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Commentary

A comparison between traditional kernel-based methods and network analysis: an example from two nearshore shark species

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Understanding how marine species use their environment has become increasingly important in management and conservation. Acoustic monitoring allows long-term tracking of marine animal movement that is traditionally analysed using kernel-based home range estimators. These traditional methods, however, are limited because they do not examine movement pathways within activity spaces. Network analysis (NA) provides an alternative approach to traditional home range analysis that treats acoustic receivers as network nodes and analyses movement between nodes. To investigate the utility of NA in identifying core use areas and compare the results with traditional analysis, a case study using acoustically monitored coastal sharks was conducted. To make direct comparisons with static traditional analysis a temporal scale was not explicitly explored. Comparison of traditional analysis and NA demonstrated that both methods provided similar results for identifying core use areas (50% kernel utilization distribution (KUD) equivalent), but that NA tended to overestimate general use areas (95% KUD equivalent) compared to kernel-based methods. Furthermore, frequent bidirectional movements within core use areas were identified by NA, indicating the importance of movement corridors within or between core areas. Movements between acoustic receivers outside core use areas were less frequent and unidirectional suggesting transiting movements. Therefore, NA may be a practical alternative to traditional home range metrics by providing useful data interpretation that allows for a comprehensive picture of animal movement, including identifying core use areas and pathways used.

Data on animal movement patterns, connectivity and habitat use have become crucial elements in effective management and conservation (Greene et al., 2009; Rayfield, Fortin, & Fall, 2011). A complete understanding of animal movement must consider how biological functions (e.g. foraging, reproduction, predator avoidance) and environmental factors (e.g. salinity, temperature, competition) influence movement (Acevedo-Gutiérrez, 2009; Rogers & White, 2007). Empirical analysis of spatial and temporal changes in location and distribution of animals has traditionally applied activity space measures including, but not restricted to, home range metrics, random walks or theoretical models such as Lévy flight and dispersal measures (Greenwood & Swingland, 1983; Turchin, 1998). However, understanding drivers for movement and interactions between marine species and their environment remains a challenge (Croft, James, & Krause, 2008).

Technological advances such as acoustic monitoring have allowed scientists to obtain long-term movement and behaviour data for marine organisms (Simpfendorfer, Heupel, & Collins, 2008; Voegeli, Smale, Webber, Andrade, & O'Dor, 2001). Acoustic monitoring provides data sets of significant size and quality, but few standardized methods have been developed to analyse the data produced (Heupel, Semmens, & Hobday, 2006; Rogers & White, 2007). Researchers either use coarse data (i.e. widely spaced acoustic receiver locations) or interpolate data using methods such as positioning algorithms (Hedger et al., 2008; Simpfendorfer, Heupel, & Hueter, 2002). However, interpolation methods do not produce high accuracy in calculated positions due to aggregation of data at the detection range of a receiver and across relatively long time periods (Hedger et al., 2008). A standardized method for analysing acoustic data using raw detections could reduce data processing requirements and decrease the possibility of introducing errors. Furthermore, a standardized method would provide consistency in the analysis and

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interpretation of acoustic monitoring data that may increase the ability to compare studies.

Network analysis investigates the relationship between nodes, with connections between nodes called edges, and the combined connections represented as a network (West, 2001) and may provide a standardized approach to acoustic monitoring data sets. Applied to acoustic monitoring, nodes represent acoustic receivers deployed in the study area and edges represent movement (trajectory) of an animal between nodes (Jacoby, Brooks, Croft & Sims, 2012). Thus, networks can be constructed from detection data obtained from acoustic receivers. Node and edge properties can also be complemented with additional information. For example, physical and environmental attributes such as habitat type, salinity or depth can be included in analyses. Consequently, NA can be adapted to various situations and scales (Stehfest et al., 2013) depending on what is examined (Croft et al., 2008). Network analysis can also provide information that traditional methods do not. For example, weighted directional movement patterns may highlight corridors of movement between important habitats/areas. Recent NA studies have used acoustic monitoring data to look at social behaviour of sharks (Jacoby, Croft & Sims, 2012; Mourier, Vercelloni, & Planes, 2012), fish aggregations (Stehfest et al., 2013), animal movements (Finn et al., 2014; Jacoby, Brooks, et al., 2012) and spatial utilization (Stehfest, Patterson, Barnett, & Semmens, 2014). The use of NA in acoustic monitoring studies, however, is still in its infancy and its utility in analysing animal movement is yet to be well established.

Since NA has rarely been applied to acoustic monitoring data, it is important to test and compare outputs against traditional analyses and understand where differences occur, what benefits may be generated and why. Therefore, the aims of this study were to determine the utility of NA in identifying core use areas of two species of acoustically monitored coastal sharks, compare results with traditional kernel-based analysis, and identify additional information that could be generated by NA to extend the interpretation of animal movement data. Finally, to make direct comparisons with static traditional analysis a temporal scale was not explicitly explored.

METHODS

Acoustic monitoring data from Cleveland Bay, north Queensland, Australia, previously analysed by Knip, Heupel, and Simpfendorfer (2012), Knip, Heupel, Simpfendorfer, Tobin, and Moloney (2011) were used to test the efficacy of the NA approach. Methods below describe the acoustic array, methods of Knip et al. (2012; 2011) and the NA approach applied to this data set. Details on deployment locations and settings of acoustic receivers can be found in Knip et al. (2012; 2011). The data used in this study will be stored in the AATAMS database https://aatams.emii.org.au/aatams/.

Ethical Note

In research by Knip et al. (2012; 2011) sharks were captured on 500 m bottom-set longlines soaked for 1 h. Gangions included 1 m of 5 mm nylon cord, 1 m of wire leader and a 14/0 Mustad tuna circle hook. Captured sharks were measured to the nearest cm, sexed and tagged with a rototag in the first dorsal fin for identification and an acoustic transmitter implanted. Transmitters (V16 16 mm × 65 mm acoustic transmitters (Vemco Ltd) which were less than 1% of shark body weight) were surgically implanted into the body cavity. Sharks were restrained using tonic immobility, a 3–4 cm incision made in the abdomen, a transmitter inserted and the incision sutured with running stitches using absorbable sutures and disposable needles to ensure healing. All passively monitored animals were in good condition upon capture and released in good condition within 10 min of landing at their site of capture.

All Knip et al. (2012; 2011) research activities were conducted under the GBRMPA permit number G10/33315.1, Queensland DPIF permit number 90911 and James Cook University animal ethics approval no. A1566.

Study Site

Cleveland Bay on the northeast coast of Queensland, Australia, has an area of about 225 km^2, is relatively shallow (<10 m) and has varied coastal habitats including coral reef, sand bank, intertidal mudflats, sea grass and mangrove habitats (Knip et al., 2011). Acoustic monitoring was used to track 43 pigeye sharks, *Carcharhinus amboinensis*, and 29 spottail sharks, *Carcharhinus sorrah* between 2008 and 2010 (Knip et al., 2012; 2011). Sixty-five acoustic receivers (VR2W Vemco Ltd), 28 in the western section and 37 in the eastern section (Fig. 1), were deployed to track shark movements. Acoustic receivers were deployed on average 2 km apart and had a detection range of about 900 m, so there was no overlap in detection ranges.

Data Analysis

Receiver data were downloaded quarterly and used to describe activity space and movement patterns (Knip et al., 2012; 2011). Prior analysis using traditional activity space approaches (kernel utilization distributions, KUD; extent of movement (95% KUD) and core use area (50% KUD) of *C. amboinensis* and *C. sorrah*) were compared with NA results. All NA and statistical analyses were conducted in the R environment (R Development Core Team, 2014) using the sna (Butts, 2013; CRAN: sna), igraph (Csardi & Nepusz, 2006; CRAN: igraph) and tnet (Opsahl, 2009; CRAN: tnet) packages. UCINet (Borgatti, Everett, & Freeman, 2002) and Netdraw (Borgatti, 2002) were used for network representation. Imported data were used to create square movement matrices that counted the presence at, and movements between, receivers, regardless of time required to reach the next receiver. Only detections at the same receiver that were 5 min or more apart were included in the network. Square matrices were used to create directed and weighted networks which represented the activity space of an individual. Each network was tested for nonrandom associations of receivers, based on observed movements, using a modified version of the Bejder–Manly method (Mourier et al., 2012; Whitehead, Bejder, & Andrea Ottensmeyer, 2005). The Bejder–Manly method randomized receivers' associations to create null random networks to control for the sampling design of the receiver array. Receiver community memberships (i.e. group number of the community/cluster in the network) were calculated from the observed matrix to obtain group size and numbers of communities in the network and then permuted within each new matrix. The observed matrix was randomized 10 000 times with 1000 flips (i.e. receiver community membership was randomly flipped within each new matrix) per permutation within sampling periods (Whitehead et al. 2005). Coefficient of variation and likelihood ratio tests (χ^2_2, $P < 0.05$) were used to determine whether receivers' associations in the study area were significantly different from random. Data distribution and normality were tested prior to statistical analysis and if the normality assumption was violated, a nonparametric test was performed.