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FINAL PROJECT REPORT

A Genoscape Framework for Assessing the Population-Level Impacts of Renewable Energy Development on Migratory Bird Species in California

Gavin Newsom, Governor
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PREPARED BY:

Primary Authors:
Kristen C. Ruegg, Christen M. Bossu, Jasmine Rajbhandary, Trevon Fuller, Ryan Harrigan, Tom Smith

Institute of the Environment and Sustainability
Center for Tropical Research
University of California, Los Angeles
610 Charles E. Young Drive East
Los Angeles, CA 90095
310-206-6234
https://www.ioes.ucla.edu/
https://www.birdgenoscape.org

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PREPARED FOR:
California Energy Commission

David Stoms, Ph.D.
Project Manager

Jonah Steinbuck, Ph.D.
Office Manager
ENERGY GENERATION RESEARCH OFFICE

Laurie ten Hope
Deputy Director
ENERGY RESEARCH AND DEVELOPMENT DIVISION

Drew Bohan
Executive Director

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PREFACE

The California Energy Commission's Energy Research and Development Division supports energy research and development programs to spur innovation in energy efficiency, renewable energy and advanced clean generation, energy-related environmental protection, energy transmission and distribution and transportation.

In 2012, the Electric Program Investment Charge (EPIC) was established by the California Public Utilities Commission to fund public investments in research to create and advance new energy solutions, foster regional innovation and bring ideas from the lab to the marketplace. The California Energy Commission and the state's three largest investor-owned utilities—Pacific Gas and Electric Company, San Diego Gas & Electric Company and Southern California Edison Company—were selected to administer the EPIC funds and advance novel technologies, tools, and strategies that provide benefits to their electric ratepayers.

The Energy Commission is committed to ensuring public participation in its research and development programs that promote greater reliability, lower costs, and increase safety for the California electric ratepayer and include:

- Providing societal benefits.
- Reducing greenhouse gas emission in the electricity sector at the lowest possible cost.
- Supporting California's loading order to meet energy needs first with energy efficiency and demand response, next with renewable energy (distributed generation and utility scale), and finally with clean, conventional electricity supply.
- Supporting low-emission vehicles and transportation.
- Providing economic development.
- Using ratepayer funds efficiently.

A Genoscape Framework for Assessing the Population-Level Impacts of Renewable Energy Development on Migratory Bird Species in California is the final report for the Development of a Genoscape Framework for Assessing the Population-level Impacts of Renewable Energy Development on Migratory Bird Species in California project (Grant EPC-15-043) conducted by the Bird Genoscape Project team at University of California, Los Angeles. The information from this project contributes to the Energy Research and Development Division's EPIC Program.

For more information about the Energy Research and Development Division, please visit the Energy Commission's website (www.energy.ca.gov/research/) or contact the Energy Commission at 916-327-1551.

ABSTRACT

With California’s mandate to produce more clean, renewable electricity, every effort must be made to assess and mitigate the impacts of renewable energy development on California’s sensitive ecosystems and the wildlife species they support. The researchers took a three-pronged approach to assess the population-specific impacts of renewable energy development on migratory birds. First, to locate population boundaries for four species, they applied a newly developed, high-resolution genetic tagging method to map population-specific migratory pathways using the DNA from feathers collected from across the annual life cycle. Maps of fine-scale spatial structure of genetic diversity (called genoscapes) and population-specific migratory timing in two of the four species highlight the importance of understanding the population structure when developing mitigation strategies for these species. Second, they used completed genoscapes to identify the breeding populations of origin of carcasses salvaged from renewable energy facilities along the Pacific migration corridor. The results support the idea that the majority of individual birds exposed to renewable energy facilities came from the largest genetically distinct populations within each species; carcasses from rare and declining populations made up a smaller percentage of the total number of birds sampled. Finally, they created maps that combined multi-species migration hotspots with information on regions of high renewable energy potential to influence selection of renewable energy sites that minimize harm to migratory birds. The results demonstrated that prioritization of renewable energy siting practices varied across the taxonomic groups analyzed (nine target species as well as three groups: raptors, waterfowl, and songbirds), but generally supported prioritization of renewable energy siting in four California counties: Modoc, Lassen, Riverside, and San Bernardino. Overall, this work supports the idea that high-resolution genetic tagging improves identification of population-level exposure of migratory birds to wind and solar development and provides tools for siting and monitoring renewable energy facilities in the future.

Keywords: population-specific impacts, bird genoscapes, migratory hotspots, DNA, solar energy

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EXECUTIVE SUMMARY

Background

One of the greatest challenges facing California in the coming decades is how best to produce clean, renewable electricity capable of meeting the state's ever-growing electricity consumption needs while simultaneously reducing the greenhouse gas emissions that contribute to climate change. To meet this challenge, a number of state and federal policies aim to stimulate development of renewable energy technologies through incentives. These incentives have already led to the rapid development and operation of installations across the western U.S., especially wind and solar in California. While the percentage of renewable energy production in the state has increased, every effort must also be made to minimize the impacts of that development on California's sensitive ecosystems and the wildlife species they support. If these wildlife impacts are not adequately mitigated, they could potentially hobble further renewable energy development and the greenhouse gas emissions reductions it could provide. Thus, as the demand for renewable energy development in California increases, so does the need to better understand its ecological impact and minimize its effects on bird populations that either live within California or traverse the state's critical migratory corridors.

Project Purpose

A central challenge in the effort to better understand the impact of renewable energy development on bird populations has been a lack of precise knowledge about when and where those birds migrate and whether or not collisions with energy facilities kill them. Science tells us that preserving genetic diversity, expressed through different species populations, is essential for those species' long-term survival as they adapt to ever-changing environmental conditions. When a bird carcass is found at a wind or solar facility, the significance of that death will be quite different depending on whether the individual was from a stable or declining population. Previous methods to identify population-specific impacts suffered from insufficient data to map populations with a useful level of geographic detail. The overarching goal of this research was to overcome previous technological limitations by developing high-resolution genetic-tagging methods that could efficiently map genetic variations geographically and identify bird populations at finer spatial scales (that is, in greater detail); this map is what the researchers call a genoscape. The development of this methodology makes it possible to analyze the DNA from the feathers of thousands of live birds and carcasses, identify which birds live within California (for all or part of their annual cycle), and develop a clearer understanding of when particularly vulnerable bird populations come into contact with renewable energy facilities, primarily wind and solar. If the project's approach is implemented widely, the knowledge gained can better protect declining populations while increasing the efficiency of population-level monitoring at those facilities. This increased efficiency could reduce downstream costs to California ratepayers.

Project Approach

The multi-disciplinary project team of geneticists, statisticians, bioinformaticians (scientists who organize and analyze large amounts of genomic biological data), and research technicians adopted an integrated approach to achieve the following three main objectives:

- Objective 1: Identify where and when vulnerable bird populations in California migrate. Using the high-resolution genomic tagging method recently developed by the research team, the researchers built genoscapes for four target species: two migratory passerines, or songbirds (Wilson's Warbler and Common Yellowthroat) and two raptors, or predatory species (American Kestrel and Burrowing Owl). Because genoscapes reveal genetically distinct populations, they are the best-available method for identifying the breeding populations of migratory bird fatalities at renewable energy facilities. Simply put, researchers created the genoscapes by generating a draft genome assembly for each species from a single bird. They then conducted genome-wide genetic sequencing many birds from across the geographic range of each target species (between 148 and 207 individuals) before finally aligning that sequence data with the draft genomes. The combined genome assembly and genome-wide sequencing allowed researchers to identify up to millions of genetic variants across the genome; these genetic variants were invaluable in assigning individual birds to their correct breeding populations. The variants then enabled identification of bird populations at fine spatial scales used to create low-cost assays to genotype thousands of samples across the species' ranges (including samples collected at wintering sites and migratory stopovers) and then assigning each sample to a distinct breeding population. The result was an extremely high-resolution spatial map of breeding-population distributions for each species, as well as identification of specific migratory pathways and timetables of migration for each population. This information can help shape guidelines for renewable energy facility siting and mitigation to avoid or minimize avian injury or death in the vulnerable populations.

- Objective 2: Assess the population-level impacts of renewable energy development on migratory birds. In collaboration with sample collection partners at the Migratory Bird Division in Region 8 of the U. S. Fish and Wildlife Service, researchers applied the genoscapes to three of the target bird species (American Kestrel, Common Yellowthroat, and Wilson's Warbler) to identify the breeding populations of carcasses collected at renewable energy facilities along major bird flyways in the lower Colorado River Valley, the Mojave Desert, and the Imperial Valley. The renewable energy facilities sampled include Altamont Pass Wind Farm, Blythe Mesa Solar Power Project, Desert Sunlight Solar Farm, Genesis Solar Energy Project, Ivanpah Solar Electric Generating System, McCoy Solar Energy Project, and Mojave Solar Project. The collected carcasses were then curated by researchers at University of California, Los Angeles, and their DNA was extracted in the UCLA genetics laboratory. All the samples were then analyzed with the high-resolution genetic tags described in Objective 1. The researchers then assigned individual carcasses to their breeding populations of origin to determine whether the bird fatalities were concentrated in either demographically vulnerable or stable populations. Analyses of these carcasses, together with independently collected data on demographic trends of each genetically unique breeding population, allowed the researchers to determine population-level impact assessments for each species and facility within this region.
- Objective 3: Identify sites for future energy facilities that minimize wildlife impacts while maximizing renewable energy potential. Researchers then identified areas that meet essential habitat or ecological requirements for each of the target bird species and three groups (or guilds; in this case, raptors, waterfowl, and songbirds), and determined which areas were most ecologically valuable for the bird species studied in this project. The researchers spatially defined so-called "migratory hotspots," or regions within

California with the highest migratory bird conservation potential per land unit. This information, combined with spatial information on regions of high renewable energy potential, was used to prioritize regions that both maximize that potential while minimizing impacts on migrating species, ultimately resulting in promising sites for future renewable energy development from an avian wildlife conservation perspective.

Project Results

- Objective 1. The researchers successfully produced genoscape maps for three of the four targeted migratory bird species (American Kestrel, Common Yellowthroat, and Wilson's Warbler) that regularly use or traverse California for all or part of their annual cycles. The completed genoscape maps identified populations at finer spatial scales than previously possible. The spatial scale of populations fell along a continuum depending upon the life history of each species - ranging from fine-scale delineation of unique breeding populations within California in the cases of the Common Yellowthroat and Wilson's Warbler, to the American Kestrel, whose ranges span the entire western United States. The high-resolution genetic markers developed for Burrowing Owl populations distinguished between the geographically widespread migratory Burrowing Owl populations and each resident population. Distinction between different migratory populations, however, was not possible with these genetic markers. These results made it impossible to assign Burrowing Owl migrants to genetically distinct breeding populations and therefore suggest, for this species in particular, that the potential impact of renewable energy facilities will be more pronounced in small, geographically restricted resident populations rather than in widespread, genetically indistinguishable migratory populations.

  The delineation of genetically distinct populations within each species had various population management implications depending upon both the patterns of population-specific declines and the timing of population-specific migrations. For instance, researchers identified two genetically distinct groups of Common Yellowthroat breeding and migrating in California: a small California-endemic breeding population, and a larger western breeding population whose range spanned north to the Yukon and east to the Rocky Mountains. Demographic data suggests that only the genetically distinct California group is declining; however, both populations were detected across the migratory period and are thus potentially at risk from renewable energy facilities. The Wilson's Warbler also exhibited fine-scale genetic structure across its breeding range, with three of six genetically distinct populations found within California. In this species, researchers found a temporal shift in stopover-site usage. Spring migrants primarily belonged to the very large Western Boreal population that breeds in northern Canada, and fall migrants primarily belonged to the smaller declining Pacific Northwest and Sierra Nevada populations. Unlike the Common Yellowthroat and the Wilson's Warbler, most of the American Kestrels were assigned to a single, very large western U.S. genetic group.

- Objective 2. The development of high-resolution genetic tags for each species allowed researchers to assess the population-specific effects of renewable energy production on migratory birds in California. In general, the majority of carcasses recovered from renewable energy facilities were from the largest breeding populations within each species, while carcasses from rare and declining populations made up a smaller percentage of the total number of birds collected, which is expected given their declining and overall population numbers. For instance, researchers assigned all American Kestrel carcasses from Altamont and Ivanpah, and the majority from Genesis, to the western U.S. population, which covers the largest geographic area of any kestrel group and spans from the western coastal areas to the Midwestern United States and Canada. While the U.S. Geological Survey's Breeding Bird Survey status and trend data suggest that breeders in this region vary in population density and may be declining overall, the population impacts for birds in the western breeding population would be dispersed across a very large geographic area. Similarly, Common Yellowthroat carcasses found and genotyped at renewable energy facilities, while fewer in number, were primarily assigned to the largest western population rather than to the small declining California-endemic population. Although Wilson's Warbler fatalities at renewable energy facilities were also predominantly assigned to the largest western breeding population ranging from Alaska to Alberta, Canada, the researchers also detected individual birds from three of the smaller declining populations in the Pacific Northwest, the Sierra Nevada, and Coastal California.

- Objective 3. Using the relationship between a species and its habitat, researchers produced spatially explicit maps of essential migratory areas for nine target species, visually revealing migratory hotspots within California. These data were overlaid with maps of renewable energy resource potential across the state and prioritized particular regions deemed optimal for solar-facility siting from an avian wildlife perspective. For instance, the counties with the smallest numbers of the target species and highest solar potential were Lassen and Modoc, which are located in northeastern California. Moreover, an analysis of the raptor, waterfowl, and songbird guilds showed that Modoc and Lassen counties had high solar potential and relatively small numbers of raptors and songbirds, while Riverside and San Bernardino counties had high solar potential and relatively small numbers of songbirds and waterfowl.

Knowledge Transfer

A technical advisory committee was created from members from agencies, academia, and industry including First Solar, National Audubon Society, United States Fish and Wildlife Service, United States Geological Survey, California Department of Fish and Wildlife, and the California Energy Commission. A start-up meeting was held with the entirety of the advisory committee, and subsequent meetings were conducted every quarter with a subset of the committee. The researchers discussed preliminary results, updates on progress and conservation implications with the committee, and comments were incorporated into the results.

Technology and knowledge generated from this project were shared with academics, non-profit organizations, government agencies, renewable energy companies, and the general public. The main products transferred included: 1) Population maps (genoscapes) of genetic variation across geographic space for four species exposed to renewable energy development in California, 2) timetables of migration along the Pacific Flyway, 3) population-level impact assessments based upon the analysis of individual birds killed at renewable energy facilities within California, and 4) least-cost-analysis maps that can be used to help prioritize regions for renewable energy siting that maximize energy potential while minimizing risks to migratory birds. To reach broad and diverse audiences, researchers developed a multi-pronged plan to widely disseminate the project's data and conclusions.

First, to reach decision makers in agencies, industry, and non-profit organizations, the researchers have given and will continue to give presentations at conferences and symposia related to avian impacts from renewable energy production in California. Specifically, the researchers have shared versions of this report with the Avian Solar Working Group and actively communicated with its members through meeting webinars. Researchers have already published or have articles in review in high-impact journals (*Science*, *Ecology Letters*) to share this research with academics. Additional manuscripts are in preparation for target species in peer-reviewed journals (such as *Ecological Applications*, *Current Biology*). To share this report more broadly, researchers developed the Bird Genoscape website (http://www.birdgenoscape.org/), which publicizes this and related studies, provides a forum for displaying completed genoscapes, and invites ornithologists to contribute samples to sustain research beyond this study. Researchers also fostered community involvement by providing kits and training to broaden contributions of samples by the public. These community efforts are already in place and will continue beyond this study period.

This project has also been featured so far in 12 public media outlets including *Science Magazine, National Geographic, Audubon* magazine, *American Association for the Advancement of Science, New Scientist*, CBS News, and *Wildlife Society*. The researchers have also participated in the creation of videos and podcasts within the documentary filmmaker WildLen's Inc. Eyes on Conservation series (http://wildlensinc.org/eoc-single/the-bird-genoscape-project/) and are in the process of creating additional videos with Days Edge Productions (http://www.daysedge.com/) and the National Geographic Society.

Benefits to California

This project addressed the goal of lowering electricity costs for the state's electric utility ratepayers in three primary ways:

1. Reduced monitoring costs - While monitoring may be required at many facilities year round, the migration timetables developed in Objective 1 and the "migratory hotspots" identified in Objective 3 could help focus monitoring to peak migratory weeks in key migratory areas. Further exploration of the timing of migration in other guilds of birds could also broaden the reach of this research aimed at protecting birds from renewable energy production.
2. Increased compliance with wildlife protection regulations – The knowledge gained from this project, particularly the population-specific impacts of renewable energy production, the timing of population-specific migration, and new conclusions on where best to site facilities, can together minimize the potential negative impacts of renewable energy development on bird populations of conservation concern in California.
3. Increased operational time - The precise predictions of when and where target bird populations migrate can maximize electricity generation while minimizing negative wildlife impacts. The results of this project help meet this goal through both spatial recommendations for future renewable energy facilities and temporal recommendations for shutting down (curtailing) existing wind-energy facilities to more precisely avoid

peak migrations of vulnerable populations (such as the late spring migration of Wilson’s Warblers).

Overall, researchers expect that the implementation of this framework for avian wildlife monitoring can ultimately apply to a broad spectrum of wildlife affected by renewable energy development and production.

CHAPTER 1:
Introduction

Interactions of Migratory Birds and Renewable Energy Facilities

The environmental impacts of fossil-fuel consumption and the urgent need to reduce the pace of climate change have stimulated a huge rise in renewable energy development at both federal and state levels (Allison et al. 2014). According to the U.S. Energy Information Association, annual production of energy from utility-scale solar facilities in the country has spiked from 864,000 megawatt hours (MWh) in 2008 to 52,958,000 MWh in 2017 (U.S. Energy Information Administration 2018). Similarly, energy production from wind farms has risen from 30,000 gigawatt hours (GWh) in 2005 to more than 50,000 GWh in 2018 (California Energy Commission 2018). To meet ever-growing consumption needs while simultaneously addressing climate change, California aims to increase renewable energy capacity (by about 11.6 percent) from the current 7,540 megawatts (MW) to 20,000 MW by 2023 (California Energy Commission 2015b). These drivers have fueled the rapid scaling, growth, and deployment of wind and solar installations across the U.S., and especially in California.

While such shifts toward sources of energy with lower carbon footprints are essential for climate-change mitigation, they can also negatively affect wildlife, especially birds and bats (Strickland et al. 2011). Each year collisions with wind turbines kill hundreds of thousands of birds, the majority of which occur during migration (Kuvlesky et al. 2007; Arnett et al. 2008; Smallwood 2013). Bird deaths caused by collisions with monopole wind turbines in the contiguous United States number more than an estimated 200,000 per year (Loss et al. 2013).

In addition, while the nature and extent of avian mortality due to solar photovoltaic (PV) and concentrating solar-power generating facilities is not well understood because such technology has only recently been implemented at scale, recent reports of avian deaths at these facilities are concerning (Erickson et al. 2014; Kagan et al. 2014; Walston et al. 2015). Utility-scale solar energy (USSE) developments in the United States are estimated to kill between 37,800-138,600 birds annually (Walston et al. 2016). Understanding these potential ecological effects is of particular concern in California, which is home to nearly 650 species of birds, and its coastline and interior habitats serve as vital migration corridors for avian populations across the United States and Canada (Cryan and Brown 2007; Cryan 2003; Kays and Wilson 2009; DeSante 1983).

The American Bird Conservancy and other groups have suggested four methods to minimize the effects of renewable energy development on bird populations: (1) proper siting, operation, and construction; (2) mitigation; (3) effective monitoring; and (4) offset compensation (American Bird Conservancy 2015). A central challenge in the effort to achieve these goals is the lack of precise knowledge about when and where populations are migrating and whether or not fatal collisions at renewable energy facilities will have population-level effects (Ruegg et al. 2014b). More specifically, when a bird is found dead at a wind or solar facility, understanding whether the individual bird was from a stable or declining population has very different implications for mitigation strategies. Preserving the genetic diversity represented by the various populations is critical to ensuring the long-term persistence of the species in the face of continually changing environmental conditions.

Efforts to understand population-specific bird migration patterns have faced numerous limitations and technological hurdles over the last century. In the past, efforts to map population-specific bird migration patterns relied on recovery of individual birds previously captured and tagged with bird bands. However, this approach has had limited success, especially for small-bodied songbirds, because recapture rates of birds away from their original banding sites are generally very low (< 1 recapture per 10,000 birds banded; Gustafson 1999; Faaborg et al. 2010a, b). In addition, geo-locators (small tracking devices that record information on ambient light levels to estimate an individual bird's location), have increased researchers' knowledge of the migratory pathways in many songbird species (Stutchbury *et al.* 2009), but remain impractical for most large-scale (1,000's of individuals) applications due to cost, weight restrictions, and the need to recover individuals to collect data from the devices (Arlt et al. 2013; Bridge et al. 2013). Alternatively, genetic and isotopic markers that use information contained within a single feather to pinpoint an individual's population of origin have broad appeal because they are cost-effective, non-invasive, and do not require recapture (Rubenstein et al. 2002; Kelly et al. 2005; Rundel et al. 2013). However, until recently these methods yielded poor resolution data and were plagued by technical issues related to working with feather material (Wunder et al. 2005; Lovette et al. 2004; Segelbacher 2002).

In this innovative study, the researchers adopted new sequencing technologies to develop a high-resolution genetic tagging method for identifying conservation units in birds that provide significant advantages over previous methods (Ruegg et al. 2014b). Through this pilot study they demonstrated the feasibility and applicability of high-resolution genetic tagging technology for a single bird species, the Wilson's Warbler. They first used genome-scan methods to map genetic variation across geographic space, and defined conservation units at finer spatial scales than previously possible; this map is what the researchers call a genoscape. They then used the genomic information to design high-resolution genetic tags, which allowed them to screen the DNA contained within a single feather of a living bird or carcass collected away from the breeding location to identify the breeding population of origin. In other words, a feather collected at one stage of the migratory cycle was used to make essential links between where that bird may be going and where it came from. In addition, because of the low per-individual cost of screening, the high-resolution molecular tags that the researchers developed can be used to screen thousands of samples and build timetables of population-specific bird migrations.

Objectives

This project met the following objectives to overcome past obstacles:

1. Identify where and when vulnerable bird populations in California migrate.
2. Assess the population-level impacts of renewable energy development on migratory birds.
3. Identify sites for future renewable energy facilities that minimize avian impacts while maximizing energy potentials.

Organization of Report

Justification of Target Species

The bird species selected for this study (hereafter, target species) were representative of many of the groups that are particularly vulnerable to impacts from wind- and solar-energy development (Guzy and Ritchison 1999; Smallwood and Bird 2002) and for which a tremendous bank of genetic material had already been collected. The species are divided into two categories, based upon the depth of genetic analyses presented in subsequent chapters.

Group 1 Species

The first group consists of species for which the researchers used Electric Program Investment Charge (EPIC) funds to build genoscapes and screen avian fatalities from renewable energy facilities. Originally this list included, American Kestrel (*Falco sparverius*), Common Yellowthroat (*Geothlypis trichas*), and Yellow-rumped Warbler *(Setophaga coronata).* At the beginning of the project, researchers surveyed biologists in federal and state agencies, as well as members of the Technical Advisory Committee (TAC), to decide whether to substitute Common Yellowthroat and Yellow-rumped Warbler with species that garnered the most support. A summary of the species selection process follows. The American Kestrel was acceptable from the outset.

Species Selection Surveys

This species selection survey was conducted in two parts. During part one, a list of 100 species with the most genetic samples for building genoscapes was sent to biologists within the California Energy Commission's (Energy Commission) Siting Division and the United States Fish and Wildlife Service (USFWS) to request their input. In general, there was very little consensus. Some of the suggestions were for species on the original target list. There was some support for investigating common species to identify populations of concern, rather than just focusing on rare species. Based upon the results of this survey and careful deliberation, as well as the need to select at least one species in time to do fieldwork before the 2016 breeding season, the researchers selected the Common Yellowthroat as the second of the three target species.

The second part of the survey took place after forming the TAC in August 2016. Technical advisory committee members include members from agencies, academia, and industry including First Solar, National Audubon Society, United States Fish and Wildlife Service, United States Geological Survey, California Department of Fish and Wildlife, and the California Energy Commission. They were surveyed by email about candidate species in general, as well as for their particular thoughts about Burrowing Owl as a species candidate. Burrowing Owl was a particular focus because of potential synergies with other currently funded EPIC projects (and because of an outpouring of interest from the Burrowing Owl community) and their willingness to help contribute samples. TAC members were given the following criteria and asked to either give their thoughts about including Burrowing Owl or suggest alternatives that meet the following criteria (which were all met by Burrowing Owl):

1. The species should be a focus of state and federal regulations so that the tools the project developed would ultimately be useful for reducing avian wildlife monitoring costs.

2. It should be a species with demonstrated impacts from renewable energy development in some form (wind, solar, or any other).
3. It must be a species for which there are existing or easy-to-obtain DNA samples from across the geographic distribution (for construction of the base map), as well as samples from carcasses at renewable energy facilities (for identification of population-specific impacts).

Strong support was expressed for the inclusion of Burrowing Owl as the final taxa from the majority of the TAC, so Burrowing Owl became the third target species. Details on each of the final Group 1 target taxa (identified groups within a larger system) follow:

- American Kestrel (*Falco sparverius*) – Although one of the most common falcons in North America with year-round distribution throughout much of the United states, American Kestrel populations have dropped by nearly half over the last 45 years (Smallwood and Bird 2002; Sauer et al. 2017). In the United States, declines are worst in the Northeast, where there are losses up to 88 percent in some areas (Hoffman and Collopy 1988). Arguably one of the most beautiful falcons in North America, American Kestrels may also be an important early indicator species of environmental impacts and changes (Smallwood et al. 2009). While reasons for the declines are unclear, changing land use, competition from other birds, toxins like pesticides or pollution, or climate change are all potential candidates (Smallwood and Bird 2002).

  The population-level impact of renewable energy development on American Kestrels has not been assessed, but survey data indicate that it is one of the most commonly identified fatalities at renewable energy facilities in California (Kagan et al. 2014; WEST Inc 2014). Absolute counts are difficult to obtain, but estimates predict that between 195 and 332 American Kestrels are killed each year at wind facilities (ICF International 2014), and a recent report cited 22 known fatalities at solar facilities (Kagan et al. 2014; WEST Inc 2014). The researchers have built a sample base of breeding, migratory, and fatalities at renewable energy facilities through a partnership with American Kestrel biologist Julie Heath, of Boise State University. With approximately 1,000 samples from across the geographic range of this species, the researchers built a genoscape for the American Kestrel, which is presented in Chapter 2, and investigated population-level impacts of renewable energy development in Chapter 3.

- Common Yellowthroat (*Geothlypis trichas*) - The Common Yellowthroat is one of the most common and widely-distributed wood warblers in North America and breeds across much of Canada and the U.S. and south into Mexico (Guzy and Ritchison 1999). Although the species is common elsewhere in its range, in California some populations are listed as Species of Special Concern (Shuford and Gardali 2008). Once a common breeder in the Central Valley, its numbers are now much reduced due to wetlands destruction and habitat alteration (Small 1994; Guzy & Ritchison 1999). However, it does still breed in both the Sacramento and San Joaquin River valleys. It prefers marshy areas and early successional, shrubby riparian habitat, and it nests primarily in tall, emergent wetland and upland vegetation. Genetic diversity of Californian populations of this species have not yet been studied.

  While Common Yellowthroats represent a smaller overall proportion of casualties at renewable energy facilities than American Kestrels (solar, n = 8, 0.5 percent and wind, n = 25, 1 percent; see Erickson et al. 2014; Kagan et al. 2014; Walston et al. 2015), their conservation status within California makes them an important species to incorporate in renewable siting and mitigation efforts. The researchers have leveraged 5,045 blood and tissue samples from across the species range to build a genoscape for the Common Yellowthroat, which is presented in Chapter 2, and they investigated population-level impacts of renewable energy, presented in Chapter 3.

- Burrowing Owl (*Athene cunicularia*) - Burrowing Owls are a small and charismatic predatory raptor that occupy much of the Americas. Western Burrowing Owls have declined significantly in many areas due to habitat loss, secondary poisoning by rodenticides, mesopredator release, and impacts at wind-energy sites (Poulin et al. 2011). The subspecies is currently listed as endangered in Canada, for special protection in Mexico, and as a species of concern in nine states including California, Colorado, Oregon, Montana, Oklahoma, Utah, Washington, and Wyoming. Numerous captive breeding and heavy capture-and-release projects are ongoing throughout their range. While these efforts are a vital component in the protection and recovery of western Burrowing Owls, they are currently conducted without essential information about population structure. (See Desmond et al. 2000; Korfanta et al. 2005.)

  While sampling has taken place across the breeding range of Burrowing Owls, their population genomic structure impedes researchers' ability to create a genoscape. (See results in Chapter 2.)

  Thus, the researchers were unable to assign fatalities at renewable energy facilities to specific breeding populations, so were excluded from Chapter 3.

Group 2 Species

This group consists of species for which the researchers were in the process of building or had already built genoscapes for; they were also using match funds to screen fatalities from solar and wind facilities and conduct an analysis of migration hotspots. These included Common Loon (*Gavia immer*), Wilson's Warbler (*Cardellina pusilla*), Swainson's Thrush (*Catharus ustulatus*), Yellow Warbler (*Setophaga petechia*), Painted Bunting (*Passerina ciris*), and Willow Flycatcher (*Empidonax traillii*). All of these species, apart from Willow Flycatcher and Painted Bunting, had been identified as casualties at renewable energy facilities. In the case of the Willow Flycatcher, while there is no data to suggest that individual birds are particularly susceptible to impacts of renewable energy development, the southwestern Willow Flycatcher is on the endangered species list and is therefore of high conservation concern in California. The Wilson's Warbler genoscape is presented in Chapter 2 and the population-level effects of renewable energy development are described in Chapter 3. Using data from eBird (Sullivan et al. 2014), the researchers tallied the abundance of migratory birds for each Group 1 and Group 2 species since both are the subject of ongoing genomic analyses to identify population structures across their migratory cycles.

In summary, Chapter 2 presents the genoscapes and migration timetables for four target species (American Kestrel, Common Yellowthroat, and Burrowing Owl from Group 1 and Wilson's Warbler from Group 2). Chapter 3 describes the population effects of fatalities at renewable energy facilities on those target species (except for Burrowing Owl because that species does not have a genetic spatial structure that could distinguish populations). To meet the third project objective of identifying where future energy facilities could be sited to minimize avian wildlife impacts while maximizing energy potential, Chapter 4 compared abundance of the three Group 1 and six Group 2 target species with the level of solar insolation.

CHAPTER 2:
Genoscape Maps and Migration Timetables

Introduction

California is home to nearly 650 species of birds, and its coastline and interior habitats serve as vital migration corridors for avian populations across the United States and Canada (DeSante 1983; Cryan 2003; Cryan and Brown 2007; Kays and Wilson 2009). Each year collisions with wind turbines kill hundreds of thousands of birds, the majority of which occur during migration (Kuvlesky et al. 2007; Arnett et al. 2008; Smallwood 2013). In addition, while the nature and extent of avian mortality due to solar PV generating facilities is not well understood because such technology has only recently been implemented at scale, recent reports of avian deaths at these facilities are of concern (Erickson et al. 2014; Kagan et al. 2014; Walston et al. 2015). If wildlife impacts are not adequately addressed, public concern could potentially impede renewable energy development and result in a net-negative for bird populations that are also under severe threat from climate warming. Thus, as the demand for renewable energy development in California increases, so does the need to better understand the impact of their development on bird populations that reside either within California or traverse the state's critical migratory corridors.

Historically, the inability to define biologically meaningful avian population boundaries for conservation and management has limited the ability to assess the impacts of renewable energy development and other anthropogenic impacts on birds. The use of genetic data to define management units within a species now makes it possible to identify populations that are both demographically and genetically independent (Moritz 1994; Palsboll et al. 2007), thus providing a solid foundation upon which to base management decisions. Genetically distinct groups that are defined at the spatial scale of locally adapted populations are often referred to as conservation units (Moritz 1994; Allendorf and Luikart 2007; Funk et al. 2012), but in the past, it has been difficult to identify conservation units in highly mobile avian species with large population sizes, such as migratory birds where gene flow is high and the effect of genetic drift in large populations is expected to be small (Willoughby et al. 2017; Doyle et al. 2018; Medina et al. 2018). These difficulties have largely been limited by the time, technology, and sequencing costs associated with attaining the number of genetic markers needed to identify signals of local adaptation in highly mobile species such as birds. However, with the onset of new sequencing technologies, these barriers can now be overcome.

The researchers previously adopted new sequencing technologies to develop a high-resolution genetic tagging method for identifying conservation units in birds that provides a significant advantage over previous methods (Ruegg et al. 2014b). Through this pilot study they demonstrated the feasibility and applicability of genoscapes for a single bird species, the Wilson's Warbler, and then identified the breeding population of origin of migrating and wintering birds from DNA in their feathers.

Here the researchers generated bird genoscapes, which are innovative and cost-effective genomic and geographic information system (GIS)-based tools recently developed by the research team, to overcome past technological challenges, identify conservation units in migratory birds, and assess with unprecedented precision the impacts of renewable energy installations on migratory bird populations for all or part of their annual cycles. Passerines, or songbirds, are the most frequently discovered fatalities at both wind (62.5 percent) and solar (48.4 percent) facilities that have been studied in detail (Erickson et al. 2014). Diurnal raptors comprise 7.8 percent of the fatalities at wind and 1.3 percent of fatalities at solar facilities, and loons and grebes comprise 0.4 percent of fatalities at wind and 6.5 percent of fatalities at solar facilities (Erickson et al. 2014). The researchers selected species representative of many of the groups that are particularly vulnerable to impacts from wind- and solar-energy development and that allow them to take advantage of the tremendous bank of genetic material already collected by the researchers themselves and their collaborators. Specifically, they built genoscapes and defined conservation units for four species of migratory birds that regularly inhabit the Pacific migratory corridor for breeding, wintering, migrating or some combination of the three. The species they focused on in this report include: American Kestrel, Common Yellowthroat, Wilson's Warbler, and Burrowing Owl. They then used high-resolution genetic tags to screen the DNA in the feathers and build timetables of migration.

Genoscape Approach

Sampling

Collection of feather and blood samples from locations across the breeding, wintering and migratory ranges of multiple species was made possible through collaboration with bird-banding stations within and outside the Monitoring Avian Productivity and Survivorship (MAPS), the Landbird Monitoring of North America, and the Monitoreo de Sobrevivencia Invernal networks (Table 1). Overall, the researchers and their collaborators sampled and genotyped: 995 American Kestrels, including 597 breeders from 55 sites and 398 migrating birds from 47 locations (Figure A-1, Table A-1); 660 Common Yellowthroats, including 247 breeders from 42 collection sites and 413 migrants and wintering birds from 46 locations (Figure A-2, Table A-2); 1,696 Wilson's Warblers, including 407 breeders from 33 locations and 1,264 migrants from 46 locations (Figure A-3, Table A-3); and 207 Burrowing Owls including 190 breeders from 28 locations and 17 migrants from 1 renewable energy facility (Figure A-4, Table A-4).

DNA Isolation

The research team used a Qiagen DNeasy 96 blood and tissue kit (Qiagen Inc., Valencia, California) to extract DNA from each sample. Specific protocols for blood and feather extractions can be found in Appendix B and earlier manuscripts (Ruegg et al. 2014b; Bay et al. 2018; Ruegg et al. 2018).

Genoscape Construction With RAD-Seq

To construct the genoscapes for Wilson's Warbler and American Kestrel the researchers scanned the genomes of a subset of individual birds to identify genetic variants that were diagnostic or representative of populations at finer spatial scales. (See Appendix B for technical details.) They then filtered and trimmed the resulting sequence data and mapped those sequences to the species-specific genomes. For species with no available reference genome, such as the Burrowing Owl and American Kestrel, they assembled and annotated their own genome following the methods described in Ruegg et al. (2018) and Bay et al. (2018). Once the researchers mapped the sequences to the appropriate reference genome, they identified approximately 500,000 single nucleotide polymorphisms (SNPs) across the genomes of the two target taxa.

Genoscape Construction With Low Coverage Whole Genome Sequencing

To construct genoscapes for Common Yellowthroat and Burrowing Owl, the researchers a new low-coverage whole-genome sequencing protocol to take advantage of the orders of magnitude of more genetic markers that could be generated for these species and used in subsequent analyses. Details of the whole-genome sequencing pipeline can be found in Appendix B. In short, the researchers began by sequencing resident and migratory Burrowing Owl blood samples (n = 190) (Figure A-4) and Common Yellowthroat blood samples (n=150) from across the geographic range (Figure A-2). Then, in order to test the quality of genomic sequences from the low quantity of DNA collected from feathers of migratory birds, they also sequenced 17 Burrowing Owl feather samples from Altamont, a wind-energy facility in California (Bossu, Barr et al. *in prep*). After standard filtering, the researchers then aligned the reads of Burrowing Owls to the Burrowing Owl genome, and the Common Yellowthroat reads to the Common Yellowthroat genome and identified genetic variants to use in downstream analyses.

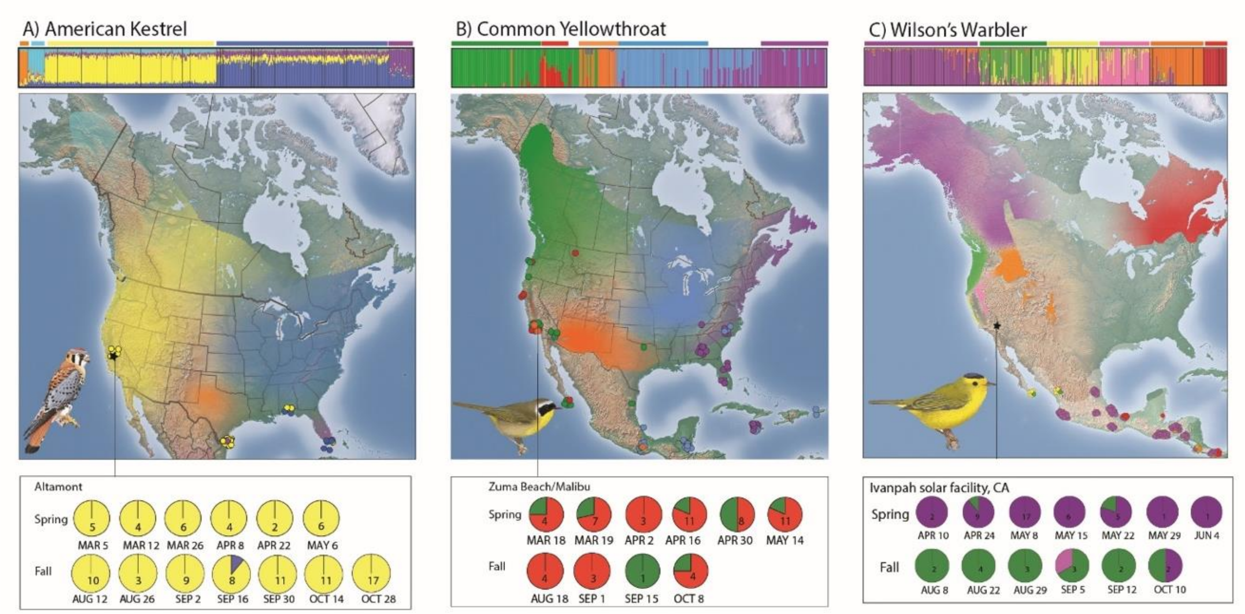
Feather Screening

From initial genome-wide sequence data, the researchers used custom R scripts to identify 96 – 192 highly divergent SNPs (Appendix B for technical details) and converted them into SNPtype Assay (Fluidigm Inc.). The researchers used the SNPtype Assays, also referred to as high-resolution molecular tags, to screen individuals collected from wintering and migratory stopover sites. The samples were screened using the Fluidigm Corporation EP1TM Genotyping System and the results were imaged on an EP1 Array Reader. The researchers used Fluidigm's automated Genotyping Analysis Software (Fluidigm Inc.) to identify genotypes for each individual with a confidence threshold of 90 percent. In addition, they visually inspected all SNP calls and removed any calls that did not fall clearly into one of three clusters—heterozygote or either homozygote cluster from the analysis. As DNA quality can affect call accuracy, they employed a stringent quality filter and dropped variants with greater than 50% missing calls. The resulting variant sets included approximately 96 variants genotyped for Wilson's Warblers and Common Yellowthroats, and 186 variants for American Kestrels. The final SNP panel was used to screen additional feather samples from across the breeding locations in the United States and Canada, as well as wintering and migratory birds (Figures A-1 through A-4 and Tables A-1 through A-4).

Genetic Screening and Building the Genoscape

The researchers removed samples with missing genotypes at more than 10 percent of SNP assays from their analyses of spatially-explicit population structure. To assess population structure across the breeding region of each species, they used the software program STRUCTURE (version 2.3.4; Pritchard et al. 2000). They visualized posterior probability of group membership estimates from STRUCTURE as transparency levels of different colors overlaid upon a base map from Natural Earth (naturalearthdata.com) and clipped to a map of each species' breeding range (NatureServe 2012). They scaled the transparency of colors within each distinguishable group, so that the highest posterior probability of membership in the group according to structure is opaque and the smallest is transparent. This creates the spatially-explicit map of genomic clustering, which they term the genoscape of each species (Figure 1).

Figure 1: Migratory Connection Maps



Migratory connections in the A) American Kestrel B) Common Yellowthroat and C) Wilson's Warbler identified using SNP-based genetic markers. (Top Panel) Results from STRUCTURE showing genetically distinct populations across the breeding grounds for each species. (Middle Panel) Spatially explicit population structure across the annual cycle. The colors across the breeding range represent the results from RUBIAS which were post-processed using R so that the density of each color reflects the relative posterior probability of membership for each pixel to the most probable of the different genetic clusters (see text). The researchers clipped the results to the species distribution map (NatureServe2012). (Bottom Panel) The proportion of individuals assigned to a specific breeding population across spring and fall migration of 2008 and 2009. Numbers in the center of the pies refer to sample sizes and the data are grouped by week with the date. American Kestrels were collected from Altamont wind facility, CA; Common Yellowthroat individuals were collected in southern California and Zuma Beach/Malibu beach, CA; Wilson's Warblers were collected at the Ivanpah Solar Electric Generating System, CA.

Source: K. Ruegg and C. Bossu

Baseline Conservation Groups and Accuracy Assignment

The researchers defined conservation units as the genetically-based breeding populations identified in the completed genoscapes of each species (Ruegg et al. 2014b; Brinkmeyer et al. in prep.). They evaluated the accuracy of individual assignment of birds to conservation units using self-assessment testing in the software package RUBIAS (Anderson et al. 2008, Anderson 2017). The self-assessment function in RUBIAS tests the accuracy of assignment by assigning individuals in the reference back to the collections in the reference using a leave-one-out cross validation approach. Accuracy is the proportion of individuals from known conservation groups that are assigned back to the correct conservation group. For each specimen, the researchers calculated the probability of assignment to a specific conservation group and defined significant assignment as > 0.8 posterior probability of assignment to the inferred collection. They designated assignments with a posterior probability < 0.8 as uncertain and filtered those individuals from the final reporting. Further details on the methods used to develop the baseline can be found in Appendix B.

Assignment of Unknown Migratory and Wintering Birds

The researchers then assigned individuals of unknown origin collected from wintering and migratory stopover locations (hereafter called 'unknown' birds; see Figures A-1 through A-4 and Tables A-1 through A-4) to conservation units using RUBIAS (Anderson and Moran 2017). They illustrate the assignment of individual wintering and migratory birds on each map by color coding each point by group membership (Figure 1; colored points on the maps), and used the assignment of migratory birds to provide a time series of migration through California during spring and fall migration. Further details on the assignment methods can be found in Appendix B.

Genoscape Results

SNP Genotyping

The researchers genotyped the DNA samples from feathers of the additional breeding, migrating and wintering birds of the target taxa using the markers developed to assign individuals to conservation units (Figures A-1 through A-4 and Tables A-1 through A-4). American Kestrel had a high genotyping success rate, with 90.8 percent of individuals successfully genotyped, followed by Common Yellowthroat (87.9 percent), and Wilson's Warbler (84.0 percent).

Population Structure and Wintering Assignment

American Kestrel

From the initial genome scan, the final variant set includes 186 variants that can be used for population delineation, and the researchers identified five genetic clusters in American Kestrels (Figure 1A). The majority of the American Kestrel breeding range is encompassed by two unique conservation units: East (blue) and West (yellow). The remaining genetic clusters represent geographically isolated populations of long-range migrants in Alaska (cyan), as well as resident breeding kestrel populations in Texas (orange) and Florida (purple). The researchers did not sample wintering birds.

Common Yellowthroat

The analyses of population structures across the breeding range of the target taxa varied in spatial scale at which the researchers were able to identify birds to conservation units. They identified five genetically unique breeding populations of Common Yellowthroat, with 96 targeted variants: West (green), Northeast (purple), Midwest (blue), Southwest (orange), and a unique genetic cluster in California (red; Figure 1B). Population structure was not so clearly defined in the East, as the researchers detected mixed ancestry between the New England and Midwest conservation units in New York, Ontario, and Quebec samples. Assignment of wintering individuals to genetically distinct breeding groups using RUBIAS indicated a clear east/west divide, suggesting a marginal level of migratory connectivity. California breeders winter in coastal Oregon and California to southern Baja. The west breeders also winter in the same area as California breeders, with the addition of wintering as far east as eastern Mexico and Texas. The researchers assigned birds wintering in California to three conservation units (West, Southwest and Central Valley, California; Figure 1B).

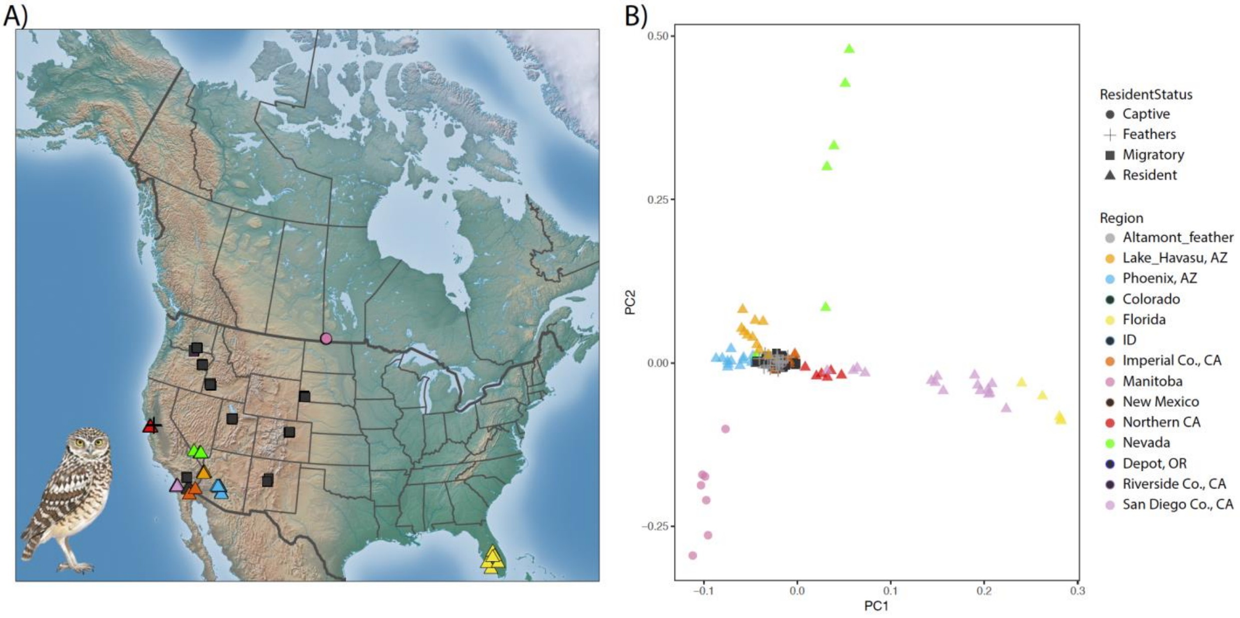
Wilson's Warbler

Ruegg et al. (2014b) identified six genetically distinct groups of Wilson's Warbler: Alaska to Alberta (purple), eastern North America (red), the Southern Rockies and Colorado Plateau (orange), the Pacific Northwest (green), Sierra Nevada (pink) and Coastal California (yellow, Figure 1C). Assignment of wintering individuals to genetically distinct breeding groups using RUBIAS indicates that Coastal California, Sierra Nevada, and Pacific Northwest breeders winter in western Mexico and southern Baja, and migrate north along the Pacific Flyway, with Coastal California and Sierra Nevada breeders found to the west of the Lower Colorado River (Ruegg et al. 2014b).

Burrowing Owl

The researchers discovered a novel genetic structure of burrowing owls, where population structure did not cluster on a spatial scale as with the other target taxa. Instead, they show that the Burrowing Owl's genetic structure is associated with migration strategy. For instance, all migratory Burrowing Owl populations, while widespread geographically, form one genetic cluster, while each resident population forms a unique genetic cluster (Figure 2). Substantial gene flow among migrant populations, contrasting with little gene flow between resident populations, would produce this pattern. Both migratory and residential breeding populations of burrowing owls can be found in California. Thus, distinguishing migratory and resident populations will be feasible; however, identifying between migratory populations is not.

Figure 2: Burrowing Owl Sampling Sites and Principle Component Analysis



A) Distribution and sampling strategy and B) principle component analysis of genomic variation within Burrowing Owls captive breeders (circle), migratory breeders (square), residential breeders (triangle), and feathers of migratory birds collected from Altamont, CA (cross).

Source: C. Bossu

Time Series of Migration Through the Pacific Flyway

To investigate the timing of migration along the Pacific Flyway, the researchers focused on species and California sites where a large number of migrating birds was sampled across the spring and fall migratory season. Therefore, this was feasible for only three of the target taxa: Wilson's Warbler, Common Yellowthroat, and American Kestrel.

Ruegg et al. (2014b) sampled 605 Wilson's Warblers at the Cibola, Arizona, site in the 2008 and 2009 migrating seasons. They assigned migrating birds to at least three conservation units; however assignment of Wilson's Warbler migrants collected in a time series from Cibola revealed a clear temporal shift in stopover site usage across the spring migratory period (Ruegg et al. 2014b; Figure A-5). They assigned early spring migrants to the southernmost conservation units, Coastal California and the Pacific Northwest, shifting to chiefly Alaska to Alberta migrants in late April. This time series also illustrated consistency between years; subsequent time series analyses of migrant birds combined sampling years and estimated the proportion of individual birds assigned to a conservation unit at weekly or bi-weekly intervals during the migrating seasons. The researchers collected an additional 63 Wilson's Warbler carcasses at the Ivanpah Solar Electric Generating System, 58 of which could be assigned with confidence to a specific conservation unit. Similar to the Cibola migrants, the majority of late April spring migrants at Ivanpah migrate through the Pacific Flyway to breeding grounds from Alaska to Alberta. While they sampled fewer birds during the fall migration, they found Pacific Northwest migrants migrate first, with the addition of Sierra Nevada birds in early September, followed by Alaska to Alberta breeding birds migrating later in the season. Further sampling of fall migrants is necessary to determine the robustness of this pattern.

To create a migration time table for Common Yellowthroat, researchers assigned 56 individual birds at Zuma Beach, California, and at nearby Malibu to two conservation units: California and the Pacific Northwest. Collections spanned March to May of the spring migrating season and August to October of the fall migration; however, researchers saw little evidence of population-specific turnover over time. During the spring migration, migrating birds are assigned to the California and Pacific Northwest conservation units consistently from March to mid-May. During the fall migrating season, the Pacific Northwest birds potentially migrate later in the season, mid-September, but much denser sampling is required to accurately determine the validity of this pattern.

The researchers did not detect any temporal shifts in migration in the third target taxa sampled. They collected 162 American Kestrel carcasses at Altamont Pass, and assigned 150 with certainty to the West conservation unit (with one individual mis-assigned to the East; Figure 1A).

Discussion

Assessing the potential impact of renewable energy development on California's bird populations has been hindered in the past by the inability to delineate conservation units below the species level. For this study researchers provided genoscape maps for four species of migratory birds that regularly use California for all or part of their annual cycle. They found with the new sequencing technologies, they were able to define conservation units in birds at finer spatial and temporal scales than previously possible. In order to understand the utility of their approach across a range of species, they focused on the following four taxa: American Kestrel, Common Yellowthroat, Burrowing Owl, and Wilson's Warbler. While completed genoscape maps for each of their target taxa demonstrated previously undefined genetic diversity, the ability of designed markers to resolve conservation units fell along a continuum, ranging from fine-scale delineation of unique breeding populations within California to little genetic structure across the range.

The researchers' approach yielded fine-scale resolution of conservation units for two of the four taxa, including the Common Yellowthroat and Wilson's Warbler. The delineation of conservation units within each species has varying implications for management of populations in California and depends upon both patterns of population declines specific to each genetically distinct conservation unit and the temporal scale upon which each conservation unit inhabits or traverses California throughout its annual cycle. Researchers outlined the results of their analysis for each species, as well as the implications for managing those avian populations in the face of increased renewable energy development.

American Kestrel

American Kestrels demonstrate little to no population structure in the West, with the exception of a distinct resident Texas conservation unit. Although it is one of the most common falcons in North America with a year-round distribution throughout much of the United States, American Kestrel populations have dropped by nearly half over the last 45 years (Smallwood and Bird 2002; Sauer et al. 2017). In the United States, declines are worst in the Northeast, where there are losses up to 88 percent in some areas (Hoffman and Collopy 1988). While the population-level impact of renewable energy development on American Kestrels has not been assessed, survey data indicate that it is one of the most commonly identified fatalities at solar- and wind-energy facilities in California (Kagan et al. 2014; WEST Inc. 2014). The researchers' data support the idea that while the impact of renewable energy on American Kestrels might result in hundreds of deaths (Kagan et al. 2014; WEST Inc. 2014), the impact is geographically diffused, spreading across the entire western conservation unit. As a result, kestrels may be more resilient to losses in any particular site within the west because of the potential for migration and exchange with other populations within the west conservation unit. For those kestrel populations experiencing significant declines such as California populations (Breeding Bird Survey [BBS] trend 1966 – 2015 = -1.81), translocation and release of birds from nearby populations (Scott and Carpenter 1987; Griffith et al. 1989) is a viable option. Therefore, in terms of management of declining populations with limited population structure, gene flow from a nearby migrant breeding population would contribute to potential recovery of localized declines or extirpations.

Common Yellowthroat

The researchers detected fine-resolution spatial structure and temporal structure of Common Yellowthroats in California, where some populations are showing marked declines and are thus particularly vulnerable to the impacts of renewable energy resources. The Central Valley of California constitutes a described conservation unit of Common Yellowthroat. While BBS survey data indicate a statewide population growth of 1.6 (Sauer et al. 2017), the Central Valley populations are among several in California that are listed as Species of Special Concern (Shuford and Gardali 2008) due to wetlands destruction and habitat alteration (Small 1994; Guzy and Ritchison 1999). They also detect a potential shift in timing during the fall migration in Southern California (Figure 1B), with the declining California conservation unit migrating through earlier than the stable Pacific Northwest conservation unit (Figure 1B; BBS Trend = 0.56). However, limited temporal sampling from mid-August to early October makes this conclusion tentative and requires further exploration. Overall, the combination of genetic and temporal structures, as well as demographic signatures, suggest that the California conservation unit is most vulnerable to the increasing development of renewable energy in California. Declines in populations in the Central Valley warrant further research to understand the evolutionary processes that maintain a distinct genetic cluster, what kind of impact renewable energy facilities may have on this population and whether mitigation early in the fall migration season could reduce the effects of renewable energy facilities on this conservation unit.

Wilson’s Warbler

The fine spatial structure and clear shift in timing of migration of Wilson’s Warblers can be combined with demographic profiles to create a strategy to mitigate population-specific effects of renewable energy facilities. Demographic signatures of Wilson’s Warbler Sierra Nevada conservation units illustrated that they have both the lowest population densities and the highest population decline (BBS Trend = -4.19, 95% CI = −5.90, −2.29; Sauer et al. 2017). On the other hand, the Coastal California breeders demonstrate one of the lowest population densities (Sauer et al. 2017), but show a mostly stable population trend (BBS trend = -0.06, 95% CI = −1.35, 1.27). The temporal shift in migration is specific to four Wilson’s Warbler conservation units that use the California corridor and have population-specific decline assessments. The Coastal California and Pacific Northwest breeders migrate earlier in spring (Ruegg et al. 2014b) and BBS trends indicate that they have markedly lower population declines (Coastal California (yellow) = -0.06, Northern Pacific Rainforest (green) = -1.72) compared with later and mid-season migrants (Northwest Interior Forest (purple) = -3.74, Sierra Nevada (pink) =. -4.19). While the spring migration time-series hints at a temporal shift of specific conservation unit migration (Figure 1C), data is limited and a survey of a greater number of migrants over the entirety of the fall migration period would help clarify this pattern. Overall, the most vulnerable Wilson’s Warbler conservation units are migrating through California later in the migrating season, suggesting Northwest Interior Forest and Sierra Nevada conservation units might require greater provisioning or safety during their migration periods.

Burrowing Owl

The Burrowing Owl, a broadly distributed species in western North America, shows no genetic structure between migrant breeding populations, but unique genetic structure of each year-round resident population. California is a breeding ground for both residential and migratory burrowing owls. BBS trend data suggest that Burrowing Owl populations are decreasing in California (1966-2015 trend = -1.79), with declines concentrated along the central and southern coast (DeSante et al. 1997, 2007) in areas undergoing rapid urbanization. It is considered a species of special concern in California (Shuford and Gardali 2008). An initial survey of genetic variation in resident and migratory populations in western North America suggests interbreeding is prevalent (Korfanta et al. 2005), which is confirmed with new genomic analyses (Barr, Bossu et al. in prep.). Given distinct genetic clustering of resident breeding populations of burrowing owls, they might be particularly vulnerable to renewable energy development compared with migrant populations. In order to interpret these results for management, one needs to consider what evolutionary processes are underlying the population structure in California. If genetic uniqueness is linked to a process that limits population resilience, such as inbreeding, which can lead to fitness effects that further reduce population size, multiple-mitigation strategies are possible. First, captive breeding using viable non-inbred individuals as breeders could maintain the genetic diversity and potentially reduce inbreeding, but if inbreeding effects are already prevalent in a population (such as disease susceptibility, infertility), immigration from an outbred population can increase depleted genetic diversity, improve population numbers, and reverse indications of inbreeding depression. This strategy has been successful with Florida panthers (Johnson et al. 2010). Ultimately, population declines of unique conservation units require further exploration into the evolutionary processes that underlie the genetic patterns of populations, and their isolation may make them vulnerable to greater threat by renewable energy facilities.

The resulting maps provide a solid framework for defining the spatial and temporal scales at which to manage California's migratory bird populations in the face of increasing renewable energy development. The researchers demonstrate that multiple conservation units across multiple species can be found breeding, wintering, and traversing California as a migratory corridor. These high-resolution genoscape maps across multiple species can also be used to assess population-level exposure of renewable energy development on migratory birds. In Chapter 3, the research team demonstrates how researchers can investigate which populations have been impacted by existing renewable energy facilities through the collection of the targeted species that have been killed at solar and wind farms in California. Assignment of those carcasses to specific breeding populations can be used to determine whether certain breeding populations are particularly impacted by renewable energy facilities. Secondly, they show how data on the timing of migration for specific populations can be used to help avoid conflicts with particularly vulnerable avian populations.

CHAPTER 3:
Population-Level Effects of Renewable Energy Development on Migratory Birds in California Assessed Using High-Resolution Genetic Markers

Introduction

Large-scale development and operation of renewable energy facilities, while representing a positive shift towards climate change mitigation, have also been linked to adverse effects on migratory birds (Strickland et al. 2011; Erickson et al. 2014). Determining the population-level effects of renewable energy development on bird populations has been difficult due to a lack of a reliable method for distinguishing populations at spatial scales that are similar to the scale of regional population declines.

In this chapter, the researchers applied the high-resolution genetic tagging method (described in Chapter 2) to identify population-specific exposure from renewable energy development on migratory birds in California; this method provides a significant advantage over previous tracking methods (Ruegg et al. 2014b). They illustrated this method on three species of birds with diverse life histories, including: Wilson's Warbler (*Cardellina pusilla*), American Kestrel (*Falco sparverius*), and Common Yellowthroat (*Geothlypis trichas*). Burrowing Owl (*Athene cunicularia*) was not included in this chapter because their migrant population did not present a spatial structure. The researchers began with previously created genoscape maps that define genetically based conservation units at regional spatial scales (Chapter 2, Ruegg et al. 2014b; Brinkmeyer et al. in prep., Bossu et al. in prep.). They then used genomic information contained within a single feather of a living bird or carcass collected away from the breeding location to identify the breeding population of origin. Feathers collected from carcasses could then provide essential links between where that bird was collected and which breeding population it came from. The researchers summarize the resulting information on population-specific effects of renewable energy development across all three species and discuss the implications of their results for management of migratory birds in California with respect to renewable energy facility development.

Methods

Sampling

To understand the population-level effects of renewable energy facilities on migratory birds, the researchers collaborated with the U.S. Fish and Wildlife Service in the Pacific Southwest Region (USFWS) and the U.S. Geological Survey's (USGS) Forest & Rangeland Ecosystem Science Center and sampled carcasses collected during routine surveys and incidentally at six solar and one wind facility (Figure 3; Table 1) in California.

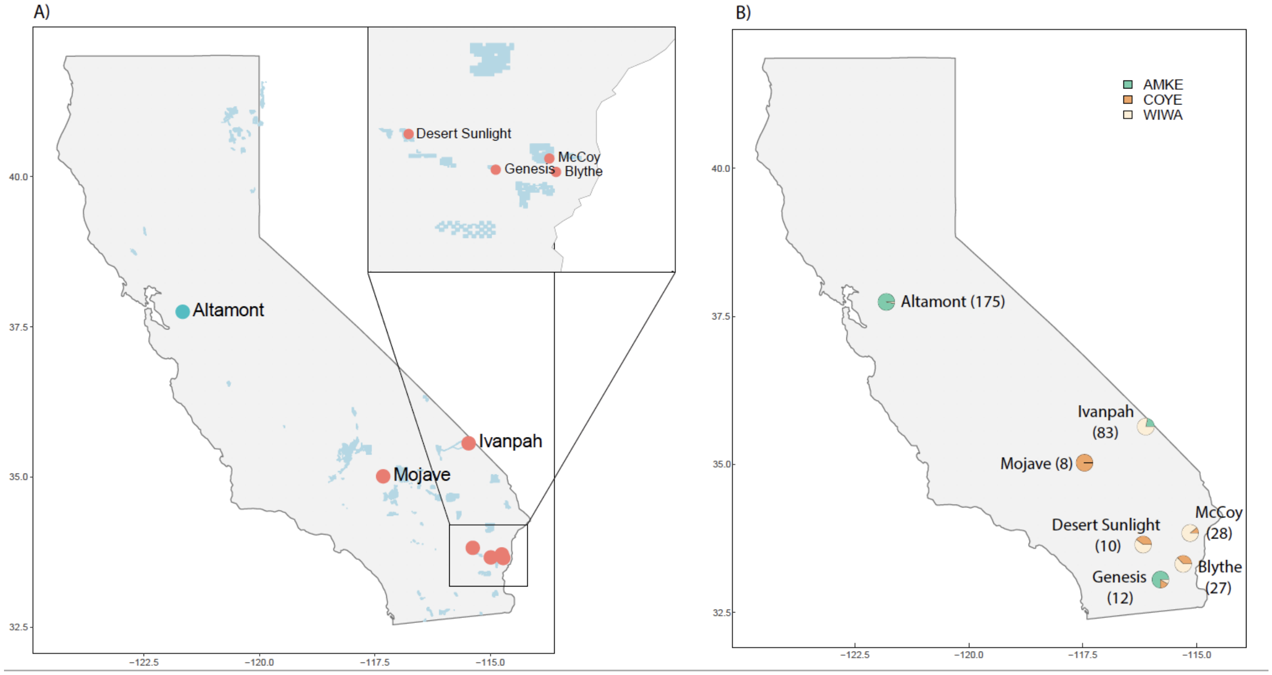
Table 1: Solar and Wind Facility Study Sites

Site	Type	State	County	Lati-tude	Long-itude	Total No. Target Taxa
Altamont Pass Wind Farm	Wind	CA	Alameda	37.75	-121.66	370
Blythe Mesa Solar Power Project	Solar PV	CA	Riverside	33.65	-114.72	27
Desert Sunlight Solar Farm	Solar PV	CA	Riverside	33.82	-115.38	10
Genesis Solar Energy Project	Solar Trough	CA	Riverside	33.66	-114.99	13
Ivanpah Solar Electric Generating System	Solar Power Tower	CA	San Bernardino	35.56	-115.47	83
McCoy Solar Energy Project	Solar PV	CA	Riverside	33.71	-114.75	28
Mojave Solar Project	Solar Trough	CA	San Bernardino	35.01	-117.32	8

Summary of solar facility and wind farms included in the study and the total number of target taxa carcasses collected at each facility.

Source: J. Rajbhandary

Figure 3: Map of Solar and Wind Facility Study Sites



A) Solar and wind facilities that collected bird carcasses (blue and red dots) as well as distribution of all renewable energy sites in California (blue polygons); and B) sample composition by three target taxa at each of the facilities. AMKE = American Kestrel, COYE = Common Yellowthroat, and WIWA = Wilson's Warbler.

Source: J. Rajbhandary

As a result of this collaborative effort they were able to collect more than 3,500 samples, birds, 539 of which were the three species referenced above, during the 3-year project (Table 2, Table A-5). Consulting firms identified carcasses to species, which were then temporarily stored in freezers on site. They then either shipped the carcasses to USGS or the University of California, Los Angeles (UCLA) for feather sampling, or had USFWS or UCLA staff sample them directly on site. Carcass quality varied significantly – some carcasses were intact, some were scavenged or singed to varying degrees and some only consisted of feathers (feather spots). From each carcass or bird remains, the researchers sampled a minimum of two feathers and transferred these to long-term storage envelopes with associated information about species, site, and collection date. In addition, they also sampled feathers from birds banded within 30 miles of seven additional facilities to get an idea of the populations that use flyways proximate to the facilities (Table 4, Figure 5). They eventually sent all feather samples to the Center for Tropical Research at UCLA and stored them in -20^{o}C freezers.

Table 2: Target Taxa Species Summary

	American Kestrel (AMKE)	Common Yellowthroat (COYE)	Wilson's Warbler (WIWA)	Total
Altamont	170 (162)		5(4)	370
Blythe		10 (4)	17 (15)	27
Desert Sunlight		4 (2)	6 (1)	10
Genesis	9 (4)		1 (0)	13
Ivanpah	18 (13)		65 (63)	83
McCoy		3 (1)	25 (17)	28
Mojave		8 (6)		8
Total	197	27	119	539

Priority taxa samples received and genotyped from solar facilities and wind farms. Numbers in parentheses reflect the number of birds genotyped successfully.

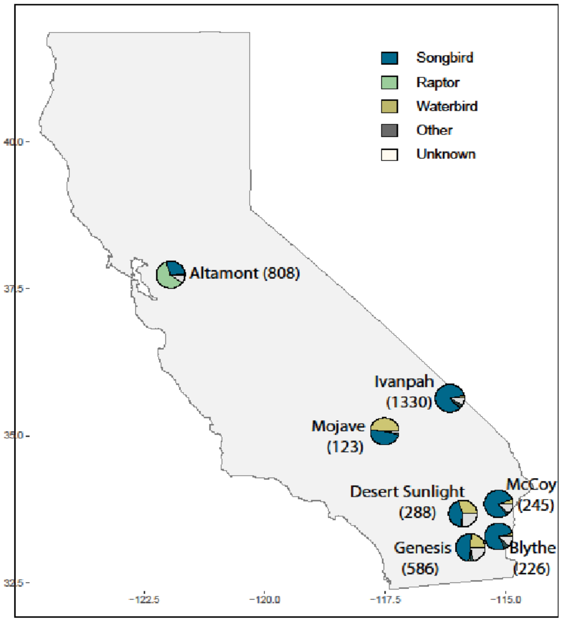
Source: J. Rajbhandary and C. Bossu

Table 3. Carcasses Sampled at Solar and Wind Facilities by Guild

Guild	Altamont	Blythe	Desert Sunlight	Genesis	Ivanpah	McCoy	Mojave
Waterbird	9	10	88	142	47	14	59
Songbird	241	176	122	285	1098	194	59
Raptor	478	0	0	12	20	0	0
Other	1	12	7	20	55	8	2
Unknown	79	28	71	127	102	29	3
Total	808	226	288	586	1322	245	123

Source: J. Rajbhandary and C. Bossu

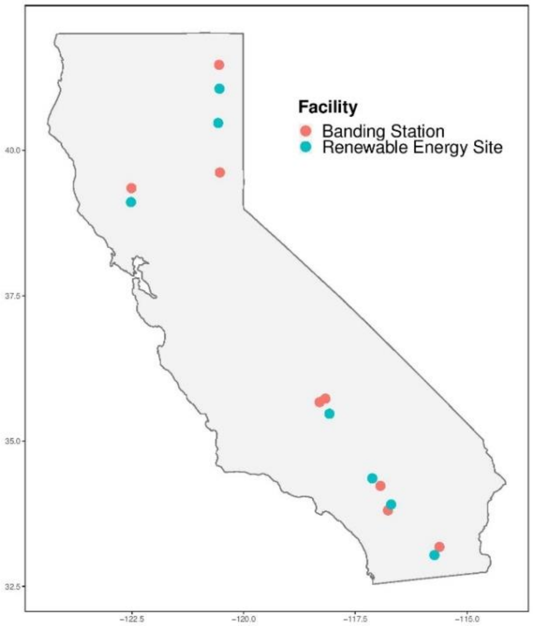
Figure 4. Sample Composition by Guild at Each Facility



Sample composition by guild at each of the facilities. Guilds were separated to songbirds, waterbirds and raptors; all others were identified as unknowns.

Source: J. Rajbhandary

Figure 5: Map of Study Sites and Banding Stations



Banding stations (red dots) within ~30 miles radius of solar/wind facilities (blue dots) where Wilson's Warbler (WIWA) and American Kestrel (AMKE) feathers were collected that the researchers genotyped to look at the populations that use flyways in close proximity to renewable facilities.

Source: J. Rajbhandary

Table 4: WIWA and AMKE Samples from Banding Stations

Near town	Near facility	Number of WIWA samples	Number of AMKE samples
Sierra City	Horizon Wind Energy	16 (16)	0
Big Bear Lake	Airtricity Wind Energy	13 (13)	0
Alturas	Padoma Wind Energy	5 (5)	0
East Park Reservoir	Alta-Gas Wind Energy	3 (3)	0
Idyllwild	FPL Solar Energy	1 (1)	0
Kern	Tehachapi Wind Energy	1 (1)	0
Onyx	Tehachapi Wind Energy	6 (6)	0
Calipatria	Sunpeak Solar Energy	13 (13)	13 (13)

Wilson's Warbler (WIWA) and American Kestrel (AMKE) feathers collected at banding stations within ~30 miles radius solar/wind facilities that the researchers genotyped to look at the populations that use flyways in close proximity to renewable facilities. Numbers in parentheses reflect the number of birds genotyped successfully.

Source: J. Rajbhandary and C. Bossu

DNA Isolation and SNP Genotyping

The researchers extracted and genotyped DNA from carcasses of the three target taxa, as outlined in Chapter 2 of this report.

Baseline Reporting Groups and Accuracy of Assignment

Researchers identified conservation units and evaluated the accuracy of individual assignments, as outlined in Chapter 2.

Assignment of Unknown Individuals Found at Solar Facilities

Individuals of unknown origin from the target taxa were collected from renewable energy locations (Tables A-3 through A-5) and assigned to conservation units defined in the completed genoscape using RUBIAS (Anderson and Moran 2017). While researchers knew the species identification of the bird carcasses collected at solar and wind facilities and birds banded near renewable energy facilities, they did not know the conservation unit the solar birds would be assigned to; therefore, they initially grouped them by mixture collection (the locations where the fatality or collection occurred), and treated them as a separate group to get its own mixing proportion estimate. The proportion of certain assignments (individuals with a posterior probability > 0.8 of being assigned to a genetic reporting group) at each renewable energy collection site were reported.

Results

Sampling

Through the researchers' collaboration with the USFWS and USGS, feather samples were collected from more than 3,500 carcasses at one wind and six solar facilities in California. The proportion of target taxa they received from each facility varied widely. American Kestrel made up a significant proportion of carcasses collected at Altamont (21 percent). On the other hand, the remaining facilities mainly collected non-targeted taxa. Altamont, Blythe, Desert Sunlight, Ivanpah, and McCoy collected two of the four target taxa; Genesis collected all four; and McCoy collected only one of the target taxa.

SNP Genotyping

The researchers genotyped DNA samples from the carcasses of three of the target taxa (197 American Kestrels, 27 Common Yellowthroats and 119 Wilson's Warblers) using the markers developed to assign individual birds to conservation units (Table 2). American Kestrel had a high genotyping success rate, with 90.8 percent of individuals successfully genotyped, followed by Wilson's Warbler (84.0 percent) and Common Yellowthroat (55.6 percent).

Baseline Reporting Groups and Accuracy of Assignment

The researchers defined baseline reporting groups from previously generated genoscapes for each target taxa described in Chapter 2.

American Kestrel

The researchers assessed American Kestrels of known origins for assignment accuracy in two sets – one with 597 individuals that were included in the design assay and one with 400 individuals that were not included in the design assay (Table A-7). They assigned all individuals to one of five genetically distinct reporting groups (Alaska, East, Florida, Texas, and West) with moderate accuracy in RUBIAS. The proportion of correct assignments for the first set of samples ranged from 71 percent (Alaska) to 92 percent (Texas). Breeding birds from Alaska were erroneously assigned to West 24 percent of the time and 5 percent of the time to the Texas conservation unit; birds from Florida were erroneously assigned to the East group 23 percent of the time.

The self-assessment of American Kestrel breeding individuals from the second set that removed the training bias had a lower accuracy of assignment, especially for Alaska. Of the six additional breeding birds collected from Alaska that were not used to design the target variants, the proportion of assignment to Alaska was only 17 percent; birds from Alaska were more likely to be erroneously assigned to the West (86 percent). Breeding kestrels from Florida showed 50 percent assignment to Florida and 50 percent erroneous assignment to the East. Assignment to the East and West showed higher accuracy with 88 percent and 91 percent correct assignments, respectively. There was only one additional individual SNP genotyped collected in Texas, so it was not included in this analysis. Birds from East, Texas and West showed greater than 0.80 posterior probability of assignment to the correct conservation unit.

Common Yellowthroat

Cross validation assignment of Common Yellowthroats indicated the ability to correctly assign individuals to five genetically distinct conservation units was high, ranging from 80.4 percent

(Midwest) to 96.7 percent (West conservation unit; Table A-8). The greatest number of incorrect assignments was between the Midwest and New England conservation units, and therefore does not impact assignment of solar birds in California.

Wilson’s Warbler

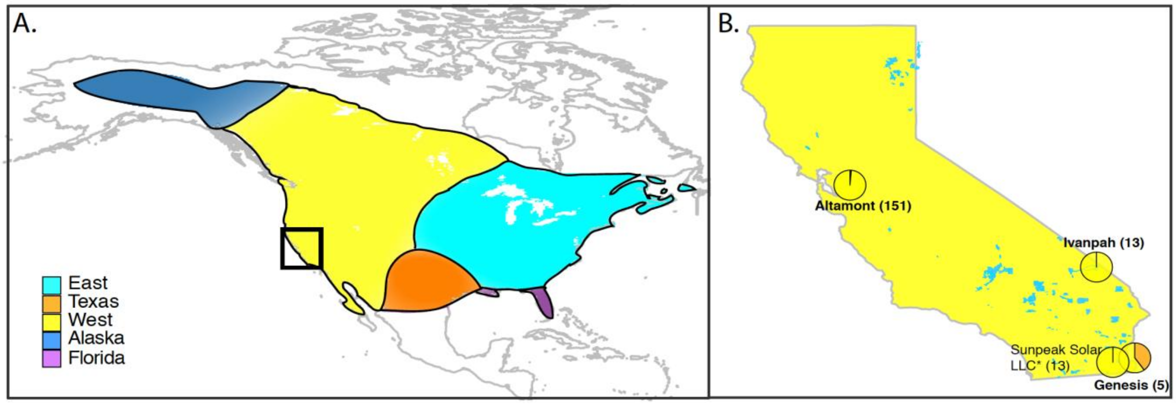
Cross validation assignment of Wilson’s Warbler indicated that the ability to correctly assign individuals to six genetically distinct reporting groups was high, ranging from 80 percent (California Coastal) to 100 percent (Eastern conservation unit; Ruegg et al. 2014b). The majority of incorrect assignments were between the California Coastal, Sierra, and Pacific Northwest groups.

Assignment of Carcasses of Unknown Populations From Solar Facilities

American Kestrel

Researchers assigned the majority of the American Kestrel carcasses collected at the wind and solar facilities to the West conservation unit, followed by Texas (Figure 6). They assigned all of the carcasses at Ivanpah and almost all at Altamont to the West, and carcasses at Genesis to either Texas or West conservation units. Altamont also had a significantly higher number of carcasses assigned with certainty to specific conservation units (n=151) compared to Ivanpah (n=13) and Genesis (5).

Figure 6: American Kestrel Assignments to Populations



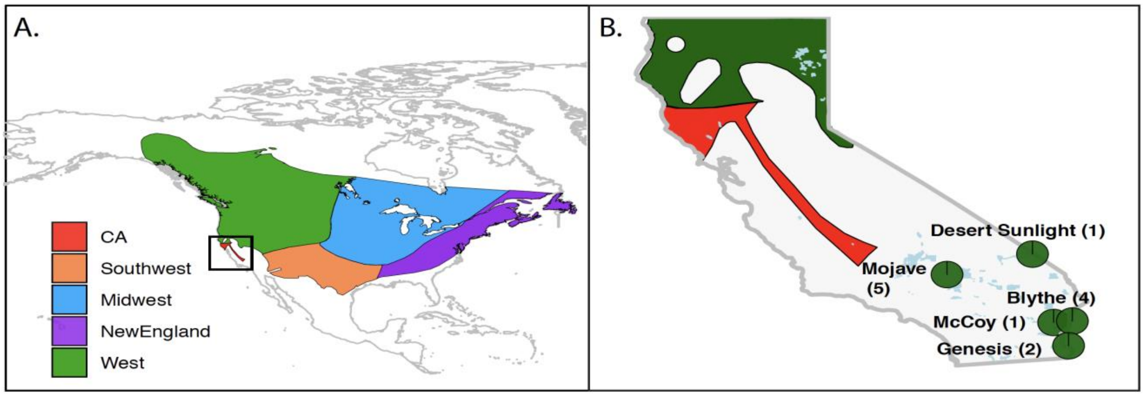
American kestrel genoscape (A) and population-specific assignment of American Kestrel carcasses collected at renewable energy facilities (bold) and birds collected near renewable energy facilities.

Source: C. Bossu

Common Yellowthroat

Researchers assigned all of the Common Yellowthroat carcasses collected at five wind and solar facilities to the West conservation unit (Figure 7). Mojave had the highest number of Common Yellowthroat carcasses assigned with certainty to the West conservation unit (n=5), followed by Blythe (n=4), Genesis (n=2) and one carcass collected at Desert Sunlight and McCoy each.

Figure 7: Common Yellowthroat Assignments to Populations



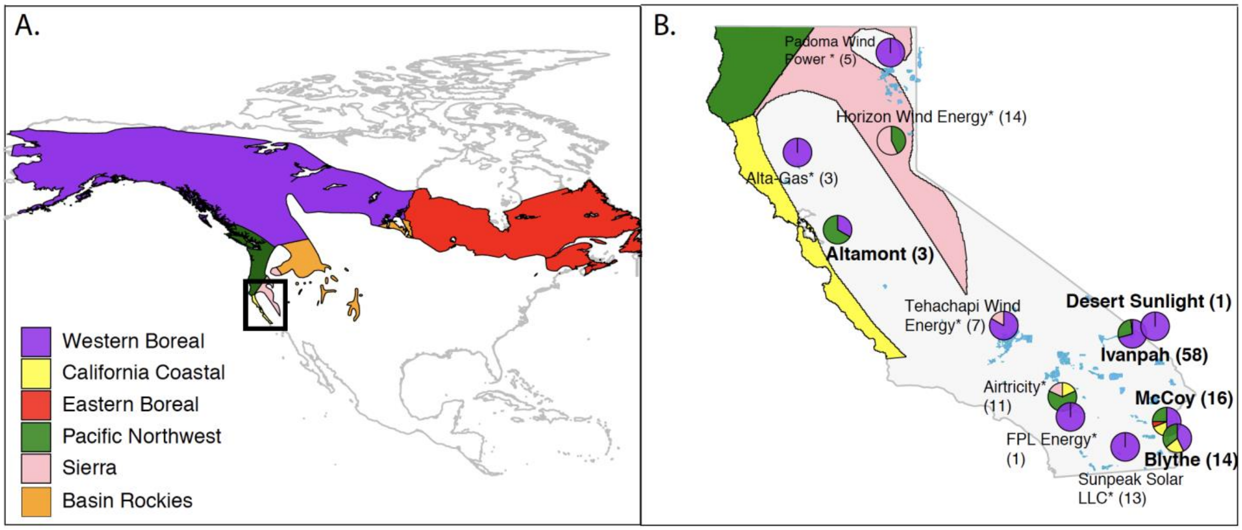
Common Yellowthroat genoscape (A) and population-specific assignment of Common Yellowthroat carcasses collected at renewable energy sites in California (B).

Source: C. Bossu

Wilson's Warbler

The researchers assigned the majority of Wilson's Warbler individuals collected at renewable energy sites in California to the Western Boreal population; however, they also found carcasses of individual birds from two of the smaller populations, California Coastal and California Sierra, at some of these facilities (Figure 8).

Figure 8: Wilson's Warbler Assignments to Populations



Wilson's warbler genoscape (A) and assignment of Wilson's Warbler individuals collected at renewable energy sites in California to genetically distinct breeding populations (B). * reference birds collected near solar sites, but are not fatalities, bold are carcasses collected at renewable energy facilities.

Source: C. Bossu

While most facilities had carcasses assigned to only one (Desert Sunlight) or two (Altamont and Ivanpah) conservation units, McCoy and Blythe had carcasses assigned to at least three conservation units. In addition to genotyping carcasses found at the wind and solar sites involved in this study, the researchers also genotyped feather samples collected at migratory bird-banding stations located near a wind or solar facility (Table 4). These additional sites show a similar pattern, with most individuals assigned to the Western Boreal population (Padoma Wind Power, Alta-Gas, Tehachapi Wind Energy, FPL Energy and Sunpeak Solar LLC).

They assigned Wilson’s Warblers caught at stations near the Horizontal Wind Energy and Tehapachi Wind Energy to two units, and those banded near Airtricity to either Pacific Northwest, California Sierra, or California Coastal.

Discussion

Using previously constructed genoscape maps (Ruegg et al. 2014b; Brinkmeyer et al. in prep.), researchers successfully assigned bird carcasses collected at solar and wind facilities to genetically distinct conservation units and identify population-specific effects. They discuss the efficacy of their methods for assigning birds to genetically distinct conservation units and the utility of those results for managing migratory birds in California in the face of increasing solar and wind development.

Efficacy of High-Resolution Markers for Genotyping Samples From Carcasses

The efficacy of the researchers’ markers for assigning carcasses collected from solar and wind facilities across California varied with the number and resolution of conservation units associated with each species. American Kestrel required a greater number of variants in order to assign individuals to populations due to lower genome-wide differentiation between conservation units. For instance, using 186 genetic variants, the researchers were able to identify five conservation units within American Kestrels. While they identified two of these units to the west (West and Alaska; F_{ST} = 0.023-0.033), the major split within the species was between eastern and western conservation units. Future research will reveal the extent to which increasing the total number of higher resolution markers used (>192) could improve their ability to assign carcasses to conservation units with greater resolution.

On the other end of the spectrum, they were able to assign both Wilson’s Warblers and Common Yellowthroats to conservation units using 96 genetic markers because patterns of population structure were strong. In Wilson’s Warblers they define six conservation units, four of which are found in the western region, with pairwise F_{ST} at outlier loci (a measure of the extent of population structure, with 1 = complete differentiation and 0 = panmixia) between the conservation units ranging from 0 to 0.68 (Ruegg et al. 2014b). In general, they observed the strongest genetic differentiation between eastern and western groups (outlier F_{ST} = 0.41–0.68) with strong genetic differentiation also seen between the Southern Rockies and Colorado Plateau and all other groups (outlier F_{ST} = 0.09–0.27; Ruegg et al*.* 2014b). Similarly, in Common Yellowthroat, they define five conservation units, with pairwise F_{ST} of outlier loci between breeding populations of the conservation units ranging from 0 to 0.83. Again, they observed the strongest genetic differentiation between eastern and westerns groups (outlier F_{ST} = 0.23-0.83), but they also show strong differentiation between the three conservation units found in western United States (outlier F_{ST} ranging from 0.13-0.66).

Utility of Feathers for Population Assignment

The ability to assign carcasses to conservation units using the researchers’ approach also varied with the species-specific technical details associated with extracting DNA from feathers. Using the markers developed, they successfully genotyped 90.8 percent of American Kestrel carcasses, 55.6 percent of Common Yellowthroats, and 84.0 percent of Wilson’s Warblers (Table 2). For all three species, they cut one calamus from a single feather to extract DNA. The larger American Kestrel feathers yielded almost twice the amount of DNA as the smaller Wilson’s warbler feathers (average DNA = 5.67ng/ul for American Kestrel versus 2.67ng/ul for

Wilson's Warbler), which could attribute to the higher genotyping success rate for kestrel carcasses. In general, the genotyping success rate across both taxa was lower than that of fresh feather DNA: American Kestrel samples from fresh feather extractions had a 93.6 percent success rate (Brinkmeyer et al. in prep.); and Wilson's warbler samples had a 96 percent success rate (Ruegg et al. 2014b). Hogan et al. (2008) found that DNA amplification success was significantly influenced by the quality of feathers, which explains the lower genotyping success rate for feathers from carcasses relative to feathers from live birds as carcass feathers are inherently of lower quality than fresh feathers.

Carcass Collection and Proportion of Species Found at Each Facility

Through the researchers' collaborative effort with USFWS and USGS, they sampled feathers from more than 3,500 carcasses collected at seven renewable facilities in California (Table A-6). Of these, they identified a little more than 3,000 carcasses, representing a broad range of species and guilds (Table 2, 3). Their three target taxa as well as the different guilds were found in varying proportions at each of the facilities (Figure 3B, 4). The biggest difference to note between solar and wind facilities is the significantly higher presence of raptors in the wind farm (Altamont). A survey conducted in 2000 at the Altamont Pass Wind Resource Area in Alameda and Contra Costa counties found that 65 percent of all dead birds found on site were raptors (Orloff and Flannery, 1992). Similarly, there is consensus that raptors are more vulnerable to collision with wind turbines than other bird groups (NWCC 2000). Studies attribute such trends to the lower displacement and avoidance by raptors to the presence of wind-energy facilities (Band et al. 2005). Orloff and Flannery (1992) also suggest that raptors keep their eyes fixed on prey while hunting, rather than being vigilant for flight hazards, which renders them more susceptible to collisions with wind turbines. While the researchers' study seems to conform to this pattern of higher raptor susceptibility to injury or death from wind farms, it is crucial to note that their collection method does not address differences in sampling efforts at each facility. Further research and analyses are needed to successfully compare the effect of wind facilities on raptors versus other bird groups.

While raptors make up the majority of carcasses found at Altamont Pass wind farms, passerine carcasses were more numerous at all of the solar facilities. One reason for this could be due to the higher number of insects attracted to the light reflected from solar projects (Horvath et al. 2009), which in turn could attract insect-foraging birds. Two such species, Yellow Warbler and the Yellow-rumped Warbler, seem to be particularly affected at the Ivanpah Solar Electric Generating System, which also had the most passerine carcasses in total. Another explanation for this could be the differences in post-construction avian mortality monitoring in wind versus solar facilities. Post-construction avian mortality monitoring at wind-energy facilities has traditionally focused strictly on wind turbines whereas monitoring at solar facilities also includes generator tie-in lines (gen-tie lines) that transmit electricity generated at a solar facility to the nearest substation. Gen-tie lines can range in length from 1 km to more than 15 km, and the project monitors around 50 percent of the gen-tie length. Wind projects have gen-tie lines too, but the project is not required to monitor this facility component. Within solar projects, USFWS staff has also observed a higher proportion of water-associated bird fatalities at solar PV arrays (i.e., panels) and a higher proportion of passerine fatalities at gen-tie lines. One hypothesis regarding mortalities of birds and particularly water-dependent species at solar PV projects is the idea that these birds may be attracted to or confused by the visual signature of solar panels (such as mistaking them for water features) which could lead to collision or other harms (for example strandings). This "lake effect" hypothesis is defined as the effect that migrating waterbirds flying across the desert perceive the reflective solar panels as water bodies and in an attempt to land, collide with panels and other project structures (Kagan et al. 2014). Researchers found water-associated bird carcasses in higher numbers at Desert Sunlight and Genesis, which use continuous long panels that may better mimic lakes (Kagan et al. 2014). Mirrors at Ivanpah are individual 4 x 8′ panels that look more speckled and may not have as much of the "lake effect." Again, while the numbers in their study reflect findings in similar reports (Kagan et al. 2014; Horvath et al. 2009), the causes of bird collisions with solar panels and bird mortalities in general at solar projects is presently under study.

Population-Specific Exposure by Species Relative to Trends and Abundance

Overall, the development of high-resolution genetic tags for each species allowed researchers to assess the population-specific effects of renewable energy on migratory birds in California with greater resolution than any method previously employed. In general, the majority of individual birds exposed to renewable energy development were from the largest conservation units within each species, while carcasses from rare and declining populations made up a smaller percentage of the total number of birds sampled. Researchers outline the species and population specific impacts relative to population density and trend estimates from the BBS in the following section. They recognize that regional BBS trend estimates are not always accurate and look forward to future work that can integrate more precise estimates of population decline and survival within each conservation unit with their data on the population-level impacts of renewable energy development in California.

American Kestrel

Researchers assigned American Kestrel carcasses from this study to two of five conservation units previously identified by Brinkmeyer et al. (in prep.). The one carcass at Altamont assigned to the East conservation unit may be explained by the 0.09 posterior probability of breeding birds from the West being mistakenly assigned to the East (Table A-9). Excluding this sample, researchers assigned all of the carcasses from Altamont and Ivanpah, and the majority from Genesis to the West conservation unit (N West = 177; Figure 6; Table A-9), which covers the largest geographic area of any kestrel conservation unit, spanning from the West Coast to the Midwestern United States and Canada. While BBS data suggest that breeders in this region vary in population density and may be declining overall (BBS Trend = -1.22, 95% CI = −1.60, −0.84; Sauer et al. 2017), the population-level impacts for birds in the West conservation unit would be dispersed across a very large geographic area. In contrast, the Texas conservation unit shows a more stable population trend (BBS Trend = 0.12, 95 percent CI = −3.23, 3.64), but the BBS relative-abundance map illustrates how sparsely distributed this population is (Sauer et al. 2017). The low number of carcasses identified as belonging to the Texas conservation unit (N Texas = 2; Table A-5) could be due to biases in the geography of the renewable energy facilities included in this study. American Kestrels found at renewable energy sites in or near Texas may show more significant impacts to the Texas conservation unit.

Common Yellowthroat

Common Yellowthroat carcasses found and genotyped at renewable facilities in this study were fewer than the other target species examined here. Researchers assigned all carcasses to the West conservation unit (Figure 7, Table A-10), where BBS estimates show a slight increasing trend (average BBS Trend = 0.43) but the density map suggests a relatively low abundance (Sauer et al. 2017). Population increases in concert with low abundances in these specific conservation units suggest that renewable energy facilities may have only a moderate impact on these species.

Wilson’s Warbler

The researchers assigned the majority of Wilson’s Warbler carcasses as well as Wilson’s Warblers banded near solar or wind facilities to the Western Boreal conservation unit (Figure 8, Table A-11). This unit covers the largest geographic area of any other conservation unit for this species and has relatively high estimated population densities across the range (BBS Summer Distribution Map 2011-2015; Sauer et al. 2017). According to 2005-2015 Breeding Bird Survey (BBS) trend estimates (Sauer et al. 2017), as well as the Birds of North America account for Wilson’s Warbler (2018), populations in the Western Boreal conservation unit are also increasing. The second and third most common assignments of carcasses and birds passing near renewable energy facilities were to the Pacific Northwest and Sierra conservation units. Although Pacific Northwest breeders have the highest population density across the range (Sauer et al. 2017), BBS survey data indicate that populations in this region are declining (BBS Trend = -1.72, 95 percent CI = −2.31, −1.14). In addition, while the researchers didn’t assign any carcasses to the Sierra conservation unit, they did identify a significant number of birds from this region near the Tehachapi wind area. Populations within the Sierra conservation unit have both the lowest population densities and the most significant population declines according to BBS data (BBS Trend = -4.19, 95 percent CI = −5.90, −2.29; Sauer et al. 2017). Lastly, researchers found carcasses assigned to the Coastal California conservation unit at two solar facilities (Blythe and McCoy) and identified live birds near one facility (Aitricity). While the total number of birds identified from the Coastal California conservation unit was smaller than for any other unit, the geographic area covered by this unit is the smallest, population densities are some of the lowest (Sauer et al. 2017), and population trends are slightly decreasing (BBS Trend = -0.06, 95 percent CI = −1.35, 1.27). In summary, while the researchers assigned fewer overall Wilson’s Warblers to the Pacific Northwest, Sierra and Coastal California conservation units, the overall smaller geographic region encompassed by these three conservation units, combined with variable estimates of population densities and signatures of population decline, suggest that the population-level effects of any one avian casualty may be greater than for birds from these areas than for the larger Western Boreal conservation unit.

CHAPTER 4: Migratory Hotspots to Inform Siting of Renewable Energy

Introduction

While an understanding of each species' migratory patterns is a valuable asset in determining whether particular avian populations or regions may be vulnerable to negative effects from renewable energy facilities at particular times of the year, it is vital to include data on multiple species across regions of California to ensure that final assessments of solar impacts are as encompassing as possible. To this end, modeling occurrence (Fink et al. 2010) or abundance (Johnston et al. 2015; Tanner et al. 2017) for individual species and combining estimates across groups or guilds can provide reliable estimates of locations important for multiple species that represent a wide variety of niches (Loman et al. 2017). These abundance estimates can also provide an understanding of temporal nuances concerning species' habitat use that might be overlooked using species distribution models alone, which often provide only static representations of a species' habitat preference. Including abundance measurements are often unrealistic, however, given the difficulty of amassing the volumes of data required to produce reliable estimates. Fortunately, the researchers were able to harness the power of a massive community science database accumulated through eBird (Sullivan et al. 2014) to estimate abundance for individual species, as well as for groups of species, and to overlay these with estimates of solar potential, to understand how each can effectively influence facility siting. The goal of this task, therefore, was to determine which possible siting regions minimize wildlife impact across multiple species while simultaneously maximizing energy potential. The researchers' results could support the planning of future renewable energy facility development.

Methods

Solar Potential Across the Study Region

To calculate overall solar potential at the county scale, the researchers downloaded the National Renewable Energy Laboratory (NREL) solar potential model from Data Basin. The NREL data set indicates the number of pixels per county that are potentially suitable for solar-energy installations due to characteristics such as total solar radiation on available lands (those not excluded from development by law or policy). The files from Data Basin were at the 10 km scale. They processed the Data Basin GIS layers by summing the solar potential in each county using the Zonal Statistics function in ArcGIS. They added up the number of suitable pixels per county, and classified the 58 counties of California into five quintiles of solar potential based on total solar potential range among the 58 counties: lowest 0-20th percentile, 20-40th, 40-60th, 60-80th, and highest 80-100th.

Multi-Species Analysis

Using data from eBird (Sullivan et al. 2014), the researchers tallied the abundance of migratory birds for the following target species: American Kestrel (*Falco sparverius*), Burrowing Owl (*Athene cunicularia*), Common Yellowthroat (*Geothlypis trichas*), Wilson's

Warbler (*Cardellina pusilla*), Common Loon (*Gavia immer*), Painted Bunting (*Passerina ciris*), Western Grebe (*Aechmophorus occidentalis*), Swainson's Thrush (*Catharus ustulatus*) and Yellow Warbler (*Setophaga petechia*). They selected these nine species (four of which are part of this report in Chapter 2 and the other five are part of the larger Bird Genoscape project) because they are the subjects of ongoing genomic analyses that characterize population structures across the migratory cycle. These nine species were selected in consultation with the Energy Commission and the TAC, as outlined in Chapter 1. Given the bias that occurs from variations in observer abundance, location, and skill/experience, particularly in community science datasets (Dickinson et al. 2010; Kelling et al. 2015), the researchers corrected all abundance models for potential bias using the method described in the following Guild Analysis section.

For each of these nine species, researchers consulted the Birds of North America volumes to determine the timing of migratory periods. They excluded eBird records outside the migratory period for each species from the analysis. They also filtered the data to exclude records before 2000.

Guild Analysis

In addition to analyzing the target species, the researchers tallied the abundance of migratory bird hotspots for three avian guilds: raptors, waterfowl, and songbirds (Tables A-12 through A-14). The analysis combined data acquired from eBird (Figure 11), and identified species belonging to each guild by consulting California Department of Fish and Wildlife bird checklists. They adjusted tallies to correct for sampling effort by regressing out the number of observers per county, as noted in the following discussion.

The TAC, with members from government, industry, and non-profits with broad expertise in avian migration and avian interactions with renewable energy facilities, requested that researchers tally the abundance of different avian guilds using the eBird data set. To follow up on this, researchers downloaded eBird abundance data for raptors, waterfowl, and songbirds (Tables A-12 through A-14) and they added up the total number of birds in each guild in each California county. In addition, the TAC pointed out that the detection rate of observations of birds in the eBird data set would be artificially higher in counties with higher human population densities since that sampling effort is correlated to the number of observers conducting the sampling (in this case, more citizens equal more citizen-science observations). In light of this fact, the TAC suggested that researchers adjust the total number of birds in each county to account for human population density. To address this, they adjusted the total abundance from eBird for each guild as follows. For each guild, they constructed a data set with 58 data points, each representing one county in California. For each county, they added up the number of birds in the guild, according to eBird. They also compiled the human population density (density here is represented by number of people per 30 second cell, approximately 1 km^2), according to the 2016 LandScan data set. (For details on the LandScan methodology, see Dobson et al. 2000.) They then fit a linear regression to the 58 points in which the independent variable was the average density of humans for that county and the dependent variable was the total number of birds in the guild according to eBird. They used the results of the regression to remove the effects of human population density on the eBird abundance counts. They classified these sampling-effort corrected abundances into five quintiles of abundance for the target species: lowest (0-86 observations) to highest (511 to 1138 observations).

Migration Hotspot Maps and Least-Cost Analysis

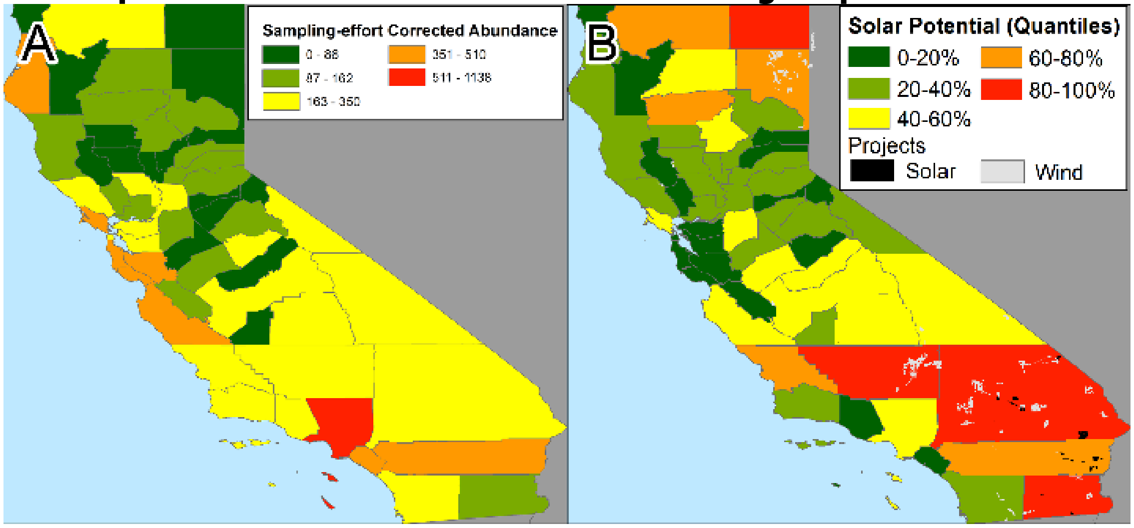
The researchers overlaid GIS layers to create a spatial map of potential wild bird exposure to renewable energy facilities. These overlaid maps were then used to prioritize areas that represent the least-cost conservation option for these species; in other words, they identified regions that would simultaneously minimize wild bird exposure and maximize energy-production potential, which essentially represents high- renewable energy-potential, low-risk-to-wildlife counties. In conjunction with this analysis, researchers also identified counties that were most likely to have conflicts between industry and conservation (that is, those counties with both high renewable energy potential as well as high risk to wildlife).

Results

Target Species Analysis

The researchers combined abundance estimates for the nine target species (listed in the prior Methods section) and compared those estimates with those of solar potential from the same study area (Figure 9).

Figure 9: Spatial Pattern of Solar Potential and Target Species of this Analysis

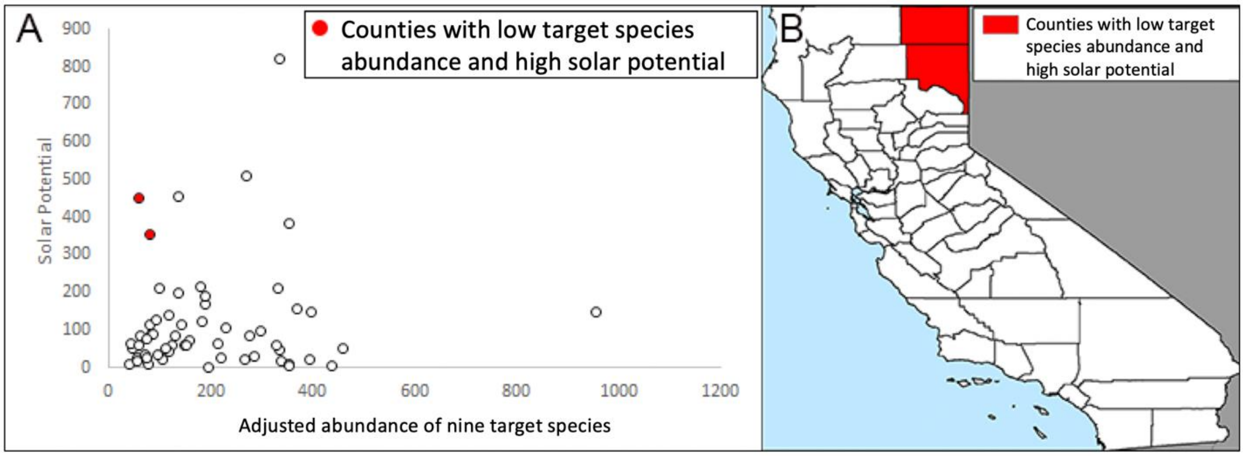


A) Abundance of nine target species according to eBird after correcting for average human population density in each county; (B) Solar potential. Potential was estimated production per 10 km grid square from the NREL Renewable Portfolio Standards (RPS) calculator. The analysis excluded Renewable Energy Transmission Initiative (RETI) Category 1: development prohibited. The researchers downloaded the data from Data Basin and calculated total potential per county using the Zonal Statistics tool in ArcGIS 10.3.1. Projects are applications submitted to BLM as of 2015 according to Data Basin. There was no relationship between abundance and solar potential in the analysis of all counties (r=0.09, p=0.52). However, there were particular counties that had high solar potential and low migratory bird abundance.

Source: (A) from UCLA; (B) modified from raw Data Basin data

By combining these results and overlaying them on the same map (Figure 10), particular regions can be identified that would be optimal for solar siting from a migratory bird perspective. For instance, the counties with the lowest abundance of the target species and highest solar potential were Lassen and Modoc, which are located in the Modoc Ecological Region in Northeastern California.

Figure 10: Least-Cost Counties for Nine Target Species



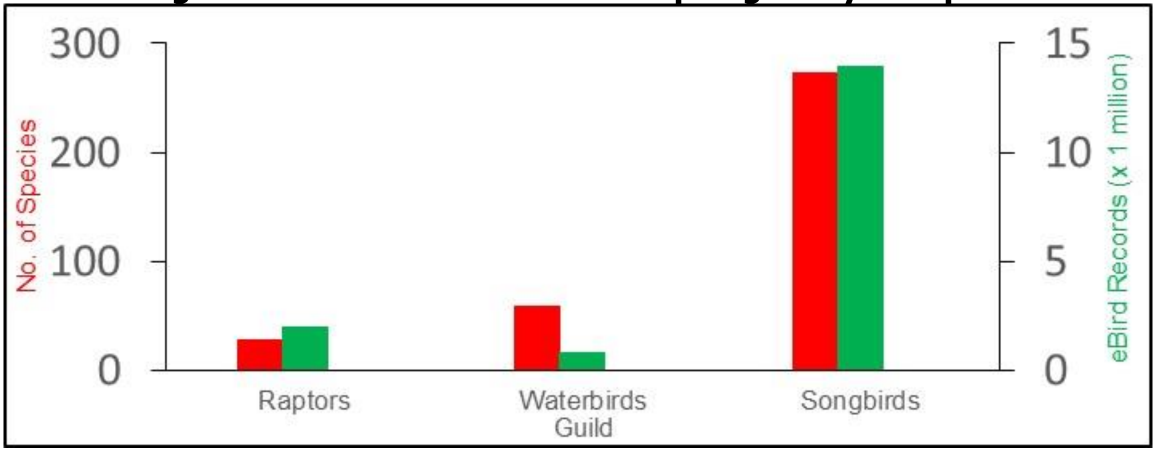
A) Scatterplot of adjusted abundance vs. solar potential indicating counties with low abundance of the target species and high solar potential. Potential was estimated production per 10 km grid square from the NREL Renewable Portfolio Standards (RPS) calculator. Low abundance was defined as the first quantile (of 5), or bottom 20% of the 58-county data set. High potential was defined as the top quantile (of 5), or 20% of the data. (B) Map of high potential, low abundance counties: Lassen and Modoc.

Source: T. Fuller

Guild Analysis

The researchers tallied the abundance of migratory bird hotspots for three avian guilds: raptors, waterfowl, and songbirds, then applied the same type of comparative analyses between these guilds and estimates of solar potential across the study region. The analysis combined data acquired from eBird (Figure 11), and full lists of species represented by each guild are provided in Tables A-12 through A-14.

Figure 11: eBird Data Used to Map Migratory Hotspots



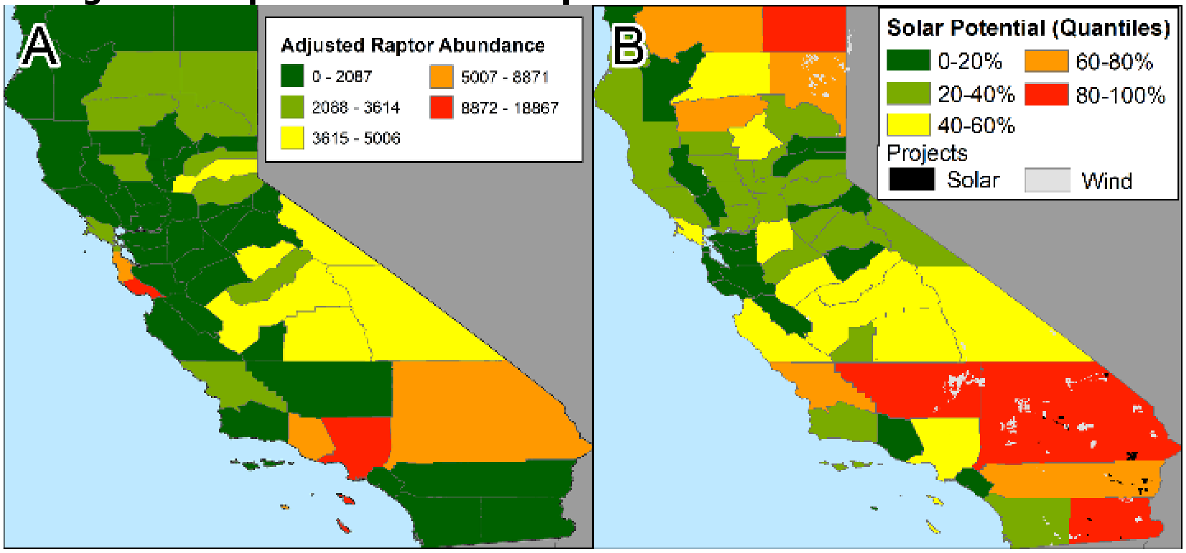
Red columns indicate the number of species that were included in each group (Raptors, Waterbirds, and Songbirds). For a full list of species included in each group, see Tables A-12 through A-14. Green columns indicate total number of unique eBird records that contributed to each group.

Source: eBird

Raptors

After adjusting for human population density, the counties with highest solar potential and lowest abundance of raptors were Lassen and Modoc (Figures 12 and 13), which were also the highest solar potential/lowest abundance for the nine target species.

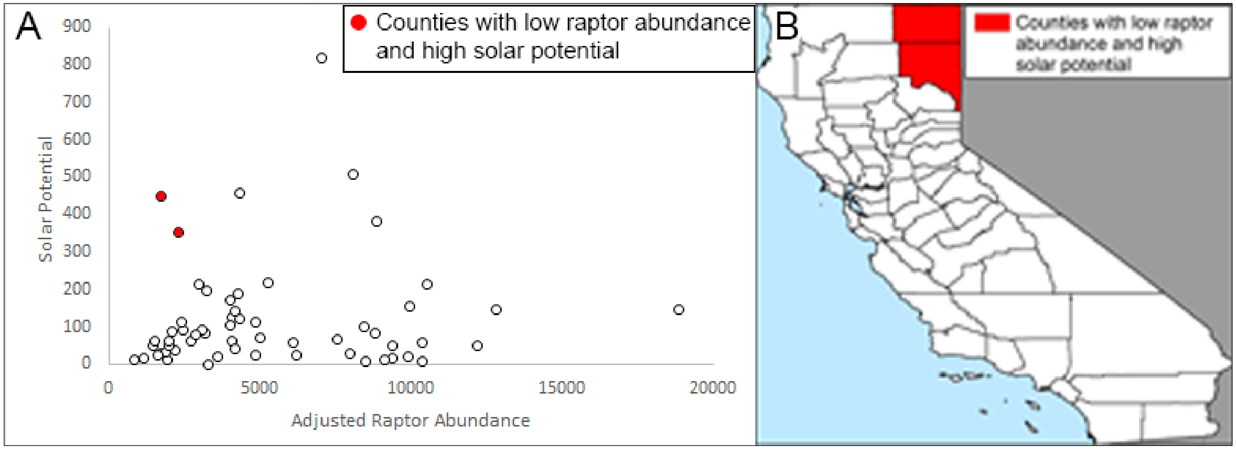
Figure 12: Spatial Pattern of Raptor Abundance and Solar Potential



A) Abundance of raptors according to eBird after correcting for average human population per km^2 (a proxy for observer density); (B) Solar potential (estimated production per 10 km grid square from the NREL Renewable Portfolio Standards (RPS) calculator). There was no relationship between abundance and solar potential in the analysis of all counties (r=-0.08, p=0.57).

Source: (A) from UCLA; (B) modified from raw Data Basin data

Figure 13: Least-Cost Counties for Raptors



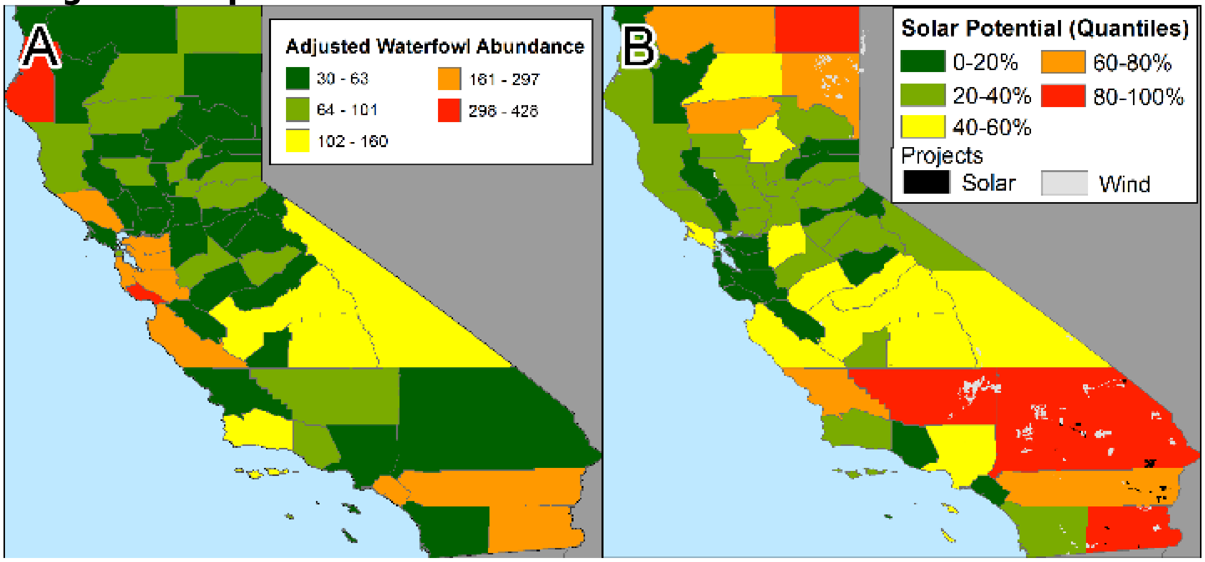
A) Scatterplot of adjusted abundance vs. solar potential (estimated production per 10 km grid square from the NREL Renewable Portfolio Standards calculator) indicating counties with low raptor abundance and high solar potential; (B) Map of high potential, low abundance counties: Lassen and Modoc.

Source: (A) from UCLA; (B) modified from raw Data Basin data

Waterfowl

After adjusting for average human population density, the counties with the lowest abundance of waterfowl and highest solar potential were Riverside and San Bernardino counties in the Mojave Desert Ecoregion (Figures 14 and 15).

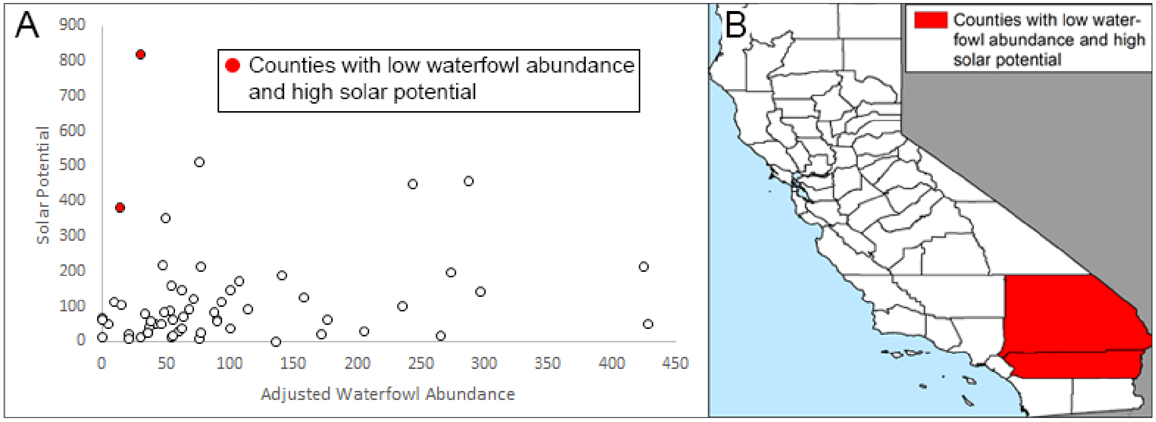
Figure 14: Spatial Pattern of Waterfowl Abundance and Solar Potential



A) Abundance of waterfowl according to eBird after correcting for observer effort; (B) Solar potential (estimated production per 10 km grid square from the NREL Renewable Portfolio Standards (RPS) calculator). There was no relationship between abundance and solar potential in the analysis of all counties (r=0.14, p=0.33).

Source: (A) from UCLA; (B) modified from raw Data Basin data

Figure 15: Least-Cost Counties for Waterfowl



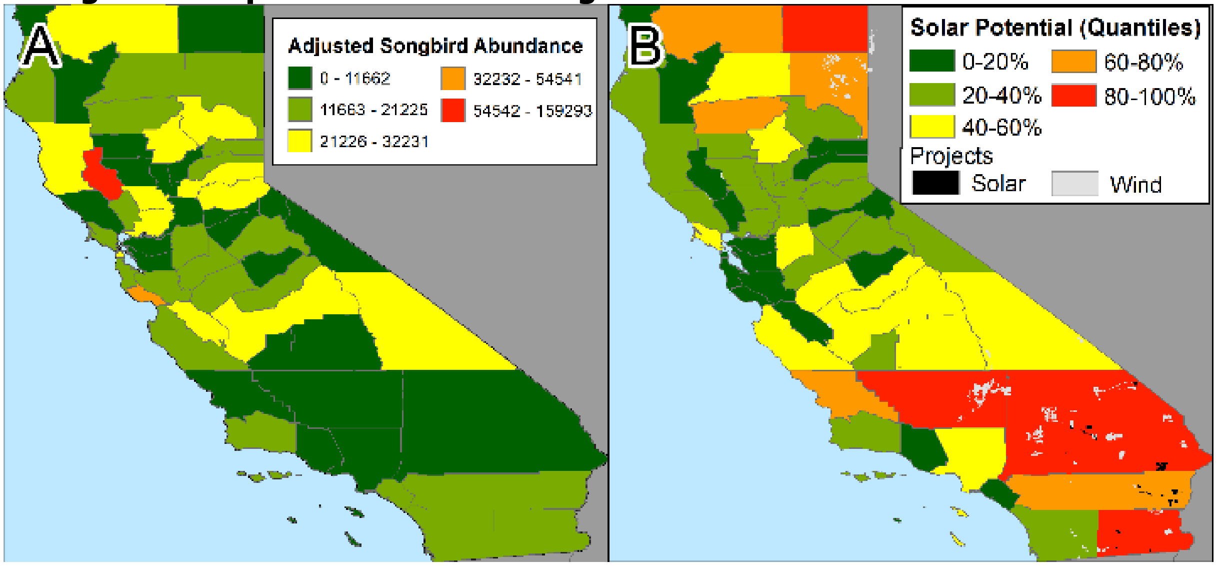
A) Scatterplot of adjusted abundance vs. solar potential (estimated production per 10 km grid square from the NREL Renewable Portfolio Standards (RPS) calculator) indicating counties with low waterfowl abundance and high solar potential; (B) Map of high potential, low abundance counties: Riverside and San Bernardino.

Source: (A) from UCLA; (B) modified from raw Data Basin data

Songbirds

After adjusting for average human population density, there were seven counties in southern California and the Modoc Ecoregion with low abundance for songbirds and high-solar potential (Figure 16 and 17).

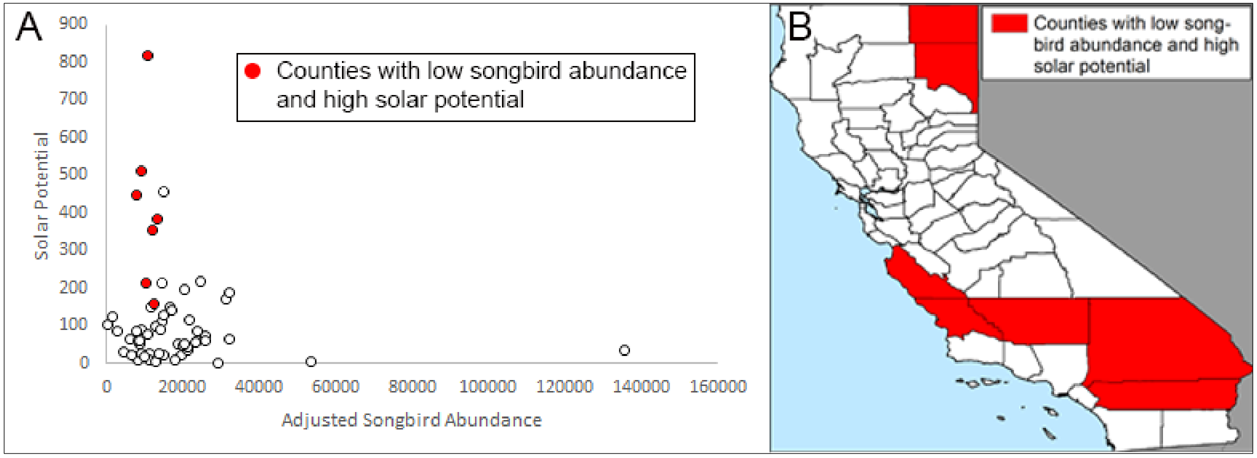
Figure 16: Spatial Pattern of Songbird Abundance and Solar Potential



A) Abundance of songbirds according to eBird after correcting for observer effort; (B) Solar potential (estimated production per 10 km grid square from the NREL Renewable Portfolio Standards (RPS) calculator). There was no relationship between abundance and solar potential in the analysis of all counties (r=-0.13, p=0.33).

Source: (A) from UCLA; (B) modified from raw Data Basin data

Figure 17: Least-Cost Counties for Songbirds



A) Scatterplot of adjusted abundance vs. solar potential (estimated production per 10 km grid square from the NREL Renewable Portfolio Standards (RPS) calculator) indicating counties with low songbird abundance and high solar potential; (B) Map of high potential, low abundance counties: Kern, Lassen, Modoc, Monterey, Riverside, San Luis Obispo, and San Bernardino.

Source: (A) from UCLA; (B) modified from raw Data Basin data

Discussion

Least-cost analyses identified counties with high solar potential and low abundance across avian guilds, according to eBird (Table 5). For instance, Modoc and Lassen counties had high solar potential and relatively low abundance of the nine target species, Raptors, and Songbirds, after adjusting for observer effort. Furthermore, Riverside and San Bernardino counties had high solar potential and relatively low abundance of songbirds and waterfowl after adjusting for the number of observers.

Table 5: Least-Cost Counties Across Guilds

County	Nine Target Species	Raptors	Waterfowl	Songbird
Kern				X
Lassen	X	X		X
Modoc	X	X		X
Monterey				X
Riverside			X	X
San Bernardino			X	X
San Luis Obispo				X

Source: Trevon Fuller

Similar analyses can identify counties that represent high-conflict areas; that is, counties with both high renewable energy potential and high risk to wildlife populations (in this case represented by the abundance of avian species in that county) (Table 6). One county in particular, Monterey, was found to have both high solar potential but also high abundance of the nine target taxa and the guild waterfowl. Conflicts with the nine target taxa could also occur in other high renewable energy potential counties, such as Kern and San Luis Obispo. Other high-risk areas are more specific in their potential conflicts, such as San Bernardino County that has high renewable energy potential and a high abundance of raptors, or Siskiyou County in Northern California, that has somewhat high renewable energy potential and a high abundance of songbirds.

Table 6: High-Conflict Counties Across Guilds

County	Nine Target Species	Raptors	Waterfowl	Songbirds
Imperial			X	
Kern	X			
Monterey	X		X	
Riverside			X	
San Bernardino		X		
San Luis Obispo	X			
Siskiyou				X

Source: Trevon Fuller

The approach that researchers used to tally abundance is subject to limitations. For example, since they added abundance across species within a guild, their approach assigns greater weight to common species, or species that are easily observed, as compared with more elusive, rare ones. Recent evidence has suggested, however, that occurrences of even common species can be an effective surrogate for the presence of rare or threatened ones (Fuller et al. 2013). Their approach also assumes that species within the same guild are equivalent; however, an ecological guild such as waterfowl includes diverse taxonomic groups that may differ with the timing of their migrations and stopovers in California. Some species may also be more reliant on stopovers in California than other species, particularly if their ranges are more restricted. Moreover, since the researchers simply tallied abundance rather than producing a predictive model, their approach did not lend itself to model cross-validation. Further efforts are warranted in this case to quantitatively compare the ability of habitat versus other biotic and abiotic factors for predicting abundance of individual species and the guilds they represent.

In light of these limitations, the researchers’ approach to tallying abundance may not have broad suitability for the design of multi-species conservation plans. Nevertheless, the approach adopted here was deemed suitable for the specific task of understanding potential avian solar conflicts at a broad scale in California, according to the expert judgment of the TAC. The researchers’ approach is a technique tailored to the specific context of understanding the geographic distribution of avian guilds given the rapid growth of renewable energy infrastructure in the state. This analysis presented here would not be suitable for site-level selection by solar energy developers or local planners because of its low spatial resolution.

This analysis included the eBird data set, which relies upon amateur bird watchers, including counts of backyard birds. Due to the nature of this data set, it may omit areas with high abundance but few reports by amateur bird watchers, such as remote sites that are difficult to access. For instance, northeastern California is renowned for raptor abundance, but according to eBird data and their estimates the abundance of raptors there is in the lowest 20 percent of counties in the state. This could reflect the nature of the eBird data set and its reliance on backyard observations. Future refinement to these maps using the opinions of wildlife managers and avifauna researchers could prove complementary to their analyses.

The researchers’ use of the NREL solar-potential model influenced which counties were classified as high solar potential. For example, according to the NREL model, while the eastern half of Riverside County has high solar potential, the western portion has lower potential. Thus, when they classified counties into quintiles based on total solar potential, Riverside falls into the second highest quantile, whereas the neighboring county of San Bernardino is classified as belonging to the highest quantile of solar potential. The west-to-east gradient in solar potential within Riverside County appears to be a robust pattern seen in multiple data sets. For example, the Photovoltaic Solar Resource layer in Data Basin also classifies eastern Riverside County as high annual solar irradiance of approximately 7 kWh/m2/day, whereas irradiance in the west is lower at 6 kWh/m2/day. To put this in context, San Bernardino County has an average irradiance of 7 kWh/m2/day, while Santa Barbara County has an average irradiance of 6 kWh/m2/day. In light of the variation in irradiance within Riverside County that is seen consistently across geographic data sets, the researchers believe it is defensible to classify Riverside County as a whole in the second quantile of solar potential, while recognizing that areas in the eastern portion of the county have among the highest solar irradiance of anywhere in the state.

CHAPTER 5:
Knowledge Transfer Activities

Purpose of Knowledge Transfer

For knowledge generated in scientific research projects to benefit society, it is crucial for the stock of accumulated knowledge to be transferred to decision makers, thereby influencing policy (Loomis and Rosenberger 2006). To reach decision makers in agencies, industry, and NGOs, the researchers have given and will continue to give presentations at conferences and symposia on the environmental dimensions of renewable energy in California. To inform academics of their findings, they have published or will publish at least one article about each of the target species in a peer-reviewed journal.

One of the biggest barriers to knowledge transfer in the sciences is that members of the project team have tacit knowledge that must be converted into explicit knowledge so that outside users will understand and apply that knowledge (Conway 2009). To make their tacit knowledge explicit and intelligible to other biologists and lay people, the researchers have developed the Bird Genoscape website http://www.birdgenoscape.org/, which publicizes their activities and invites ornithologists to contribute samples to help make the project sustainable beyond the EPIC funding. They also provided kits and training to facilitate the sharing of lawfully acquired samples.

Knowledge That the Project Created

- Population maps (Genoscapes) of genetic variation across geographic space for four species exposed to renewable energy development in California
- Timetables of migration to identify when particularly vulnerable populations are migrating through an area
- Population-level impact assessments based upon the analysis of individual birds killed at renewable energy facilities within California
- Migration hotspot maps identifying areas of highest potential exposure of wildlife populations to renewable energy development
- Least-cost analyses prioritizing regions for renewable energy siting that maximize energy potential while minimizing harmful exposure of wildlife to renewable energy facilities

Target Audiences

The audience for this project includes academics, non-profit organizations, government agencies, renewable energy companies, and the general public. Genoscape maps, timetables of migration along the Pacific Flyway, population-level impact assessments, and least-cost-analysis maps generated in this report are targeted to reach decision-makers in agencies (e.g., United States Fish and Wildlife Service and California Department of Fish and Wildlife), industry (e.g., First Solar), and non-profit organizations (e.g., National Audubon Society) to help prioritize regions for renewable energy siting with maximum energy potential and minimum risk to migratory birds. The researchers have already published or will publish articles in high-impact journals to inform academics of their findings. Finally, scientific knowledge gained from the study is disseminated to other biologists and the public through a project website: http://www.birdgenoscape.org/.

Transfer Tasks

Technical Advisory Committee

The TAC consisted of individuals from agencies, academia, and industry (Laura Abram (First Solar); Garry George (National Audubon Society); Tom Dietsch (United States Fish and Wildlife Service), Todd Katzner (United States Geological Survey), Magdalena Rodriguez (California Department of Fish and Wildlife), and David Stoms (California Energy Commission). The researchers held quarterly meetings with the subsets of the TAC throughout the project to discuss preliminary results and conservation implications. Comments from the TAC were incorporated into the results.

Conference Presentations

For conferences attended to date, the researchers have presented to an estimated 500 stakeholders and biologists; slides and presentations are also publicly available to those who did not personally attend.

- "High-resolution Mapping of Population-specific Migratory Flyways using DNA Sequencing." Presentation by Rachael Bay at the Technical Symposium on Avian-Solar Interactions, August 16, 2017. Sacramento, California
- "Incorporating Avian Migratory Hotspots into the Prioritization of Renewable Energy Siting." Presentation by Trevon Fuller at the Technical Symposium on Avian-Solar Interactions, August 16, 2017. Sacramento, California
- "The American Kestrel Genoscape Project: Using High Resolution Genomic Markers to Identify Discrete Population Structure in a Continuously Distributed Raptor Species." Presentation by Michaela Brinkmeyer at the Raptor Research Foundation Annual Meeting, November 9, 2017. Salt Lake City, Utah
- A representative from the team presented at the Avian Solar Working Group meeting December 5-6, 2017. Santa Monica, California
- Ryan Harrigan gave an invited presentation at the Los Angeles Energy Research Symposium on March 19, 2018.
- Kristen Ruegg gave an invited presentation at the Avian Solar Interactions Symposium at the American Ornithological Union meeting on April 9-14, 2018, in Tucson, Arizona.
- "Taking Flight: Bird Migration Across Hemispheres," Kristen Ruegg gave an invited presentation at the National Geographic Society on February 15, 2018.
- "Bird Genoscapes and Migratory Bird Conservation." Kristen Ruegg gave an invited presentation to the National Audubon Society board of directors in honor of Migration Science Day in Naples, Florida, on January 24, 2019.
- "Genoscapes and Avian Solar Impacts." Kristen Ruegg gave an invited web-based presentation at the Avian Solar Working Group on April 15 2019.
- "The Bird Genoscape Project." Kristen Ruegg gave an invited presentation at the Partners in Flight meeting in Fort Collins, Colorado, on April 16, 2019.

- “Bioblitz – Mapping the Flyways of the America’s Using Genomics.” Kristen Ruegg gave and IGNITE presentation for the Global Biodiversity Center in Fort Collins, Colorado, on April 23, 2019.
- “Genoscapes and Species Limits: Lessons Learned in 5 Years.” Kristen Ruegg gave an invited presentation as part of a symposium on species limits at the American Ornithological Union conference in Anchorage, Alaska, on June 26, 2019.

Websites

To provide a public, online, and dedicated portal to disseminate all genoscape and prioritization maps to a general audience, the researchers developed the Bird Genoscape project website: http://www.birdgenoscape.org/. The site provides a jargon-free description of genoscapes to explain the concept to a lay audience, and also includes search functions that enable users to query the UCLA samples database for information about the target species. The website also explains to bird biologists from the Western Hemisphere how to contribute lawfully collected blood, feather, tissue, or DNA samples. Ultimately, these contributions will allow the team to make the project sustainable beyond the project funding period and reach the team’s goal of 100 species.

- Created and made available live on 10/01/2017
- Since created, the site has had over 50,000 unique visitors, averaging a view of two pages per visit

Data Basin (https://databasin.org). Data Basin is a widely used website for making GIS data available to the public. The researchers uploaded models of migratory hotspots and the least-cost-analysis model (areas of high renewable potential and low wildlife exposure) shown in Chapter 4. The public can access the data at ArcGIS (https://arcg.is/0K0Oqz).

Journal Articles

Over the last three years, the researchers have published multiple research papers that document the activity of the project (Table 7). Several papers are also scheduled to be published within the next year.

Table 7: Publications Planned and Published From the Project

Planned or submitted publications	Target journal	Schedule/Status
Population-Level Effects of Renewable Energy Development on Migratory Birds in California Assessed Using High-Resolution Genetic Markers	Journal of Wildlife Management	Q3 2020
Conservation genomics of resident versus migrant phenotype in Burrowing Owls-does inbreeding play a role?	Ecological Applications	Q2 2020
The genomics of migratory strategies in American Kestrels	Current Biology	Q2 2020
The American Kestrel Genoscape (*Falco sparverius*): Implications for Monitoring, Management, and Subspecies Boundaries	AUK	*In review*, 2020
Individual-level niche tracking across the annual cycle of a migratory bird	PNAS	Q2 2020
Genomic signals of selection predict climate-driven population declines. Bay RA, Harrigan RJ, Underwood VL, Gibbs HL, Smith TB, Ruegg KC.	Science	Published, Q1 2018
Ecological Genomics Predicts Climate Vulnerability in an Endangered Southwestern Songbird. Ruegg K, Bay RA, Harrigan RJ, Saracco JF, Anderson EC, Whitfield M, Paxton EH, Smith TB.	Ecology Letters	Published, Q1 2018
A genoscape-network for conservation prioritization in migratory species	Conservation Biology	*In review,* 2019

Source: University of California Los Angeles

Publication Metrics

"Genomic signals of selection predict climate-driven population declines"

- Altmetric Score of 204 (as of 10/3/2018) – top 5 percent of all research scored by Altmetric
- Abstract downloaded over 15,000 times, PDF downloaded over 2,000 times
- Cited in 19 publications (as of 10/3/2018)
- Picked up by 12 news outlets, including AAAS, New Scientist, CBS News, Audubon, and Wildlife Society
- Additional interview requests, including The Conversation: (https://theconversation.com/can-this-bird-adapt-to-a-warmer-climate-read-the-genes-to-find-out-95744)

"Ecological Genomics Predicts Climate Vulnerability in an Endangered Southwestern Songbird"

- Altmetric Score of 45 (as of 10/3/2018) – top 5 percent of all research scored by Altmetric
- Cited in 2 publications (as of 10/3/2018)

Policy Development

To date, the project has not been cited in government policy publications, or used to inform regulatory bodies; however, the researchers are working in collaboration with one of the leading regulatory authorities – the U.S. Fish and Wildlife Service – to provide the sound science needed to guide policy to minimize wildlife impacts from renewable energy development.

CHAPTER 6: Conclusions and Future Work

The researchers successfully generated genoscape maps for three species of migratory birds that regularly reside in or traverse California for all or part of their annual cycles: American Kestrel, Common Yellowthroat and Wilson's Warbler. They found that with new sequencing technologies they could define avian conservation units at finer spatial and temporal scales than previously possible. The genoscape of the Burrowing Owl, for example, showed no genetic structure for migrant breeding populations, but rather a unique genetic structure for each year-round resident population. The resulting maps provide a solid framework for managing California's migratory bird populations as renewable energy development expands.

Next, researchers developed high-resolution genetic markers for the three species with successful genoscape maps that allowed researchers to assess population-specific effects of renewable energy development on migratory birds in California with greater resolution than previous methods. The precision of their high-resolution genetic tags varied with the degree of population structure inherent in each species, as well as with technical details associated with the concentration and quality of DNA samples from carcasses. Here they limited their analysis to either 96 or 192 high-resolution genetic markers, but future research is underway to reveal the extent to which additional genetic markers would allow them to increase the resolution of assignments of birds to conservation units. Comparisons of the population-specific effects of exposure to renewable energy development, relative to population size and trends, suggest that the majority of carcasses are from the largest, most abundant breeding populations for each species. Researchers also documented examples of exposure of unique genetic breeding populations that are small and declining, particularly for the Wilson's Warbler. Overall, this work demonstrates the value of high-resolution genetic tags for managing and protecting migratory birds in California as renewable energy facilities continue to expand. The Bird Genoscape Project plans to expand this genoscape analysis to at least 100 avian species.

As part of this work, the researchers estimated abundance for target avian species, as well as for several encompassing guilds of avifauna, and combined this with estimates of solar development potential; this helped identify possible sites that would minimize avian wildlife exposure across multiple species while maximizing energy potential. They found that Lassen and Modoc counties have low avian abundance and high solar potential for three of the five avian groups. Riverside and San Bernardino were identified as low-avian-abundance, high-solar-potential counties for two out of the five groups. While songbirds seemed to occupy more regions across California in higher abundance relative to other groups, this might be expected given their vast numbers when compared with other birds such as raptors or waterfowl, the relatively larger number of species included in this group (Figure 11), and the fact that they are readily observable by community scientists. Most importantly, the research revealed that for many migratory species, California's wildlands provide crucial stopover habitat during particularly vulnerable points in their life cycles. While the researchers' results suggest that avian wildlife and solar-energy development can effectively coexist, additional research into the impacts of renewable energy production on migratory hotspots could further refine and improve management siting decisions.

Although the researchers’ scope of work focused on the exposure of avian populations to renewable energy development, there are a number of opportunities to broaden this analysis. For example, future work could analyze aspects of landscape intactness developed by the Conservation Biology Institute, including: agricultural density, brown-field sites, invasive species, mining, pollution, habitat fragmentation, urban development, and roads (Conservation Biology Institute 2013). Maps of ecological intactness could be overlaid on solar photovoltaic (PV) potential and permit applications for the construction of renewable energy facilities. This type of analysis could identify counties with very low levels of intactness and high PV potential. Such counties could become future sites for renewable energy projects with low risks of further harming their landscapes.

CHAPTER 7:
Benefits to Ratepayers

This project addressed the EPIC goal of lowering costs for California investor-owned utility ratepayers in three main ways.

First, a science-based understanding of when bird populations migrate through California (Chapter 2), combined with the identification of migratory hotspots (Chapter 4), can ultimately reduce environmental monitoring costs of renewable energy facilities. While at many facilities monitoring may need to be conducted weekly throughout the year, researchers showed that migration variations throughout the Pacific Flyway could focus essential monitoring windows in some areas. Of the four target species investigated, Wilson's Warbler populations migrate through the Pacific Flyway at different times during their spring and fall migrating seasons. Since the goal was to monitor the effects of renewable energy facilities on vulnerable breeding populations, evidence that the small Coastal California conservation unit migrates in early spring (Ruegg et al 2014b), and that the Sierra migrants use the Pacific Flyway later in the fall migration season (Figure 1), would make it possible to confine monitoring efforts to those critical times. In addition, these results can reduce the spatial breadth of necessary monitoring to sites that overlap with vulnerable migrating populations. Broader exploration of the timing of migration in other guilds of birds would further clarify the spatial and temporal patterns of population-specific migrations.

Second, the population-specific impacts of renewable energy sources, when integrated with projections of where new sites would have minimal impacts on avian wildlife populations, would ultimately increase compliance with wildlife protection regulations for species of special concern**.** At this time, the target species in this report are neither federally nor state listed; however, two of them are listed as bird species of special concern in California: the Common Yellowthroat, which inhabits the Bay Area, and the Burrowing Owl. It is also clear, based on the completed genoscapes described in Chapter 2, that the genetic structure of each species has been underestimated. The genoscape framework detected conservation units below the species level, which opens an avenue of investigation into greater protections for local adaption of these smaller management units. This knowledge can improve siting and development of future renewable energy facilities to avoid or minimize harmful avian ecological impacts.

Finally, the precise predictions of when and where these targeted species will migrate, detailed in Chapters 2 – 4, can ultimately maximize energy operations while minimizing avian wildlife impacts. This would increase operational time, at least for wind energy. The results of this project help meet this goal through both spatial recommendations for future renewable energy facilities and temporal recommendations to manage operational times to avoid peak migrations of vulnerable populations. For example, changes in operational time to avoid impacts with the vulnerable Sierra Nevada breeding population of the Wilson's Warbler could be limited to the late spring migration. Further, siting facilities in counties such Modoc and Lassen, which are not hotspots of migration, would help avoid potential conflicts that could reduce operational time. The genoscape framework proposed in this report provides the robust, scientific framework necessary for management to make informed, targeted decisions.

Overall, the report authors expect implementation of this framework for avian wildlife monitoring can also apply to a broad spectrum of other wildlife affected by renewable energy development.

LIST OF ACRONYMS

Term	Definition
AMKE	American Kestrel
BBS	Breeding Bird Survey
BUOW	Burrowing Owl
COYE	Common Yellowthroat
DNA	DeoxyriboNucleic Acid
EPIC	Electric Program Investment Charge
GIS	Geographic Information System
NREL	National Renewable Energy Laboratory
PV	photovoltaic
RETI	Renewable Energy Transmission Initiative
RPS	Renewable Portfolio Standard
SNPs	Single Nucleotide Polymorphisms
TAC	Technical Advisory Committee
UCLA	University of California, Los Angeles
USFWS	U.S. Fish and Wildlife Service
USGS	U.S. Geological Survey
USSE	Utility-Scale Solar Energy
WIWA	Wilson’s Warbler

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APPENDIX A:
Supplemental Figures and Tables

Figure A-1: Distribution of American Kestrel with Sampling Locations

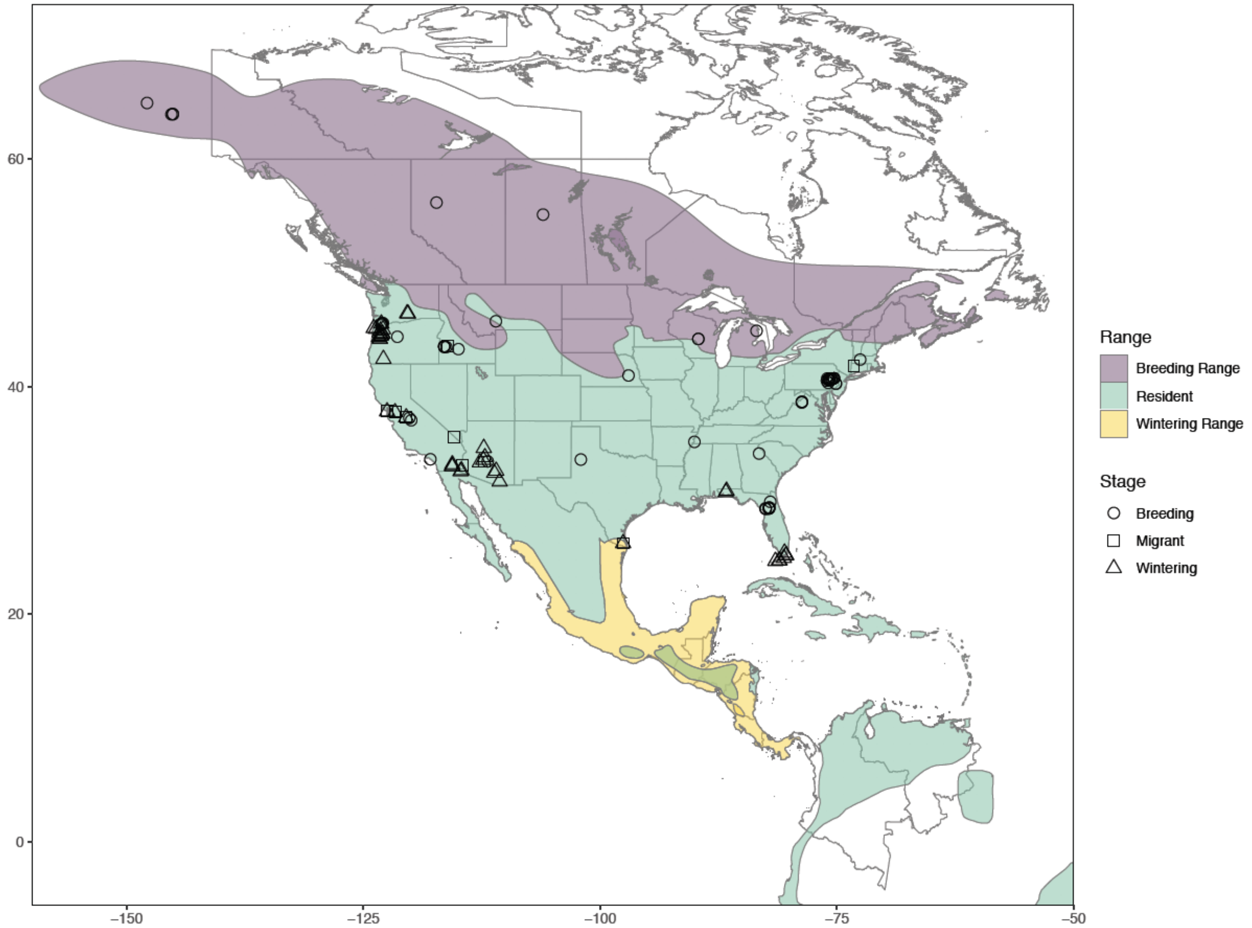


Figure A-2: Distribution of the Common Yellowthroat with Sampling Locations

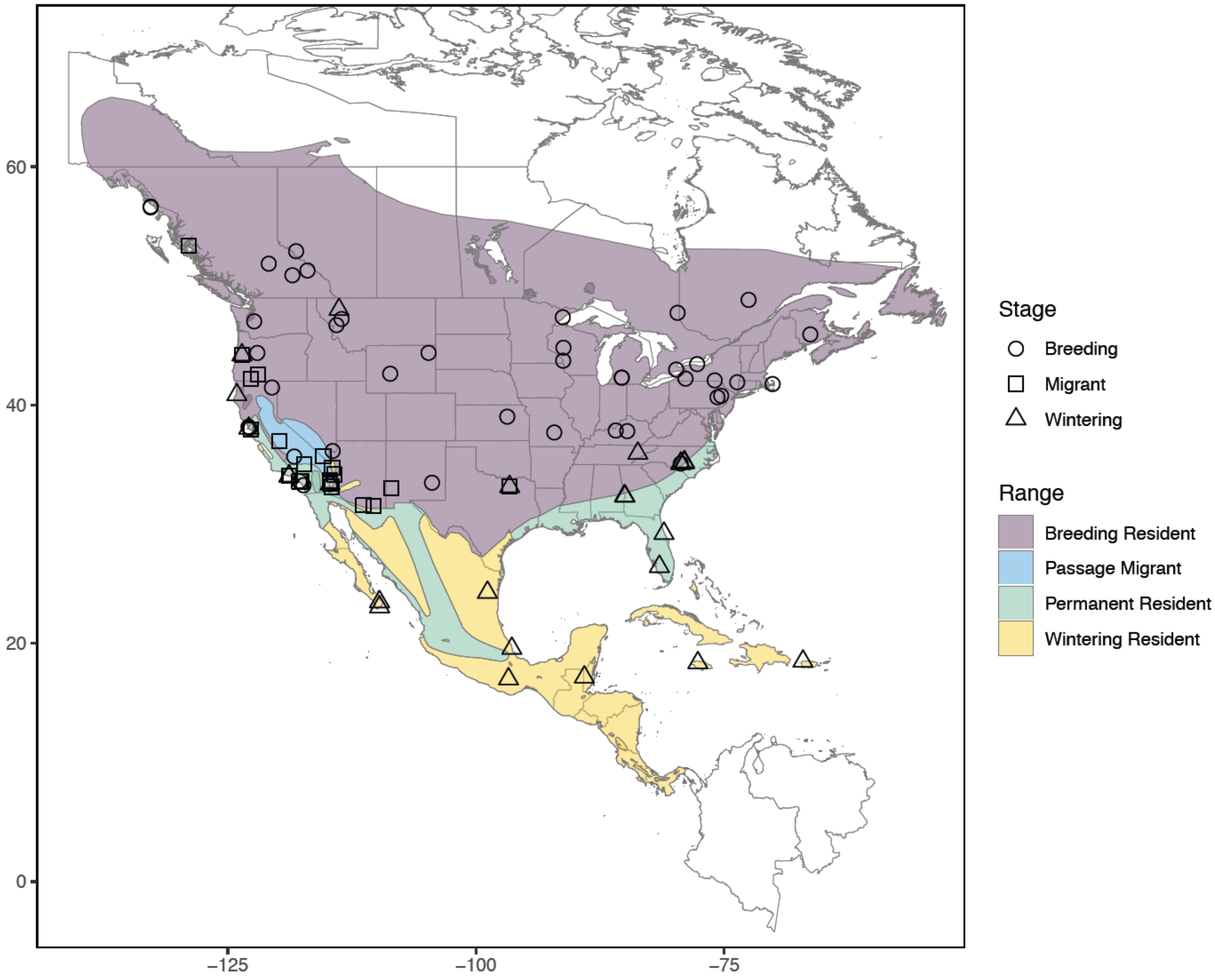


Figure A-3: Distribution of the Wilson's Warbler with Sampling Locations

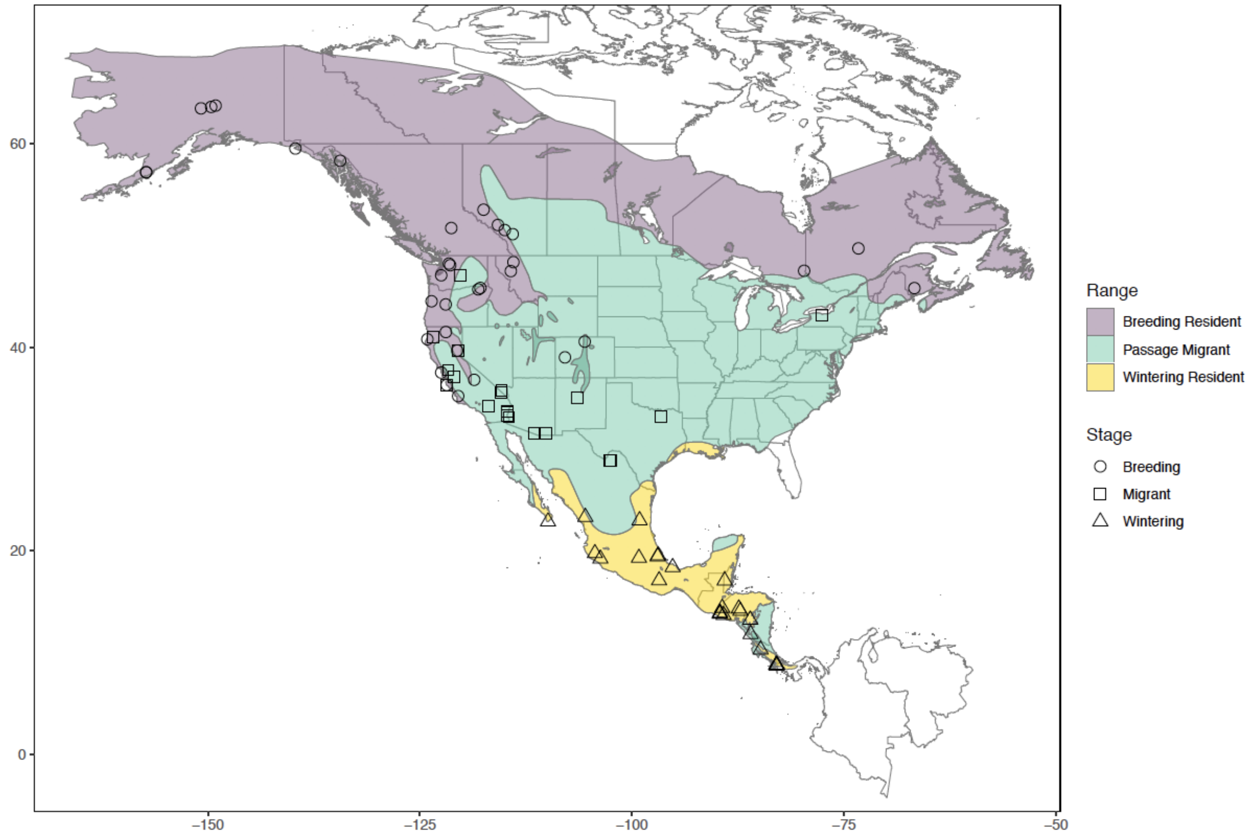
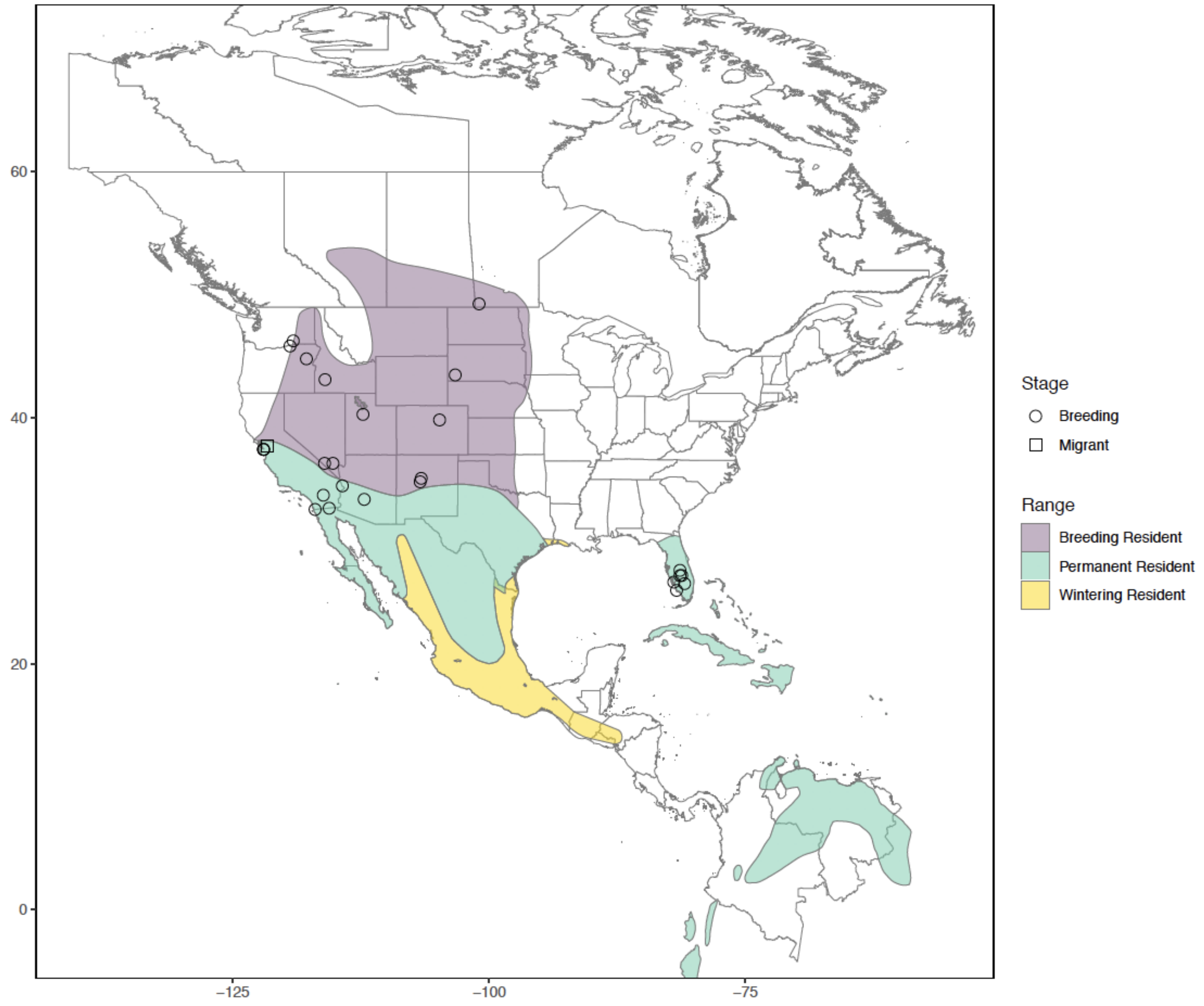


Figure A-4: Distribution of the Burrowing Owl with sampling locations



Breeders (blood =red and DNA aliquots = green) and feathers from migrant birds (blue).

Figure A-5: Time series of spring migration for Wilson's Warbler at Cibola National Wildlife Refuge, AZ and CA

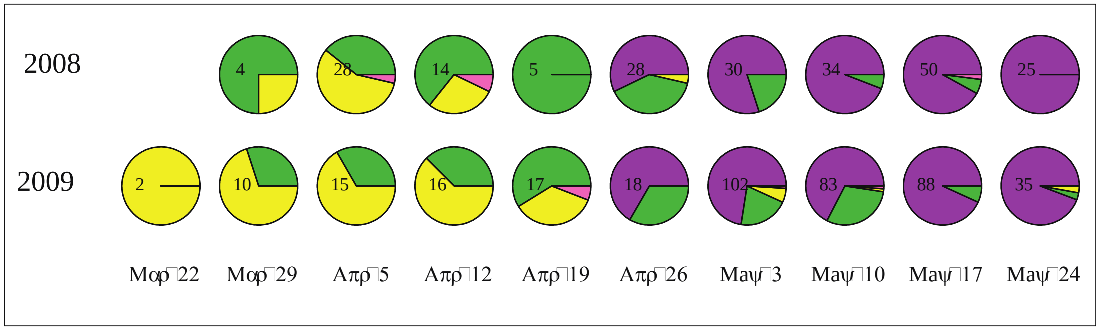


Table A-1: American Kestrel Blood and Feather Sample Locations, Stage, Sample Type and Number of Samples

Location	Latitude	Longitude	Stage	Sample	Number
Alaska, AK	63.95	-145.27	Breeding	Blood	7
Albany, PA	40.62	-75.90	Breeding	Blood	3
Alberta, AB	56.19	-117.29	Breeding	Feather	12
Anthony, FL	29.28	-82.17	Breeding	Blood	2
Bath, PA	40.73	-75.39	Breeding	Feather	1
Besnard Lake, SK	55.13	-106.03	Breeding	Blood	39
Boise, ID	43.49	-116.25	Breeding	Blood	27
Boise, ID	43.56	-116.48	Breeding	Feather	14
Bronson, FL	29.30	-82.55	Breeding	Blood	1
CentralWest, MT	45.75	-111.01	Breeding	Feather	63
Coastal, CA	37.05	-119.95	Breeding	Blood	17
Coastal, OR	44.39	-121.42	Breeding	Feather	37
Cornelius, OR	45.48	-123.05	Breeding	Blood	1
Danielsville, PA	34.12	-83.22	Breeding	Feather	1
Delta Junction, AK	63.98	-145.13	Breeding	Blood	14
Delta Junction, AK	63.95	-145.11	Breeding	Feather	2
Fairbanks, AK	64.95	-147.85	Breeding	Blood	2
Fairfield, ID	43.31	-114.97	Breeding	Blood	7
Florida, FL	29.88	-82.04	Breeding	Feather	20
Forest Grove, OR	45.56	-123.08	Breeding	Blood	7
Gaston, OR	45.40	-123.10	Breeding	Blood	1
GreatLakes, MI	44.91	-83.49	Breeding	Feather	35
Hamburg, PA	40.53	-76.07	Breeding	Blood	2
Hillsboro, OR	45.59	-122.93	Breeding	Blood	3
Kempton, PA	40.63	-75.85	Breeding	Blood	6
Kempton, PA	40.63	-75.85	Breeding	Feather	3
Klinesville, PA	40.59	-75.84	Breeding	Blood	1
Kuna, ID	43.48	-116.45	Breeding	Blood	2
Kutztown, PA	40.55	-75.73	Breeding	Blood	1
Lowell, FL	29.35	-82.20	Breeding	Blood	2
Lubbock, TX	33.59	-102.04	Breeding	Blood	13
Lynnport, PA	40.68	-75.81	Breeding	Blood	2
Meridian, ID	43.54	-116.45	Breeding	Blood	2
Midwest, NE	40.99	-97.01	Breeding	Feather	23
Nazareth, PA	40.74	-75.31	Breeding	Blood	1
NAZARETH, PA	40.74	-75.31	Breeding	Feather	1
New Ringgold, PA	40.72	-76.02	Breeding	Blood	1
New Tripoli, PA	40.71	-75.78	Breeding	Blood	1
NewEngland, MA	42.38	-72.55	Breeding	Feather	74
Newport Beach, CA	33.62	-117.93	Breeding	Feather	1
North Plains, OR	45.59	-123.02	Breeding	Blood	2

Location	**Latitude**	**Longitude**	**Stage**	**Sample**	**Number**
NORTHAMPTON, PA	40.69	-75.50	Breeding	Blood	1
Ocala, FL	29.30	-82.17	Breeding	Blood	1
Orange County, CA	0.00	0.00	Breeding	Blood	3
Orefield, PA	40.64	-75.58	Breeding	Blood	2
Orefield, PA	40.64	-75.58	Breeding	Feather	2
Orwigsburg, PA	40.65	1.00	Breeding	Blood	1
Plainfield, WI	44.20	-89.64	Breeding	Blood	18
Plainfield, WI	44.20	-89.64	Breeding	Feather	9
Raymond, CA	37.25	-120.16	Breeding	Blood	2
Reading, PA	40.34	-75.93	Breeding	Blood	1
Reddick, FL	29.38	-82.18	Breeding	Blood	3
Reinholds, PA	40.27	-75.12	Breeding	Blood	2
Reinholds, PA	40.27	-75.12	Breeding	Feather	2
Rockingham, VA	38.64	-78.72	Breeding	Blood	24
Shenandoah, VA	38.69	-78.69	Breeding	Blood	10
Southeast, TN	35.15	-90.05	Breeding	Feather	32
Southeast, VA	38.61	-78.71	Breeding	Blood	2
Southwest, AZ	33.43	-111.88	Breeding	Feather	20
Sparr, FL	29.37	-82.12	Breeding	Blood	1
Steinsville, PA	40.66	-75.86	Breeding	Blood	1
Williston, FL	29.24	-82.52	Breeding	Blood	6
Altamont, CA	37.75	-121.66	Migrant	Feather	123
Blythe, CA	33.13	-114.51	Migrant	Feather	4
Boise, ID	43.61	-116.06	Migrant	Feather	40
Cameron, TX	26.24	-97.58	Migrant	Feather	9
Goshen, CT	41.83	-73.22	Migrant	Feather	1
Merced, CA	37.30	-120.48	Migrant	Blood	1
Nipton, CA	35.56	-115.47	Migrant	Feather	13
Phoenix, AZ	33.41	-112.20	Migrant	Feather	6
Sacramento, CA	37.30	-120.48	Migrant	Blood	2
Sausalito, CA	37.84	-122.49	Migrant	Feather	32
Airlic, OR	44.75	-123.31	Wintering	Feather	1
Altamont, CA	37.75	-121.66	Wintering	Feather	39
Alvadore, OR	44.19	-123.25	Wintering	Feather	3
Baker, FL	30.85	-86.66	Wintering	Feather	6
Bellfountain, OR	44.36	-123.36	Wintering	Feather	1
Brawley, CA	32.99	-115.60	Wintering	Feather	1
Brooks, OR	45.05	-122.94	Wintering	Feather	4
Bueno, WA	46.42	-120.28	Wintering	Feather	1
Bumstead, AZ	33.57	-112.34	Wintering	Feather	1
Calipatria, CA	33.18	-115.61	Wintering	Feather	11
Cameron, TX	26.24	-97.58	Wintering	Feather	26
Cheshire, OR	44.23	-123.29	Wintering	Feather	2

Location	Latitude	Longitude	Stage	Sample	Number
Corvallis, OR	44.54	-123.12	Wintering	Feather	24
Crabtree, OR	44.66	-122.97	Wintering	Feather	1
Cudjoe Key, FL	24.68	-81.50	Wintering	Feather	1
Dalles, OR	44.93	-123.20	Wintering	Feather	2
Forest Grove, OR	45.55	-123.11	Wintering	Feather	2
Grande Ronde, OR	45.15	-123.91	Wintering	Feather	1
Hassayampa, AZ	33.35	-112.71	Wintering	Feather	3
Holt, FL	30.72	-86.74	Wintering	Feather	1
Homestead, FL	25.41	-80.54	Wintering	Feather	4
Islamorada, FL	24.94	-80.61	Wintering	Feather	1
Key Largo, FL	25.15	-80.39	Wintering	Feather	2
Knight Key, FL	24.71	-81.12	Wintering	Feather	1
Marana, AZ	32.43	-111.19	Wintering	Feather	1
Marathon Key, FL	24.73	-81.06	Wintering	Feather	3
Medford, OR	42.44	-122.89	Wintering	Feather	3
Merced, CA	37.30	-120.48	Wintering	Blood	2
Millersburg, OR	44.67	-123.02	Wintering	Feather	1
North key, FL	25.19	-80.36	Wintering	Feather	1
Oco Valley, AZ	32.60	-110.98	Wintering	Feather	1
Pacific City, OR	45.09	-123.67	Wintering	Feather	2
Phoenix, AZ	33.80	-112.17	Wintering	Feather	2
Prescott Valley, AZ	34.61	-112.29	Wintering	Feather	1
Sanoita, AZ	31.66	-110.62	Wintering	Feather	1
Sausalito, CA	37.83	-122.50	Wintering	Feather	1
Shedd, OR	44.47	-123.17	Wintering	Feather	3
Somerton, AZ	32.57	-114.74	Wintering	Feather	1
Wapato, WA	46.45	-120.38	Wintering	Feather	1
Westmorland, CA	33.02	-115.66	Wintering	Feather	1
Yuma, AZ	32.64	-114.65	Wintering	Feather	3

Source: University of California Los Angeles

Table A-2: Common Yellowthroat Blood, DNA and Feather Sample Locations, Stage, Sample Type and Number of Samples

Location	Latitude	Longitude	Stage	Sample	Number
Alturas, CA, US	41.47	-120.54	Breeding	Feather	3
Ashley Heights, NC, US	35.09	-79.37	Breeding	Feather	6
Atlantic City, WY, US	42.63	-108.63	Breeding	Feather	3
Augusta, MI, USA	42.30	-85.32	Breeding	Feather	4
Augusta, MI, USA	42.30	-85.30	Breeding	Blood	13
Boulder City, NV, US	36.14	-114.43	Breeding	Feather	4
Brewster, MA, US	41.76	-70.12	Breeding	Feather	5
Brighton, NJ, USA	42.07	-75.95	Breeding	Feather	8
Burpee Wildlife Refuge,	45.93	-66.32	Breeding	Blood	10

Location	Latitude	Longitude	Stage	Sample	Number
NB, CAN					
Bush River Road 3, BC, CAN	51.30	-116.97	Breeding	Blood	13
Cibola, AZ, USA	33.35	-114.67	Breeding	Feather	8
Devil's Elbow, MO, USA	37.69	-92.11	Breeding	Feather	3
Eagle Creek, BC, CAN	51.86	-120.87	Breeding	Feather	1
Eau Claire, WI, USA	44.81	-91.18	Breeding	Feather	4
Finland, MN, US	47.37	-91.25	Breeding	Feather	5
Frog Falls 1, BC, CAN	50.90	-118.48	Breeding	Blood	3
Graham, WA, USA	47.03	-122.34	Breeding	Feather	6
Haldimand, ON, CAN	42.98	-79.83	Breeding	Feather	8
Hardin, KY, USA	37.86	-85.92	Breeding	Feather	5
Harrodsburg, KY, USA	37.81	-84.76	Breeding	Blood	13
Hilliardton, ON, CAN	47.74	-79.70	Breeding	Blood	9
Hilton, NY, USA	43.43	-77.72	Breeding	Blood	7
Holter Dam, MT, USA	43.72	-91.21	Breeding	Feather	3
Irvine, CA, US	33.60	-117.78	Breeding	Feather	4
Jasper National Park, AB, CAN	52.91	-118.11	Breeding	Blood	2
Junction City, KS, US	39.02	-96.84	Breeding	Feather	7
Kern, CA, US	35.67	-118.30	Breeding	Feather	1
Keyhole Banding Station, WY, USA	44.38	-104.77	Breeding	Blood	5
Marion Forks, OR, US	44.37	-122.02	Breeding	Feather	8
Marshall, CA, USA	38.17	-122.90	Breeding	Blood	3
Mitkof Island, AK, USA	56.66	-132.77	Breeding	Feather	10
Mitkof Island, AK, USA	56.59	-132.76	Breeding	Blood	14
MPG Ranch, MT, USA	46.71	-114.04	Breeding	Blood	1
Napoli, NY, USA	42.22	-78.89	Breeding	Feather	7
Nazareth, PA, USA	40.78	-75.30	Breeding	Blood	2
NO INFO, NB, CA	0.00	0.00	Breeding	Feather	1
Normandin, QUE, CAN	48.83	-72.54	Breeding	Blood	8
Oceanside, CA, USA	33.27	-117.37	Breeding	Blood	7
Olema, CA, USA	38.06	-122.81	Breeding	Blood	3
Roswell, NM, USA	33.48	-104.42	Breeding	Feather	5
Schnecksville, PA, USA	40.66	-75.67	Breeding	Blood	11
Seely Lake, MT, USA	47.22	-113.53	Breeding	Blood	1
Stanfordville, NY, USA	41.91	-73.68	Breeding	Feather	2
Vancouver BC, CA	0.00	0.00	Breeding	Feather	1
Ashland, OR, USA	42.20	-122.69	Migrant	Feather	37
Blythe, CA, USA	33.65	-114.72	Migrant	Feather	4
Bolinas, CA, US	37.92	-122.69	Migrant	Feather	13
Chiloquin, OR, US	42.59	-121.93	Migrant	Feather	12

Location	Latitude	Longitude	Stage	Sample	Number
Cibola, AZ, US	33.37	-114.68	Migrant	Feather	9
Fairview, TX, USA	33.15	-96.60	Migrant	Feather	85
Fresno, CA, US	36.99	-119.82	Migrant	Feather	30
Gila, NM, US	33.01	-108.55	Migrant	Feather	4
Hinkley, CA, USA	35.01	-117.32	Migrant	Feather	6
Laguna Beach, CA, US	33.57	-117.78	Migrant	Feather	4
Los Banos, CA, USA	44.20	-123.57	Migrant	Feather	5
Malibu, CA, USA	34.04	-118.75	Migrant	Feather	18
Mohave, AZ, US	34.73	-114.49	Migrant	Feather	7
NA, BC, US	53.39	-128.93	Migrant	Feather	4
Orange, CA, US	33.63	-117.56	Migrant	Feather	5
Parker, AZ, US	34.17	-114.28	Migrant	Feather	9
Picacho, CA, USA	33.13	-114.51	Migrant	Feather	2
Pima, AZ, USA	31.58	-111.34	Migrant	Feather	4
Riverside, CA, US	35.72	-115.38	Migrant	Feather	3
Saint David, AZ, USA	31.55	-110.30	Migrant	Feather	6
Zuma Beach, CA, US	34.05	-118.81	Migrant	Feather	48
Aeropuerto, OAX, MX	17.00	-96.72	Wintering	Feather	7
Arcata, CA, USA	40.86	-124.08	Wintering	Feather	1
Ashley Heights, NC, USA	35.09	-79.37	Wintering	Feather	3
Chattahoochee, GA, USA	32.37	-85.04	Wintering	Feather	2
Cibola, AZ, USA	33.37	-114.68	Wintering	Feather	4
Corkscrew Swamp Sanctuary Bird Banding Station, FL, USA	26.44	-81.52	Wintering	Feather	3
Cumberland, NC, USA	35.23	-79.00	Wintering	Feather	1
El Cedro, mpio. Actopan, Veracruz, Mexico	19.57	-96.38	Wintering	Feather	1
Fairview, TX, USA	33.15	-96.60	Wintering	Feather	1
Flathead National Forest, MT, USA	48.02	-113.79	Wintering	Feather	1
Ft Bragg, NC, USA	35.14	-79.00	Wintering	Feather	1
Hoke, NC, US	35.11	-79.35	Wintering	Feather	1
Jobos, PR	18.49	-67.06	Wintering	Feather	2
Knox, TN, USA	35.94	-83.69	Wintering	Feather	1
Los Banos, CA, USA	44.20	-123.57	Wintering	Feather	3
Malibu, CA, USA	34.02	-118.83	Wintering	Feather	4
Ormond Beach - Tomoka State Park, FL, USA	29.22	-81.06	Wintering	Feather	4
Point Reyes Station, CA, USA	38.05	-122.87	Wintering	Feather	2
Russell, AL, USA	32.34	-84.98	Wintering	Feather	10
San Carlos, Tamaulipas, Mexico	24.27	-98.84	Wintering	Feather	1

Location	Latitude	Longitude	Stage	Sample	Number
San Ignacio, 0, BE	17.15	-89.08	Wintering	Feather	8
San Jose Del Cabo, BCS, MX	23.05	-109.70	Wintering	Feather	7
Santiago, BCS, MX	23.48	-109.71	Wintering	Feather	1
Sherwood Content, Trelawny, Jamaica	18.36	-77.65	Wintering	Feather	13
Zuma Beach, CA, USA	34.05	-118.81	Wintering	Feather	16

Source: University of California Los Angeles

Table A-3: Wilson's Warbler Blood and Feather Sample Locations, Stage, Sample Type and Number of Samples

Location	Latitude	Longitude	Stage	Sample	Number
Ugashik_2, AK	57.18	-157.28	Breeding	Blood	16
Ugashik_1, AK	57.18	-157.27	Breeding	Blood	10
Cantwell_1, Denali National Park, AK	63.45	-150.81	Breeding	Blood	10
Cantwell_2, Denali National Park, AK	63.59	-149.61	Breeding	Blood	11
Denali, Denali National Park, AK	63.72	-149.09	Breeding	Blood	8
Yakutat, AK	59.51	-139.68	Breeding	Blood	21
Juneau, AK	58.30	-134.40	Breeding	Blood	10
Eureka, CA	40.78	-124.12	Breeding	Blood	18
Harlan, OR	44.51	-123.63	Breeding	Blood	23
Half Moon Bay, CA	37.51	-122.49	Breeding	Blood	17
Roy, WA	47.06	-122.49	Breeding	Blood	4
McKenzie Bridge, OR	44.20	-121.96	Breeding	Blood	22
Tennant, CA	41.49	-121.94	Breeding	Blood	25
Big Sur, CA	36.29	-121.84	Breeding	Blood	15
Darrington, WA	48.21	-121.58	Breeding	Blood	3
Silverton, WA	48.05	-121.43	Breeding	Blood	5
100 Mile House, BC	51.70	-121.30	Breeding	Blood	13
Clio, CA	39.67	-120.60	Breeding	Blood	15
San Luis Obispo, CA	35.20	-120.49	Breeding	Blood	23
Hume, CA	36.80	-118.60	Breeding	Blood	16
Elgin_2, OR	45.68	-118.12	Breeding	Blood	21
Elgin_1, OR	45.82	-117.87	Breeding	Blood	4
Hardisty Creek, Calgary, AB	53.50	-117.50	Breeding	Blood	2
Ram Falls, Calgary, AB	52.00	-115.80	Breeding	Blood	5
Benjamin Creek, Calgary, AB	51.50	-115.00	Breeding	Blood	2
Crow Creek, MT	47.47	-114.28	Breeding	Blood	1
Beaver Dam, Calgary, AB	51.10	-114.06	Breeding	Blood	16

Location	Latitude	Longitude	Stage	Sample	Number
Hillary Meadow, MT	48.35	-113.98	Breeding	Blood	2
Grand Mesa, CO	39.00	-107.90	Breeding	Blood	11
Pingree Park, Fort Colins, CO	40.55	-105.57	Breeding	Blood	19
Hilliardton, ON	47.50	-79.70	Breeding	Blood	4
Camp Myrica, QC	49.70	-73.30	Breeding	Blood	17
Fredericton, NB	45.80	-66.70	Breeding	Blood	4
Denny, CA	40.96	-123.49	Migrant	Feather	9
Big Sur, CA	36.29	-121.84	Migrant	Feather	10
Altamont, CA	37.75	-121.66	Migrant	Feather	3
O'neil Forbay Wildlife Area, CA	37.08	-121.02	Migrant	Feather	75
Sierra City, CA	39.62	-120.53	Migrant	Feather	9
Wild Horse Wind Facility, WA	47.01	-120.20	Migrant	Feather	1
Big Bear Lake, CA	34.23	-116.94	Migrant	Feather	11
Ivanpah Solar, CA	35.56	-115.47	Migrant	Feather	18
Desert Sunlight, CA	35.72	-115.38	Migrant	Feather	3
McCoy Solar, CA	33.71	-114.75	Migrant	Feather	18
Blythe Solar, CA	33.65	-114.72	Migrant	Feather	11
Colorado River Delta, Cibola, CA	33.30	-114.68	Migrant	Feather	604
Genesis Solar, CA	33.13	-114.51	Migrant	Feather	1
Buenos Aires National Wildlife Refuge, AZ	31.55	-111.55	Migrant	Feather	71
San Pedro Riparian National Conservation Area, AZ	31.58	-110.13	Migrant	Feather	52
San Jose del Cabo, Baja California Sur, MX	22.88	-109.90	Wintering	Feather	8
Albuquerque, NM	35.01	-106.47	Migrant	Feather	12
Chupaderos, Sinaloa, MX	23.33	-105.50	Wintering	Feather	8
Las Joyas, Autlan, Jalisco, MX	19.77	-104.37	Wintering	Feather	25
Nevado de Colima, Colima, Jalisco, MX	19.23	-103.72	Wintering	Feather	3
Sierra del Carmen #2, Coahuila, MX	28.86	-102.65	Migrant	Feather	3
Sierra del Carmen #1, Coahuila, MX	28.91	-102.55	Migrant	Feather	4
University of Mexico, San Angel, Distrito Federal, MX	19.31	-99.18	Wintering	Feather	9
El Cielo Biosphere Reserve, Tamulipas, MX	23.00	-99.10	Wintering	Feather	15
Coatapec, Veracruz, MX	19.45	-96.97	Wintering	Feather	13

Location	Latitude	Longitude	Stage	Sample	Number
Parque Macuiltepec, Xalapa, Veracruz, MX	19.55	-96.92	Wintering	Feather	7
Aeropuerto, Oaxaca, MX	17.10	-96.80	Wintering	Feather	14
Fairview, Tx	33.15	-96.60	Migrant	Feather	43
Tuxtlas, Veracruz, MX	18.40	-95.20	Wintering	Feather	9
Izalco, Sonsonate, SV	13.82	-89.65	Wintering	Feather	17
Los Andes National Park, Santa Ana, SV	13.85	-89.62	Wintering	Feather	7
Las Lajas, Santa Ana, SV	13.94	-89.62	Wintering	Feather	7
Metapan, Santa Ana, SV	14.40	-89.36	Wintering	Feather	9
San Salvador Volcano, SV	13.70	-89.20	Wintering	Feather	12
Chaa Creek, San Ignacio, BE	17.09	-89.07	Wintering	Feather	1
Cantoral, Tegucigalapa, HN	14.33	-87.40	Wintering	Feather	11
La Tigra National Park, Tegucigalpa, HN	14.10	-87.22	Wintering	Feather	15
El Jaguar Cafetal, Jinotega, NI	13.23	-86.05	Wintering	Feather	10
Volcan Mombacho, Granada, NI	11.83	-86.01	Wintering	Feather	2
Monteverde Cloud Forest, Santa Elena, CR	10.31	-84.83	Wintering	Feather	9
San Vito #3, Puntarenaus, CR	8.78	-82.98	Wintering	Feather	5
San Vito #5, Puntarenaus, CR	8.82	-82.97	Wintering	Feather	12
San Vito #2, Puntarenaus, CR	8.77	-82.94	Wintering	Feather	2
San Vito #1, Puntarenaus, CR	8.75	-82.93	Wintering	Feather	2
San Vito #4, Puntarenaus, CR	8.81	-82.92	Wintering	Feather	1
Braddock Bay, NY	43.16	-77.61	Migrant	Feather	19

Source: University of California Los Angeles

Table A-4: Burrowing Owl Blood, DNA and Feather Sample Location, Stage, Sample Type and Number of Samples

Nearest Town	Latitude	Longitude	Stage	Sample	Number
Albuquerque, NM	35.08	-106.63	Breeding	Blood	1
Alviso, CA	37.43	-122.01	Breeding	Blood	4
Avon Park, FL	27.60	-81.39	Breeding	Blood	1
Baker, OR	44.80	-117.83	Breeding	DNA	9
Buffalo Gap, SD	43.49	-103.31	Breeding	DNA	12
Cape Coral, FL	26.64	-81.99	Breeding	Blood	1
Clewiston, FL	26.52	-80.94	Breeding	Blood	1

Nearest Town	Latitude	Longitude	Stage	Sample	Number
Depot, OR	45.84	-119.43	Breeding	DNA	10
Fremont, CA	37.43	-122.01	Breeding	Blood	4
Grand View, ID	43.11	-116.01	Breeding	Blood	12
Lake Havasu City, AZ	34.47	-114.32	Breeding	Blood, Feather	12
Lake Placid, FL	27.18	-81.22	Breeding	Blood	1
Las Vegas, NV	36.30	-115.24	Breeding	Blood	7
Los Lunas, NM	34.80	-106.73	Breeding	Blood	5
Marco Island, FL	25.97	-81.72	Breeding	Blood	1
Melita, MAN	49.27	-100.99	Breeding	Blood	14
Moffett Field Mountain View, CA	37.43	-122.01	Breeding	Blood	6
Otay Mesa, CA	32.55	-116.98	Breeding	Blood, DNA	16
Pahrump, NV	36.30	-116.06	Breeding	Blood	1
Pasco, WA	46.26	-119.11	Breeding	DNA	7
Phoenix, AZ	33.37	-112.19	Breeding	Blood	14
Rocky Mountain Arsenal, CO	39.83	-104.84	Breeding	DNA	10
Spotlight 29, Coachella, CA	33.71	-116.18	Breeding	Blood, DNA	15
Tooele, UT	40.28	-112.31	Breeding	Blood	10
Venus, FL	27.17	-81.39	Breeding	Blood	1
Wistaria, CA	32.65	-115.61	Breeding	Blood, DNA	15
Altamont Pass Wind Farm, CA	37.75	-121.66	Migrant	Feather	17

Source: University of California Los Angeles

Table A-5: Summary of Bird Carcasses Collected From Each Solar Facility and Wind Farms

Site	Type	State	County	Latitude	Longitude	No. Birds	No. Species
Altamont Pass Wind Farm	Wind	CA	Alameda	37.75	-121.66	808	50
Blythe Mesa Solar Power Project	Solar PV	CA	Riverside	33.65	-114.72	226	51
Desert Sunlight Solar Farm	Solar PV	CA	Riverside	33.82	-115.38	288	69
Genesis Solar Energy Project	Solar Trough	CA	Riverside	33.66	-114.99	586	103
Ivanpah Solar Electric Generating	Solar Power	CA	San Bernardino	35.56	-115.47	1330	105

Site	Type	State	County	Lati-tude	Long-itude	No. Birds	No. Species
System	Tower						
McCoy Solar Energy Project	Solar PV	CA	Riverside	33.71	-114.75	245	58
Mojave Solar Project	Solar Trough	CA	San Bernardino	35.01	-117.32	123	36

Source: University of California Los Angeles

Table A-6: Samples Shipped Per Collection Date

Site	Mar 2016	Jun 2016	Mar 2017	May 2017	Jun 2017	Jul 2017	Oct 2017	Jun 2018	Jul 2018	Sep 2018	Oct 2018	Total
Altamont					54	131	76	434			113	808
Blythe				78				127		21+		226
Desert Sunlight		204								84+		288
Genesis	358*				185+			25		18+		586
Ivanpah				441*					889+			1330
McCoy					83+			146		16+		245
Mojave			123									123
Total per shipment	358	204	123	519	322	131	76	732	889	139	113	3606

Numbers with * were sampled on site; numbers with + were sampled at UCLA; all others were sampled at USGS then shipped to UCLA.

Source: University of California Los Angeles

Table A-7: Assignment Accuracy of American Kestrel Breeding Individuals Using 186 SNPs - First Assessment

Group of known-origin	Total	Alaska	East	Florida	Texas	West
Alaska	21	**0.71**	0.00	0.00	0.05	0.24
East	221	0.0051	**0.88**	0.02	0.00	0.10
Florida	30	0.00	0.23	**0.77**	0.00	0.00
Texas	12	0.00	0.00	0.00	**0.92**	0.08
West	217	0.03	0.05	0.01	0.00	**0.91**

Known-origin American Kestrels were assigned to one of five genetically distinct reporting groups: Alaska, East, Florida, Texas, West. Assignment accuracies were assessed for all individuals, including those used to design the assay (top), and for individuals of a known-origin not included in the design assay, reducing training bias (bottom). The proportion of individuals assigned to each group with certainty (>0.8 posterior probability) is shown. Bold values are correct assignments. There were not enough samples to test the assignment of Texas in the second assessment.

Source: University of California Los Angeles

Table A-8: Assignment Accuracy of American Kestrel Breeding Individuals Using 186 SNPs – Second Assessment

Group of known-origin	Total	Alaska	East	Florida	Texas	West
Alaska	6	**0.17**	0.00	0.00	-	0.83
East	158	0.00	**0.84**	0.03	-	0.14
Florida	14	0.00	0.50	**0.50**	-	0.00
Texas	1	0.00	0.00	0.00	-	1.00
West	150	0.01	0.05	0.02	-	**0.91**

Known-origin American Kestrels were assigned to one of five genetically distinct reporting groups: Alaska, East, Florida, Texas, West. Assignment accuracies were assessed for all individuals, including those used to design the assay (top), and for individuals of a known-origin not included in the design assay, reducing training bias (bottom). The proportion of individuals assigned to each group with certainty (>0.8 posterior probability) is shown. Bold values are correct assignments. There were not enough samples to test the assignment of Texas in the second assessment.

Source: University of California Los Angeles

Table A-9: Assignment Accuracy of Common Yellowthroat Breeding Individuals Using 96 SNPs

Group of known-origin	Total	California	South-west	Mid-west	New England	West
California	19	**15**	1	0	0	3
Midwest	107	0	0	**86**	21	0
New England	30	0	0	4	**26**	0
Southwest	25	0	**19**	1	0	5
West	61	1	1	0	0	**59**

Known-origin Common Yellowthroats were assigned to one of five genetically distinct reporting groups: California, West, Southwest, Midwest, New England (see Figure 1). Assignment accuracies were assessed for all individuals, included those used to design the assay. The proportion of individuals assigned to each group with certainty (>0.8 posterior probability) is shown. Bold values are correct assignments.

Source: University of California Los Angeles

Table A-10: Successfully Genotyped American Kestrel Carcasses from Wind and Solar Facilities or Live Birds Collected Near Facilities and The Posterior Probability of Assignment of Each Sample to One of 6 Genetic Groups

Sample	Carcass (Y/N)	Site	State	Lat	Long	Month	Day	Year	AK	East	FL	TX	West
201602377	**Y**	Altamont	CA	37.75	-121.66	APR	2	2007	0	0.018	0	0	**0.982**
201602388	**Y**	Altamont	CA	37.75	-121.66	APR	9	2007	0	0.542	0	0	0.458
201602392	**Y**	Altamont	CA	37.75	-121.66	APR	10	2007	0	0.018	0	0	**0.982**
201602410	**Y**	Altamont	CA	37.75	-121.66	MAY	15	2007	0	0.475	0	0	0.525
201602414	**Y**	Altamont	CA	37.75	-121.66	MAY	21	2007	0	0.006	0	0	**0.994**
201602415	**Y**	Altamont	CA	37.75	-121.66	MAY	21	2007	0.001	0.002	0	0	**0.997**
201602441	**Y**	Altamont	CA	37.75	-121.66	JUN	26	2007	0	0.195	0	0	**0.805**
201602442	**Y**	Altamont	CA	37.75	-121.66	JUN	26	2007	0.096	0.014	0	0	**0.889**
201602457	**Y**	Altamont	CA	37.75	-121.66	JUL	9	2007	0.001	0	0	0	**0.998**
201602490	**Y**	Altamont	CA	37.75	-121.66	AUG	15	2007	0	0.001	0	0	**0.999**
201602496	**Y**	Altamont	CA	37.75	-121.66	AUG	22	2007	0	0	0	0	**1**
201602497	**Y**	Altamont	CA	37.75	-121.66	AUG	22	2007	0	0.059	0	0	**0.941**
201602498	**Y**	Altamont	CA	37.75	-121.66	AUG	22	2007	0	0.003	0	0	**0.997**
201602499	**Y**	Altamont	CA	37.75	-121.66	AUG	22	2007	0	0.064	0	0	**0.936**
201602500	**Y**	Altamont	CA	37.75	-121.66	AUG	22	2007	0	0.008	0	0	**0.992**
201602511	**Y**	Altamont	CA	37.75	-121.66	SEP	10	2007	0	0.004	0	0	**0.996**
201602513	**Y**	Altamont	CA	37.75	-121.66	SEP	11	2007	0	0.003	0	0	**0.997**

Sample	Carcass (Y/N)	Site	State	Lat	Long	Month	Day	Year	AK	East	FL	TX	West
201602518	**Y**	Altamont	CA	37.75	-121.66	SEP	26	2007	0	0.011	0	0	**0.989**
201602523	**Y**	Altamont	CA	37.75	-121.66	OCT	2	2007	0	0.008	0	0	**0.992**
201602538	**Y**	Altamont	CA	37.75	-121.66	OCT	29	2007	0	0.037	0	0	**0.963**
201602553	**Y**	Altamont	CA	37.75	-121.66	NOV	6	2007	0.003	0	0	0	**0.997**
201602564	**Y**	Altamont	CA	37.75	-121.66	NOV	20	2007	0	0.011	0	0	**0.988**
201602569	**Y**	Altamont	CA	37.75	-121.66	NOV	29	2007	0	0.1	0	0	**0.9**
201602571	**Y**	Altamont	CA	37.75	-121.66	DEC	3	2007	0.115	0.023	0	0	**0.863**
201602573	**Y**	Altamont	CA	37.75	-121.66	DEC	4	2007	0	0.461	0	0	0.539
201602579	**Y**	Altamont	CA	37.75	-121.66	DEC	27	2007	0	0.012	0	0	**0.988**
201602580	**Y**	Altamont	CA	37.75	-121.66	DEC	27	2007	0	0.001	0	0	**0.999**
201602581	**Y**	Altamont	CA	37.75	-121.66	DEC	27	2007	0	0.718	0.116	0	0.166
201602584	**Y**	Altamont	CA	37.75	-121.66	JAN	3	2008	0.001	0.009	0	0	**0.99**
201602590	**Y**	Altamont	CA	37.75	-121.66	JAN	15	2008	0	0.003	0	0	**0.997**
201602591	**Y**	Altamont	CA	37.75	-121.66	JAN	16	2008	0	0.828	0	0	0.172
201602603	**Y**	Altamont	CA	37.75	-121.66	JAN	28	2008	0	0.034	0	0	**0.966**
201602605	**Y**	Altamont	CA	37.75	-121.66	JAN	29	2008	0	0.013	0	0	**0.987**
201602606	**Y**	Altamont	CA	37.75	-121.66	JAN	29	2008	0	0	0	0	**1**
201602609	**Y**	Altamont	CA	37.75	-121.66	JAN	31	2008	0	0	0	0	**1**
201602616	**Y**	Altamont	CA	37.75	-	FEB	18	2008	0.003	0.036	0	0	**0.961**

Sample	Carcass (Y/N)	Site	State	Lat	Long	Month	Day	Year	AK	East	FL	TX	West
					121.66								
201602617	**Y**	Altamont	CA	37.75	-121.66	FEB	18	2008	0	0	0	0	**1**
201602619	**Y**	Altamont	CA	37.75	-121.66	FEB	19	2008	0	0.032	0	0	**0.968**
201602621	**Y**	Altamont	CA	37.75	-121.66	FEB	19	2008	0	0.001	0	0	**0.999**
201602622	**Y**	Altamont	CA	37.75	-121.66	FEB	20	2008	0	0	0	0	**1**
201602623	**Y**	Altamont	CA	37.75	-121.66	FEB	21	2008	0	0.014	0.04	0	**0.946**
201602624	**Y**	Altamont	CA	37.75	-121.66	FEB	21	2008	0	0.012	0	0	**0.988**
201602627	**Y**	Altamont	CA	37.75	-121.66	FEB	25	2008	0.002	0	0	0	**0.998**
201602654	**Y**	Altamont	CA	37.75	-121.66	APR	24	2008	0	0.005	0	0	**0.995**
201602657	**Y**	Altamont	CA	37.75	-121.66	MAY	27	2008	0	0.166	0	0	**0.834**
201602660	**Y**	Altamont	CA	37.75	-121.66	JUN	2	2008	0	0.005	0	0	**0.995**
201602661	**Y**	Altamont	CA	37.75	-121.66	JUN	4	2008	0	0.002	0	0	**0.998**
201602677	**Y**	Altamont	CA	37.75	-121.66	JUL	8	2008	0	0.001	0	0	**0.999**
201602679	**Y**	Altamont	CA	37.75	-121.66	JUL	8	2008	0	0.161	0	0	**0.839**
201602685	**Y**	Altamont	CA	37.75	-121.66	AUG	12	2008	0.009	0.012	0	0	**0.978**
201602695	**Y**	Altamont	CA	37.75	-121.66	SEP	10	2008	0	0	0	0	**1**
201602698	**Y**	Altamont	CA	37.75	-121.66	SEP	11	2008	0	0.005	0	0	**0.995**
201602703	**Y**	Altamont	CA	37.75	-121.66	SEP	18	2008	0	0	0	0	**1**
201602728	**Y**	Altamont	CA	37.75	-121.66	OCT	21	2008	0	0	0	0	**1**

Sample	**Carcass (Y/N)**	**Site**	**State**	**Lat**	**Long**	**Month**	**Day**	**Year**	**AK**	**East**	**FL**	**TX**	**West**
201602733	**Y**	Altamont	CA	37.75	-121.66	OCT	29	2008	0	0.091	0	0	**0.909**
201602734	**Y**	Altamont	CA	37.75	-121.66	OCT	29	2008	0	0.017	0	0	**0.982**
201602737	**Y**	Altamont	CA	37.75	-121.66	JAN	10	2008	0	0.019	0	0	**0.981**
201602738	**Y**	Altamont	CA	37.75	-121.66	OCT	30	2008	0	0	0	0	**1**
201602740	**Y**	Altamont	CA	37.75	-121.66	NOV	10	2008	0	0	0	0	**1**
201602749	**Y**	Altamont	CA	37.75	-121.66	NOV	26	2008	0.001	0.005	0	0	**0.994**
201602755	**Y**	Altamont	CA	37.75	-121.66	JAN	13	2009	0	0	0	0	**1**
201602758	**Y**	Altamont	CA	37.75	-121.66	JAN	14	2009	0	0	0	0	**1**
201602767	**Y**	Altamont	CA	37.75	-121.66	FEB	5	2009	0	0.001	0	0	**0.999**
201602771	**Y**	Altamont	CA	37.75	-121.66	MAR	5	2009	0	0.003	0	0	**0.997**
201602772	**Y**	Altamont	CA	37.75	-121.66	MAR	6	2009	0	0.003	0	0	**0.997**
201602776	**Y**	Altamont	CA	37.75	-121.66	MAR	11	2009	0	0.053	0	0	**0.947**
201602787	**Y**	Altamont	CA	37.75	-121.66	MAR	26	2009	0	0	0	0	**1**
201602788	**Y**	Altamont	CA	37.75	-121.66	MAR	26	2009	0.002	0.096	0	0	**0.903**
201602796	**Y**	Altamont	CA	37.75	-121.66	APR	13	2009	0	0.012	0	0	**0.987**
201602807	**Y**	Altamont	CA	37.75	-121.66	MAY	21	2009	0	0.005	0	0	**0.995**
201602811	**Y**	Altamont	CA	37.75	-121.66	JUN	1	2009	0	0.169	0.004	0	**0.827**
201602815	**Y**	Altamont	CA	37.75	-121.66	JUN	12	2009	0.635	0.108	0	0	0.257
201602816	**Y**	Altamont	CA	37.75	-	JUN	16	2009	0	0	0	0	**1**

Sample	Carcass (Y/N)	Site	State	Lat	Long	Month	Day	Year	AK	East	FL	TX	West
					121.66								
201602829	**Y**	Altamont	CA	37.75	-121.66	AUG	5	2009	0.475	0	0	0	0.525
201602835	**Y**	Altamont	CA	37.75	-121.66	AUG	20	2009	0	0.003	0	0	**0.997**
201602836	**Y**	Altamont	CA	37.75	-121.66	SEP	2	2009	0	0.001	0	0	**0.999**
201602842	**Y**	Altamont	CA	37.75	-121.66	OCT	5	2009	0.001	0.056	0.035	0	**0.908**
201602848	**Y**	Altamont	CA	37.75	-121.66	OCT	8	2009	0	0.006	0	0	**0.994**
201602850	**Y**	Altamont	CA	37.75	-121.66	OCT	14	2009	0	0	0	0	**1**
201602866	**Y**	Altamont	CA	37.75	-121.66	NOV	16	2009	0.707	0	0	0	0.293
201602869	**Y**	Altamont	CA	37.75	-121.66	NOV	17	2009	0	0	0	0	**1**
201602871	**Y**	Altamont	CA	37.75	-121.66	NOV	18	2009	0	0.002	0	0	**0.998**
201602872	**Y**	Altamont	CA	37.75	-121.66	NOV	18	2009	0	0.008	0	0	**0.992**
201602874	**Y**	Altamont	CA	37.75	-121.66	NOV	19	2009	0	0	0	0	**1**
201602882	**Y**	Altamont	CA	37.75	-121.66	DEC	9	2009	0	0.013	0	0	**0.987**
201602889	**Y**	Altamont	CA	37.75	-121.66	JAN	7	2010	0	0.001	0	0	**0.999**
201602890	**Y**	Altamont	CA	37.75	-121.66	JAN	7	2010	0	0	0	0	**0.999**
201602895	**Y**	Altamont	CA	37.75	-121.66	FEB	11	2010	0	0	0	0	**1**
201602901	**Y**	Altamont	CA	37.75	-121.66	MAR	10	2010	0	0.002	0	0	**0.998**
201602912	**Y**	Altamont	CA	37.75	-121.66	APR	5	2010	0	0	0	0	**1**
201602913	**Y**	Altamont	CA	37.75	-121.66	APR	5	2010	0	0.001	0	0	**0.999**

Sample	Carcass (Y/N)	Site	State	Lat	Long	Month	Day	Year	AK	East	FL	TX	West
201602916	**Y**	Altamont	CA	37.75	-121.66	APR	8	2010	0	0.028	0	0	**0.972**
201602918	**Y**	Altamont	CA	37.75	-121.66	MAY	3	2010	0.029	0.003	0	0	**0.969**
201602931	**Y**	Altamont	CA	37.75	-121.66	JUN	1	2010	0	0.001	0	0	**0.999**
201602934	**Y**	Altamont	CA	37.75	-121.66	JUN	9	2010	0	0	0	0	**1**
201602950	**Y**	Altamont	CA	37.75	-121.66	AUG	17	2010	0	0	0	0	**1**
201602958	**Y**	Altamont	CA	37.75	-121.66	AUG	26	2010	0	0.004	0	0	**0.996**
201602959	**Y**	Altamont	CA	37.75	-121.66	AUG	30	2010	0	0	0	0	**1**
201602966	**Y**	Altamont	CA	37.75	-121.66	SEP	21	2010	0	0	0	0	**1**
201602988	**Y**	Altamont	CA	37.75	-121.66	OCT	26	2010	0	0.001	0	0	**0.999**
201603047	**Y**	Altamont	CA	37.75	-121.66	FEB	3	2010	0	0	0	0	**1**
201603097	**Y**	Altamont	CA	37.75	-121.66	MAR	8	2011	0	0	0	0	**1**
201603103	**Y**	Altamont	CA	37.75	-121.66	MAR	15	2011	0	0	0	0	**1**
201603107	**Y**	Altamont	CA	37.75	-121.66	MAR	16	2011	0	0.002	0	0	**0.998**
201603126	**Y**	Altamont	CA	37.75	-121.66	APR	20	2011	0	0	0	0	**1**
201603187	**Y**	Altamont	CA	37.75	-121.66	OCT	4	2011	0	0.001	0	0	**0.999**
201603228	**Y**	Altamont	CA	37.75	-121.66	MAR	12	2012	0	0.061	0.002	0	**0.936**
201603233	**Y**	Altamont	CA	37.75	-121.66	MAR	13	2012	0	0	0	0	**1**
201603253	**Y**	Altamont	CA	37.75	-121.66	JUN	20	2012	0.011	0.006	0	0	**0.983**
201603273	**Y**	Altamont	CA	37.75	-	SEP	10	2012	0	0	0	0	**1**

Sample	Carcass (Y/N)	Site	State	Lat	Long	Month	Day	Year	AK	East	FL	TX	West
					121.66								
201603274	**Y**	Altamont	CA	37.75	-121.66	SEP	11	2012	0	0.001	0	0	**0.999**
201603275	**Y**	Altamont	CA	37.75	-121.66	SEP	12	2012	0	0	0	0	**1**
201603281	**Y**	Altamont	CA	37.75	-121.66	OCT	8	2012	0	0	0	0	**1**
201603283	**Y**	Altamont	CA	37.75	-121.66	OCT	10	2012	0.004	0	0	0	**0.996**
201603293	**Y**	Altamont	CA	37.75	-121.66	OCT	30	2012	0	0.001	0	0	**0.999**
201702052	**Y**	Altamont	CA	37.75	-121.66	FEB	1	2012	0	0.267	0.001	0	0.733
201603307	**Y**	Altamont	CA	37.75	-121.66	JAN	10	2013	0	0	0	0	**1**
201603313	**Y**	Altamont	CA	37.75	-121.66	JAN	22	2013	0	0.004	0	0	**0.996**
201603316	**Y**	Altamont	CA	37.75	-121.66	JAN	31	2013	0.065	0.59	0	0	0.345
201603334	**Y**	Altamont	CA	37.75	-121.66	MAY	9	2013	0	0.003	0	0	**0.997**
201603339	**Y**	Altamont	CA	37.75	-121.66	JUN	6	2013	0	0	0	0	**1**
201603342	**Y**	Altamont	CA	37.75	-121.66	JUN	19	2013	0	0.03	0	0	**0.97**
201603345	**Y**	Altamont	CA	37.75	-121.66	JUN	27	2013	0	0.006	0	0	**0.994**
201603351	**Y**	Altamont	CA	37.75	-121.66	JUL	8	2013	0	0	0	0	**1**
201603366	**Y**	Altamont	CA	37.75	-121.66	AUG	28	2013	0	0	0	0	**1**
201603375	**Y**	Altamont	CA	37.75	-121.66	SEP	18	2013	0	0.091	0	0	**0.909**
201603377	**Y**	Altamont	CA	37.75	-121.66	SEP	18	2013	0	0.001	0	0	**0.999**
201603384	**Y**	Altamont	CA	37.75	-121.66	SEP	26	2013	0	0	0	0	**0.999**

Sample	Carcass (Y/N)	Site	State	Lat	Long	Month	Day	Year	AK	East	FL	TX	West
201603385	**Y**	Altamont	CA	37.75	-121.66	SEP	30	2013	0	0	0	0	**1**
201603396	**Y**	Altamont	CA	37.75	-121.66	OCT	21	2013	0	0	0	0	**1**
201603398	**Y**	Altamont	CA	37.75	-121.66	OCT	21	2013	0	0	0	0	**1**
201603403	**Y**	Altamont	CA	37.75	-121.66	OCT	22	2013	0	0.001	0	0	**0.999**
201603404	**Y**	Altamont	CA	37.75	-121.66	OCT	22	2013	0	0	0	0	**1**
201603408	**Y**	Altamont	CA	37.75	-121.66	OCT	24	2013	0	0	0	0	**1**
201603415	**Y**	Altamont	CA	37.75	-121.66	NOV	13	2013	0	0	0	0	**1**
201603422	**Y**	Altamont	CA	37.75	-121.66	JAN	15	2014	0	0.002	0	0	**0.998**
201603430	**Y**	Altamont	CA	37.75	-121.66	FEB	24	2014	0	0.001	0	0	**0.999**
201603438	**Y**	Altamont	CA	37.75	-121.66	APR	2	2014	0	0.003	0	0	**0.997**
201603446	**Y**	Altamont	CA	37.75	-121.66	MAY	29	2014	0	0.014	0	0	**0.985**
201603454	**Y**	Altamont	CA	37.75	-121.66	JUN	16	2014	0	0.001	0	0	**0.999**
201603457	**Y**	Altamont	CA	37.75	-121.66	JUN	23	2014	0	0.017	0	0	**0.983**
201603471	**Y**	Altamont	CA	37.75	-121.66	SEP	29	2014	0	0.007	0	0	**0.993**
201603472	**Y**	Altamont	CA	37.75	-121.66	OCT	13	2014	0	0.003	0	0	**0.997**
201603476	**Y**	Altamont	CA	37.75	-121.66	OCT	15	2014	0	0.008	0	0	**0.992**
201603477	**Y**	Altamont	CA	37.75	-121.66	OCT	20	2014	0	0	0	0	**1**
201603482	**Y**	Altamont	CA	37.75	-121.66	NOV	10	2014	0	0	0	0	**1**
201600578	**Y**	Altamont	CA	37.75	-	NOV	23	2015	0	0.012	0	0	**0.988**

Sample	Carcass (Y/N)	Site	State	Lat	Long	Month	Day	Year	AK	East	FL	TX	West
					121.66								
201603487	**Y**	Altamont	CA	37.75	-121.66	JAN	7	2015	0	0.779	0	0	0.221
201603489	**Y**	Altamont	CA	37.75	-121.66	JAN	14	2015	0	0	0	0	**1**
201603495	**Y**	Altamont	CA	37.75	-121.66	FEB	24	2015	0	0	0	0	**1**
16N3353	**Y**	Altamont	CA	37.75	-121.66	DEC	13	2016	0.003	0	0	0	**0.997**
201700016	**Y**	Altamont	CA	37.75	-121.66	OCT	10	2016	0	0.001	0	0	**0.999**
201708209_b	**Y**	Altamont	CA	37.75	-121.66	AUG	22	2017	0	0	0	0	**1**
201708224_b	**Y**	Altamont	CA	37.75	-121.66	SEP	8	2017	0.001	0.01	0	0	**0.989**
201708234_b	**Y**	Altamont	CA	37.75	-121.66	SEP	26	2017	0	**0.993**	0.003	0	0.004
201708235_b	**Y**	Altamont	CA	37.75	-121.66	SEP	27	2017	0	0	0	0	**1**
201800104_b	**Y**	Altamont	CA	37.75	-121.66	OCT	2	2017	0	0.005	0	0	**0.995**
201800115_b	**Y**	Altamont	CA	37.75	-121.66	OCT	9	2017	0	0	0	0	**1**
201800130_b	**Y**	Altamont	CA	37.75	-121.66	OCT	18	2017	0	0	0	0	**1**
201800135_b	**Y**	Altamont	CA	37.75	-121.66	OCT	26	2017	0	0.444	0	0	0.556
201800142_b	**Y**	Altamont	CA	37.75	-121.66	NOV	8	2017	0	0	0	0	**1**
201800151_b	**Y**	Altamont	CA	37.75	-121.66	NOV	29	2017	0	0	0	0	**1**
18N00021	**N**	Calipatria	CA	33.18	-115.61	JAN	28	2018	0	0	0.003	0	**0.997**
18N00022	**N**	Calipatria	CA	33.17	-115.62	JAN	28	2018	0	0.001	0	0	**0.999**
18N00023	**N**	Calipatria	CA	33.15	-115.61	JAN	28	2018	0	0	0	0	**1**

Sample	**Carcass (Y/N)**	**Site**	**State**	**Lat**	**Long**	**Month**	**Day**	**Year**	**AK**	**East**	**FL**	**TX**	**West**
18N00024	**N**	Calipatria	CA	33.15	-115.64	JAN	28	2018	0.001	0	0	0	**0.999**
18N00025	**N**	Calipatria	CA	33.14	-115.65	JAN	28	2018	0	0	0	0	**1**
18N00026	**N**	Calipatria	CA	33.13	-115.65	JAN	28	2018	0	0.013	0	0	**0.987**
18N00027	**N**	Calipatria	CA	33.12	-115.6	JAN	28	2018	0	0	0	0	**1**
18N00028	**N**	Calipatria	CA	33.1	-115.49	JAN	28	2018	0	0.042	0	0.002	**0.956**
18N00031	**N**	Calipatria	CA	33.07	-115.66	JAN	29	2018	0	0	0	0	**1**
18N00032	**N**	Calipatria	CA	33.07	-115.66	JAN	29	2018	0	0	0	0	**1**
18N00033	**N**	Calipatria	CA	33.06	-115.61	JAN	29	2018	0	0.076	0	0	**0.924**
15N2520	**Y**	Genesis	CA	33.13	-114.51	OCT	19	2015	0	0.105	0	0	**0.894**
15N2537	**Y**	Genesis	CA	33.13	-114.51	OCT	19	2015	0	0.009	0	0	**0.991**
15N2562	**Y**	Genesis	CA	33.13	-114.51	OCT	2	2015	0	0	0	0	**1**
15N2585	**Y**	Genesis	CA	33.13	-114.51	JUL	2	2015	0	0	0	**0.928**	0.072
15N2585	**Y**	Genesis	CA	33.13	-114.51	JUL	2	2015	0	0	0	**0.928**	0.072
15N3259	**Y**	Ivanpah	CA	35.56	-115.47	JUN	30	2015	0	0.002	0	0	**0.998**
15N3260	**Y**	Ivanpah	CA	35.56	-115.47	AUG	5	2015	0	0.019	0	0	**0.981**
15N3266	**Y**	Ivanpah	CA	35.56	-115.47	SEP	8	2015	0.051	0.009	0	0	**0.94**
15N3268	**Y**	Ivanpah	CA	35.56	-115.47	SEP	13	2015	0.001	0.001	0.001	0	**0.997**
15N3269	**Y**	Ivanpah	CA	35.56	-115.47	OCT	8	2015	0	0.06	0	0	**0.94**
15N3753	**Y**	Ivanpah	CA	35.56	-115.47	SEP	1	2015	0	0	0	0.001	**0.999**

Sample	Carcass (Y/N)	Site	State	Lat	Long	Month	Day	Year	AK	East	FL	TX	West
15N3754	**Y**	Ivanpah	CA	35.56	-115.47	AUG	25	2015	0	0.012	0	0	**0.988**
15N3755	**Y**	Ivanpah	CA	35.56	-115.47	APR	7	2015	0	0	0	0	**1**
15N3756	**Y**	Ivanpah	CA	35.56	-115.47	SEP	8	2015	0	0	0	0	**1**
15N3757	**Y**	Ivanpah	CA	35.56	-115.47	SEP	13	2015	0	0	0	0	**1**
15N3758	**Y**	Ivanpah	CA	35.56	-115.47	SEP	22	2015	0	0	0	0	**1**
15N3759	**Y**	Ivanpah	CA	35.56	-115.47	OCT	1	2015	0	0.045	0	0	**0.955**
15N3760	**Y**	Ivanpah	CA	35.56	-115.47	NOV	17	2015	0.001	0.005	0.007	0	**0.988**

Source: University of California Los Angeles

Table A-11: Successfully Genotyped Common Yellowthroat Carcasses from Wind and Solar Facilities or Live Birds Collected Near Facilities and the Posterior Probability of Assignment of Each Sample to One of 5 Genetic Groups

Sample	Carcass (Y/N)	Site	State	Lat	Long	Month	Day	Year	California	Midwest	New England	South-west	West
15N2874	Y	Desert Sunlight	CA	35.72	-115.38	SEP	22	2015	0.000	0.000	0.000	0.000	**1.000**
15N2875	Y	Desert Sunlight	CA	35.71506	-115.38	SEP	22	2015	0.000	0.000	0.000	0.000	**1.000**
16N2381	Y	Mojave	CA	35.012	-117.32	AUG	30	2016	0.004	0.000	0.000	0.000	**0.996**
16N2384	Y	Mojave	CA	35.012	-117.32	SEP	20	2016	0.003	0.000	0.000	0.000	**0.997**
16N2385	Y	Mojave	CA	35.012	-117.32	SEP	21	2016	0.001	0.000	0.000	0.000	**0.999**
16N2386	Y	Mojave	CA	35.012	-117.32	SEP	26	2016	0.000	0.000	0.000	0.000	**1.000**
16N2387	Y	Mojave	CA	35.012	-117.32	SEP	27	2016	0.000	0.000	0.000	0.000	**1.000**
16N2388	Y	Mojave	CA	35.012	-117.32	OCT	6	2016	0.634	0.000	0.000	0.000	0.366

Sample	Carcass (Y/N)	Site	State	Lat	Long	Month	Day	Year	California	Midwest	New England	South-west	West
16N2877	Y	Genesis	CA	33.127	-114.51	AUG	31	2016	0.000	0.000	0.000	0.000	**1.000**
16N2881	Y	Genesis	CA	33.127	-114.51	AUG	30	2016	0.002	0.000	0.000	0.000	**0.998**
16N2966	Y	McCoy	CA	33.71	-114.75	SEP	16	2016	0.000	0.000	0.000	0.000	**1.000**
17N00569	Y	Blythe	CA	33.65	-114.72	MAR	28	2017	0.031	0.000	0.000	0.000	**0.969**
17N00600	Y	Blythe	CA	33.65	-114.72	MAR	22	2017	0.001	0.000	0.000	0.000	**0.999**
17N02946	Y	Blythe	CA	33.65	-114.72	SEP	6	2017	0.000	0.000	0.000	0.000	**1.000**
17N02970	Y	Blythe	CA	33.65	-114.72	SEP	28	2017	0.000	0.000	0.000	0.000	**1.000**

Source: University of California Los Angeles

Table A-12: Successfully Genotyped Wilson's Warbler Carcasses from Wind and Solar Facilities or Live Birds Collected Near Facilities and the Posterior Probability of Assignment of Each Sample to One of 6 Genetic Groups

Sample	Carcass (Y/N)	Site	State	Lat	Long	Month	Day	Year	Western Boreal	Coastal CA	Eastern Boreal	Pacific Northwest	Basin Rockies	Sierra
17N00743	**Y**	Altamont	CA	37.75	-121.66	MAY	17	2017	**1**	0	0	0	0	0
17N01293	**Y**	Altamont	CA	37.75	-121.66	JUN	1	2017	0	0.552	0	0.448	0	0
17N02875	**Y**	Altamont	CA	37.75	-121.66	SEP	20	2017	0	0.005	0	**0.991**	0	0.004
17N02876	**Y**	Altamont	CA	37.75	-121.66	SEP	25	2017	0	0	0	1	0	0
15N3818	**Y**	Blythe	CA	33.65	-114.72	MAY	6	2015	**0.997**	0	0	0	0.003	0
15N3819	**Y**	Blythe	CA	33.65	-114.72	MAY	7	2015	**1**	0	0	0	0	0
16N2987	**Y**	Blythe	CA	33.65	-114.72	APR	14	2016	0	**0.999**	0	0	0	0.001
16N2992	**Y**	Blythe	CA	33.65	-114.72	MAY	19	2016	**1**	0	0	0	0	0

Sample	Carcass (Y/N)	Site	State	Lat	Long	Month	Day	Year	Western Boreal	Coastal CA	Eastern Boreal	Pacific Northwest	Basin Rockies	Sierra
16N3204	**Y**	Blythe	CA	33.65	-114.72	SEP	15	2016	0	**0.999**	0	0.001	0	0
16N3213	**Y**	Blythe	CA	33.65	-114.72	OCT	6	2016	0	0	0	**0.995**	0	0.005
17N00570	**Y**	Blythe	CA	33.65	-114.72	MAR	28	2017	0	**0.815**	0	0.148	0	0.037
17N00576	**Y**	Blythe	CA	33.65	-114.72	APR	18	2017	0.006	0	0	**0.994**	0	0
17N00584	**Y**	Blythe	CA	33.65	-114.72	APR	25	2017	**1**	0	0	0	0	0
17N00585	**Y**	Blythe	CA	33.65	-114.72	MAY	1	2017	0	0.025	0	**0.906**	0	0.07
17N00587	**Y**	Blythe	CA	33.65	-114.72	MAY	2	2017	0.545	0	0	0.455	0	0
17N00590	**Y**	Blythe	CA	33.65	-114.72	MAY	2	2017	**1**	0	0	0	0	0
17N00596	**Y**	Blythe	CA	33.65	-114.72	MAY	16	2017	**1**	0	0	0	0	0
17N02953	**Y**	Blythe	CA	33.65	-114.72	SEP	12	2017	0	0	0	**1**	0	0
17N02978	**Y**	Blythe	CA	33.65	-114.72	OCT	2	2017	0	0.001	0	**0.999**	0	0
16N0935	**Y**	Desert Sunlight	CA	35.72	-115.38	MAY	19	2016	**1**	0	0	0	0	0
15N3246	**Y**	Ivanpah	CA	35.56	-115.47	APR	30	2015	**1**	0	0	0	0	0
15N3248	**Y**	Ivanpah	CA	35.56	-115.47	MAY	13	2015	**1**	0	0	0	0	0
15N3249	**Y**	Ivanpah	CA	35.56	-115.47	MAY	13	2015	**1**	0	0	0	0	0
15N3250	**Y**	Ivanpah	CA	35.56	-115.47	MAY	28	2015	0.001	0.004	0	**0.995**	0	0.001
15N3251	**Y**	Ivanpah	CA	35.56	-115.47	AUG	8	2015	0.001	0	0	**0.998**	0	0
15N3252	**Y**	Ivanpah	CA	35.56	-115.47	AUG	12	2015	0	0	0	**1**	0	0
15N3253	**Y**	Ivanpah	CA	35.56	-	AUG	19	2015	0	0.324	0	0.625	0	0.051

Sample	Carcass (Y/N)	Site	State	Lat	Long	Month	Day	Year	Western Boreal	Coastal CA	Eastern Boreal	Pacific Northwest	Basin Rockies	Sierra
					115.47									
15N3254	**Y**	Ivanpah	CA	35.56	-115.47	AUG	26	2015	0	0.001	0	**0.999**	0	0
15N3256	**Y**	Ivanpah	CA	35.56	-115.47	AUG	26	2015	0	0.101	0	**0.878**	0	0.021
15N3258	**Y**	Ivanpah	CA	35.56	-115.47	SEP	9	2015	0	0.001	0	**0.999**	0	0
15N3770	**Y**	Ivanpah	CA	35.56	-115.47	APR	20	2015	**1**	0	0	0	0	0
15N3771	**Y**	Ivanpah	CA	35.56	-115.47	APR	28	2015	0	0.004	0	**0.991**	0	0.005
15N3772	**Y**	Ivanpah	CA	35.56	-115.47	APR	30	2015	**1**	0	0	0	0	0
15N3773	**Y**	Ivanpah	CA	35.56	-115.47	AUG	26	2015	0.021	0.002	0	**0.977**	0	0
15N3774	**Y**	Ivanpah	CA	35.56	-115.47	SEP	16	2015	0	0	0	0.546	0	0.454
16N2934	**Y**	Ivanpah	CA	35.56	-115.47	APR	10	2016	**0.999**	0	0	0.001	0	0
16N4393	**Y**	Ivanpah	CA	35.56	-115.47	MAY	10	2016	**1**	0	0	0	0	0
16N4395	**Y**	Ivanpah	CA	35.56	-115.47	MAY	10	2016	0.21	0	0	0.79	0	0
16N4396	**Y**	Ivanpah	CA	35.56	-115.47	MAY	10	2016	**1**	0	0	0	0	0
16N4400	**Y**	Ivanpah	CA	35.56	-115.47	MAY	11	2016	**1**	0	0	0	0	0
16N4401	**Y**	Ivanpah	CA	35.56	-115.47	MAY	13	2016	**0.993**	0	0	0	0.007	0
16N4405	**Y**	Ivanpah	CA	35.56	-115.47	MAY	16	2016	**1**	0	0	0	0	0
16N4407	**Y**	Ivanpah	CA	35.56	-115.47	MAY	16	2016	**1**	0	0	0	0	0
16N4408	**Y**	Ivanpah	CA	35.56	-115.47	MAY	16	2016	**1**	0	0	0	0	0
16N4491	**Y**	Ivanpah	CA	35.56	-115.47	AUG	26	2016	0	0.003	0	**0.838**	0	0.159

Sample	Carcass (Y/N)	Site	State	Lat	Long	Month	Day	Year	Western Boreal	Coastal CA	Eastern Boreal	Pacific Northwest	Basin Rockies	Sierra
16N4499	**Y**	Ivanpah	CA	35.56	-115.47	AUG	29	2016	0	0.001	0	0.23	0	0.769
16N4503	**Y**	Ivanpah	CA	35.56	-115.47	AUG	29	2016	0	0	0	**1**	0	0
16N4519	**Y**	Ivanpah	CA	35.56	-115.47	AUG	30	2016	0.004	0	0	**0.996**	0	0
16N4524	**Y**	Ivanpah	CA	35.56	-115.47	AUG	30	2016	0	0.316	0	0.542	0	0.142
16N4551	**Y**	Ivanpah	CA	35.56	-115.47	SEP	5	2016	0	0.001	0	0.008	0	**0.991**
16N4608	**Y**	Ivanpah	CA	35.56	-115.47	SEP	13	2016	0	0.018	0	**0.973**	0	0.009
16N4653	**Y**	Ivanpah	CA	35.56	-115.47	SEP	21	2016	0	0.018	0	**0.982**	0	0
17N03215	**Y**	Ivanpah	CA	35.56	-115.47	MAY	15	2017	**1**	0	0	0	0	0
17N03217	**Y**	Ivanpah	CA	35.56	-115.47	MAY	16	2017	**1**	0	0	0	0	0
17N03223	**Y**	Ivanpah	CA	35.56	-115.47	MAY	30	2017	**1**	0	0	0	0	0
17N03302	**Y**	Ivanpah	CA	35.56	-115.47	AUG	29	2017	0	0.015	0	**0.985**	0	0
17N03319	**Y**	Ivanpah	CA	35.56	-115.47	SEP	6	2017	0.001	0	0	**0.999**	0	0
17N03407	**Y**	Ivanpah	CA	35.56	-115.47	OCT	18	2017	0.019	0.08	0	**0.901**	0	0
17N03410	**Y**	Ivanpah	CA	35.56	-115.47	OCT	18	2017	**1**	0	0	0	0	0
18N00637	**Y**	Ivanpah	CA	35.56	-115.47	APR	24	2018	**1**	0	0	0	0	0
18N00644	**Y**	Ivanpah	CA	35.56	-115.47	APR	24	2018	**1**	0	0	0	0	0
18N00653	**Y**	Ivanpah	CA	35.56	-115.47	APR	28	2018	**1**	0	0	0	0	0
18N00654	**Y**	Ivanpah	CA	35.56	-115.47	APR	28	2018	**1**	0	0	0	0	0
18N00655	**Y**	Ivanpah	CA	35.56	-	APR	28	2018	**0.975**	0	0	0.025	0	0

Sample	Carcass (Y/N)	Site	State	Lat	Long	Month	Day	Year	Western Boreal	Coastal CA	Eastern Boreal	Pacific Northwest	Basin Rockies	Sierra
					115.47									
18N00662	**Y**	Ivanpah	CA	35.56	-115.47	MAY	7	2018	**1**	0	0	0	0	0
18N00663	**Y**	Ivanpah	CA	35.56	-115.47	MAY	8	2018	**0.999**	0	0	0.001	0	0
18N00668	**Y**	Ivanpah	CA	35.56	-115.47	MAY	9	2018	**1**	0	0	0	0	0
18N00669	**Y**	Ivanpah	CA	35.56	-115.47	MAY	9	2018	**1**	0	0	0	0	0
18N00677	**Y**	Ivanpah	CA	35.56	-115.47	MAY	10	2018	**1**	0	0	0	0	0
18N00679	**Y**	Ivanpah	CA	35.56	-115.47	MAY	10	2018	**1**	0	0	0	0	0
18N00681	**Y**	Ivanpah	CA	35.56	-115.47	MAY	10	2018	**1**	0	0	0	0	0
18N00687	**Y**	Ivanpah	CA	35.56	-115.47	MAY	10	2018	**1**	0	0	0	0	0
18N00688	**Y**	Ivanpah	CA	35.56	-115.47	MAY	10	2018	**1**	0	0	0	0	0
18N00689	**Y**	Ivanpah	CA	35.56	-115.47	MAY	10	2018	**1**	0	0	0	0	0
18N00690	**Y**	Ivanpah	CA	35.56	-115.47	MAY	10	2018	**0.989**	0	0	0.011	0	0
18N00691	**Y**	Ivanpah	CA	35.56	-115.47	MAY	10	2018	**0.995**	0	0	0.005	0	0
18N00698	**Y**	Ivanpah	CA	35.56	-115.47	MAY	16	2018	**0.971**	0	0	0.029	0	0
18N00699	**Y**	Ivanpah	CA	35.56	-115.47	MAY	22	2018	**1**	0	0	0	0	0
18N00705	**Y**	Ivanpah	CA	35.56	-115.47	MAY	22	2018	**1**	0	0	0	0	0
18N00706	**Y**	Ivanpah	CA	35.56	-115.47	MAY	22	2018	**1**	0	0	0	0	0
18N00713	**Y**	Ivanpah	CA	35.56	-115.47	MAY	22	2018	**1**	0	0	0	0	0
18N00719	**Y**	Ivanpah	CA	35.56	-115.47	JUN	7	2018	**1**	0	0	0	0	0

Sample	Carcass (Y/N)	Site	State	Lat	Long	Month	Day	Year	Western Boreal	Coastal CA	Eastern Boreal	Pacific Northwest	Basin Rockies	Sierra
18N00726	**Y**	Ivanpah	CA	35.56	-115.47	JUN	25	2018	**0.999**	0	0	0.001	0	0
15N3875	**Y**	McCoy	CA	33.71	-114.75	SEP	28	2015	0	0	**1**	0	0	0
16N2937	**Y**	McCoy	CA	33.71	-114.75	MAR	21	2016	0	**1**	0	0	0	0
16N2948	**Y**	McCoy	CA	33.71	-114.75	APR	29	2016	**1**	0	0	0	0	0
16N2949	**Y**	McCoy	CA	33.71	-114.75	MAY	3	2016	**1**	0	0	0	0	0
16N2950	**Y**	McCoy	CA	33.71	-114.75	MAY	4	2016	0	0.002	0	**0.918**	0	0.08
16N2952	**Y**	McCoy	CA	33.71	-114.75	MAY	9	2016	**1**	0	0	0	0	0
16N2953	**Y**	McCoy	CA	33.71	-114.75	MAY	10	2016	0	0.002	0.498	0.398	0	0.103
16N2962	**Y**	McCoy	CA	33.71	-114.75	SEP	6	2016	0	0.019	0	**0.981**	0	0
17N00479	**Y**	McCoy	CA	33.71	-114.75	APR	14	2017	0	0.001	0	**0.995**	0	0.004
17N00485	**Y**	McCoy	CA	33.71	-114.75	APR	27	2017	0	0.015	0	**0.982**	0	0.003
17N00486	**Y**	McCoy	CA	33.71	-114.75	MAY	15	2017	**1**	0	0	0	0	0
17N00487	**Y**	McCoy	CA	33.71	-114.75	MAY	15	2017	0.008	**0.941**	0	0.015	0	0.035
17N00617	**Y**	McCoy	CA	33.71	-114.75	MAY	8	2017	**0.978**	0	0	0.002	0.02	0
17N00618	**Y**	McCoy	CA	33.71	-114.75	MAY	8	2017	**0.996**	0	0	0.004	0	0
17N00619	**Y**	McCoy	CA	33.71	-114.75	MAY	1	2017	**0.998**	0.002	0	0	0	0
17N00621	**Y**	McCoy	CA	33.71	-114.75	MAY	2	2017	**1**	0	0	0	0	0
17N03066	**Y**	McCoy	CA	33.71	-114.75	SEP	9	2017	0	**0.999**	0	0.001	0	0
97N5441	**N**	Altruras	CA	41.47	-	MAY	25	1997	**1**	0	0	0	0	0

Sample	**Carcass (Y/N)**	**Site**	**State**	**Lat**	**Long**	**Month**	**Day**	**Year**	**Western Boreal**	**Coastal CA**	**Eastern Boreal**	**Pacific Northwest**	**Basin Rockies**	**Sierra**
					120.55									
97N5442	**N**	Altruras	CA	41.47	-120.55	MAY	25	1997	**1**	0	0	0	0	0
97N5443	**N**	Altruras	CA	41.47	-120.55	MAY	18	1997	**1**	0	0	0	0	0
97N5444	**N**	Altruras	CA	41.47	-120.55	MAY	25	1997	**0.999**	0	0	0	0.001	0
97N5445	**N**	Altruras	CA	41.47	-120.55	MAY	25	1997	**1**	0	0	0	0	0
96N0621	**N**	Big Bear Lake	CA	34.23	-116.94	MAY	23	1996	0	0.029	0	0.01	0	**0.962**
96N0624	**N**	Big Bear Lake	CA	34.23	-116.94	MAY	23	1996	0	0	0	0.037	0	**0.963**
96N0627	**N**	Big Bear Lake	CA	34.23	-116.94	AUG	15	1996	0	0	0	**1**	0	0
96N0628	**N**	Big Bear Lake	CA	34.23	-116.94	AUG	15	1996	0	**0.997**	0	0	0	0.003
96N0629	**N**	Big Bear Lake	CA	34.23	-116.94	AUG	22	1996	0	0.234	0	0.746	0	0.019
96N0630	**N**	Big Bear Lake	CA	34.23	-116.94	AUG	22	1996	0	0.002	0	**0.998**	0	0
96N0631	**N**	Big Bear Lake	CA	34.23	-116.94	AUG	22	1996	0	0	0	**0.994**	0	0.005
96N0633	**N**	Big Bear Lake	CA	34.23	-116.94	AUG	22	1996	0	0	0	**1**	0	0
96N0634	**N**	Big Bear Lake	CA	34.23	-116.94	AUG	22	1996	0	0.78	0	0.22	0	0
96N0635	**N**	Big Bear Lake	CA	34.23	-116.94	AUG	22	1996	0	0	0	**1**	0	0
96N0636	**N**	Big Bear Lake	CA	34.23	-116.94	AUG	22	1996	0	0.002	0	**0.997**	0	0
96N0637	**N**	Big Bear Lake	CA	34.23	-116.94	AUG	22	1996	0	0.066	0	**0.921**	0	0.013
96N0638	**N**	Big Bear Lake	CA	34.23	-116.94	AUG	22	1996	0	**0.969**	0	0.03	0	0.001
10N12197	**N**	Calipatria	CA	33.18	-115.62	APR	30	2010	**1**	0	0	0	0	0

Sample	Carcass (Y/N)	Site	State	Lat	Long	Month	Day	Year	Western Boreal	Coastal CA	Eastern Boreal	Pacific Northwest	Basin Rockies	Sierra
10N12198	**N**	Calipatria	CA	33.18	-115.62	APR	30	2010	**1**	0	0	0	0	0
10N12199	**N**	Calipatria	CA	33.18	-115.62	MAY	1	2010	**1**	0	0	0	0	0
10N12200	**N**	Calipatria	CA	33.18	-115.62	MAY	1	2010	**1**	0	0	0	0	0
10N12201	**N**	Calipatria	CA	33.18	-115.62	MAY	1	2010	**1**	0	0	0	0	0
10N12202	**N**	Calipatria	CA	33.18	-115.62	MAY	2	2010	**1**	0	0	0	0	0
10N12203	**N**	Calipatria	CA	33.18	-115.62	MAY	2	2010	**1**	0	0	0	0	0
10N12204	**N**	Calipatria	CA	33.18	-115.62	MAY	2	2010	**1**	0	0	0	0	0
10N12205	**N**	Calipatria	CA	33.18	-115.62	MAY	2	2010	**1**	0	0	0	0	0
10N12206	**N**	Calipatria	CA	33.18	-115.62	MAY	2	2010	**1**	0	0	0	0	0
10N12207	**N**	Calipatria	CA	33.18	-115.62	MAY	3	2010	**1**	0	0	0	0	0
10N12208	**N**	Calipatria	CA	33.18	-115.62	MAY	4	2010	**1**	0	0	0	0	0
10N12209	**N**	Calipatria	CA	33.18	-115.62	MAY	4	2010	**1**	0	0	0	0	0
97N5584	**N**	Colusa County	CA	39.37	-122.5	MAY	18	1997	**0.974**	0	0	0	0.026	0
97N5585	**N**	Colusa County	CA	39.37	-122.5	MAY	18	1997	**1**	0	0	0	0	0
97N5586	**N**	Colusa County	CA	39.37	-122.5	MAY	18	1997	**1**	0	0	0	0	0
03N4361	**N**	Idyllwild	CA	33.81	-116.77	MAY	23	2003	**0.999**	0	0	0.001	0	0
03N5650	**N**	Kern	CA	35.67	-118.3	MAY	16	2003	**1**	0	0	0	0	0
06N30554	**N**	Onyx	CA	35.73	-118.17	MAY	19	2007	**0.91**	0	0	0	0.09	0
06N30580	**N**	Onyx	CA	35.73	-118.17	MAY	19	2007	**0.998**	0	0	0	0.002	0

Sample	Carcass (Y/N)	Site	State	Lat	Long	Month	Day	Year	Western Boreal	Coastal CA	Eastern Boreal	Pacific Northwest	Basin Rockies	Sierra
06N23927	**N**	Onyx	CA	35.73	-118.17	MAY	12	2008	**0.951**	0	0	0	0.049	0
06N23930	**N**	Onyx	CA	35.73	-118.17	MAY	12	2008	**1**	0	0	0	0	0
06N23937	**N**	Onyx	CA	35.73	-118.17	MAY	12	2008	0	0	0	0.007	0	**0.992**
06N23939	**N**	Onyx	CA	35.73	-118.17	MAY	12	2008	**1**	0	0	0	0	0
92N0002	**N**	Sierra City	CA	39.62	-120.53	AUG	17	1992	0	0.007	0	**0.993**	0	0
92N0003	**N**	Sierra City	CA	39.62	-120.53	AUG	17	1992	0	0	0	0	0	1
92N0004	**N**	Sierra City	CA	39.62	-120.53	AUG	17	1992	0	0	0	1	0	0
92N0005	**N**	Sierra City	CA	39.62	-120.53	AUG	17	1992	0	0.131	0	0.008	0	**0.861**
92N0006	**N**	Sierra City	CA	39.62	-120.53	AUG	17	1992	0	0	0	0.003	0	**0.997**
92N0007	**N**	Sierra City	CA	39.62	-120.53	AUG	17	1992	0	0	0	**1**	0	0
92N0008	**N**	Sierra City	CA	39.62	-120.53	AUG	17	1992	0	0	0	**1**	0	0
92N0009	**N**	Sierra City	CA	39.62	-120.53	AUG	17	1992	0	0	0	**1**	0	0
92N0010	**N**	Sierra City	CA	39.62	-120.53	AUG	NA	1992	0	0.063	0	0	0	**0.937**
92N0060	**N**	Sierra City	CA	39.62	-120.53	APR	7	1992	0	0	0	0	0	**1**
92N0061	**N**	Sierra City	CA	39.62	-120.53	APR	7	1992	0	0.001	0	0	0	**0.999**
92N0062	**N**	Sierra City	CA	39.62	-120.53	APR	7	1992	0	0.003	0	0.353	0	0.644
92N0063	**N**	Sierra City	CA	39.62	-120.53	APR	7	1992	0	0.003	0	**0.997**	0	0
92N0064	**N**	Sierra City	CA	39.62	-120.53	APR	7	1992	0	0.004	0	0.003	0	**0.994**
92N0065	**N**	Sierra	CA	39.62	-	APR	7	1992	0	0	0	0.25	0	0.75

Sample	**Carcass (Y/N)**	**Site**	**State**	**Lat**	**Long**	**Month**	**Day**	**Year**	**Western Boreal**	**Coastal CA**	**Eastern Boreal**	**Pacific Northwest**	**Basin Rockies**	**Sierra**
		City			120.53									
92N0066	**N**	Sierra City	CA	39.62	-120.53	APR	7	1992	0	0	0	0.078	0	**0.922**

Table A-13: Raptor Species Used in the Analysis

Common Name	Scientific Name
American Kestrel	*Falco sparverius*
Bald Eagle	*Haliaeetus leucocephalus*
Barn Owl	*Tyto alba*
Broad-winged Hawk	*Buteo platypterus*
Burrowing Owl	*Athene cunicularia*
California Condor	*Gymnogyps californianus*
Cooper's Hawk	*Accipiter cooperii*
Elf Owl	*Micrathene whitneyi*
Ferruginous Hawk	*Buteo regalis*
Golden Eagle	*Aquila chrysaetos*
Great Horned owl	*Bubo virgianus*
Long-eared Owl	*Asio otus*
Merlin	*Falco columbarius*
Northern Goshawk	*Accipiter gentilis*
Northern Harrier	*Circus hudsonius*
Osprey	*Pandion haliaetus*
Peregrine Falcon	*Falco peregrinus*
Prairie Falcon	*Falco mexicanus*
Red-shouldered Hawk	*Buteo lineatus*
Red-tailed Hawk	*Buteo jamaicensis*
Rough-legged Hawk	*Buteo lagopus*
Sharp-shinned Hawk	*Accipiter striatus*
Short-eared Owl	*Asio flammeus*
Spotted Owl	*Strix occidentalis*
Swainson's Hawk	*Buteo swainsoni*
Turkey Vulture	*Cathartes aura*
Western Screech-Owl	*Megascops kennicottii*
White-tailed Kite	*Elanus leucurus*

These species were included because they are the raptors in the California Checklist of Birds (California Bird Records Committee 2018).

Source: University of California Los Angeles

Table A-14: Waterfowl Species

Common Name	Scientific Name
American black duck	*Anas rubripes*
American coot	*Fulica americana*
American wigeon	*Mareca americana*
Baikal teal	*Sibirionetta formosa*
Barrow's goldeneye	*Bucephala islandica*
Black rail	*Laterallus jamaicensis*
Black scoter	*Melanitta americana*
Black-bellied whistling-duck	*Dendrocygna autumnalis*
Blue-winged teal	*Spatula discors*
Brant	*Branta bernicla*
Bufflehead	*Bucephala albeola*
Cackling goose	*Branta hutchinsii*
Canada goose	*Branta canadensis*
Canvasback	*Aythya valisineria*
Cinnamon teal	*Spatula cyanoptera*
Common eider	*Somateria mollissima*
Common gallinule	*Gallinula galeata*
Common goldeneye	*Bucephala clangula*
Common merganser	*Mergus merganser*
Common pochard	*Aythya ferina*
Common scoter	*Melanitta nigra*
Emperor goose	*Anser canagicus*
Eurasian wigeon	*Mareca penelope*
Falcated duck	*Mareca falcata*
Fulvous whistling-duck	*Dendrocygna bicolor*
Gadwall	*Mareca strepera*
Garganey	*Spatula querquedula*
Greater scaup	*Aythya marila*
Greater white-fronted goose	*Anser albifrons*
Green-winged teal	*Anas crecca*
Harlequin duck	*Histrionicus histrionicus*
Hooded merganser	*Lophodytes cucullatus*
King eider	*Somateria spectabilis*
Lesser scaup	*Aythya affinis*
Long-tailed duck	*Clangula hyemalis*
Mallard	*Anas platyrhynchos*
Northern pintail	*Anas acuta*
Northern shoveler	*Spatula clypeata*
Purple gallinule	*Porphyrio martinicus*
Red-breasted merganser	*Mergus serrator*
Redhead	*Aythya Americana*
Ridgway's rail	*Rallus obsoletus*
Ring-necked duck	*Aythya collaris*
Ross's goose	*Anser rossii*
Ruddy duck	*Oxyura jamaicensis*
Smew	*Mergullus albellus*

Common Name	Scientific Name
Snow goose	*Anser caerulescens*
Sora	*Porzana Carolina*
Steller's eider	*Polysticta stelleri*
Surf scoter	*Melanitta perspicillata*
Trumpeter swan	*Cygnus buccinators*
Tufted duck	*Aythya fuligula*
Tundra bean-goose	*Anser serrirostris*
Tundra swan	*Cygnus columbianus*
Virginia rail	*Rallus limicola*
White-winged scoter	*Melanitta deglandi*
Whooper swan	*Cygnus Cygnus*
Wood duck	*Aix sponsa*
Yellow rail	*Coturnicops noveboracensis*

These species were included because they are on the waterfowl list of the California Department of Fish and Wildlife (ducks, geese, swans, rails, gallinules, and coots).

Source: University of California Los Angeles

Table A-15: Songbird Species

Common Name	**Scientific Name**
Abert's towhee	*Melozone aberti*
Alder flycatcher	*Empidonax alnorum*
American crow	*Corvus brachyrhynchos*
American dipper	*Cinclus mexicanus*
American goldfinch	*Spinus tristis*
American pipit	*Anthus rubescens*
American redstart	*Setophaga ruticilla*
American robin	*Turdus migratorius*
American tree sparrow	*Spizella arborea*
Arctic warbler/Kamchatka leaf warbler	*Phylloscopus borealis*
Ash-throated flycatcher	*Myiarchus cinerascens*
Baird's sparrow	*Ammodramus bairdii*
Baltimore oriole	*Icterus galbula*
Bank swallow	*Riparia riparia*
Barn swallow	*Hirundo rustica*
Bay-breasted warbler	*Setophaga castanea*
Bell's sparrow	*Artemisiospiza belli*
Bell's vireo	*Vireo bellii*
Bendire's thrasher	*Toxostoma bendirei*
Bewick's wren	*Thryomanes bewickii*
Black phoebe	*Sayornis nigricans*
Black rosy-finch	*Leucosticte atrata*
Black-and-white warbler	*Mniotilta varia*
Black-backed oriole	*Icterus abeillei*
Black-billed magpie	*Pica hudsonia*
Blackburnian warbler	*Setophaga fusca*
Black-capped chickadee	*Poecile atricapillus*
Black-chinned sparrow	*Spizella atrogularis*
Black-headed grosbeak	*Pheucticus melanocephalus*
Blackpoll warbler	*Setophaga striata*
Black-tailed gnatcatcher	*Polioptila melanura*
Black-throated blue warbler	*Setophaga caerulescens*
Black-throated gray warbler	*Setophaga nigrescens*
Black-throated green warbler	*Setophaga virens*
Black-throated sparrow	*Amphispiza bilineata*
Blue grosbeak	*Passerina caerulea*
Blue jay	*Cyanocitta cristata*
Blue mockingbird	*Melanotis caerulescens*
Blue-gray gnatcatcher	*Polioptila caerulea*
Blue-headed vireo	*Vireo solitarius*
Bluethroat	*Luscinia svecica*
Blue-winged warbler	*Vermivora cyanoptera*
Bobolink	*Dolichonyx oryzivorus*
Bohemian waxwing	*Bombycilla garrulus*
Brambling	*Fringilla montifringilla*
Brewer's blackbird	*Euphagus cyanocephalus*

Common Name	**Scientific Name**
Brewer's sparrow	*Spizella breweri*
Bronzed cowbird	*Molothrus aeneus*
Brown creeper	*Certhia Americana*
Brown shrike	*Lanius cristatus*
Brown thrasher	*Toxostoma rufum*
Brown-crested flycatcher	*Myiarchus tyrannulus*
Brown-headed cowbird	*Molothrus ater*
Buff-breasted flycatcher	*Empidonax fulvifrons*
Bullock's oriole	*Icterus bullockii*
Bushtit	*Psaltriparus minimus*
Cactus wren	*Campylorhynchus brunneicapillus*
California gnatcatcher	*Polioptila californica*
California scrub-jay	*Aphelocoma californica*
California thrasher	*Toxostoma redivivum*
California towhee	*Pipilo crissalis*
Canada warbler	*Cardellina canadensis*
Canyon wren	*Catherpes mexicanus*
Cape May warbler	*Setophaga tigrina*
Cassin's finch	*Haemorhous cassinii*
Cassin's kingbird	*Tyrannus vociferans*
Cassin's sparrow	*Peucaea cassinii*
Cassin's vireo	*Vireo cassinii*
Cave swallow	*Petrochelidon fulva*
Cedar waxwing	*Bombycilla cedrorum*
Cerulean warbler	*Setophaga cerulea*
Chestnut-backed chickadee	*Poecile rufescens*
Chestnut-collared longspur	*Calcarius ornatus*
Chestnut-sided warbler	*Setophaga pensylvanica*
Chipping sparrow	*Spizella passerina*
Clark's nutcracker	*Nucifraga columbiana*
Clay-colored sparrow	*Spizella pallida*
Cliff swallow	*Petrochelidon pyrrhonota*
Common grackle	*Quiscalus quiscula*
Common raven	Corvus corax
Common redpoll	Acanthis flammea
Common rosefinch	Carpodacus erythrinus
Common yellowthroat	Geothlypis trichas
Connecticut warbler	Oporornis agilis
Cordilleran flycatcher	Empidonax occidentalis
Couch's kingbird	Tyrannus couchii
Crissal thrasher	Toxostoma crissale
Curve-billed thrasher	Toxostoma curvirostre
Dark-eyed junco	Junco hyemalis
Dickcissel	Spiza americana
Dusky flycatcher	Empidonax oberholseri
Dusky warbler	Phylloscopus fuscatus
Dusky-capped flycatcher	Myiarchus tuberculifer

Common Name	Scientific Name
Eastern kingbird	Tyrannus tyrannus
Eastern phoebe	Sayornis phoebe
Eastern wood-pewee	Contopus virens
Eastern yellow wagtail	Motacilla tschutschensis
Eurasian skylark	Alauda arvensis
European starling	Sturnus vulgaris
Evening grosbeak	Coccothraustes vespertinus
Eyebrowed thrush	Turdus obscurus
Field sparrow	Spizella pusilla
Fork-tailed flycatcher	Tyrannus savana
Fox sparrow	Passerella iliaca
Golden-cheeked warbler	Setophaga chrysoparia
Golden-crowned kinglet	Regulus satrapa
Golden-crowned sparrow	Zonotrichia atricapilla
Golden-winged warbler	Vermivora chrysoptera
Grace's warbler	Setophaga graciae
Grasshopper sparrow	Ammodramus savannarum
Gray catbird	Dumetella carolinensis
Gray flycatcher	Empidonax wrightii
Gray jay	Perisoreus canadensis
Gray silky-flycatcher	Ptiliogonys cinereus
Gray vireo	Vireo vicinior
Gray wagtail	Motacilla cinerea
Gray-cheeked thrush	Catharus minimus
Gray-crowned rosy-finch	Leucosticte tephrocotis
Great crested flycatcher	Myiarchus crinitus
Greater pewee	Contopus pertinax
Great-tailed grackle	Quiscalus mexicanus
Green-tailed towhee	Pipilo chlorurus
Hammond's flycatcher	Empidonax hammondii
Harris's sparrow	Zonotrichia querula
Hepatic tanager	Piranga flava
Hermit thrush	Catharus guttatus
Hermit warbler	Setophaga occidentalis
Hooded oriole	Icterus cucullatus
Hooded warbler	Setophaga citrina
Horned lark	Eremophila alpestris
House finch	Haemorhous mexicanus
House sparrow	Passer domesticus
House wren	Troglodytes aedon
Hutton's vireo	Vireo huttoni
Indigo bunting	Passerina cyanea
Island scrub-jay	Aphelocoma insularis
Juniper titmouse	Baeolophus ridgwayi
Kentucky warbler	Geothlypis formosa
Lanceolated warbler	Locustella lanceolata
Lapland longspur	Calcarius lapponicus

Common Name	Scientific Name
Lark bunting	Calamospiza melanocorys
Lark sparrow	Chondestes grammacus
Lawrence's goldfinch	Spinus lawrencei
Lazuli bunting	Passerina amoena
Least flycatcher	Empidonax minimus
LeConte's sparrow	Ammodramus leconteii
LeConte's thrasher	Toxostoma lecontei
Lesser goldfinch	Spinus psaltria
Lincoln's sparrow	Melospiza lincolnii
Little bunting	Emberiza pusilla
Loggerhead shrike	Lanius ludovicianus
Louisiana waterthrush	Parkesia motacilla
Lucy's warbler	Oreothlypis luciae
MacGillivray's warbler	Geothlypis tolmiei
Magnolia warbler	Setophaga magnolia
Marsh wren	Cistothorus palustris
McCown's longspur	Rhynchophanes mccownii
Mountain bluebird	Sialia currucoides
Mountain chickadee	Poecile gambeli
Mourning warbler	Geothlypis philadelphia
Nashville warbler	Oreothlypis ruficapilla
Nelson's sparrow	Ammodramus nelsoni
Northern cardinal	Cardinalis cardinalis
Northern mockingbird	Mimus polyglottos
Northern parula	Setophaga americana
Northern rough-winged swallow	Stelgidopteryx serripennis
Northern shrike	Lanius borealis
Northern waterthrush	Parkesia noveboracensis
Northern wheatear	Oenanthe oenanthe
Nutting's flycatcher	Myiarchus nuttingi
Oak titmouse	Baeolophus inornatus
Olive-backed pipit	Anthus hodgsoni
Olive-sided flycatcher	Contopus cooperi
Orange-crowned warbler	Oreothlypis celata
Orchard oriole	Icterus spurius
Oriental greenfinch	Chloris sinica
Ovenbird	Seiurus aurocapilla
Pacific wren	Troglodytes pacificus
Pacific-slope flycatcher	Empidonax difficilis
Painted bunting	Passerina ciris
Painted redstart	Myioborus pictus
Palm warbler	Setophaga palmarum
Phainopepla	Phainopepla nitens
Philadelphia vireo	Vireo philadelphicus
Pine grosbeak	Pinicola enucleator
Pine siskin	Spinus pinus
Pine warbler	Setophaga pinus

Common Name	**Scientific Name**
Pinyon jay	Gymnorhinus cyanocephalus
Plumbeous vireo	Vireo plumbeus
Prairie warbler	Setophaga discolor
Prothonotary warbler	Protonotaria citrea
Purple finch	Haemorhous purpureus
Purple martin	Progne subis
Pygmy nuthatch	Sitta pygmaea
Pyrrhuloxia	Cardinalis sinuatus
Red crossbill	Loxia curvirostra
Red-breasted nuthatch	Sitta canadensis
Red-eyed vireo	Vireo olivaceus
Red-faced warbler	Cardellina rubrifrons
Red-flanked bluetail	Tarsiger cyanurus
Red-throated pipit	Anthus cervinus
Red-winged blackbird	Agelaius phoeniceus
Rock wren	Salpinctes obsoletus
Rose-breasted grosbeak	Pheucticus ludovicianus
Ruby-crowned kinglet	Regulus calendula
Rufous-backed robin	Turdus rufopalliatus
Rufous-crowned sparrow	Aimophila ruficeps
Rustic bunting	Emberiza rustica
Rusty blackbird	Euphagus carolinus
Sage thrasher	Oreoscoptes montanus
Sagebrush sparrow	Artemisiospiza nevadensis
Savannah sparrow	Passerculus sandwichensis
Say's phoebe	Sayornis saya
Scaly-breasted munia	Lonchura punctulata
Scarlet tanager	Piranga olivacea
Scissor-tailed flycatcher	Tyrannus forficatus
Scott's oriole	Icterus parisorum
Sedge wren	Cistothorus stellaris
Smith's longspur	Calcarius pictus
Snow bunting	Plectrophenax nivalis
Song sparrow	Melospiza melodia
Spotted towhee	Pipilo maculatus
Sprague's pipit	Anthus spragueii
Steller's jay	Cyanocitta stelleri
Stonechat	Saxicola rubicola
Streak-backed oriole	Icterus pustulatus
Sulphur-bellied flycatcher	Myiodynastes luteiventris
Summer tanager	Piranga rubra
Swainson's thrush	Catharus ustulatus
Swamp sparrow	Melospiza georgiana
Taiga flycatcher	Ficedula albicilla
Tennessee warbler	Oreothlypis peregrina
Thick-billed kingbird	Tyrannus crassirostris
Townsend's solitaire	Myadestes townsendi

Common Name	Scientific Name
Townsend's warbler	Setophaga townsendi
Tree swallow	Tachycineta bicolor
Tricolored blackbird	Agelaius tricolor
Tropical kingbird	Tyrannus melancholicus
Varied bunting	Passerina versicolor
Varied thrush	Ixoreus naevius
Veery	Catharus fuscescens
Verdin	Auriparus flaviceps
Vermilion flycatcher	Pyrocephalus obscurus
Vesper sparrow	Pooecetes gramineus
Violet-green swallow	Tachycineta thalassina
Virginia's warbler	Oreothlypis virginiae
Warbling vireo	Vireo gilvus
Western bluebird	Sialia mexicana
Western kingbird	Tyrannus verticalis
Western meadowlark	Sturnella neglecta
Western tanager	Piranga ludoviciana
Western wood-pewee	Contopus sordidulus
White wagtail	Motacilla alba
White-breasted nuthatch	Sitta carolinensis
White-crowned sparrow	Zonotrichia leucophrys
White-eyed vireo	Vireo griseus
White-throated sparrow	Zonotrichia albicollis
White-winged crossbill	Loxia leucoptera
Willow flycatcher	Empidonax traillii
Wilson's warbler	Cardellina pusilla
Winter wren	Troglodytes hiemalis
Wood thrush	Hylocichla mustelina
Woodhouse's scrub-jay	Aphelocoma woodhouseii
Worm-eating warbler	Helmitheros vermivorum
Wrentit	Chamaea fasciata
Yellow warbler	Setophaga petechia
Yellow-bellied flycatcher	Empidonax flaviventris
Yellow-billed magpie	Pica nuttalli
Yellow-breasted chat	Icteria virens
Yellow-green vireo	Vireo flaviviridis
Yellow-headed blackbird	Xanthocephalus xanthocephalus
Yellow-rumped warbler	Setophaga coronata
Yellow-throated vireo	Vireo flavifrons
Yellow-throated warbler	Setophaga dominica

These species were included because they are Passerine birds listed in the Checklist of California Birds (California Bird Records Committee 2018).

Source: University of California Los Angeles

APPENDIX B: Technical Methods

DNA Isolation

The research team used Qiagen DNeasy 96 blood and tissue kit (Qiagen Inc., Valencia, CA, USA) to extract DNA from each sample. For blood, they combined 20 ul of blood suspended in Queens lyses buffer with 20ul of Proteinase K. For feathers, they cut at least one calamus per sample using sterile razor blades and incubated them overnight in 200ul of tissue lysis buffer (ATL) and 20ul of digestive enzyme (Proteinase K). They also added 10ul of Dithiothreitol (DTT) to the lysis mix to break down the keratin in feathers. They then eluted the samples the next day as per the manufacturer's protocol, yielding a final elution of 120ul of DNA solution per sample.

Genoscape Construction with RAD-Seq

To construct the genoscapes for Wilson's Warbler, and American Kestrel the researchers scanned the genomes of a subset of individuals to identify genetic variants that were diagnostic or representative of populations at finer spatial scales using a methodology known as RAD-Seq. RAD-Seq methodological details are described in earlier manuscripts (Ruegg et al. 2014b, 2018; Ali et al. 2016). In short, the researchers digested genomic DNA with restriction enzymes, then barcoded, sheared, size selected, amplified in a PCR-enrichment step, and finally sequenced them on an Illumina HiSeq2000 (Illumina) using paired-end 100-bp sequencing reads. They filtered and trimmed reads using the program Stacks (Catchen et al. 2013) and mapped the resulting sequences to the species-specific genome assembly using bowtie2 (Langmead and Salzberg 2012). For species with no available reference genome, such as Yellow Warbler, Burrowing Owl, and American Kestrel, they assembled and annotated their own genome following the methods described in Ruegg et al. (2018) and Bay et al. (2018).

Once the researchers mapped RAD fragments to the appropriate reference genome, they used the HaplotypeCaller in the Genome Analysis Toolkit to identify single nucleotide polymorphisms (SNPs), following best practices from the Broad Institute (http://www.broadinstitute.org). Finally, they discarded low quality variants, indels and non-biallelic SNPs using vcftools (Danecek *et al.* 2011). Using this quality filtered set, they further filtered based on missingness, discarding SNPs with low coverage and discarding individuals with missing genotypes. In total, they identified ~500,000 SNPs across the genomes of the target taxa.

Genoscape Construction with Low Coverage Whole Genome Sequencing

To construct genoscapes for Common Yellowthroats and Burrowing Owls, the researchers implemented a new low coverage whole genome sequencing protocol, modified from Illumina's Nextera Protocol. They switched to this new protocol in order to take advantage of the orders of magnitude more genetic markers that could be generated for these species and used in their subsequent analyses. In short, the first step in library prep is the tagmentation reaction that fragmented DNA and then tagged the DNA with adapter sequences in a single step. The researchers amplified the library using a limited-cycle PCR program, followed by a reconditioning PCR step, and a cleaning step with AMPure XP beads that size selects short library fragments. They quantified the library with a Qubit plate reader and normalized the quantity of libraries to be pooled together. Final libraries with a volume of at least 20 ul and a concentration of at least 2ng/ul was sequenced on an Illumina HiSeq4000 (Illumina).

First, the researchers sequenced resident and migratory Burrowing Owls blood samples (n = 190) and Common Yellowthroat blood samples (n=150) to ~1.0× coverage by pooling 75 multiplexed individuals per lane. Second, to test the quality of prepared libraries from the low quantity of DNA collected from feathers of migratory birds, they also sequenced 17 Burrowing Owl feather samples from Altamont, a renewable energy facility in California to ~1.0× coverage (Bossu, Barr et al. *in prep*).

After processing the sequencing reads (removing PCR duplicates and trimming low quality fragments and adapters), the researchers mapped the reads of Burrowing Owls to the Burrowing Owl genome, and Common Yellowthroat reads to the Yellow Warbler genome assembly using hisat2 (Kim *et al.* 2015). Given genotype calls from low coverage whole genome sequencing are unreliable due to multiple sources of uncertainty (i.e. mapping and sequencing error), they instead calculated genotype likelihoods using ANGSD (Korneliussen *et al.* 2014), a program that incorporates statistical uncertainty regarding genotypes. They filtered within ANGSD for max read depth (> 500), minimum mapped quality of 20, minimum phred score of 30, minor allele frequency of 0.05, as well as discarding indels and non-biallelic SNPs.

Feather Screening

From initial genome-wide RAD-sequencing for American Kestrels and Wilson's Warbler (see methods within Ruegg et al. 2014b; Ruegg et al. 2108; Bay et al. 2018), the researchers used custom R scripts to identify 96 – 192 highly divergent SNPs. To identify highly divergent variants from low coverage whole genome sequencing datasets of the Common Yellowthroat, they estimated pairwise F_{ST} using ngsTools between the major genetic groups (Fumagalli et al. 2014). From these initial divergent variants lists, they used custom R scripts to create a low-cost assay to screen additional individuals from across the range, and create a high-resolution population map. They then used the R package SNPS2ASSAYS (Anderson 2015) to evaluate which of their top-ranking SNPs would generate designable assays for each conservation unit. They considered variants designable if GC content was less than 0.65, there were no insertions or deletions (indels) within 30bp, and there were no additional variants within 20bp of the targeted variable site. Additionally, they filtered out designable SNPs that mapped to multiple locations. They used this subset of SNPs to develop a SNPtype Assay (Fluidigm Inc.) that they used to screen individuals collected from wintering and migratory stopover sites for assignment to breeding population of origin.

Genetic Screening and Building the Genoscape

The researchers removed samples with missing genotypes at more than 10 percent of SNP assays from their analyses of spatially-explicit population structure. To assess population structure across the breeding region of each species, they used the admixture model in structure (version 2.3.4; Pritchard et al. 2000), a model-based clustering method. While model-based approaches describe continuous patterns of variation using discrete clusters, and may therefore overestimate the number of discrete clusters present, the objective is to describe the greatest number of genetically unique breeding populations, (i.e. conservation units). Therefore, they implemented the locprior model that used sampling locations as prior information if the genetic data was weak, uncorrelated allele frequencies, a burn-in period of 50,000, and total run length of 150,000. They ran 5 iterations of each assumed number of genetic clusters (K), where K ranged from 1:10 (Pritchard et al. 2000).

They visualized posterior probability of group membership estimates from structure as transparency levels of different colors overlaid upon a base map from Natural Earth (naturalearthdata.com) and clipped to a map of each species breeding range (NatureServe 2012), making use of the R packages sp, RGDAL, and raster (Bivand et al. 2013, 2017; Hijmans 2017). Thus, they scaled the transparency of colors within each distinguishable group, so that the highest posterior probability of membership in the group according to structure is opaque and the smallest is transparent. This creates the spatially-explicit map of genomic clustering, which they term the genoscape of each species (Figure 1).

Baseline Conservation Groups and Accuracy Assignment

The researchers defined conservation units (i.e., genetically distinct populations for assignment purposes as defined in the literature Kalinowski et al. 2007; Bradbury et al. 2018) as the genetically-based breeding populations identified in the completed genoscapes of each species (Ruegg et al. 2014b; Brinkmeyer et al. in prep.). They evaluated the accuracy of individual assignment analysis using self - assessment testing in RUBIAS (Anderson et al. 2008, Anderson 2017), a Bayesian hierarchical genetic identification approach which accounts for population structure and differences in the number of populations grouped into baseline conservation units. The self-assessment function in RUBIAS tests the accuracy of assignment by assigning individuals in the reference back to the collections in the reference using a leave-one-out cross validation approach. Accuracy is the proportion of individuals from known conservation groups that are assigned back to the correct conservation group. For each specimen, the researchers calculated the probability of assignment to a specific conservation group and defined significant assignment as > 0.8 posterior probability of assignment to the inferred collection. They designated assignments with a posterior probability < 0.8 as uncertain, and filtered those individuals from the final reporting.

Assignment of Unknown Migratory and Wintering Birds

The researchers assigned individuals of unknown origin collected from wintering and migratory stopover locations (hereafter called ‘unknown’ birds; see Figures A-1 through A-4, and Tables A-1 through A-4) to conservation units characterized by the genoscape using RUBIAS (Anderson and Moran 2017). They defined the unknown birds by the mixture collection that corresponded to the state where the collection occurred, and treated it as a separate sample group, thus getting its own mixing proportion estimate or combined into one ‘mixture’ category. They saw no difference in assignment under these two strategies. Here, they report the certain assignment of wintering individuals (individuals with a posterior probability > 0.8 (and > 0.9) of being assigned to a genetic conservation group) and the proportion of individuals assigned to conservation units of each migratory stopover site. They illustrate the assignment of individual wintering birds on each genoscape (colored points on the wintering grounds), and they used the assignment of migratory birds to provide a time series of migration through the Pacific Flyway in California during spring and fall migration.