

Pygmy Blue Whale Home Ranges and Their Overlaps with Indonesian and Australian Marine Protected Areas: Comparison between a-LoCoH and BBMM Methods

Achmad Sahri^{1*}, Charlotte Jak², Albertinka J Murk³, Ron J van Lammeren²

¹Research Center for Oceanography, National Research and Innovation Agency, Jl. Pasir Putih 1, Ancol Timur, Jakarta 14430, Indonesia

²Laboratory of Geo-Information Science and Remote Sensing, Wageningen University and Research, P.O. Box 47, 6700 AA Wageningen, the Netherlands

³Marine Animal Ecology Group, Wageningen University and Research, Droevendaalsesteeg 1, 6708 PB Wageningen, the Netherlands

Abstract. Information on the distribution of marine migratory species is lacking, and for a long time, these species have been overlooked in the designation of Marine Protected Areas (MPAs). This study analysed the home range of pygmy blue whales (PBWs) from western Australia to eastern Indonesia to be able to assess the overlap with current MPAs. In this study, data from 11 individual PBWs tagged in the Perth Canyon were used. Two home range methods, adaptive Local Convex Hull (a-LoCoH) and Brownian Bridge Movement Model (BBMM), were performed and compared to identify core use areas and connections between these areas (i.e., migration corridors). By assessing the relative properties and visually inspecting the home ranges, 90% BBMM (home range and migration corridor) and 50% BBMM (core use area) are chosen as the best results, because they cover the connected core-use areas to a large extent. The home ranges that were covered by current MPAs were only 2% in Indonesia and 16% in Australia. Important migration corridors without current protection are in the east Savu Sea, south of Timor Island, and wider Banda Sea. It is noteworthy that comparing methods is relevant to be able to choose the most suitable method for the data used and the goal of this study. The limited overlap between the calculated home ranges and the MPAs of the Indonesian waters articulates the importance of in-depth scientific studies to be able to evaluate, implement and develop marine conservation planning.

1 Introduction

The Pygmy Blue Whale (*Balaenoptera musculus brevicauda* [1], hereafter PBW) is one of the subspecies of blue whales in the southern hemisphere [2]. The current IUCN Red List status of the species is uncertain due to data deficiency (<https://www.iucnredlist.org/>), since

* Corresponding author: achmad.sahri@brin.go.id

the species was targeted by 18th-19th centuries' commercial whaling after which the recovery was slow [3]. Compared to its bigger sister, the Antarctic blue whale (*Balaenoptera musculus intermedia*), the PBW is found further north [4]. At least four populations of PBW are identified ranging from the northern Indian Ocean, Madagascar to the Sub Antarctic, the equator to New Zealand, and Indonesia to western and southern Australia [3]. The latter population is the focus of the current study.

The PBW is a migratory filter-feeding species which uses different areas for breeding and foraging, because they store energy to provide for their offspring [5]. Different studies using recorded acoustics or visual surveys of the PBWs have shown the presence of this species in Australia to be only six months of the year, i.e., from November to June [3], [6-9]. The whales mainly forage in Australian waters [8], [10], [11]. They migrate north along the west coast of Australia to eastern Indonesia presumably to breed during the Austral fall and winter [3], [8], [12]. It has also been suggested that PBWs are feeding in the highly productive waters of Indonesia around the Banda, Molucca and Savu Seas [8], and other migrating marine species also use these areas to forage [13]. The distribution and migration corridors of the PBW are poorly understood, which makes conservation and management challenging [14]. This applies especially to Indonesia as no in-depth analyses have been performed to assess the complete distribution of this population.

Indonesia is the biggest archipelagic state of the world with a maritime area of 5.8 million km² and could therefore have a big influence on the protection of marine ecosystems [15]. Internationally, cetaceans are recognized as protected species under CITES, CMS, and UNCLOS [16]. In Indonesia, they are also protected under several regulations (e.g., fisheries and ban on commercial hunting) and area-based management tools such as Marine Protected Areas (MPAs) and Marine Spatial Planning (MSP) (*sensu* [16]). For the PBW, as a migratory species, protection of the habitat as well as of migration corridors are essential. This discrimination is mentioned, because for migratory species, it is important to identify core areas where individuals spend most of the time, as well as areas that are used to connect these areas, also known as migration corridors [17-19]. In 2018, 16 of the 34 provinces in Indonesia have MSP in place, and 12 provinces have designated marine mammal migration corridors implemented [16]. However, most of the current MPAs in Indonesia are not intentionally designated for migratory species such as marine mammals, and for a long time, these species have been overlooked in MPA designation. Marine migratory corridors within provincial MSP development as mandated by the country's regulations are, however, mostly not based on scientific-proved but on practical consideration.

Disturbance of the PBW can have cascading effects on the lower trophic levels of the marine ecosystem [20], [21], e.g., for fertilization of surface waters, phytoplankton depends on whale's feces. Knowledge on the distribution of this species in Indonesian waters can help to evaluate the current MPAs and could be provide input for those provinces that have not yet finished their MSP. With the use of the satellite telemetry acquired data, the overlap between PBW habitat and the currently assigned MPAs can be investigated. Double et al. [8] used biotelemetric data of 11 individual PBWs to assess the rough distribution and movement on the basis of presence only information, which does not represent the complete species distribution but rather only fragmented points of the species occurrence [22], [23]. The satellite telemetry data gathered by Double et al. [8] can, however, be used for further analyses to map out the home range of PBWs.

This study investigated the core areas and migration corridors of the PBW using the home range approach [24]. This approach is necessary, because it is not known what happened between measured locations [25]. A home range is the conversion of the tracked movement into a spatial representation in which the animal can find the requirements to grow, survive and reproduce [26]. Taking uncertainties of the measured locations and the trajectory in between into account is important to estimate the migration corridors of the complete

population [17]. Several methods to construct a home range are developed, but careful consideration is needed before applying a method [27], since wrong conclusions can have big impacts on the conservation of a species.

Home ranges constructed directly from the points are the most common methods. Examples of this approach are the grid cell method [28], Minimum Convex Polygon (MCP; [29], [30]), Kernel Density Estimators (KDE; [31]), and Characteristic Hull Polygon (CHP; [32]). Problems with these methods are over- or underestimating the size of the home range and failing to identify core areas [33]. These core areas are important to be able to identify high-use area and migration corridors. Also, most methods need regular interval tracking data or temporally independent location data [34], [35] and this is not the case for telemetry data, as used in this study. Newer methods such as adaptive Local Convex Hull (a-LoCoH; [36]) are able to overcome some problems such as like the evenly distribution of observation points and the including of non-visited areas. To further overcome the issue with irregularity of the tracking data and the independence assumption, there are two methods developed: the Brownian Bridge Movement Model (BBMM; [24] and Time-Geographic Density Estimation (TGDE; [37]).

This study aimed to provide information about the home range (core use areas and migration corridors) of the tagged PBW and its overlap with current MPAs in eastern Indonesia and western Australia. Two different methods, adaptive Local Convex Hull (a-LoCoH) and a Brownian Bridge Movement Model (BBMM), were tested and compared to acquire the best possible assessment of the overlap between calculated home ranges of PBWs and MPAs.

2 Materials and methods

2.1 Study area

The study area covers the eastern Indonesian and western Australian waters (Figure 1). The whales migrate north from the Perth Canyon or Naturaliste Plateau via the North West Cape/Ningaloo Reef to the Savu, Timor, Banda and Molucca Seas in Indonesia [8], [12]. The Perth Canyon is one of the areas in West Australia with the highest primary productivity [38]. The North West Cape/Ningaloo Reef has low productivity; however, feeding has been observed here and primary production are the same as in upwelling regions [39]. The regions occupied in Indonesia have similar primary productivity compared to the subtropical frontal zone near the West Australia characterized with high phytoplankton concentration, especially in the Banda and Molucca Seas where upwelling take place [8].

2.2 Telemetry data and marine protected area data

In this study, telemetry data of the PBW was used (Figure 1A) where the tagged whales travelled from the western Australian coast to eastern Indonesia waters [8], [12]. Eleven individual PBWs were employed with satellite tags in 2009 and 2011 in March or April at Perth Canyon, western Australia [8]. The satellite tags were custom-designed and manufactured by Wildlife Computers. There was a difference in duty cycles and transmission periods between the employment years. In 2009, the duty cycle was 6 hours on (every 30 seconds when surfacing during 6 hours the location was retrieved), with 18 hours off cycle. In 2011, this changed to a duty cycle of 4 hours and 8 hours off cycle. Points located at unlikely locations, i.e., the points that did not conform to swimming speed, distance between successive locations, and turning angles, were filtered out from the data [8]. For the home range analysis, 2 individuals (98106 and 98141) were excluded because the number of

relocations was too low [40]. The telemetry data gave the opportunity to study the movement of these small blue whales and to use the results to assess the home range (core use areas and migration corridors). The coordinate projection of Universal Transverse Mercator zone 50 (UTM 50) in ArcGIS software was used in this study.

To acquire information on the overlap between the PBW home ranges and current Marine Protected Areas (MPAs) in Indonesia and Australia, polygons of the boundaries of the MPAs were used. The current MPA boundary data was available from the Indonesian Ministry of Marine Affairs and Fisheries (MMAF) website (<https://kkp.go.id/djprl/kkhl/page/2023-data-kawasan-konservasi-perairan>). The MPA boundary data from west Australia was available from UNEP-WCMC website (<https://www.protectedplanet.net/country/AU>).

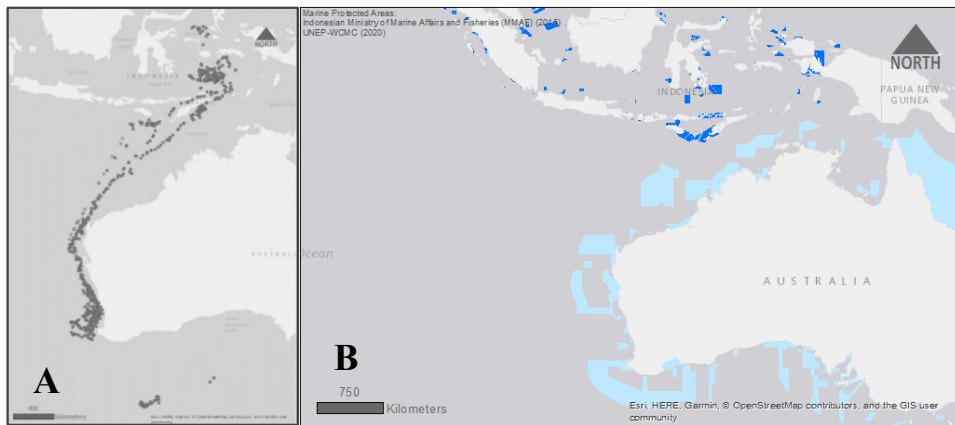


Fig. 1. (A). Recorded locations ($n=1,378$) of the 11 tagged individuals of pygmy blue whales from Double et al. (2014). (B). Marine Protected Areas in Indonesia and Australia. Dark blue shows the MPAs in Indonesia from the Indonesian Ministry of Marine Affairs and Fisheries (MMAF) and light blue shows the MPAs of Australia from UNEP-WCMC website.

2.3 Home range methods

Two different methods were used and compared for predicting the home range of the PBWs in western Australia and eastern Indonesia: adaptive Local Convex Hull (a-LoCoH; [36]) and Brownian Bridge Movement Model (BBMM; [24]). For the two methods, parameters had to be estimated first. The methods use different probabilities to obtain the home ranges. A-LoCoH uses 95%, 90% and 50% probabilities [17], [41] and the Brownian Bridge Movement Model uses 95%, 90%, 75%, 50% and 25% probabilities [17] to estimate the home ranges. The 95%, 90%, and 75% probabilities represent migration corridors, while 50% and 25% probabilities represent core use areas.

The first method used was a-LoCoH, and for this method, parameter alpha (a) had to be estimated. This 'a value' was used as the radius in which the points were utilized to construct the kernels [36]. The 'Minimum Spurious Hole Covering' (MSHC) rule was applied to estimate each individual 'a value' [36]. This rule was used in many studies constructing home ranges using a-LoCoH [41-43]. To estimate the 'a value', the maximum distance between locations per individual was first calculated. From the maximum distance for the 'a value', the further development of the area size with an increasing 'a value' was used to evaluate what the optimum 'a value' was. By using the area function, plateaus were identified in the home range construction and this indicated if all spurious holes were filled. These plateaus were caused by filling up of the spurious holes, however, by increasing the 'a value', further real holes were filled up and different plateaus were identified. Finding the balance between

not filling in the real holes (areas not used by the PBWs such as land) and filling up spurious holes was challenging. To overcome this challenge, the home ranges were constructed using different plateaus and were evaluated for increase in overlap. From this, it was decided which ‘a value’ (connected to plateaus) was most suitable to construct the home ranges (Table A1; Figure A1 in Appendices). However, if the first plateau was connected to a lower ‘a value’ compared to maximum distance, the maximum distance was chosen. In case of two individuals 53791 and 98141 (Table A1), this rule has not been followed due to large differences with species behavior. In these cases, we selected a best fitting value.

a-LoCoH is developed for using data in projected coordinate systems, however when using meters or km the graphs do not show any plateaus, because the scale of the home ranges was too big. Therefore, degrees were used to have a clear overview on the development of the area sizes when the ‘a value’ changed. The home ranges were constructed using degrees and were then re-projected to UTM 50 afterwards. The home ranges were combined by overlaying raster datasets of all individuals and per probabilities (95%, 90%, and 50%) and the total amount of individuals per cell was calculated.

The second method used was a Brownian Bridge Movement Model (BBMM). When using the BBMM, different parameters had to be estimated. First, the error of the locations was assigned by the Argos system [8] and ranged between 250 and 2000 meters [8]. However, the highest value (i.e., 2000) was chosen for the error, because 916 out of 1281 data points had an undefined error and the chosen error accommodated the highest location errors. Differences between taking a variable error and a static error were compared; taking the differences of the error assigned by Argos into account makes a maximum of 336 meters difference compared to a static error. Second, the optimal cell size was estimated, where 10 km was chosen. Differences between using 1 km and 10 km cell sizes were assessed and small shifts (2.5 - 5 km) in the contours were visible. The small shifts were measured using random points in the contour of the home range using 10 km cell size and the home range using 1 km cell size. Changing the error into a variable value and decreasing the cell size increases the computing time extremely (134 times), and for some of the individuals with a high number of relocations and big distances between relocations the computations take 20 hours when using a 10 km cell size (1 km would take 111 days). Home ranges were assessed per individual and were combined by overlaying the home ranges and counting the number of individuals per area. From these counts the overall home ranges were constructed.

2.4 Comparing methods

To compare the different methods, the characteristics (relative properties) of the home ranges were assessed, i.e., area size, boundary complexity and barrier detection [43]. Boundary complexity was assessed by comparing the edge size with the area size (called ‘edge density’). This comparison was performed per individual and also for the overall home range. For estimating the home ranges using the a-LoCoH kernel method, a minimum of 30 relocations per individuals was used as recommended by Seaman et al. [40], and when comparing the different methods, the individuals with a low number of relocations showed outlying values for area size.

2.5 Comparing home ranges and marine protected areas

The current marine protected area (MPA) boundary data was used to assess the overlap of these protected areas with the areas used by the PBWs. The calculated home ranges (core use areas and migration corridors) were assumed to represent the areas used by the whales. The proportion and size of the home range areas inside and outside an MPA were assessed.

3 Results

3.1 Home ranges

The home ranges estimated using a-LoCoH method were separated into 95% or 90% probabilities for migration corridors and 50% probability for core use areas (Figure 2). The number of overlapping individuals of PBWs were also shown. The 95% home range was visually similar to that of 90%. The smallest 50% core areas were located in the middle of the Banda Sea and off the coast of Perth (Figure 2). The total core use area (50%) from the a-LoCoH method was 235,840.61 km², which entails only 25% of the total area of 95% home range (Table 1).

The home ranges estimated using the BBMM were separated into 95%, 90% and 75% probabilities for migration corridors and 50% and 25% probabilities for core use area (Figures 3). The 95% and 90% home ranges were visually similar. The 50% core areas were located not only in the middle of the Banda Sea and off the coast of Perth, but also in the international waters between two countries (Figure 3). The variability of areas among home range probabilities was very high, with the core use area of 25% probability (357,931.58 km²) only accounting for 5% of the total 95% home range area (Table 1).

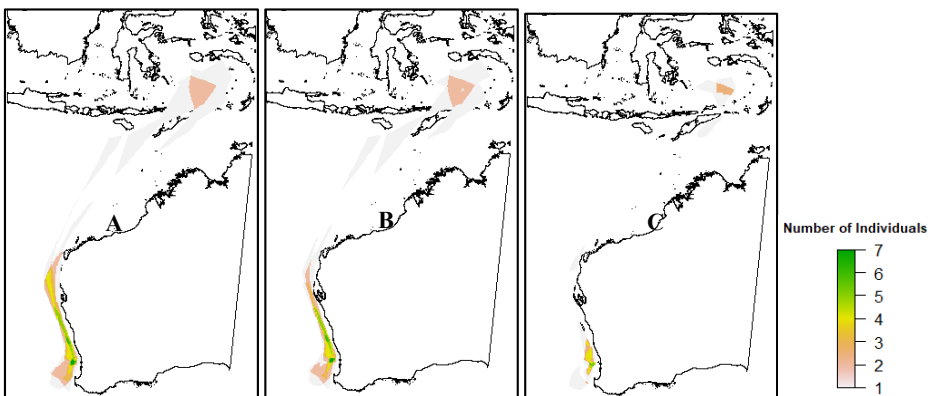


Fig. 2. Home ranges as calculated using the a-LoCoH method: 95% (A) and 90% (B) probabilities represent migration corridors and 50% (C) probability represents the core area. The different colors indicate the number of overlapping individuals.

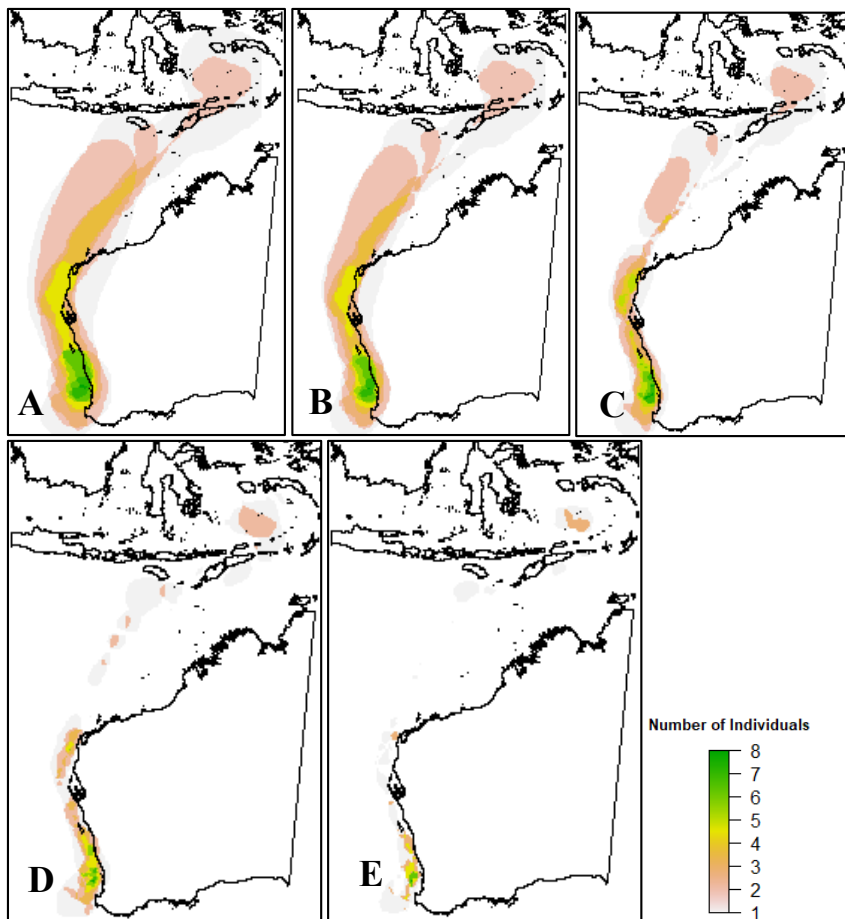


Fig. 3. Home ranges resulted from BBMM: 95% (A), 90% (B), and 75% (C) probabilities represent migration corridors and 50% (D) and 25% (E) probabilities represent core use area. The different colors indicate the number of overlapped individuals.

Table 1. Home range area (km²) gained from a-LoCoH and BBMM with different probabilities.

Tag ID	Area (km ²) in a-LoCoH probabilities			Area (km ²) in BBMM probabilities				
	95%	90%	50%	95%	90%	75%	50%	25%
53734	5,148.99	4,807.42	2,368.31	123,836.30	77,385.00	43,714.45	16,394.00	5,978.63
53791	71,782.70	63,744.67	30,803.21	1,258,060.00	627,523.00	568,546.10	248,358.00	84,181.22
88731	5,403.73	5,403.73	5,403.73	49,184.99	35,756.00	19,879.45	8,948.00	3,509.13
88739	271,759.60	204,920.20	77,921.40	891,401.90	623,759.00	366,076.70	131,126.00	40,794.16
88740	47,496.87	42,252.30	11,436.56	126,244.50	99,380.00	63,436.59	31,577.00	9,729.46
98106*								
98108	148,786.20	148,786.20	27,513.98	1,984,318.00	1,286,448.00	850,485.50	328,466.00	112,938.30
98115	13,473.97	8,383.61	4,611.39	357,333.10	180,083.00	114,684.30	43,085.00	15,833.49
98134	68,298.69	50,327.65	9,084.70	358,008.80	244,392.00	168,430.70	76,997.00	25,740.09
98135	301,673.50	266,749.00	66,697.33	1,501,799.00	964,815.00	478,166.60	188,238.00	59,227.13
98141*								
Total	933,824.25	795,374.70	235,840.61	6,650,187.33	4,139,541.00	2,673,420.40	1,073,189.00	357,931.58
Mean	103,758.30	88,374.97	26,204.51	738,909.70	459,949.00	297,046.70	119,243.22	39,770.18

Tag ID	Area (km ²) in a-LoCoH probabilities			Area (km ²) in BBMM probabilities				
	95%	90%	50%	95%	90%	75%	50%	25%
SD	113,146.0 0	95,849.82	28,096.81	702,308.20	443,565.07	287,868.60	113,665.88	38,461.87

3.2 Comparing methods

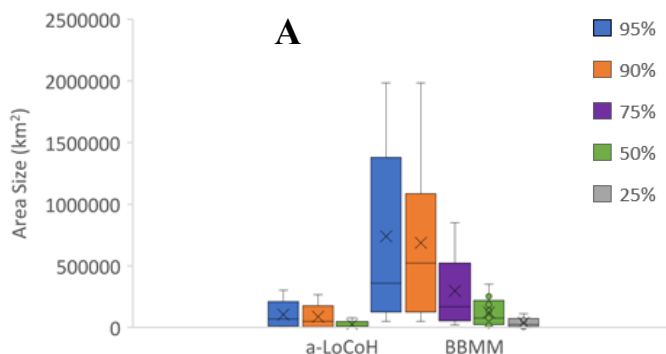
Different metrics were used to compare the a-LoCoH and BBMM home ranges (Figure 4). The average home range area and average area-on-land (the percentage of home ranges overlapping with land) were bigger in the BBMM (Figure 4), while the average edge density was larger when using the a-LoCoH method (Figure 4). The BBMM home ranges with the 90% and 95% probabilities (migration corridors) were successfully connecting the core areas in Australia and Indonesia (Figure 3). Contrarily, the a-LoCoH home ranges with 90% and 95% probabilities (migration corridors) did not connect the core areas in the two countries (Figure 2). The total area of migration corridors from the 95% BBMM home range was seven times higher than that of the 95% a-LoCoH home range (Figures 2 and 3; Table 1). Similarly, the total core use area of the 50% BBMM home range was more than four times larger than that of the 50% a-LoCoH home range (Figures 2 and 3; Table 1).

3.3 Overlap of home ranges with marine protected areas

The results for the home ranges were used to assess the overlap between the current Marine Protected Areas and the calculated home range of the pygmy blue whales (PBWs) in eastern Indonesia and western Australia. The total MPAs in Indonesia and Australia cover 887,092 km², of which 794,451 km² (90%) fall under Australian jurisdiction and 92,640.94 km² (10%) under Indonesian jurisdiction.

The different methods (a-LoCoH and BBMM) showed similar proportions of overlap with the MPAs, however, the absolute area size inside and outside using the BBMM method was larger. In Indonesia, only up to 2% of home ranges (90%) and core use areas (50%) were inside of MPAs using both methods, and in Australia this was 12-19% (Table 2 and Figure 5).

When assessing the number of individuals inhabiting the same area, the shape of home ranges was highly variable among individuals and differed in degree of overlap (Figure 6). The overlapping individual home ranges represented areas that were used by several individuals during migration. Seven out of nine whales were calculated to have overlapping home ranges using the a-LoCoH method (Figure 6 A-B), and all nine whales were calculated to have overlapping home ranges using BBMM (Figure 6 C-D). When visually inspecting the home ranges, unlike a-LoCoH, BBMM well-connected the core use areas in the two countries (Figures 5 and 6).



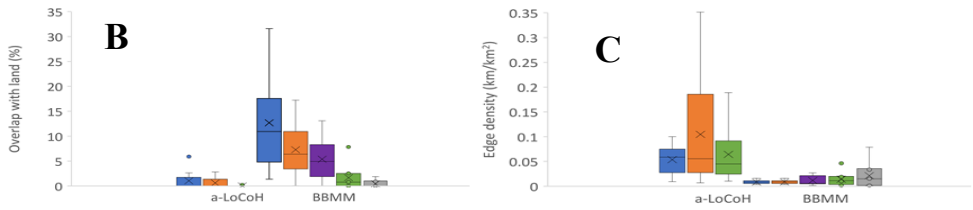


Fig. 4. Boxplots of the (A) area size (km²), (B) area-on-land (the percentage of home ranges overlapping with land, in %) and (C) edge density (km/km²) for a-LoCoH and BBMM home range methods and different probabilities (95%, 90%, 75%, 50% or 25%).

Table 2. Area (km²) and proportion (%) of home range (including migration corridors) and core use areas of 11 individual whales combined calculated to occur within and outside MPAs in Indonesia and Australia using the two methods.

	a-LoCoH		BBMM	
	90%	50%	90%	50%
Indonesia				
- Within MPAs	12,987 km ² (2%)	0 km ² (0%)	37,857 km ² (2%)	4,381 km ² (1%)
- Outside MPAs	539,813 km ² (98%)	182,100 km ² (100%)	2,272,943 km ² (98%)	700,919 km ² (99%)
Australia				
- Within MPAs	67,800 km ² (12%)	34,983 km ² (19%)	371,588 km ² (16%)	134,248 km ² (19%)
- Outside MPAs	485,000 km ² (88%)	147,117 km ² (81%)	1,939,212 km ² (84%)	571,052 km ² (81%)

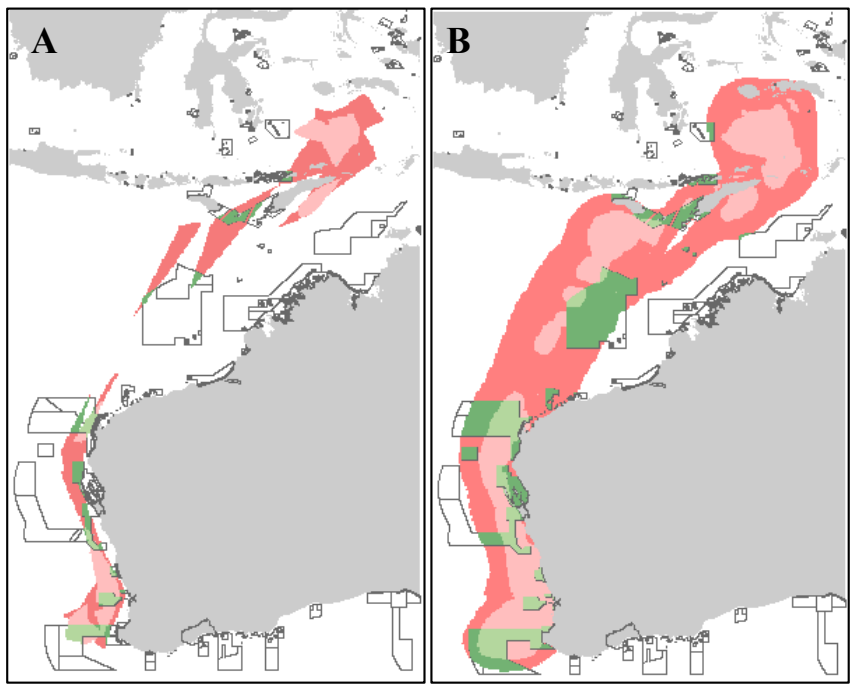


Fig. 5. Core use area and home range (including migration corridors) using the a-LoCoH method (A) and BBMM (B) inside (green) and outside (red) Marine Protected Areas in Australia and Indonesia.

4 Discussion

4.1 Home ranges

By comparing the home ranges and core use areas using area size, area-on-land and edge density, it is clear that the area size and area-on-land is significantly larger for the home range and core areas calculated using BBMM. This may cause some uncertainty about the reliability of the BBMM method. The considerably large error of the Argos system, a system that provides access to satellite data around the globe (<https://www.argos-system.org/>), is likely to have caused this difference in area size and area-on-land. In addition, the changes in BBMM variance generated by differences in trajectories (elapsed time between relocations) is also likely to have caused this. It is important to consider that with increasing time intervals between relocations, the distances between connected observations become larger having a “flattening” effect on the home range and increases spatial uncertainty of it [24]. This, however, does not discredit the BBMM in its usefulness to model the movement process in the absence of other information [24]. The predicted home ranges in Australia and Indonesia were not connected using the a-LoCoH method and also not in the 75% BBMM probability home range. For effective conservation management of this highly migratory species, it is important to identify the complete movement pattern and habitat used [44]–[46]. The patchiness of the a-LoCoH home ranges (95% and 90%) suggests overfitting of the data, meaning underestimating the home ranges [43]. The higher edge density and higher levels of boundary complexity show the same tendency of overfitting, because of the fragmented and concave edges [47].

The a-LoCoH method has the advantage to identify hard boundaries (in this case land), but in accordance with earlier studies, it did not reliably estimate home ranges for species covering large areas in short periods such as PBWs [48], [49]. Using the core area (50%), the stopover site in Ningaloo Reef was clearly distinguished by the BBMM method (4 individuals) but not by the a-LoCoH method (only one individual) (Figures 5 and 6). These core areas identified using BBMM can therefore also be identified as hotspots and extensively used corridors [17]–[19]. The function of these core areas is to accumulate energy reserves to complete the migration [50], [51]. These core areas are important to be identified to be able to manage these sites and to connect the migration corridors [17]. The a-LoCoH method, as a kernel-based method, exhibited a mechanism assuming a sample from a probability distribution instead of a movement path, which was used in the BBMM [24]. The different migration corridors used by the whales are therefore best captured using the BBMM method, using 90% as the home range (including migration corridors) estimation and 50% as the core area estimation.

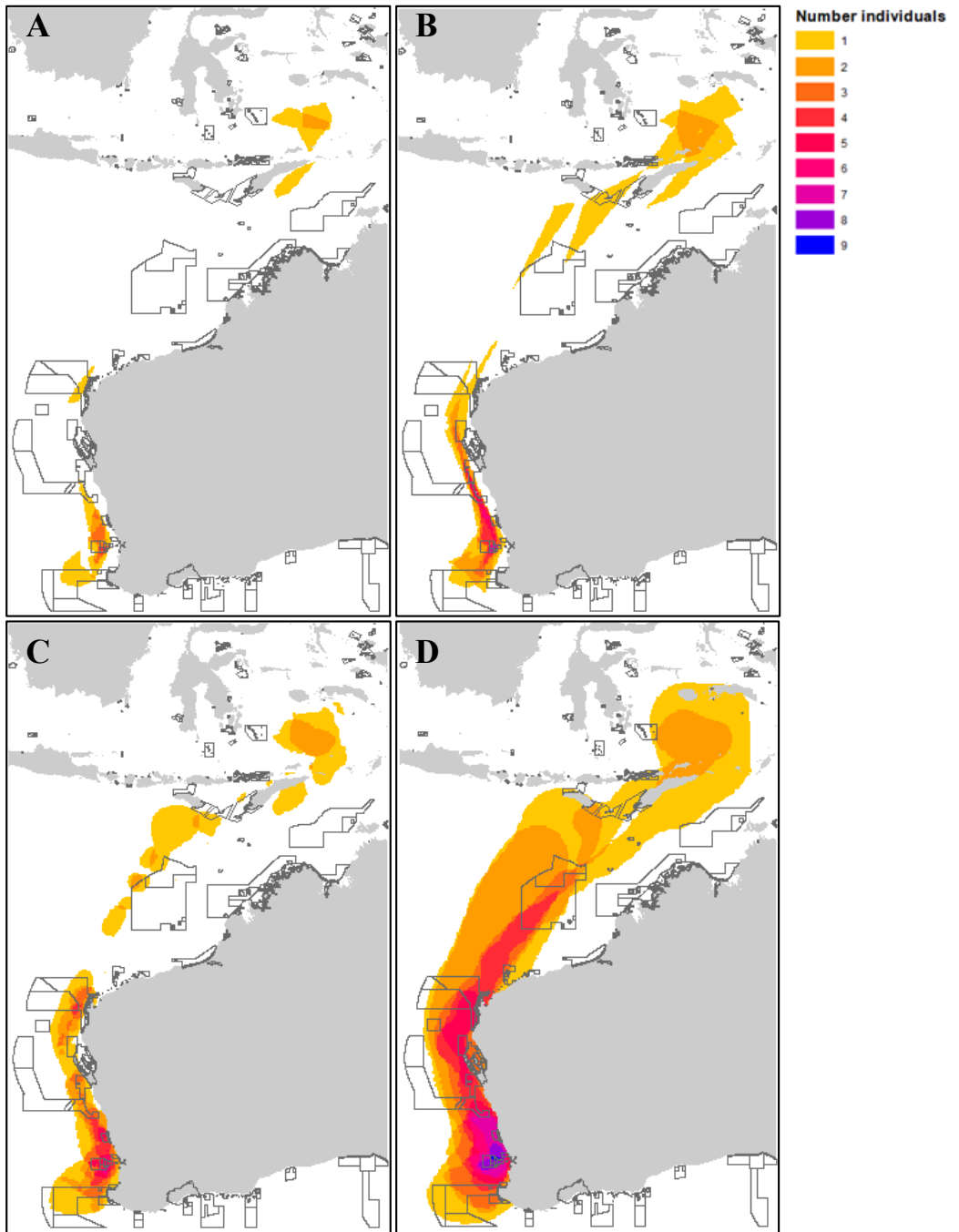


Fig. 6. The number of individuals inhabiting the same areas ranging from 1-9 individuals (yellow to blue) in the home range/migration corridors (A) and core use areas (B) calculated using the a-LOCOH method, and home range/migration corridors (C) and core use area (D) calculated using BBMM.

For home range analysis, a minimum of 30 relocations was needed, therefore 2 individuals were excluded from the analysis. It is important to consider that individual 98141 was the only individual using the Molucca Sea and was not used for the home range analysis

due to the limited number of relocations; however, this area is important to consider for conservation management and policies, since with just only limited relocations already inform us the occurrence of the animal. The Molucca Sea is currently not part of a protected area or migration corridors.

4.2 Overlap with marine protected areas

Superimposing home ranges with MPAs resulted in a low overlap, especially in Indonesia with only 2% overlap with the migration corridors and 0-1% overlap with the core use areas. Essential migration corridors without any protection in eastern Indonesia were found in the eastern Savu Sea, south of Timor Island, and the wider Banda Sea (Figure 5). The area south of Timor Island and the wider Banda Sea were identified as core areas for the whales. In other studies, sightings of PBWs around Komodo National Park were reported [3], [52]. This could be caused by the fact that these previous studies were based on sightings from boat observation and this study on telemetric data, where the tagged individuals were not using Komodo waters, at least not during the time of the study.

In Australia, a higher total number of MPAs are in place and the sizes of the protected areas are significantly larger compared to Indonesia (Figure 1). 68% of the area where nine of the individuals overlapped in their home ranges was covered by Australian MPAs. In Indonesia, only 2 individuals overlapped in their home ranges, and only 1% of these 50% probability home ranges overlaps with MPAs (Table 2). Although only 16% of the total home range overlaps with MPAs, from visual inspection the core areas in Australia are in or close to MPAs. Essential for migratory species is to be able to have the core areas connected to each other, in this case connecting by safeguarded areas in which the disturbance is limited.

One minor problem with the calculated area sizes and overlap was the used projection system. Universal Transverse Mercator zone 50 was used in this study, however some of the study area fell into zones 49, 51 and 52. This caused distortion in the area sizes in the other zones. However, the area of MPAs is also following the projection distortion and therefore the percentage of overlap will be negligible. To overcome the distortion problem, an equal area projection like Lambert azimuthal equal area could be used in future studies.

This study has tried to evaluate the Indonesian and Australian MPAs regarding their coverage of home ranges (migration corridors and core use areas) of the PBW. Important migration corridors are without current protection, including in the east Savu Sea, south of Timor Island, and the wider Banda Sea. The BBMM technique made it possible to connect the core areas (high use areas) with migration corridors. The home range derived using BBMM (90%) may be an overestimate due to high location uncertainty and high variance but connects the BBMM core areas (50%) with each other. Important to state from the outcomes of this study is the relevance of comparing methods to be able to choose the right method for the data used and the study goal. Also, the unforeseen low overlap of the home ranges with MPAs in Indonesia shows the importance of in-depth scientific studies to be able to evaluate, implement and develop conservation and management planning.

We thank Virginia Andrews-Goff and Michael Double from the Australian Antarctic Division for the satellite data used in this study.

References

1. T. Ichihara, *Norsk Hvalfangst-Tid*, **50** (1961)
2. M. Carwardine, (London: Bloomsbury Publishing Plc., 2020)
3. T. A. Branch et al., *Mamm Rev*, **37** (2007)

4. T. Ichihara, (Berkley and Los Angeles: Univ. Calif. Press, 1966)
5. A. I. Houston, P. A. Stephens, I. L. Boyd, K. C. Harding, and J. M. McNamara, *Behavioral Ecology*, **18** (2007)
6. F. Samaran et al., *PLoS One*, **8** (2013)
7. A. N. Gavrilov, R. D. McCauley, C. Salgado-Kent, J. Tripovich, and C. Burton, *J Acoust Soc Am*, **130** (2011)
8. M. C. Double et al., *PLoS One*, **9** (2014)
9. K. M. Stafford, E. Chapp, D. R. Bohnenstiel, and M. Tolstoy, *Mar Mamm Sci*, **27** (2011)
10. S. Rennie et al., *Journal of Marine Systems*, **77** (2009)
11. P. C. Gill, M. G. Morrice, P. Brad, P. Rebecca, A. H. Levings, and C. Michael, *Mar Ecol Prog Ser*, **421** (2011)
12. A. Sahri et al., *Biol Conserv*, **272** (2022)
13. S. R. Benson et al., *Ecosphere*, **2** (2011)
14. K. D. Hyrenbach, K. A. Forney, and P. K. Dayton, *Aquat Conserv*, **10** (2000)
15. T. Josse, M. Hadiwinata, H. Pratama, Z. W. Brent, and M. Barbesgaard, (Amsterdam: Transnational Institute, 2019)
16. A. Sahri, P. L. K. Mustika, H. Y. Dewanto, and A. J. Murk, *Mar Policy*, **117** (2020)
17. H. Sawyer, M. J. Kauffman, R. M. Nielson, and J. S. Horne, *Ecological Applications*, **19** (2009)
18. C. J. Farmer, K. Safi, D. R. Barber, I. Newton, M. Martell, and K. L. Bildstein, *Auk*, **127** (2010)
19. J. Y. Takekawa et al., *Avian Dis*, **54** (2010)
20. R. A. Myers and B. Worm, *Nature*, **423** (2003)
21. M. Scheffer, S. Carpenter, and B. De Young, *Trends in Ecology and Evolution*, **20** (2005)
22. B. A. Block et al., *Nature*, **475** (2011)
23. T. Mazar, M. Beger, J. McGowan, H. P. Possingham, and S. Kark, *Global Ecology and Biogeography*, **25** (2016)
24. J. S. Horne, E. O. Garton, S. M. Krone, and J. S. Lewis, *Ecology*, **88** (2007)
25. T. Patterson, L. Thomas, C. Wilcox, O. Ovaskainen, and J. Matthiopoulos, *Trends Ecol Evol*, **23** (2008)
26. W. H. Burt, *J Mammal*, **24** (1943)
27. G. Péron, *Biological Reviews*, **94** (2019)
28. A. O. Haugen, *Ecology*, **23** (1942)
29. C. O. Mohr, *American Midland Naturalist*, **37** (1947)
30. D. W. Hayne, *J Mammal*, **30** (1949)
31. B. J. Worton, *Ecology*, **70** (1989)
32. J. A. Downs and M. W. Horner, *Transactions in GIS*, **13** (2009)
33. G. C. White and R. A. (San Diego: Academic Press, 1990)
34. J. Fieberg, *Ecology*, **88** (2007)
35. J. Fieberg, J. Matthiopoulos, M. Hebblewhite, M. S. Boyce, and J. L. Frair, *Philosophical Transactions of the Royal Society B: Biological Sciences*, **365** (2010)

36. W. M. Getz, S. Fortmann-Roe, P. C. Cross, A. J. Lyons, S. J. Ryan, and C. C. Wilmers, *PLoS One*, **2** (2007)
37. J. A. Downs, M. W. Horner, and A. D. Tucker, *Ann GIS*, **17** (2011)
38. J. K. Moore and M. R. Abbott, *J Geophys Res Oceans*, **105** (2000)
39. M. Furnas, *Cont Shelf Res*, **27** (2007)
40. D. E. Seaman, J. J. Millspaugh, B. J. Kernohan, G. C. Brundige, K. J. Raedeke, and R. A. Gitzen, *J Wildl Manage*, **63** (1999)
41. P. Scull, M. Palmer, F. Frey, and E. Kraly, *International Journal of Geographical Information Science*, **26** (2012)
42. A. J. Bengsen, J. A. Butler, and P. Masters, *Wildlife Research*, **39** (2012)
43. D. J. Stark, I. P. Vaughan, D. A. Ramirez Saldivar, S. K. S. S. Nathan, and B. Goossens, *PLoS One*, **12** (2017)
44. D. P. Costa, G. A. Breed, and P. W. Robinson, *Annu Rev Ecol Evol Syst*, **43** (2012)
45. G. C. Hays et al., *Trends Ecol Evol*, **31** (2016)
46. R. Schuster et al., *Nat Commun*, **10** (2019)
47. P. A. Pebsworth, H. R. Morgan, and M. A. Huffman, *Primates*, **53** (2012)
48. J. W. Fischer, W. D. Walter, and M. L. Avery, *Condor*, **115** (2013)
49. M. Huck, J. Davison, and T. J. Roper, *Wildlife Biol*, **14** (2008)
50. T. Alerstam and A. Hedenstrom, *J Avian Biol*, **29** (1998)
51. A. Hedenström, *Anim Behav*, **66** (2003)
52. T. A. Branch, E. M. N. Abubaker, S. Mkango, and D. S. Butterworth, *Mar Mamm Sci*, **23** (2007)