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Density-based clustering method for detecting space use patterns, forays, and dispersal in animal tracking data: Case study of translocated desert and Rocky Mountain bighorn sheep

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Research Article

Keywords: Bighorn sheep, excursion, extra-home range movements, Ovis canadensis, space use, translocation

Posted Date: September 10th, 2026

DOI: https://doi.org/10.21203/rs.3.rs-10963067/v1

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Additional Declarations: The authors declare no competing interests.

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Dylan G. Stewart: Conceptualization, Data curation, Formal analysis, Investigation, Methodology, Software, Validation, Visualization, Writing – original draft. **Marcus E. Blum:** Writing – review & editing. **Teresa J. Frink:** Writing – review & editing. **Jonathan A. Jenks:** Funding acquisition, Project administration, Writing – review & editing. **John T. Kanta:** Project administration, Writing – review & editing. **Chadwick P. Lehman:** Writing – review & editing. **E. Alejandro Lozano-Cavazos:** Project administration; resources; supervision; writing – review & editing. **Autumn D. Patterson:** Writing – review & editing. **Ty J. Werdel:** Data curation, Project administration, Supervision, Writing – review & editing. **Stephen L. Webb:** Funding acquisition; project administration; resources; supervision; writing – review & editing.

Acknowledgements

Project funding for the desert sheep project was provided by Texas A&M Natural Resources Institute and the Wild Sheep Foundation (GIA 2425-73). We thank the Artee family, Sierra El Alamo Sonora Wildlife Conservation, and Alcampo Hunting Adventures for their partnership,

and logistical and field support. We thank I.A. Lozano-Sifuentes for assisting with data collection. Financial support for the Rocky Mountain bighorn sheep project was provided by Federal Aid to Wildlife Restoration administered through the South Dakota Department of Game, Fish and Parks (Study Number 7556). We thank the South Dakota Department of Game, Fish and Parks, the Civil Air Patrol, the Deadwood Police Department, the Lawrence County Sheriff's Office, and private landowners in the Deadwood region for their assistance and access to property. We also acknowledge J. Smith and B. Simpson for their contributions during earlier phases of the project, and T. Haffley, K. Cudmore, J. Doyle, J. Clark, and C. Werdel for their support with the monitoring, capture, and humane euthanasia of bighorn sheep throughout the study period. D.G. Stewart was supported by a Merit Fellowship and a Future Faculty Fellowship and A.D. Patterson by a Dr. Dionel Avilés and Dr. James Johnson Fellowship, both through the College of Agriculture and Life Sciences and the Department of Rangeland, Wildlife, and Fisheries Management at Texas A&M University. Scholarships were provided to D.G. Stewart and A.D. Patterson by the Wild Sheep Foundation and Houston Safari Club Foundation.

Declaration of competing interests

The authors declare no competing interests. The funders had no role in the design of the study; in the collection, analyses, or interpretation of data; in the writing of the manuscript; or in the decision to publish the results.

Data availability statement

Reasonable requests for the location data may be made by contacting the corresponding author, Dylan G. Stewart, or through Movebank (Movebank ID 3002591901) for the desert sheep data.

Highlights

- Foraying differed in timing and spatial scale between populations
- Foray occurrence and characteristics differed among range estimators
- Spatial density-based clustering (S-DBC) identified clusters, stopovers, and forays
- S-DBC balanced conservative core delineation with contiguous spatial representation
- S-DBC may facilitate consistent comparisons of forays across populations and species

Abstract

Home range-independent approaches for detecting space use patterns, forays, and dispersal may improve upon home range-based methods, yet comparisons among approaches remain limited. We leveraged location data from 13 (7 F; 6 M) desert bighorn sheep (*Ovis canadensis mexicana*; DBS) restocked in Sonora, Mexico and 18 female Rocky Mountain bighorn sheep (*O. c. canadensis*; RMBS) reintroduced in South Dakota, USA to identify space use patterns and forays. We used a multivariate Bayesian generalized linear mixed-effects model to compare a spatial density-based clustering (S-DBC) framework with fixed-period methods using range isopleths generated from five range estimators. We detected 144 forays for DBS and 91 for RMBS with S-DBC, with maximum distances of 13.7 and 51.1 km, respectively. Forays differed in timing and spatial scale between populations, suggesting influences of environmental conditions, post-release exploration, and resource availability. Foray occurrence and characteristics were sensitive to how areas of use were defined, with substantial differences among range estimators in the number and extent of detected forays. In contrast, S-DBC identified multiple components of space use, including primary and secondary clusters, stopovers, and distance-based forays. S-DBC balanced the conservative delineation of core areas associated with movement-model estimators with the contiguous spatial representation of kernel-

based methods. S-DBC generally detected fewer forays than movement-model estimators but identified forays that were more extensive in duration and distance. Our results demonstrate that S-DBC provides an alternative to fixed-range approaches for characterizing movements beyond areas of use and may facilitate more consistent comparisons of foraying behavior across populations and species.

Keywords

Bighorn sheep, excursion, extra-home range movements, *Ovis canadensis*, space use, translocation

1. Introduction

Animal tracking data have transformed our understanding of animal behavior by revealing where animals move, how they use landscapes, and when these activities occur (Nathan et al. 2008; Cagnacci et al. 2010; Kays et al. 2015). A foundational concept in spatial ecology is the home range, defined by Burt (1943) as “that area traversed by the individual in its normal activities of food gathering, mating, and caring for young.” More recently, the home range has been conceptualized as part of an animal's cognitive map that is maintained for future use, emphasizing spatial memory and dynamic resource use (Powell 2000; Powell and Mitchell 2012; Fagan et al. 2013; Powell 2025). Movements extending beyond an individual's typical area of use, termed extra-home-range movements (hereafter, forays to consolidate terminology; Conradt et al. 2003), were explicitly excluded from Burt's (1943) original home range concept but represent an important component of animal movement ecology (Avril et al. 2014; Debeffe et al. 2014; Gastón et al. 2016).

Approaches for detecting forays can be broadly categorized according to whether they are home range-based or home range-independent and whether they rely primarily on spatial or

116 spatiotemporal information (Fig. 1). Home range-based approaches identify movements
117 extending beyond a boundary of estimated area of use, whereas home range-independent
118 approaches identify atypical movements directly from animal locations or movement trajectories
119 without requiring a predefined spatial boundary. Home range-based approaches include fixed-
120 period and moving-window home range methods (Jacobsen et al. 2020), whereas home range-
121 independent approaches include clustering-based methods (Ester et al. 1996; Birant and Kut
122 2007; Damiani et al. 2014, 2015, 2018), such as density-based spatial clustering of applications
123 with noise (DBSCAN), spatiotemporal-DBSCAN (ST-DBSCAN), and sequential scan
124 (SeqScan), as well as behavioral-state models such as hidden Markov models (Langrock et al.
125 2012). These approaches can be further distinguished by their treatment of time. Spatial methods
126 rely primarily on the spatial distribution of locations, whereas spatiotemporal methods
127 incorporate both the spatial arrangement and temporal sequence of movements. Under this
128 framework, spatial methods include fixed-period methods and DBSCAN, whereas
129 spatiotemporal methods include moving-window methods, ST-DBSCAN, and SeqScan. Spatial
130 methods may therefore be particularly useful for quantifying the extent and distribution of
131 forays, whereas spatiotemporal methods can provide additional information about movement
132 timing, duration, and behavioral context, which may be particularly valuable for understanding
133 the spatial ecology of migrations (Sawyer and Kauffman 2011; Blum et al. 2015; Monteith et al.
134 2018; Kauffman et al. 2023).
135 A common home range-based approach is the fixed-period method, which estimates an
136 individual's area of use over a predefined period, typically at seasonal or annual scales
137 (Kolodzinski et al. 2010; Sullivan et al. 2017; Kamler et al. 2019), and identifies movements
138 extending beyond the resulting range boundary as forays (Lovari et al. 2008; Karns et al. 2011;

Jacobsen et al. 2020). Alternatively, moving-window methods estimate an individual's area of use from a user-defined temporal window and evaluate subsequent locations relative to this dynamically updated boundary (Messinger et al. 2019; Jacobsen et al. 2020). The window then advances sequentially through the movement trajectory, allowing forays to be evaluated continuously through time (Jacobsen et al. 2020). Thus, fixed-period methods rely primarily on the spatial distribution of locations within a predefined period, whereas moving-window methods incorporate temporal information by repeatedly updating the area of use as new locations are collected. Both approaches commonly incorporate spatial and temporal thresholds, individually or in combination, to distinguish forays from other movement behaviors (Messier 1985; Olson et al. 2015; Lutz et al. 2016).

Despite their utility, home range-based approaches have several limitations. Fixed-period methods can incorporate forays into the estimated home range, hindering the ability to detect some forays (Jacobsen et al. 2020). Moving-window methods address this limitation by allowing home ranges to change through time but cannot evaluate forays occurring during the initial window, which commonly spans 30–60 days (Jacobsen et al. 2020; Hooven et al. 2023). This limitation is particularly important following capture, release, or translocation when animals may exhibit pronounced exploratory movements in unfamiliar environments (Liang et al. 2026; Stewart et al. 2026*e*,*f*,*i*) and movement responses may be of ecological and management interest (Berger-Tal et al. 2014; Berger-Tal and Saltz 2014; Berger-Tal and Blumstein 2024). Additionally, all home range-based methods are sensitive to estimator selection, bandwidth, data retention, and other methodological decisions, which may produce varying estimates of space use (Powell 2000; Powell and Mitchell 2012; Signer et al. 2015; Werdel et al. 2021). For example, foray classification can be an artifact of the selected home range boundary (Mancinelli

and Ciucci 2018). A 100% isopleth encompasses all observed locations and identifies no forays, whereas a 95% isopleth excludes approximately 5% of locations, by definition, without necessarily identifying biologically meaningful excursions. Thus, whether a movement is classified as a foray may depend more on the selected estimator and isopleth than on characteristics of the movement itself (Mancinelli and Ciucci 2018). Home range-independent approaches, which identify forays directly from movement data without requiring a predefined home range boundary, may overcome these limitations, but their application to foray detection remains limited (Cisneros-Araujo et al. 2024; Ricci et al. 2024; Pantelić et al. 2026).

Bighorn sheep (*Ovis canadensis*) provide a useful system for evaluating such approaches. Populations have declined and experienced substantial range contraction since the late 1800s because of habitat degradation, disease, competition, and other factors (Valdez et al. 2026; Lutz et al. 2026). Translocations have become an important conservation tool for restoring and reconnecting populations (Krausman 2000; WSWG 2015; Whiting et al. 2023*b*; Lutz and Bleich 2026); however, disease, particularly respiratory disease associated with pneumonia, remains a major threat to population persistence (Sells et al. 2015; Cassirer et al. 2018; Miller et al. 2026). Forays may facilitate connectivity and gene flow among isolated populations (Festa-Bianchet 1986; Epps et al. 2018) but may also increase opportunities for pathogen transmission (Carpenter et al. 2014; O'Brien et al. 2014; Anderson et al. 2022). Translocated animals frequently undertake exploratory movements following release into unfamiliar environments (Le Gouar et al. 2012; Bell 2016; Lutz and Bleich 2026), making translocated populations especially useful for evaluating foray detection methods and movement patterns.

Home range-independent approaches for detecting forays have the potential to improve upon traditional home range-based methods; however, these approaches remain relatively

185 untested, and structured comparisons among methods are needed (Cisneros-Araujo et al. 2024;
186 Ricci et al. 2024; Pantelić et al. 2026). Therefore, we leveraged location data from a desert
187 bighorn sheep (*O. c. mexicana*; hereafter, DBS; proposed reclassification to *O. c. nelsoni*; Epps
188 et al. 2026; Jahner et al. 2026) restocking effort in Sonora, Mexico, and a Rocky Mountain
189 bighorn sheep (*O. c. canadensis*; hereafter, RMBS) reintroduction effort in South Dakota, USA,
190 to evaluate the performance of a spatial density-based clustering framework (hereafter, S-DBC
191 method) for detecting forays. Specifically, our objectives were to: (1) apply the S-DBC method
192 to identify patterns of space use and detect forays and dispersal movements in bighorn sheep
193 location data; and (2) compare space use and foray characteristics between the S-DBC method, a
194 spatial, home range-independent method, and fixed-period methods, a spatial, home range-based
195 approach, using range polygons generated from autocorrelated kernel density estimation
196 (AKDE), Brownian bridge movement models (BBMMs), dynamic Brownian bridge movement
197 models (dBBMMs), fixed kernel density estimation (KDE), and minimum convex polygons
198 (MCPs; Fig. 1).

199 **2. Materials and methods**

200 **2.1 Desert bighorn sheep**

201 **2.1.1 Study area**

202 The source population of DBS was located at Alcampo Ranch (29.127397º N,
203 111.377069º W), a 15.6-km² property enclosed by a 2.4-m-high chain-link fence near
204 Hermosillo, northwestern Sonora, Mexico (Ordoñez 1936). Here, we provide a consolidated
205 description of the study area, capture and handling procedures, and data collection protocols for
206 the case study. Additional details for the DBS case study are available in Acosta et al. (2026) and
207 Stewart et al. (2026*a–e*), and detailed descriptions of the RMBS case study are provided by

Werdel et al. (2018, 2020, 2021, 2023) and Stewart et al. (2026*f*). The elevation ranged from 129 to 465 m above sea level and the slope varied from 0 to 38 degrees (USGS 2021). Average monthly temperatures ranged from a low of 16°C in December and January to a high of 32°C in July and August; monthly precipitation ranged from lows in March through June (mean of 2 mm) to highs in July through September (mean of 54 mm; CD n.d.*a*). Plant growth cycles were assumed to be comparable to those observed at Sierra El Alamo.

We translocated the cohort of DBS to Sierra El Alamo (30.655912º N, 112.587282º W), located near Caborca in the Sonoran Desert of northwestern Sonora, Mexico, to augment (restock) a high-density resident population of ~300 individuals (Ordóñez 1936). The property contained a network of 30 low-elevation, permanent water sources constructed for wildlife, with a local density of 1 source per 1.44 km². The study area was comprised of several desert vegetation communities, including sandy desert vegetation, sarcocaule scrub, microphyllous desert scrub, and halophytic desert scrub (INEGI 2010). The flora was dominated by creosotebush (*Larrea tridentata*), white bursage (*Ambrosia dumosa*), cardón (*Pachycereus pringlei*), paloverde (*Parkinsonia* spp.), tree ocotillo (*Fouquieria* spp.), ironwood (*Olneya tesota*), elephant tree (*Bursera microphylla*), and limberbush (*Jatropha cardiophylla*; Tarango et al. 2002; Dimmitt 2015). The elevation ranged from 31 to 889 m above sea level and the slope varied from 0 to 48 degrees (USGS 2021). Average monthly temperatures ranged from a low of 14°C in December to a high of 33°C in July and August; monthly precipitation ranged from lows in April through June (mean of 2 mm) to highs in July through September (mean of 32 mm; CD n.d.*b*). Vegetation greenness was lowest in July, greatest in September, and relatively high from October through February (Drusch et al. 2012).

2.1.2 Capture & handling

We used alfalfa (*Medicago sativa*) and protein pellets as supplemental feed to attract DBS to capture corrals beginning in September 2022; we captured 16 individuals (9 F, 7 M) on 16 November 2022 for subsequent translocation. Following capture, we recorded the sex of each individual and estimated age based on horn characteristics for males and teeth wear methods for females described in Geist (1966). We fitted each individual with a Vectronic Aerospace Vertex Lite or Plus Iridium neck collar (Vectronic Aerospace GmbH, Berlin, Germany), programmed to acquire one GPS fix every 3 hours, beginning at 0200 MST daily. Prior to capture, we conducted stationary tests and used the centroid method described by Stewart et al. (2026*g*) to estimate horizontal GPS error (m) for each collar. Following capture and initial processing, we held the DBS in a 1-ha holding pen at Alcampo Ranch for 4 days (16–20 November). On 21 November, we transported the animals approximately 200 km northwest to Sierra El Alamo where we placed them in an 8-ha acclimation enclosure to facilitate a soft-release protocol (Lonner et al. 2024). Sheep remained in the acclimation enclosure for 7 days (21–28 November) before release. Upon release, individuals promptly exited the enclosure and ascended the nearest mountain, generally moving in groups (Stewart et al. 2026*c*).

2.2 Rocky Mountain bighorn sheep

2.2.1 Study area

The source population of RMBS was located at the Luscar Mine in Alberta, Canada (53.065939º N, 117.412967º W), where approximately 1,000 resident RMBS resided at the reclaimed mine site (Teck 2012). Mining operations created a series of benches across the landscape that provided suitable escape terrain adjacent to reclaimed grasslands (MacCallum and Geist 1992). Elevations ranged from 1,680 to 1,860 m above sea level (MacCallum 2012).

We translocated the RMBS to a private property (44.349597° N, 103.707955° W) in the Deadwood ecoregion of the northern Black Hills, Lawrence County, South Dakota, USA, approximately 3.5 km SW of Deadwood (SDGFP 2013). The region comprised a heterogeneous landscape of canyons, mountains, and valleys (Hoffman and Alexander 1987), interspersed with areas of reclaimed mining activity, including the Homestake and Gilt Edge mines. Elevations ranged from 1,073 to 2,209 m above sea level, with mean annual snowfall and precipitation of 379 cm and 34–46 cm, respectively (Hoffman and Alexander 1987; NOAA 2017). The landscape was dominated by ponderosa pine (*Pinus ponderosa*) forests, with stands of quaking aspen (*Populus tremuloides*) and paper birch (*Betula papyrifera*) occurring throughout the region (McIntosh 1949; Orr 1959; Hoffman and Alexander 1987; Thilenius 1972; Richardson and Peterson 1974). Bighorn sheep historically inhabited the region but were extirpated by the early 1900s (Valdez 2026), and no established population was present in the area prior to our study.

2.2.2 Capture & handling

We used alfalfa hay to attract RMBS to 2 capture sites at the Luscar Mine beginning one week prior to the initial capture. We captured 26 RMBS on the morning of 11 February 2015 using modified 18 × 18-m electromagnetic drop nets positioned over bait sites (Jedrzejewski and Kamler 2004). We determined sex and estimated age using the same procedures described for DBS (Geist 1966; Hemming 1969; Krausman and Bowyer 2003). We fitted 22 adult RMBS (21 F, 1 M) with Advanced Telemetry Systems (ATS) Model 2110D GPS collars (Advanced Telemetry Systems, Isanti, Minnesota, USA), programmed to acquire and store a GPS location fix every 5 h. We released the RMBS onto private property on 12 February 2015. All capture, handling, marking, and transport procedures were approved by the Texas A&M AgriLife Animal Care and Use Committee (AUP #2022-022A; AUP #2025-024A) for DBS and by the South

Dakota State University Institutional Animal Care and Use Committee (Approval No. 14-096A) for RMBS. All procedures followed guidelines established by the American Society of Mammalogists (Sikes and the ACUC-ASM 2016).

2.3 Data collection & preparation

We remotely downloaded GPS location data from collars deployed on DBS and retrieved location data from collars deployed on RMBS upon collar recovery. We calculated straight-line (Euclidean) distance and the time elapsed between sequential locations. To standardize the length of deployment between studies, we truncated location data to one year beginning the day after release (DBS: 29 November 2022–28 November 2023; RMBS: 13 February 2015–12 February 2016). All data processing was conducted in R statistical software (v. 4.3.0; R Core Team 2023); we primarily used the move (v. 4.2.6; Kranstauber et al. 2024) and sf packages (v. 1.0-19; Pebesma 2018; Pebesma and Bivand 2023).

2.4 Spatial Density-based clustering method

To address our first objective, we developed a S-DBC framework to classify GPS location data into biologically meaningful space-use and movement patterns, including primary and secondary clusters, stopovers, transient movements, and forays (Fig. 2). Forays were further categorized as short-, mid-, or long-distance based on population-specific distance breakpoints and classified according to their relationship with established space-use networks as returning forays, non-returning forays, or start and end forays when network associations could not be identified due to the beginning or end of the monitoring period. The framework combined spatial density-based clustering, breakpoint analyses, and spatial relationships among recursive space-use areas and movement sequences to distinguish persistent space use from forays and dispersal events.

First, location data for each individual were clustered independently using the DBSCAN algorithm (Ester et al. 1996). The DBSCAN algorithm identifies clusters of locations based on a specified neighborhood distance (ε) and minimum number of neighboring locations, while assigning isolated locations to noise. The minimum number of locations required to form a cluster was standardized among individuals by converting a user-defined minimum cluster duration into an equivalent number of GPS fixes using each individual's median sampling interval. For both case studies, we used a minimum cluster duration of 2 days. To identify an appropriate ε, we conducted a population-level sensitivity analysis by iteratively fitting DBSCAN across neighborhood distances ranging from 50 to 2,000 m in 50-m increments. For each neighborhood distance, we calculated the number of clusters identified for each individual and modeled the relationship between neighborhood distance and mean cluster number using segmented regression. The estimated breakpoint was obtained by bootstrapping individuals with replacement (1,000 iterations) and was selected as the optimal neighborhood distance because it represented the point beyond which increasing ε produced relatively small reductions in the number of detected clusters (DBS: 362 m [95% CI: 285–411]; RMBS: 781 m [95% CI: 482–879]).

Second, using the selected neighborhood distance, DBSCAN was rerun independently for each individual to identify spatial clusters representing areas of repeated use. Cluster duration was calculated as the number of days represented by each cluster while accounting for individual-specific sampling intervals. Cluster durations were modeled using Gaussian finite mixture models to identify natural groupings in persistence. Confidence intervals around mixture means were estimated using nonparametric bootstrap resampling (1,000 iterations). The models identified four mixture components for each population (DBS: 2.9 d [95% CI: 2.0–3.3], 8.9 d

[95% CI: 3.2–12.6], 47.6 d [95% CI: 8.4–82.2], and 291.2 d [95% CI: 148.8–326.2]; RMBS: 2.3 d [95% CI: 1.9–10.4], 5.5 d [95% CI: 3.8–10.4], 28.7 d [95% CI: 5.5–99.9], and 312.0 d [95% CI: 182.7–333.1]). Because the confidence intervals of the two shortest-duration components overlapped substantially, they were combined into a single short-duration class. Clusters were subsequently classified according to duration, with clusters ≤ the upper 95% confidence limit of the second mixture classified as stopovers, clusters > the upper 95% confidence limit of the second mixture and ≤ the upper 95% confidence limit of the third mixture classified as secondary clusters, and clusters > the upper 95% confidence limit of the third mixture classified as primary clusters. Locations not assigned to clusters were initially classified as transient movements, representing periods of movement between recursively used areas. This approach provided an objective, data-driven framework for distinguishing classes of spatial persistence and defining stopovers and longer-duration recursively used areas based on the empirical distribution of cluster durations rather than relying on a priori or subjective thresholds.

Third, to distinguish forays from movements occurring within an individual's established space-use network, distances between transient movement sequences or stopover locations and primary or secondary clusters were calculated. For stopovers, straight-line distance was calculated between stopover centroids and the nearest primary or secondary cluster. For transient movement sequences, the maximum distance between any location within the sequence and the nearest primary or secondary cluster was calculated. Distances were ranked and analyzed using segmented regression with two estimated breakpoints to identify thresholds (DBS: 1,061-m, 3,127-m; RMBS: 3,198-m, 10,165-m) used to classify excursions into three distance-based foray categories: short-, mid-, and long-distance forays. Short-distance forays represented excursions with the smallest displacement from established space-use areas and may represent movements

along the periphery of established ranges, whereas mid- and long-distance forays represented progressively greater departures from these areas. Consecutive locations classified as forays were combined into biological foray events. Each foray was extended by one location before departure and one location after the excursion to capture the complete movement sequence. Isolated single-location excursions were classified as noise to reduce the potential for erroneous GPS fixes to be classified as forays (Deuel et al. 2017; Ryder 2026). Thus, a foray was defined as a discrete movement event extending beyond the established primary and secondary space-use network, containing >1 consecutive location classified according to the population-specific distance thresholds.

Fourth, because individuals frequently maintained multiple spatially distinct primary and secondary clusters, clusters separated by less than the threshold distinguishing short- from mid-distance forays were connected into common primary–secondary cluster networks using graph theory. An adjacency matrix was constructed by connecting clusters when their minimum inter-cluster distance was less than the distance threshold. Connected components of the resulting undirected graph defined discrete primary–secondary cluster networks. Forays were then classified according to their relationship with primary–secondary cluster networks. Forays that originated and terminated within the same cluster network were classified as returning forays. Forays that originated and terminated in different cluster networks were classified as non-returning forays. In rare cases where a foray occurred at the beginning or end of the monitoring period, such that an associated cluster network could not be identified before departure or after termination, these events were classified as start forays or end forays, respectively. Thus, unlike fixed-period approaches in which forays are conceptualized around returns to the area of departure (home range; Singer et al. 2001; Jacobsen et al. 2020) and classification can depend on

368 the selected range estimator and isopleth, we defined forays as movements beyond established
369 cluster networks, representing subcomponents of an individual's broader range. Non-returning
370 forays therefore represented movements between discrete established networks (Resop et al.
371 2024; Stewart et al. 2026*j*). Dispersal events, defined as one-way movements resulting in
372 establishment of a new area of use, typically observed in adolescent animals (Howard 1960;
373 Debeffe et al. 2013; Ellis et al. 2025), were not observed during the study, although the
374 framework could be used to identify them. For each foray, we recorded type (short-, mid-, long-
375 distance; non-returning, returning, start, end), start and end times, duration (d), total distance
376 traveled (km), maximum displacement from primary or secondary clusters (km), and associated
377 cluster networks (Jacobsen et al. 2020; Ladd et al. 2024).

378 Fifth, to quantify the spatial extent and fragmentation of S-DBC-derived space-use areas
379 for comparison with conventional home-range estimators, we delineated a concave hull around
380 the locations comprising each primary and secondary cluster. For each individual, locations
381 assigned to primary and secondary clusters were grouped by cluster, and a concave hull was
382 generated around the locations within each cluster using a concavity ratio of 0.2 (Downs and
383 Horner 2009). Hulls were calculated independently for each cluster to retain the spatial
384 separation among discrete areas of repeated use. Hull area was calculated (km^2), and the areas of
385 all primary and secondary cluster hulls were summed for each individual to obtain total S-DBC
386 space-use area. We also recorded the number of discrete primary and secondary cluster hulls for
387 each individual. These measures quantified the total spatial extent and fragmentation of
388 recursively used areas and facilitated comparison with the annual 95% home-range area and
389 number of spatial components derived from the fixed-period estimators. The S-DBC framework
390 was primarily implemented using the R packages boot (v. 1.3-32; Davison and Hinkley 1997;

Canty and Ripley 2025), dbscan (v. 1.2.5; Hahsler et al. 2019; Hahsler and Piekenbrock 2026), igraph (v. 2.1.4; Csárdi and Nepusz 2006; Csárdi et al. 2025), mclust (v. 6.1.2; Scrucca et al. 2023), and segmented (v. 2.1-4; Fasola et al. 2018; Muggeo 2003; 2008; 2016; 2017; Muggeo et al. 2014).

2.5 Fixed-period method

To address our second objective, comparing our S-DBC method to the conventional fixed-period method, we identified forays using five commonly applied home-range estimators: fixed KDE (Worton 1987; 1989; Seaman and Powell 1996), MCP (Schoener 1981), BBMM (Horne et al. 2007), dBBMM (Kranstauber et al. 2012), and AKDE (Fleming et al. 2015) output from continuous time movement modeling. We selected these estimators based on their widespread use in studies evaluating EHRMs (Kamler and Gipson 2000; Skuldt et al. 2008; Ward et al. 2014; Foley et al. 2015; Celis-Murillo et al. 2017; Gaughran et al. 2018) and, more broadly, in animal movement ecology (Seaman and Powell 1996; Powell 2000; Fleming et al. 2015; Stewart et al. 2026*h*). Home ranges were estimated independently for each individual using all available locations.

Fixed KDE home ranges were estimated using the reference bandwidth (href) smoothing parameter and a 100-cell grid. BBMMs were parameterized by estimating the Brownian motion variance through maximum likelihood while fixing location error at 2 m. dBBMMs were estimated using a sliding window of 33 locations with an 11-location margin and a location error of 2 m. AKDEs were generated by fitting continuous-time movement models to each individual's telemetry data and estimating the 95% utilization distribution. For all estimators, 95% utilization distributions were extracted and annual home-range area (km^2) was calculated. We also quantified the number of spatially discrete polygon components comprising each 95% home-

range estimate. Component number was calculated independently for each individual and estimator by counting the discrete polygon features within each 95% home-range estimate. These measures provided estimates of both the spatial extent and fragmentation of home ranges for comparison among estimators and with the space-use areas identified by S-DBC.

For each estimator, telemetry locations were classified as either inside or outside the corresponding 95% home-range polygon. Consecutive sequences containing at least two locations outside the home range were identified as forays (Deuel et al. 2017; Ryder 2026). For each foray, maximum displacement from the corresponding home-range polygon was calculated as the maximum straight-line distance between any location in the foray and the nearest point on the home-range boundary. Forays were retained regardless of displacement and subsequently classified according to the species-specific distance thresholds previously identified from the S-DBC distance breakpoint analysis. These thresholds were used to distinguish short-, mid-, and long-distance forays, with movements at or below the short-foray threshold classified as short forays, movements greater than the short-foray threshold and at or below the mid-foray threshold classified as mid forays, and movements exceeding the mid-foray threshold classified as long forays.

For each foray, the movement sequence was extended by one telemetry location immediately preceding departure from the home range and one location immediately following re-entry to capture movement associated with departure and return. Total distance traveled was calculated along the observed movement path, including distances between telemetry locations and the estimated points at which the movement path crossed the home-range boundary. Foray duration was calculated as the elapsed time between the beginning and end locations of the extended sequence. The same foray metrics calculated for the S-DBC method were recorded,

including number of forays, foray duration (d), total distance traveled (km), and maximum displacement (km) (Jacobsen et al. 2020; Ladd et al. 2024). For each estimator, forays were subsequently categorized as short-, mid-, or long-distance using the population-specific S-DBC distance thresholds. This procedure was repeated independently for each of the five home-range estimators to facilitate direct comparison with the S-DBC framework. The fixed-period method was implemented primarily using the R packages adehabitatHR (v. 0.4.22; Calenge 2024*a*), adehabitatLT (v. 0.3.28; Calenge 2024*b*), and ctmm (v. 1.1.0; Fleming and Calabrese 2022; Fleming et al. 2015; Fleming and Calabrese 2017).

2.6 Statistical analysis

To address our second objective, we used a multivariate Bayesian generalized linear mixed-effects model to evaluate how foray characteristics varied among space-use estimators and study populations and whether variation in foray behavior was associated with characteristics of the estimated home range. For each individual–estimator combination, we quantified four characteristics of detected forays: number of forays, foray duration (d), total distance traveled during forays (km), and maximum distance traveled during a foray (km). Each response included fixed effects for estimator (six levels: S-DBC, AKDE, BBMM, dBBMM, KDE, and MCP), home-range area, home-range complexity (number of spatial components), and study population (two levels: DBS, RMBS). We modeled the number of forays using a Poisson distribution with a log link and foray duration, total distance, and maximum distance using Gamma distributions with log links. We included individual sheep identifier as a random intercept, with a shared multivariate grouping structure allowing individual-level random effects to be estimated jointly among response variables.

459 The multivariate formulation allowed correlations among individual-level variation in the
460 four foray characteristics to be estimated simultaneously rather than treating each response as an
461 independent analysis. We fitted the models using four Markov chain Monte Carlo chains with
462 4,000 iterations per chain, including 2,000 warm-up iterations. We assessed model convergence
463 using the Gelman–Rubin potential scale reduction factor ($\hat{R}$) and evaluated sampling efficiency
464 using bulk and tail effective sample sizes (ESS) (Gelman and Rubin 1992; Vehtari et al. 2021).
465 Model adequacy was evaluated using posterior predictive checks, comparing observed response
466 distributions with distributions generated from the posterior predictive distribution. Posterior
467 predictive checks were conducted separately for each response, using replicated frequency
468 distributions for the number of forays and density overlays for foray duration, total distance
469 traveled, and maximum distance traveled.
470 We summarized posterior parameter estimates using posterior means and 95% credible
471 intervals. For categorical predictors, we calculated estimated marginal means for each estimator
472 and population, with predictions averaged over the remaining model predictors. We evaluated
473 pairwise differences among estimators and populations from the posterior distributions of the
474 marginal means. To facilitate interpretation and visualization, we generated compact letter
475 displays from posterior pairwise comparisons using a 0.05 probability threshold. For continuous
476 predictors, we generated marginal predictions across the observed ranges of home-range area and
477 home-range complexity while averaging over estimator, population, and the remaining model
478 terms. We back-transformed predictions and associated 95% credible intervals to the response
479 scale for presentation. All analyses were conducted in R using the brms (v. 2.22.0; Bürkner 2017;
480 2018; 2021) and emmeans packages (v. 1.10.7; Lenth 2025); compact letter displays were

generated using the multcomp (v. 1.4.-28; Hothorn et al. 2008) and multcompView packages (v. 0.1-10; Graves et al. 2024).

3. Results

The DBS dataset comprised 13 adults (7 F, 6 M) (≥2.5 years old at capture) after excluding 3 individuals that died before completing the first year of data collection (Stewart et al. 2026*a*). The RMBS dataset comprised 18 adult females after excluding individuals based on censoring criteria, including premature mortality, delayed initiation of data collection, and an unrecoverable collar (Stewart et al. 2026*f*). The mean fix success rates of the DBS and RMBS datasets were 98.3% and 97.0%, respectively, and the mean horizontal location error of the DBS dataset was 2.0 m.

3.1 Desert bighorn sheep

We detected 98 short- (max distance from primary or secondary cluster = ≤1,061-m), 34 mid- (1,062–3,127-m), and 12 long-distance forays (≥3,128-m), resulting in 144 forays among 13 DBS (Fig. 3a). Of the 13 DBS, 86% of females (6 of 7 individuals) and 100% of males (6 of 6 individuals) conducted short-distance forays, 86% (6) of females and 67% (4) of males conducted mid-distance forays, and 43% (3) of females and 67% (4) of males conducted long-distance forays. Across individuals, females conducted an average of 9.6 forays (SE = 3.1; range = 3–23), whereas males conducted an average of 12.8 forays (SE = 3.6; range = 5–28), resulting in an overall mean of 11.1 forays per individual (SE = 2.3; range = 3–28). Of the 144 forays detected, 97.2% (140) were returning, 1.4% (2) were non-returning, and 1.4% (2) were end forays. Mean total distance traveled during forays was 6,850 m (SE = 843; range = 477–38,087) for females and 5,707 m (SE = 1,027; range = 132–65,070) for males. Mean maximum distance traveled among forays was 1,542 m (SE = 200; range = 37–7,710) for females and 1,110 m (SE

= 202; range = 48–13,749) for males. We detected that 10 (5 F; 5 M) individuals visited 34 stopovers 116 times. Mean duration per visit at stopovers was 1.3 d (SE = 0.2; range = 0.1–10.0) for females and 1.4 d (SE = 0.2; range = 0.1–8.1) for males.

Foray initiation and termination times exhibited unimodal distributions, with peak initiation occurring at approximately 1100 and termination occurring from 0800 to 2000 (Fig. 4). Following release, the proportion of individuals residing in primary clusters increased to >80% at approximately 165 days (12 May 2023), coinciding with an apparent inverse pattern in the proportion of individuals residing in secondary clusters (Fig. 5a). Short-distance forays occurred sporadically throughout the study period, whereas mid- and long-distance forays occurred primarily between 39 and 166 days post-release (6 January–13 May).

3.2 Rocky Mountain bighorn sheep

We detected 48 short- (max distance = 0–3,198-m), 27 mid- (3,199–10,165-m), and 16 long-distance forays (≥10,166-m), resulting in 91 forays among 18 RMBS (Fig. 3b). Of the 18 individuals, 94% (17 of 18 individuals), 89% (16), and 67% (12) conducted short-, mid-, and long-distance forays, respectively. Across individuals, RMBS conducted an average of 5.1 forays (SE = 0.7; range = 2–10). Of the 91 forays detected, 85.7% (78) were returning, 1.1% (1) was non-returning, and 13.2% (12) were start forays. Mean total and max distance traveled during forays was 17,804 m (SE = 2,068; range = 539–142,619) and 5,213 m (SE = 670; range = 509–51,147), respectively. We detected that 17 individuals visited a total of 47 stopovers 101 times, averaging 1.9 d/visit (SE = 0.1; range = 0.2–6.9) at stopovers. Following release, the proportion of individuals residing in primary clusters increased to 100% at 155 days post-release (17 July 2015), coinciding with an apparent inverse pattern in the proportions of individuals residing in

secondary clusters and conducting short-distance forays (Fig. 5b). Mid- and long-distance forays occurred mostly between 1 and 128 days post-release (13 February–20 June).

3.3 Methods comparison

The multivariate Bayesian model showed good convergence and sampling performance, with $\hat{R}$ values ranging from 0.999 to 1.002 across all model parameters. Bulk ESS ranged from approximately 2,500 to 13,600, while tail ESS ranged from approximately 4,100 to 7,100, indicating adequate sampling efficiency. Posterior predictive checks indicated that the model generally reproduced the observed distributions of all four foray characteristics, supporting the adequacy of the model for inference. Full model results are available in Table S1.

Foray characteristics varied among space use estimators and between populations, although the magnitude and direction of differences depended on the response variable (Fig. 6; Table S1). Movement models (BBMM: 8.8 [95% CrI: 6.5–11.3]; dBBMM: 22.4 [95% CrI: 18.4–26.5]) estimated more forays than kernel estimators (KDE: 4.8 [95% CrI: 3.8–6.0]; AKDE: 4.9 [95% CrI: 3.8–6.2]), with S-DBC intermediate (6.7 [95% CrI: 5.3–8.2]; Fig. 6a). An opposite pattern was observed for maximum distance, with kernel estimators (KDE: 1.8 km [95% CrI: 1.4–2.3]; AKDE: 2.0 km [95% CrI: 1.5–2.6]) generally estimating greater maximum distances than movement models (BBMM: 1.1 km [95% CrI: 0.7–1.6]; dBBMM: 1.0 km [95% CrI: 0.7–1.2]; Fig. 6g). A similar pattern was observed for total distance, although most Bayesian pairwise comparisons indicated no credible differences among estimators (Fig. 6d). S-DBC estimated the greatest foray duration (2.9 d [95% CrI: 2.2–3.7]; Fig. 6c), total distance (10.1 km [95% CrI: 7.5–13.4]; Fig. 6e), and maximum distance (2.4 km [95% CrI: 1.8–3.2]; Fig. 6g). Foray characteristics also differed between populations. DBS had a greater estimated number of forays (10.5 [95% CrI: 8.1–13.7]) than RMBS (6.5 [95% CrI: 5.2–8.2]; Fig. 6b), whereas foray duration

549 (Fig. 6d), total distance (Fig. 6f), and maximum distance (Fig. 6h) were lower for DBS (1.5 d
550 [95% CrI: 1.2–1.9], 3.4 km [95% CrI: 2.5–4.5], 0.8 km [95% CrI: 0.6–1.1], respectively) than
551 RMBS (2.6 d [95% CrI: 2.2–3.2], 10.0 km [95% CrI: 7.8–12.7], 2.9 km [95% CrI: 2.3–3.7],
552 respectively).

553 After accounting for space use estimator and population, the number of forays decreased
554 with increasing home range area (β = -0.30, 95% CrI: -0.44 –-0.18), with 9.5 forays (95% CrI:
555 7.8–11.3) predicted at 0.9 km^2 compared with 0.5 forays (95% CrI: 0.1–1.4) at 861.4 km^2 (Fig.
556 7a; Table S2). In contrast, total distance (β = 0.10, 95% CrI: -0.03–0.23; Fig. 7e) and maximum
557 distance (β = 0.11, 95% CrI: -0.01–0.24; Fig. 7g) showed positive associations with home range
558 area, although their 95% credible intervals included zero. Foray duration decreased with
559 increasing number of range components (β = -0.18, 95% CrI: -0.35–-0.01), with predicted
560 duration declining from 2.2 d (95% CrI: 1.8–2.7) at one range component to 0.8 d (95% CrI: 0.3–
561 1.7) at 21 components (Fig. 7d). The number of forays showed a positive association with the
562 number of range components (β = 0.08, 95% CrI: -0.02–0.17; Fig. 7b), whereas maximum
563 distance (β = -0.12, 95% CrI: -0.30–0.06; Fig. 7h) showed a negative association; however, the
564 credible interval for the effect included zero.

565 **4. Discussion**

566 Our results demonstrate that forays are an important component of space use in bighorn
567 sheep populations (Bleich et al. 1990; 1996; Singer et al. 2000*a*; 2000*b*; 2001; Whiting et al.
568 2023*a*), but the timing and spatial scale of foraying differed between restocked DBS and
569 reintroduced RMBS. The contrasting timing of foraying between populations further suggests
570 that movement beyond established areas of use may reflect intrinsic and environmental drivers,
571 including post-release exploration, resource availability, landscape composition and structure,

and thermal and abiotic conditions. Foray occurrence and characteristics were also sensitive to how areas of use were defined, with substantial differences among range estimators in the number and spatial extent of detected forays. In contrast, S-DBC provided a flexible framework for identifying multiple components of movement and space use, including primary and secondary clusters, stopovers, and distance-based forays, while capturing forays that were generally fewer than those identified by movement-model estimators but more extensive in duration and distance. By deriving spatial and temporal thresholds from population-level movement distributions, S-DBC provides an alternative to fixed-range approaches for characterizing movement beyond areas of use and may facilitate more consistent comparisons of foraying behavior among populations and species.

Across all foray classes, we observed an annual foray probability (O'Brien et al. 2014) of 1.00 for DBS and RMBS, with corresponding annual foray rates (number of forays/individual/animal-year; Singer et al. 2001) of 11.1 and 5.1 forays, respectively. When restricted to mid- and long-distance forays, annual foray probability decreased to 0.85 for DBS (11 of 13 individuals) and 0.94 for RMBS (17 of 18 individuals), with corresponding annual foray rates of 3.5 and 2.4 forays, respectively. These annual foray probabilities and rates were generally greater than those reported in previous studies of bighorn sheep (Singer et al. 2001; DeCesare and Pletscher 2006; Carpenter et al. 2014; O'Brien et al. 2014; Marcisz 2021; Dekelaita et al. 2023; Ryder 2026), although direct comparisons among studies are difficult because of differences in foray criteria, particularly duration and distance thresholds, definitions, temporal scope, and reporting metrics. The relatively high foray probabilities and rates observed in our study likely reflect, at least in part, our broader definition of a foray as movement outside an individual's core area of use rather than beyond a population boundary, which can result in

595 greater foray detection (Marcisz 2021), inclusion of long-distance movements between discrete
596 established networks (Resop et al. 2024; Stewart et al. 2026*j*), as well as the increased
597 exploratory behavior expected following introduction into a novel environment (Le Gouar et al.
598 2012; Bell 2016; Liang et al. 2026; Lutz and Bleich 2026; Stewart et al. 2026*e*,*f*). Variation in the
599 spatial and temporal thresholds used to distinguish forays from other movements can make
600 comparisons among studies challenging (Jacobsen et al. 2020). We therefore suggest that foray
601 thresholds either be defined from the observed distribution of movement distances, as in our
602 study, or evaluated relative to standardized distance-based criteria, such as fixed buffer zones
603 (O'Brien et al. 2014; Marcisz 2021).
604 We found that DBS primarily conducted mid- and long-distance forays 39–166 days post-
605 release (25 Jan.–13 May), with long-distance forays peaking 149–153 days post release (26
606 April–01 May), whereas RMBS forayed 1–128 days post-release (6 Jan.–20 June). The
607 immediate and elevated foray activity exhibited by reintroduced RMBS was expected, as animals
608 introduced into novel environments often exhibit a short-term period of exploration to acquire
609 knowledge about the location and distribution of resources (Le Gouar et al. 2012; Berger-Tal et
610 al. 2014; Clapp et al. 2014; Bell 2016; Lutz and Bleich 2026). This period closely matched the
611 exploration phase and settlement timing identified by Stewart et al. (2026*f*) for the population. In
612 contrast, the absence of substantial foraying immediately following DBS release is consistent
613 with evidence that these animals settled within days to weeks (Stewart et al. 2026*c*,*e*), likely
614 facilitated by conspecific attraction resulting from the high density of resident bighorn sheep
615 (Clapp et al. 2014; Stewart et al. 2026*j*). For DBS, the period of increased long-distance forays
616 coincided with declining NDVI and precipitation, increasing temperatures, expanded range size
617 and movement distances (Stewart et al. 2026*c*), and increased revisitation and residence time

(Stewart et al. 2026*b*), suggesting that seasonal changes, particularly the onset of forage limitation and thermal stress, may have triggered foraying behavior. This interpretation is supported by Krausman et al. (1989), who documented short-term (≤10-day), long-distance exploratory movements by desert bighorn sheep during spring and summer that were hypothesized to facilitate familiarization with the spatial distribution of resources. However, several previous studies have reported that most forays occur during the late summer and fall breeding season (Rubin et al. 1998; Borg et al. 2017; Lassis et al. 2022; Dekelaita et al. 2023; Ricci et al. 2024; Ryder 2026), contrasting with our findings. This discrepancy may, at least partially, reflect differences in the relatively young age structure of males in our study (2.5–4.5 y at release; Ricci et al. 2024), environmental conditions, resident population density, or a delayed post-release response that may have been difficult to detect in previous analyses (Cohen et al. 2015; Bleisch et al. 2017).

The S-DBC method provided a framework for identifying multiple aspects of movement and space use, including primary and secondary clusters, stopovers, and forays that were further classified as short-, mid-, or long-distance movements, as well as returning and non-returning forays (Fig. 8). These additional movement classifications provide ecological information that is generally unavailable from fixed-range methods. For example, range fracture, or the presence of discrete spatial segments within an individual's broader area of use, has been documented across taxa, with some studies linking these spatial components to differences in movement strategies (Resop et al. 2024; Lowrey 2026; Stewart et al. 2026*j*). By quantifying population-level spatial and temporal thresholds for distinguishing primary and secondary clusters, S-DBC provides an objective framework for identifying these spatial components and investigating their relationships with ecological or life-history processes, such as post-capture movements or other

641 major biological events. Similarly, identifying stopovers as temporary, extended stays during
642 forays provides an opportunity to investigate locations that may represent important resources or
643 behavioral responses to landscape conditions (Krausman et al. 1989; Pantelić et al. 2026), similar
644 to that observed during migrations (Sawyer and Kauffman 2011; Blum et al. 2015; Monteith et
645 al. 2018; Kauffman et al. 2023), which could be incorporated into behavior-specific resource
646 selection analyses (Bakner et al. 2023; Egan et al. 2025; Stewart et al. 2026*b*). The model-based
647 classification of short-, mid-, and long-distance forays may be particularly useful for
648 comparisons among populations and species because movement categories are derived from the
649 observed distribution of movement distances rather than imposed a priori thresholds. In our
650 study, for example, the distance separating mid- and long-distance forays was more than three
651 times greater for RMBS (10.2 km) than for DBS (3.1 km), highlighting the differences in the
652 spatial scale of foraying behavior between populations. Applying this approach across
653 populations could facilitate comparisons of movement strategies while allowing movement
654 thresholds to reflect population-specific distributions.
655 Differences in home-range estimates attributed to estimator choice represent a major
656 challenge for comparisons among studies (Boulanger and White 1990; Walter et al. 2015;
657 Noonan et al. 2019). Consistent with the broader literature (Powell 2000; Powell and Mitchell
658 2012; Signer et al. 2015; Werdel et al. 2021), estimators differed in the spatial structure of home-
659 range isopleths, with kernel estimators generally producing larger, more contiguous estimates
660 and movement models producing smaller, more fragmented estimates (Fig. 9). We found that
661 foray characteristics also varied among estimators, with kernel estimators generally producing
662 fewer forays but greater maximum foray distances than movement models. The predicted
663 number of forays decreased with increasing home-range area and tended to increase with the

number of discrete range components, although credible intervals overlapped zero for the latter relationship. Similar but opposite trends were observed for maximum foray distance, as maximum foray distance increased with increasing range area and decreased with number of range components, although these relationships were also uncertain. Differences in range size and complexity (number of components) influence whether movements are classified as occurring within or outside the estimated home range and their distance from the range boundary; therefore, estimator choice can propagate into downstream measures of movement behavior (Fig. 10). Thus, estimator selection is an important consideration not only for quantifying space use but also for interpreting and comparing foray behavior across studies. These limitations highlight the potential value of S-DBC, which defines use areas using population-level parameters of clustering (recursive use) and may provide a more consistent framework for identifying movement beyond core areas across studies.

The S-DBC method identified more forays than the kernel estimator but generally fewer forays than the movement-model estimators. Additionally, foray duration, total distance, and maximum distance were greatest when using S-DBC compared with all other estimators, although some uncertainty remained in these relationships. These findings align with our expectations based on how location data were assigned to areas of use and the resulting spatial distribution of those areas. Specifically, S-DBC incorporated characteristics of both kernel and movement-model estimators. Like movement-model estimators, S-DBC defined primary and secondary clusters as core areas of use while minimizing their spatial extent, potentially allowing for more consistent identification of the first and last locations occurring outside these core areas. At the same time, grouping locations into discrete primary and secondary clusters and evaluating stopovers and transient movements as potential forays maintained relatively contiguous areas of

687 core use, a characteristic more similar to kernel estimators. By combining these characteristics,
688 S-DBC may provide a useful balance between the conservative delineation of core areas
689 associated with movement-model estimators and the contiguous spatial representation
690 characteristic of kernel-based methods, potentially improving the identification of movements
691 extending beyond primary areas of use and capturing a greater proportion of their full spatial and
692 temporal extent.

693 The evaluation of two non-migratory subspecies of translocated bighorn sheep provided a
694 valuable case study for evaluating the S-DBC method and comparing its performance with fixed-
695 range methods. The method appears promising for broader applications in ecology; however, the
696 use of clustering approaches to identify forays and dispersal remains in its infancy (Cisneros-
697 Araujo et al. 2024; Pantelić et al. 2026). Bighorn sheep are habitat specialists that typically
698 concentrate movements in areas associated with escape terrain and rugged slopes (Whiting et al.
699 2023*a*; Krausman 2026; Stewart et al. 2026*e*,*f*). These relatively discrete areas of use may make
700 S-DBC particularly well suited for characterizing clusters in bighorn sheep compared with more
701 mobile species that have less clearly defined areas of use. Consequently, evaluation across a
702 broader range of species and movement strategies is needed to determine the generality of the
703 approach. Our implementation identifies the distance inputs for the clustering algorithm,
704 breakpoints used to define clusters, and distance cutoffs used to classify forays from population-
705 level movement distributions. Thus, the method, as described, requires further evaluation to
706 determine whether these parameters can be reliably estimated at the individual level, particularly
707 when movement distributions vary substantially among individuals. In addition, because the
708 algorithm uses spatial relationships among locations to identify clusters, its performance may be
709 sensitive to the amount of location data available for each individual. When applying S-DBC

across a population, we therefore recommend that individuals have similar amounts of tracking data when possible. Whether and how differences in the quantity of data collected among individuals affect S-DBC outputs should be formally evaluated. Finally, our method has not been evaluated for migratory or semi-migratory species, for which seasonal shifts in space use may challenge the identification of persistent clusters and forays. Testing S-DBC, and spatiotemporal-DBC methods, across migratory and semi-migratory systems will be important for determining its broader utility for movement ecology.

5. Conclusions

Our results demonstrate that forays represent an important component of space use in bighorn sheep, with their occurrence, timing, and spatial extent varying between populations. The contrasting seasonal patterns of foraying further suggest that movements beyond established areas of use may arise from different ecological processes. Reintroduced RMBS forayed immediately following release, likely reflecting exploratory movements associated with acquiring information about a novel environment (Stewart et al. 2026*f*), whereas restocked DBS exhibited increased mid- and long-distance foraying during spring and early summer, coinciding with warmer, drier conditions and declining forage availability (Stewart et al. 2026*c*). The S-DBC method provided an alternative framework for characterizing these movements by identifying spatially distinct areas of use, stopovers, and forays across multiple distance classes using thresholds derived from observed movement distributions. Compared with fixed-range estimators, S-DBC generally identified fewer forays than movement-model estimators but captured forays of greater duration and spatial extent, suggesting that its combination of contiguous clustering and conservative delineation of core areas may improve characterization of movements extending beyond primary areas of use. More broadly, our findings highlight that

methodological decisions used to delineate space use can influence subsequent inference about movement behavior and underscore the importance of considering how home-range structure affects foray identification. Although S-DBC shows promise for improving the characterization and comparison of foraying behavior, further evaluation across species, movement strategies, and tracking regimes, including migratory and semi-migratory systems, is needed to determine its broader applicability and limitations.

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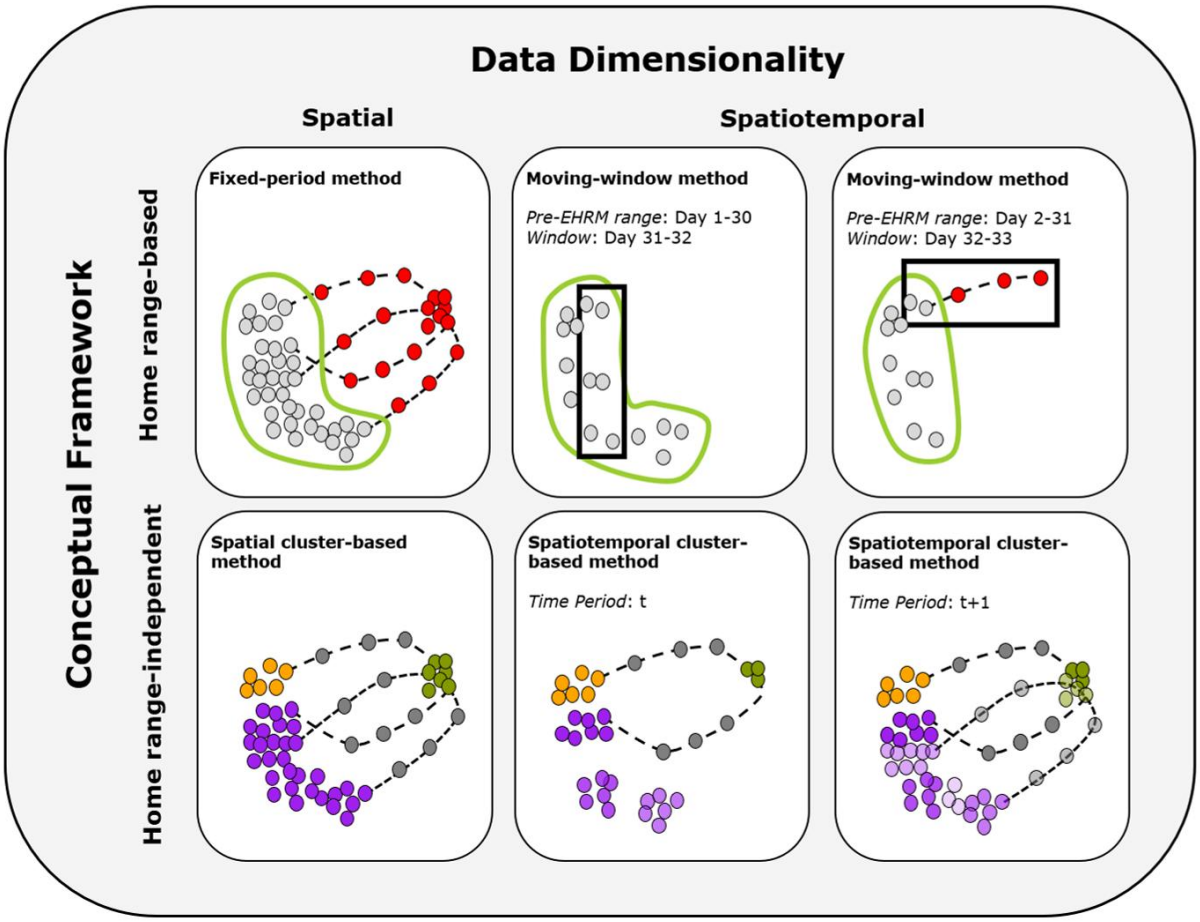


Fig. 1. Conceptual framework for classifying foray-detection approaches by their dependence on an estimated home range (Conceptual Framework) and use of spatial versus spatiotemporal information (Data Dimensionality). Home range-based approaches identify forays beyond an estimated area of use, whereas home range-independent approaches identify atypical movements directly from animal locations or trajectories. Spatial approaches rely primarily on the spatial distribution of locations, whereas spatiotemporal approaches incorporate their temporal sequence. In the first row, red points represent detected forays, gray points represent locations within the estimated range, and black boxes indicate locations evaluated for forays within the moving window. In the second row, purple points represent primary clusters and yellow points

represent secondary clusters, both representing range components; green points represent temporary stopovers, and gray points represent transition movements.

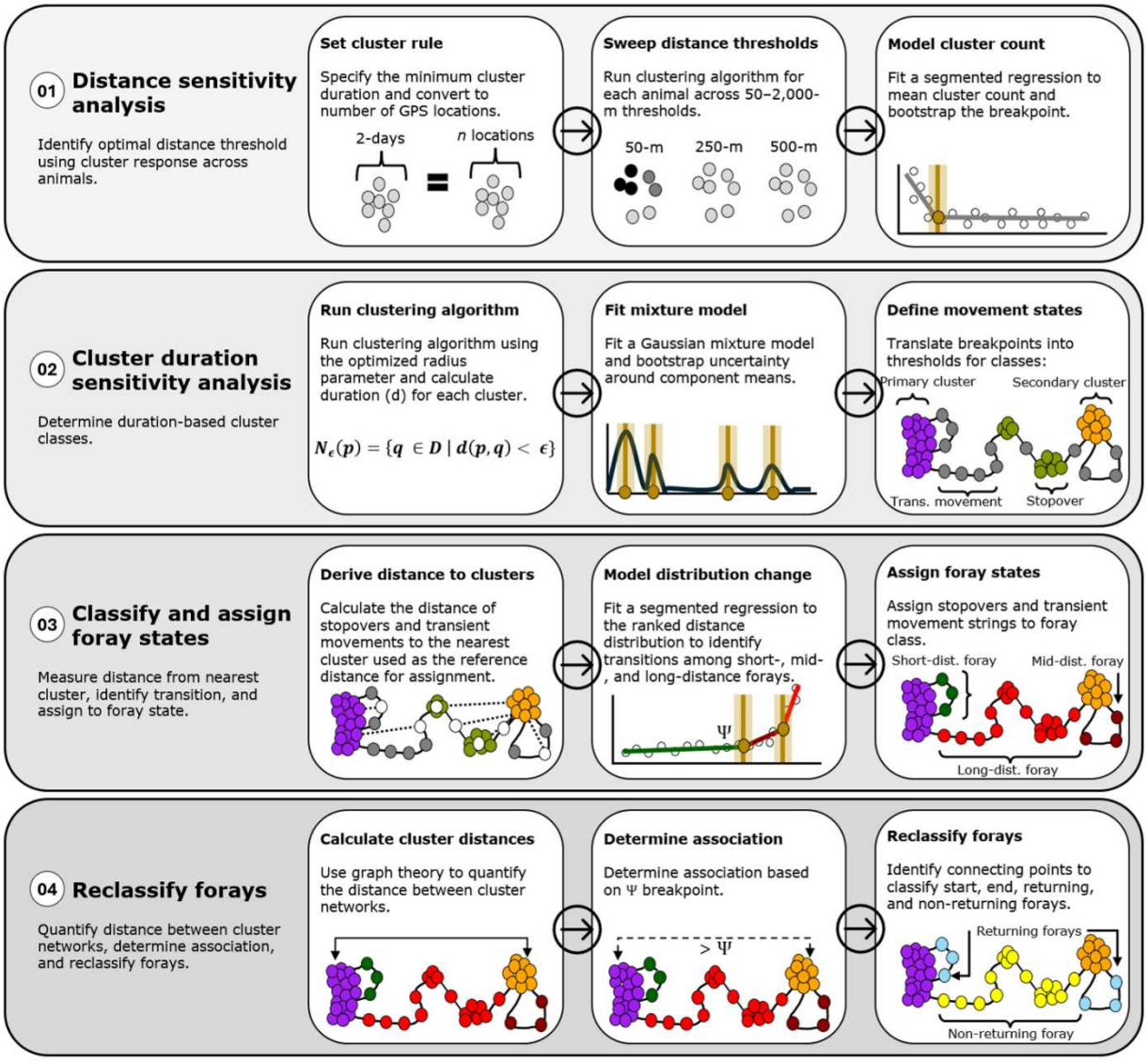


Fig. 2. Conceptual workflow for the spatial density-based clustering (S-DBC) framework used to classify GPS locations into biologically meaningful space-use states and identify forays. (1) Distance sensitivity analysis: density-based spatial clustering of applications with noise (DBSCAN) was applied across a range of neighborhood distances (ε) to identify the population-specific distance threshold at which the number of detected clusters stabilized. (2) Cluster duration sensitivity analysis: DBSCAN was rerun using the optimized distance threshold, and cluster durations were modeled with a Gaussian mixture model to

identify duration-based classes representing stopovers, secondary clusters, and primary clusters; non-clustered locations were classified as transient movements. (3) Classification and assignment of foray states: Distances between transient movements or stopovers and the nearest primary or secondary cluster were calculated, and segmented regression of ranked distances identified population-specific thresholds used to classify short-, mid-, and long-distance forays. (4) Foray reclassification: Spatial relationships among primary and secondary clusters were quantified using graph theory to define connected cluster networks, which were used to classify forays as returning, non-returning, start, or end forays. Each step incorporated population-specific breakpoint estimates to distinguish persistent space-use from transient movements and increasingly distant excursions.

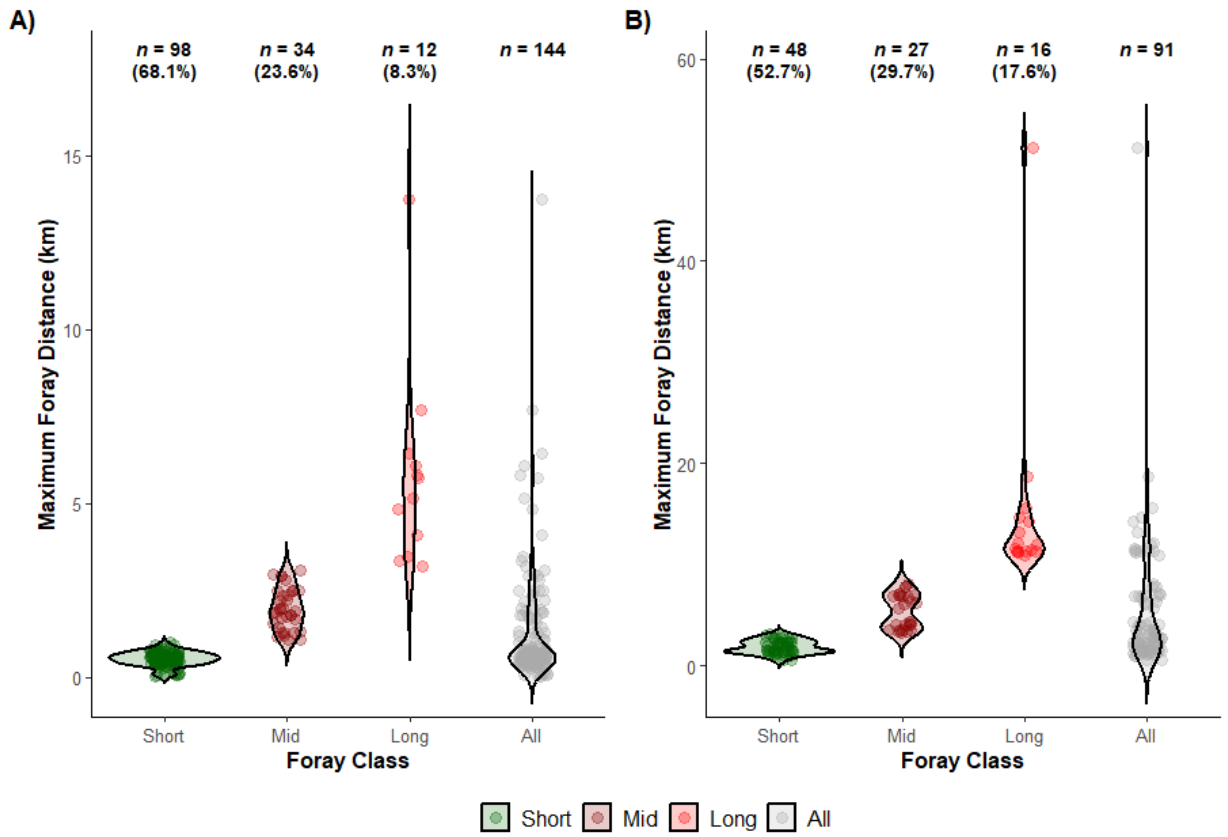


Fig. 3. Maximum foray distances (km) of (A) desert bighorn sheep (n = 13; *Ovis canadensis mexicana*) restocked in Sonora, Mexico, during 2022–2023 and (B) Rocky Mountain bighorn sheep (n = 18; *O. c. canadensis*) reintroduced in South Dakota, USA, during 2015–2016, classified within the spatial density-based clustering (S-DBC) framework by predicted foray class: short-distance (green), mid-distance (dark red), long-distance (light red), and all forays (gray). For desert bighorn sheep, predicted foray classes corresponded to maximum distances from the nearest primary or secondary cluster of 0.00–1.06, 1.06–3.13, and ≥3.13 km for short-, mid-, and long-distance forays, respectively. For Rocky Mountain bighorn sheep, corresponding thresholds were 0.00–3.20, 3.20–10.17, and ≥10.17 km. Numbers in bin headings indicate the number and percentage of forays within each class.

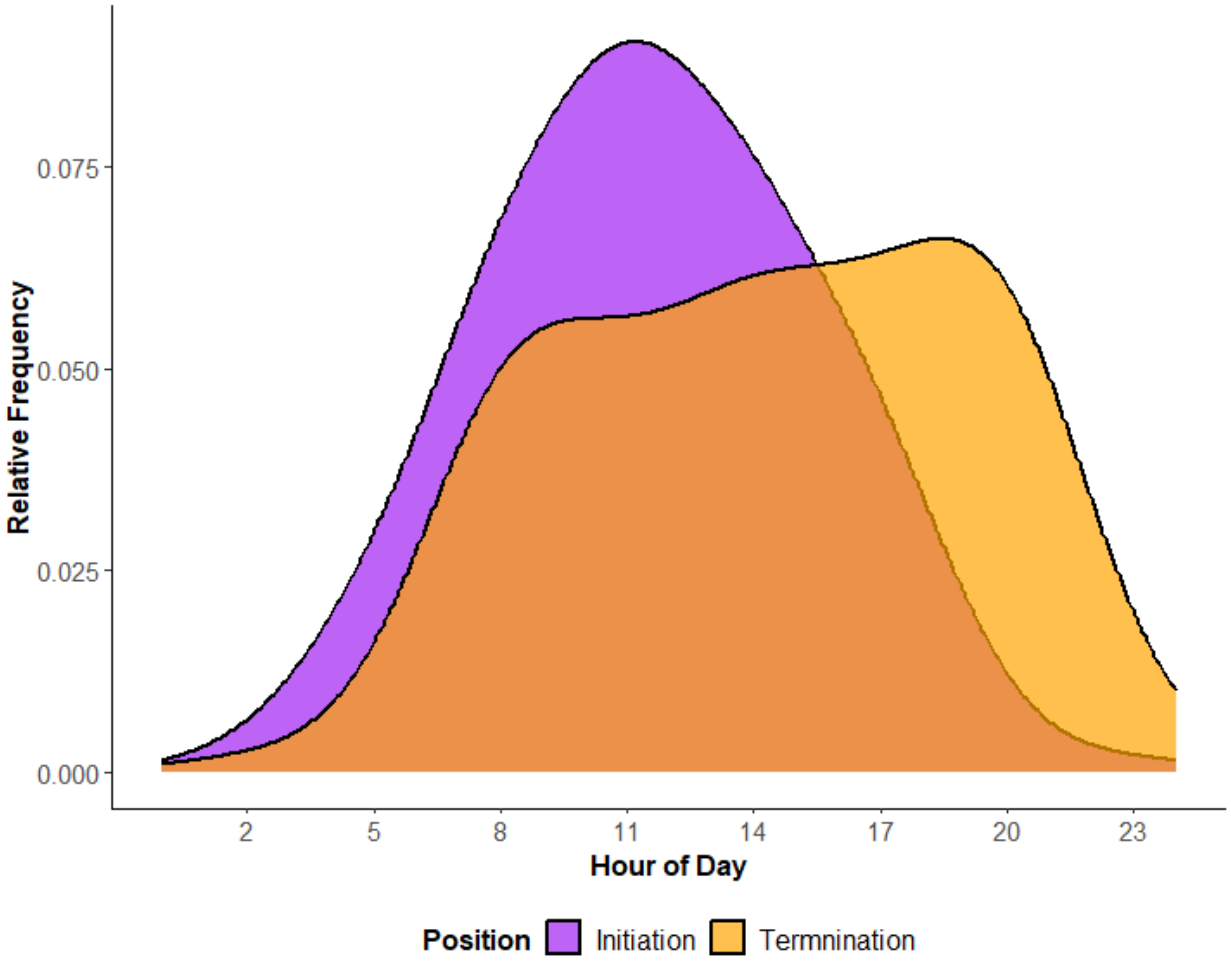


Fig. 4. Relative frequency of foray initiation (purple) and termination (orange) by hour (0200–2300, 3-h intervals) for predicted forays identified using the spatial density-based clustering (S-DBC) framework for desert bighorn sheep (n = 13; *Ovis canadensis mexicana*) restocked in Sonora, Mexico, during 2022–2023.

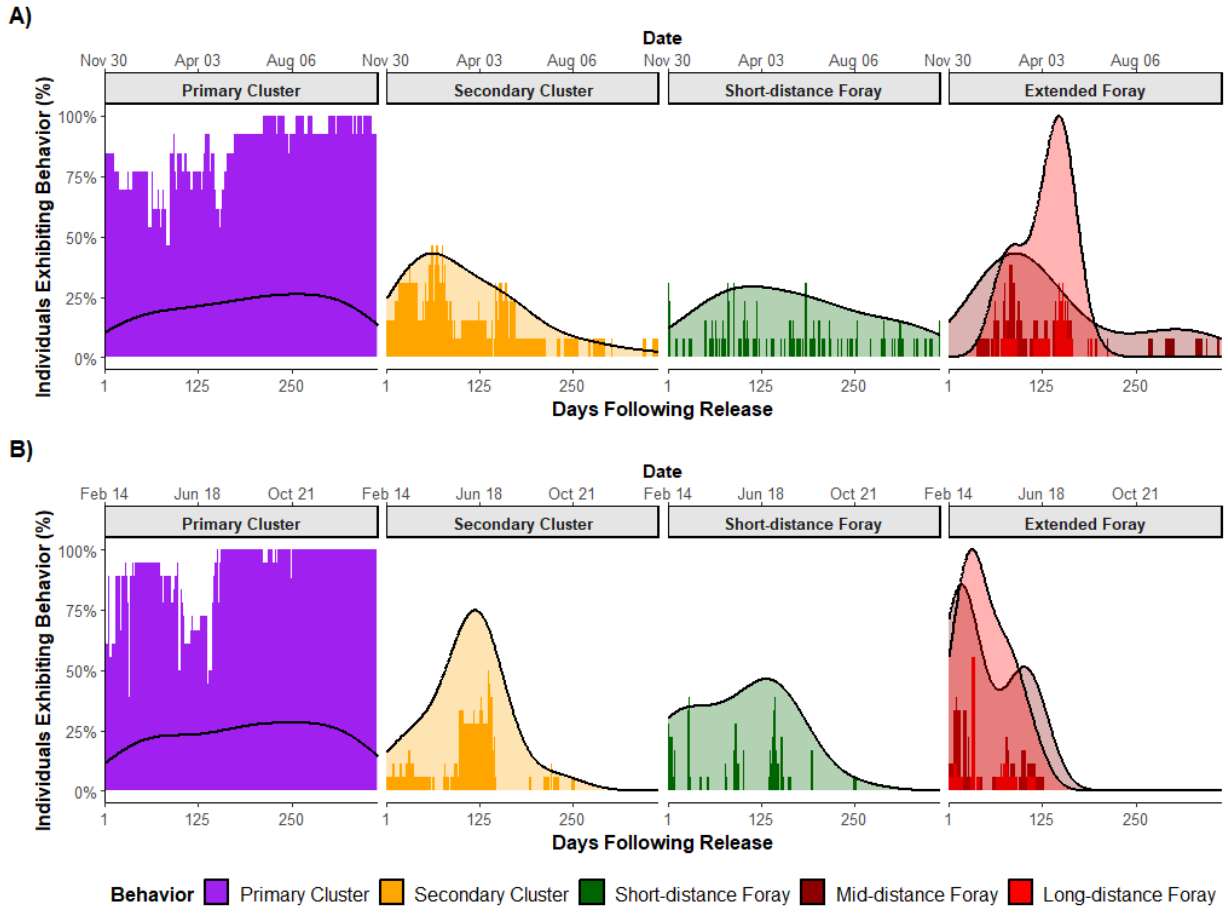
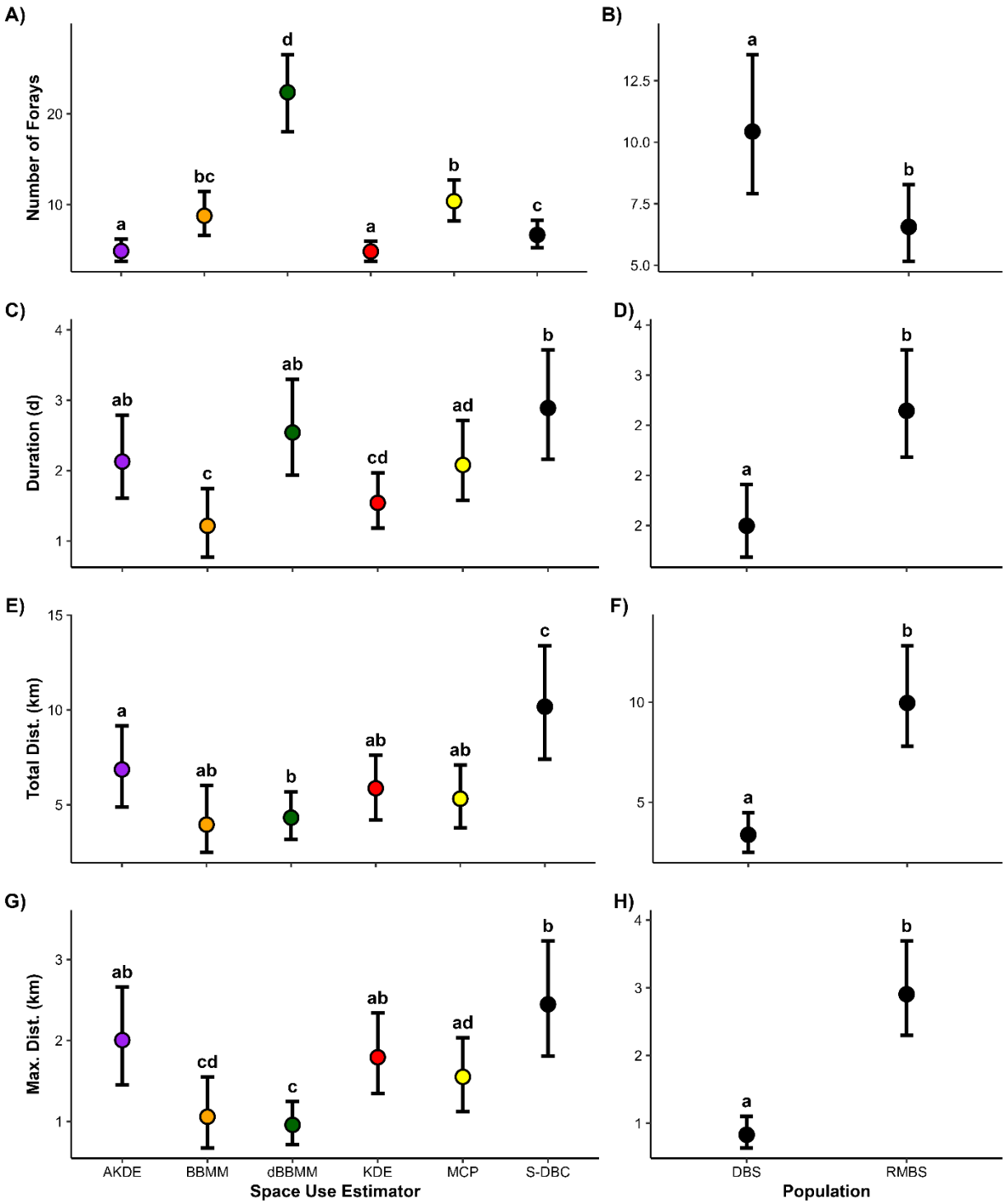


Fig. 5. Percentage (bars) and density distributions (density curves) of locations classified by the spatial density-based clustering (S-DBC) framework as primary clusters (purple), secondary clusters (orange), short-distance forays (green), mid-distance forays (dark red), or long-distance forays (light red) for (A) desert bighorn sheep (n = 13; *Ovis canadensis mexicana*) restocked in Sonora, Mexico, during 2022–2023 and (B) Rocky Mountain bighorn sheep (n = 18; *O. c. canadensis*) reintroduced in South Dakota, USA, during 2015–2016. Mid- and long-distance forays were combined as extended forays. The x-axis represents days since release, and the secondary x-axis represents the corresponding calendar date.



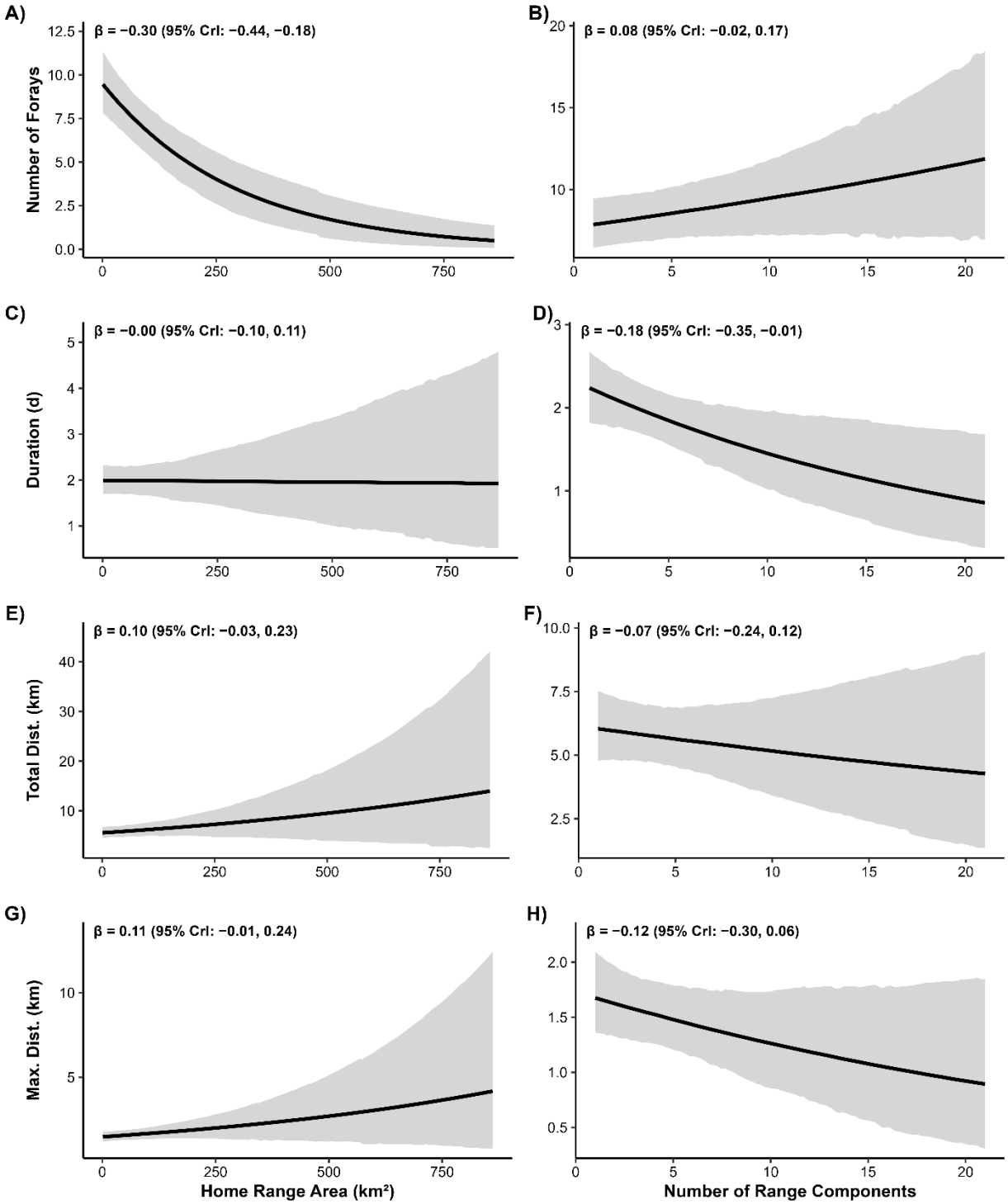
1402

1403 **Fig. 6.** Posterior estimated marginal means (points) and 95% credible intervals (error bars) for

1404 response variables: (A, B) number of forays, (C, D) foray duration (d), (E, F) total distance

1405 traveled (km), and (G, H) maximum foray distance (km) by (A, C, E, G) space-use estimator and

(B, D, F, H) population. For each response, estimates are shown for six space-use estimators: autocorrelated kernel density estimate (AKDE; purple), Brownian bridge movement model (BBMM; orange), dynamic Brownian bridge movement model (dBBMM; dark green), kernel density estimate (KDE; red), minimum convex polygon (MCP; yellow), and spatial density-based clustering (S-DBC; black). Population-level estimates represent desert bighorn sheep (n = 13; *Ovis canadensis mexicana*) restocked in Sonora, Mexico, during 2022–2023 and Rocky Mountain bighorn sheep (n = 18; *O. c. canadensis*) reintroduced in South Dakota, USA, during 2015–2016. Groups with the same letter did not differ based on posterior pairwise comparisons ($\alpha = 0.05$); mean comparisons are specific to each fixed effect (space use estimator and population).



1429

1430 **Fig. 7.** Posterior predicted relationships between (A, C, E, G) home range area (km^2) and (B, D,

1431 F, H) complexity (number of range components) and (A, B) number of forays, (C, D) foray

1432 duration (d), (E, F) total distance traveled (km), and (G, H) maximum foray distance (km) for

desert bighorn sheep (*n* = 13; *Ovis canadensis mexicana*) restocked in Sonora, Mexico, during 2022–2023 and Rocky Mountain bighorn sheep (*n* = 18; *O. c. canadensis*) reintroduced in South Dakota, USA, during 2015–2016. Lines represent posterior mean estimates, and shaded ribbons represent 95% credible intervals. Values within panels indicate posterior effect estimates (β) and 95% credible intervals.

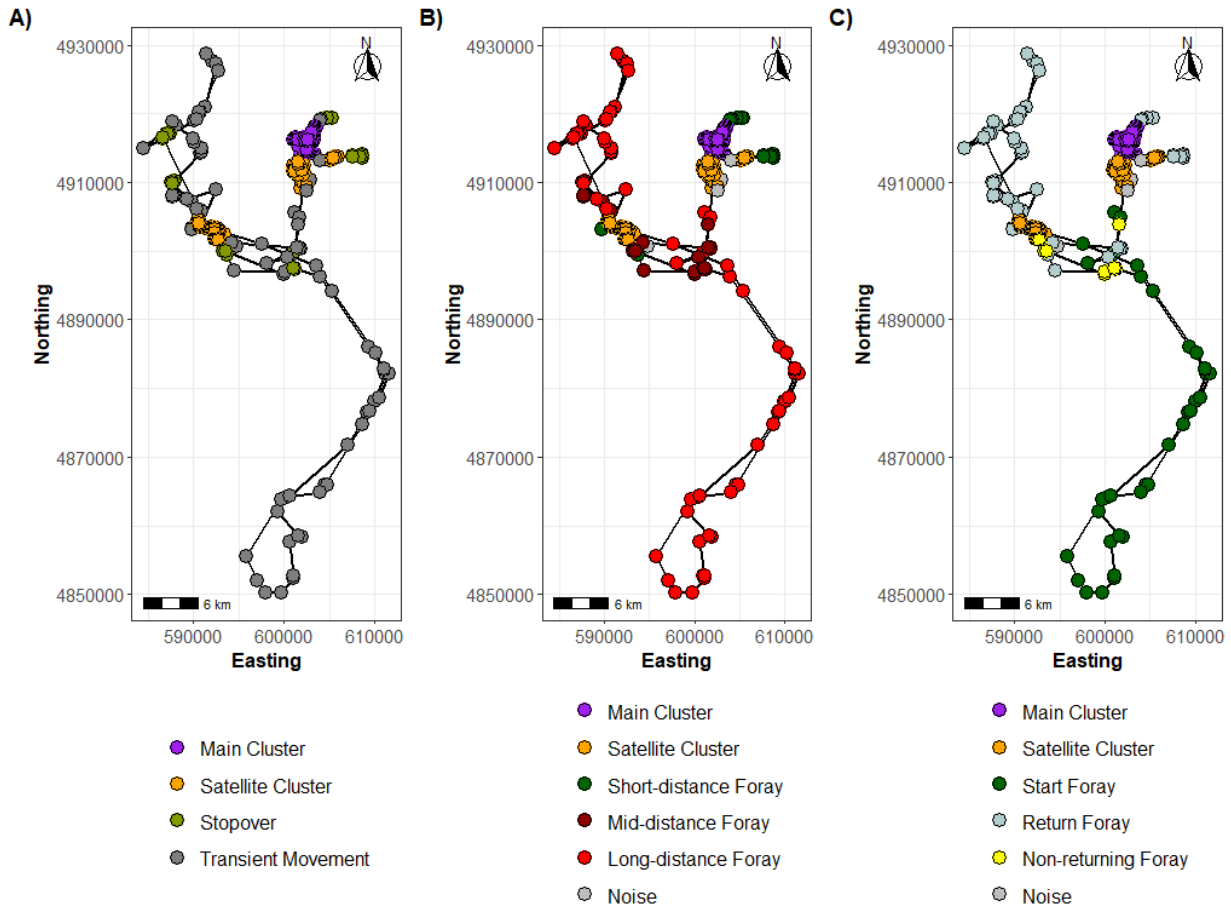


Fig. 8. Movement trajectory and classification of GPS locations for a Rocky Mountain bighorn sheep (*Ovis canadensis canadensis*) reintroduced in South Dakota, USA using three stages of the spatial density-based clustering (S-DBC) framework. (A) Locations classified as primary clusters (purple), secondary clusters (orange), stopovers (olive), or transient movements (gray). (B) Locations further classified by predicted foray distance as short-distance (dark green), mid-distance (dark red), or long-distance (red) forays, in addition to primary and secondary clusters and noise (gray). (C) Foray locations classified by movement role as foray initiation (dark green), returning foray (light blue), non-returning foray (yellow), or foray termination (red), in addition to primary and secondary clusters and noise. Black lines represent the observed

movement trajectory. Maps illustrate the sequential classification of locations within the S-DBC framework.

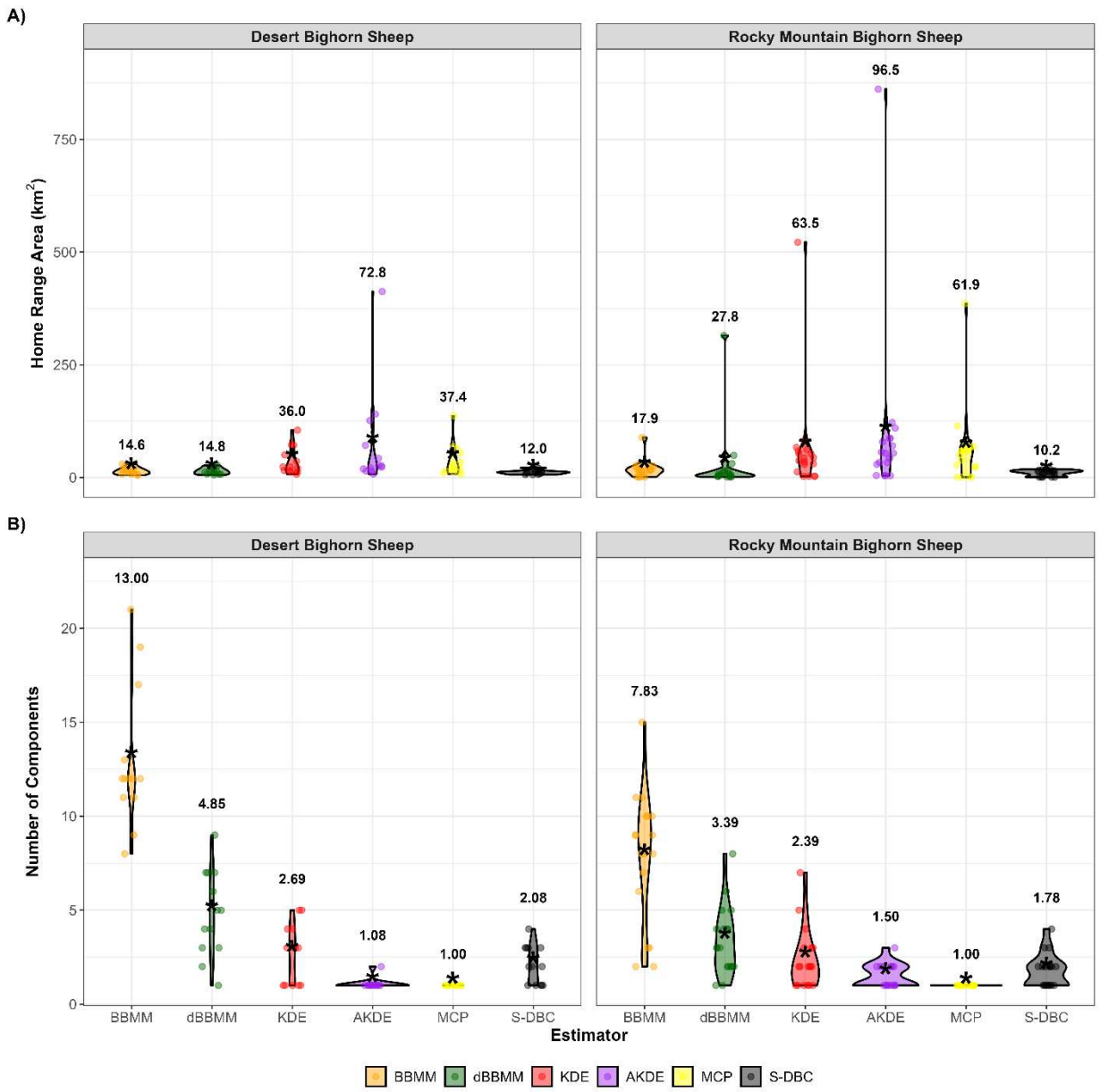
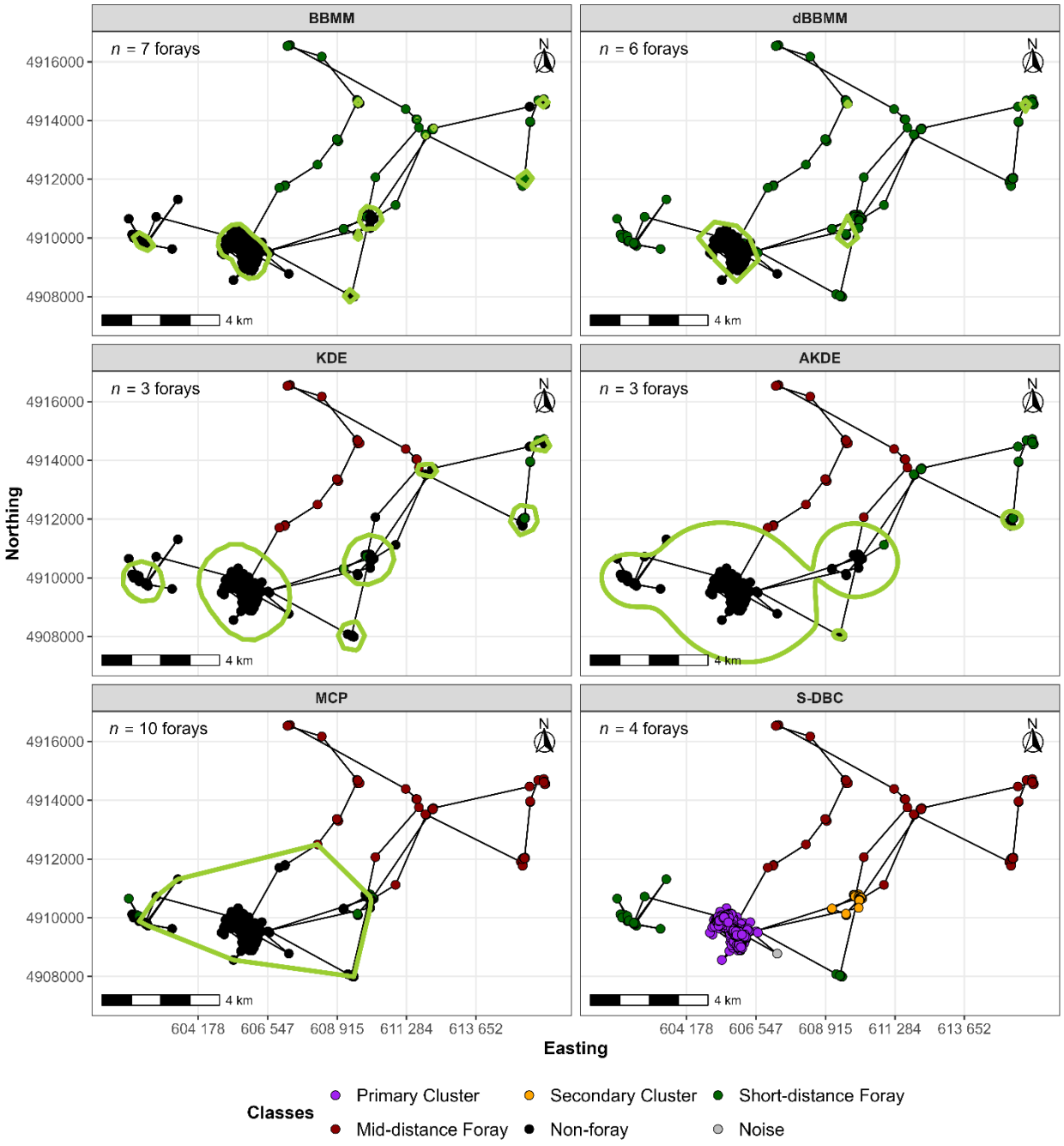


Fig. 9. Distributions of (A) home range area (km^2) and (B) number of range components for desert bighorn sheep (n = 13; *Ovis canadensis mexicana*) restocked in Sonora, Mexico, during 2022–2023 and Rocky Mountain bighorn sheep (n = 18; *O. c. canadensis*) reintroduced in South Dakota, USA, during 2015–2016 among six space-use estimators: Brownian bridge movement model (BBMM), dynamic Brownian bridge movement model (dBBMM), kernel density estimate (KDE), autocorrelated kernel density estimate (AKDE), minimum convex polygon (MCP), and

spatial density-based clustering (S-DBC). Violin plots represent the distributions of individual estimates, points represent individual animals, asterisks indicate mean estimates, and values above each distribution indicate mean home range area or number of range components.



1517

1518 **Fig. 10.** Movement trajectory and foray classification for a Rocky Mountain bighorn sheep (*Ovis*

1519 *canadensis canadensis*) reintroduced in South Dakota, USA across six space-use estimators:

1520 kernel density estimate (KDE), autocorrelated kernel density estimate (AKDE), Brownian bridge

movement model (BBMM), dynamic Brownian bridge movement model (dBBMM), minimum convex polygon (MCP), and spatial density-based clustering (S-DBC). Colored GPS locations represent primary clusters (purple), secondary clusters (orange), short-distance forays (dark green), mid-distance forays (dark red), non-foray locations (black), and noise (gray). Green outlines represent the 95% utilization distribution or home range isopleth estimated by each respective method. Black lines represent the observed movement trajectory. Numbers in each panel indicate the number of forays identified by the corresponding method.

Supplementary Files

This is a list of supplementary files associated with this preprint. Click to download.

- SupplementaryInformation.docx