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An Integrated Population Model for Greater Sage-Grouse (*Centrocercus urophasianus*) in the Bi-State Distinct Population Segment, California and Nevada, 2003–17

Open-File Report 2018–1177

U.S. Department of the Interior
U.S. Geological Survey

Cover photographs:

Background: Photograph showing greater sage-grouse nesting habitat at Parker Meadows, California, by Mary Meyerpeter, U.S. Geological Survey, June 25, 2017.

Inset: Photograph of male greater sage-grouse (*Centrocercus urophasianus*) in flight, by Tatiana Gettelman, U.S. Geological Survey, June 10, 2013.

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Conversion Factors

International System of Units to U.S. customary units

Multiply	By	To obtain
	Length	
meter (m)	3.281	foot (ft)
kilometer (km)	0.6214	mile (mi)
	Area	
hectare (ha)	2.471	acre

Datums

Vertical coordinate information is referenced to the North American Vertical Datum of 1988 (NAVD 88).
Horizontal coordinate information is referenced to the North American Datum of 1983 (NAD 83).

Abbreviations

AI	Artificial Insemination
BH	Bodie Hills
BLM	Bureau of Land Management
CDFW	California Department of Fish and Wildlife
CI	confidence interval
CRI	credible interval
CSTG	Columbian sharp-tailed grouse (*Tympanuchus phasianellus columbianus*)
DC	Desert Creek
DPS	distinct population segment
ESA	Endangered Species Act
FA	Fales
GPS	Global Positioning System
h	hour
IPM	integrated population model
ISU	Idaho State University
LADWP	Los Angeles Department of Water and Power
LV	Long Valley
MG	Mount Grant
min	minute
NDOW	Nevada Department of Wildlife
OR	odds ratio
PJ	pinyon and juniper
PM	Parker Meadows
PMU	Population Management Unit
PN	Pine Nut Mountains
PTT	Platform Transmitter Terminal
RRHL	Raptor, Raven, Horse and Livestock survey
SH	Sagehen
UD	utilization distribution
USFS	U.S. Forest Service
USFWS	U.S. Fish and Wildlife Service

USGS	U.S. Geological Survey
VHF	very high frequency
WERC	Western Ecological Research Center
WMC	White Mountains California
WMN	White Mountains Nevada

An Integrated Population Model for Greater Sage-Grouse (*Centrocercus urophasianus)* in the Bi-State Distinct Population Segment, California and Nevada, 2003–17

By Steven R. Mathews[1,2], Peter S. Coates[1], Brian G. Prochazka[1], Mark A. Ricca[1], Mary B. Meyerpeter[1,2], Shawn P. Espinosa[3], Sherri Lisius[4], Scott C. Gardner[5], and David J. Delehanty[2]

Abstract

The Bi-State Distinct Population Segment (DPS) of greater sage-grouse (*Centrocercus urophasianus,* hereinafter “sage-grouse”) occupies parts of Alpine, Mono, and Inyo Counties in California, and parts of Douglas, Esmeralda, Lyon, Carson City, and Mineral Counties in Nevada and was proposed for listing as threatened under the Endangered Species Act (ESA) by the U.S. Fish and Wildlife Service (USFWS) in October 2013. In April 2015, the USFWS determined that the Bi-State DPS did not warrant listing under the ESA, but monitoring continued for assessment of long-term population stability (U.S. Fish and Wildlife Service, 2015a). Threats to this population include geographic isolation, expansion of single-leaf pinyon (*Pinus monophylla*) and Utah juniper (*Juniperus osteosperma*), anthropogenic activities, changes in historical wildfire cycles and the conversion of native shrubs to invasive annual grasslands, and recent changes in predator communities. As part of a broad long-term monitoring program, we used an integrated population model to estimate finite rate of population change (λ) of each subpopulation within the Bi-State DPS from 2003 to 2017. Since 2012, the Bi-State DPS experienced multiple years of drought conditions associated with periods of population decline across multiple populations. The 14-year average (λ) for the Bi-State DPS is 0.98 (95 percent CRI=0.70–1.31). Three subpopulations (Mount Grant, Fales, Bodie Hills) showed continued evidence of stability and growth as the average λ exceeded 1.0. Moreover, we implemented the first year of an experimental pre-nesting female and brood translocation program to bolster a critically low population of sage-grouse in Parker Meadows, California. Finally, we report summary statistics describing sage-grouse movements and relative abundance of avian predators across all years of the study.

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[1] U.S. Geological Survey.

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[3] Nevada Department of Wildlife.

[4] Bureau of Land Management.

[5] California Department of Fish and Wildlife.

Background

Greater sage-grouse (*Centrocercus urophasianus,* hereinafter “sage-grouse”) require large continuous areas of sagebrush for population persistence (Patterson, 1952; Knick and others, 2013) and are considered an umbrella species for the conservation of sagebrush ecosystems at landscape scales (Rowland and others, 2006). Populations of sage-grouse have declined concomitantly with the loss and fragmentation of sagebrush ecosystems across western North America (Connelly and others, 2004; Schroeder and others, 2004), and management actions aimed at understanding and ameliorating these declines are at the forefront of national conservation policy (Bureau of Land Management, 2015; U.S. Fish and Wildlife Service, 2015b).

The sage-grouse population in the extreme southwestern part of sage-grouse range along the border of California and Nevada (hereinafter, “Bi-State DPS”) is genetically distinct from Great Basin populations owing to geographic isolation and loss of contiguous sagebrush habitat (Oyler-McCance and others, 2005, 2015) and may require different vegetation types than those required within other parts of the species range (Kolada and others, 2009). Because of these reasons, in part, the U.S. Fish and Wildlife Service classified the Bi-State population as a Distinct Population Segment (DPS) under the Endangered Species Act (ESA). Threats to the Bi-State DPS include geographic isolation, wildfire and subsequent invasion by annual grasses (Coates and others, 2016a), encroachment by single-leaf pinyon pine (*Pinus monophylla*) and Utah juniper (*Juniperus osteosperma*; hereinafter, “PJ”; Coates and others, 2017; Severson and others, 2017), anthropogenic activities, and recent changes in predator communities (Coates and Delehanty, 2008, 2010; Bi-State Action Plan, 2012; Howe and others, 2014). Although the Bi-State DPS was nominated for protection under the ESA in 2015, the U.S. Fish and Wildlife Service (USFWS) decided listing was not warranted (U.S. Fish and Wildlife Service, 2015a) owing largely to a suite of conservation measures and science-based adaptive management listed in the Bi-State Action Plan (2012). This plan, which represented a collaborative effort between State and Federal resource and science agencies, identified a suite of threats to the persistence of the Bi-State DPS for the multiple Population Management Units (PMU) that comprise the DPS. The plan then outlines potential management actions designed to ameliorate those threats.

Following guidelines from the Bi-State Action Plan (2012), and in the subsequent Bi-State Monitoring Plan (2015), the U.S. Geological Survey (USGS) Western Ecological Research Center (WERC) led an interagency field research effort to monitor sage-grouse populations across multiple study sites in the Bi-State DPS designed to identify long-term population trends, habitat associations, and ultimately quantify responses to management action. These efforts are conducted in collaboration and partnership with Federal, State, and local agencies that include the Bureau of Land Management (BLM), U.S. Forest Service (USFS), USFWS, Natural Resource Conservation Service, Nevada Department of Wildlife (NDOW), California Department of Fish and Wildlife (CDFW), Idaho State University (ISU), Los Angeles Department of Water and Power (LADWP), and Great Basin Bird Observatory.

In tandem with these efforts, we initiated an experimental translocation program to restore critically low populations of sage-grouse in Parker Meadows, California, during 2017. This work was identified as a specific management action in the Bi-State Action Plan (2012). For this augmentation, sage-grouse were captured from the Bodie Hills subpopulation, translocated overnight, and released the following morning at Parker Meadows using a modified soft-release (Rodgers, 1992). As part of this program, we used artificial insemination (AI) techniques to ensure that a subsample of pre-nesting females were inseminated prior to release at Parker Meadows. We also used a novel brood translocation where female sage-grouse were translocated with their brood to Parker Meadows. To our knowledge, this is the first time that brood translocations have been attempted in sage-grouse.

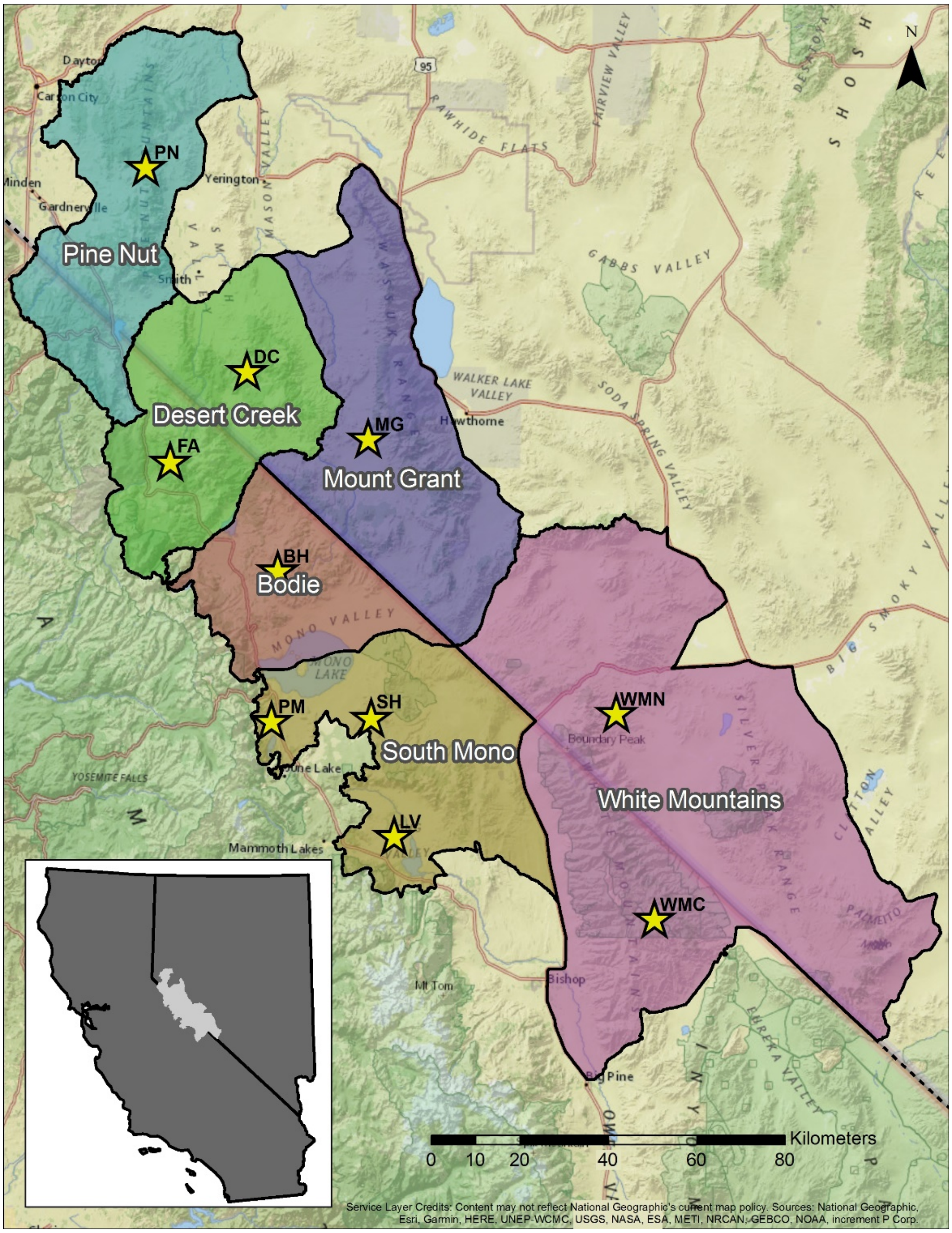
The broad and long-term objectives of research reported in this study are as follows:

A. Develop an effective collaboration between land and wildlife administrators and research agencies to improve our knowledge of the Bi-State DPS of greater sage-grouse.
B. Estimate population vital rates for subpopulations comprising the Bi-State DPS.
C. Monitor lek attendance.
D. Identify seasonal and annual movement patterns and calculate utilization distributions of subpopulations.
E. Monitor spatial and temporal abundance of avian predators.
F. Evaluate the effectiveness of experimental translocation procedures at stabilizing the population in Parker Meadows.
G. Estimate the long-term viability of the Bi-State DPS and representative subpopulations through use of an integrated population model (IPM) informed by lek count and vital rate data.

This report presents updated findings regarding the Bi-State DPS from 2003 to 2017 and incorporates data reported by Coates and others (2014, 2016b, 2018) as part of an ongoing long-term research effort. We coupled data from contemporary studies that began in 2013 with archived data from previous studies to inform demographic estimates of the IPM spanning 2003 to 2017.We only report summary data and results for sage-grouse captures, movements, utilization distributions (UDs), and avian predator abundance from the contemporary studies. Reported translocation results began in 2017. The findings contained in this report are reported to provide managers with timely science from this ongoing research effort.

Study Areas

We studied multiple sage-grouse subpopulations in the Bi-State DPS from 2003 to 2017. The following is a brief description of study areas associated with these populations and associated PMUs, beginning with the most northern population and progressing southward. We monitored sage-grouse subpopulations at Pine Nut Mountains, Mount Grant, Desert Creek, Fales, Bodie Hills, Long Valley, Sagehen, Parker Meadows, and the California and Nevada sides of the White Mountains (fig. 1). Cheatgrass (*Bromus tectorum*), an invasive annual grass that can profoundly alter sagebrush ecosystem processes such as fire regimes (Chambers and others, 2014), is present in many areas throughout the Bi-State DPS and is present at all field sites to varying degrees.



Service Layer Credits: Content may not reflect National Geographic's current map policy. Sources: National Geographic, Esri, Garmin, HERE, UNEP-WCMC, USGS, NASA, ESA, METI, NRCAN, GEBCO, NOAA, increment P Corp.

Figure 1. The Bi-State Distinct Population Segment (DPS) of greater sage-grouse (*Centrocercus urophasianus)* identified by population management units (PMUs) across Nevada and California. Stars indicate approximate center-points of subpopulations monitored: PN (Pine Nut Mountains), Desert Creek (DC), Fales (FA), Mount Grant (MG), Bodie Hills (BH), Parker Meadows (PM), Sagehen (SH), Long Valley (LV), White Mountains Nevada (WMN), White Mountains California (WHC).

The Pine Nut Mountains study area is located at the northernmost boundary of the Bi-State DPS within the Pine Nut PMU (fig. 1). The Pine Nut Mountains subpopulation is topographically diverse and encompasses 232,695 hectares (ha; Bi-State Local Planning Group, 2004) of the Bi-State DPS study area. Dominant plant communities consist of sagebrush-steppe (*Artemisia* spp.) and mixed mountain shrub communities with extensive single-leaf pinyon and Utah juniper woodlands throughout the study area. Overstory of sagebrush communities is characterized by big sagebrush (*Artemisia tridentata* spp.) and dwarf sagebrush (*Artemisia arbuscula* spp). Other shrub cover consists of a variety of rabbitbrush (*Chrysothamnus* and *Ericameria* spp.), Bailey's greasewood (*Sarcobatus baileyi*), and horsebrush (*Tetradymia* spp.). Mountain shrub communities are characterized by big sagebrush and a variety of mountain shrubs including Utah serviceberry (*Amelanchier utahensis*), common snowberry (*Symphoricarpos albus*), and desert bitterbrush (*Purshia glandulosa*). Dominant forbs consist of wooly mule-ears (*Wyethia mollis*), lupine (*Lupinus* spp.), and arrowleaf balsamroot (*Balsamorhiza sagittata*). Grasses include bluebunch wheatgrass (*Pseudoroegneria spicata*), crested wheatgrass (*Agropyron cristatum*), Great Basin wild rye (*Elymus cinereus*), needle-and-thread grass (*Hesperostipa comata*) and Indian ricegrass (*Achnatherum hymenoides*).

In the mid-northern regions of the Bi-State DPS, we intensively monitored sage-grouse within the Mount Grant and Desert Creek PMUs (fig. 1). Additional lek-count only monitoring occurred for the Fales subpopulation within Desert Creek. Mount Grant consists of low elevation leks surrounded by the high elevation habitats of Aurora Crater, Powell Mountain, and Big Indian Mountain. The northernmost leks are Rough Creek and China Camp 2 and the southernmost lek is Aurora, near the site's namesake, Mount Grant, a mountain owned by the United States Army. One common use area is Nine Mile Ranch, owned by The Nature Conservancy and located within Nine Mile Flat. Here, sage-grouse use the Walker River as a water source. High elevation areas with stands of PJ encompass large parts of the Mount Grant field site. Desert Creek extends in a north-south orientation south of Wellington, Nevada, to Sweetwater Ranch, and east of the Sweetwater Mountains to west of State Highway 338. Annual grasses dominate parts of the ranchland and surrounding areas but eventually transition to a mix of shrubs and perennial grasses at higher elevations. Black (*Artemisia nova)* and low sagebrush (*Artemisia arbuscula*) are the dominant species within the study area. On the western side of the Sweetwater Mountains, sage-grouse are typically associated with shrubs, forbs, and grasses at higher elevation in Jackass Flat.

In the central and mid-southern regions of the Bi-State DPS in Mono County, Calif., we monitored the Bodie Hills PMU and three populations (Long Valley, Sagehen, and Parker Meadows) within the South Mono PMU (fig. 1). Bodie Hills is located about 12.87 km east of Bridgeport; Long Valley is located approximately 11.27 km southeast of Mammoth Lakes, Calif. Sagehen is geographically located between the Bodie Hills and Long Valley field sites, approximately 16.09 km southeast of Lee Vining. Parker Meadows is about 9.66 km south of Lee Vining, Calif., along U.S. Highway 395. All four sites consist of sagebrush communities with major land cover types comprised of Wyoming (*A. t. wyomingensis*) and mountain big sagebrush (*A. t. vaseyana*), low sage, rabbitbrush, bitterbrush, snowberry, and other non-sagebrush shrubs at lower elevation, as well as coniferous forests dominated by single-leaf pinyon pine, Utah juniper, and in many areas Jeffrey Pine (*Pinus jeffreyi*).

In the southern extreme of the Bi-State DPS, we monitored the White Mountains PMU (fig. 1). Little is known about sage-grouse behavior and ecology in the White Mountains. On the California side, a pilot movement study was initiated in the fall of 2016 and 2017 with GPS (Global Positioning System)-Platform Transmitting Terminal (PTT) units. Intensive field study of reproductive ecology to estimate demographic vital rates on both the California and Nevada side with VHF (very high frequency) and GPS-PTT (hereinafter, GPS) marked sage-grouse began in March 2018. The White Mountains lie along the border of Nevada and California and stretch for about 97 kilometers (km), but grouse are primarily located on a large plateau ranging from 3,048 to 3,962 meters (m), which extends for about 32 km (Elliot-Fisk, 1991), just south of White Mountain Peak (4,342 m). There are only a few known leks in the White Mountains, and sage-grouse on the Nevada side reside at low elevations, which are composed of several species of conifer tree (bristlecone pine, *Pinus longaeva*; limber pine, *Pinus flexilis*; and PJ) intermixed with stands of mountain mahogany (Genus *Cercocarpus*) and sage brush. Various species of sagebrush and conifer trees make up the vegetation at high elevations.

Methods

Lek Surveys

We followed a modified version of published protocols for lek counts (Connelly and others, 2003). A team of interagency personnel from CDFW, NDOW, BLM, USFS, USGS, ISU, LADWP, University of Nevada Reno, and University of Idaho conducted annual surveys of leks across the full extent of the Bi-State across at least three separate and equally spaced occasions from March to May that corresponded to peak lek attendance by males. Counts were conducted between 30 minutes (hereinafter, min) before and 90 min after sunrise and used binoculars, spotting scopes, or both from a suitable viewing location. For each survey occasion, a total of three counts were conducted at 10 min intervals, and the highest count for three separate categories (male, female, unknown) recorded. Many leks within the central and southern Bi-State DPS, which include Fales, Bodie Hills, and Long Valley on the California side, were surveyed using a “saturation count” method, which required that all known active leks be counted simultaneously by experienced observers on a single day and then repeated across the lekking season. For the IPM (see section “Estimating Population Growth Using an Integrated Population Model”), we used the maximum male lek count for each lek and year and then calculated the average maximum lek count for each subpopulation by year. We used averaged counts because model inferences occurred at the subpopulation level, and thus, we sought to prevent underestimates during years of missing data and for subpopulations consisting of different numbers of leks. Leks with a recorded integer value of zero or greater were included in the analysis, and leks with a blank value (that is, not surveyed) were not included.

Capturing and Handling Sage-Grouse

All sage-grouse were captured and handled in accordance with the USGS WERC Animal Care and Use Protocol WERC-2015-02. We captured sage-grouse during the fall (September–November) and spring (March–May) seasons of 2003 to 2017. Sage-grouse were captured at night at nocturnal roosting locations using spotlights and hand-held nets attached to 3-m extension handles. White noise was broadcast from predator callers to dampen observer noise and help prevent sage-grouse from flushing (Wakkinen and others, 1992). Sage-grouse were fitted with battery powered necklace-style VHF transmitters (less than 3 percent body mass; Schroeder and others, 1999; Advanced Telemetry Systems, Isanti, Minnesota) equipped with mortality sensors that would activate after 8 hours (hereinafter, h) of inactivity. A subsample of sage-grouse were fitted with harness-style rump-mounted PTTs (less than 5 percent body mass; Northstar Science and Technology LLC, King George, Virginia) equipped with GPS and VHF transmitters. The GPS collects and remotely transmits locations to a central database via satellites, requiring no post-release pressure from researchers, and the VHF transmitters were used to relocate the device in the field after mortality or if the GPS failed to transmit data.

Captured sage-grouse were weighed, and multiple morphometric measurements were recorded. Measurements included length of the metatarsal bone, flattened wing chord, and length of the culmen. We classified sage-grouse age as juvenile (pre-breeding; fall captures only), yearling (first year breeding), or adult (greater than 1 breeding year) based on plumage characteristics of the 9th and 10th primaries (Ammann, 1944). Photographs of the extended primaries were taken for each individual to confirm age. Sage-grouse were processed and released within 30 min of capture. During release, sage-grouse were gently placed under a shrub greater than or equal to 50 m from the processing location and were allowed to walk or fly from the area at will.

Experimental Sage-Grouse Translocation to Parker Meadows

Sage-Grouse Capture, Handling, and Transport

In the spring of 2017, we initiated an experimental translocation program to restore a critically low population of sage-grouse in Parker Meadows. Sage-grouse translocated to Parker Meadows were captured on leks in Bodie Hills using the methods described in section, “Capturing and Handling Sage-Grouse.” Initially, we attempted to trap at leks with greater than or equal to 20 males and translocate no more than 5 percent of the high male count from 2016 for each lek. However, the winter of 2016 to 2017 yielded record snowfall and a snowpack that lingered through the spring of 2017, which precluded access to many leks and led to the translocation of greater than 5 percent of the high male count for some of the target leks in 2017. Once captured, sage-grouse were placed into a cardboard box lined with non-clumping diatomaceous earth litter or paper towels to absorb fecal matter and keep their plumage clean. Captured sage-grouse were transported from their capture locations to a processing station at Parker Meadows where they underwent processing (morphometric measurements and transmitter attachment), and a subsample of females were artificially inseminated. After processing, all sage-grouse were placed in a compartmentalized release box (figs. 2*A* and 2*B*) prior to release and moved to the Parker Meadows lek.

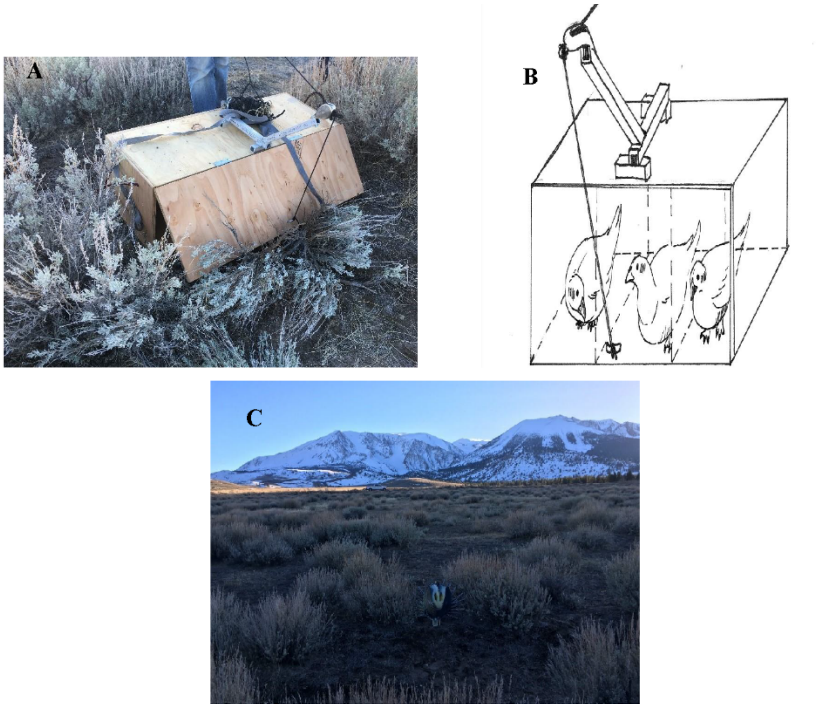


Figure 2. Compartmentalized release box used for releasing greater sage-grouse (*Centrocercus urophasianus*) (*A*); illustration of release box showing interior compartments (*B*); and silhouette used to enhance the lek for the Parker Meadows, California, translocation, 2017 (*C*). Illustration in *B* courtesy of Diana Muñoz.

Semen Collection and Artificial Insemination Procedures

To obtain semen for AI of female sage-grouse translocated to Parker Meadows, we captured male sage-grouse on leks in Bodie Hills using the capture methods described in section “Capturing and Handling Sage-Grouse.” After transport to the processing station at Parker Meadows, male sage-grouse were aged, weighed, and given leg bands with unique ID numbers. Semen was collected using the massage method (Quinn and Burrows, 1936), which has recently been used with success in other grouse translocations (Helena Schnieder, Justus-Liebig University of Giessen, written commun., 2018). We assessed semen volume and spermatozoa density following collection, and samples were buffered according to the quality of the ejaculate. The purpose of semen buffer is to provide sperm cells with energy to remain alive and active for potentially several hours prior to artificial insemination. After semen collection, donor males were released back onto their respective capture leks and were not translocated to Parker Meadows, precluding the possibility of natural mating between a donor-male and an AI female after translocation. From the time of capture to the time of release, male semen donors were held in captivity for less than 8 h, but most were held less than 6 h.

Buffered semen samples were deposited into the female’s vagina using a 1-mL (milliliter) syringe with a flexible rubber tip. To evaluate the effectiveness of AI, translocated females were divided into three groups, AI, SHAM-AI, and Control, following a random block design upon capture. SHAM-AI females were inseminated with a buffer-only solution, and control females were not inseminated. The purpose of three treatment groups was to test the effects of additional handling and stimulation of the AI procedure upon translocated female sage-grouse. Analyses are underway to test differences between treatment groups with regards to nest initiation, nest survival, and sage-grouse survival.

Soft-Release of Translocated Sage-Grouse

After processing, sage-grouse were placed into a compartmentalized release box (figs. 2*A* and 2*B*), which facilitated the release of several sage-grouse at once, following recommendations by Musil (1989). The release site at Parker Meadows was selected because of its proximity to the lek and dense vegetative cover to reduce the likelihood of sage-grouse flushing when released. Sage-grouse silhouettes, along with playback of lek sounds, were placed near the release site based on design of Rodgers (1992). The purpose of these methodologies were to (1) create an “artificial lek” for newly released sage-grouse in the event resident males at Parker Meadows were absent and (2) enhance the appearance of the existing lek to released sage-grouse (fig. 2*C*). The release box was placed at the release site before sunrise and opened remotely by an observer in a blind ~50 m from the release boxes. Observational data were collected on behavior of birds at release, including exit behavior from the box (flushing, walking, time-to-release once the box is open) and behavioral interactions with silhouettes or resident grouse.

Experimental Brood Capture and Translocation

Following a strict experimental design as part of a first year-pilot study, we translocated three females with broods from Bodie Hills to Parker Meadows before chicks reached an age of 10-days post-hatch. The rationale behind this translocation technique was females with young broods have already succeeded in nest initiation and nest survival, a critical and risky stage of the breeding season. Thus, these females translocated at later stages of reproduction likely will contribute to growth of the translocated population more than females translocated at earlier stages, who must still initiate nests and successfully produce young before progressing to the next reproductive stage. Radio-marked females with broods were captured at night using spotlighting methods described in section “Capturing and Handling Sage-Grouse.” Chicks were captured by hand and placed into a small insulated cardboard box with heat sources, and females were placed in separate cardboard boxes lined with paper towels (Thompson and others, 2015). The female and chicks were transported to the release site separately to prevent injury to chicks by the female but were allowed to comingle prior to their ultimate release at Parker Meadows. Translocated females with broods were released into high-quality brood habitat based on prior telemetry locations and observations of resident brood use (Cassaza and others, 2011).

Prior to release, the female and chicks were placed in a specialized brood release box wherein the female was separated from her chicks by a removable plexiglass partition (fig. *3A*. The partition protected the chicks from potential injury from the female but still allowed audiovisual contact between the female and her chicks. When the box was in place at the release site and the female was sufficiently calm, the partition was removed, allowing the female to interact with her chicks for at least 2 h prior to release. Cameras were placed inside and around the outside of the box to record release behavior of the female and her chicks.

Figure 3. The interior of a brood release box after the brood exited the box (*A*) the arrow indicates the placement of a removable partition. The soft-release enclosure used to release translocated greater sage-grouse (*Centrocercus urophasianus;* hereinafter sage-grouse) broods (*B*) as part of a sage-grouse translocation project at Parker Meadows, California, from 2017-18. Photographs by Mary Meyerpeter, U.S. Geological Survey.

For the first release, we placed the release box on site several hours before sunrise and opened it remotely at dawn by an observer in a blind. For all subsequent releases, a secondary wire and mesh enclosure was built around the release box (fig. 3*B*) to ensure the female would remain in the immediate vicinity of her chicks until the chicks exited the box. Dried mealworms were placed inside the enclosure to allow the female and chicks forage material directly after release. The secondary enclosure was opened 2–3 h after sunrise, allowing the brood to exit and disperse into brood-rearing habitat, while still allowing for a full day to familiarize with the novel environment.

Estimating the Probability of Nest Initiation and Permanent Movement Away from the Restoration Site of Translocated Sage-Grouse

To calculate the probabilities of nest initiation and dispersal of translocated sage-grouse, we used generalized linear models in JAGS (Plummer, 2003) within Program R (R-Core-Team, 2018), and assumed that the response variable (nest initiation: nest or no-nest; dispersal: permanent movement away from restoration site or no-permanent movement) followed binomial distributions, and probabilities were derived from intercept-only models. We removed sage-grouse that died or went missing during the first 16 days post-release from the analyses (but they were retained for the survival analysis). We used a 16-day criterion following recent findings of an intensive translocation effort on a different species of grouse, Columbian sharp-tailed grouse (*Tympanuchus phasianellus columbianus;* hereinafter, CSTG), in which nest incubation was not observed until greater than or equal to 16 days post-release (Mathews and others, in press). Thus, nest initiation probabilities only represent sage-grouse with known histories (that is, not missing) that were alive and presumably had the opportunity to nest at the release site.

We estimated the probability of dispersing away from the release site for individuals that survived the first 30 d following release. We chose this criterion based on extensive (that is, 5 years) movement data for reintroduced CSTG in Nevada (Steven Mathews, U.S. Geological Survey, written commun., 2018) where most grouse dispersed away from the release site within 30 days. Therefore, individuals that died prior to 30 days could have still dispersed away from the release site and represent “unknown” dispersal responses. Furthermore, sage-grouse routinely travel several kilometers from their lek of capture to their nest location as a seasonal movement in a normal population (Coates and others, 2013). After 30 days at the release site, we were not capable of distinguishing between dispersal, seasonal movement patterns, or exploratory movement behavior, whereas movement away from the release site in less than or equal to 30 days was viewed as a distinct behavioral choice to attempt to return to the capture location.

Monitoring of Sage-Grouse

Radio and GPS Telemetry

We conducted intensive monitoring of sage-grouse movement, survival, and reproduction each spring and summer season following the release of marked individuals. We used a three-element Yagi antenna (Advanced Telemetry Systems Inc., Isanti, Minn.) and a portable receiver (Communication Specialist Inc., Orange, Calif.) to track radio-marked sage-grouse. Throughout the nesting and brood-rearing period, we attempted to visually locate female sage-grouse once per week for general locations, and up to three times per week if the female was nesting. We attempted to locate sage-grouse that went missing during this period with fixed-wing telemetry.

Grouse Use of Conifer Treatments and Irrigated Pasture

We conducted a preliminary analysis of sage-grouse use of conifer (that is, PJ) removal treatments outlined in the Bi-State Action Plan (2012). Removal treatments occurred in areas of phase 1 (less than approximately 10 percent conifer) or phase 2 (approximately 10–20 percent conifer) encroached habitats where shrub understories are still relatively intact. We restricted our data analysis to treatments implemented in 2014 to correspond with the initiation of sage-grouse telemetry monitoring efforts described in this report. We also restricted the analysis to GPS-PTT marked sage-grouse. For each year, we calculated the average number of locations for each sage-grouse located in the following areas: (1) any planned but not yet implemented treatments, (hereinafter, “pre-treatment”); (2) any implemented treatments (hereinafter, “post-treatment”); and (3) no treatments. We also evaluated sage-grouse use of treatments at three scales: (1) within the perimeter of any treatment (0-m), (2) within 439 m of any treatment, and (3) within 1,451 m of any treatment. The latter two scales represent the average and average maximum daily distance traveled by sage-grouse, respectively (Coates and others, 2017), and were calculated to approximate use of edge or periphery habitat relative to treatments. We stress that this is a preliminary, cursory examination of the data.

We also conducted a preliminary assessment of sage-grouse use of two extensive irrigated pastures in Long Valley, California. We leveraged past telemetry data collected by USGS and collaborators going back to 2007 and calculated the number of all telemetry locations, number of nests, and number of brood locations inside and within 1 km of the two pastures.

Utilization Distribution

We estimated utilization distributions (hereinafter, UDs; Kernohan and others, 2001), which interpolate animal use of space across unknown areas based on the distribution and density of known location telemetry data and GPS location data (Worton, 1989). Utilization distributions allow for estimation of the total area used by individual sage-grouse while accounting for imperfect monitoring efforts that are common to radio-telemetry studies. To calculate UDs, we used a kernel density estimator with likelihood to estimate the most appropriate smoothing parameter (Horne and Garton, 2006). Utilization distributions were calculated at the population level for spring (March–May), summer (June–August), fall (September–November), winter (December–February), and cumulatively for the entire year. We defined the population core-use area as the 50 percent contour (isopleth) from the UD and the population home range as the 95 percent contour. We only report cumulative UDs for sage-grouse marked at Sagehen, Bodie Hills, Parker Meadows, Long Valley subpopulations since at least fall 2014, and those at the Mount Grant and Desert Creek subpopulations since fall 2013.

Monitoring of Nests and Broods

For nest survival analysis, we developed a daily encounter history for individuals that included the date that a nest was first found, the last date a nest was known to be alive, and the fate (confirmed success or failure). A nest was considered successful if greater than or equal to one chick hatched determined by visual assessment of eggshell remains or observing greater than or equal to one chick in the nest bowl. Nests were considered unsuccessful when the entire clutch failed to hatch. Failed nests were scored as depredated, partially depredated and subsequently abandoned (greater than or equal to one intact egg), or abandoned. After confirming incubation (first found), each nest was monitored every 3 days until nest fate could be determined.

For brood survival analysis, we recorded hatch date, number of hatched eggs (initial brood size), and number of live chicks at the end of the brood monitoring period (final brood size). We monitored broods every 10 days, both during daytime and nighttime hours for up to 50 days after hatch. We determined a successful brood if greater than or equal to one chick survived to an age of 50 days post-hatch. We flushed the female and all her chicks to obtain an accurate chick count on day 50. However, brood monitoring periods varied (50, 28, and 35 days) between years, and thus, we corrected for unequal monitoring intervals in the modeling procedures (see section, "Modeling Equations of the IPM").

Avian Predator Monitoring

We followed a consistent predator survey protocol we developed for common raven (*Corvus corax*), raptor, horse, and livestock surveys (hereinafter, RRHL) from March to August. Briefly, we conducted point-count surveys with binoculars at each telemetry, lek, nest, brood, mortality, and habitat location from approximately 0 (directly at the point) to 100 m (brood rearing female). Surveys were conducted over a 10-min period wherein all four directional quadrants around the location were scanned for an equal amount of time. The time, bearing, and distance from the survey point of each observation were recorded for each avian predator detected, and all birds were classified to species. We performed the survey upon arrival to each location between 30 min prior to sunrise and 30 min following sunset, which provided a representative sample of avian predator abundance during diel and crepuscular periods. The same survey technique was conducted at randomly generated RRHL points throughout the study site, with an attempt to obtain one random RRHL point for each nest and brood location. We only report RRHL summary statistics for the same subpopulations and time periods where UDs were reported.

Estimating Population Growth Using an Integrated Population Model

Integrating Data for the IPM

Integrated population models (IPMs) provide an empirically driven framework to investigate population dynamics by incorporating multiple sources of data within a single unified framework (Schaub and Abadi, 2011; Kéry and Schaub, 2012). We developed a stochastic stage-based and age-structured IPM to estimate finite annual rates of population change (hereinafter, λ) among subpopulations and across the Bi-State DPS (that is, the metapopulation). The IPM closely followed methods described by Coates and others (2018), was informed by annual demographic and lek survey datasets for seven sage-grouse subpopulations, and implemented with JAGS (Plummer, 2003) within Program R (R-Core-Team, 2018). Combining lek-survey and stage-based demographic data for each subpopulation within the IPM framework allows for more precise estimation of λ and better understanding of processes and patterns influencing λ, even in circumstances when data were missing or disparate (Schaub and Abadi, 2011). Notably, our framework also allowed for inclusion of random effects (for example, subpopulation and year) and density dependence structures for each life stage to refine the demographic process models (Coates and others, 2018).

Modeling Equations of the IPM

Yearling and adult survival models. For each sage-grouse, encounter histories were created using telemetry data and modeled as a continuous process observed at discrete monthly intervals. We right censored individuals from the data if we did not observe their fate but included them when their fate was known. We considered censoring to be a random process in that all individuals either died or were eventually right censored (alive or status unknown). We allowed for yearling sage-grouse to graduate to the adult age class between years. Inference was based on a constant hazard model, meaning the probability of mortality did not change across months. Each encounter interval for each unit hazard (*UH*) represented a Bernoulli process per-month, following modeling procedures described in Halstead and others (2012). The additive effect model was expressed as the following:

$$UH_{hkij} = exp(\alpha_i + \beta_{age} * x_{age,hik} + \gamma_j + \zeta_{ij}) \tag{1}$$

$$\alpha_i \sim Normal(0, \sigma_\alpha^2)$$

$$\gamma_j \sim Normal\left(0, \sigma_\gamma^2\right)$$

$$\zeta_{ij} \sim Normal\left(0, \sigma_\zeta^2\right)$$

where *UH* was a function of random effect for subpopulation α_i, a random effect for year γ_j, a random effect for subpopulation and year ζ_{ij}, each of which were assumed to arise from Normal distributions with mean zero, and variances $\sigma_\alpha^2, \sigma_\gamma^2$, and σ_ζ^2, respectively. The magnitude of β_{age} was modeled as the expected change in the ln(hazard ratio), where the indicator of age was equal to one for adults. The hazard ratio represented the ratio of hazard rates (in this case, monthly risk of morality) between the two age classes. Subscripts *h*, *k*, *i*, and *j* reference sage-grouse, month, subpopulation, and year. Following the modeling process, we derived the annual (*an*) survival parameter (*s*) as the following:

$$s_{an,ij} = e^{-CH_{ij}} \tag{2}$$

$$CH_{ij} = \sum_{j=1}^{T=12} UH_{ki} \tag{3}$$

where *CH* represented the cumulative hazard (*T*=12 months represented annual survival).

First nest propensity. We used estimates from Taylor and others (2012) of 0.96 (95 percent confidence interval [CI]=0.94–0.97) and 0.89 (95 percent CI=0.87–0.91) as informative priors for nest propensity for adults and yearlings, respectively. These values were considered reliable because of the large number of studies used in the analysis (Taylor and others, 2012). However, we used priors that were slightly wider as a more conservative approach (adults = Beta [97,5] and yearlings = Beta [90,12]) and assumed these proportions to be constant among subpopulation and years.

Clutch size. Data for clutch size of first (*c1*) and second (*c2*) nests were modeled as arising from the Poisson distribution as follows:

$$y_{c,cj} \sim Poisson\left(\mu_{c,cj}\right)$$

$$log\left(\mu_{c,cj}\right) = \beta_{age} * x_{age,cj} + \gamma_j \tag{4}$$

$$\gamma_j \sim Normal\left(0, \sigma_\gamma^2\right)$$

Thus, the log expected count of clutch size μ_c at clutch *c* and year *j* is a linear function of the random effect of year, γ_j, which was assumed to arise from a Normal distribution with mean zero, and variance σ_γ^2. The magnitude of β_{age} was modeled as the change in the expected count where the indicator of age was equal to one for adults.

Nest survival. Survival parameters of first (*ns1*) and second (*ns2*) nests were derived separately and modeled as proportional hazards as expressed in equation 1. We modeled nest survival at discrete daily intervals (*T*=38) to estimate cumulative survival during the laying and incubation phases and included random effects for subpopulation and year; female age was used as a fixed effect. Separate analyses did not support the inclusion of random effects in the nest survival models (Coates and others, 2018), so estimates by site and year are not reported.

Egg hatchability. Egg hatchability (*h*) was modeled from successful nests as arising from a Binomial distribution (logit-link function) that took the following form:

$$y_{h,eij} \sim Binomial(p_{h,eij}, n_{h,eij})$$

$$\text{logit}\left(p_{h,eij}\right) = a_i + \beta_{age} * x_{age,eij} + \gamma_j + \zeta_{ij} \tag{5}$$

$$\alpha_i \sim Normal(0, \sigma_\alpha^2)$$

$$\gamma_j \sim Normal\left(0, \sigma_\gamma^2\right)$$

$$\zeta_{ij} \sim Normal\left(0, \sigma_\zeta^2\right)$$

where $y_{h,eij}$ represents the number of hatched eggs (successes) out of the initial number (that is, number of trials; $n_{h,eij}$) of eggs in a clutch *e,* at subpopulation *i* and year *j.* The logit-link ($p_{h,eij}$) is a linear function of random subpopulation effects a_i, random year effects γ_j, as well as subpopulation and year effects combined ζ_{ij}; all were assumed to arise from normal distributions with mean zero and variances $\sigma_\alpha^2, \sigma_\gamma^2$, and σ_ζ^2, respectively. The magnitude of β_{age} was modeled as the change in the expected count of successfully hatched eggs where the indicator of age was equal to one for adults.

Second nest initiation. Parameters were derived for the probability of second nest attempt (*np2*) directly from data collected in the Bi-State DPS. Second-nest propensity data were modeled as arising from a Binomial distribution as follows:

$$y_{np,ij} \sim Binomial(p_{np2,ij}, n_{np2,ij})$$

$$logit(p_{np2,ij}) = a_i + \beta_{age} * x_{age,ij} + \beta_{dd} * x_{dd,ij} + \gamma_j + \zeta_{ij} \tag{6}$$

$$\alpha_i \sim Normal(0, \sigma_\alpha^2)$$

$$\gamma_j \sim Normal(0, \sigma_\gamma^2)$$

$$\zeta_{ij} \sim Normal(0, \sigma_\zeta^2)$$

where the number of unsuccessful nests at each subpopulation in each year were denoted by $n_{np2,ij}$. In this model, $y_{np2,ij}$ represents the number of renests and logit($p_{np2,ij}$) is a linear function of random subpopulation effects a_i, random year effects γ_j, as well as random subpopulation and year effects combined ζ_{ij}, each of which were assumed to arise from Normal distributions with mean zero, and variances $\sigma_\alpha^2, \sigma_\gamma^2, \sigma_\zeta^2$, respectively. The influences of age and density dependence on *np2* were measured as fixed effects with magnitude β_{age} and β_{dd}, where the indicator of age was equal to one for adults, and the density dependent variable was the natural log of abundance with a 1-year lag.

Chick survival. Chick survival (*cs*) probabilities were derived from two brood counts with time interval lengths that varied across the 15-year study period. However, the number of days elapsed from nest hatch to brood count varied by study year (2003–05, 50 days; 2007–09, 35 days; 2010–11, 28 days; 2012–17, 50 days). Therefore, we used an adjustment in estimating survival probabilities depending on the year of study. We modeled chick survival based on brood count data as arising from a Binomial distribution where the initial brood size was scored as the number of trials, and chicks that survived to days *d* were scored as successes and took the following form:

$$y_{cs,bij} \sim Binomial(p_{cs,bijd}, n_{cs,bij}) \tag{7}$$

where *d* on the binomial probability *p* is *d*=*d*(*j*) and represents one of three survival periods depending on the year *j* of data collection (*d*=28, 35, or 50). For a 35-day interval, the probability of survival is modeled by this logistic relationship:

$$\text{logit}(p_{cs,bi,35}) = a_i + \beta_{age} * x_{age,bi} + \beta_{dd} * x_{dd,bi} \tag{8}$$

$$\alpha_i \sim Normal(0, \sigma_\alpha^2)$$

In this model, $y_{cs,bi}$ represents the number of chicks that survived for each brood, b, at subpopulation i. The logit($p_{cs,bi,35}$) is a linear function of random subpopulation effects a_i. The influence of age and density dependence on chick survival were measured as fixed effects with magnitude β_{age} and β_{dd}, where the indicator of age was equal to one for adults, and the density dependent variable was the natural log of abundance with a 1-year lag. We assumed a constant hazard function, and consistent with this assumption, the probabilities of survival for the other intervals are related as follows:

`

$$p_{cs,bid} = \begin{cases} \left(p_{cs,bi,35}\right)^{28/35}, & t = 28 \\ p_{cs,bi,35}, & t = 35 \\ \left(p_{cs,bi,35}\right)^{50/35}, & t = 50 \end{cases} \tag{9}$$

Juvenile survival. Juvenile sage-grouse (*js*; post-fledging, greater than 35 days and less than 1 year old) were not radio-marked and tracked in the Bi-State DPS. However, we derived a posterior distribution of juvenile survival rates (*js*) during this period by using an informative prior of 0.75 (95 percent CI=0.67–0.82) reported in Taylor and others (2012) in the form of Beta (100,34).

Estimating Population Size and λ. Coates and others (2018) provide detailed methods for the final step of the IPM where joint likelihoods for lek counts informed the observation process (equation 11 in Coates and others, 2018) and demographic data informed the state process (equations 2 and 10 in Coates and others, 2018). In brief, this process produced posterior distributions of abundance (*N)* for each subpopulation that were used to derive λ, which took the following form:

$$\lambda_{ij} = \frac{N_{ij+1}}{N_{ij}} \tag{10}$$

where *i* represents subpopulation, *j* represents year, and *j*+1 represents the following year. We also calculated the instantaneous per capita rate of change (*r*) as the following:

$$r_{ij} = ln(\lambda_{ij}) \tag{11}$$

We also calculated an annual estimate of *N* at the regional level (that is, across the Bi-State DPS) by summing the annual abundance estimates across the seven subpopulations and estimated regional λ and *r* using equations 10 and 11, respectively. For each subpopulation, we then calculated the probability that the subpopulation was increasing, stable, or decreasing based on the posterior distributions of derived parameters. We calculated the odds of increase from the probability values, where the odds of increase represented the probability of increase divided by the sum of the probability of decrease and stability. Likewise, we calculated the odds of decrease. We then created a ratio of the two odds (OR; increase:decrease) and applied natural logarithmic transformation to that ratio (ln[OR]). A value equal to zero indicates stability, values greater than zero indicate higher odds of increase, and values less than zero indicate higher odds of decrease. Posterior distributions of all parameters were summarized as median and 95 percent credible intervals (CRI), expressed as 0.025–0.975 quantile.

Translocated grouse were censored from contributing to IPM estimates for Bodie Hills, Parker Meadows, and the Bi-State DPS. We report estimates from translocated grouse to better inform translocation methodologies (see section, "Estimates of Population Growth from an Integrated Population Model"), but we did not allow grouse within the experimental translocation to influence subpopulation trends because their survival and demographic rates were likely altered by the translocation.

Preliminary Results

The following sections provide preliminary findings of an ongoing monitoring program of sage-grouse in the Bi-State DPS. We provide summary capture statistics, area sizes of UDs, relative raven abundance, and estimates of demographic vital rates across each of the subpopulations. We do not report the varying random effect structures for each vital rate, but we indicate that specific parameters (for instance, chick survival) varied across subpopulations. We provide tables of estimated parameters pooled across years and subpopulations. Data for some subpopulations were too sparse to reliably estimate vital rate parameters. For example, we marked a small sample of sage-grouse in the White Mountains PMU during the fall of 2016 for exploratory analysis of movement patterns, and then we marked a much larger sample in the fall of 2017 and spring of 2018. Thus, we did not have sufficient data to estimate population vital rates for the White Mountains PMU, and we only report preliminary movement summaries. Also, sage-grouse comprising the Sagehen subpopulation were monitored by the BLM and CDFW during 2015 and 2016, so results from this subpopulation are reported episodically throughout the report as data allowed.

Capture Summary and Sage-Grouse Space Use by Subpopulation

General telemetry locations of sage-grouse and the location of mortalities are shown in figure 4; nest and brood locations are shown in figure 5.

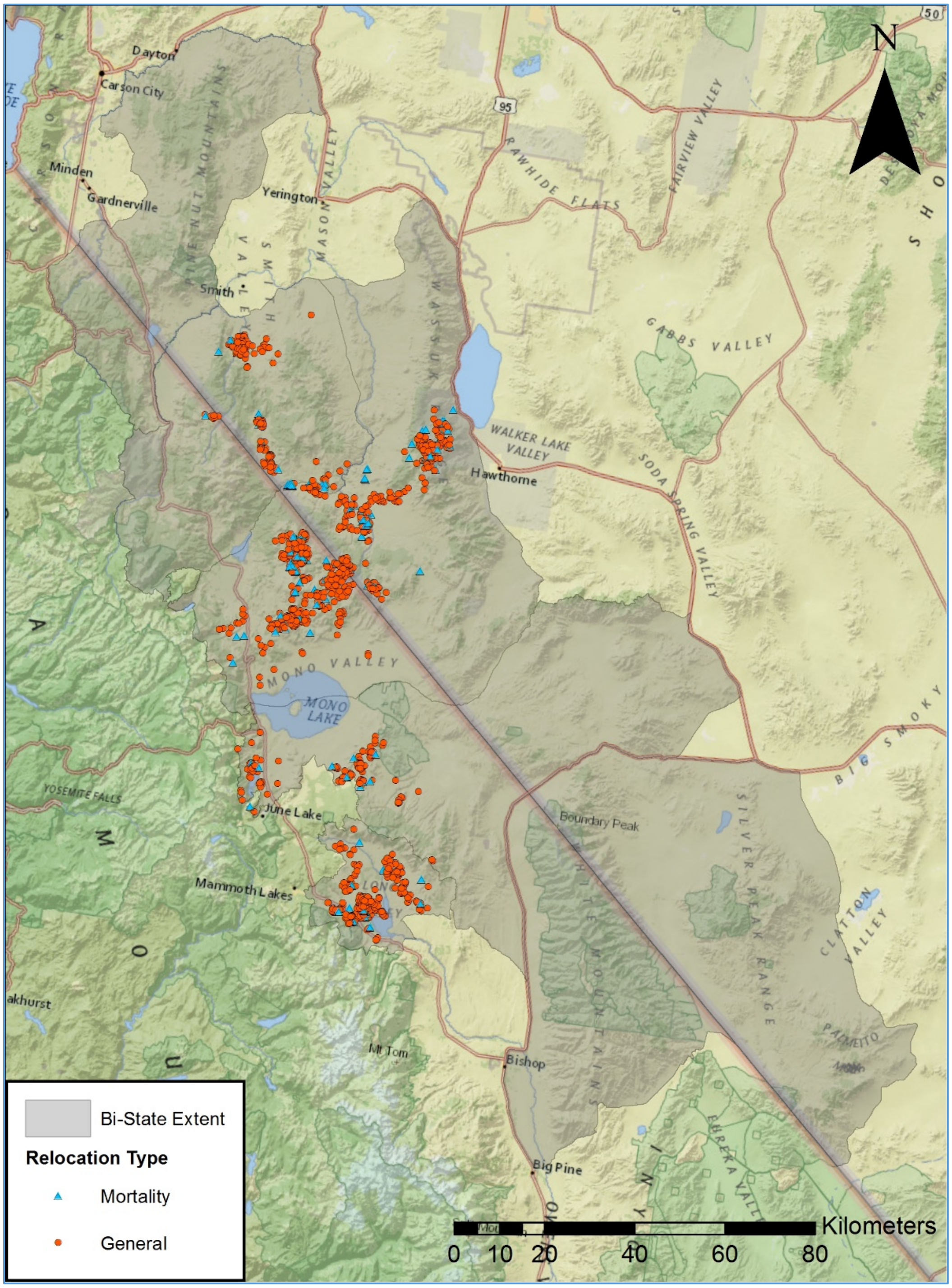


Figure 4. General and mortality telemetry locations of VHF-marked greater sage-grouse (*Centrocercus urophasianus)* across the Bi-State Distinct Population Segment study area California and Nevada, 2015–17.

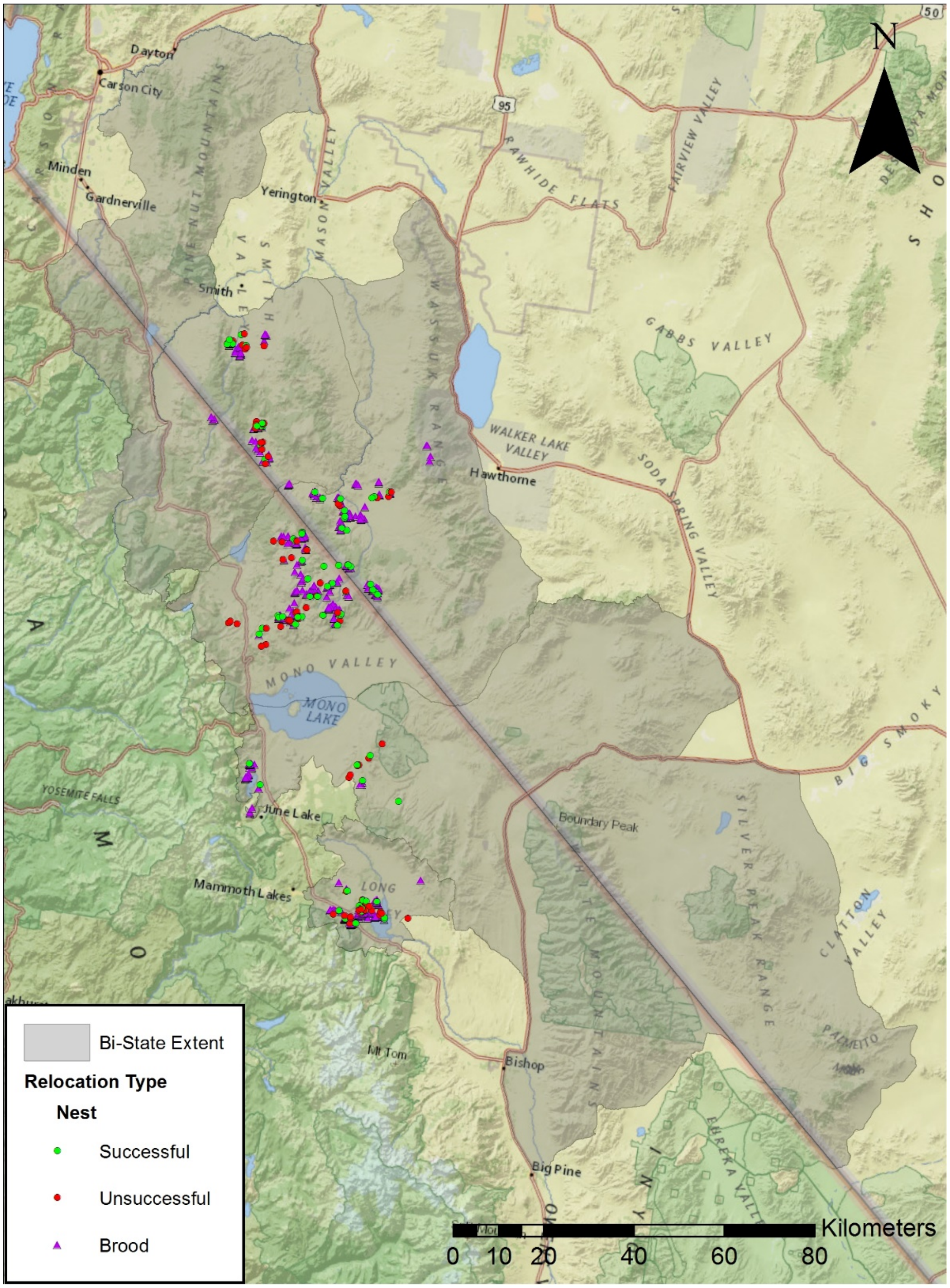


Figure 5. Nest and brood locations of greater sage-grouse (*Centrocercus urophasianus)* across the Bi-State Distinct Population Segment study area California and Nevada, 2015–17.

Capture Summary and Sage-Grouse Space Use at Mount Grant and Desert Creek

We deployed 11 GPS transmitters during 2013–14 at Mount Grant as part of a pilot study and then initiated full monitoring during spring of 2016. During the fall of 2015, we captured 12 females at Mount Grant and 8 at Desert Creek. In the spring of 2016, we radio-marked 10 females at Mount Grant and 13 at Desert Creek and an additional 21 females at Mount Grant and 18 at Desert Creek during the fall of 2016. In the spring of 2017, we captured and marked 9 females and 1 male at Desert Creek and 10 females and 1 male at Mount Grant. In the fall of 2017, we captured 9 females at Desert Creek and an additional 15 females and 1 male at Mount Grant. During spring (March–May), summer (June–August), fall (September–November), and winter (December–February) of 2013–17, we obtained 16,916 GPS locations or marked sage-grouse at Mount Grant and Desert Creek (figs. 6–13).

We calculated utilization distributions by season for GPS and VHF-marked sage-grouse. The UDs for Mount Grant and Desert Creek were jointly calculated and presented on the same map owing to the proximity of the two subpopulations. The core area of sage-grouse activity and the population level home range across all seasons were 1,389 and 13,013 ha, respectively (table 1). During the spring, Desert Creek and Mount Grant sage-grouse concentrated at Nine Mile Flat, a valley southeast of Bald Mountain and southwest of Mount Grant (figs. 6–7). Many sage-grouse used the area surrounding the East Walker River and Rough Creek, and some remained on Mount Grant. Sage-grouse were primarily located at Nine Mile Flat during the summer as well, with the highest concentrations located near Rough Creek, but there was some light utilization of high elevation areas such as the Bodie Hills and Mount Grant (figs. 8–9). During the fall, sage-grouse once again primarily utilized Nine Mile Flat but also used Bald Mountain and the Wassuk Range (figs. 10–11). Sage-grouse again primarily congregated in Nine Mile Flat during the winter; they made less use of Bald Mountain but made more use of areas within and around the Wassuk Range (figs. 12–13).

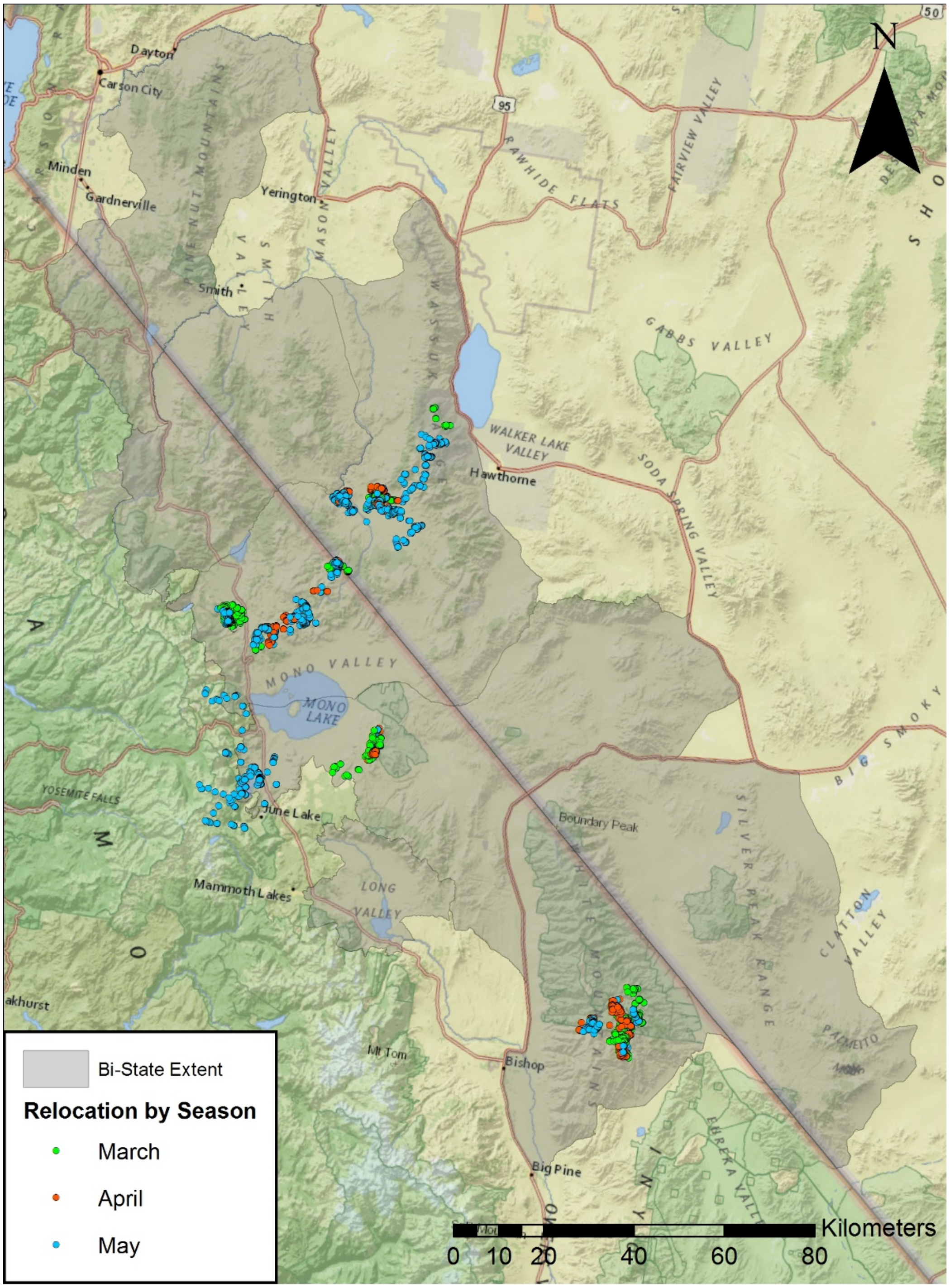


Figure 6. Monthly GPS locations of greater sage-grouse (*Centrocercus urophasianus)* during spring, across the Bi-State Distinct Population Segment study area California and Nevada, 2015–17.

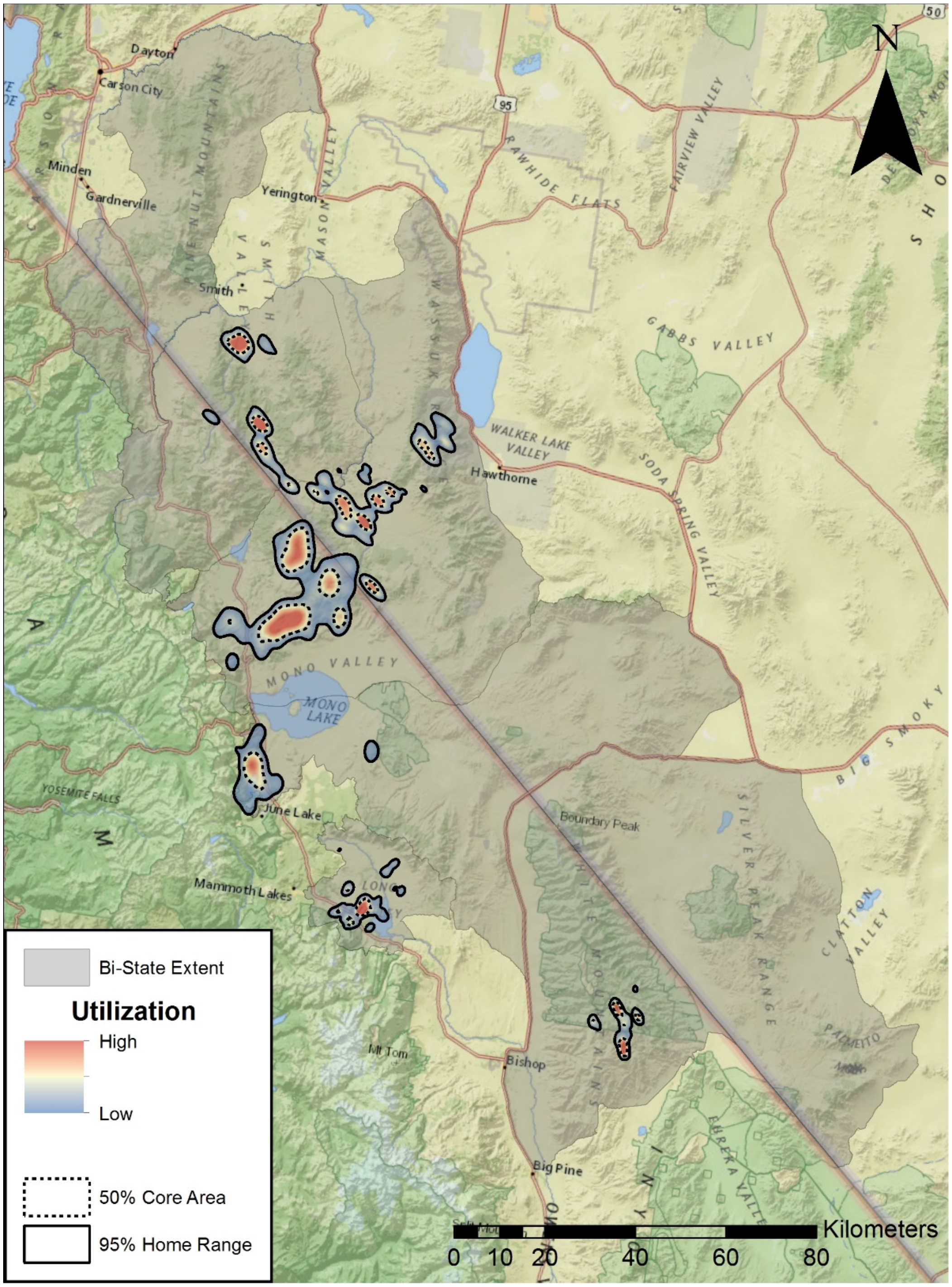


Figure 7. Cumulative utilization distribution of greater sage-grouse (*Centrocercus urophasianus*) during the spring season across the Bi-State Distinct Population Segment study area California and Nevada, 2015–17. Utilization distribution was approximated by using kernel density estimators.

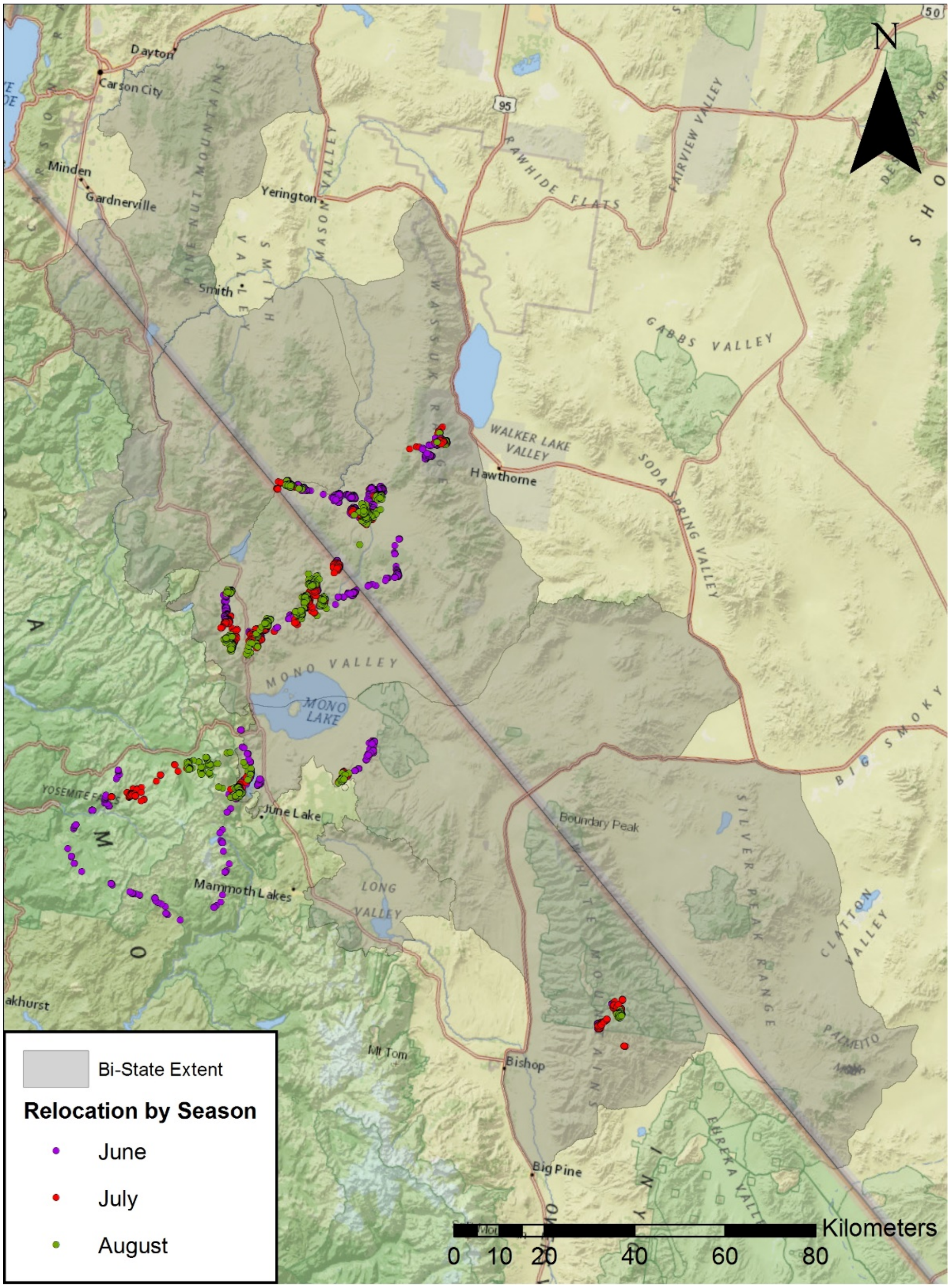


Figure 8. Monthly GPS locations of greater sage-grouse (*Centrocercus urophasianus)* during summer, across the Bi-State Distinct Population Segment study area California and Nevada, 2015–17.

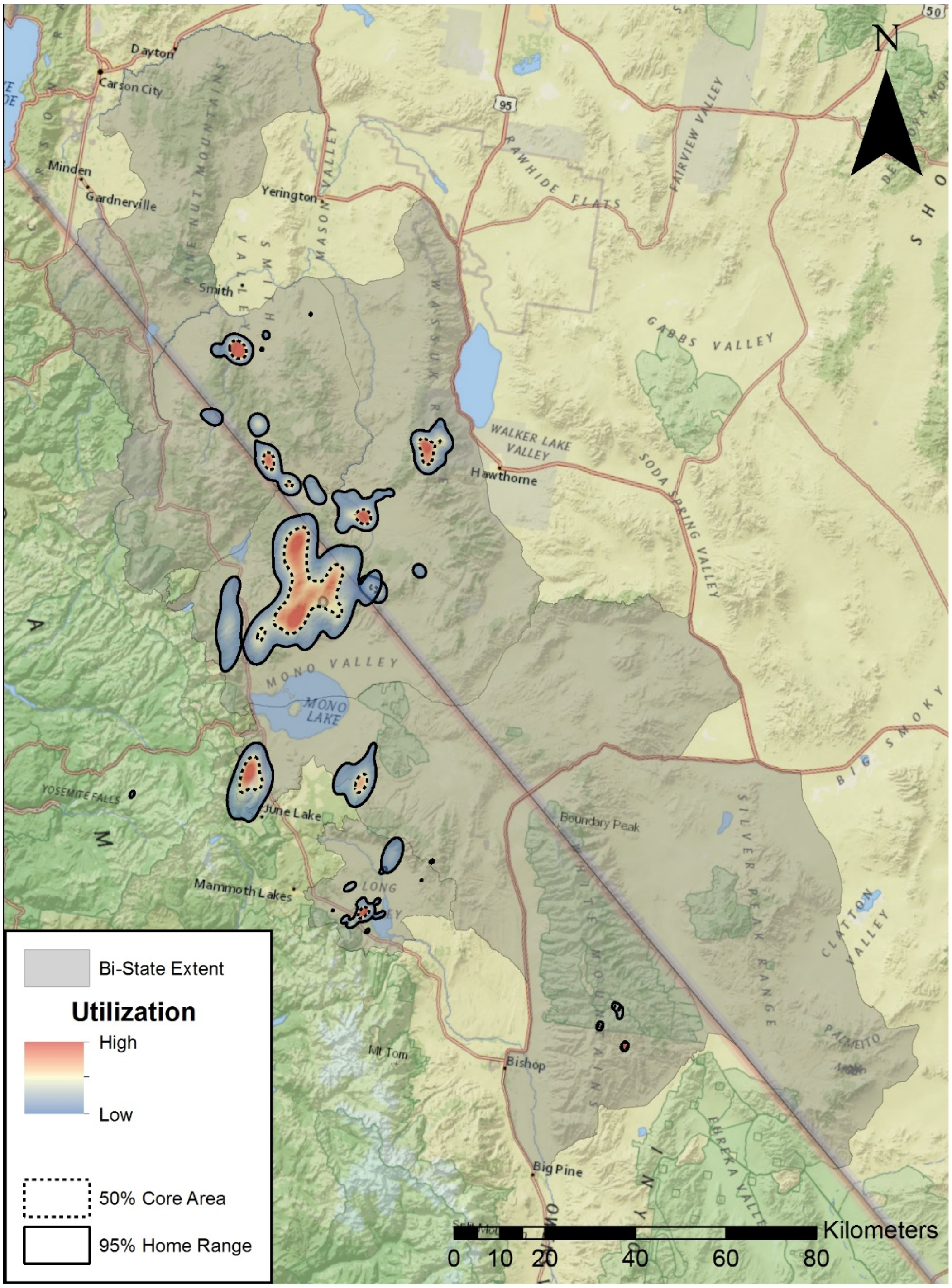


Figure 9. Cumulative utilization distribution of greater sage-grouse (*Centrocercus urophasianus*) during the summer season across the Bi-State Distinct Population Segment study area California and Nevada, 2015–17. Utilization distribution was approximated by using kernel density estimators.

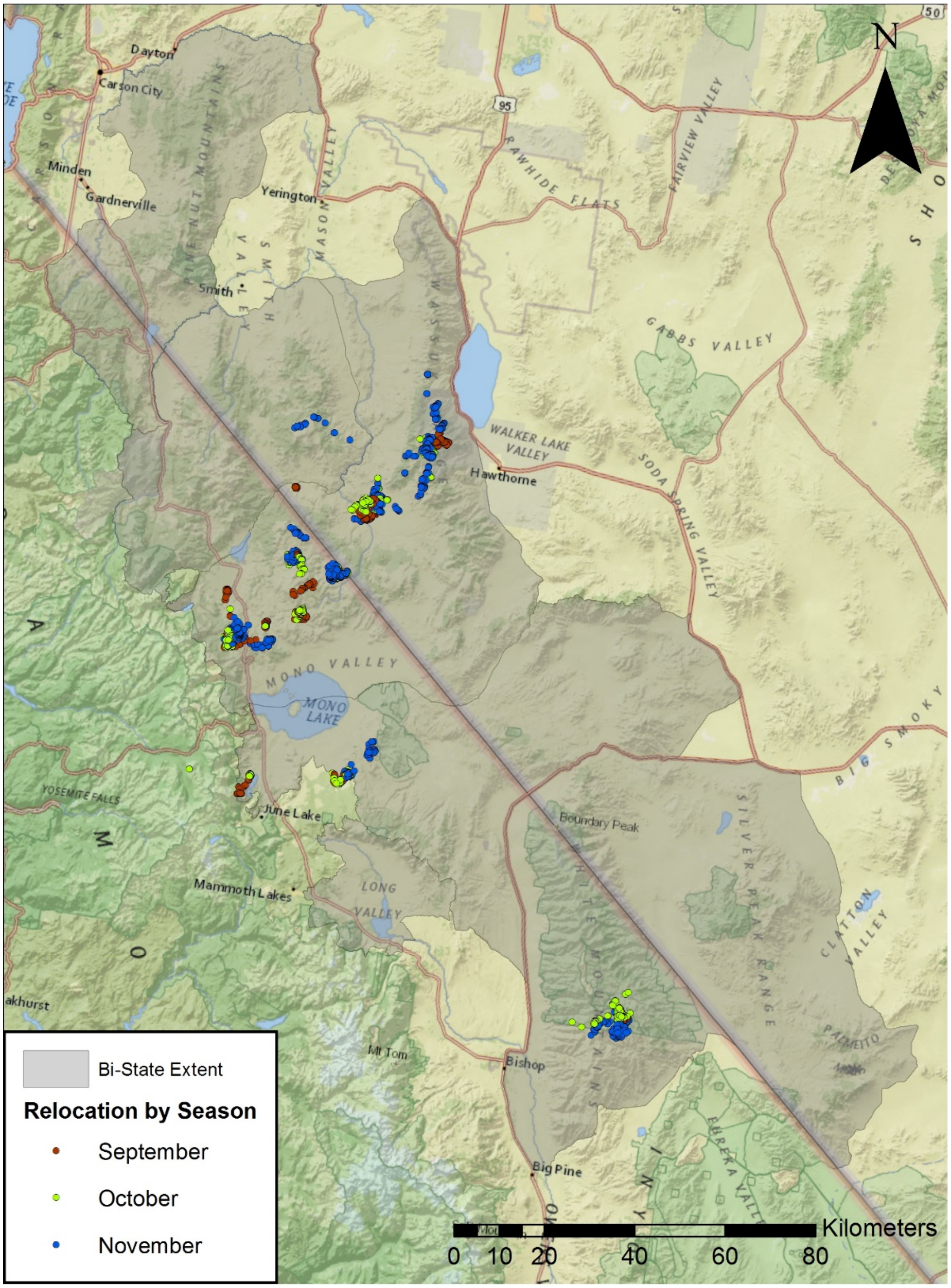


Figure 10. Monthly GPS locations of greater sage-grouse (*Centrocercus urophasianus)* during fall, across the Bi-State Distinct Population Segment study area California and Nevada, 2015–17.

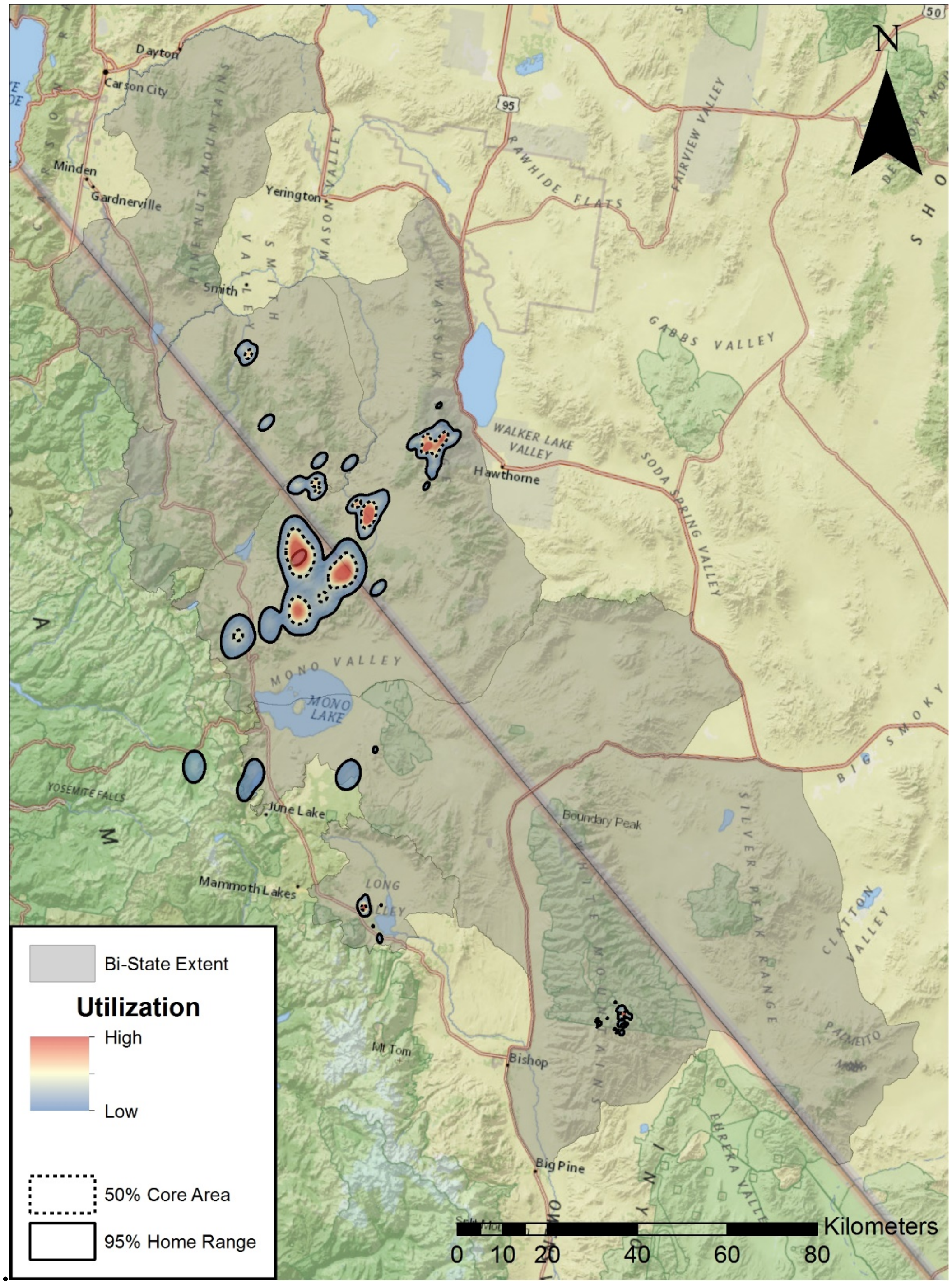


Figure 11. Cumulative utilization distribution of greater sage-grouse (*Centrocercus urophasianus*) during the fall season across the Bi-State Distinct Population Segment study area California and Nevada, 2015–17. Utilization distribution was approximated by using kernel density estimators.

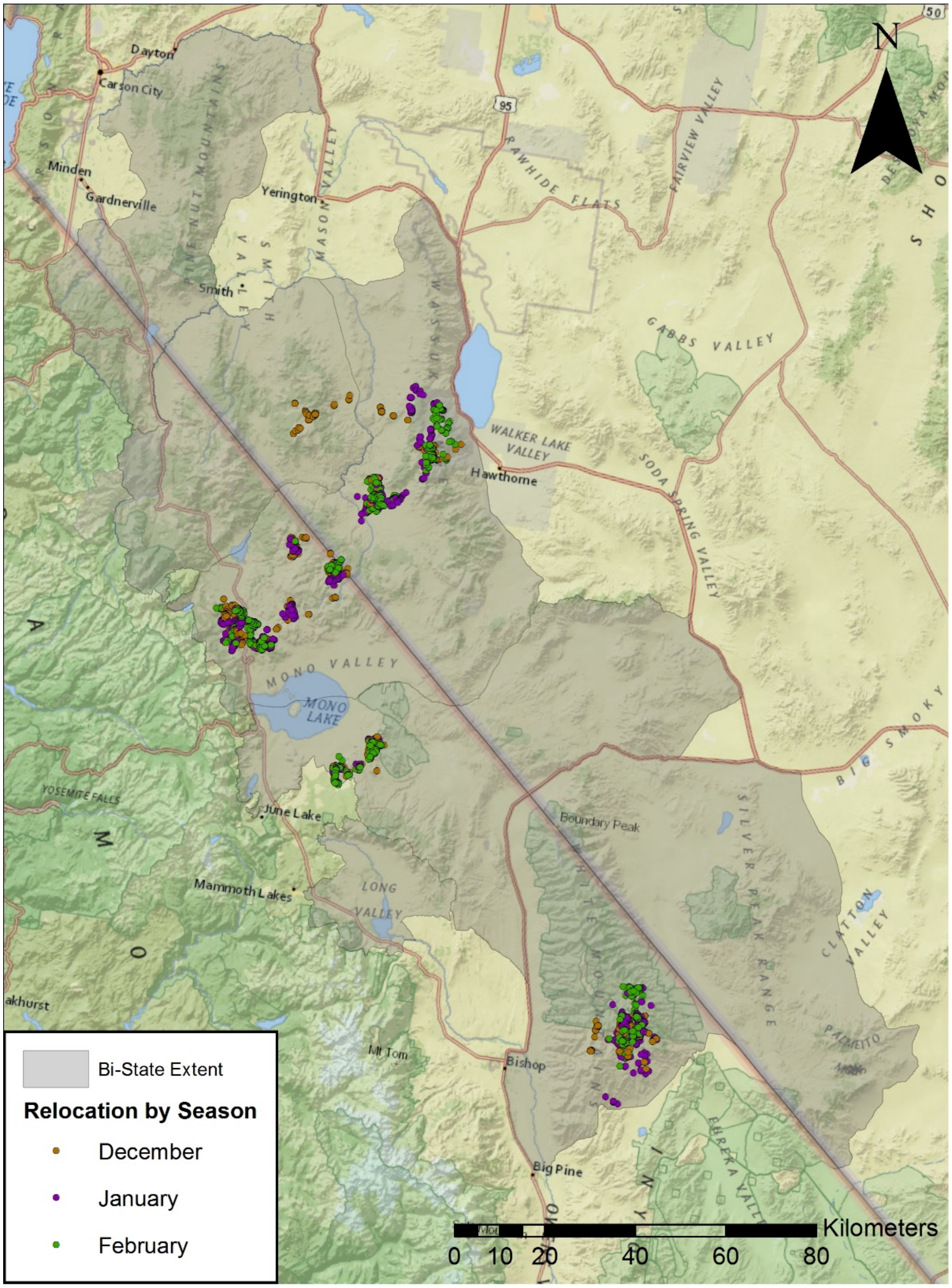


Figure 12. Monthly GPS locations of greater sage-grouse (*Centrocercus urophasianus)* during winter, across the Bi-State Distinct Population Segment study area California and Nevada, 2015–17.

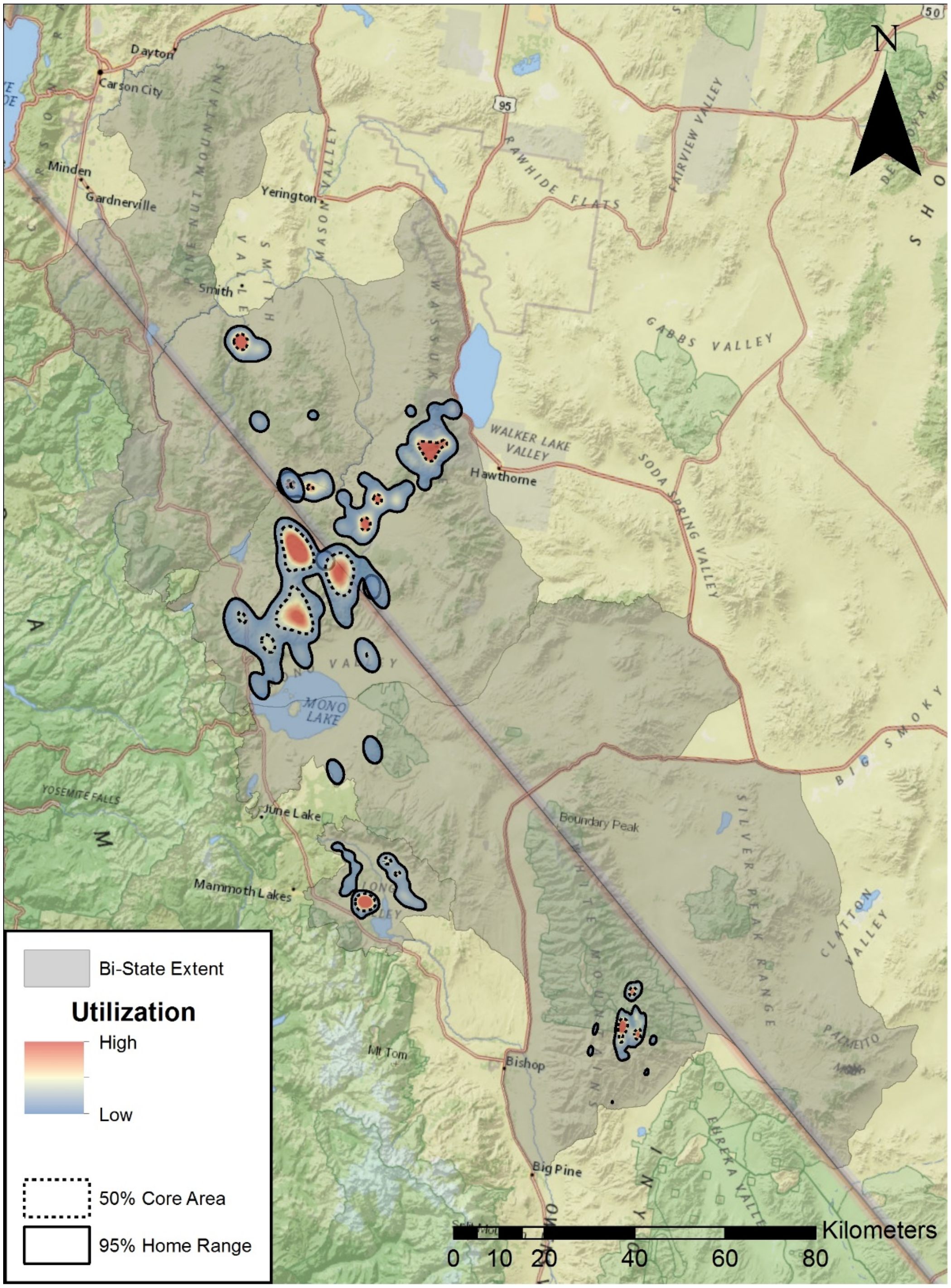


Figure 13. Cumulative utilization distribution of greater sage-grouse (*Centrocercus urophasianus*) during winter, across the Bi-State Distinct Population Segment study area California and Nevada, 2015–17. Utilization distribution was approximated by using kernel density estimators.

Table 1. Seasonal utilization distributions (UD) of GPS-marked greater sage-grouse (*Centrocercus urophasianus*) across the Bi-State Distinct Population Segment study area California and Nevada, 2017.

Subpopulation	Season	50 percent core area (hectare)	95 percent home range (hectare)
Mount Grant and Desert Creek	All	1,389	13,013
	Winter	1,019	11,662
	Spring	882	6,574
	Summer	510	3,653
	Fall	1,001	10,839
Bodie Hills	All	58,839	228,533
	Winter	15,891	63,322
	Spring	12,301	47,595
	Summer	19,498	69,250
	Fall	11,148	48,365
Long Valley	All	3,114	22,127
	Winter	1,570	10,542
	Spring	1,036	7,037
	Summer	396	3,323
	Fall	109	1,223
Sagehen	All	1,651	15,828
	Winter	354	2,788
	Spring	317	7,037
	Summer	766	4,665
	Fall	214	1,338
Parker Meadows	All	2,959	32,600
	Winter	No data	No data
	Spring	2,266	19,143
	Summer	693	13,457
	Fall	No data	No data
White Mountains[1]	All	2,490	14,398
	Winter	1,006	7,274
	Spring	1,055	4,991
	Summer	299	1,006
	Fall	130	1,126

[1] Estimates presented only pertain to GPS-marked sage-grouse.

Capture Summary and Sage-Grouse Space Use at Bodie Hills, Sagehen, and Long Valley

Trapping efforts began at Bodie Hills in the fall of 2014, and monitoring began in the spring of 2015. During the fall of 2014–16, we radio-marked 55 sage-grouse with VHF transmitters and seven sage-grouse with GPS transmitters. At Long Valley, trapping began in the fall of 2015, and monitoring began in the spring of 2016. We radio-marked 45 sage-grouse at Long Valley with VHF transmitters during the fall of 2015–16.

During March–April 2017, we captured and radio-marked an additional 17 sage-grouse at Bodie Hills and 8 at Long Valley with VHF transmitters; we marked 7 sage-grouse with GPS transmitters at Bodie Hills. In fall 2017 (September–October), we radio-marked 37 sage-grouse at Bodie Hills (*n*=5 GPS) and 25 at Long Valley.

From 2015 to 2017, we monitored a total of 69 and 50 female sage-grouse and obtained 617 and 406 VHF locations at Bodie and Long and Long Valley, respectively (fig. 4). At Bodie Hills, we obtained 5,064 GPS locations during winter (December–February), 9,743 during spring (March–May), 7,248 during summer (June–August), and 4,654 during fall (September–November) for a total of 26,709 locations from 2015 to 2017.

We calculated UDs by season for VHF and GPS-marked sage-grouse (table 1). At Bodie Hills, the core area of sage-grouse activity and population level home range during winter encompassed 15,891 and 63,332 ha (table 1), respectively, and core winter use areas were concentrated on the Dry Lakes plateau, near Big Flat, and near Biedeman lek (figs. 12–13). The core area of sage-grouse activity (50 percent UD) during spring and summer was 12,301 and 19,498 ha (table 1), respectively, and the population level home range (95 percent UD) was 47,595 and 69,250 ha (figs. 6–9; table 1), respectively. Spring and summer use areas were primarily centered around leks, especially Bridgeport Canyon, Big Flat, 7-troughs, Dry Lakes, and Little Mormon Meadow. During fall, the core area of sage-grouse activity (50 percent UD) and population level home range (95 percent UD) encompassed 11,148 and 48,365 ha, respectively (figs. 10–11; table 1). Fall use areas were similar to those used in winter.

At Long Valley, the core area of sage-grouse activity and population level home range during winter encompassed 1,570 and 10,542 ha (figs. 12–13; table 1), respectively. The core area of sage-grouse activity during spring and summer was 1,036 and 396 ha (table 1), respectively, and the population level home range was 7,037 and 3,323 ha (figs. 6–9; table 1), respectively. In the spring, use was concentrated in two main areas—Tobacco Flat (west of Highway 395) and areas near leks between Crowley Lake and Benton Crossing Road. In summer, sage-grouse congregated in the fields near Convict Creek (north of Lake Crowley and south of Benton Crossing Road). During fall, the core area of sage-grouse activity and population level home range encompassed 1,109 and 1,223 ha (figs. 10–11; table 1), respectively. In the fall and winter seasons, sage-grouse primarily used areas along Benton Crossing Road, although winter use was more dispersed to the northeast and northwest than fall use.

At Sagehen, the core area of sage-grouse activity and population level home range during winter encompassed 354 and 1,714 ha (figs. 12–13; table 1), respectively. The core area of sage-grouse activity during spring and summer was 317 and 766 ha (table 1), respectively, and the population level home range was 2,788 and 4,665 ha (figs. 6–9; table 1), respectively. During fall, the core area of sage-grouse activity and population level home range encompassed 214 and 1,338 ha (figs. 10–11; table 1), respectively.

Capture Summary and Sage-Grouse Space Use in the White Mountains

In the fall of 2016, we trapped eight sage-grouse on the California side of the White Mountains (*n*=5 female, *n*=3 male), all of which were fitted with rump-mounted GPS-PTTs. Of these, one female continued to provide movement data through spring of 2018. In the fall of 2017, we trapped 23 female sage-grouse and fitted all sage-grouse with necklace-style VHF radio transmitters. Within the White Mountains, sage-grouse exhibited a population level home range of 14,398 ha, and the core area of sage-grouse activity was 2,490 ha (figs. 6–13; table 1). In the spring, sage-grouse exhibited a 95 percent home range of 4,991 ha and a core use area of

1,055 ha (figs. 6–7; table 1). In the summer, sage-grouse used the smallest home range of any season with only 1,006 ha used at the 95 percent population level, and a core area of 299 ha (figs. 8–9; table 1). In the fall, the population level home range (95 percent home range) was 1,126 ha, and the core area was only 130 ha (figs. 10–11; table 1). In the winter, sage-grouse used the largest population level home range of any season of 7,274 ha and used a core area of 1,006 ha (figs. 12–13; table 1).

Sage-Grouse Space Use in Relation to Conifer Removal Treatments and Irrigated Pastures

Descriptive statistics for sage-grouse use of conifer removal treatments across the Bi-State DPS during the study period are presented in table 2. Overall, preliminary analyses indicate that average proportions of GPS locations in post-treatment areas tended to increase over time and across spatial scales. For example, average proportions of pre-treatment locations appeared higher than those for post-treatments in 2015, but patterns appeared to reverse thereafter. As of 2017, 3, 10, and 18 percent of locations averaged across individual sage-grouse occurred within post-treatment areas at the 0, 439, and 1,451 scales, respectively.

At Long Valley, long-term data indicated uneven spatial patterns of irrigated pasture use, whereby use appears to be linked to pasture edges more so than pasture interiors. Overall, 13 (n=707), 9 (n=156), and 18 (n=1,554) percent of general telemetry, nests, and brood locations, respectively, occurred within the pastures. However, within 1 km of the pasture edge, 62 (n=3,451), 51 (n=156), and 63 (n=989) general telemetry locations (of 5,579; 62 percent), 80 nests (of 156; 51 percent), and 989 brood locations (of 1,554; 63 percent). Locations of females with broods at Long Valley in relation to the pastures are shown in figure 14.

Table 2. GPS-marked greater sage-grouse (*Centrocercus urophasianus*) space use in relation to conifer removal (that is, single-leaf pinyon, *Pinus monophylla*, and Utah juniper, *Juniperus osteosperma*) treatments across the Bi-State Distinct Population Segment study area, California and Nevada, 2014–17.

[**Average proportion of sage-grouse GPS locations:** Calculations assume that hectares cut within a year are available for sage-grouse the following years. Hectares cut and number marked grouse are presented for 2014 without use estimates to indicate availability to sage-grouse in 2015 and thereafter. **Scale:** 0-m, 439-m, and 1,451-m indicates location within perimeter, 439 m, and 1,451 m any treatment perimeter. NA not applicable]

Year	Number of grouse marked	Hectares cut	Average proportion of sage-grouse GPS locations								
			0-m			439-m			1,451-m		
			Pre-treatment	Post-treatment	No-treatment	Pre-treatment	Post-treatment	No-treatment	Pre-treatment	Post-treatment	No-treatment
2014	22	3,260	NA	NA	NA	NA	NA	NA	NA	NA	NA
2015	10	2,223	0.09	0.02	0.89	0.13	0.06	0.81	0.31	0.16	0.53
2016	13	6,306	0.01	0.04	0.95	0.07	0.07	0.86	0.15	0.16	0.69
2017	24	4,923	0.00	0.04	0.96	0.03	0.14	0.83	0.16	0.20	0.64
Total	48	16,712	0.02	0.03	0.94	0.06	0.10	0.84	0.19	0.18	0.63

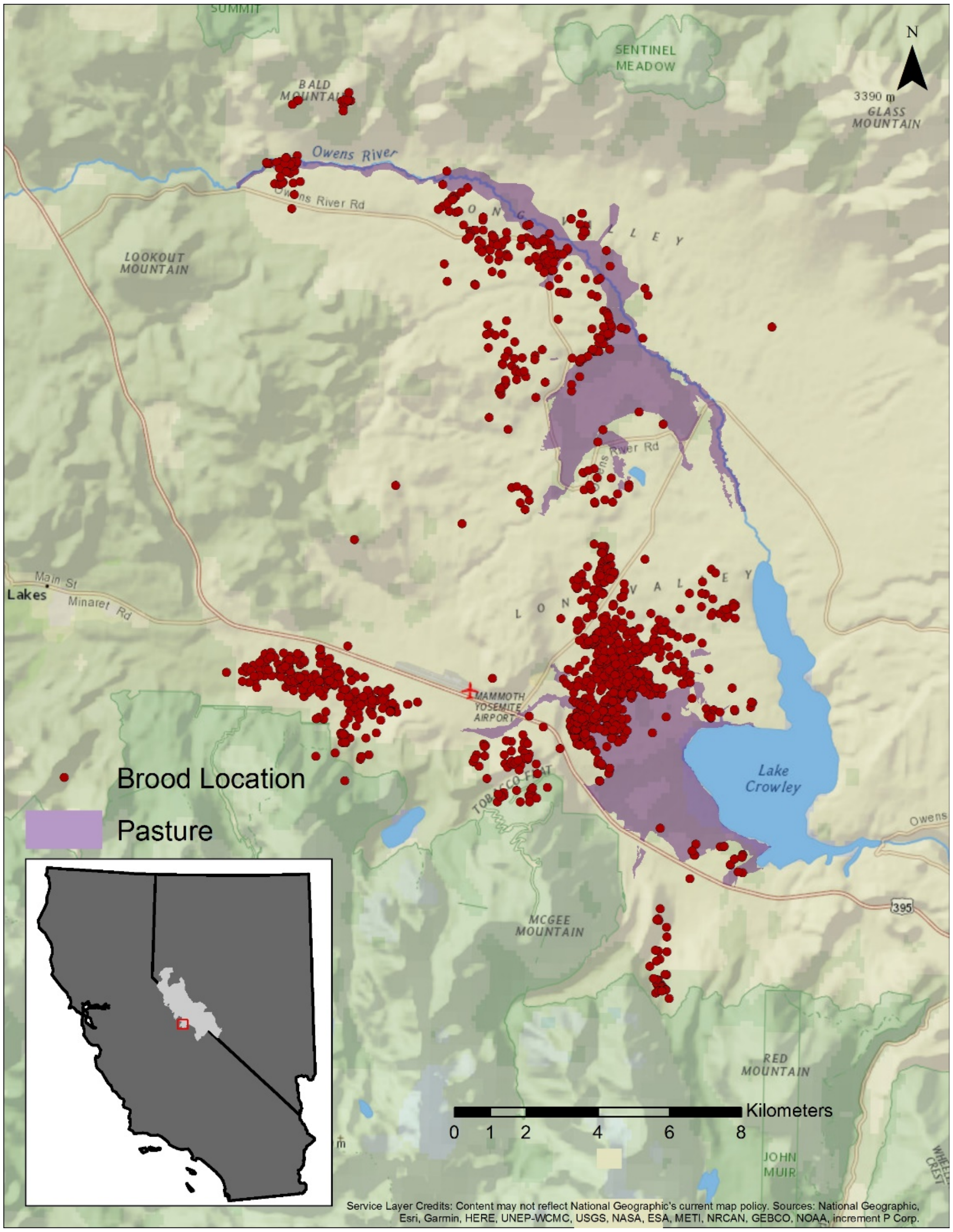


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Figure 14. Locations of greater sage-grouse (*Centrocercus urophasianus*) females with broods (*n*=1,554) in relation of two irrigated pastures in Long Valley, California, 2007–17.

Initial Results from the Experimental Translocation to Parker Meadows

Capture, Translocation, and Space Use of Translocated Pre-Nesting Sage-Grouse

We translocated 25 (n=17 pre-nesting female; n=8 male) sage-grouse to Parker Meadows from 7 leks at Bodie Hills. Of those, one male was observed at the release site with a broken wing 5 days after translocation and was trapped, euthanized, and censored from survival analyses after the injury was deemed to likely have occurred during the translocation process rather than post-release. We translocated sage-grouse primarily from the leks of Biedeman and satellites (7.5 percent), Big Flat (10 percent), Bridgeport Canyon (15 percent), and Dry Lakes (6 percent). Big Flat and Bridgeport Canyon were targeted extensively for translocations. Big Flat had a higher count during the translocation period in 2017 (48 males) than in 2016, and several of the birds captured at Bridgeport Canyon were males. In 2018, we plan to capture sage-grouse from leks that were not targeted in 2017 to minimize impacts on the source population.

At Parker Meadows, we obtained 575 GPS locations during spring, 1,061 locations during summer, and 252 locations during fall for a total of 1,888 locations in 2017. Translocated sage-grouse had a population level home range in the spring (95 percent UD) of 19,143 ha, and the core area of sage-grouse activity (50 percent UD) was 2,226 ha (table 1). In the summer, population level home range (95 percent UD) was 13,457 ha, and the core area of sage-grouse activity (50 percent UD) was 693 ha (table 1). In the spring, translocated sage-grouse exhibited exploratory movements, whereas in the summer, most locations were composed of females with broods utilizing Parker Meadows. Translocated sage-grouse that stayed at Parker Meadows primarily used the meadow and surrounding sagebrush hillsides, although some sage-grouse dispersed to Sagehen.

Annual Survival of Translocated Sage-Grouse

Using a shared frailty model described in equations 1–3, translocated sage-grouse had an annual probability of survival of 0.19 (95 percent CRI=0.05–0.46; table 3). Six mortalities of translocated sage-grouse occurred after release at Parker Meadows. Cause of death was mammalian predation (n=3) and unknown (n=3). Two mortalities occurred after sage-grouse dispersed to other study areas (Sagehen and Bodie Hills). Two others occurred in snowbound alpine areas west of Parker Meadows, and we were not able to access these areas to determine cause of death.

Table 3. Annual survival of greater sage-grouse (*Centrocercus urophasianus*) translocated to Parker Meadows, California, in 2017, and the probability that a translocated sage-grouse would permanently move away from the release location during the first 30 days following translocation.

Parameter	Median estimate	Credible interval (CRI)	
		Lower (0.025)	Upper (0.975)
Annual survival of translocated sage-grouse	0.19	0.05	0.46
Probability of nest initiation at Parker Meadows	0.21	0.1	0.32
Probability of movement away from Parker Meadows	0.49	0.41	0.73

Nest Initiation and Survival by Translocated Sage-Grouse at Parker Meadows

We translocated 17 female sage-grouse to Parker Meadows during the spring of 2017. Of those, 3 died less than or equal to 16 days post-release and were removed from nest-initiation analysis because of the potential confounding effects of capture and translocation. Of the remaining 14 sage-grouse, 3 initiated a nest. The probability of nest initiation at Parker Meadows by translocated sage-grouse was 0.21 (95 percent CRI=0.10–0.32; table 3), derived from an intercept-only model. Apparent nest survival at Parker Meadows was 100 percent (3/3 successes).

For the AI experiment, we captured 23 males to serve as semen donors from 2 leks in Bodie Hills. Of those, five males produced viable semen samples that were used to artificially inseminate four females.

Brood Survival at Parker Meadows of Resident and Translocated Broods

At Parker Meadows, we monitored six broods in 2017: three broods from translocated pre-nesting females and three females translocated with post-hatch broods. Of the three females translocated with post-hatch broods, the first brood failed likely owing to not using the secondary enclosure. The second and third translocated broods survived to 40 and 50 days post hatch, respectively. Although these data are insufficient to accurately model differences in brood survival between the “type” of translocations (that is, broods from translocated pre-nesting hens versus translocated hens with post-hatch brood), these preliminary data provide evidence that brood translocation may require fewer females moved to produce proportionally more surviving broods (in this case 2 out of 3) compared to pre-nesting hens (in this case, 2 out of 17). In 2017, chick survival (*cs*) at Parker Meadows was 0.20 (95 percent CRI=0.08–0.40); we did not include the first translocated brood in this calculation because it is not an accurate reflection of chick survival in Parker Meadows.

Probability of Movement Away from Parker Meadows by Translocated Sage-Grouse

After mortalities and missing individuals were censored from the analysis, we quantified the probability of permanent movement away from Parker Meadows using movement data from 19 sage-grouse (*n*=14 female, *n*=5 male). The probability that any sage-grouse would disperse from the release site within 30 days of release was 0.49 (95 percent CRI=0.41–0.73; table 3).

Avian Predator Monitoring

Avian Predator Monitoring at Mount Grant and Desert Creek

We conducted 248 and 296 raptor and raven surveys throughout Mount Grant and Desert Creek, respectively, for a total of 544 surveys during March–August 2016–17 (fig. 15). At Mount Grant, raptors or ravens were detected during 67 of 248 surveys (27.0 percent; table 4), of which 26 included common raven detections (10.5 percent; table 4). In total, we recorded 59 raptors and 41 raven detections, and we did not detect any target species during 176 surveys (71.0 percent; table 4). Raptor species included golden eagle (*Aquila chrysaetos*; *n*=2), northern harrier (*Circus cyaneus; n*=5), rough-legged hawk (*Buteo lagopus*; *n*=3), red-tailed hawk (*Buteo jamaicensis*; *n*=5), and turkey vulture (*Cathartes aura*; *n*=33). American kestrel (*Falco sparverius*), osprey (*Pandion haliaetus*), prairie falcon (*Falco mexicanus*), and sharp-shinned hawk (*Accipiter striatus*) were identified only once. Of the 26 surveys that detected ravens, 22 of these detected only 1 raven per survey (84.6 percent; table 4), and 4 detected from 3 to 8 ravens, likely pairs with broods, fledged broods, or small juvenile flocks (15.4 percent; table 4).

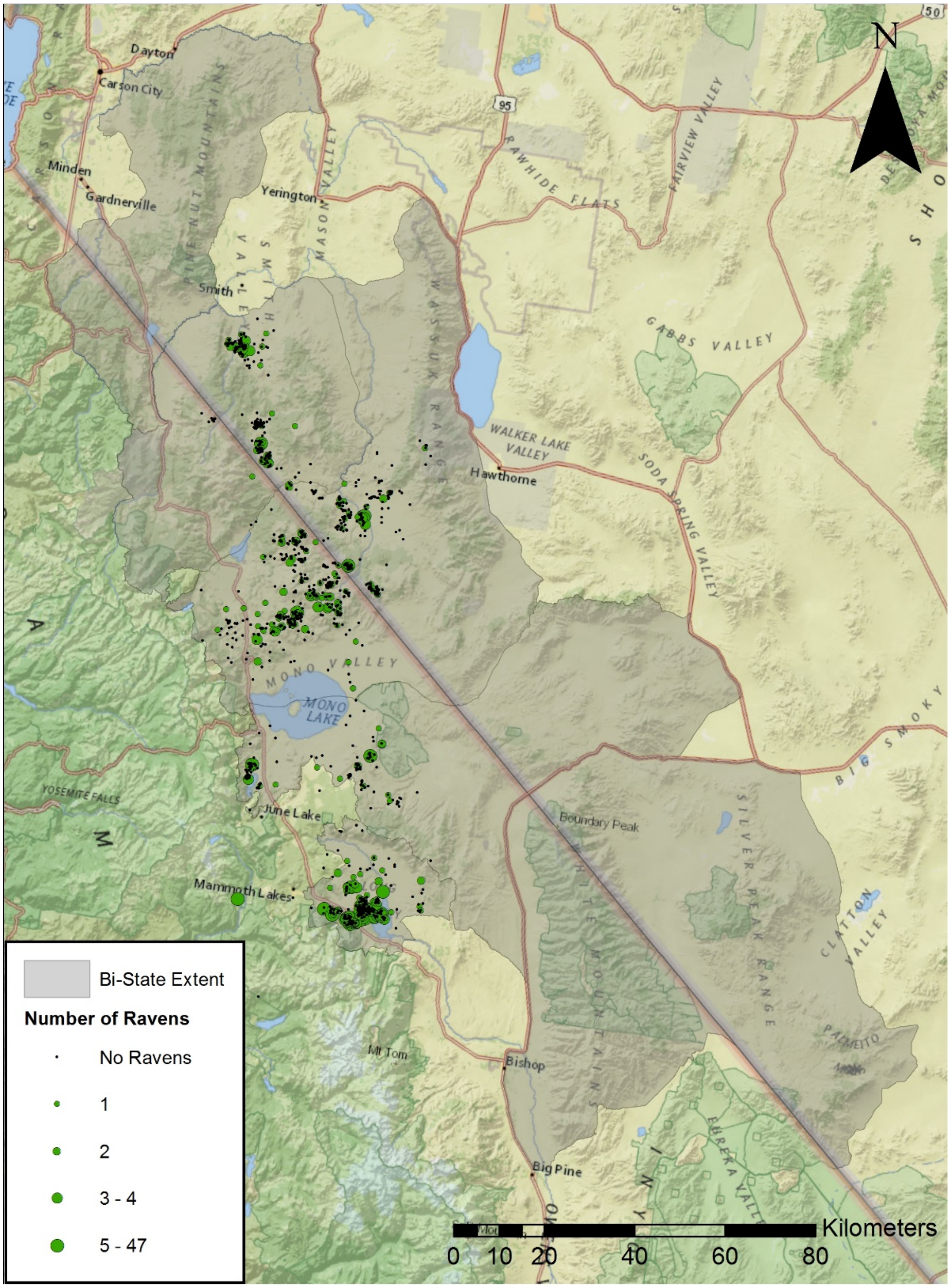

Figure 15. Survey locations and corresponding number of raven (*Corvus corax*) detections from March to August across the Bi-State Distinct Population Segment study area California and Nevada, 2015–17. Black dots indicate that no ravens were detected.

Table 4. Number of raptor, common raven (*Corvus corax)*, and livestock surveys (for example, RRHL) across the Bi-State Distinct Population Segment study area, California and Nevada, 2014– 17.

[Only the number of surveys in which ravens were observed were reported, but the number of surveys with raptor or livestock observations is available upon request]

Subpopulation	Year	Total surveys	Surveys with 1 raven	Surveys ≥2 ravens
Mount Grant	2016	104	4	0
	2017	144	18	0
	2016–17	248	22	0
Desert Creek	2016	109	12	2
	2017	187	10	5
	2016–17	296	22	7
Bodie Hills	2014	11	1	2
	2015	39	6	0
	2016	266	17	12
	2017	300	42	7
	2014–17	616	66	21
Long Valley	2016	273	48	19
	2017	265	61	20
	2016–17	538	109	39
Parker Meadows	2017	67	5	2

At Desert Creek, raptors or ravens were detected during 85 of 296 surveys (28.7 percent; table 4), of which 35 included raven detections (11.8 percent; fig. 15; table 4). In total, we recorded 95 raptors and 63 raven detections, and we did not detect any target species during 191 surveys (64.5 percent; table 4). Raptor species included golden eagle (*n*=4), northern harrier (*n*=4), red-tailed hawk (*n*=9), and turkey vulture (*n*=75). American kestrel and bald eagle were identified once each. Other non-raptor or corvid avian species included American crow (*Corvus brachyrhynchos*) and black-billed magpie (*Pica hudsonia*), both of which were identified once. Of the 35 surveys that detected ravens, 22 detected only 1 raven per survey (62.9 percent), 7 detected 2 ravens, likely a territorial pair (20.0 percent; table 4), and 6 detected 3 or more ravens, likely pairs with broods, fledged broods, or small juvenile flocks (17.1 percent; table 4).

Avian Predator Monitoring at Bodie Hills, Parker Meadows, and Long Valley

We conducted a total of 616 raptor RRHL surveys during March–August 2015–17 throughout the Bodie Hills (fig. 15). Avian predators were detected on 201 (32.6 percent; table 4) surveys, and 95 of these surveys (15.4 percent; table 4) detected ravens. No observations were detected in 415 surveys except livestock (67.4 percent). In total, we recorded 138 raptor and 83 raven detections. Frequently observed raptor species included red-tailed hawk (*n*=67), turkey vulture (*n*=80), American kestrel (*n*=29), northern harrier (*n*=9), golden eagle (*n*=6), and prairie falcon (*n*=5). Of the 95 surveys that detected ravens, 66 detected only 1 raven per survey (69.4 percent; table 4), and 29 detected greater than 1 raven (30.5 percent; table 4).

We conducted 538 raptor and raven surveys during March–August 2016–17, throughout Long Valley (fig. 15). Aerial predators were detected during 248 surveys (46.0 percent), and 148 of these included raven sightings (27.5 percent; table 4). No observations were detected in 290 surveys except livestock (54.0 percent). In total, we recorded 206 raptor and 339 raven detections. Frequently, observed raptor species included turkey vulture (*n*=309), American kestrel (*n*=17), red-tailed hawk (*n*=14), bald eagle (*n*=12*),* golden eagle (*n*=8*),* northern harrier (*n*=9), and osprey (*n*=4). Of the 148 surveys that detected ravens, 109 detected only 1 raven (73.6 percent; table 4), and 39 detected greater than 1 raven per survey (26.4 percent; table 4).

We conducted 67 raptor and raven surveys during March–August 2017, throughout Parker Meadows (fig. 15). Raptors or ravens were detected during 31 surveys (46.3 percent; table 4), and 7 included raven sightings (10.4 percent; table 4). Thirty-two surveys detected no target species (47.7 percent). In total, we recorded 32 raptor and 7 raven detections. Raptor species included turkey vulture (*n*=6), American kestrel (*n*=6), and red-tailed hawk (*n*=6), and unidentified accipiters (*n*=2). Of the seven surveys that detected ravens, five detected only one raven per survey (71.4 percent; table 4), and two detected four ravens (28.4 percent; table 4).

Estimates of Population Growth from an Integrated Population Model

We report summary information for observed lek counts, population vital-rate estimates, IPM-derived estimates of *N*, λ, and probabilities of increasing population growth versus declining population growth (that is, odds ratios) for the Bi-State DPS (appendix 1) and each subpopulation (appendix 2) from 2003 to 2017. Derived parameters were averaged across years and listed by site and averaged across fecundity (*F*) for adults (*a*) and yearlings (*y*) for each subpopulation. We also report annual rates of change and vital rates for some subpopulations that appear to differ from inferences at the regional scale across the Bi-State DPS.

Overall Bi-State Estimates (Regional Inferences)

From 2003 to 2017, the Bi-State DPS has averaged a finite rate of change (λ) of 0.98 (95 percent CRI=0.70–1.31; fig. 16; table 5), and the corresponding per capita rate (*r*) was –0.03 (95 percent CRI=–0.36–0.27, table 5). Since 2013, observed males on leks have decreased across the Bi-State DPS (fig. 17), but trends in lek counts appear to follow cyclical patterns. Model predictions of the Bi-State DPS support annual fluctuations in population growth, likely with overall (all subpopulations combined) declines. The 14-year *ln*(odds ratio) provides slightly more evidence of decrease than that of increase (fig. 18). We also found that across the Bi-State DPS, adult sage-grouse averaged higher survival (0.73, 95 percent CRI=0.55–0.87; table 5) and fecundity (0.39, 95 percent CRI=0.16–0.65; table 5) than yearlings (survival=0.61, 95 percent CRI=0.39–0.80; fecundity=0.27, 95 percent CRI=0.12–0.50; table 5).

Table 5. Summary of posterior distributions of derived population vital rate parameters for greater sage-grouse (*Centrocercus urophasianus*) in the Bi-State Distinct Population Segment study area California and Nevada, 2003–17.

[NA, not applicable]

Population vital rate	Age	Median estimate	Credible interval (CRI) Lower (0.025)	Credible interval (CRI) Upper (0.975)
Per capita growth (*r*)	NA	-0.03	-0.36	0.27
Annual growth rate (λ)	NA	0.98	0.70	1.31
Nest propensity (*np1*)	Adult	0.96	0.91	0.99
	Yearling	0.89	0.82	0.94
Nest propensity (*np2*)	Adult	0.27	0.07	0.67
	Yearling	0.19	0.04	0.59
Nest survival (*ns1*)	Adult	0.40	0.33	0.49
	Yearling	0.44	0.33	0.55
Clutch size (*c1*)	Adult	6.53	5.48	7.72
	Yearling	5.99	4.86	7.29
Nest survival (*ns2*)	Adult	0.40	0.23	0.63
	Yearling	0.41	0.11	0.76
Clutch size (*c2*)	Adult	5.74	2.81	16.65
	Yearling	4.32	1.82	20.50
Hatchability (*h*)	Adult	0.92	0.45	0.98
	Yearling	0.96	0.56	0.99
Chick survival (*cs*)	Adult	0.38	0.32	0.45
	Yearling	0.29	0.22	0.37
Fecundity (*f*)	Adult	0.39	0.16	0.65
	Yearling	0.27	0.12	0.50
Survival (*s*)	Adult	0.73	0.55	0.87
	Yearling	0.61	0.39	0.80
	Juvenile	0.79	0.72	0.84

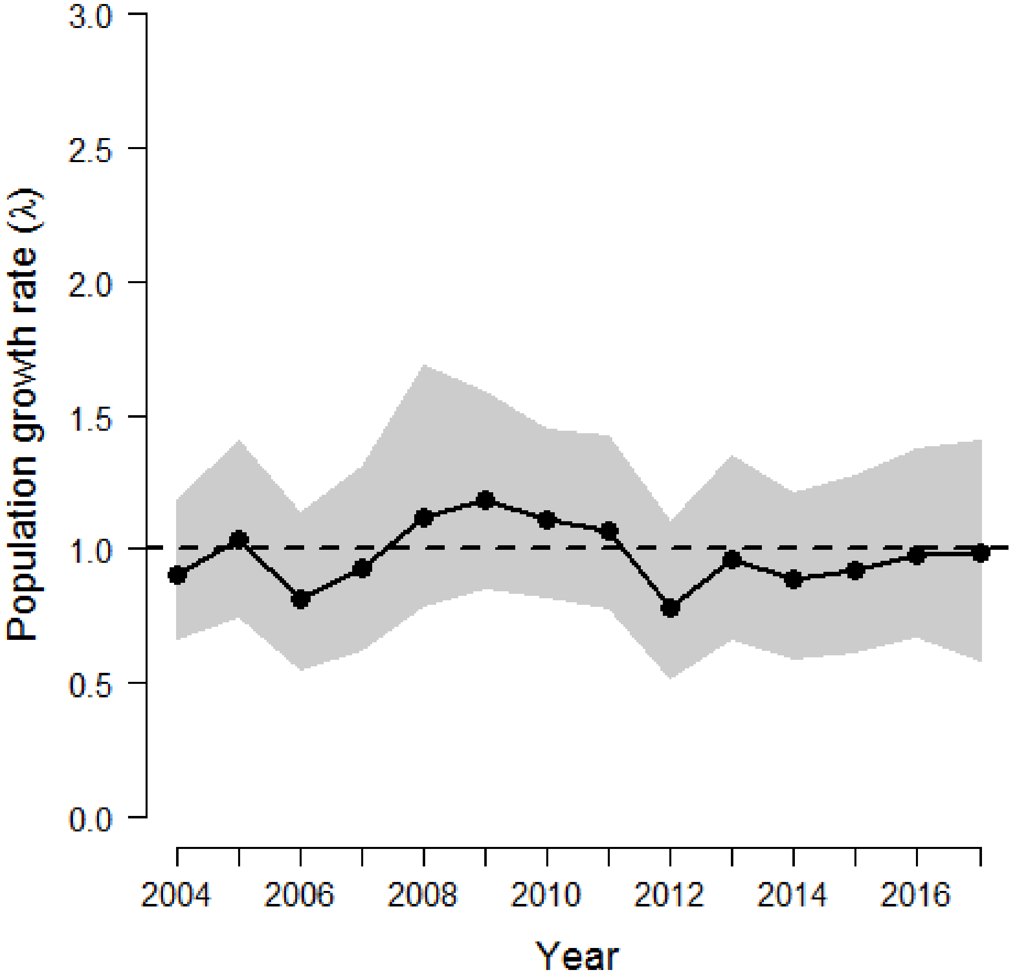

Figure 16. Graph showing annual population growth rate (λ) of greater sage-grouse (*Centrocercus urophasianus*) across all Bi-State Distinct Population Segment study area sites, California and Nevada, 2003–17 (λ=0.98, 95 percent CRI=0.70–0.1.31). Gray shading represents the 95 percent credible interval. The dashed line represents a stable population (λ=1.0).

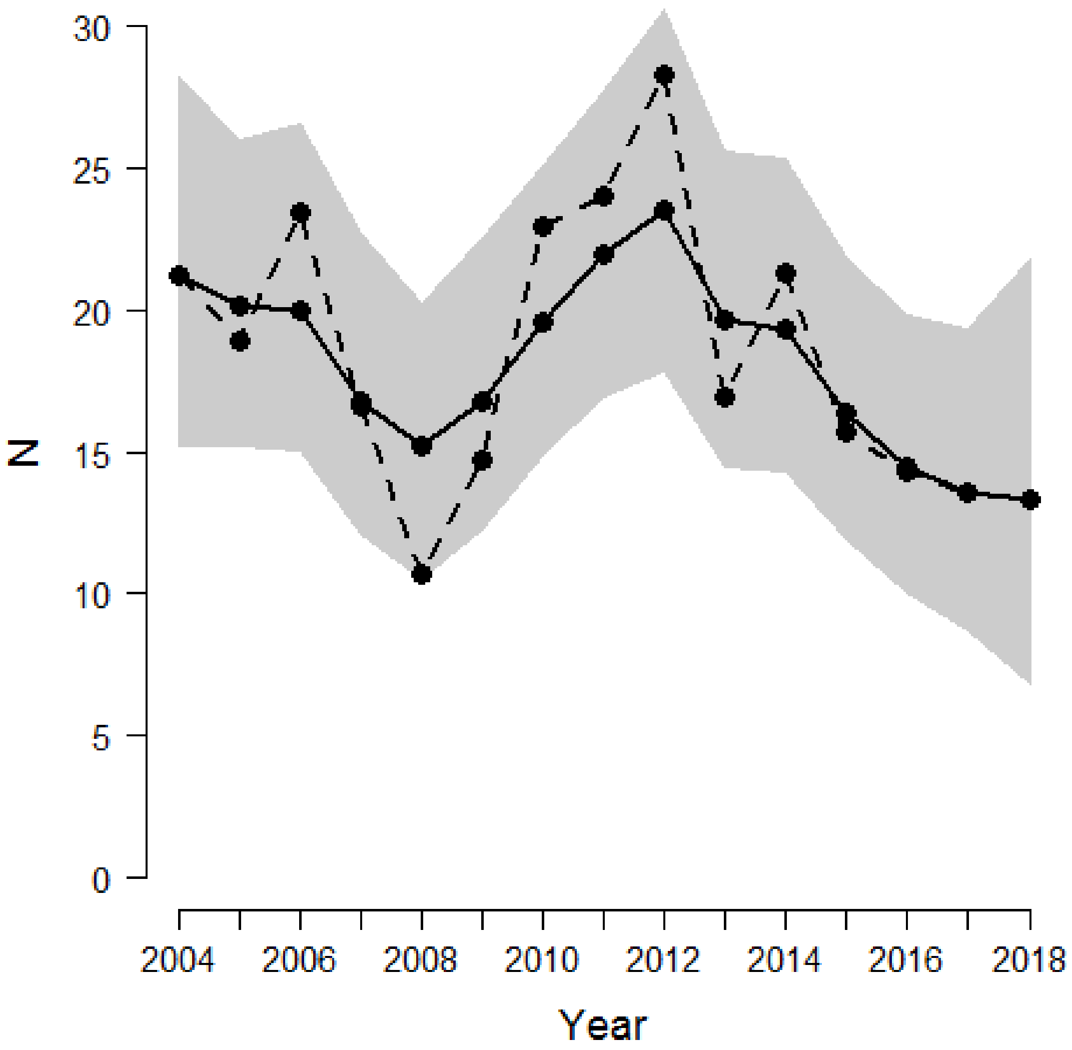

Figure 17. Graph showing annual counts (dashed line) of male greater sage-grouse (*Centrocercus urophasianus*) attending leks and estimates (solid line) across all Bi-State Distinct Population Segment study sites in California and Nevada, 2003–17. Gray shading represents the 95 percent credible interval. Estimated and observed values represent the average predicted and observed counts per lek within the Bi-State DPS on an annual basis.

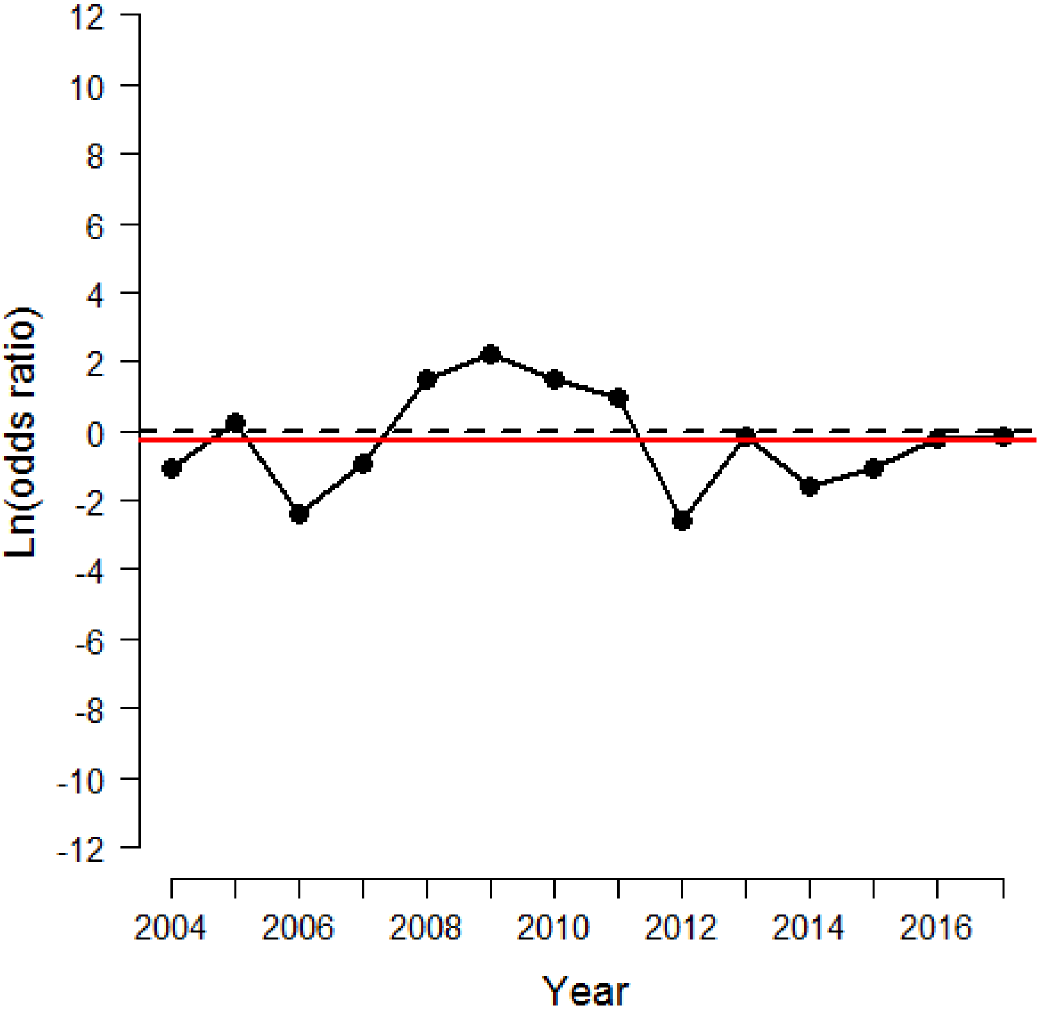

Figure 18. Graph showing *ln*(odds ratio) of population increase to decrease of greater sage-grouse (*Centrocercus urophasianus*) of all Bi-State Distinct Population Segment study area subpopulations across California and Nevada, 2003–17. The ratio consisted of the odds of the population increasing to that of decreasing. The dashed horizontal line represents a stable population. The solid red line is the overall average for the 14-year period.

Pine Nut Subpopulation

From 2003 to 2017, the average number of observed males on all leks was 8.8 (95 percent CRI=0.5–19.7; table 6), which was similar to the average estimate of *N* at 8.3 (95 percent CRI=5.3–12.1; fig. 19; appendix 1) during the same period. The pattern of *N* across years is similar to that of *N* averaged across the entire Bi-State DPS (fig. 19). From 2003 to 2017, sage-grouse in the Pine Nut Mountains had an average annual probability of survival of 0.66 (95 percent CRI=0.44–0.83; appendix 1), and adults experienced higher survival (0.72, 95 percent CRI=0.52–0.86; appendix 1) than yearlings (0.60, 95 percent CRI=0.35–0.80; appendix 1). The average fecundity rate for adults (F_a=0.39, 95 percent CRI=0.10–0.69; appendix 1) and yearlings ($F_{y=}$0.28, 95 percent CRI=0.09–0.55; appendix 1) from 2003–17 was similar to the rates for other subpopulations. The finite rate of change (λ) for the Pine Nut Mountains was 0.90 (95 percent CRI=0.53–1.38; fig. 20; appendix 1), and the corresponding per capita rate (*r*) was –0.10 (95 percent CRI=–0.63–0.32; appendix 1). Population declines at the Pine Nut Mountains were more pronounced than that of the Bi-State DPS overall (fig. 20), and the *ln*(odds ratio) provides evidence of likely decrease for this subpopulation over the 14-year study period (fig. 21).

Table 6. Summary of lek survey data averaged across years for greater sage-grouse (*Centrocercus urophasianus*) in the Bi-State Distinct Population Segment study area, California and Nevada, 2003–17.

[Number pairs in parentheses are lower and upper limits of the 95-percent credible interval]

Subpopulation	Average number of leks	Average number of males per lek	Average number of active leks	Percentage of active leks
Bodie Hills	17.3 (12.3, 20.0)	24.0 (12.1, 37.4)	13.1 (9.7, 16.7)	76.6% (56.8%, 96.6%)
Desert Creek	8.9 (5.0, 11.0)	15.8 (5.5, 29.8)	4.4 (3.0, 6.7)	53.8% (27.3%, 100.0%)
Fales	3.9 (3.3, 4.0)	11.2 (6.7, 14.9)	2.4 (2.0, 3.0)	62.5% (50.0%, 91.9%)
Long Valley	12.3 (10.0, 14.0)	28.0 (13.4, 40.1)	11.4 (10.0, 13.7)	92.9% (80.9%, 100.0%)
Mount Grant	9.6 (5.0, 11.0)	15.6 (3.3, 32.4)	4.4 (1.3, 7.0)	47.7% (14.0%, 89.2%)
Parker Meadows	3.3 (2.3, 5.0)	5.4 (1.9, 10.0)	1.9 (1.0, 3.0)	59.8% (33.3%, 100.0%)
Pine Nut Mountains	7.3 (2.0, 9.0)	8.8 (0.5, 19.7)	1.8 (0.3, 4.7)	31.1% (4.1%, 94.6%)

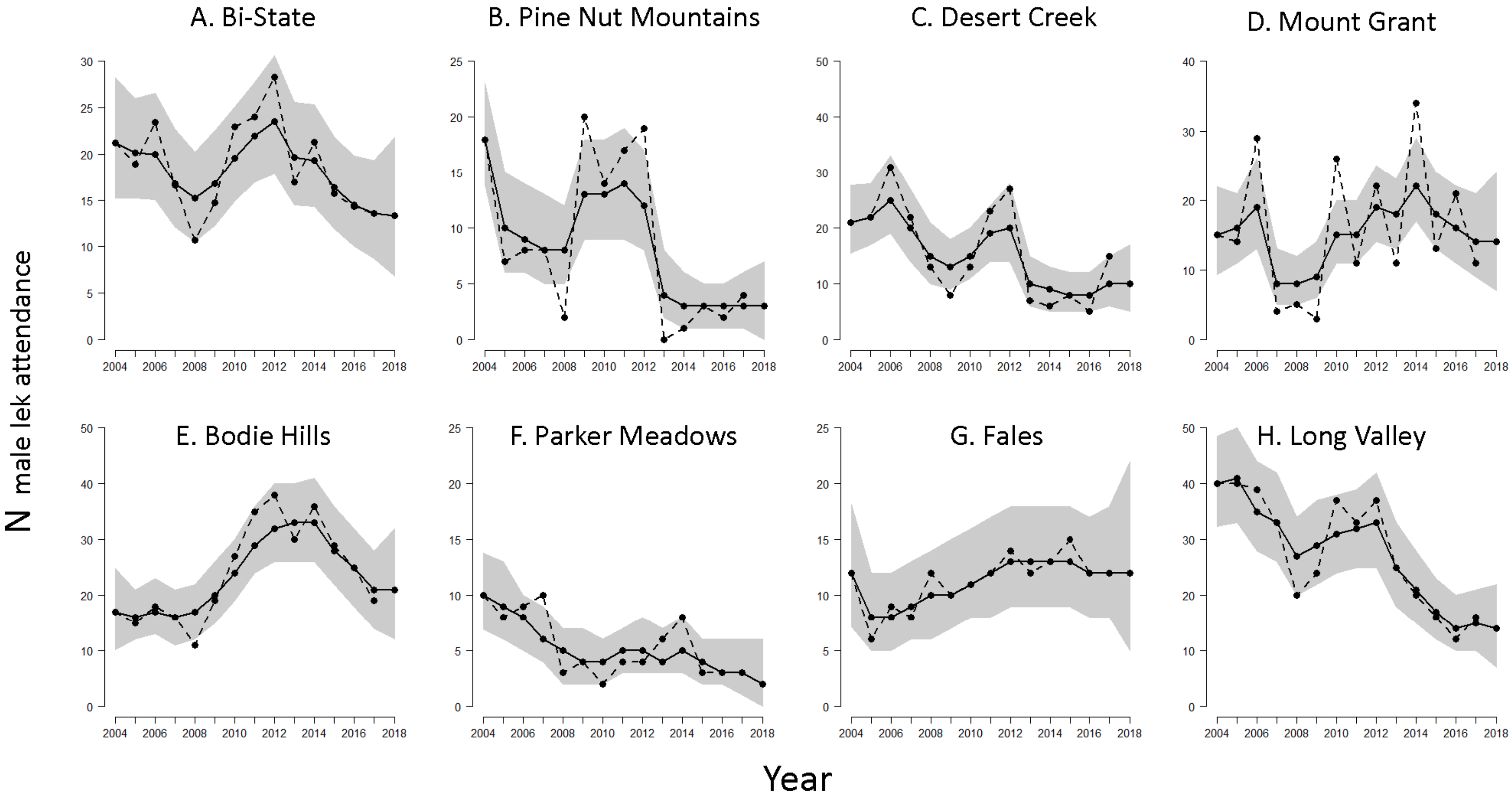

Figure 19. Graphs showing estimated number of male sage-grouse (*Centrocercus urophasianus*) per lek (solid line) and lek observations (dashed line) of the Bi-State Distinct Population Segment study area overall (A) and at subpopulations (B–H), California and Nevada, 2003–17. Gray shading represents the 95 percent credible intervals.

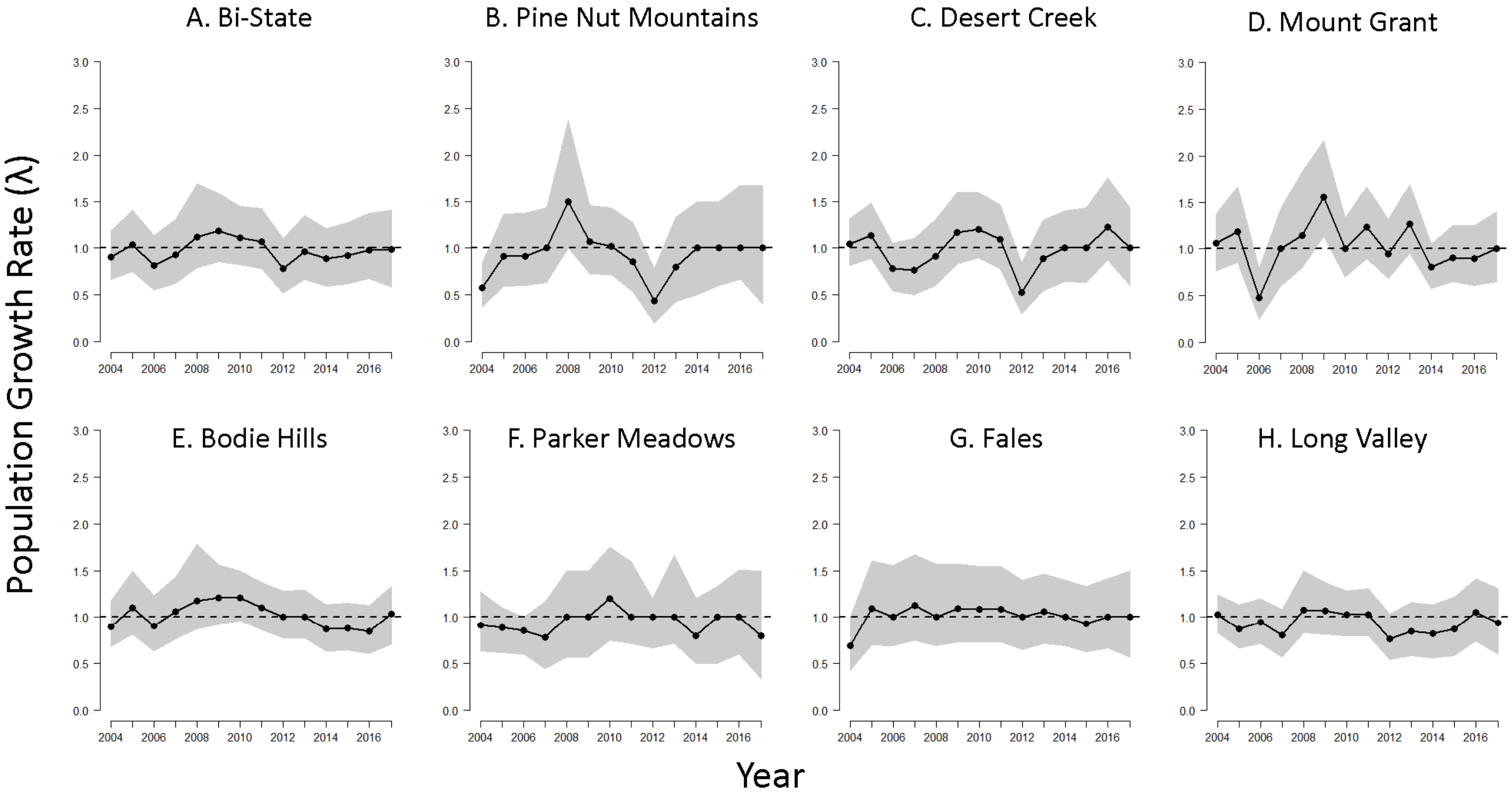

Figure 20. Graphs showing population growth rate (λ) of greater sage-grouse (*Centrocercus urophasianus*) for the Bi-State Distinct Population Segment overall (A) and for each monitored subpopulation (B-H), California and Nevada, 2003–17. Gray shading represents the 95 percent credible intervals. The dashed line represents a stable population (λ=1.0).

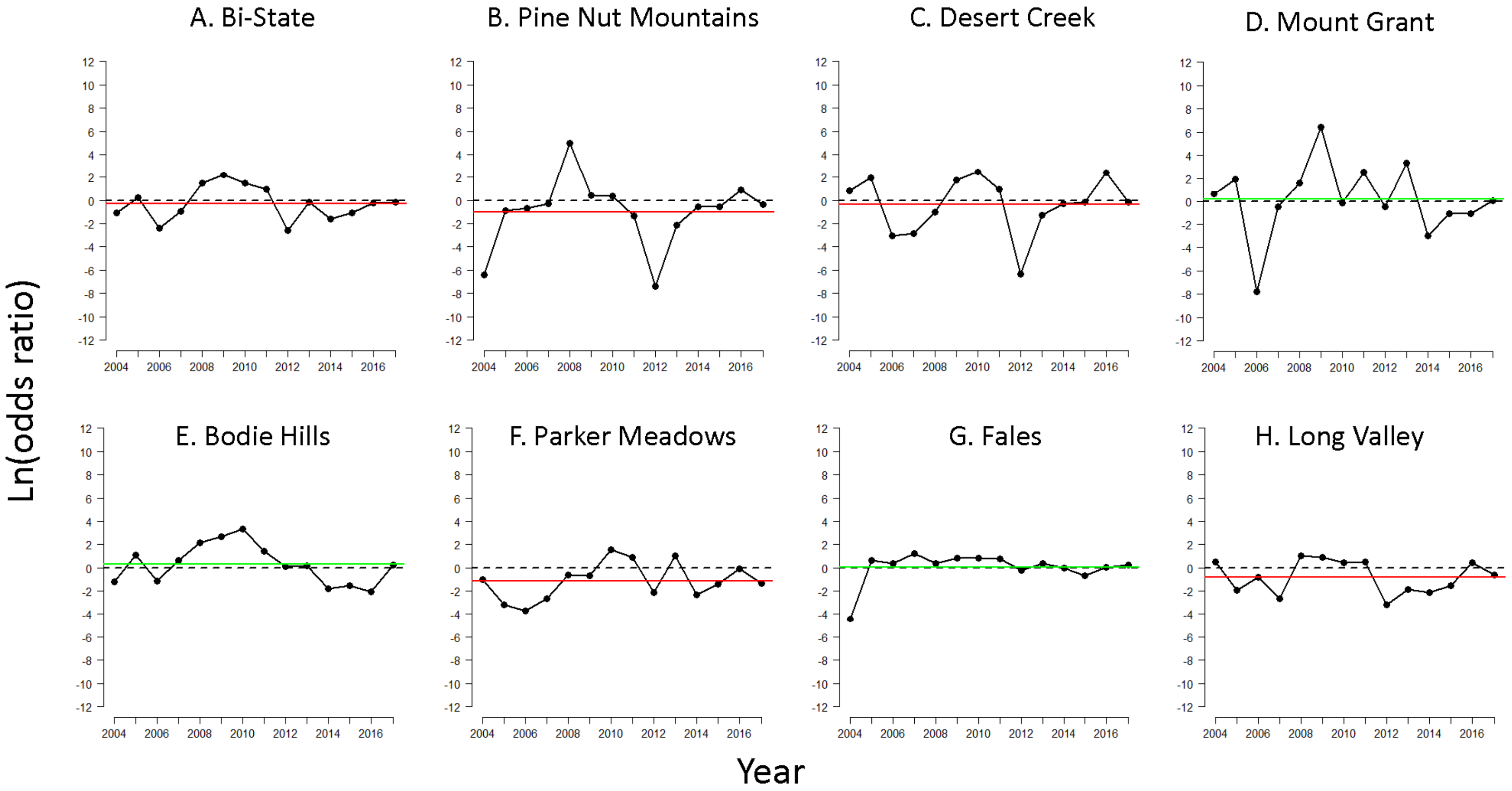

Figure 21. Graphs showing *ln*(odds ratio) of population increase to decrease of greater sage-grouse (*Centrocercus urophasianus*) for the Bi-State Distinct Population Segment overall (A) and for each monitored subpopulation (B–H) area, California and Nevada, 2003–17. The ratio consisted of the odds of the population increasing to that of decreasing. The dashed horizontal line represents a stable population. The solid line represents the overall average for the 14-year period (red=relatively higher odds of decrease, green=relatively higher odds of increase).

Desert Creek Subpopulation

From 2003 to 2017, the average number of observed males on leks at Desert Creek was 15.8 (95 percent CRI=5.5–29.8; table 6), which was similar to the average estimate of *N* during the same period (15.0, 95 percent CRI=10.6–20.3; fig. 19; appendix 1). The pattern of *N* across years is similar to that of *N* averaged across the entire Bi-State DPS (fig. 19). The fecundity rate for adults (F_a= 0.38, 95 percent CRI=0.10–0.62; appendix 1) and yearlings (F_y=0.26, 95 percent CRI=0.09–0.48; appendix 1) at Desert Creek was similar to the rates for other subpopulations. Survival for adults (S_a) was 0.74 (95 percent CRI=0.55–0.88; appendix 1), and survival for yearlings (S_y) was 0.63 (95 percent CRI=0.39–0.82; appendix 1). The finite rate of change (λ) for Desert Creek was 0.96 (95 percent CRI=0.65–1.34; fig. 20; appendix 1), and the corresponding per capita rate (*r*) was –0.04 (95 percent CRI= –0.43–0.29; appendix 1). Population growth at Desert Creek is similar to that of the Bi-State DPS overall (fig. 20), and the *ln*(odds ratio) provides slightly more evidence of decrease than that of increase for this subpopulation over the 14-year study period (fig. 21).

Mount Grant Subpopulation

From 2003 to 2017, the average number of observed males on leks at Mount Grant was 15.6 (95 percent CRI=3.3–32.4; table 6), which was similar to the average estimate of *N* during the same period (15.1, 95 percent CRI=10.7–20.7; fig. 19; appendix 1). The pattern of *N* across years is similar to that of *N* averaged across the entire Bi-State DPS (fig. 19). The fecundity rate for adults (F_a=0.40, 95 percent CRI=0.13–0.71; appendix 1) and yearlings (F_y=0.28, 95 percent CRI=0.11–0.54; appendix 1) at Mount Grant was similar to the rates for other subpopulations. Survival for adults (S_a) was 0.75 (95 percent CRI=0.57–0.89; appendix 1), and survival for yearlings (S_y) was 0.64 (95 percent CRI=0.41–0.83; appendix 1). The finite rate of change (λ) for Mount Grant was 1.00 (95 percent CRI=0.69–1.40; fig. 20; appendix 1), and the corresponding per capita rate (*r*) was 0.003 (95 percent CRI=-0.37–0.34; appendix 1). Population growth at Mount Grant showed greater interannual variation relative to the Bi-State DPS overall (fig. 20), but the *ln*(odds ratio) also indicates more evidence of stability or increase for this subpopulation over the 14-year study period (fig. 21).

Fales Subpopulation

From 2003 to 2017, the average number of observed males on leks at Fales was 11.2 (95 percent CRI=6.7–14.9; table 6), which was identical to the average estimate of *N* during the same period (95 percent CRI=7.53–16.07; fig. 19; appendix 1). At Fales, the pattern of *N* across years is different compared to *N* averaged across the entire Bi-State DPS (fig. 19) in that lek counts have increased after a sharp decrease in 2003–05. The fecundity rate for adults (F_a=0.48, 95 percent CRI=0.17–0.85; appendix 1) and yearlings (F_y=0.34, 95 percent CRI=0.15–0.66; appendix 1) at Fales was similar to the rates for other subpopulations. Survival for adults (S_a) was 0.72 (95 percent CRI=0.49–0.87; appendix 1), and survival for yearlings (S_y) was 0.60 (95 percent CRI=0.33–0.81; appendix 1). The finite rate of change (λ) for Fales was 1.00 (95 percent CRI=0.66–1.46; fig. 20; appendix 1), and the corresponding per capita rate (*r*) was 0.00 (95 percent CRI=–0.41–0.38; appendix 1). Population growth at Fales appeared less variable relative to the Bi-State DPS overall (fig. 20), and the *ln*(odds ratio) indicates more evidence for stability for this subpopulation over the 14-year study period (fig. 21).

Bodie Hills Subpopulation

From 2003 to 2017, the average number of observed males on leks at Bodie Hills was 24.0 (95 percent CRI=12.1–37.4; table 6), which was similar to the average estimate of *N* at 23.3 (95 percent CRI=17.7–29.7; fig. 19; appendix 1) during the same period. The pattern of *N* across years is similar to that of *N* averaged across the entire Bi-State DPS (fig. 19). The fecundity rate for adults (F_a= 0.39, 95 percent CRI=0.24–0.65; appendix 1) and yearlings ($F_{y=}$0.27, 95 percent CRI=0.24–0.65; appendix 1) at Bodie Hills was similar to the rates for other subpopulations. Survival for adults (S_a) was 0.72 (95 percent CRI=0.56–0.85; appendix 1), and survival for yearlings (S_y) was 0.60 (95 percent CRI=0.40–0.78; appendix 1). The finite rate of change (λ) for Bodie Hills was 1.01 (95 percent CRI=0.75–1.34; fig. 20; appendix 1), and corresponding per capita growth (*r*) was 0.01 (95 percent CRI= –0.28–0.29; appendix 1). Population growth at Bodie Hills tended to track trends across the Bi-State DPS overall (fig. 20), and the *ln*(odds ratio) indicates more evidence for stability or increase for this subpopulation over the 14-year study period (fig. 21).

Parker Meadows Subpopulation

From 2003 to 2017, the average number of observed males on leks at Parker Meadows was 5.4 (95 percent CRI=1.9–10.0; table 6), which was similar to the average estimate of *N* at 5.1 (95 percent CRI=3.1–7.8; fig. 19; appendix 1) during the same period. Estimates of *N* at Parker Meadows decreased continually across years, which differed from the more cyclic pattern exhibited across the entire Bi-State DPS (fig. 19). The fecundity rate for adults (F_a= 0.23, 95 percent CRI=0.06–0.45; appendix 1) and yearlings (F_y=0.19, 95 percent CRI=0.04–0.37; appendix 1) at Parker Meadows was greatly reduced compared with the rates for other subpopulations. Survival for adults (S_a) was 0.74 (95 percent CRI=0.52–0.89; appendix 1), and survival for yearlings (S_y) was 0.63 (95 percent CRI=0.36–0.83; appendix 1), which is similar to other subpopulations. The finite rate of change (λ) for Parker Meadows was 0.94 (95 percent CRI=0.58–1.36; fig. 20; appendix 1), and corresponding per capita growth (*r*) was –0.06 (95 percent CRI= –0.55–0.31; appendix 1). Population growth at Parker Meadows differs from that of the Bi-State DPS overall (fig. 20), and the *ln*(odds ratio) indicates more evidence of decrease for this subpopulation over the 14-year study period (fig. 21).

Long Valley Subpopulation

From 2003 to 2017, the average number of observed males on leks at Long Valley was 28.0 (95 percent CI=13.4–40.1; table 6), which was similar to the average estimate of *N* at 27.1 (95 percent CRI=20.9–34.3; fig. 19; appendix 1) over the same period. The pattern of *N* across years is similar to that of *N* averaged across the entire Bi-State DPS (fig. 19). The fecundity rate for adults (F_a= 0.38, 95 percent CRI=0.20–0.61; appendix 1) and yearlings (F_y=0.26, 95 percent CRI=0.13–0.46; appendix 1) at Long Valley was similar to the rates for other subpopulations. Survival for adults (S_a) was 0.72 (95 percent CRI=0.54–0.85; appendix 1), and survival for yearlings (S_y) was 0.60 (95 percent CRI=0.38–0.78; appendix 1). The finite rate of change (λ) for Long Valley was 0.93 (95 percent CRI=0.68–1.24; fig. 20; appendix 1), and the corresponding per capita growth (*r*) was –0.07 (95 percent CRI= –0.39–0.21; appendix 1). Population growth at Long Valley differs from that of the Bi-State DPS overall (fig. 20), and the *ln*(odds ratio) of the Long Valley subpopulation indicates more evidence of decrease for this subpopulation over the 14-year study period (fig. 21).

Interpretation of Demographic Estimates

A strength of the IPM is its ability to borrow information across sites and years to produce precise estimates when data are sparse (Schaub and Abadi, 2011; Coates and others, 2018). Lek count data were collected from all subpopulations across all years of the study, but vital rate data were less consistently collected (owing largely to the expense of collecting such data). Thus, we focus interpretation of vital rate estimates from populations with relatively consistent field data collection across the entire study. We also briefly discuss the Parker Meadows translocation.

Bi-State Region

From 2003 to 2017, the average rate of population change was less than 1.0 (λ=0.98; table 5), but estimates of uncertainty widely overlap 1.00 (95 percent CRI=0.70–1.31; table 5). Variability in population change was high among years and subpopulations. The Pine Nut Mountains, Parker Meadows (prior to translocation), and Long Valley had the most evidence of long-term decreasing trends, whereas Desert Creek had relatively less evidence of such a decrease (fig. 21). Population contractions at the Pine Nut Mountains and Long Valley are likely a result of the adverse effects caused by severe drought from 2012 to 2015. The long-term population decreases in Parker Meadows are partially explained by low hatchability, as reflected in low fecundity rates by females (appendix 1). In contrast, the large and increasing (1 percent annual) subpopulation at Bodie Hills contributes strongly to overall near term population stability of the Bi-State DPS. Based on the greater availability of springs and associated upland wet meadows, water does not appear to be as strong of a limiting resource for Bodie Hills populations during drought periods. Thus, this population appears to be at least moderately buffered from adverse effects of drought on population growth.

Mount Grant and Desert Creek

Small differences in demographic rates between Mount Grant and Desert Creek indicate that the average λ at Mount Grant was 1.00 (95 percent CRI=0.69–1.40; appendix 1), and λ at Desert Creek was 0.96 (95 percent CRI=0.65–1.34) from 2003 to 2017 (appendix 1). Sage-grouse at Desert Creek reside much closer to agriculture and anthropogenic structures compared with sage-grouse at Mount Grant, potentially exposing them to a higher number of predators, particularly nest predators (that is, ravens; table 4). Fecundity, female survival, and chick survival were slightly lower at Desert Creek compared with Mount Grant (appendix 1), and with larger samples sizes after more years of data collection, sensitivity and elasticity analyses will allow for a better determination of variation in specific vital rates driving population rates of change.

Bodie Hills and Long Valley

Bodie Hills and Long Valley represent the two largest subpopulations of sage-grouse in the Bi-State DPS, and also possibly represent two diverging populations. From 2003 to 2017, the Bodie Hills subpopulation increased annually by an average of 1 percent, while the Long Valley populations decreased by annual average of 7 percent (appendix 1). However, we note that credible intervals surrounding average λ for both subpopulations widely overlapped 1.0 (appendix 1), which indicated uncertainty over the absolute rate of change direction for these subpopulations. We hypothesize that population shrinkage at Long Valley may be partially attributed to increased corvid populations (table 4) supported by subsidies provided by nearby landfills. For example, the Benton Crossing landfill provides food subsidies for ravens throughout the year and is located about 5 km from the highest density of nest locations in the study site. Alternatively, the prolonged drought that began in 2012 is associated with population declines at Long Valley but not at Bodie Hills. Coates and others (2018) reasoned that sage-grouse at Bodie Hills associated with high elevation and more mesic habitats are better buffered from drought, whereas sage-grouse at Long Valley are associated with low elevation and xeric habitats where drought effects are exacerbated and they likely rely on irrigated pastures during the late summer brood rearing. Patterns from this study continue to support that reasoning.

Adult survival in 2017 was lower than long-term averages for both Bodie Hills and Long Valley (appendix 2). Preliminary nest survival estimates at these sites were also lower than long-term averages (Steven Mathews, U.S. Geological Survey, written commun., 2018). The winter of 2016–17 deposited a record volume of snowfall throughout the region, which persisted well into the nesting season. At Bodie Hills, snow depths greater than 0.3 m were observed on several leks on April 1, 2017, which could have potentially limited the available habitat for nesting throughout the region. Similarly due to the record snow year, sage-grouse could simply have been in poor body condition entering the spring 2017 season, which might have had lingering effects throughout the remainder of the year, but this is mainly conjecture.

In addition, 2017 estimates of brood survival should be noted with some caution because at Long Valley, all of the brooding females monitored, regardless of nest location, moved to the agricultural fields north-northwest of Crowley Lake for the late brood-rearing period. Field crews anecdotally reported a remarkably high abundance of arthropods, especially caterpillars (order Lepidoptera) and grasshoppers (family Acrididae), which likely supported high densities of sage-grouse in these areas. Brood mixing is known to occur in sage-grouse (Dahlgren and others, 2010) and has been observed in Long Valley. In one instance, a radio-marked female was observed with chicks ranging in age from 20 to 40 days post-hatch, and no other female was observed in the vicinity. The high density of broods and the occurrence of brood-mixing made determination of brood fate difficult in some cases and could confound estimates of brood survival. Females with broods also used habitats within 1 km of the irrigated pastures 63 percent of the time. This might indicate that broods forage on the edge of the pastures but then use the sagebrush areas outside of the pastures for cover and roosting. Anecdotal field observations also suggest that broods not located near the pastures seemed to be located near mesic sources such as natural springs or pasture irrigation canals, especially at the southern pasture near Lake Crowley. For these reasons, sage-grouse broods may be affected by management actions that affect the size or shape of irrigated pastures and similar mesic habitats.

Experimental Translocation to Parker Meadows

At Parker Meadows, we translocated 17 females and 8 males to rescue the critically low population as recommended by the Bi-State Action Plan (2012). However, translocated pre-nesting females had a high probability of permanent movement away from the release site within 30 days of translocation (table 4) despite the availability of suitable habitat as measured by resource selection functions (Ricca and others, 2018). Six of these females were known to return to their lek of capture, and several other females dispersed to neighboring populations (for example, Sagehen) or were never found post-release. One male sage-grouse dispersed to a high-elevation peak composed of conifer forest overlooking the Yosemite Valley and perished shortly thereafter (figs. 4 and 6).

If a female stayed and nested at Parker Meadows, both nest and brood survival were high. However, only 3 of 17 translocated females attempted to nest (and all were successful), whereas all other dispersed or died. These data indicate that translocation of pre-nesting females may be an inefficient tool to increase fecundity. In contrast, brood translocations might provide a more efficient tool. The three broods translocated represent the first such effort that we know of for sage-grouse. We feel that use of the secondary enclosure (which we determined was necessary after the first failed brood) greatly enhanced the success of the technique. Moreover, the second and third brood translocated hens both successfully reared greater than one chick to an age of 40 and 50 days post-hatch, respectively. If the goal of translocating females is to produce offspring at the release site, preliminary results provide some evidence that brood translocations are more efficient than translocating pre-nesting females. This ongoing research includes planned 2018 translocation efforts to help corroborate these preliminary findings based on limited small sample size.

Near the conclusion of the 2017 field season, crews anecdotally reported at least three broods from non-marked females at Parker Meadows, all of which survived to an age of 35 days or older. This indicates that egg fertility, a known problem at Parker Meadows, was likely high in 2017 and may warrant the continued translocation of males providing an influx of new genetic information from surrounding populations.

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Appendix 1. Summary of Derived Posterior Distributions for Greater Sage-Grouse (*Centrocercus urophasianus*) Population Vital Rates by Subpopulation in the Bi-State Distinct Population Segment Study Area, 2003–17

[Propensity of first nest and juvenile survival were derived from informative priors reported by Taylor and others, 2012.

Vital rates not listed (nest survival) did not very by field site during initial analyses and are included in the estimation of fecundity. Their values are reported in table 5.

Bold values indicate the overall average of the median estimate for a parameter and its respective credible intervals, and non-bolded values represent median estimates and credible intervals based on the age of grouse]

Subpopulation	Vital rate	Age	Median estimate	Credible interval (CRI)	
				Lower (0.025)	Upper (0.975)
Pine Nut Mountains	Abundance (*N*)	Overall	**8.27**	**5.33**	**12.13**
	Lambda (*λ*)	Overall	**0.90**	**0.53**	**1.38**
	r	Overall	**-0.10**	**-0.63**	**0.32**
	Chick survival (*cs*)	Overall	**0.36**	**0.28**	**0.48**
		Adult	0.41	0.33	0.53
		Yearling	0.32	0.23	0.44
	Fecundity (*f*)	Overall	**0.34**	**0.09**	**0.62**
		Adult	0.39	0.10	0.69
		Yearling	0.28	0.09	0.55
	Hatchability (*h*)	Overall	**0.94**	**0.31**	**0.99**
		Adult	0.91	0.25	0.99
		Yearling	0.96	0.37	1.00
	Nest propensity (*np2*)	Overall	**0.17**	**0.02**	**0.56**
		Adult	0.20	0.02	0.60
		Yearling	0.14	0.01	0.51
	Survival (*s*)	Overall	**0.66**	**0.44**	**0.83**
		Adult	0.72	0.52	0.86
		Yearling	0.60	0.35	0.80
Desert Creek	Abundance (*N*)	Overall	**15.00**	**10.67**	**20.33**
	Lambda (*λ*)	Overall	**0.96**	**0.65**	**1.34**
	r	Overall	**-0.04**	**-0.43**	**0.29**
	Chick survival (*cs*)	Overall	**0.33**	**0.27**	**0.40**
		Adult	0.38	0.32	0.44
		Yearling	0.29	0.22	0.37
	Fecundity (*f*)	Overall	**0.32**	**0.09**	**0.55**
		Adult	0.38	0.10	0.62
		Yearling	0.26	0.09	0.48
	Hatchability (*h*)	Overall	**0.95**	**0.31**	**1.00**
		Adult	0.93	0.25	0.99
		Yearling	0.97	0.37	1.00
	Nest propensity (*np2*)	Overall	**0.22**	**0.03**	**0.67**
		Adult	0.26	0.04	0.71
		Yearling	0.18	0.02	0.63
	Survival (*s*)	Overall	**0.69**	**0.47**	**0.85**

Subpopulation	Vital rate	Age	Median estimate	Credible interval (CRI)	
				Lower (0.025)	Upper (0.975)
		Adult	0.74	0.55	0.88
		Yearling	0.63	0.39	0.82
Mount Grant	Abundance (*N*)	Overall	**15.07**	**10.67**	**20.67**
	Lambda (λ)	Overall	**1.00**	**0.69**	**1.40**
	r	Overall	**0.00**	**-0.37**	**0.34**
	Chick survival (*cs*)	Overall	**0.34**	**0.26**	**0.42**
		Adult	0.38	0.31	0.47
		Yearling	0.29	0.22	0.38
	Fecundity (*f*)	Overall	**0.34**	**0.12**	**0.63**
		Adult	0.40	0.13	0.71
		Yearling	0.28	0.11	0.54
	Hatchability (*h*)	Overall	**0.96**	**0.39**	**1.00**
		Adult	0.94	0.32	0.99
		Yearling	0.98	0.46	1.00
	Nest propensity (*np2*)	Overall	**0.26**	**0.04**	**0.75**
		Adult	0.31	0.06	0.79
		Yearling	0.22	0.03	0.72
	Survival (*s*)	Overall	**0.70**	**0.49**	**0.86**
		Adult	0.75	0.57	0.89
		Yearling	0.64	0.41	0.83
Fales	Abundance (*N*)	Overall	**11.20**	**7.53**	**16.07**
	Lambda (λ)	Overall	**1.00**	**0.66**	**1.46**
	r	Overall	**0.00**	**-0.41**	**0.38**
	Chick survival (*cs*)	Overall	**0.40**	**0.30**	**0.58**
		Adult	0.45	0.35	0.63
		Yearling	0.35	0.25	0.53
	Fecundity (*f*)	Overall	**0.41**	**0.16**	**0.75**
		Adult	0.48	0.17	0.85
		Yearling	0.34	0.15	0.66
	Hatchability (*h*)	Overall	**0.98**	**0.47**	**1.00**
		Adult	0.98	0.38	1.00
		Yearling	0.99	0.55	1.00
	Nest propensity (*np2*)	Overall	**0.23**	**0.04**	**0.68**
		Adult	0.27	0.05	0.72
		Yearling	0.19	0.03	0.64
	Survival (*s*)	Overall	**0.66**	**0.41**	**0.84**
		Adult	0.72	0.49	0.87
		Yearling	0.60	0.33	0.81
Bodie Hills	Abundance (*N*)	Overall	**23.27**	**17.73**	**29.73**
	Lambda (λ)	Overall	**1.01**	**0.75**	**1.34**
	r	Overall	**0.01**	**-0.28**	**0.29**
	Chick survival (*cs*)	Overall	**0.32**	**0.27**	**0.37**
		Adult	0.36	0.32	0.40
		Yearling	0.27	0.22	0.34
	Fecundity (*f*)	Overall	**0.33**	**0.20**	**0.57**
		Adult	0.39	0.24	0.65

Subpopulation	Vital rate	Age	Median estimate	Credible interval (CRI)	
				Lower (0.025)	Upper (0.975)
		Yearling	0.27	0.15	0.49
	Hatchability (*h*)	Overall	**0.97**	**0.72**	**0.99**
		Adult	0.96	0.67	0.99
		Yearling	0.99	0.78	1.00
	Nest propensity (*np2*)	Overall	**0.24**	**0.08**	**0.58**
		Adult	0.28	0.10	0.63
		Yearling	0.20	0.05	0.54
	Survival (*s*)	Overall	**0.66**	**0.48**	**0.81**
		Adult	0.72	0.56	0.85
		Yearling	0.60	0.40	0.78
Parker Meadows	Abundance (*N*)	Overall	**5.13**	**3.13**	**7.80**
	Lambda (λ)	Overall	**0.94**	**0.58**	**1.36**
	r	Overall	**-0.06**	**-0.55**	**0.31**
	Chick survival (*cs*)	Overall	**0.34**	**0.26**	**0.43**
		Adult	0.38	0.31	0.47
		Yearling	0.29	0.22	0.38
	Fecundity (*f*)	Overall	**0.21**	**0.05**	**0.41**
		Adult	0.23	0.06	0.45
		Yearling	0.19	0.04	0.37
	Hatchability (*h*)	Overall	**0.63**	**0.18**	**0.83**
		Adult	0.57	0.16	0.80
		Yearling	0.70	0.20	0.87
	Nest propensity (*np2*)	Overall	**0.18**	**0.04**	**0.56**
		Adult	0.22	0.05	0.60
		Yearling	0.15	0.03	0.51
	Survival (*s*)	Overall	**0.69**	**0.44**	**0.86**
		Adult	0.74	0.52	0.89
		Yearling	0.63	0.36	0.83
Long Valley	Abundance (*N*)	Overall	**27.13**	**20.93**	**34.27**
	Lambda (λ)	Overall	**0.93**	**0.68**	**1.24**
	r	Overall	**-0.07**	**-0.39**	**0.21**
	Chick survival (*cs*)	Overall	**0.31**	**0.26**	**0.37**
		Adult	0.36	0.31	0.41
		Yearling	0.27	0.21	0.34
	Fecundity (*f*)	Overall	**0.32**	**0.17**	**0.54**
		Adult	0.38	0.20	0.61
		Yearling	0.26	0.13	0.46
	Hatchability (*h*)	Overall	**0.96**	**0.63**	**0.99**
		Adult	0.95	0.58	0.98
		Yearling	0.98	0.67	1.00
	Nest propensity (*np2*)	Overall	**0.26**	**0.09**	**0.62**
		Adult	0.30	0.11	0.66
		Yearling	0.22	0.06	0.58
	Survival (*s*)	Overall	**0.66**	**0.46**	**0.82**
		Adult	0.72	0.54	0.85
		Yearling	0.60	0.38	0.78

Appendix 2. Summary of Derived Posterior Distribution for Greater Sage-Grouse (*Centrocercus urophasianus*) Population Vital Rates by Year, 2003–17

[**Population vital rate:** Propensity of first nest and juvenile survival were derived from informative priors reported by Taylor and others, 2012. Vital rates not listed (Nest Survival) were not supported by initial analyses but are included in the estimation of fecundity and are reported in table 5. **Median estimate:** Estimates of the abundance parameter represent the averaged median estimate per lek in a given year]

Subpopulation	Population vital rate	Age	Year	Median estimate	Credible interval (CRI)	
					Lower (0.025)	Upper (0.975)
Bi-State	Lambda (λ)	NA	2003	0.90	0.79	1.02
			2004	0.97	0.84	1.16
			2005	0.89	0.75	1.04
			2006	0.88	0.71	1.05
			2007	1.09	0.93	1.49
			2008	1.11	0.94	1.29
			2009	1.12	0.97	1.27
			2010	1.05	0.91	1.21
			2011	0.78	0.64	0.93
			2012	0.94	0.79	1.12
			2013	0.88	0.72	1.05
			2014	0.89	0.73	1.07
			2015	0.98	0.82	1.17
			2016	0.99	0.79	1.19
	r	NA	2003	-0.11	-0.24	0.02
			2004	-0.03	-0.17	0.15
			2005	-0.12	-0.29	0.04
			2006	-0.13	-0.34	0.05
			2007	0.09	-0.08	0.40
			2008	0.11	-0.06	0.25
			2009	0.11	-0.03	0.24
			2010	0.04	-0.10	0.19
			2011	-0.25	-0.44	-0.07
			2012	-0.06	-0.24	0.12
			2013	-0.13	-0.32	0.05
			2014	-0.11	-0.31	0.07
			2015	-0.02	-0.20	0.16
			2016	-0.01	-0.23	0.17
Pine Nut Mountains	Abundance (*N*)	NA	2003	18.00	17.00	19.00
			2004	10.00	6.00	15.00
			2005	9.00	6.00	14.00
			2006	8.00	5.00	13.00

Subpopulation	Population vital rate	Age	Year	Median estimate	Credible interval (CRI)	
					Lower (0.025)	Upper (0.975)
			2007	8.00	5.00	12.00
			2008	13.00	9.00	18.00
			2009	13.00	9.00	18.00
			2010	14.00	9.00	19.00
			2011	12.00	8.00	17.00
			2012	4.00	2.00	8.00
			2013	3.00	1.00	6.00
			2014	3.00	1.00	5.00
			2015	3.00	1.00	5.00
			2016	3.00	1.00	6.00
			2017	3.00	0.00	7.00
	Lambda (λ)	NA	2003	0.58	0.37	0.84
			2004	0.91	0.59	1.36
			2005	0.92	0.60	1.38
			2006	1.00	0.64	1.43
			2007	1.50	1.00	2.38
			2008	1.07	0.72	1.45
			2009	1.02	0.71	1.43
			2010	0.86	0.53	1.27
			2011	0.44	0.20	0.78
			2012	0.80	0.43	1.33
			2013	1.00	0.50	1.50
			2014	1.00	0.60	1.50
			2015	1.00	0.67	1.67
			2016	1.00	0.40	1.67
	r	NA	2003	-0.55	-1.00	-0.17
			2004	-0.10	-0.53	0.31
			2005	-0.09	-0.51	0.32
			2006	0.00	-0.45	0.36
			2007	0.41	0.00	0.86
			2008	0.06	-0.33	0.37
			2009	0.02	-0.34	0.36
			2010	-0.15	-0.63	0.24
			2011	-0.83	-1.61	-0.25
			2012	-0.22	-0.85	0.29
			2013	0.00	-0.69	0.41
			2014	0.00	-0.51	0.41
			2015	0.00	-0.41	0.51
			2016	0.00	-0.92	0.51
	Chick survival (*cs*)	Yearling	NA	0.32	0.23	0.44
		Adult	NA	0.41	0.33	0.53
	Fecundity (*f*)	Yearling	2003	0.29	0.02	0.51

Subpopulation	Population vital rate	Age	Year	Median estimate	Credible interval (CRI)	
					Lower (0.025)	Upper (0.975)
		Adult	2003	0.40	0.01	0.66
		Yearling	2004	0.26	0.02	0.59
		Adult	2004	0.37	0.01	0.73
		Yearling	2005	0.25	0.03	0.44
		Adult	2005	0.36	0.02	0.57
		Yearling	2006	0.27	0.02	0.48
		Adult	2006	0.37	0.01	0.63
		Yearling	2007	0.32	0.19	1.41
		Adult	2007	0.46	0.26	1.78
		Yearling	2008	0.34	0.12	0.57
		Adult	2008	0.49	0.08	0.73
		Yearling	2009	0.31	0.09	0.50
		Adult	2009	0.43	0.06	0.64
		Yearling	2010	0.33	0.03	0.57
		Adult	2010	0.47	0.02	0.74
		Yearling	2011	0.31	0.19	0.51
		Adult	2011	0.43	0.24	0.64
		Yearling	2012	0.28	0.17	0.48
		Adult	2012	0.38	0.25	0.58
		Yearling	2013	0.26	0.16	0.42
		Adult	2013	0.37	0.26	0.54
		Yearling	2014	0.23	0.12	0.39
		Adult	2014	0.25	0.13	0.41
		Yearling	2015	0.26	0.06	0.44
		Adult	2015	0.37	0.03	0.58
		Yearling	2016	0.26	0.04	0.43
		Adult	2016	0.36	0.02	0.54
		Yearling	2017	0.27	0.10	0.44
		Adult	2017	0.38	0.07	0.56
	Hatchability (*h*)	Yearling	2003	0.96	0.05	1.00
		Adult	2003	0.89	0.02	1.00
		Yearling	2004	0.95	0.06	1.00
		Adult	2004	0.86	0.02	1.00
		Yearling	2005	0.97	0.11	1.00
		Adult	2005	0.93	0.04	1.00
		Yearling	2006	0.97	0.07	1.00
		Adult	2006	0.93	0.03	1.00
		Yearling	2007	0.99	0.80	1.00
		Adult	2007	0.99	0.60	1.00
		Yearling	2008	0.99	0.32	1.00
		Adult	2008	0.97	0.14	1.00
		Yearling	2009	0.98	0.26	1.00

Subpopulation	Population vital rate	Age	Year	Median estimate	Credible interval (CRI)	
					Lower (0.025)	Upper (0.975)
		Adult	2009	0.95	0.11	1.00
		Yearling	2010	0.96	0.08	1.00
		Adult	2010	0.90	0.03	1.00
		Yearling	2011	0.95	0.73	1.00
		Adult	2011	0.86	0.50	0.99
		Yearling	2012	0.96	0.87	0.99
		Adult	2012	0.90	0.75	0.97
		Yearling	2013	1.00	0.96	1.00
		Adult	2013	0.99	0.91	1.00
		Yearling	2014	0.81	0.52	0.95
		Adult	2014	0.60	0.34	0.82
		Yearling	2015	0.99	0.20	1.00
		Adult	2015	0.96	0.08	1.00
		Yearling	2016	0.98	0.13	1.00
		Adult	2016	0.95	0.05	1.00
		Yearling	2017	1.00	0.38	1.00
		Adult	2017	0.99	0.18	1.00
	Nest propensity (*np2*)	Yearling	2003	0.13	0.01	0.51
		Adult	2003	0.20	0.02	0.62
		Yearling	2004	0.13	0.01	0.51
		Adult	2004	0.21	0.02	0.60
		Yearling	2005	0.17	0.01	0.59
		Adult	2005	0.25	0.02	0.70
		Yearling	2006	0.09	0.00	0.74
		Adult	2006	0.15	0.00	0.82
		Yearling	2007	0.06	0.00	0.53
		Adult	2007	0.10	0.00	0.65
		Yearling	2008	0.21	0.02	0.64
		Adult	2008	0.31	0.03	0.73
		Yearling	2009	0.08	0.01	0.42
		Adult	2009	0.14	0.01	0.55
		Yearling	2010	0.42	0.05	0.84
		Adult	2010	0.55	0.08	0.88
		Yearling	2011	0.37	0.04	0.79
		Adult	2011	0.50	0.07	0.85
		Yearling	2012	0.04	0.00	0.21
		Adult	2012	0.06	0.00	0.30
		Yearling	2013	0.04	0.00	0.30
		Adult	2013	0.07	0.00	0.38
		Yearling	2014	0.10	0.01	0.49
		Adult	2014	0.17	0.01	0.58
		Yearling	2015	0.13	0.01	0.62

Subpopulation	Population vital rate	Age	Year	Median estimate	Credible interval (CRI)	
					Lower (0.025)	Upper (0.975)
		Adult	2015	0.20	0.01	0.74
		Yearling	2016	0.04	0.00	0.24
		Adult	2016	0.06	0.00	0.32
		Yearling	2017	0.04	0.00	0.25
		Adult	2017	0.07	0.00	0.33
	Survival (*s*)	Yearling	2003	0.44	0.17	0.68
		Adult	2003	0.59	0.33	0.78
		Yearling	2004	0.62	0.34	0.83
		Adult	2004	0.74	0.51	0.89
		Yearling	2005	0.59	0.31	0.82
		Adult	2005	0.72	0.49	0.88
		Yearling	2006	0.63	0.36	0.84
		Adult	2006	0.74	0.52	0.89
		Yearling	2007	0.69	0.46	0.87
		Adult	2007	0.79	0.62	0.92
		Yearling	2008	0.65	0.40	0.84
		Adult	2008	0.76	0.56	0.90
		Yearling	2009	0.67	0.42	0.86
		Adult	2009	0.77	0.58	0.90
		Yearling	2010	0.59	0.28	0.81
		Adult	2010	0.71	0.46	0.87
		Yearling	2011	0.56	0.34	0.75
		Adult	2011	0.69	0.50	0.84
		Yearling	2012	0.58	0.41	0.72
		Adult	2012	0.71	0.58	0.81
		Yearling	2013	0.50	0.32	0.66
		Adult	2013	0.64	0.49	0.76
		Yearling	2014	0.63	0.44	0.79
		Adult	2014	0.75	0.60	0.86
		Yearling	2015	0.64	0.43	0.82
		Adult	2015	0.75	0.59	0.88
		Yearling	2016	0.66	0.36	0.85
		Adult	2016	0.76	0.53	0.90
		Yearling	2017	0.59	0.25	0.82
		Adult	2017	0.71	0.43	0.88
Desert Creek	Abundance (*N*)	NA	2003	21.00	20.00	22.00
			2004	22.00	17.00	28.00
			2005	25.00	19.00	33.00
			2006	20.00	14.00	27.00
			2007	15.00	10.00	21.00
			2008	13.00	9.00	18.00

Subpopulation	Population vital rate	Age	Year	Median estimate	Credible interval (CRI)	
					Lower (0.025)	Upper (0.975)
			2009	15.00	11.00	20.00
			2010	19.00	14.00	24.00
			2011	20.00	14.00	28.00
			2012	10.00	6.00	15.00
			2013	9.00	5.00	13.00
			2014	8.00	5.00	12.00
			2015	8.00	5.00	12.00
			2016	10.00	6.00	15.00
			2017	10.00	5.00	17.00
	Lambda (λ)	NA	2003	1.05	0.82	1.32
			2004	1.14	0.88	1.48
			2005	0.78	0.55	1.05
			2006	0.76	0.50	1.11
			2007	0.92	0.60	1.31
			2008	1.17	0.83	1.60
			2009	1.20	0.89	1.60
			2010	1.10	0.78	1.47
			2011	0.53	0.29	0.84
			2012	0.89	0.55	1.30
			2013	1.00	0.64	1.40
			2014	1.00	0.64	1.43
			2015	1.22	0.88	1.75
			2016	1.00	0.60	1.43
	r	NA	2003	0.04	-0.20	0.28
			2004	0.13	-0.12	0.39
			2005	-0.25	-0.61	0.05
			2006	-0.27	-0.69	0.10
			2007	-0.09	-0.51	0.27
			2008	0.15	-0.18	0.47
			2009	0.18	-0.11	0.47
			2010	0.09	-0.25	0.38
			2011	-0.64	-1.22	-0.17
			2012	-0.12	-0.61	0.26
			2013	0.00	-0.44	0.34
			2014	0.00	-0.45	0.36
			2015	0.20	-0.13	0.56
			2016	0.00	-0.51	0.36
	Chick survival (cs)	Yearling		0.29	0.22	0.37
		Adult		0.38	0.32	0.44
	Fecundity (f)	Yearling	2003	0.30	0.19	0.48
		Adult	2003	0.44	0.31	0.63
		Yearling	2004	0.27	0.17	0.68

Subpopulation	Population vital rate	Age	Year	Median estimate	Credible interval (CRI)	
					Lower (0.025)	Upper (0.975)
		Adult	2004	0.37	0.27	0.87
		Yearling	2005	0.25	0.15	0.40
		Adult	2005	0.35	0.23	0.51
		Yearling	2006	0.23	0.01	0.42
		Adult	2006	0.33	0.01	0.57
		Yearling	2007	0.28	0.04	0.84
		Adult	2007	0.40	0.02	1.05
		Yearling	2008	0.32	0.15	0.51
		Adult	2008	0.48	0.14	0.67
		Yearling	2009	0.29	0.16	0.45
		Adult	2009	0.42	0.16	0.59
		Yearling	2010	0.32	0.10	0.54
		Adult	2010	0.48	0.06	0.68
		Yearling	2011	0.25	0.01	0.45
		Adult	2011	0.34	0.00	0.59
		Yearling	2012	0.24	0.02	0.43
		Adult	2012	0.34	0.01	0.56
		Yearling	2013	0.22	0.04	0.37
		Adult	2013	0.32	0.03	0.49
		Yearling	2014	0.24	0.02	0.40
		Adult	2014	0.34	0.01	0.53
		Yearling	2015	0.25	0.12	0.40
		Adult	2015	0.37	0.11	0.55
		Yearling	2016	0.24	0.04	0.38
		Adult	2016	0.34	0.02	0.49
		Yearling	2017	0.25	0.09	0.39
		Adult	2017	0.36	0.07	0.51
	Hatchability (*h*)	Yearling	2003	0.98	0.90	1.00
		Adult	2003	0.95	0.79	1.00
		Yearling	2004	0.95	0.86	0.98
		Adult	2004	0.86	0.75	0.94
		Yearling	2005	0.95	0.81	0.99
		Adult	2005	0.88	0.65	0.98
		Yearling	2006	0.96	0.04	1.00
		Adult	2006	0.88	0.01	1.00
		Yearling	2007	0.99	0.12	1.00
		Adult	2007	0.97	0.05	1.00
		Yearling	2008	0.99	0.48	1.00
		Adult	2008	0.98	0.27	1.00
		Yearling	2009	0.99	0.61	1.00
		Adult	2009	0.97	0.37	1.00
		Yearling	2010	0.98	0.27	1.00

Subpopulation	Population vital rate	Age	Year	Median estimate	Credible interval (CRI)	
					Lower (0.025)	Upper (0.975)
		Adult	2010	0.95	0.12	1.00
		Yearling	2011	0.88	0.03	1.00
		Adult	2011	0.73	0.01	1.00
		Yearling	2012	0.98	0.09	1.00
		Adult	2012	0.94	0.03	1.00
		Yearling	2013	0.98	0.18	1.00
		Adult	2013	0.95	0.08	1.00
		Yearling	2014	0.97	0.10	1.00
		Adult	2014	0.92	0.04	1.00
		Yearling	2015	0.99	0.54	1.00
		Adult	2015	0.97	0.31	1.00
		Yearling	2016	0.98	0.15	1.00
		Adult	2016	0.95	0.06	1.00
		Yearling	2017	1.00	0.38	1.00
		Adult	2017	0.99	0.18	1.00
	Nest propensity (*np2*)	Yearling	2003	0.17	0.02	0.55
		Adult	2003	0.25	0.03	0.65
		Yearling	2004	0.19	0.02	0.65
		Adult	2004	0.28	0.04	0.73
		Yearling	2005	0.23	0.04	0.64
		Adult	2005	0.34	0.07	0.73
		Yearling	2006	0.13	0.00	0.82
		Adult	2006	0.20	0.01	0.88
		Yearling	2007	0.09	0.00	0.56
		Adult	2007	0.14	0.01	0.67
		Yearling	2008	0.28	0.04	0.75
		Adult	2008	0.39	0.07	0.81
		Yearling	2009	0.12	0.01	0.57
		Adult	2009	0.19	0.02	0.67
		Yearling	2010	0.51	0.10	0.89
		Adult	2010	0.64	0.18	0.92
		Yearling	2011	0.48	0.08	0.89
		Adult	2011	0.61	0.15	0.92
		Yearling	2012	0.06	0.00	0.49
		Adult	2012	0.10	0.00	0.62
		Yearling	2013	0.07	0.00	0.56
		Adult	2013	0.11	0.00	0.65
		Yearling	2014	0.14	0.01	0.67
		Adult	2014	0.21	0.02	0.75
		Yearling	2015	0.18	0.01	0.72
		Adult	2015	0.28	0.02	0.82
		Yearling	2016	0.05	0.00	0.32

Subpopulation	Population vital rate	Age	Year	Median estimate	Credible interval (CRI)	
					Lower (0.025)	Upper (0.975)
		Adult	2016	0.08	0.01	0.41
		Yearling	2017	0.06	0.01	0.34
		Adult	2017	0.09	0.01	0.44
	Survival (*s*)	Yearling	2003	0.62	0.42	0.80
		Adult	2003	0.74	0.57	0.87
		Yearling	2004	0.72	0.54	0.87
		Adult	2004	0.81	0.68	0.92
		Yearling	2005	0.50	0.28	0.70
		Adult	2005	0.65	0.45	0.79
		Yearling	2006	0.56	0.27	0.80
		Adult	2006	0.70	0.44	0.86
		Yearling	2007	0.61	0.33	0.83
		Adult	2007	0.73	0.50	0.89
		Yearling	2008	0.68	0.44	0.87
		Adult	2008	0.78	0.61	0.91
		Yearling	2009	0.72	0.51	0.88
		Adult	2009	0.81	0.65	0.92
		Yearling	2010	0.68	0.43	0.86
		Adult	2010	0.78	0.60	0.91
		Yearling	2011	0.42	0.13	0.69
		Adult	2011	0.58	0.29	0.79
		Yearling	2012	0.63	0.33	0.84
		Adult	2012	0.75	0.50	0.90
		Yearling	2013	0.63	0.37	0.84
		Adult	2013	0.75	0.54	0.89
		Yearling	2014	0.64	0.38	0.85
		Adult	2014	0.76	0.54	0.90
		Yearling	2015	0.71	0.48	0.88
		Adult	2015	0.80	0.63	0.92
		Yearling	2016	0.71	0.53	0.86
		Adult	2016	0.80	0.67	0.90
		Yearling	2017	0.63	0.40	0.80
		Adult	2017	0.74	0.57	0.87
Mount Grant	Abundance (*N*)	NA	2003	15.00	14.00	16.00
			2004	16.00	11.00	21.00
			2005	19.00	13.00	26.00
			2006	8.00	5.00	13.00
			2007	8.00	5.00	12.00
			2008	9.00	6.00	14.00
			2009	15.00	11.00	20.00
			2010	15.00	11.00	20.00

Subpopulation	Population vital rate	Age	Year	Median estimate	Credible interval (CRI)	
					Lower (0.025)	Upper (0.975)
			2011	19.00	14.00	25.00
			2012	18.00	13.00	23.00
			2013	22.00	17.00	29.00
			2014	18.00	13.00	24.00
			2015	16.00	11.00	22.00
			2016	14.00	9.00	21.00
			2017	14.00	7.00	24.00
	Lambda (λ)	NA	2003	1.06	0.76	1.38
			2004	1.19	0.86	1.67
			2005	0.48	0.25	0.79
			2006	1.00	0.60	1.43
			2007	1.14	0.80	1.83
			2008	1.56	1.13	2.17
			2009	1.00	0.70	1.33
			2010	1.24	0.89	1.67
			2011	0.95	0.68	1.31
			2012	1.26	0.95	1.69
			2013	0.81	0.58	1.05
			2014	0.90	0.65	1.25
			2015	0.90	0.61	1.25
			2016	1.00	0.65	1.40
	r	NA	2003	0.06	-0.27	0.32
			2004	0.17	-0.15	0.51
			2005	-0.74	-1.39	-0.24
			2006	0.00	-0.51	0.36
			2007	0.13	-0.22	0.61
			2008	0.44	0.13	0.77
			2009	0.00	-0.36	0.29
			2010	0.21	-0.11	0.51
			2011	-0.05	-0.39	0.27
			2012	0.23	-0.05	0.53
			2013	-0.21	-0.55	0.05
			2014	-0.10	-0.43	0.22
			2015	-0.11	-0.49	0.22
			2016	0.00	-0.44	0.34
	Chick survival (*cs*)	Yearling	NA	0.29	0.22	0.38
		Adult	NA	0.38	0.31	0.47
	Fecundity (*f*)	Yearling	2003	0.31	0.13	0.51
		Adult	2003	0.45	0.11	0.68
		Yearling	2004	0.28	0.14	0.87
		Adult	2004	0.41	0.13	1.09
		Yearling	2005	0.23	0.01	0.41

Subpopulation	**Population vital rate**	**Age**	**Year**	**Median estimate**	**Credible interval (CRI)**	
					Lower (0.025)	**Upper (0.975)**
		Adult	2005	0.33	0.01	0.55
		Yearling	2006	0.26	0.02	0.46
		Adult	2006	0.37	0.01	0.63
		Yearling	2007	0.30	0.13	1.34
		Adult	2007	0.43	0.11	1.68
		Yearling	2008	0.35	0.21	0.55
		Adult	2008	0.52	0.32	0.72
		Yearling	2009	0.29	0.06	0.46
		Adult	2009	0.42	0.04	0.62
		Yearling	2010	0.34	0.17	0.58
		Adult	2010	0.51	0.16	0.73
		Yearling	2011	0.30	0.04	0.49
		Adult	2011	0.44	0.02	0.66
		Yearling	2012	0.27	0.16	0.51
		Adult	2012	0.39	0.21	0.69
		Yearling	2013	0.22	0.13	0.36
		Adult	2013	0.28	0.16	0.44
		Yearling	2014	0.25	0.07	0.42
		Adult	2014	0.36	0.05	0.57
		Yearling	2015	0.25	0.03	0.40
		Adult	2015	0.35	0.02	0.56
		Yearling	2016	0.26	0.16	0.39
		Adult	2016	0.36	0.25	0.49
		Yearling	2017	0.26	0.17	0.41
		Adult	2017	0.39	0.28	0.55
	Hatchability (*h*)	Yearling	2003	0.99	0.43	1.00
		Adult	2003	0.97	0.21	1.00
		Yearling	2004	0.98	0.52	1.00
		Adult	2004	0.96	0.29	1.00
		Yearling	2005	0.96	0.04	1.00
		Adult	2005	0.88	0.01	1.00
		Yearling	2006	0.98	0.07	1.00
		Adult	2006	0.94	0.03	1.00
		Yearling	2007	0.99	0.46	1.00
		Adult	2007	0.98	0.23	1.00
		Yearling	2008	1.00	0.85	1.00
		Adult	2008	0.99	0.68	1.00
		Yearling	2009	0.99	0.20	1.00
		Adult	2009	0.96	0.09	1.00
		Yearling	2010	0.99	0.51	1.00
		Adult	2010	0.96	0.28	1.00
		Yearling	2011	0.97	0.11	1.00

Subpopulation	Population vital rate	Age	Year	Median estimate	Credible interval (CRI)	
					Lower (0.025)	Upper (0.975)
		Adult	2011	0.93	0.04	1.00
		Yearling	2012	0.99	0.76	1.00
		Adult	2012	0.98	0.54	1.00
		Yearling	2013	0.90	0.68	0.98
		Adult	2013	0.76	0.51	0.92
		Yearling	2014	0.98	0.26	1.00
		Adult	2014	0.95	0.12	1.00
		Yearling	2015	0.98	0.12	1.00
		Adult	2015	0.95	0.05	1.00
		Yearling	2016	0.97	0.88	0.99
		Adult	2016	0.91	0.77	0.98
		Yearling	2017	1.00	0.99	1.00
		Adult	2017	1.00	0.97	1.00
	Nest propensity (*np2*)	Yearling	2003	0.22	0.03	0.75
		Adult	2003	0.32	0.05	0.83
		Yearling	2004	0.23	0.03	0.74
		Adult	2004	0.33	0.06	0.81
		Yearling	2005	0.26	0.04	0.78
		Adult	2005	0.38	0.07	0.84
		Yearling	2006	0.17	0.01	0.87
		Adult	2006	0.25	0.01	0.91
		Yearling	2007	0.11	0.00	0.67
		Adult	2007	0.18	0.01	0.76
		Yearling	2008	0.34	0.06	0.84
		Adult	2008	0.46	0.10	0.88
		Yearling	2009	0.15	0.02	0.65
		Adult	2009	0.23	0.03	0.75
		Yearling	2010	0.58	0.12	0.93
		Adult	2010	0.69	0.21	0.95
		Yearling	2011	0.54	0.11	0.94
		Adult	2011	0.67	0.20	0.96
		Yearling	2012	0.08	0.00	0.67
		Adult	2012	0.14	0.00	0.75
		Yearling	2013	0.09	0.00	0.65
		Adult	2013	0.14	0.01	0.73
		Yearling	2014	0.17	0.01	0.78
		Adult	2014	0.26	0.02	0.83
		Yearling	2015	0.22	0.02	0.80
		Adult	2015	0.32	0.03	0.87
		Yearling	2016	0.07	0.01	0.32
		Adult	2016	0.11	0.02	0.42
		Yearling	2017	0.07	0.01	0.39

Subpopulation	Population vital rate	Age	Year	Median estimate	Credible interval (CRI)	
					Lower (0.025)	Upper (0.975)
		Adult	2017	0.11	0.02	0.49
	Survival (*s*)	Yearling	2003	0.63	0.39	0.84
		Adult	2003	0.75	0.55	0.90
		Yearling	2004	0.69	0.47	0.87
		Adult	2004	0.79	0.63	0.92
		Yearling	2005	0.40	0.11	0.68
		Adult	2005	0.56	0.26	0.78
		Yearling	2006	0.64	0.35	0.85
		Adult	2006	0.75	0.52	0.90
		Yearling	2007	0.67	0.42	0.87
		Adult	2007	0.78	0.58	0.91
		Yearling	2008	0.72	0.52	0.89
		Adult	2008	0.81	0.66	0.92
		Yearling	2009	0.68	0.43	0.86
		Adult	2009	0.78	0.59	0.91
		Yearling	2010	0.70	0.47	0.88
		Adult	2010	0.80	0.63	0.92
		Yearling	2011	0.63	0.37	0.84
		Adult	2011	0.74	0.54	0.89
		Yearling	2012	0.73	0.54	0.89
		Adult	2012	0.82	0.67	0.93
		Yearling	2013	0.61	0.43	0.77
		Adult	2013	0.73	0.59	0.84
		Yearling	2014	0.54	0.33	0.72
		Adult	2014	0.68	0.51	0.81
		Yearling	2015	0.69	0.47	0.87
		Adult	2015	0.79	0.62	0.92
		Yearling	2016	0.67	0.48	0.82
		Adult	2016	0.78	0.64	0.88
		Yearling	2017	0.62	0.39	0.81
		Adult	2017	0.74	0.55	0.87
Fales	Abundance (*N*)	NA	2003	12.00	11.00	13.00
			2004	8.00	5.00	12.00
			2005	8.00	5.00	12.00
			2006	9.00	6.00	13.00
			2007	10.00	6.00	14.00
			2008	10.00	7.00	15.00
			2009	11.00	8.00	16.00
			2010	12.00	8.00	17.00
			2011	13.00	9.00	18.00
			2012	13.00	9.00	18.00

Subpopulation	Population vital rate	Age	Year	Median estimate	Credible interval (CRI)	
					Lower (0.025)	Upper (0.975)
			2013	13.00	9.00	18.00
			2014	13.00	9.00	18.00
			2015	12.00	8.00	17.00
			2016	12.00	8.00	18.00
			2017	12.00	5.00	22.00
	Lambda (*λ*)	NA	2003	0.69	0.43	1.00
			2004	1.09	0.70	1.60
			2005	1.00	0.69	1.56
			2006	1.13	0.75	1.67
			2007	1.00	0.69	1.57
			2008	1.09	0.73	1.57
			2009	1.08	0.73	1.55
			2010	1.08	0.73	1.55
			2011	1.00	0.65	1.40
			2012	1.06	0.71	1.47
			2013	1.00	0.69	1.40
			2014	0.93	0.63	1.33
			2015	1.00	0.67	1.42
			2016	1.00	0.57	1.50
	r	NA	2003	-0.37	-0.85	0.00
			2004	0.09	-0.36	0.47
			2005	0.00	-0.37	0.44
			2006	0.12	-0.29	0.51
			2007	0.00	-0.37	0.45
			2008	0.09	-0.31	0.45
			2009	0.08	-0.31	0.44
			2010	0.08	-0.31	0.44
			2011	0.00	-0.44	0.34
			2012	0.06	-0.34	0.38
			2013	0.00	-0.37	0.34
			2014	-0.07	-0.47	0.29
			2015	0.00	-0.41	0.35
			2016	0.00	-0.56	0.41
	Chick survival (*cs*)	Yearling	NA	0.35	0.25	0.53
		Adult	NA	0.45	0.35	0.63
	Fecundity (*f*)	Yearling	2003	0.38	0.23	0.66
		Adult	2003	0.53	0.34	0.85
		Yearling	2004	0.34	0.20	0.83
		Adult	2004	0.47	0.30	1.04
		Yearling	2005	0.31	0.10	0.55
		Adult	2005	0.44	0.07	0.72
		Yearling	2006	0.33	0.12	0.60

Subpopulation	Population vital rate	Age	Year	Median estimate	Credible interval (CRI)	
					Lower (0.025)	Upper (0.975)
		Adult	2006	0.46	0.09	0.79
		Yearling	2007	0.37	0.21	1.31
		Adult	2007	0.52	0.31	1.67
		Yearling	2008	0.40	0.20	0.69
		Adult	2008	0.58	0.19	0.90
		Yearling	2009	0.36	0.16	0.60
		Adult	2009	0.50	0.12	0.79
		Yearling	2010	0.41	0.15	0.73
		Adult	2010	0.58	0.12	0.92
		Yearling	2011	0.37	0.11	0.64
		Adult	2011	0.52	0.07	0.84
		Yearling	2012	0.32	0.13	0.60
		Adult	2012	0.45	0.10	0.78
		Yearling	2013	0.29	0.12	0.50
		Adult	2013	0.40	0.10	0.65
		Yearling	2014	0.30	0.05	0.54
		Adult	2014	0.42	0.03	0.70
		Yearling	2015	0.31	0.11	0.53
		Adult	2015	0.44	0.07	0.71
		Yearling	2016	0.32	0.20	0.54
		Adult	2016	0.45	0.32	0.68
		Yearling	2017	0.32	0.19	0.54
		Adult	2017	0.45	0.31	0.70
	Hatchability (*h*)	Yearling	2003	0.98	0.87	1.00
		Adult	2003	0.94	0.73	1.00
		Yearling	2004	0.97	0.86	1.00
		Adult	2004	0.93	0.70	1.00
		Yearling	2005	0.99	0.35	1.00
		Adult	2005	0.98	0.15	1.00
		Yearling	2006	0.99	0.38	1.00
		Adult	2006	0.98	0.18	1.00
		Yearling	2007	1.00	0.84	1.00
		Adult	2007	0.99	0.64	1.00
		Yearling	2008	1.00	0.53	1.00
		Adult	2008	0.99	0.30	1.00
		Yearling	2009	0.99	0.43	1.00
		Adult	2009	0.98	0.23	1.00
		Yearling	2010	0.99	0.36	1.00
		Adult	2010	0.97	0.18	1.00
		Yearling	2011	0.99	0.27	1.00
		Adult	2011	0.96	0.12	1.00
		Yearling	2012	0.99	0.41	1.00

Subpopulation	Population vital rate	Age	Year	Median estimate	Credible interval (CRI)	
					Lower (0.025)	Upper (0.975)
		Adult	2012	0.98	0.21	1.00
		Yearling	2013	0.99	0.45	1.00
		Adult	2013	0.98	0.22	1.00
		Yearling	2014	0.99	0.15	1.00
		Adult	2014	0.96	0.06	1.00
		Yearling	2015	0.99	0.35	1.00
		Adult	2015	0.98	0.15	1.00
		Yearling	2016	1.00	0.97	1.00
		Adult	2016	0.99	0.94	1.00
		Yearling	2017	1.00	0.99	1.00
		Adult	2017	1.00	0.97	1.00
	Nest propensity (*np2*)	Yearling	2003	0.20	0.03	0.61
		Adult	2003	0.29	0.06	0.71
		Yearling	2004	0.18	0.02	0.55
		Adult	2004	0.27	0.04	0.66
		Yearling	2005	0.23	0.03	0.71
		Adult	2005	0.33	0.05	0.79
		Yearling	2006	0.14	0.00	0.83
		Adult	2006	0.22	0.01	0.88
		Yearling	2007	0.09	0.00	0.59
		Adult	2007	0.15	0.01	0.70
		Yearling	2008	0.28	0.04	0.74
		Adult	2008	0.40	0.07	0.81
		Yearling	2009	0.12	0.01	0.57
		Adult	2009	0.19	0.02	0.67
		Yearling	2010	0.52	0.10	0.90
		Adult	2010	0.65	0.18	0.92
		Yearling	2011	0.49	0.10	0.90
		Adult	2011	0.62	0.17	0.93
		Yearling	2012	0.07	0.00	0.54
		Adult	2012	0.11	0.00	0.64
		Yearling	2013	0.07	0.00	0.57
		Adult	2013	0.12	0.00	0.66
		Yearling	2014	0.14	0.01	0.68
		Adult	2014	0.22	0.02	0.76
		Yearling	2015	0.19	0.01	0.73
		Adult	2015	0.28	0.02	0.82
		Yearling	2016	0.05	0.00	0.33
		Adult	2016	0.09	0.01	0.43
		Yearling	2017	0.06	0.01	0.37
		Adult	2017	0.10	0.01	0.47
	Survival (*s*)	Yearling	2003	0.29	0.08	0.57

Subpopulation	Population vital rate	Age	Year	Median estimate	Credible interval (CRI)	
					Lower (0.025)	Upper (0.975)
		Adult	2003	0.46	0.21	0.69
		Yearling	2004	0.54	0.28	0.74
		Adult	2004	0.68	0.44	0.82
		Yearling	2005	0.61	0.34	0.83
		Adult	2005	0.73	0.51	0.89
		Yearling	2006	0.64	0.39	0.85
		Adult	2006	0.76	0.55	0.90
		Yearling	2007	0.60	0.32	0.81
		Adult	2007	0.72	0.48	0.87
		Yearling	2008	0.64	0.38	0.84
		Adult	2008	0.75	0.54	0.89
		Yearling	2009	0.67	0.40	0.85
		Adult	2009	0.77	0.57	0.91
		Yearling	2010	0.62	0.34	0.82
		Adult	2010	0.73	0.52	0.88
		Yearling	2011	0.59	0.32	0.81
		Adult	2011	0.71	0.49	0.87
		Yearling	2012	0.65	0.39	0.84
		Adult	2012	0.76	0.55	0.90
		Yearling	2013	0.61	0.36	0.83
		Adult	2013	0.73	0.53	0.89
		Yearling	2014	0.60	0.32	0.82
		Adult	2014	0.72	0.50	0.88
		Yearling	2015	0.64	0.38	0.84
		Adult	2015	0.76	0.55	0.90
		Yearling	2016	0.65	0.36	0.85
		Adult	2016	0.76	0.53	0.90
		Yearling	2017	0.59	0.26	0.82
		Adult	2017	0.71	0.43	0.88
Bodie Hills	Abundance (*N*)	NA	2003	17.00	16.00	18.00
			2004	16.00	12.00	21.00
			2005	17.00	13.00	23.00
			2006	16.00	11.00	21.00
			2007	17.00	12.00	22.00
			2008	20.00	15.00	26.00
			2009	24.00	19.00	30.00
			2010	29.00	24.00	36.00
			2011	32.00	26.00	40.00
			2012	33.00	26.00	40.00
			2013	33.00	26.00	41.00
			2014	28.00	22.00	36.00

Subpopulation	Population vital rate	Age	Year	Median estimate	Credible interval (CRI)	
					Lower (0.025)	Upper (0.975)
			2015	25.00	18.00	32.00
			2016	21.00	14.00	28.00
			2017	21.00	12.00	32.00
	Lambda (λ)	NA	2003	0.89	0.68	1.18
			2004	1.10	0.81	1.50
			2005	0.90	0.64	1.24
			2006	1.06	0.76	1.43
			2007	1.18	0.88	1.79
			2008	1.21	0.92	1.56
			2009	1.21	0.97	1.50
			2010	1.10	0.87	1.37
			2011	1.00	0.77	1.29
			2012	1.00	0.78	1.29
			2013	0.87	0.63	1.13
			2014	0.88	0.65	1.15
			2015	0.85	0.61	1.13
			2016	1.03	0.71	1.33
	r	NA	2003	-0.11	-0.38	0.16
			2004	0.10	-0.21	0.41
			2005	-0.10	-0.45	0.21
			2006	0.06	-0.27	0.36
			2007	0.16	-0.13	0.58
			2008	0.19	-0.08	0.45
			2009	0.19	-0.04	0.41
			2010	0.10	-0.14	0.32
			2011	0.00	-0.26	0.25
			2012	0.00	-0.25	0.25
			2013	-0.14	-0.46	0.13
			2014	-0.13	-0.44	0.14
			2015	-0.17	-0.50	0.12
			2016	0.03	-0.34	0.29
	Chick survival (*cs*)	Yearling	NA	0.27	0.22	0.34
		Adult	NA	0.36	0.32	0.40
	Fecundity (*f*)	Yearling	2003	0.29	0.19	0.46
		Adult	2003	0.44	0.31	0.62
		Yearling	2004	0.27	0.18	0.77
		Adult	2004	0.40	0.30	1.04
		Yearling	2005	0.25	0.16	0.39
		Adult	2005	0.38	0.28	0.54
		Yearling	2006	0.25	0.09	0.43
		Adult	2006	0.37	0.06	0.58
		Yearling	2007	0.28	0.18	1.28

Subpopulation	Population vital rate	Age	Year	Median estimate	Credible interval (CRI)	
					Lower (0.025)	Upper (0.975)
		Adult	2007	0.42	0.29	1.67
		Yearling	2008	0.31	0.20	0.47
		Adult	2008	0.46	0.34	0.59
		Yearling	2009	0.28	0.18	0.41
		Adult	2009	0.39	0.28	0.51
		Yearling	2010	0.32	0.20	0.50
		Adult	2010	0.44	0.32	0.59
		Yearling	2011	0.30	0.20	0.46
		Adult	2011	0.46	0.33	0.61
		Yearling	2012	0.25	0.13	0.42
		Adult	2012	0.36	0.14	0.58
		Yearling	2013	0.22	0.08	0.35
		Adult	2013	0.32	0.07	0.47
		Yearling	2014	0.23	0.04	0.37
		Adult	2014	0.34	0.03	0.49
		Yearling	2015	0.24	0.15	0.36
		Adult	2015	0.34	0.24	0.48
		Yearling	2016	0.25	0.17	0.36
		Adult	2016	0.36	0.28	0.47
		Yearling	2017	0.24	0.16	0.36
		Adult	2017	0.36	0.27	0.47
	Hatchability (*h*)	Yearling	2003	1.00	0.92	1.00
		Adult	2003	0.99	0.80	1.00
		Yearling	2004	0.99	0.94	1.00
		Adult	2004	0.96	0.87	0.99
		Yearling	2005	1.00	0.97	1.00
		Adult	2005	0.99	0.92	1.00
		Yearling	2006	0.99	0.36	1.00
		Adult	2006	0.98	0.16	1.00
		Yearling	2007	1.00	0.93	1.00
		Adult	2007	0.99	0.82	1.00
		Yearling	2008	0.98	0.92	1.00
		Adult	2008	0.94	0.84	0.99
		Yearling	2009	0.96	0.90	0.99
		Adult	2009	0.91	0.77	0.97
		Yearling	2010	0.94	0.81	0.99
		Adult	2010	0.84	0.69	0.94
		Yearling	2011	1.00	0.90	1.00
		Adult	2011	0.99	0.78	1.00
		Yearling	2012	0.99	0.60	1.00
		Adult	2012	0.98	0.35	1.00
		Yearling	2013	0.99	0.37	1.00

Subpopulation	Population vital rate	Age	Year	Median estimate	Credible interval (CRI)	
					Lower (0.025)	Upper (0.975)
		Adult	2013	0.98	0.19	1.00
		Yearling	2014	0.99	0.17	1.00
		Adult	2014	0.96	0.07	1.00
		Yearling	2015	0.96	0.88	0.99
		Adult	2015	0.90	0.78	0.97
		Yearling	2016	1.00	0.99	1.00
		Adult	2016	1.00	0.98	1.00
		Yearling	2017	1.00	0.99	1.00
		Adult	2017	1.00	0.98	1.00
	Nest propensity (*np2*)	Yearling	2003	0.18	0.03	0.55
		Adult	2003	0.28	0.05	0.65
		Yearling	2004	0.23	0.06	0.57
		Adult	2004	0.33	0.12	0.66
		Yearling	2005	0.24	0.06	0.59
		Adult	2005	0.35	0.11	0.70
		Yearling	2006	0.14	0.01	0.81
		Adult	2006	0.22	0.01	0.86
		Yearling	2007	0.10	0.00	0.53
		Adult	2007	0.16	0.01	0.64
		Yearling	2008	0.26	0.08	0.55
		Adult	2008	0.37	0.16	0.62
		Yearling	2009	0.13	0.02	0.40
		Adult	2009	0.20	0.04	0.51
		Yearling	2010	0.57	0.26	0.85
		Adult	2010	0.69	0.44	0.88
		Yearling	2011	0.52	0.22	0.83
		Adult	2011	0.65	0.38	0.86
		Yearling	2012	0.07	0.00	0.46
		Adult	2012	0.11	0.01	0.58
		Yearling	2013	0.08	0.00	0.49
		Adult	2013	0.13	0.01	0.60
		Yearling	2014	0.14	0.01	0.55
		Adult	2014	0.22	0.02	0.64
		Yearling	2015	0.20	0.03	0.62
		Adult	2015	0.30	0.05	0.75
		Yearling	2016	0.05	0.01	0.17
		Adult	2016	0.08	0.02	0.23
		Yearling	2017	0.06	0.01	0.18
		Adult	2017	0.10	0.03	0.23
	Survival (*s*)	Yearling	2003	0.48	0.27	0.67
		Adult	2003	0.63	0.43	0.78
		Yearling	2004	0.63	0.45	0.79

Subpopulation	Population vital rate	Age	Year	Median estimate	Credible interval (CRI)	
					Lower (0.025)	Upper (0.975)
		Adult	2004	0.75	0.61	0.86
		Yearling	2005	0.48	0.27	0.66
		Adult	2005	0.63	0.44	0.77
		Yearling	2006	0.66	0.43	0.86
		Adult	2006	0.77	0.58	0.91
		Yearling	2007	0.56	0.37	0.72
		Adult	2007	0.69	0.53	0.81
		Yearling	2008	0.59	0.41	0.74
		Adult	2008	0.72	0.58	0.83
		Yearling	2009	0.74	0.57	0.87
		Adult	2009	0.82	0.70	0.91
		Yearling	2010	0.65	0.47	0.81
		Adult	2010	0.76	0.62	0.87
		Yearling	2011	0.64	0.43	0.83
		Adult	2011	0.75	0.59	0.89
		Yearling	2012	0.66	0.45	0.85
		Adult	2012	0.77	0.61	0.90
		Yearling	2013	0.59	0.35	0.80
		Adult	2013	0.72	0.52	0.87
		Yearling	2014	0.60	0.39	0.79
		Adult	2014	0.72	0.55	0.86
		Yearling	2015	0.56	0.37	0.72
		Adult	2015	0.69	0.54	0.81
		Yearling	2016	0.69	0.51	0.83
		Adult	2016	0.79	0.66	0.89
		Yearling	2017	0.52	0.31	0.70
		Adult	2017	0.66	0.49	0.79
Parker Meadows	Abundance (*N*)	NA	2003	10.00	9.00	11.00
			2004	9.00	6.00	13.00
			2005	8.00	5.00	10.00
			2006	6.00	4.00	9.00
			2007	5.00	2.00	7.00
			2008	4.00	2.00	7.00
			2009	4.00	2.00	6.00
			2010	5.00	3.00	7.00
			2011	5.00	3.00	8.00
			2012	4.00	3.00	7.00
			2013	5.00	3.00	8.00
			2014	4.00	2.00	6.00
			2015	3.00	2.00	6.00
			2016	3.00	1.00	6.00

Subpopulation	Population vital rate	Age	Year	Median estimate	Credible interval (CRI)	
					Lower (0.025)	Upper (0.975)
			2017	2.00	0.00	6.00
	Lambda (λ)	NA	2003	0.91	0.64	1.27
			2004	0.89	0.62	1.10
			2005	0.86	0.60	1.00
			2006	0.78	0.44	1.17
			2007	1.00	0.57	1.50
			2008	1.00	0.57	1.50
			2009	1.20	0.75	1.75
			2010	1.00	0.71	1.60
			2011	1.00	0.67	1.20
			2012	1.00	0.71	1.67
			2013	0.80	0.50	1.20
			2014	1.00	0.50	1.33
			2015	1.00	0.60	1.50
			2016	0.80	0.33	1.50
	r	NA	2003	-0.10	-0.45	0.24
			2004	-0.12	-0.49	0.10
			2005	-0.15	-0.51	0.00
			2006	-0.25	-0.81	0.15
			2007	0.00	-0.56	0.41
			2008	0.00	-0.56	0.41
			2009	0.18	-0.29	0.56
			2010	0.00	-0.34	0.47
			2011	0.00	-0.41	0.18
			2012	0.00	-0.34	0.51
			2013	-0.22	-0.69	0.18
			2014	0.00	-0.69	0.29
			2015	0.00	-0.51	0.41
			2016	-0.22	-1.10	0.41
	Chick survival (*cs*)	Yearling	NA	0.29	0.22	0.38
		Adult	NA	0.38	0.31	0.47
	Fecundity (*f*)	Yearling	2003	0.26	0.01	0.45
		Adult	2003	0.34	0.00	0.59
		Yearling	2004	0.02	0.00	0.14
		Adult	2004	0.01	0.00	0.08
		Yearling	2005	0.02	0.00	0.10
		Adult	2005	0.01	0.00	0.06
		Yearling	2006	0.18	0.00	0.40
		Adult	2006	0.18	0.00	0.52
		Yearling	2007	0.25	0.01	0.76
		Adult	2007	0.33	0.00	0.93
		Yearling	2008	0.26	0.01	0.47

Subpopulation	Population vital rate	Age	Year	Median estimate	Credible interval (CRI)	
					Lower (0.025)	Upper (0.975)
		Adult	2008	0.34	0.00	0.62
		Yearling	2009	0.29	0.18	0.44
		Adult	2009	0.40	0.27	0.56
		Yearling	2010	0.22	0.11	0.40
		Adult	2010	0.22	0.11	0.37
		Yearling	2011	0.02	0.00	0.11
		Adult	2011	0.01	0.00	0.08
		Yearling	2012	0.22	0.01	0.42
		Adult	2012	0.29	0.00	0.54
		Yearling	2013	0.18	0.00	0.34
		Adult	2013	0.21	0.00	0.45
		Yearling	2014	0.18	0.00	0.37
		Adult	2014	0.19	0.00	0.48
		Yearling	2015	0.25	0.15	0.39
		Adult	2015	0.36	0.20	0.53
		Yearling	2016	0.20	0.00	0.36
		Adult	2016	0.25	0.00	0.46
		Yearling	2017	0.25	0.16	0.40
		Adult	2017	0.36	0.25	0.51
	Hatchability (*h*)	Yearling	2003	0.90	0.03	1.00
		Adult	2003	0.77	0.01	1.00
		Yearling	2004	0.07	0.00	0.43
		Adult	2004	0.03	0.00	0.17
		Yearling	2005	0.06	0.00	0.37
		Adult	2005	0.02	0.00	0.14
		Yearling	2006	0.69	0.01	1.00
		Adult	2006	0.44	0.00	1.00
		Yearling	2007	0.91	0.02	1.00
		Adult	2007	0.78	0.01	1.00
		Yearling	2008	0.87	0.02	1.00
		Adult	2008	0.69	0.01	1.00
		Yearling	2009	0.96	0.87	0.99
		Adult	2009	0.91	0.74	0.98
		Yearling	2010	0.66	0.35	0.88
		Adult	2010	0.41	0.21	0.62
		Yearling	2011	0.06	0.00	0.31
		Adult	2011	0.02	0.00	0.15
		Yearling	2012	0.91	0.03	1.00
		Adult	2012	0.78	0.01	1.00
		Yearling	2013	0.81	0.01	1.00
		Adult	2013	0.60	0.00	1.00
		Yearling	2014	0.73	0.01	1.00

Subpopulation	Population vital rate	Age	Year	Median estimate	Credible interval (CRI)	
					Lower (0.025)	Upper (0.975)
		Adult	2014	0.49	0.00	1.00
		Yearling	2015	0.98	0.74	1.00
		Adult	2015	0.95	0.54	1.00
		Yearling	2016	0.84	0.01	1.00
		Adult	2016	0.66	0.01	1.00
		Yearling	2017	0.99	0.90	1.00
		Adult	2017	0.98	0.78	1.00
	Nest propensity (*np2*)	Yearling	2003	0.13	0.02	0.44
		Adult	2003	0.20	0.03	0.55
		Yearling	2004	0.13	0.02	0.44
		Adult	2004	0.21	0.03	0.53
		Yearling	2005	0.18	0.02	0.59
		Adult	2005	0.27	0.04	0.69
		Yearling	2006	0.10	0.00	0.75
		Adult	2006	0.17	0.01	0.82
		Yearling	2007	0.07	0.00	0.48
		Adult	2007	0.11	0.00	0.59
		Yearling	2008	0.21	0.03	0.58
		Adult	2008	0.32	0.06	0.68
		Yearling	2009	0.09	0.01	0.36
		Adult	2009	0.14	0.02	0.46
		Yearling	2010	0.45	0.14	0.79
		Adult	2010	0.58	0.25	0.83
		Yearling	2011	0.44	0.12	0.81
		Adult	2011	0.57	0.22	0.85
		Yearling	2012	0.05	0.00	0.39
		Adult	2012	0.08	0.00	0.50
		Yearling	2013	0.06	0.00	0.43
		Adult	2013	0.09	0.00	0.52
		Yearling	2014	0.11	0.01	0.56
		Adult	2014	0.17	0.02	0.65
		Yearling	2015	0.14	0.01	0.57
		Adult	2015	0.21	0.02	0.70
		Yearling	2016	0.04	0.00	0.24
		Adult	2016	0.06	0.01	0.33
		Yearling	2017	0.04	0.00	0.24
		Adult	2017	0.07	0.01	0.33
	Survival (*s*)	Yearling	2003	0.54	0.30	0.76
		Adult	2003	0.68	0.47	0.84
		Yearling	2004	0.65	0.42	0.83
		Adult	2004	0.76	0.59	0.88
		Yearling	2005	0.62	0.37	0.83

Subpopulation	Population vital rate	Age	Year	Median estimate	Credible interval (CRI)	
					Lower (0.025)	Upper (0.975)
		Adult	2005	0.74	0.54	0.89
		Yearling	2006	0.60	0.28	0.82
		Adult	2006	0.72	0.45	0.88
		Yearling	2007	0.63	0.34	0.84
		Adult	2007	0.75	0.50	0.90
		Yearling	2008	0.65	0.38	0.86
		Adult	2008	0.76	0.56	0.90
		Yearling	2009	0.66	0.41	0.83
		Adult	2009	0.77	0.57	0.89
		Yearling	2010	0.70	0.47	0.88
		Adult	2010	0.80	0.63	0.92
		Yearling	2011	0.66	0.40	0.86
		Adult	2011	0.77	0.57	0.90
		Yearling	2012	0.67	0.40	0.86
		Adult	2012	0.77	0.57	0.91
		Yearling	2013	0.60	0.29	0.82
		Adult	2013	0.72	0.46	0.88
		Yearling	2014	0.62	0.32	0.83
		Adult	2014	0.74	0.49	0.89
		Yearling	2015	0.66	0.41	0.84
		Adult	2015	0.77	0.58	0.90
		Yearling	2016	0.57	0.25	0.78
		Adult	2016	0.70	0.43	0.85
		Yearling	2017	0.58	0.28	0.80
		Adult	2017	0.71	0.45	0.87
Long Valley	Abundance (*N*)	NA	2003	40.00	39.00	41.00
			2004	41.00	33.00	50.00
			2005	35.00	28.00	44.00
			2006	33.00	26.00	42.00
			2007	27.00	20.00	34.00
			2008	29.00	22.00	37.00
			2009	31.00	24.00	38.00
			2010	32.00	25.00	39.00
			2011	33.00	25.00	42.00
			2012	25.00	18.00	33.00
			2013	21.00	15.00	28.00
			2014	17.00	12.00	23.00
			2015	14.00	10.00	20.00
			2016	15.00	10.00	21.00
			2017	14.00	7.00	22.00
	Lambda (λ)	NA	2003	1.03	0.83	1.24

Subpopulation	Population vital rate	Age	Year	Median estimate	Credible interval (CRI)	
					Lower (0.025)	Upper (0.975)
			2004	0.87	0.67	1.13
			2005	0.94	0.71	1.20
			2006	0.81	0.57	1.09
			2007	1.08	0.83	1.50
			2008	1.07	0.82	1.37
			2009	1.03	0.80	1.29
			2010	1.03	0.80	1.31
			2011	0.77	0.54	1.04
			2012	0.84	0.59	1.16
			2013	0.83	0.56	1.13
			2014	0.87	0.58	1.21
			2015	1.05	0.74	1.41
			2016	0.94	0.60	1.31
	r	NA	2003	0.02	-0.19	0.22
			2004	-0.14	-0.41	0.12
			2005	-0.06	-0.34	0.18
			2006	-0.22	-0.57	0.08
			2007	0.07	-0.19	0.41
			2008	0.07	-0.20	0.32
			2009	0.03	-0.22	0.25
			2010	0.03	-0.22	0.27
			2011	-0.27	-0.62	0.04
			2012	-0.17	-0.53	0.15
			2013	-0.19	-0.58	0.13
			2014	-0.14	-0.54	0.19
			2015	0.05	-0.31	0.34
			2016	-0.06	-0.51	0.27
	Chick survival (*cs*)	Yearling	NA	0.27	0.21	0.34
		Adult	NA	0.36	0.31	0.41
	Fecundity (*f*)	Yearling	2003	0.29	0.19	0.47
		Adult	2003	0.44	0.32	0.62
		Yearling	2004	0.25	0.14	0.61
		Adult	2004	0.34	0.16	0.75
		Yearling	2005	0.25	0.16	0.39
		Adult	2005	0.38	0.28	0.53
		Yearling	2006	0.23	0.02	0.41
		Adult	2006	0.34	0.01	0.56
		Yearling	2007	0.28	0.18	1.02
		Adult	2007	0.42	0.29	1.39
		Yearling	2008	0.33	0.21	0.50
		Adult	2008	0.50	0.38	0.66
		Yearling	2009	0.28	0.18	0.41

Subpopulation	**Population vital rate**	**Age**	**Year**	**Median estimate**	**Credible interval (CRI)**	
					Lower (0.025)	**Upper (0.975)**
		Adult	2009	0.41	0.30	0.54
		Yearling	2010	0.30	0.19	0.48
		Adult	2010	0.40	0.28	0.54
		Yearling	2011	0.31	0.20	0.48
		Adult	2011	0.48	0.36	0.64
		Yearling	2012	0.24	0.05	0.41
		Adult	2012	0.35	0.03	0.55
		Yearling	2013	0.22	0.05	0.35
		Adult	2013	0.31	0.03	0.46
		Yearling	2014	0.23	0.04	0.37
		Adult	2014	0.33	0.02	0.51
		Yearling	2015	0.24	0.11	0.37
		Adult	2015	0.36	0.10	0.52
		Yearling	2016	0.23	0.15	0.34
		Adult	2016	0.31	0.23	0.41
		Yearling	2017	0.24	0.16	0.36
		Adult	2017	0.36	0.27	0.48
	Hatchability (*h*)	Yearling	2003	0.99	0.92	1.00
		Adult	2003	0.97	0.84	1.00
		Yearling	2004	0.94	0.61	1.00
		Adult	2004	0.84	0.40	0.99
		Yearling	2005	1.00	0.98	1.00
		Adult	2005	1.00	0.95	1.00
		Yearling	2006	0.98	0.07	1.00
		Adult	2006	0.95	0.03	1.00
		Yearling	2007	1.00	0.96	1.00
		Adult	2007	1.00	0.90	1.00
		Yearling	2008	1.00	0.99	1.00
		Adult	2008	1.00	0.97	1.00
		Yearling	2009	0.98	0.94	1.00
		Adult	2009	0.95	0.88	0.98
		Yearling	2010	0.90	0.76	0.97
		Adult	2010	0.77	0.62	0.88
		Yearling	2011	1.00	0.97	1.00
		Adult	2011	0.99	0.93	1.00
		Yearling	2012	0.99	0.18	1.00
		Adult	2012	0.97	0.07	1.00
		Yearling	2013	0.99	0.21	1.00
		Adult	2013	0.97	0.09	1.00
		Yearling	2014	0.98	0.15	1.00
		Adult	2014	0.95	0.06	1.00
		Yearling	2015	0.99	0.50	1.00

Subpopulation	Population vital rate	Age	Year	Median estimate	Credible interval (CRI)	
					Lower (0.025)	Upper (0.975)
		Adult	2015	0.98	0.27	1.00
		Yearling	2016	0.94	0.86	0.98
		Adult	2016	0.86	0.78	0.92
		Yearling	2017	1.00	0.99	1.00
		Adult	2017	1.00	0.98	1.00
	Nest propensity (*np2*)	Yearling	2003	0.23	0.06	0.60
		Adult	2003	0.34	0.10	0.69
		Yearling	2004	0.21	0.05	0.49
		Adult	2004	0.31	0.10	0.57
		Yearling	2005	0.26	0.08	0.55
		Adult	2005	0.37	0.14	0.66
		Yearling	2006	0.16	0.01	0.82
		Adult	2006	0.24	0.01	0.88
		Yearling	2007	0.10	0.00	0.47
		Adult	2007	0.16	0.01	0.58
		Yearling	2008	0.36	0.13	0.70
		Adult	2008	0.49	0.25	0.76
		Yearling	2009	0.15	0.03	0.44
		Adult	2009	0.23	0.05	0.55
		Yearling	2010	0.56	0.26	0.83
		Adult	2010	0.69	0.44	0.86
		Yearling	2011	0.60	0.25	0.90
		Adult	2011	0.72	0.41	0.93
		Yearling	2012	0.08	0.00	0.50
		Adult	2012	0.13	0.01	0.62
		Yearling	2013	0.09	0.00	0.53
		Adult	2013	0.14	0.01	0.64
		Yearling	2014	0.17	0.02	0.66
		Adult	2014	0.25	0.03	0.73
		Yearling	2015	0.22	0.02	0.71
		Adult	2015	0.32	0.04	0.81
		Yearling	2016	0.06	0.01	0.22
		Adult	2016	0.09	0.01	0.29
		Yearling	2017	0.07	0.01	0.22
		Adult	2017	0.11	0.02	0.28
	Survival (*s*)	Yearling	2003	0.67	0.48	0.85
		Adult	2003	0.78	0.62	0.90
		Yearling	2004	0.56	0.37	0.72
		Adult	2004	0.69	0.54	0.81
		Yearling	2005	0.64	0.44	0.82
		Adult	2005	0.75	0.59	0.88
		Yearling	2006	0.56	0.31	0.79

Subpopulation	Population vital rate	Age	Year	Median estimate	Credible interval (CRI)	
					Lower (0.025)	Upper (0.975)
		Adult	2006	0.70	0.48	0.86
		Yearling	2007	0.64	0.45	0.80
		Adult	2007	0.75	0.60	0.87
		Yearling	2008	0.52	0.34	0.68
		Adult	2008	0.66	0.51	0.78
		Yearling	2009	0.65	0.46	0.80
		Adult	2009	0.76	0.61	0.87
		Yearling	2010	0.65	0.46	0.82
		Adult	2010	0.76	0.62	0.88
		Yearling	2011	0.45	0.23	0.66
		Adult	2011	0.60	0.41	0.76
		Yearling	2012	0.60	0.34	0.81
		Adult	2012	0.72	0.50	0.88
		Yearling	2013	0.57	0.31	0.79
		Adult	2013	0.70	0.48	0.86
		Yearling	2014	0.60	0.32	0.81
		Adult	2014	0.72	0.50	0.88
		Yearling	2015	0.68	0.47	0.85
		Adult	2015	0.78	0.62	0.90
		Yearling	2016	0.64	0.46	0.80
		Adult	2016	0.76	0.62	0.86
		Yearling	2017	0.52	0.29	0.71
		Adult	2017	0.66	0.46	0.80

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