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RESEARCH ARTICLE

Separating biological signal from methodological noise in home range estimates

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Abstract

1. Space use is commonly estimated in animal ecology and has become a cornerstone of evidence-based conservation planning, with animal tracking increasingly used to underpin the designation of protected areas with high conservation value. However, tracking technologies and analytical methods may introduce biases in home range size estimates. We assessed these potential biases using simulated tracking data and published home range size estimates from empirical animal tracking studies.
2. We first simulated animal movement data and added published location error estimates for different technologies used for tracking sea turtles. Location data were analysed using common space use estimation methods (minimum convex polygon, fixed and autocorrelated kernel density estimation, biased random bridge and dynamic Brownian bridge movement model). Second, we reviewed home range size estimates obtained using different technologies to track hawksbill (*Eretmochelys imbricata*) and green (*Chelonia mydas*) turtles to assess the relative impacts on home range estimates due to (i) tracking accuracy and (ii) analytical methods.
3. For both simulated data and empirical values of space use from the literature ($n=90$ studies), relatively large home range estimates tended to be generated from lower resolution Argos tracking compared to higher-resolution Fastloc-GPS tracking. These findings reflect inaccuracies in location data providing spuriously large movements. For example, Argos and Fastloc-GPS home range size estimates for adult green turtles averaged 393 and 53 km^2 respectively ($n=64$ and 39 individuals). For simulated data, biases introduced by tracking accuracy had a far greater impact on home range size estimation than the analytical method used, apart from when using autocorrelated kernel density estimation (AKDE) which compensated for positional error very well.
4. Our results suggest that in many cases, hawksbill and green turtles have relatively small home ranges (<10 km^2 and in some cases, <1 km^2), with this picture of their limited space use only emerging through high-accuracy tracking. These general conclusions likely apply broadly across taxa and will impact attempts to

assess patterns of home range sizes recorded for individuals across studies in different regions.

KEYWORDS
foraging, GPS, kernel analysis, marine turtle, satellite tracking, spatial ecology, utilisation distribution

1 | INTRODUCTION

Home range is a popular index of space use, defined as the area traversed by an animal for its regular activities of mating, foraging and caring for its young (Burt, 1943). The size of an animal's home range is influenced by various intrinsic and extrinsic factors including body size, metabolic requirements, food quality and availability (Chambault et al., 2020; Tamburello et al., 2015; Wood et al., 2017). In addition to such biological considerations, however, home range size estimates may also be affected by scientific decisions such as the tracking device technology and analytical methodology used to study space use (e.g. Börger et al., 2006; Thomson et al., 2017). For example, studies of space use by various taxa such as wild boar (Peris et al., 2020), baboons (Pebsworth et al., 2012) and reptiles (Silva et al., 2020) have reported that variable tracking technologies, analytical methods and sample size introduced methodological and analytical noise that led to over- or underestimated home range size estimates (Dwyer et al., 2015; Shimada et al., 2021; Signer et al., 2015). Therefore, it is important to be able to quantify the relative importance of biological signal versus methodological and analytical noise when assessing home ranges. Here, we consider these issues with respect to some widely used tracking technologies and analytical methods. In this way, we show some key considerations when comparing home range estimates across different studies.

Since the 1980s, satellite tracking has been used for many terrestrial, aerial and marine animals, most typically using the Argos satellite system (Fancy et al., 1988). This global system allows remote acquisition of animal location data and is used for species that range over broad areas. More recently, Argos satellite tracking has been supplemented with the relay of high-accuracy global positioning system (GPS) locations and a derivative of GPS, Fastloc-GPS (Kuhn et al., 2009). Unlike traditional GPS, which requires several seconds to generate a location estimate, Fastloc-GPS acquires high-accuracy location fixes within milliseconds, enabling GPS tracking technology to be used even for marine animals that surface briefly (Dujon et al., 2014). For animals with smaller ranges, tracking technologies might include very high frequency (VHF) radio (e.g. bats; Gottwald et al., 2022) and acoustic tracking for aquatic species (e.g. sharks, turtles; Lea et al., 2016). Satellite telemetry has led to the identification of space use patterns, species distributions and connectivity between habitats, often with strong conservation benefits (Crego et al., 2024; Katzner & Arlettaz, 2020; Kot et al., 2022). For example, in marine systems, information on space use patterns has led to the designation of marine protected areas (Sahri et al., 2022) and approaches to reduce harmful interactions between humans and wildlife, such as boat strikes (Hays et al., 2019). It has been shown that less accurate tracking, for example, Argos compared to Fastloc-GPS, will lead to larger home range estimates (Martinez-Estevez et al., 2021; Tanabe et al., 2023; Thomson et al., 2017).

Analytical approaches to process location data and estimate space use have evolved over the last 40 years. Minimum convex polygon (MCP; Mohr, 1947) is a traditional method that calculates home range as the extent of the smallest polygon without concave angles that contains the outermost locations and is still widely reported in comparative studies (e.g. Hardy et al., 2023; Wilson et al., 2020). Kernel density estimation (KDE; Worton, 1989) is commonly used to estimate the home range of an individual by calculating the probability that an animal occurred in a particular area over a specified period of time. Autocorrelated kernel density estimation (AKDE) builds on KDE and addresses common issues with animal location data such as autocorrelation and sampling biases (Fleming et al., 2015). Other commonly used analytical methods include biased random bridge (BRB), which relies on movement-based KDE via location interpolation (Benhamou, 2011), and the Brownian bridge movement model (BBMM; Horne et al., 2007), which estimates an animal's path using interpolation and accounts for time gaps and movement uncertainty. The dynamic Brownian bridge movement model (dBBMM) builds on BBMM by detecting behaviour changes, and both BBMM methods estimate an animal's occurrence distribution (rather than range distribution) by quantifying uncertainty in the movement path using likelihood statistics (Alston et al., 2022; Kranstauber et al., 2012). Unlike the traditional MCP and KDE methods, AKDE, BRB and dBBMM consider biological factors like behaviour and technical factors like location error that are known to influence animal movement and space use estimation.

The interaction between tracking resolution of Fastloc-GPS vs. Argos location data and commonly used analytical methods for home range estimation has not yet been considered. Following theoretical considerations for how tracking resolution and analytical method impact space use estimation using simulated data, we then explore empirical home range estimates across studies of two commonly tracked species, hawksbill (*Eretmochelys imbricata*; Ei) and green turtles (*Chelonia mydas*; Cm). The hard shells of Cheloniid species facilitate transmitter attachment, and their pantropical distribution and conservation dependence means that tracking studies are available from many parts of the globe, which are increasingly used in the designation of marine protected areas (e.g. Davies et al., 2021; Hays et al., 2019). Both species inhabit productive but vulnerable foraging habitats such as coral reefs and seagrass beds (Christianen et al., 2023; Hoenner et al., 2015) and variations in their spatial behaviour can inform the need for ecosystem protection (Hardy et al., 2023). We consider how these data can be directly compared to assess global patterns of home range size for broadly distributed species.

2 | MATERIALS AND METHODS

2.1 | Data simulation

To quantify and compare variation in home range size estimation that can arise due to tracking technology and analytical method, we simulated movement data based on the Ornstein–Uhlenbeck foraging (OUF) Gaussian process (Fleming et al., 2014a, 2014b; Uhlenbeck & Ornstein, 1930), a correlated random walk that accounts for autocorrelation and generates movement tending toward a central location (e.g. Noonan et al., 2019), resembling behaviour at foraging grounds. Data were generated using the simulate function from package *ctmm* (Calabrese et al., 2016) in R version 4.2.3 (R Core Team, 2023) for 10 distinct individuals to ensure computational feasibility whilst obtaining reasonable estimates of variability. We chose an isotropic model (equal movement in all directions), and movement variance was set to 200,000 m^2 in order to generate realistic home range sizes (<4 km^2) based on published estimates using Fastloc-GPS locations (Hardy et al., 2023; Hays et al., 2021). We based the other model parameters on results extracted from publicly available tracking datasets for foraging hawksbill (n = 5; Hays et al., 2021) and green (n = 5; Hardy et al., 2023) turtles, ensuring realistic autocorrelation parameters for position and velocity. The resulting autocorrelation values were 126,000 s (35 h) for the home range crossing time, a measure of long-term spatial autocorrelation, and 3300 s (55 min) for the velocity autocorrelation time, which reflects short-term consistency in movement direction and speed (mean values, n = 10). Times were similar across species (Table S1).

The number of simulated locations (n = 1441) was selected to achieve a sampling duration of 6 months to emulate typical mean tracking durations (e.g. Maurer et al., 2024; Shaver et al., 2013) and transmission frequency (one location every 3 h, see Hays et al., 2021) for sea turtles. Timestamps (range: 01/01/2024 00:00:00–29/06/2024 00:00:00) were generated using the R package *lubridate* (Grolemund & Wickham, 2011).

To generate mock tracking datasets from our simulated animal movement data, we added randomly generated, independent location errors for each location fix drawn from bivariate (x and y) normal distributions typical of Fastloc-GPS and Argos data. The spatial error estimate used for Fastloc-GPS was 70 m (i.e. mean = 0 m, SD = 29 m, 95% of locations with ≥6 satellites, Dujon et al., 2014). For Argos tracking data, each positional fix is assigned a location class (LC) based on the number of messages received and the estimated positional accuracy, with four or more messages required for standard locations (LC 3, 2, 1, 0, spatial accuracies ranging from <250 m to >1500 m) and auxiliary locations assigned in the case of fewer than four messages (LC A and B, spatial accuracy unknown) (CLS, 2016). Argos tracking data for sea turtles can often be dominated by LC B owing to their brief surfacing pattern; two levels of accuracy were therefore simulated for mock Argos datasets to reflect typical filtering criteria used in empirical studies (often determined by the number of high-quality locations available): high accuracy (LC 3, 2, 1, A; spatial error: 2500 m, SD: 1000 m) and low accuracy (LC 3, 2, 1, 0, A, B; spatial error: 10000 m, SD: 6000 m). Spatial error was assigned according to independent tests of location accuracy (Hays et al., 2001; Witt et al., 2010).

2.2 | Home range estimation using simulated data

We calculated the 50% and 95% utilisation distribution (UD), commonly referred to as the 'core' and 'full' home range, for each mock tracking dataset (Fastloc-GPS, Argos high-accuracy and Argos low accuracy for each simulated animal) using each of the following analytical methods: (1) MCP, (2) fixed KDE, (3) AKDE, (4) BRB and (5) dBBMM (see Supporting Information: Extended methods). We used the area encompassing 95% of simulated animal locations as a theoretical reference area against which 95% UDs calculated from each mock tracking dataset were compared, using the following formula (see Noonan et al., 2019):

$$\text{reference area} = -2^{*}\log(0.05) * \text{pi}^{*}\text{movement variance}$$

2.3 | Comparison of published home range estimates for hawksbill and green turtles

We searched for peer-reviewed literature on foraging home ranges of hawksbill and green turtles on Web of Science and Google Scholar between 16 January 2023–12 March 2023, and again on 17 February 2024 to update the list, using a combination of keywords: (("*Eretmochelys imbricata*" OR "*Chelonia mydas*") OR (("hawksbill" OR "green") AND "turtle")) AND ("home range" OR "space use") AND (("foraging" OR "feeding") AND ("ground" OR "site")) (1980–2024). We examined available studies for information on methods and metrics of home range sizes. We conducted backwards and forward searches by scanning the reference lists of shortlisted papers and checking articles that had cited the shortlisted papers. We excluded studies that did not provide either mean values or data for individual turtles, used recapture distance to measure habitat use or focused on migration or the inter-nesting period.

For each study, we extracted information on tracking technology used, location data filtering parameters, analytical method, foraging site (or approximate location; if available), species, life stage, sex and estimated home range size (mean ± SD) as 50% and 95% UDs or 100% MCPs, as well as sample size and seasonal/diel variation. For comparisons of estimated space use across published home range sizes, we categorised tracking technology by Fastloc-GPS, Argos-only, acoustic and radio.

After finding that Argos data tended to overestimate home range size, we selected Fastloc-GPS-derived estimates for tests of difference in space use patterns among life stage groups and between the two species, in order to better reveal underlying patterns without added noise from varying location accuracy. We ran these tests of difference on published Fastloc-GPS-derived estimates using a single metric—KDE (95% KDE UD, hereafter 'KUD') was selected for comparisons across life stages and between species because it was the most frequently used analytical method in the reviewed literature, providing adequate sample size.

2.4 | Data analysis

All analyses were performed in R version 4.2.3 (R Core Team, 2023). To assess the accuracy of tracking technologies and analytical methods in estimating home ranges, we measured bias in full home range size estimates derived from our mock tracking datasets using each method. To do this, we calculated bias as the difference between the estimated 95% UD and the reference area.

Literature-gleaned data were checked for normality using the Shapiro–Wilk test and for homogeneity of variance using the Levene test (95% KUDs and 100% MCPs for Fastloc-GPS, Argos and acoustic tracking technologies, and Fastloc-GPS-derived 95% KUDs of hawksbill and green turtles for each life stage). Non-parametric tests were used to compare groups owing to non-normally distributed data.

We used the Kruskal–Wallis test and a post hoc pairwise Wilcoxon test adjusted with Bonferroni correction to compare home range estimates of individual turtles from the literature across tracking technologies for each species and each estimator (95% KUD and 100% MCP). We then used the Mann–Whitney *U*-test to compare Fastloc-GPS 95% KUD estimates for individual turtles between independent groups, that is across life stages for each species and between the two species to check for space use patterns.

3 | RESULTS

3.1 | Home range estimation using simulated animal movement data

The 95% reference area for each simulated animal was 3.76 km^2 (Figure 1). The reference area was the same across all ten simulations because this is set by the movement variance parameter.

Tracking accuracy generally had far greater impact on home range size estimates than analytical method, except for AKDE (Figure 2, Figure S1). For example, Argos data increased bias by orders of magnitude relative to Fastloc-GPS data (Fastloc-GPS mean ± SD: $0.1 \pm 0.3\,km^2$; Argos high accuracy: $20.9 \pm 13.5\,km^2$; Argos low accuracy: $769 \pm 466\,km^2$), while most of the analytical methods (except AKDE) had relatively modest impact by comparison (Figure 2). In contrast to the other methods, AKDE compensated for variable accuracy

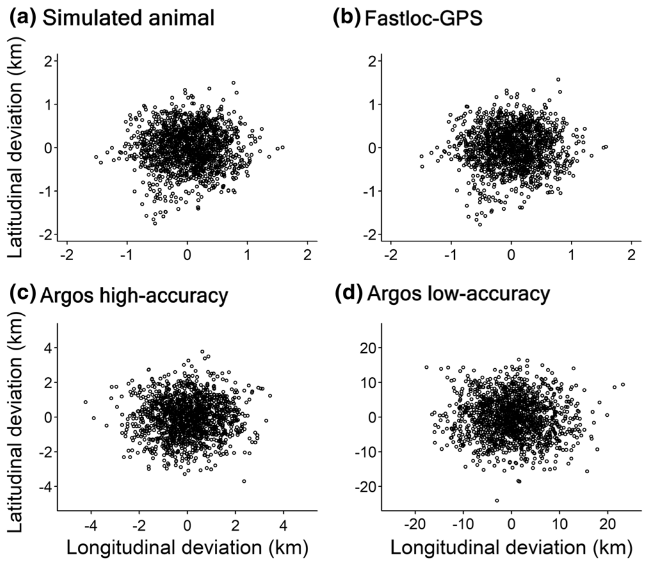

FIGURE 1 Example of (a) simulated animal movement locations and (b–d) corresponding mock tracking locations incorporating typical error estimates associated with (b) Fastloc-GPS and (c, d) Argos tracking technology, assuming high and low filtering based on location class (c: 3, 2, 1, A; d: 3, 2, 1, 0, A, B). Note the difference in scale between panels.

in simulated movement data, giving much closer size estimates across tracking technologies than the other methods (Fastloc-GPS with AKDE: $3.7 \pm 0.2\,km^2$; Argos high-accuracy with AKDE: $2.4 \pm 0.5\,km^2$; Argos low accuracy with AKDE: $8.3 \pm 12.9\,km^2$).

Full home range estimates for simulated Argos data (1.3–1368 km^2) were often substantially larger than those for simulated Fastloc-GPS data (3.1–4.2 km^2; Figure S2, Table S2), the largest difference per simulated individual being 438 times the Fastloc-GPS estimate (1338 km^2 Argos low accuracy cf. 3.05 km^2 Fastloc-GPS, BRB and dBBMM estimates respectively, simulated animal 7). Within each tracking technology, estimates across the four methods excluding AKDE fell within a comparable range, varying by at most a factor of around two. AKDE accounted for low accuracy in the simulated data very successfully, producing size estimates close to the reference area for Argos low-accuracy data—up to 495 times smaller than the other methods (Table S2). Methods often performed inconsistently across tracking technologies; dBBMM and BRB produced the largest estimates with Argos tracking data but gave relatively small estimates for Fastloc-GPS data (Figure 2).

3.2 | Published home range estimates of hawksbill and green turtles

We found 90 studies that reported home range sizes for hawksbill (Ei: $n = 30$) and green turtles (Cm: $n = 60$) at their foraging grounds (Figure 3, Tables S3 and S4) in the Atlantic ($n = 47$), Pacific ($n = 24$) and Indian ($n = 17$) Oceans and in the Mediterranean Sea ($n = 2$). The country accounting for the highest number of studies was the United States ($n = 24$), followed by Australia ($n = 10$) and Mexico

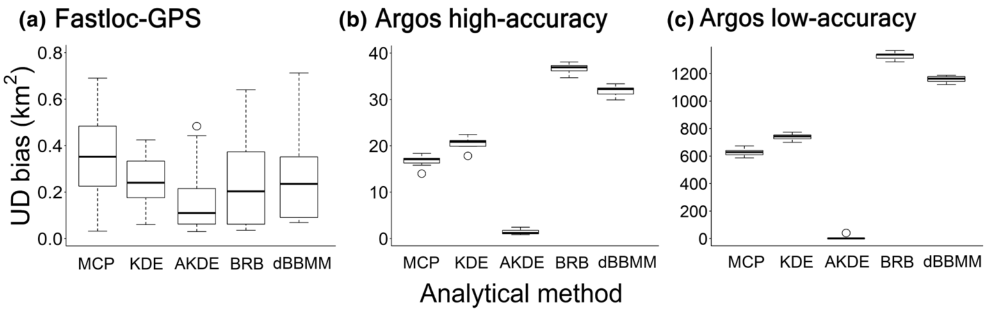

FIGURE 2 Bias—the difference between the 95% utilisation distribution (UD) derived using five analytical methods from simulated data representing (a) Fastloc-GPS, (b) Argos high-accuracy and (c) Argos low-accuracy tracking data and the reference area. Tracking accuracy inflated full home range size estimates by orders of magnitude, while most analytical methods had a more modest impact (namely minimum convex polygon, MCP; fixed kernel density estimation, KDE; autocorrelated kernel density estimation, AKDE; biased random bridge, BRB; and dynamic Brownian bridge movement model, dBBMM). AKDE compensated for lower-accuracy data, giving size estimates close to the reference area for Argos data. Note the variation in y-axis scales.

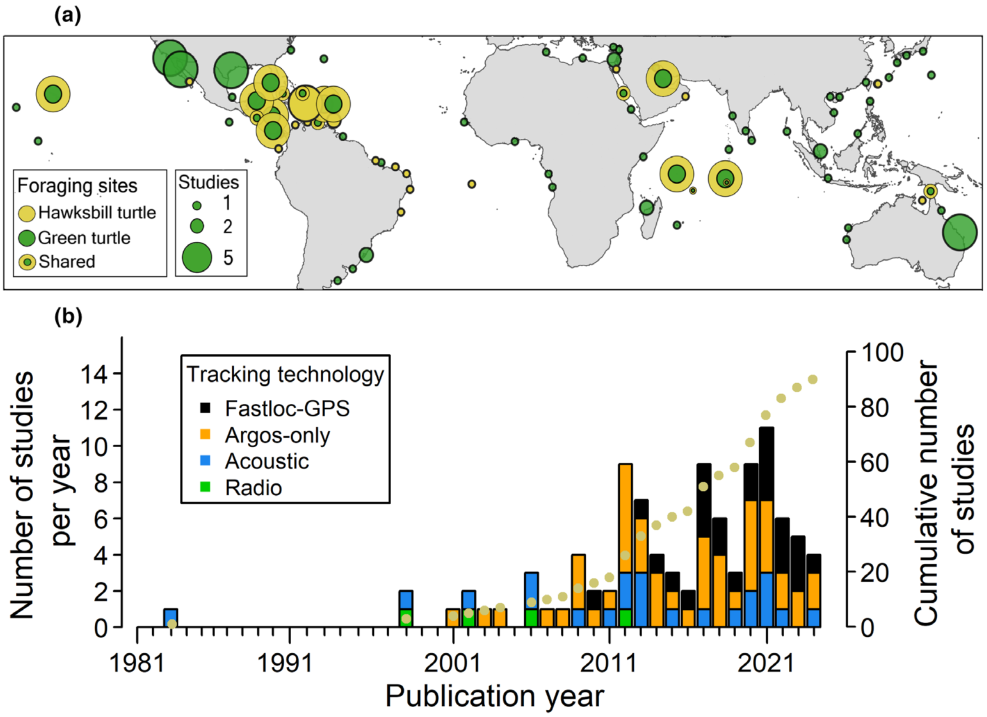

FIGURE 3 (a) Number of foraging home range studies on hawksbill ($n=30$) and green turtles ($n=60$) in 43 countries across the world. (b) Hawkbill and green turtle home range studies by year and by tracking technology. Bars indicate the number of studies; yellow circles show the cumulative number of studies. See Tables S3 and S4 for details.

($n=6$) (Figure 3a). Overall, 41 studies included home range estimates for adult sea turtles (Ei: $n=15$; Cm: $n=26$), 34 for juvenile turtles (Ei: $n=10$; Cm: $n=24$), 11 for subadults (Ei: $n=4$; Cm: $n=7$) and 10 for mixed life stages (Ei: $n=2$; Cm: $n=8$). The number of studies published yearly has grown over time, with the use of Fastloc-GPS tracking technology increasing in the last decade (Figure 3b).

Location data were collected using Fastloc-GPS ($n=24$ studies), Argos ($n=48$), acoustic ($n=22$) and radio transmitters ($n=4$) (Figure 3b). One study used observations reported by SCUBA divers via a smartphone GIS application (Baumbach et al., 2019). In studies that used Argos tracking, filtering of location data ranged from no filtering (LC 3, 2, 1, 0, A, B, Z; $n=2$), low filtering (LC 3, 2, 1, 0, A, B, or 3, 2, 1, A, B; $n=30$), medium filtering (LC 3, 2, 1, 0, or 3, 2, 1, 0, A; $n=5$) to high filtering (LC 3, 2, 1, or 3, 2, 1, A; $n=7$). The most widely used analytical methods for home range estimation were MCP ($n=30$, 1983–2024) and KDE ($n=65$, 1998–2024), with several studies using both ($n=18$, 2002–2023). KDE analyses used different types of smoothing (e.g. fixed, $n=32$; adaptive, $n=1$) and bandwidths (least squared cross validation, LSCV, $n=16$; the Gaussian reference function *href*, $n=10$; plug-in h, $n=10$; ad hoc, $n=4$). While traditional MCP and KDE methods continue to be widely used, studies increasingly adopted new methods: localised convex hull ($n=4$,

TABLE 1 Home range size varies with tracking technology for hawksbill and green turtles.

HR estimator	Tracking technology	Hawksbill turtle HR (mean ± SD, range) km^2	Number of individuals (number of studies)	Green turtle HR (mean ± SD, range) km^2	Number of individuals (number of studies)
95% KUD	Fastloc-GPS	11.5 ± 25.50, 0.01–96.90	28 (5)	27.70 ± 135, 0.09–931.01	72 (8)
	Argos-only	204 ± 194, 38.70–861	48 (5)	540 ± 1081, 0.17–5148	135 (16)
	Acoustic	0.56 ± 0.34, 0.07–1.26	15 (2)	6.60 ± 9.42, 0.73–53.40	164 (8)
	Radio	NA	NA	3.15 ± 2.72, 0.84–8.5	6 (1)
100% MCP	Fastloc-GPS	8.20 ± 7.10, 1.10–19.00	8 (2)	4.66 ± 8.30, 0.01–45.75	30 (4)
	Argos-only	3726 ± 5860, 1.96–27,001	33 (5)	3024 ± 11,738, 0.10–92,734	68 (10)
	Acoustic	0.66 ± 1.07, 0.05–4.04	17 (1)	7.21 ± 8.89, 0.06–39.08	41 (5)
	Radio	0.36 ± 0.17, 0.15–0.55	6 (1)	NA	NA

Note: Tracking datasets with higher estimated accuracy (acoustic and Fastloc-GPS) resulted in small home range sizes relative to those with lower estimated accuracy (Argos). See Tables S3 and S4 for more details.

Abbreviations: HR, home range; KUD, kernel density estimation utilisation distribution; MCP, minimum convex polygon.

2012–2019), BRB (n = 5, 2016–2024), Autocorrelated KDE (n = 4, 2019–2024) and dBBMM (n = 1, 2024).

3.3 | Comparison of published space use estimates for hawksbill and green turtles

Published home range size estimates using 95% KUD and 100% MCP for individual turtles of both species varied significantly between tracking technologies, specifically Argos and acoustic, and Argos and Fastloc-GPS data, but not between acoustic and Fastloc-GPS estimates (Tables 1 and 2). Fastloc-GPS studies recorded 95% KUD home range estimates <40 km^2 across life stages for both species (n = 12 out of 14 studies, range: 0.15–193.9 km^2), whereas Argos-derived 95% KUD estimates were often >50 km^2 for green turtles (n = 10 out of 17 studies, range: 4.8–5148 km^2) and >100 km^2 for hawksbill (n = 6 out of 7 studies, range: 48.7–8474.5 km^2; Figure 4a). Only one example combined Argos data with AKDE, giving a home range estimate of 198 km^2 (Hardin et al., 2024).

There were significant differences in home range size estimates of adults and juveniles of the two species (Fastloc-GPS; Ei: U_{17} = 85, p < 0.05; Cm: U_{49} = 648.5, p < 0.05). Juveniles were recorded occupying mean home ranges <4 km^2 (Ei: 3.01 ± 5.06 km^2, n = 11; Cm: 1.97 ± 1.94 km^2, n = 19), while adults had larger home range sizes of 28.60 km^2 (±37.70, n = 10) and 53.40 km^2 (±187, n = 39) for hawksbills and green turtles respectively. Subadult life stages were excluded due to insufficient data. Between the two species, there was no significant difference in the home range sizes of adults (U = 190, p = 0.91) or juveniles (U = 118, p = 0.58).

4 | DISCUSSION

We have shown here, through theoretical considerations and analysis of empirical data collected across studies, that the accuracy of tracking likely introduces far more variability into animal home range size estimates than the analytical methods used to process the data. This is an important finding when the goal is to synthesise data from across studies to make regional or global comparisons of space use. AKDE provided excellent compensation for low accuracy in simulated animal movement data; however, only a single example in the literature for hawksbill and green turtles used AKDE with Argos data. The accuracy of different tracking technologies, such as Fastloc-GPS and Argos, is often well known (e.g. Douglas et al., 2012; Dujon et al., 2014; Thomson et al., 2017) but is usually not considered explicitly in tracking studies. We conceptualised this issue by considering simulated animal movement data and the likely pattern of locations that would be received from Fastloc-GPS and Argos transmitters. This type of conceptualisation of location error has been considered before, for example, when developing procedures to reliably estimate the speed of travel from low-quality Argos tracking (Hays et al., 2001).

A broad range of analytical methods are routinely used to assess space use, such as MCP (Mohr, 1947), KDE (Worton, 1989), AKDE (Fleming et al., 2015), BRB (Benhamou, 2011) and dBBMM (Kranstauber et al., 2012). Home range estimates are known to vary depending on the analytical method used. For example, AKDE estimates of jaguar home ranges in South America were up to 5 times larger than KUD estimates (Morato et al., 2016), while home range estimates for hawksbill turtles in Florida were 10–30 times larger when using MCP than KDE (Wood et al., 2017). However, we provide evidence that these differences are much smaller than the impact of location accuracy of tracking technologies, except for AKDE which gave home range size estimates close to the reference area even for low-accuracy mock tracking datasets.

Our results suggest that home range estimates from Argos tracking are often likely gross overestimates of an animal's true space use. This limitation of Argos tracking has sometimes been recognised (see Martinez-Estevez et al., 2021) but is often not considered (see Hawkes et al., 2012). Argos tracking provides several benefits that make it an extremely popular option, including global coverage and no recapture requirement, and also has the advantages of lower cost and power

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TABLE 2 Comparison of home range size estimates between tracking technologies for hawksbill and green turtles.

Species	Estimator	Kruskal–Wallis *H*	df	*p*	Technology comparison	Pairwise Wilcoxon test *n*	*p*
Hawksbill turtle	95% KUD	63.84	2	**<0.05**	Argos versus Acoustic	63	**<0.05**
					Argos versus Fastloc-GPS	76	**<0.05**
					Acoustic versus Fastloc-GPS	43	0.16
	100% MCP	43.17	2	**<0.05**	Argos versus Acoustic	50	**<0.05**
					Argos versus Fastloc-GPS	41	**<0.05**
					Acoustic versus Fastloc-GPS	25	**<0.05**
Green turtle	95% KUD	161.37	2	**<0.05**	Argos versus Acoustic	309	**<0.05**
					Argos versus Fastloc-GPS	209	**<0.05**
					Acoustic versus Fastloc-GPS	228	1
	100% MCP	52.22	2	**<0.05**	Argos versus Acoustic	109	**<0.05**
					Argos versus Fastloc-GPS	98	**<0.05**
					Acoustic versus Fastloc-GPS	71	0.06

Note: Significant values ($p<0.05$) are indicated in bold.

Abbreviations: KUD, kernel density estimation utilisation distribution; MCP, minimum convex polygon; *n*, total number of individuals.

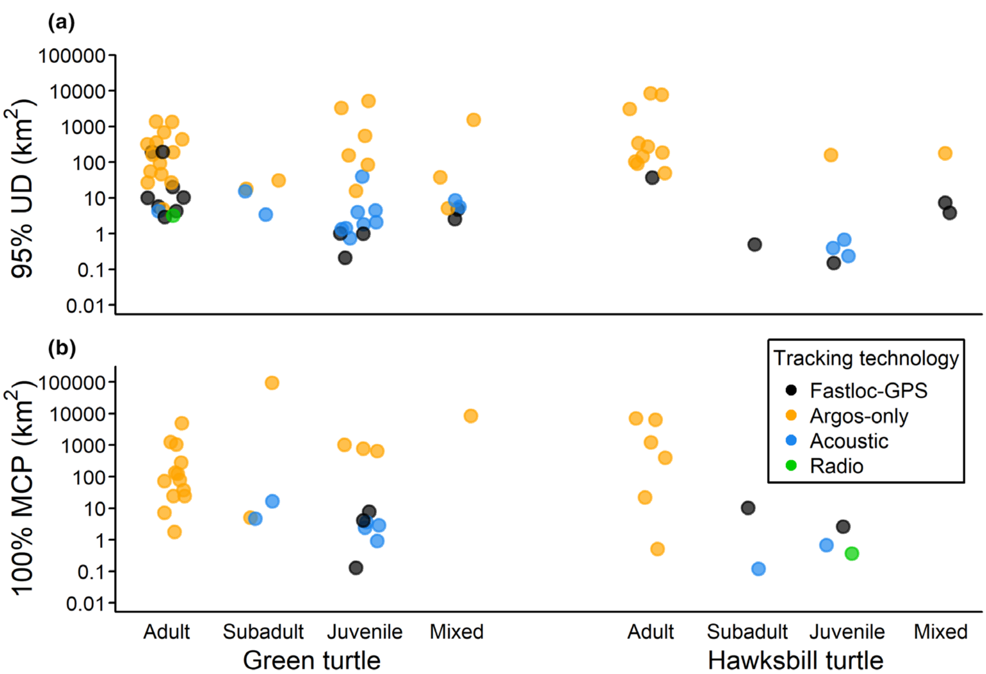

FIGURE 4 Published home range estimates of hawksbill and green turtles at their foraging sites by life stage, tracking technology and analytical method, reported as (a) 95% kernel density estimation utilisation distribution (KUD) and (b) 100% minimum convex polygon (MCP). Home range estimates using 95% KUD <10 km^2 were reported in 71% of Fastloc-GPS studies across life stages of both species and <1 km^2 in 36% of the studies, while only 8% of Argos studies resulted in estimates <10 km^2.

usage than Fastloc-GPS tracking (Witt et al., 2010). However, a key message from our theoretical considerations is that to compare home range sizes across studies, a good starting point is to exclude Argos tracking and focus on high-accuracy Fastloc-GPS tracking, unless AKDE sees broader adoption in future studies. Such analyses synthesising data from across studies may be increasingly important to determine biological factors influencing animal space use. For example, there are concerns that in some parts of the world, high densities of adult green turtles following population recoveries may lead to overgrazing of seagrass meadows, on which this species feeds (Christianen et al., 2023; Gangal et al., 2021). Comparisons of space use patterns using high-accuracy tracking may provide an approach to identifying the occurrence of such habitat destruction (Hardy et al., 2023; Hays et al., 2024). While local productivity and ecosystem health are expected to influence home range size, varying among sites and regions, we show that the much larger influence of tracking accuracy will obscure any such pattern until sufficient high accuracy (Fastloc-GPS) datasets are available to contrast habitat use across regions using comparable datasets, unless data are shared for re-processing using AKDE and further testing using empirical data provides results consistent with those from our simulated assessments.

Once across-study comparisons are distilled down to those using high-resolution tracking (e.g. Fastloc-GPS), the next stage to allow inter-comparison of results is to consider the magnitude of the differences in home range sizes likely introduced by the analytical methods. For example, our theoretical considerations suggest that BRB and dBBMM analyses provide relatively high estimates of space use when used with Argos data, around 350 times larger than the reference area, and 500 times larger than AKDE estimates. Studies on elephants and terrestrial reptiles found that dBBMM analysis reduced type I and type II errors compared with MCP and KDE (Silva et al., 2018; Wilson et al., 2020) and BRB performed better than KDE and MCP in estimating chimpanzee home ranges in Gabon (Martínez-Íñigo et al., 2021). Notably, these studies collected data using radio and GPS devices, suggesting that these movement models perform better relative to other estimators when location accuracy is high—as reflected in our analysis of simulated datasets. It is crucial to note, however, that dBBMM estimates an animal's occurrence distribution rather than its range distribution and that this distinction is important. An occurrence distribution is based on likelihood statistics, has radically different properties and responds differently to increased sampling frequency, which will reduce uncertainty and produce smaller estimates (Alston et al., 2022). While dBBMM has been used to predict home range in the past, the recommendation is that this estimator is intended to answer different ecological questions and should be regarded as distinct from home range estimators, particularly as continuing improvements in tracking technology allow sampling at increasingly high frequencies (Alston et al., 2022).

Our analysis showed that AKDE produced home range size estimates that are comparable to conventional methods such as MCP and KDE for simulated Fastloc-GPS data. This has also been shown for empirical data where AKDE home range size estimates of Perth red foxes (*Vulpes vulpes*) recorded using GPS closely aligned with those of MCP (Kobryn et al., 2023). Furthermore, AKDE estimates for our simulated Argos high- and low-accuracy datasets were similar to those of Fastloc-GPS, indicating the method's efficacy in accounting for varying levels of telemetry error (Fleming et al., 2020). Beyond error correction, AKDE offers advantages by addressing key statistical assumptions. Traditional approaches like MCP and KDE assume locations are independently and identically distributed (IID), while the newer approaches of BRB and dBBMM incorporate Brownian motion (BM) as the underlying movement process. In contrast, AKDE enables selection of the optimal movement model from multiple candidate processes including IID, BM and OUF (Fleming et al., 2015). Our findings underscore the robustness of AKDE in accounting for variable location accuracy when generating estimates of animal space use.

With our simulated Fastloc-GPS data, home range estimates across analytical methods differed by less than a factor of two, although this might be expected to vary with patterns of space use. So, where Fastloc-GPS has been used, across studies we might expect that differences in home range estimates greater than twofold might reflect real differences between regions, rather than different methodologies. For example, for juvenile green turtles tracked using Fastloc-GPS, the mean home range size was 24 km^2 in Florida compared with 0.21 km^2 in the South-West Indian Ocean (Chambault et al., 2020; Wildermann et al., 2019), suggesting that the difference in home range estimates could be linked to biological factors. Similarly, the mean home range size of adult hawksbill females was 1.39 km^2 in the Torres Strait (Barr et al., 2021) compared with 37 km^2 in the Gulf of Carpentaria due to the use of large offshore foraging grounds by some turtles (Hoenner et al., 2015). Such comparisons in home ranges of different populations recorded using high-accuracy Fastloc-GPS technology would indicate that extrinsic factors influencing space use such as habitat characteristics may require conservation attention.

The results of our comparison of home range estimates from the literature are consistent with our findings from theoretical considerations. Generally, high home range estimates were provided by studies for all life stages that used Argos tracking, for example, 5148 km^2 for a juvenile green turtle in the South China Sea (Ng et al., 2018) and 6289 km^2 for adult female hawksbills in the Caribbean (Hawkes et al., 2012). These home range estimates are likely gross overestimates due to noise from low-accuracy tracking. State space models (SSMs) have been recommended for animal tracking data to correct location inaccuracies introduced by Argos technology (Jonsen et al., 2005). Eight out of forty-five Argos tracking studies describing hawksbill and green turtle 95% KUD home ranges in the last 20 years have used SSMs to ameliorate tracking inaccuracy, but only one resulted in a mean home range estimate <100 km^2 (Hart et al., 2017), and three gave estimates >1000 km^2 (e.g. Metz et al., 2020; Sloan et al., 2022). Despite these limitations, Argos tracking has great value for determining migratory destinations (e.g. Maurer et al., 2022) and establishing connectivity between regions (e.g. Attum et al., 2014). Argos-only data should not be used to derive home range size estimates unless AKDE is used to compensate for location accuracy, although this has not yet been tested using real tracking data. Overinflated space use estimates are likely to dilute the actual protection afforded across the estimated range of a species, as conservation measures must be balanced with human access to marine resources. High-accuracy tracking can highlight restricted hotspots of space use where the strictest conservation efforts could be enforced.

As expected from theoretical consideration, high-accuracy Fastloc-GPS tracking revealed generally small home ranges across life stages. For example, Wood et al. (2017) showed that the mean space use of six subadult hawksbill turtles in Southeast Florida was 0.49 km^2, that is these turtles maintained very small foraging areas. Similarly, six adult hawksbills in Australia were reported to occupy a mean home range of 1.38 km^2 (Barr et al., 2021). High-accuracy Fastloc-GPS data can also reveal inter-individual variability in space use such as described by Gredzens et al. (2014) and Tanabe et al. (2023), where most adult green turtles occupied small home range sizes except one turtle in each case that was transient and occupied multiple foraging sites. These high-resolution studies often reveal a diel pattern in space use by turtles. For example, Hays et al. (2024) reported that the mean distance between the centre of day versus night areas occupied was around 1.57 km for 32 green turtles across different foraging grounds. Such studies, along with direct observations, are revealing that ideal foraging areas for sea turtles likely provide both good forage availability as well as protection (e.g. caves or other structures) where turtles have a lower risk of predation (Smulders et al., 2023). Using space use estimates from Fastloc-GPS tracking studies, our review indicates that home range sizes vary between juvenile and adult green turtle populations. For example, immature green turtles in the Chagos Archipelago occupied a mean home range of 1.13 km^2 (Hays et al., 2021), whereas post-nesting green turtles tagged in Chagos occupied a mean day home range of 20 km^2 at their respective foraging grounds spread across the Western Indian Ocean (Christiansen et al., 2017). High-accuracy tracking can clarify differences in space use strategies across life stages and lead to a better understanding of habitat use patterns across regions and species.

While our findings allow more informed comparisons of existing home range estimates from across different studies, an important point to note is that data-sharing and archiving raw data in freely available repositories such as Movebank (www.movebank.org; Kranstauber et al., 2011) will facilitate meta-analysis of location data to determine patterns in space use across the globe. Examples of data deposition in Movebank are already starting to appear (Hays et al., 2021, 2024). The benefits of collaboration and data-sharing are also evident in recent global examinations of movement patterns for particular taxa that are driving informed conservation decisions (e.g. Queiroz et al., 2019; Womersley et al., 2022). While processing raw tracking data from across studies in a consistent manner is ultimately the best data analysis solution, there will always be published studies where the raw data are unavailable. It is in these cases that we emphasise our key message of appreciating the impact of location accuracy when estimating animal space use.

Our study provides evidence that tracking technologies introduce far greater variation in home range size estimates than the analytical methods used on the data they collect. High-resolution technologies like Fastloc-GPS provide reliable estimates of fine-scale space use of animals, while Argos tracking is effective for recording broad movements like migratory paths. These differences can influence decisions in spatial planning and are particularly relevant for global conservation initiatives such as the 30 × 30 Biodiversity Target 3 of the Kunming-Montreal Global Biodiversity Framework (WWF & IUCN WCPA, 2023), or in designating areas for species and habitat protection such as Important Shark and Ray Areas (ISRAs; Kyne et al., 2023). Where sufficient animals have been tracked, high-accuracy tracking can allow the strictest conservation measures to be applied where they are most needed, rather than diluted across larger areas that may reflect location inaccuracy rather than animal space use. We emphasise that method selection is crucial for obtaining reliable ecological insights that can guide evidence-based management strategies.

AUTHOR CONTRIBUTIONS

Nicole Esteban, Graeme C. Hays, and Kimberley L. Stokes conceived the study. Nupur Kale compiled and analysed data supported by Kimberley L. Stokes. All authors contributed critically to the manuscript text and gave final approval for publication.

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The authors declare no financial or competing interests.

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DATA AVAILABILITY STATEMENT

Data and code available via the Dryad Digital Repository https://doi.org/10.5061/dryad.31zcrjf0b (Kale et al., 2025).

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REFERENCES

Alston, J. M., Fleming, C. H., Noonan, M. J., Tucker, M. A., Silva, I., Folta, C., Akre, T. S. B., Ali, A. H., Belant, J. L., Beyer, D., Blaum, N., Böhning-Gaese, K., Cunha de Paula, R., Dekker, J., Drescher-Lehman, J., Farwig, N., Fichtel, C., Fischer, C., Ford, A. T., … Calabrese, J. M. (2022). Clarifying space use concepts in ecology: Range vs. occurrence distributions. *BioRxiv*, 2022, 09 https://doi.org/10.1101/2022.09.29.509951

Attum, O., Kramer, A., Mahmoud, T., & Fouda, M. (2014). Post-nesting migrations patterns of Green Turtles (*Chelonia mydas*) from the Egyptian Red Sea. *Zoology in the Middle East*, *60*, 299–305. https://doi.org/10.1080/09397140.2014.962833

Barr, C. E., Hamann, M., Shimada, T., Bell, I., Limpus, C. J., & Ferguson, J. (2021). Post-nesting movements and feeding ground distribution by the hawksbill turtle (*Eretmochelys imbricata*) from rookeries in Torres Strait. *Wildlife Research*, *48*, 598–608. https://doi.org/10.1071/WR20183

Baumbach, D. S., Anger, E. C., Collado, N. A., & Dunbar, S. G. (2019). Identifying sea turtle home ranges utilizing citizen-science data from novel web-based and smartphone GIS applications. *Chelonian Conservation and Biology*, *18*, 133–144. https://doi.org/10.2744/CCB-1355.1

Benhamou, S. (2011). Dynamic approach to space and habitat use based on biased random bridges. *PLoS One*, *6*, e14592. https://doi.org/10.1371/journal.pone.0014592

Börger, L., Franconi, N., De Michele, G., Gantz, A., Meschi, F., Manica, A., Lovari, S., & Coulson, T. (2006). Effects of sampling regime on the mean and variance of home range estimates. *Journal of Animal Ecology*, *75*, 1393–1405. https://www.jstor.org/stable/4125081

Burt, W. H. (1943). Territoriality and home range concepts as applied to mammals. *Journal of Mammalogy*, *24*, 346–352. https://doi.org/10.2307/1374834

Calabrese, J. M., Fleming, C. H., & Gurarie, E. (2016). Ctmm: An r package for analyzing animal relocation data as a continuous-time stochastic process. *Methods in Ecology and Evolution*, *7*, 1124–1132. https://doi.org/10.1111/2041-210x.12559

Chambault, P., Dallaeau, M., Nicet, J. B., Mouquet, P., Ballorain, K., Jean, C., Ciccione, S., & Bourjea, J. (2020). Contrasted habitats and individual plasticity drive the fine scale movements of juvenile green turtles in coastal ecosystems. *Movement Ecology*, *8*, 1–15. https://doi.org/10.1186/s40462-019-0184-2

Christianen, M. J. A., Smulder, F. O. H., Vonk, J. A., Becking, L. E., Bouma, T. J., Engel, S. M., James, R. K., Nava, M. I., de Smit, J. C., van der Zee, J. P., Palsbøll, P. J., & Bakker, E. S. (2023). Seagrass ecosystem multifunctionality under the rise of a flagship marine megaherbivore. *Global Change Biology*, *29*, 215–230. https://doi.org/10.1111/gcb.16464

Christiansen, F., Esteban, N., Mortimer, J. A., Dujon, A. M., & Hays, G. C. (2017). Diel and seasonal patterns in activity and home range size of green turtles on their foraging grounds revealed by extended Fastloc-GPS tracking. *Marine Biology*, *164*, 1–11. https://doi.org/10.1007/s00227-016-3048-y

CLS. (2016). Argos User's Manual: Worldwide tracking and environmental monitoring by satellite. https://www.argos-system.org/cls-argos-system-user-manual/

Crego, R. D., Fennessy, J., Brown, M. B., Connette, G., Stacy-Dawes, J., Masiaine, S., & Stabach, J. A. (2024). Combining species distribution models and moderate resolution satellite information to guide conservation programs for reticulated giraffe. *Animal Conservation*, *27*, 160–170. https://doi.org/10.1111/acv.12894

Davies, T. E., Carneiro, A. P. B., Campos, B., Hazin, C., Dunn, D. C., Gjerde, K. M., Johnson, D. E., & Dias, M. P. (2021). Tracking data and the conservation of the high seas: Opportunities and challenges. *Journal of Applied Ecology*, *58*, 2703–2710. https://doi.org/10.1111/1365-2664.14032

Douglas, D. C., Weinzierl, R. C., Davidson, S., Kays, R., Wikelski, M., & Bohrer, G. (2012). Moderating Argos location errors in animal tracking data. *Methods in Ecology and Evolution*, *3*, 999–1007. https://doi.org/10.1111/j.2041-210X.2012.00245.x

Dujon, A. M., Lindstrom, R. T., & Hays, G. C. (2014). The accuracy of Fastloc-GPS locations and implications for animal tracking. *Methods in Ecology and Evolution*, *5*, 1162–1169. https://doi.org/10.1111/2041-210X.12286

Dwyer, R. G., Campbell, H. A., Irwin, T. R., & Franklin, C. E. (2015). Does the telemetry technology matter? Comparing estimates of aquatic animal space-use generated from GPS-based and passive acoustic tracking. *Marine and Freshwater Research*, *66*, 654–664. https://doi.org/10.1071/MF14042

Fancy, S. G., Pank, L. F., Douglas, D. C., Curby, C. H., Garner, G. W., Amstrup, S. C., & Regelin, W. L. (1988). *Satellite telemetry: A new tool for wildlife research and management*. US Fisheries and Wildlife Services Research Publication. https://pubs.usgs.gov/publication/70185511

Fleming, C. H., Calabrese, J. M., Mueller, T., Olson, K. A., Leimgruber, P., & Fagan, W. F. (2014). Data from: From fine-scale foraging to home ranges: A semi-variance approach to identifying movement modes across spatiotemporal scales. *Dryad Digital Repository*. https://doi.org/10.5061/dryad.45157

Fleming, C. H., Drescher-Lehman, J., Noonan, M. J., Akre, T. S. B., Brown, D. J., Cochrane, M. M., Dejid, N., DeNicola, V., DePerno, C. S., Dunlop, J. N., Gould, N. P., Harrison, A.-L., Hollins, J., Ishii, H., Kaneko, Y., Kays, R., Killen, S. S., Koeck, B., Lambertucci, S. A., … Calabrese, J. M. (2020). A comprehensive framework for handling location error in animal tracking data. *BioRxiv*, 2022 https://doi.org/10.1101/2020.06.12.130195

Fleming, C. H., Fagan, W. F., Mueller, T., Olson, K. A., Leimgruber, P., & Calabrese, J. M. (2015). Rigorous home range estimation with movement data: A new autocorrelated kernel density estimator. *Ecology*, *96*, 1182–1188. https://doi.org/10.1890/14-2010.1

Gangal, M., Gafoor, A., D'Souza, E., Kelkar, N., Karkarey, R., Marbà, N., Arthur, R., & Alcoverro, T. (2021). Sequential overgrazing by green turtles causes archipelago-wide functional extinctions of seagrass meadows. *Biological Conservation*, *260*, 109195. https://doi.org/10.1016/j.biocon.2021.109195

Gottwald, J., Royauté, R., Becker, M., Geitz, T., Höchst, J., Lampe, P., Leister, L., Lindner, K., Maier, J., Rösner, S., Schabo, D. G., Freisleben, B., Brandl, R., Müller, T., Farwig, N., & Nauss, T. (2022). Classifying the activity states of small vertebrates using automated VHF telemetry. *Methods in Ecology and Evolution*, *14*, 252–264. https://doi.org/10.1111/2041-210X.14037

Gredzens, C., Marsh, H., Fuentes, M. M. P. B., Limpus, C. J., Shimada, T., & Hamann, M. (2014). Satellite tracking of sympatric marine megafauna can inform the biological basis for species co-management. *PLoS One*, *9*, e98944. https://doi.org/10.1371/journal.pone.0098944

Grolemund, G., & Wickham, H. (2011). Dates and times made easy with lubridate. *Journal of Statistical Software*, *40*, 1–25. https://doi.org/10.18637/jss.v040.i03

Hardin, E. E., Cullen, J. A., & Fuentes, M. M. P. B. (2024). Comparing acoustic and satellite telemetry: An analysis quantifying the space use of *Chelonia mydas* in Bimini, Bahamas. *Royal Society Open Science*, *11*, 231152. https://doi.org/10.1098/rsos.231152

Hardy, R. F., Meylan, A. B., Gray, J. A., & Meylan, P. A. (2023). Daily, seasonal, and long-distance movements inferred from Fastloc-GPS telemetry of immature green turtles (*Chelonia mydas*) at a high-latitude, mid-ocean developmental site. *PLoS One*, *18*, e0292235. https://doi.org/10.1371/journal.pone.0292235

Hart, K. M., Iverson, A. R., Benscoter, A. M., Fujisaki, I., Cherkiss, M. S., Pollock, C., Lundgren, I., & Hillis-Starr, Z. (2017). Resident areas and migrations of female green turtles nesting at Buck Island reef National Monument, St. Croix, US Virgin Islands. *Endangered Species Research*, *32*, 89–101. https://doi.org/10.3354/esr00793

Hawkes, L. A., Tómas, J., Revuelta, O., León, Y. M., Blumenthal, J. M., Broderick, A. C., Fish, M., Raga, J. A., Witt, M. J., & Godley, B. J. (2012). Migratory patterns in hawksbill turtles described by satellite tracking. *Marine Ecology Progress Series*, *461*, 223–232. https://doi.org/10.3354/meps09778

Hays, G. C., Åkesson, S., Godley, B. J., Luschi, P., & Santidrian, P. (2001). The implications of location accuracy for the interpretation of satellite-tracking data. *Animal Behaviour*, *61*, 1035–1040. https://doi.org/10.1006/anbe.2001.1685

Hays, G. C., Bailey, H., Bograd, S. J., Don Bowen, W., Campagna, C., Carmichael, R. H., Casale, P., Chiaradia, A., Costa, D. P., Cuevas, E., Nico de Bruyn, P. J., Dias, M. P., Duarte, C. M., Dunn, D. C., Dutton, P. H., Esteban, N., Friedlander, A., Goetz, K. T., Godley, B. J., … Sequeira, A. M. M. (2019). Translating marine animal tracking data into conservation policy and management. *Trends in Ecology & Evolution*, *34*, 459–473. https://doi.org/10.1016/j.tree.2019.01.009

Hays, G. C., Mortimer, J. A., Rattray, A., Shimada, T., & Esteban, N. (2021). High accuracy tracking reveals how small conservation areas can protect marine megafauna. *Ecological Applications*, *31*, e02418. https://doi.org/10.1002/eap.2418

Hays, G. C., Rattray, A., Shimada, T., & Esteban, N. (2024). Individual variation in home-range across an ocean basin and links to habitat quality and management. *Journal of Applied Ecology*, *61*, 658–668. https://doi.org/10.1111/1365-2664.14599

Hoenner, X., Whiting, S. D., Hamann, M., Limpus, C. J., Hindell, M. A., & McMahon, C. R. (2015). High-resolution movements of critically endangered hawksbill turtles help elucidate conservation requirements in northern Australia. *Marine and Freshwater Research*, *67*, 1263–1278. https://doi.org/10.1071/MF15013

Horne, J. S., Garton, E. O., Krone, S. M., & Lewis, J. S. (2007). Analyzing animal movements using brownian bridges. *Ecology*, *88*, 2354–2363. https://doi.org/10.1890/06-0957.1

Jonsen, I. D., Mills Flemming, J., & Myers, R. A. (2005). Robust state-space modeling of animal movement data. *Ecology*, *86*, 2874–2880. https://doi.org/10.1890/04-1852

Kale, N., Stokes, K. L., Hays, G. C., & Esteban, N. (2025). Data from: Separating biological signal from methodological noise in home range estimates. *Dryad Digital Repository*. https://doi.org/10.5061/dryad.31zcrjf0b

Katzner, T. E., & Arlettaz, R. (2020). Evaluating contributions of recent tracking-based animal movement ecology to conservation management. *Frontiers in Ecology and Evolution*, *7*, 519. https://doi.org/10.3389/fevo.2019.00519

Kobryn, H. T., Swinhoe, E. J., Bateman, P. W., Adams, P. J., Shepard, J. M., & Fleming, P. A. (2023). Foxes at your front door? Habitat selection and home range estimation of suburban red foxes (*Vulpes vulpes*). *Urban Ecosystems*, *26*, 1–17. https://doi.org/10.1007/s11252-022-01252-5

Kot, C. Y., Åkesson, S., Alfaro-Shigueto, J., Amorocho Llanos, D. F., Antonopoulou, M., Balazs, G. H., Baverstock, W. R., Blumenthal, J. M., Broderick, A. C., Bruno, I., Canbolat, A. F., Casale, P., Cejudo, D., Coyne, M. S., Curtice, C., DeLand, S., DiMatteo, A., Dodge, K., Dunn, D. C., … Halpin, P. N. (2022). Network analysis of sea turtle movements and connectivity: A tool for conservation prioritization. *Diversity and Distributions*, *28*, 810–829. https://doi.org/10.1111/ddi.13485

Kranstauber, B., Cameron, A., Weinzerl, R., Fountain, T., Tilak, S., Wikelski, M., & Kays, R. (2011). The Movebank data model for animal tracking. *Environmental Modelling & Software*, *26*, 834–835. https://doi.org/10.1016/j.envsoft.2010.12.005

Kranstauber, B., Kays, R., LaPoint, S. D., Wikelski, M., & Safi, K. (2012). A dynamic Brownian bridge movement model to estimate utilization distributions for heterogeneous animal movement. *Journal of Animal Ecology*, *81*, 738–746. https://doi.org/10.1111/j.1365-2656.2012.01955.x

Kuhn, C. E., Johnson, D. S., Ream, R. R., & Gelatt, T. S. (2009). Advances in the tracking of marine species: Using GPS locations to evaluate satellite track data and a continuous-time movement model. *Marine Ecology Progress Series*, *393*, 97–109. https://doi.org/10.3354/meps08229

Kyne, P. M., di Sciara, G. N., Morera, A. B., Charles, R., Rodríguez, E. G., Fernando, D., Pestana, A. G., Priest, M., & Jabado, R. W. (2023). Important shark and ray areas: A new tool to optimize spatial planning for sharks. *Oryx*, *57*, 145–148. https://doi.org/10.1017/S0030605322001624

Lea, J. S. E., Humphries, N. E., von Brandis, R. G., Clarke, C. R., & Sims, D. W. (2016). Acoustic telemetry and network analysis reveal the space use of multiple reef predators and enhance marine protected area design. *Proceedings of the Royal Society B: Biological Sciences*, *283*, 20160717. https://doi.org/10.1098/rspb.2016.0717

Martinez-Estevez, L., Amador, J. P. C., Amador, F. C., Zilliacus, K. M., Pacheco, A. M., Seminoff, J. A., Lucero, J., Oceguera, K., Tershy, B. R., & Croll, D. A. (2021). Spatial ecology of hawksbill sea turtles (*Eretmochelys imbricata*) in foraging habitats of the Gulf of California, Mexico. *Global Ecology and Conservation*, *27*, e01540. https://doi.org/10.1016/j.gecco.2021.e01540

Martínez-Íñigo, L., Baas, P., Klein, H., Pika, S., & Deschner, T. (2021). Home range size in central chimpanzees (*Pan troglodytes troglodytes*) from Loango National Park, Gabon. *Primates*, *62*, 723–734. https://doi.org/10.1007/s10329-021-00927-5

Maurer, A. S., Dawson, C., Bjorkland, R., Donaldson, A., Stapleton, S. P., Richardson, J. I., Parker, D. M., Balazs, G. H., & Schroeder, B. A. (2022). Satellite telemetry elucidates migratory pathways and foraging areas for hawksbill sea turtles, *Eretmochelys imbricata*, in the Caribbean. *Caribbean Journal of Science*, *52*, 126–141. https://doi.org/10.18475/cjos.v52i1.a10

Metz, T. L., Gordon, M., Mokrech, M., & Guillen, G. (2020). Movements of juvenile green turtles (*Chelonia mydas*) in the nearshore waters of the northwestern Gulf of Mexico. *Frontiers in Marine Science*, *7*, 647. https://doi.org/10.3389/fmars.2020.00647

Mohr, C. O. (1947). Table of equivalent populations of northern American small mammals. *The American Midland Naturalist*, *37*, 223–249. https://doi.org/10.2307/2421652

Morato, R. G., Stabach, J. A., Fleming, C. H., Calabrese, J. M., De Paula, R. C., Ferraz, K. M. P. M., Kantek, D. L. Z., Miyazaki, S. S., Pereira, T. D. C., Araujo, G. R., Paviolo, A., De Angelo, C., Di Bitetti, M. S., Cruz, P., Lima, F., Cullen, L., Sana, D. A., Ramalho, E. E., Carvalho, M. M., … Leimgruber, P. (2016). Space use and movement of a neotropical top predator: The endangered jaguar. *PLoS One*, *11*, e0168176. https://doi.org/10.1371/journal.pone.0168176

Ng, C. K. Y., Gu, H. X., Li, T. H., Ye, M. B., Xia, Z. R., Zhang, F. Y., Duan, J. X., Hsu, C. K., Balazs, G. H., & Murphy, M. B. (2018). Insights into identifying habitat hot spots and migratory corridors of green turtles in the South China region. *Aquatic Conservation: Marine and Freshwater Ecosystems*, *28*, 1181–1191. https://doi.org/10.1002/aqc.2923

Noonan, M. J., Tucker, M. A., Fleming, C. H., Akre, T. S., Alberts, S. C., Ali, A. H., Altmann, J., Antunes, P. C., Belant, J. L., Beyer, D., Blaum, N., Böhning-Gaese, K., Cullen, L., Jr., de Paula, R. C., Dekker, J., Drescher-Lehman, J., Farwig, N., Fichtel, C., Fischer, C., … Calabrese, J. M. (2019). A comprehensive analysis of autocorrelation and bias in home range estimation. *Ecological Monographs*, *89*, e01344. https://doi.org/10.1002/ecm.1344

Pebsworth, P. A., Morgan, H. R., & Huffman, M. A. (2012). Evaluating home range techniques: Use of global positioning system (GPS) collar data from chacma baboons. *Primates*, *53*, 345–355. https://doi.org/10.1007/s10329-012-0307-5

Peris, A., Closa, F., Marco, I., Acevedo, P., Barasona, J. A., & Casas-Díaz, E. (2020). Towards the comparison of home range estimators obtained from contrasting tracking regimes: The wild boar as a case study. *European Journal of Wildlife Research*, *66*, 1–10. https://doi.org/10.1007/s10344-020-1370-7

Queiroz, N., Humphries, N. E., Couto, A., Vedor, M., Da Costa, I., Sequeira, A. M. M., Mucientes, G., Santos, A. M., Abascal, F. J., Abercrombie, D. L., Abrantes, K., Acuña-Marrero, D., Afonso, A. S., Afonso, P., Anders, D., Araujo, G., Arauz, R., Bach, P., Barnett, A., … Sousa, L. L. (2019). Global spatial risk assessment of sharks under the footprint of fisheries. *Nature*, *572*, 461–466. https://doi.org/10.1038/s41586-019-1444-4

R Core Team. (2023). *R: A language and environment for statistical computing*. R Foundation for Statistical Computing. https://www.R-project.org/

Sahri, A., Jak, C., Putra, M. I. H., Murk, A. J., Andrews-Goff, V., Double, M. C., & Van Lammeren, R. J. (2022). Telemetry-based home range and habitat modelling reveals that the majority of areas important for pygmy blue whales are currently unprotected. *Biological Conservation*, *272*, 109594. https://doi.org/10.1016/j.biocon.2022.109594

Shimada, T., Thums, M., Hamann, M., Limpus, C. J., Hays, G. C., FitzSimmons, N. N., Wildermann, N. E., Duarte, C. M., & Meekan, M. G. (2021). Optimising sample sizes for animal distribution analysis using tracking data. *Methods in Ecology and Evolution*, *12*, 288–297. https://doi.org/10.1111/2041-210X.13506

Signer, J., Balkenhol, N., Ditmer, M., & Fieberg, J. (2015). Does estimator choice influence our ability to detect changes in home-range size? *Animal Biotelemetry*, *3*, 1–9. https://doi.org/10.1186/s40317-015-0051-x

Silva, I., Crane, M., Marshall, B. M., & Strine, C. T. (2020). Reptiles on the wrong track? Moving beyond traditional estimators with dynamic

Brownian Bridge Movement Models. *Movement Ecology*, *8*, 1–13. https://doi.org/10.1186/s40462-020-00229-3

Silva, I., Crane, M., Suwanwaree, P., Strine, C., & Goode, M. (2018). Using dynamic Brownian Bridge Movement Models to identify home range size and movement patterns in king cobras. *PLoS One*, *13*, e0203449. https://doi.org/10.1371/journal.pone.0203449

Sloan, K. A., Addison, D. S., Glinsky, A. T., Benscoter, A. M., & Hart, K. M. (2022). Inter-nesting movements, migratory pathways, and resident foraging areas of green sea turtles (*Chelonia mydas*) satellite-tagged in Southwest Florida. *Frontiers in Marine Science*, *8*, 775367. https://doi.org/10.3389/fmars.2021.775367

Smulders, F. O. H., Bakker, E. S., O'Shea, O. R., Campbell, J. E., Rhoades, O. K., & Christianen, M. J. A. (2023). Green turtles shape the seascape through grazing patch formation around habitat features: Experimental evidence. *Ecology*, *104*, e3902. https://doi.org/10.1002/ecy.3902

Tamburello, N., Côté, I. M., & Dulvy, N. K. (2015). Energy and the scaling of animal space use. *The American Naturalist*, *186*, 196–211. https://doi.org/10.1086/682070

Tanabe, L. K., Cochran, J. E., & Berumen, M. (2023). Inter-nesting, migration, and foraging behaviors of green turtles (*Chelonia mydas*) in the central-southern Red Sea. *Scientific Reports*, *13*, 11222. https://doi.org/10.1038/s41598-023-37942-z

Thomson, J., Börger, L., Christianen, M., Esteban, N., Laloë, J.-O., & Hays, G. C. (2017). Implications of location accuracy and data volume for home range estimation and fine-scale movement analysis: Comparing Argos and Fastloc-GPS tracking data. *Marine Biology*, *164*, 1–9. https://doi.org/10.1007/s00227-017-3225-7

Uhlenbeck, G. E., & Ornstein, L. S. (1930). On the theory of the Brownian motion. *Physical Review*, *36*, 823–841.

Wildermann, N. E., Sasso, C. R., Stokes, L. W., Snodgrass, D., & Fuentes, M. M. P. B. (2019). Habitat use and behaviour of multiple species of marine turtles at a foraging area in the northeastern Gulf of Mexico. *Frontiers in Marine Science*, *6*, 155. https://doi.org/10.3389/fmars.2019.00155

Wilson, G., Gray, R. J., & Sofyan, H. (2020). Identifying the variation in utilization density estimators and home ranges of elephant clans in Aceh, Sumatra, Indonesia. *European Journal of Wildlife Research*, *66*, 88. https://doi.org/10.1007/s10344-020-01426-6

Witt, M. J., Åkesson, S., Broderick, A. C., Coyne, M. S., Ellick, J., Formia, A., Hays, G. C., Luschi, P., Stroud, S., & Godley, B. J. (2010). Assessing accuracy and utility of satellite-tracking data using Argos-linked Fastloc-GPS. *Animal Behaviour*, *80*, 571–581. https://doi.org/10.1016/j.anbehav.2010.05.022

Womersley, F. C., Humphries, N. E., Queiroz, N., Vedor, M., da Costa, I., Furtado, M., Tyminski, J. P., Abrantes, K., Araujo, G., Bach, S. S., Barnett, A., Berumen, M. L., Lion, S. B., Braun, C. D., Clingham, E., Cochran, J. E. M., de la Parra, R., Diamant, S., Dove, A. D. M., … Sims, D. W. (2022). Global collision-risk hotspots of marine traffic and the world's largest fish, the whale shark. *Ecology*, *119*, e2117440119. https://doi.org/10.1073/pnas.2117440119

Wood, L. D., Brunnick, B., & Milton, S. L. (2017). Home range and movement patterns of subadult hawksbill sea turtles in Southeast Florida. *Journal of Herpetology*, *51*, 58–67. https://doi.org/10.1670/15-133

Worton, B. J. (1989). Kernel methods for estimating the utilization distribution in home-range studies. *Ecology*, *70*, 164–168. https://doi.org/10.2307/1938423

WWF & IUCN WCPA. (2023). A guide to inclusive, equitable and effective implementation of Target 3 of the Kunming-Montreal Global Biodiversity Framework: Version 1, August 2023.

Additional Data Sources

Balazs, G. H., Parker, D. M., & Marc, R. R. (2017). Ocean pathways and residential foraging locations for satellite tracked green turtles breeding at French Frigate Shoals in the Hawaiian Islands. *Micronesica*, *4*, 1–19. https://georgehbalazs.com/wp-content/uploads/2018/10/Balazs_Parker_Rice2017_OceanPathwaysFFS_Hawaii_Micronesica-1.pdf

Berube, M. D., Dunbar, S. G., Rützler, K., & Hayes, W. K. (2012). Home range and foraging ecology of juvenile hawksbill sea turtles (*Eretmochelys imbricata*) on inshore reefs of Honduras. *Chelonian Conservation and Biology*, *11*, 33–43. https://doi.org/10.2744/CCB-0898.1

Blanco, G. S., Morreale, S. J., Bailey, H., Seminoff, J. A., Paladino, F. V., & Spotila, J. R. (2012). Post-nesting movements and feeding grounds of a resident East Pacific green turtle *Chelonia mydas* population from Costa Rica. *Endangered Species Research*, *18*, 233–245. https://doi.org/10.3354/esr00451

Broderick, A. C., Coyne, M. S., Fuller, W. J., Glen, F., & Godley, B. J. (2007). Fidelity and over-wintering of sea turtles. *Proceedings of the Royal Society B: Biological Sciences*, *274*, 1533–1538. https://doi.org/10.1098/rspb.2007.0211

Carman, V. G., Falabella, V., Maxwell, S., Albareda, D., Campagna, C., & Mianzan, H. (2012). Revisiting the ontogenetic shift paradigm: The case of juvenile green turtles in the SW Atlantic. *Journal of Experimental Marine Biology and Ecology*, *429*, 64–72. https://doi.org/10.1016/j.jembe.2012.06.007

Carrión-Cortez, J., Canales-Cerro, C., Arauz, R., & Riosmena-Rodríguez, R. (2013). Habitat use and diet of juvenile eastern Pacific hawksbill turtles (*Eretmochelys imbricata*) in the north Pacific coast of Costa Rica. *Chelonian Conservation and Biology*, *12*, 235–245. https://doi.org/10.2744/CCB-1024.1

Chan, S. K., Chan, J., Lo, L., & Balazs, G. H. (2003). Satellite tracking of the post-nesting migration of a green turtle (*Chelonia mydas*) from Hong Kong. *Marine Turtle Newsletter*, *102*, 2–4. www.seaturtle.org/mtn/archives/mtn102/mtn102p2.shtml

Craig, P., Parker, D., Brainard, R., Rice, M., & Balazs, G. (2007). Migrations of green turtles in the central South Pacific. *Biological Conservation*, *116*, 433–438. https://doi.org/10.1016/S0006-3207(03)00217-9

Crear, D. P., Lawson, D. D., Seminoff, J. A., Eguchi, T., LeRoux, R. A., & Lowe, C. G. (2017). Habitat use and behaviour of the East Pacific green turtle, *Chelonia mydas*, in an urbanized system. *Bulletin of the Southern California Academy of Sciences*, *116*, 17–32. https://doi.org/10.3160/soca-116-01-17-32.1

Cuevas, E., Abreu-Grobois, F. A., Guzmán-Hernández, V., Liceaga-Correa, M. A., & Van Dam, R. P. (2008). Post-nesting migratory movements of hawksbill turtles *Eretmochelys imbricata* in waters adjacent to the Yucatan Peninsula, Mexico. *Endangered Species Research*, *10*, 123–133. https://doi.org/10.3354/esr00128

Eguchi, T., Bredvik, J., Graham, S., LeRoux, R., Saunders, B., & Seminoff, J. A. (2020). Effects of a power plant closure on home ranges of green turtles in an urban foraging area. *Endangered Species Research*, *41*, 265–277. https://doi.org/10.3354/esr01027

Fujisaki, I., Hart, K. M., & Sartain-Iverson, A. R. (2016). Habitat selection by green turtles in a spatially heterogenous benthic landscape in dry Tortugas National Park, Florida. *Aquatic Biology*, *24*, 185–199. https://doi.org/10.3354/ab00647

Gaos, A. R., Lewison, R. L., Wallace, B. P., Yañez, I. L., Liles, M. J., Nichols, W. J., Baquero, A., Hasbún, C. R., Vasquez, M., Urteaga, J., & Seminoff, J. A. (2012). Spatial ecology of critically endangered hawksbill turtles *Eretmochelys imbricata*: Implications for management and conservation. *Marine Ecology Progress Series*, *450*, 181–194. https://doi.org/10.3354/meps09591

Griffin, L. P., Smith, B. J., Cherkiss, M. S., Crowder, A. G., Pollock, C. G., Hillis-Starr, Z., Danylchuk, A. J., & Hart, K. M. (2020). Space use and relative habitat selection for immature green turtles within a Caribbean marine protected area. *Animal Biotelemetry*, *8*, 22. https://doi.org/10.1186/s40317-020-00209-9

Hart, K. M., & Fujisaki, I. (2010). Satellite tracking reveals habitat use by juvenile green sea turtles *Chelonia mydas* in the Everglades, Florida, USA. *Endangered Species Research*, *11*, 221–232. https://doi.org/10.3354/esr00284

Hart, K. M., Iverson, A. R., Benscoter, A. M., Fujisaki, I., Cherkiss, M. S., Pollock, C., Lundgren, I., & Hillis-Starr, Z. (2019). Satellite tracking of hawksbill turtles nesting at Buck Island Reef National Monument, US Virgin Islands: Inter-nesting and foraging period movements and migrations. *Biological Conservation*, *229*, 1–13. https://doi.org/10.1016/j.biocon.2018.11.011

Hart, K. M., Sartain, A. R., Fujisaki, I., Pratt, H. L., Jr., Morley, D., & Feeley, M. W. (2012). Home range, habitat use, and migrations of hawkbill turtles tracked from Dry Tortugas National Park, Florida, USA. *Marine Ecology Progress Series*, *457*, 193–207. https://doi.org/10.3354/meps09744

Hazel, J., Hamann, M., & Lawler, I. R. (2013). Home range of immature green turtles tracked at an offshore tropical reef using automated passive acoustic technology. *Marine Biology*, *160*, 617–627. https://doi.org/10.1007/s00227-012-2117-0

Horrocks, J. A., Vermeer, L. A., Krueger, B., Coyne, M., Schroeder, B. A., & Balazs, G. H. (2001). Migration routes and destination characteristics of post-nesting hawksbill turtles satellite-tracked from Barbados, West Indies. *Chelonian Conservation and Biology*, *4*, 107–114. https://www.widecast.org/What/Country/Barbados/Docs/Horrocks_et_al_(2001)_Migratory_Hawksbills.pdf

Lamont, M. M., Benscoter, A. M., & Hart, K. M. (2023). Green turtle movements in the Gulf of Mexico: Tracking reveals new migration corridor and habitat use suggestive of MPA expansion. *Global Ecology and Conservation*, *42*, e02380. https://doi.org/10.1016/j.gecco.2023.e02380

Lamont, M. M., Fujisaki, I., Stephens, B. S., & Hackett, C. (2015). Home range and habitat use of juvenile green turtles (*Chelonia mydas*) in the northern Gulf of Mexico. *Animal Biotelemetry*, *3*, 53. https://doi.org/10.1186/s40317-015-0089-9

Lamont, M. M., & Iverson, A. R. (2018). Shared habitat use by juveniles of three sea turtle species. *Marine Ecology Progress Series*, *606*, 187–200. https://doi.org/10.3354/meps12748

Lamont, M. M., Johnson, D., & Catizone, D. J. (2021). Movements of marine and estuarine turtles during Hurricane Michael. *Scientific Reports*, *11*, 1577. https://doi.org/10.1038/s41598-021-81234-3

Levy, Y., Keren, T., Leader, N., Weil, G., Tchernov, D., & Rilov, G. (2017). Spatiotemporal hotspots of habitat use by loggerhead (*Caretta caretta*) and green (*Chelonia mydas*) sea turtles in the Levant basin as tools of conservation. *Marine Ecology Progress Series*, *575*, 165–179. https://doi.org/10.3354/meps12146

MacDonald, B. D., Lewison, R. L., Madrak, S. V., Seminoff, J. A., & Eguchi, T. (2012). Home ranges of East Pacific green turtles *Chelonia mydas* in a highly urbanized temperate foraging ground. *Marine Ecology Progress Series*, *461*, 211–221. https://doi.org/10.3354/meps09820

MacDonald, B. D., Madrak, S. V., Lewison, R. L., Seminoff, J. A., & Eguchi, T. (2013). Fine scale diel movement of the east Pacific green turtle, *Chelonia mydas*, in a highly urbanized foraging environment. *Journal of Experimental Marine Biology and Ecology*, *443*, 56–64. https://doi.org/10.1016/j.jembe.2013.02.033

Makowski, C., Seminoff, J. A., & Salmon, M. (2006). Home range and habitat use of juvenile Atlantic green turtles (*Chelonia mydas* L.) on shallow reef habitats in Palm Beach, Florida, USA. *Marine Biology*, *148*, 1167–1179. https://doi.org/10.1007/s00227-005-0150-y

Marcovaldi, M. Â., Lopez, G. G., Soares, L. S., & López-Mendilaharsu, M. (2012). Satellite tracking of hawksbill turtles *Eretmochelys imbricata* nesting in northern Bahia, Brazil: Turtle movements and foraging destinations. *Endangered Species Research*, *17*, 123–132. https://doi.org/10.3354/esr00421

Marshall, C. D., Cullen, J. A., Al-Ansi, M., Hamza, S., & Abdel-Moati, M. A. R. (2020). Environmental drivers of habitat use by hawksbill turtles (*Eretmochelys imbricata*) in the Arabian Gulf (Qatar). *Frontiers in Marine Science*, *7*, 549575. https://doi.org/10.3389/fmars.2020.549575

Matley, J. K., Eanes, R. S., Nemeth, R. S., & Jobsis, P. D. (2019). Vulnerability of sea turtles and fishes in response to two catastrophic Caribbean hurricanes, Irma and Maria. *Scientific Reports*, *9*, 14254. https://doi.org/10.1038/s41598-019-50523-3

Matley, J. K., Johansen, L. K., Klinard, N. V., Eanes, S. T., & Jobsis, P. D. (2021). Habitat selection and 3D space use partitioning of resident juvenile hawksbill sea turtles in a small Caribbean bay. *Marine Biology*, *168*, 120. https://doi.org/10.1007/s00227-021-03912-0

Matley, J. K., Jossart, J., Johansen, L., & Jobsis, P. D. (2020). Environmental drivers of diving behaviour and space-use of juvenile endangered Caribbean hawksbill sea turtles identified using acoustic telemetry. *Marine Ecology Progress Series*, *652*, 157–171. https://doi.org/10.3354/meps13466

Maurer, A. S., Seminoff, J. A., Reiskind, M. O. B., & Stapleton, S. P. (2024). Diverse migratory strategies for a hawksbill sea turtle population. *Aquatic Conservation: Marine and Freshwater Ecosystems*, *34*, e4080. https://doi.org/10.1002/aqc.4080

McClellan, C. M., & Read, A. J. (2009). Confronting the gauntlet: Understanding incidental capture of green turtles through fine-scale movement studies. *Endangered Species Research*, *10*, 165–179. https://doi.org/10.3354/esr00199

Mendonca, M. T. (1983). Movements and feeding ecology of immature green turtles (*Chelonia mydas*) in a Florida lagoon. *Copeia*, *1983*, 1013–1023. https://doi.org/10.2307/1445104

Metcalfe, K., Bréheret, N., Bal, G., Chauvet, E., Doherty, P. D., Formia, A., Girard, A., Mavoungou, J., Parnell, R. J., & Pikesley, S. K. (2020). Tracking foraging green turtles in the Republic of the Congo: Insights into spatial ecology from a data poor region. *Oryx*, *54*, 299–306. https://doi.org/10.1017/S0030605319000309

Mettler, E. K., Clyde-Brockway, C. E., Sinclair, E. M., Paladino, F. V., & Honarvar, S. (2020). Determining critical inter-nesting, migratory, and foraging habitats for the conservation of East Atlantic green turtles (*Chelonia mydas*). *Marine Biology*, *167*, 106. https://doi.org/10.1007/s00227-020-03724-8

Meylan, P. A., Meylan, A. B., & Gray, J. A. (2011). The ecology and migrations of sea turtles. 8. Tests of the developmental habitat hypothesis. *Bulletin of the American Museum of Natural History*, *2011*, 1–70. https://doi.org/10.1206/357.1

Naro-Maciel, E., Arengo, F., Galante, P., Vintinner, E., Holmes, K. E., Balazs, G., & Sterling, E. J. (2018). Marine protected areas and migratory species: Residency of green turtles at Palmyra Atoll, Central Pacific. *Endangered Species Research*, *37*, 165–182. https://doi.org/10.3354/esr00922

Niviere, M., Chambault, P., Pérez, E. D., Bonola, M., Martin, J., Barnérias, V. F., Mailles, J., Dumont-Dayot, E., Gresser, J., Hiélard, G., Régis, S., Lecerf, N., Thieulle, L., Duru, M., Lefebvre, F., Milet, G., Guillemot, B., Bildan, B., de Montgolfier, B., … Chevallier, D. (2018). Identification of marine key areas across the Caribbean to ensure the conservation of the critically endangered hawksbill turtle. *Biological Conservation*, *223*, 170–180. https://doi.org/10.1016/j.biocon.2018.05.002

Okuyama, J., Nakajima, K., Noda, T., Kimura, S., Kamihata, H., Kobayashi, M., Arai, N., Kagawa, S., Kawabata, Y., & Yamada, H. (2013). Ethogram of immature green turtles: Behavioral strategies for somatic growth in large marine herbivores. *PLoS One*, *8*, e65783. https://doi.org/10.1371/journal.pone.0065783

Parker, D. M., Balazs, G. H., King, C. S., Katahira, L., & Gilmartin, W. (2009). Short-range movements of hawksbill turtles (*Eretmochelys imbricata*) from nesting to foraging areas within the Hawaiian islands. *Pacific Science*, *63*, 371–382. https://doi.org/10.2984/049.063.0306

Pilcher, N. J., Antonopoulou, M., Perry, L., Abdel-Moati, M. A., Al Abdessalaam, T. Z., Albeldawi, M., Al Ansi, M., Al-Mohannadi, S. F., Al Zhlawi, N., & Baldwin, R. (2014). Identification of important sea turtle areas (ITAs) for hawksbill turtles in the Arabian region. *Journal of Experimental Marine Biology and Ecology*, *460*, 89–99. https://doi.org/10.1016/j.jembe.2014.06.009

Pilcher, N. J., Antonopoulou, M. A., Rodriguez-Zarate, C. J., Mateos-Molina, D., Das, H. S., Bugla, I., & Al Ghais, S. M. (2021). Movements of green turtles from foraging areas of The United Arab Emirates: Regional habitat connectivity and use of marine protected areas. *Marine Biology*, *168*, 1–15. https://doi.org/10.1007/s00227-020-03815-6

Pillans, R. D., Fry, G. C., Haywood, M. D., Rochester, W., Limpus, C. J., Patterson, T., & Babcock, R. C. (2021). Residency, home range and tidal habitat use of Green Turtles (*Chelonia mydas*) in Port Curtis, Australia. *Marine Biology*, *168*, 88. https://doi.org/10.1007/s00227-021-03898-9

Pillans, R. D., Whiting, S. D., Tucker, A. D., & Vanderklift, M. A. (2022). Fine-scale movement and habitat use of juvenile, subadult, and adult green turtles (*Chelonia mydas*) in a foraging ground at Ningaloo Reef, Australia. *Aquatic Conservation: Marine and Freshwater Ecosystems*, *32*, 1323–1340. https://doi.org/10.1002/aqc.3832

Rees, A. F., Hafez, A. A., Lloyd, J. R., Papathansopoulou, N., & Godley, B. J. (2013). Green turtles, *Chelonia mydas*, in Kuwait: Nesting and movements. *Chelonian Conservation and Biology*, *12*, 157–163. https://doi.org/10.2744/CCB-1030.1

Revuelta, O., Hawkes, L. A., León, Y. M., Godley, B. J., Raga, J. A., & Tómas, J. (2015). Evaluating the importance of marine protected areas for the conservation of hawksbill turtles *Eretmochelys imbricata* nesting in The Dominican Republic. *Endangered Species Research*, *27*, 169–180. https://doi.org/10.3354/esr00660

Richardson, P. B., Broderick, A. C., Coyne, M. S., Ekanayake, L., Kapurusinghe, T., Premakumara, C., Ranger, S., Saman, M. M., Witt, M. J., & Godley, B. J. (2013). Satellite telemetry reveals behavioural plasticity in a green turtle population nesting in Sri Lanka. *Marine Biology*, *160*, 1415–1426. https://doi.org/10.1007/s00227-013-2194-8

Robinson, D. P., Jabado, R. W., Rohner, C. A., Pierce, S. J., Hyland, K. P., & Baverstock, W. R. (2017). Satellite tagging of rehabilitated green sea turtles *Chelonia mydas* from The United Arab Emirates, including the longest tracked journey for the species. *PLoS One*, *12*, e0184286. https://doi.org/10.1371/journal.pone.0184286

Scales, K. L., Lewis, J. A., Lewis, J. P., Castellanos, D., Godley, B. J., & Graham, R. T. (2011). Insights into habitat utilisation of the hawksbill turtle, *Eretmochelys imbricata* (Linnaeus, 1766), using acoustic telemetry. *Journal of Experimental Marine Biology and Ecology*, *407*, 122–129. https://doi.org/10.1016/j.jembe.2011.07.008

Seminoff, J. A., & Jones, T. T. (2006). Diel movements and activity ranges of green turtles (*Chelonia mydas*) at a temperate foraging area in the Gulf of California, Mexico. *Herpetological Conservation and Biology*, *1*, 81–86. www.researchgate.net

Seminoff, J. A., Resendiz, A., & Nichols, W. J. (2002). Home range of green turtles *Chelonia mydas* at a coastal foraging area in the Gulf of California, Mexico. *Marine Ecology Progress Series*, *242*, 253–265. https://doi.org/10.3354/meps242253

Senko, J., Koch, V., Megill, W. M., Carthy, R. R., Templeton, R. P., & Nichols, W. J. (2010). Fine scale daily movements and habitat use of east Pacific green turtles at a shallow coastal lagoon in Baja California Sur, Mexico. *Journal of Experimental Marine Biology and Ecology*, *391*, 92–100. https://doi.org/10.1016/j.jembe.2010.06.017

Shaver, D. J., Hart, K. M., Fujisaki, I., Rubio, C., & Sartain, A. R. (2013). Movement mysteries unveiled: Spatial ecology of juvenile green sea turtles. In W. I. Lutterschmidt (Ed.), *Reptiles in research*. Nova Science Publishers, Inc.

Shimada, T., Jones, R., Limpus, C., Groom, R., & Hamann, M. (2016). Long-term and seasonal patterns of sea turtle home ranges in warm coastal foraging habitats: Implications for conservation. *Marine Ecology Progress Series*, *562*, 163–179. https://doi.org/10.3354/meps11972

Siegwalt, F., Benhamou, S., Girondot, M., Jeantet, L., Matin, J., Bonola, M., Lelong, P., Grande, C., Chambault, P., Benhalilou, A., Murgale, C., Maillet, T., Andreani, L., Campistron, G., Jacaria, F., Hiélard, G., Arqué, A., Etienne, D., Gresser, J., … Chevallier, D. (2020). High fidelity of sea turtles to their foraging grounds revealed by satellite tracking and capture-mark-recapture: New insights for the establishment of key marine conservation areas. *Biological Conservation*, *250*, 108742. https://doi.org/10.1016/j.biocon.2020.108742

Soanes, L. M., Johnson, J., Eckert, K., Gumbs, K., Halsey, L. G., Hughes, G., Levasseur, K., Quattro, J., Richardson, R., Skinner, J. P., Wynne, S., & Mukhida, F. (2022). Saving the sea turtles of Anguilla: Combining scientific data with community perspectives to inform policy decisions. *Biological Conservation*, *268*, 109493. https://doi.org/10.1016/j.biocon.2022.109493

Tanabe, L. K., Cochran, J. E. M., Williams, C. T., Garzon, F., Langer, U., Hardenstine, R. S., Hawkes, L. A., Brainard, R. E., Eweida, A. A., Marshall, P. A., & Berumen, M. (2023b). Case report: Tracking data from foraging hawksbill turtles in the northern Red Sea. *Animal Biotelemetry*, *11*, 1. https://doi.org/10.1186/s40317-022-00314-x

Uribe-Martínez, A., Liceaga-Correa, M. D. L. A., & Cuevas, E. (2021). Critical in-water habitats for post-nesting sea turtles from the southern Gulf of Mexico. *Journal of Marine Science and Engineering*, *9*, 793. https://doi.org/10.3390/jmse9080793

van Dam, R. P., & Diez, C. E. (1998). Home range of immature hawksbill turtles (*Eretmochelys imbricata* (Linnaeus)) at two Caribbean islands. *Journal of Experimental Marine Biology and Ecology*, *220*, 15–24. https://doi.org/10.1016/S0022-0981(97)00080-4

van de Merwe, J. P., Ibrahim, K., Lee, S. Y., & Whittier, J. M. (2009). Habitat use by green turtles (*Chelonia mydas*) nesting in Peninsular Malaysia: Local and regional conservation implications. *Wildlife Research*, *36*, 637–645. https://doi.org/10.1071/WR09099

Weber, S. B., Weber, N., Godley, B. J., Pelembe, T., Stroud, S., Williams, N., & Broderick, A. C. (2017). Ascension Island as a mid-Atlantic developmental habitat for juvenile hawksbill turtles. *Journal of the Marine Biological Association of the United Kingdom*, *97*, 813–820. https://doi.org/10.1017/S0025315414001258

Webster, E. G., Hamann, M., Shimada, T., Limpus, C., & Duce, S. (2022). Space-use patterns of green turtles in industrial coastal foraging habitat: Challenges and opportunities for informing management with a large satellite tracking dataset. *Aquatic Conservation: Marine and Freshwater Ecosystems*, *32*, 1041–1056. https://doi.org/10.1002/aqc.3813

Whiting, S. D., & Miller, J. D. (1998). Short term foraging ranges of adult green turtles (*Chelonia mydas*). *Journal of Herpetology*, *32*, 330–337. https://doi.org/10.2307/1565446

Yeh, F. C., Balazs, G. H., Parker, D., Ng, C., & Shi, H. (2014). Novel use of satellite tracking as a forensic tool to determine foraging ground of a rescued green turtle (*Chelonia mydas*). *Marine Turtle Newsletter*, *142*, 1–3. https://chinaturtleconservation.hainnu.edu.cn/attachment/files/2024/03/05/Novel%20Use%20of%20Satellite%20Tracking%20as%20a%20Forensic%20Tool%20to%20Determine%20Foraging%20Ground%20of%20a%20Rescued%20Green%20Turtle%20(Chelonia%20mydas).pdf

SUPPORTING INFORMATION

Additional supporting information can be found online in the Supporting Information section at the end of this article.

Figure S1. Example space use estimates showing core (50% utilisation distribution, UD; yellow) and full home ranges (95% UD; green) generated from simulated Fastloc-GPS (a–e), Argos high-accuracy (f–j), and Argos low-accuracy (k–o) datasets using (a, f, k) Minimum Convex Polygon, (b, g, l) Kernel Density Estimation, (c, h, m) Autocorrelated Kernel Density Estimation, (d, i, n) Biased Random Bridge, and (e, j, o) dynamic Brownian Bridge Movement Model. Simulated animal locations are shown in black. Note the variation in axis scales between the tracking technologies (panel rows).

Figure S2. Home range estimates derived using five analytical methods from simulated data representing (a, d) Fastloc-GPS, (b, e) Argos high-accuracy and (c, f) Argos low-accuracy tracking. Red dotted line indicates the reference area used by the simulated animal (3.76 km^2).

Table S1. Autocorrelation parameters extracted from publicly available Fastloc-GPS datasets: home range crossing time (positional autocorrelation) and velocity autocorrelation time.

Table S2. Mean home range size estimates using 50% and 95% utilisation distributions (UDs) from simulated datasets resembling commonly used tracking technologies, analysed with Minimum Convex Polygon (MCP), Kernel Density Estimation (KDE), Autocorrelated Kernel Density Estimation (AKDE), Biased Random Bridge (BRB), and dynamic Brownian Bridge Movement Model (dBBMM).

Table S3. Global home range size estimates of green turtles (*Chelonia mydas*) from the literature, grouped by tracking technology and life stage.

Table S4. Global home range size estimates of hawksbill turtles (*Eretmochelys imbricata*) grouped by tracking technology and life stage.

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