78	5.81
14	Cypseloides niger	Black swift	S2	38.62	5.76
15	Colaptes chrysoides	Gilded flicker	S 1	18.15	5.72
16	Rallus obsoletus yumanensis	Yuma Ridgway's rail	S1S2	23.36	5.62
17	Pelecanus erythrorhynchos	American white pelican	S1S2	22.78	5.59
18	Coturnicops noveboracensis	Yellow rail	S1S2	19.95	5.47
19	Ixobrychus exilis	Least bittern	S2	27.83	5.44
20	Aphelocoma insularis	Island scrub-jay	S 1	12.16	5.35
21	Lanius ludovicianus anthonyi	Island loggerhead shrike	S 1	11.65	5.31
21	Lanius ludovicianus mearnsi	San Clemente loggerhead shrike	S 1	11.65	5.31
22	Antigone canadensis tabida	Greater sandhill crane	S2	24.16	5.30
23	Oceanodroma homochroa	Ashy storm-petrel	S 2	23.40	5.27
24	Mycteria americana	Wood stork	S2?	23.38	5.27
25	Strix occidentalis caurina	Spotted owl	S2S3	32.93	5.26
26	Riparia riparia	Bank swallow	S 2	22.40	5.23

27	Vireo bellii arizonae	Arizona bell's vireo	S1S2	14.77	5.18
28	Empidonax traillii extimus	Willow flycatcher	S 1	9.87	5.16
29	Vireo huttoni unitti	Hutton's vireo	S2?	20.56	5.15
30	Leucophaeus atricilla	Laughing gull	S 1	9.54	5.13
31	Chaetura vauxi	Vaux's swift	S2S3	27.00	5.07
32	Numenius americanus	Long-billed curlew	S2	18.46	5.05
33	Charadrius montanus	Mountain plover	S2S3	26.09	5.03
34	Brachyramphus marmoratus	Marbled murrelet	S 1	8.49	5.02
35	Callipepla californica catalinensis	Catalina California quail	S2	17.79	5.01
36	Aquila chrysaetos	Golden eagle	S 3	36.44	5.01
37	Piranga flava	Hepatic tanager	S 1	8.14	4.99
38	Charadrius alexandrinus nivosus	Kentish plover	S2S3	24.71	4.98
39	Strix occidentalis occidentalis	Spotted owl	S 3	32.93	4.91
40	Vireo vicinior	Gray vireo	S 2	15.41	4.88
41	Polioptila californica californica	Coastal California gnatcatcher	S2	15.20	4.86
42	Piranga rubra	Summer tanager	S 1	7.01	4.85
43	Asio otus	Long-eared owl	S3?	30.59	4.84
44	Vireo bellii pusillus	Least bell's vireo	S2	14.77	4.84
45	Asio flammeus	Short-eared owl	S 3	30.52	4.84
46	Picoides arcticus	Black-backed woodpecker	S2	14.60	4.83
47	Empidonax traillii	Willow flycatcher	S1S2	9.87	4.81
47	Empidonax traillii brewsteri	Willow flycatcher	S1S2	9.87	4.81
48	Cardinalis cardinalis	Northern cardinal	S 1	6.63	4.80
49	Elanus leucurus	White-tailed kite	S3S4	41.97	4.80
50	Histrionicus histrionicus	Harlequin duck	S 1	6.39	4.77
51	Bucephala islandica	Barrow's goldeneye	S 1	6.27	4.76
52	Melospiza melodia graminea	Channel island song sparrow	S 1	6.27	4.76
53	Artemisiospiza belli clementeae	San Clemente sage sparrow	S 1	6.25	4.75
54	Junco hyemalis caniceps	Gray-headed junco	S 1	6.20	4.75
55	Selasphorus rufus	Rufous hummingbird	S1S2	8.58	4.69
56	Cistothorus palustris clarkae	Clark's marsh wren	S2S3	17.97	4.68
57	Athene cunicularia	Burrowing owl	S 3	25.18	4.65
58	Psiloscops flammeolus	Flammulated owl	S2S4	24.97	4.64
59	Circus hudsonius	Northern harrier	S 3	24.02	4.61
60	Progne subis	Purple martin	S 3	23.26	4.58
61	Fratercula cirrhata	Tufted puffin	S1S2	7.46	4.56
62	Dendragapus fuliginosus howardi	Mount Pinos sooty grouse	S2S3	15.33	4.53
63	Poecile atricapillus	Black-capped chickadee	S 3	21.98	4.52
64	Buteo swainsoni	Swainson's hawk	S 3	21.98	4.52
65	Centrocercus urophasianus	Greater sage-grouse	S2S3	14.99	4.51

66	Agelaius phoeniceus	Kern red-winged blackbird	S1S2	6.91	4.49
67	Agelaius tricolor	Tricolored blackbird	S1S2	6.89	4.49
68	Accipiter gentilis	Northern goshawk	S 3	21.18	4.49
69	Pipilo maculatus clementae	San Clemente spotted towhee	S1S2	6.33	4.42
70	Botaurus lentiginosus	American bittern	S3S4	28.30	4.42
71	Gelochelidon nilotica	Gull-billed tern	S 1	4.18	4.42
72	Icteria virens	Yellow-breasted chat	S 3	19.66	4.41
73	Synthliboramphus scrippsi	Scripps's murrelet	S2	8.84	4.37
74	Pelecanus occidentalis californicus	California brown pelican	S3S4	26.29	4.35
75	Haliaeetus leucocephalus	Bald eagle	S 3	17.63	4.31
76	Branta bernicla	Brant	S2?	8.04	4.28
77	Pyrocephalus rubinus	Vermilion flycatcher	S2S3	11.71	4.28
78	Antigone canadensis canadensis	Lesser sandhill crane	S3S4	24.16	4.26
79	Plegadis chihi	White-faced ibis	S3S4	23.69	4.25
80	Pandion haliaetus	Osprey	S4	33.80	4.24
81	Chlidonias niger	Black tern	S2	7.66	4.24
82	Nycticorax nycticorax	Black-crowned night-heron	S4	31.45	4.17
83	Buteo regalis	Ferruginous hawk	S3S4	21.52	4.15
84	Egretta thula	Snowy egret	S 4	30.54	4.14
85	Passerculus sandwichensis rostratus	Large-billed savannah sparrow	S2	6.76	4.13
86	Setophaga petechia sonorana	Yellow warbler	S 2	6.65	4.11
87	Toxostoma lecontei	Le Conte's thrasher	S 3	14.24	4.11
88	Ardea alba	Great egret	S4	29.13	4.10
89	Aythya valisineria	Canvasback	S2	6.48	4.09
90	Toxostoma crissale	Crissal thrasher	S 3	13.92	4.09
91	Ardea herodias	Great blue heron	S4	28.58	4.08
92	Toxostoma bendirei	Bendire's thrasher	S 3	13.66	4.07
93	Melospiza melodia samuelis	San Pablo song sparrow	S2	6.27	4.06
93	Melozone crissalis eremophilus	Inyo California towhee	S2	6.27	4.06
94	Campylorhynchus brunneicapillus sandiegensis	Coastal cactus wren	S3	13.37	4.05
95	Oreothlypis virginiae	Virginia's warbler	S2	6.10	4.04
96	Rynchops niger	Black skimmer	S2	5.92	4.01
97	Pica nuttalli	Yellow-billed magpie	S3S4	18.48	4.01
98	Sternula antillarum browni	California least tern	S 2	5.88	4.01
99	Bonasa umbellus	Ruffed grouse	S3S4	18.41	4.01
100	Phalacrocorax auritus	Double-crested cormorant	S 4	26.31	4.00
101	Falco peregrinus anatum	American peregrine falcon	S3S4	17.63	3.96
102	Melanerpes lewis	Lewis' woodpecker	S4	24.71	3.94
103	Falco columbarius	Merlin	S3S4	16.91	3.92
104	Eremophila alpestris actia	California horned lark	S 4	23.54	3.89

105	Polioptila melanura	Black-tailed gnatcatcher	S3S4	14.95	3.81
106	Passerculus sandwichensis alaudinus	Bryant's savannah sparrow	S2S3	6.76	3.78
107	Sphyrapicus ruber	Red-breasted sapsucker	S 4	20.87	3.78
108	Accipiter cooperii	Cooper's hawk	S 4	20.78	3.77
109	Thalasseus elegans	Elegant tern	S2	4.39	3.76
110	Aimophila ruficeps obscura	Santa Cruz Island rufous- crowned sparrow	S2S3	6.47	3.74
111	Baeolophus inornatus	Oak titmouse	S 4	19.98	3.74
112	Melospiza melodia pusilluls	Alameda song sparrow	S2S3	6.27	3.72
113	Accipiter striatus	Sharp-shinned hawk	S 4	19.31	3.70
114	Oreothlypis luciae	Lucy's warbler	S2S3	6.11	3.69
115	Anser albifrons elgasi	Tule greater white-fronted goose	S2S3	5.72	3.64
116	Branta hutchinsii leucopareia	Cackling (Aleutian Canada) goose	S 3	8.08	3.59
117	Cerorhinca monocerata	Rhinoceros auklet	S 3	8.05	3.59
118	Falco mexicanus	Prairie falcon	S 4	15.52	3.50
119	Ptychoramphus aleuticus	Cassin's auklet	S2S4	7.12	3.48
120	Ammodramus savannarum	Grasshopper sparrow	S 3	7.10	3.48
121	Myiarchus tyrannulus	Brown-crested flycatcher	S 3	7.06	3.47
122	Passerculus sandwichensis beldingi	Belding's savannah sparrow	S 3	6.76	3.43
123	Calypte costae	Costa's hummingbird	S 4	14.20	3.41
124	Xanthocephalus xanthocephalus	Yellow-headed blackbird	S 3	6.47	3.40
125	Aimophila ruficeps canescens	Southern California rufous- crowned sparrow	S 3	6.47	3.40
126	Pooecetes gramineus affinis	Oregon vesper sparrow	S3?	6.40	3.39
127	Spinus lawrencei	Lawrence's goldfinch	S3S4	9.39	3.38
128	Melospiza melodia	Song sparrow (Modesto population)	S3?	6.27	3.37
128	Melospiza melodia maxillaris	Suisun song sparrow	S 3	6.27	3.37
128	Melozone aberti	Aber's towhee	S 3	6.27	3.37
129	Artemisiospiza belli belli	Bell's sage sparrow	S 3	6.25	3.37
130	Geothlypis trichas sinuosa	Saltmarsh common yellowthroat	S 3	6.05	3.34
131	Larus californicus	California gull	S 4	11.88	3.25
132	Lanius ludovicianus	Loggerhead shrike	S 4	11.65	3.23
133	Contopus cooperi	Olive-sided flycatcher	S 4	11.18	3.19
134	Aythya americana	Redhead	S3S4	6.82	3.10
135	Setophaga petechia	Yellow warbler	S3S4	6.65	3.08
136	Spizella breweri	Brewer's sparrow	S 4	6.14	2.66
137	Hydroprogne caspia	Caspian tern	S4	4.40	2.38

Appendix C

California Mammal Species Ranked by RED-E Score. Species names are from the California Special Animals List (California Department of Fish and Wildlife 2019). RED-E scores are rounded to two decimal places but differences in ranks represent actual differences in RED-E scores.

Rank	Species	Common Name	State Threat	ED	RED-E
1	Aplodontia rufa nigra	Point arena mountain beaver	S1	57.69	6.84
2	Choeronycteris mexicana	Hog-nosed bat/Mexican long- tongued bat	S 1	45.64	6.62
3	Puma concolor browni	Yuma mountain lion	S 1	40.33	6.49
4	Aplodontia rufa phaea	Point Reyes mountain beaver	S2	57.69	6.15
5	Sylvilagus bachmani riparius	Riparian brush rabbit	S 1	27.75	6.13
6	Gulo gulo	Wolverine/ California wolverine	S 1	22.27	5.92
7	Ovis canadensis nelsone pop. 2	Peninsular bighorn sheep	S 1	21.15	5.87
8	Thomomys bottae operarius	Owens Lake pocket gopher	S1?	20.86	5.86
9	Zapus trinotatus orarius	Point Reyes jumping mouse	S1S3	40.89	5.81
10	Aplodontia rufa californica	Sierra Nevada mountain beaver	S2S3	57.69	5.81
11	Reithrodontomys megalotis distichlis	Salinas harvest mouse	S 1	19.64	5.80
11	Reithrodontomys megalotis santacruzae	Santa Cruz harvest mouse	S 1	19.64	5.80
12	Arctocephalus townsendi	Guadalupe fur seal	S 1	19.55	5.80
12	Callorhinus ursinus	Northern fur-seal	S 1	19.55	5.80
13	Neotoma fuscipes riparia	Riparian/San Joaquin valley woodrat	S 1	19.51	5.79
14	Lontra canadensis sonora	Southwestern river otter	S 1	18.57	5.75
15	Vulpes vulpes necator	Sierra Nevada red fox	S 1	18.25	5.73
16	Perognathus inornatus psammophilus	Salinas pocket mouse	S 1	17.45	5.69
16	Perognathus longimembris pacificus	Pacific pocket mouse	S 1	17.45	5.69
16	Perognathus longimembris salinensis	Saline Valley pocket mouse	S 1	17.45	5.69
16	Perognathus longimembris tularensis	Tulare pocket mouse	S 1	17.45	5.69
17	Sigmodon arizonae plenus	Colorado River cotton rat	S1S2	23.82	5.64
18	Sorex ornatus relictus	Buena Vista Lake ornate shrew	S 1	16.49	5.63
18	Sorex ornatus salicornicus	Southern California saltmarsh shrew	S 1	16.49	5.63
18	Sorex ornatus willetti	Santa Catalina shrew	S 1	16.49	5.63
19	Urocyon littoralis	Island gray fox/island fox	S 1	16.25	5.62
19	Urocyon littoralis clementae	San Clemente island fox	S 1	16.25	5.62
19	Urocyon littoralis dickeyi	San Nicolas island fox	S 1	16.25	5.62

19	Urocyon littoralis littoralis	San Miguel island fox	S 1	16.25	5.62
19	Urocyon littoralis santacruzae	Santa Cruz island fox	S 1	16.25	5.62
19	Urocyon littoralis santarosae	Santa Rosa island fox	S 1	16.25	5.62
19	Urucyon littoralis catalinae	Santa Catalina island fox	S 1	16.25	5.62
20	Ochotona princeps schisticeps	Gray-headed pika	S2S4	67.35	5.61
21	Canis lupus	Gray wolf	S 1	15.60	5.58
22	Erethizon dorsatum	Common porcupine/ north	S 3	63.58	5.55
23	Sorex vagrans halicoetes	American porcupine Salt-marsh wandering shrew	S 1	14.71	5.53
23	Sorex vagrans paludivagus	Monterey vagrant shrew	S 1	14.71	5.53
24	Reithrodontomys raviventris	Salt-marsh harvest mouse	S1S2	19.64	5.45
25	Onychomys torridus tularensis	Tulare grasshopper mouse	S1S2	18.31	5.39
26	Myotis velifer	Cave myotis	S 1	12.31	5.36
27	Perognathus alticola inexpectatus	Tehachapi pocket mouse	S1S2	17.45	5.34
27	Perognathus longimembris brevinasus	Los Angeles pocket mouse	S1S2	17.45	5.34
28	Sigmodon hispidus eremicus	Yuma hispid cotton rat	S2	23.82	5.29
29	Sorex ornatus salarius	Monterey shrew	S1S2	16.49	5.29
29	Sorex ornatus sinuosus	Suisun shrew	S1S2	16.49	5.29
30	Callospermophilus lateralis bernardinus	San Bernardino golden-mantled ground squirrel	S 1	10.79	5.24
31	Macrotus californicus	California leaf-nosed bat	S 3	45.64	5.23
32	Microtus californicus halophilus	Monterey vole	S 1	10.20	5.19
32	Microtus californicus mohavensis	Mohave River vole	S1	10.20	5.19
32	Microtus californicus scirpensis	Amargosa vole	S 1	10.20	5.19
33	Ovis canadensis sierrae	Sierra Nevada bighorn sheep	S2	21.15	5.18
34	Lepus americanus klamathensis	Oregon snowshoe hare	S2	20.49	5.15
34	Lepus americanus tahoensis	Sierra Nevada snowshoe hare	S2	20.49	5.15
35	Neotamias panamintinus acrus	Kingston Mountain chipmunk	S1S2	13.76	5.12
36	Lynx rufus pallescens	Pallid bobcat	S 3?	40.33	5.11
37	Eumetopias jubatus	Northern (Steller) sea-lion	S2	19.55	5.10
38	Neotoma albigula venusta	Colorado Valley woodrat	S1S2	13.33	5.09
39	Mustela frenata inyoensis	Inyo long-tailed weasel	S 2	18.69	5.06
40	Enhydra lutris nereis	Southern sea otter	S 2	18.57	5.05
41	Vulpes vulpes patwin	Sacramento valley red fox	S2	18.25	5.04
42	Dipodomys merriami parvus	San Bernardino kangaroo rat	S 1	8.36	5.01
43	Perognathus longimembris bangsi	Palm Springs pocket mouse	S2	17.45	4.99
43	Perognathus longimembris internationalis	Jacumba pocket mouse	S2	17.45	4.99
44	Peromyscus maniculatus anacapae	Anacapa Island deer mouse	S1S2	11.82	4.98
44	Peromyscus maniculatus	San Clemente deer mouse	S1S2	11.82	4.98

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45	Dipodomys venustus venustus	Santa Cruz kangaroo rat	S 1	7.97	4.97
46	Dipodomys heermanni berkelevensis	Berkeley kangaroo rat	S 1	7.23	4.88
47	Brachylagus idahoensis	Pygmy rabbit	S 3	31.21	4.86
48	Pekania pennanti	Fisher	S2S3	21.57	4.85
49	Microtus californicus sanpabloensis	San Pablo vole	S1S2	10.20	4.84
49	Microtus californicus stephensi	South Coast marsh vole	S1S2	10.20	4.84
50	Dipodomys ingens	Giant kangaroo rat	S1S2	9.50	4.78
51	Neotoma fuscipes annectens	San Francisco dusky-footed woodrat	S2S3	19.51	4.75
52	Mustela frenata xanthogenys	San Joaquin long-tailed weasel	S2S3	18.69	4.71
53	Neotamias speciosus callipeplus	Mount Pinos chipmunk	S2	12.91	4.71
54	Nyctinomops femorosaccus	Pocketed free-tailed bat	S 3	26.60	4.70
54	Nyctinomops macrotis	Big free-tailed bat	S 3	26.60	4.70
55	Dipodomys californicus eximius	Marysville California kangaroo rat	S1S2	8.55	4.68
56	Dipodomys merriami collinus	Earthquake Merriam's kangaroo rat	S1S2	8.36	4.66
56	Dipodomys nitratoides brevinasus	Short-nosed kangaroo rat	S1S2	8.36	4.66
56	Dipodomys nitratoides nitratoides	Tipton kangaroo rat	S1S2	8.36	4.66
57	Perognathus inornatus	San Joaquin pocket mouse	S2S3	17.45	4.65
58	Taxidea taxus	American badger	S 3	22.95	4.56
59	Eumops perotis californicus	Western mastiff bat	S3S4	32.85	4.56
60	Dipodomys heermanni arenae	Lompoc kangaroo rat	S1S2	7.23	4.53
61	Ovis canadensis nelsoni	Desert bighorn sheep	S 3	21.15	4.48
62	Arborimus albipes	White-footed vole	S 2	10.03	4.48
63	Antrozous pallidus	Pallid bat	S 3	20.11	4.44
63	Euderma maculatum	Spotted bat	S 3	20.11	4.44
64	Xerospermophilus tereticaudus chlorus	Palm Springs round-tailed ground squirrel	S2	9.54	4.43
65	Neotamias speciosus speciosus	Lodgepole chipmunk	S2S3	12.91	4.37
66	Onychomys torridus ramona	Southern grasshopper mouse	S 3	18.31	4.35
67	Myotis lucifugus	Little brown bat	S2S3	12.31	4.32
68	Dipodomys merriami trinidadensis	Valle del la Trinidad kangaroo rat	S2	8.36	4.32
69	Dipodomys venustus elephantinus	Big-eared kangaroo rat	S2	7.97	4.27
70	Chaetodipus californicus femoralis	Dulzura pocket mouse	S 3	16.88	4.27
71	Dipodomys panamintinus argusensis	Argus Mountains kangaroo rat	S1S3	7.88	4.26
72	Dipodomys heermanni heermanni	Heermann's kangaroo rat	S2	7.23	4.19
72	Dipodomys stephensi	Stephen's kangaroo rat	S 2	7.23	4.19

73	Ammospermophilus nelsoni	Nelson's antelope squirrel	S2S3	10.62	4.19
74	Xerospermophilus mohavensis	Mohave ground squirrel	S2S3	10.21	4.15
75	Lepus townsendii townsendii	Western white-tailed jackrabbit	S3S4	21.39	4.15
76	Myotis evotis	Long-eared myotis	S 3	14.62	4.13
76	Myotis thysanodes	Fringed myotis	S 3	14.62	4.13
77	Lepus californicus bennettii	San Diego black-tailed jackrabbit	S3S4	20.49	4.11
78	Lasionycteris noctivagans	Silver-haired bat	S3S4	20.11	4.09
79	Myotis volans	Long-legged myotis	S 3	12.31	3.98
80	Chaetodipus fallax fallax	Northwestern San Diego pocket mouse	S3S4	16.78	3.92
80	Chaetodipus fallax pallidus	Pallid San Diego pocket mouse	S3S4	16.78	3.92
81	Dipodomys heermanni dixoni	Merced kangaroo rat	S2S3	7.23	3.84
81	Dipodomys heermanni goldmani	Salinas kangaroo rat	S2S3	7.23	3.84
82	Neotamias alpinus	Alpine chipmunk	S 3	10.26	3.81
83	Microtus californicus callicola	Owens valley vole	S 3	10.20	3.80
84	Arborimus pomo	Sonoma red tree vole	S 3	10.03	3.79
85	Lasiurus cinereus	Hoary bat	S 4	20.11	3.74
86	Neotoma lepida intermedia	San Diego desert woodrat	S3S4	13.33	3.70
87	Urocitellus mollis	Piute ground squirrel	S 3	8.79	3.67
88	Dipodomys panamintinus panamintinus	Panamint kangaroo rat	S 3	7.88	3.57
89	Myotis yumanensis	Yuma myotis	S 4	12.31	3.28