Drivers of change in social networks of bottlenose dolphins (*Tursiops truncatus*) in Cardigan Bay, Wales

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Drivers of change in social networks of bottlenose dolphins (Tursiops truncatus)

in Cardigan Bay, Wales

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- Highlights
- Social differentiation was within the entire social network was relatively high (Poisson: S =
 - 2.026, SE = 0.169; r = 0.850, SE = 0.007) demonstrating the presence of diverse, non-random
- social bonds.
- - Temporal associations best fit the model of "preferred companions and casual acquaintances"
 - (QAIC = 74290.0489) against the standardised lagged association rates (SLAR). The standard
 - deviation (SD) and coefficient of variation (CV) values of the real association indices were
 - higher (SDo = 16.96985, CVo = 14.16834) compared to those of random datasets (SDr =
 - 13.17329, CVr = 11.30411). This implies a strong presence of long-term (between-sampling
 - period) preferred associations between individuals over time.

- Key words: Bottlenose dolphin, Tursiops truncatus, social network analysis, SOCPROG, photo-
- identification, association strength, social bonds, Cardigan Bay.

ABSTRACT

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Although previous studies have demonstrated the variability within delphinid social structures, it is important to analyse how association strength and patterns have changed over time and whether this correlates to fluctuations in population status, sex, social group, and changes in geographic location due to movement of individuals. This study describes the first long-term assessment, spanning almost two decades, of differences in association strength between individuals, whether preferential associations are maintained over the long-term, and the drivers of change within social networks of the bottlenose dolphin (Tursiops truncatus) using a compiled version of SOCPROG 2.9. A 16-year dataset was created by extracting unique identification features from high-resolution photographic images of the dorsal fin of bottlenose dolphin individuals within the Cardigan Bay, west Wales social network. Photo-identifications were collated using the research charity Sea Watch Foundation (SWF) annual monitoring database dating from 1990 to the present in the waters around Wales, but particularly within Cardigan Bay. This study identified a total of 505 dolphins. The social analysis was restricted to 305 individuals (sampled ≥5 times) which are suggested to be part of an open population as represented by the discovery curve generated using photo-identification data. Social differentiation was within the entire social network was relatively high (Poisson: S = 2.026, SE = 0.169; r = 0.850, SE = 0.007) demonstrating the presence of diverse, non-random social bonds. Temporal associations best fit the model of "preferred companions and casual acquaintances" (QAIC = 74290.0489) against the standardised lagged association rates. Most bottlenose dolphin associations were between pairs of individuals that preferentially associate which is constant over, and between pairs of individuals who associate for some time, dissociate, and may reassociate forming nonpermanent associations. The present study demonstrates that among bottlenose dolphins, long-term associations are more favored over short-term non-permanent companionship, correlating to a society governed by fission-fusion dynamics. These results help develop the existing knowledge of social structure obtained for oceanic dolphin species.

INTRODUCTION

Animal societies

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A species social structure is comprised of groups of individuals living and interacting cooperatively via inter- or intra-specific relationships, in which members form associations with specific individuals of varying strength and are maintained for certain periods of time (Whitehead 2008a). Individuals are considered part of a 'society' when the social structure of a same-species group enables members to associate with one another in a coordinated manner (Hamilton 1964). Regardless of relatedness, members within a society benefit from close associations formed during group living in comparison to a solitary lifestyle (Croft et al., 2008). Typical advantages include increased vigilance and protection from predators, higher survival rates through enhanced acquisition of resources, and greater reproductive success due to larger aggregations of suitable mates or increased offspring survival rates (Krause et al., 2007). Group living can also induce detrimental fitness trade-offs such as vulnerability to infectious disease or increased resource competition. Thus, group formation will only occur if the cost-benefit analysis favours most individuals within a population (Sih et al., 2009). Whilst the benefits of group living facilitate sociality, the development of social structure within animal societies is determined by a range of factors such as population distribution and density, individual fitness, and predation pressure (Wilson 2000; Croft et al., 2011; Farine and Whitehead 2015). The structure of social systems can influence the behaviour, ecology, biology, physiology, genetics, and rate of transmission of disease or infection within a species population (Silk 2007; Bertulli et al., 2021). Consequently, societies will usually demonstrate diverse grouping, mating, and spacing patterns, and show variation in the strength and quality of relationships between individuals (Aureli et al., 2008).

Cetacean social structures

Cetaceans are an excellent taxonomic group to evaluate how social networks and association patterns within a society have changed over time, as well as investigating potential drivers of change in social networks, due to the great diversification between species and the extensive continuum of sociality among delphinids (Mann *et al.*, 2000; Gero *et al.*, 2005; Rendell *et al.*, 2019; Bertulli *et al.*, 2021). Social structures vary between and within groups of cetacean species depending on a range of factors including habitat preference, environmental conditions, predator presence, and anthropogenic pressures (Gowans *et al.*, 2007). Across the broad spectrum of social structures there are: (i) long-term and constant associates with stable social bonds, as demonstrated amongst sperm whales (*Physeter macrocephalus*) and orca (*Orcinus orca*) for example, (ii) fluid societies with fission-fusion dynamics characterised by fluctuating and temporary associations, observed within striped dolphin

- 99 (Stenella coeruleoalba), and (iii) groups exhibiting social attributes of both societies, such as
- bottlenose (*Tursiops* spp.,) and Risso's dolphin (*Grampus griseus*) (Girvan and Newman 2002;
- 101 Newman 2006; Denkinger et al. 2020; Bertulli et al., 2021).
- It is imperative to investigate the drivers of change in social networks and association patterns over
- time across a wide range of cetacean species, especially those inhabiting extreme or changing
- environments, such as the bottlenose dolphin (*Tursiops truncatus*), if one is to effectively conserve
- and manage populations (Newman and Girvan 2004; Bertulli et al., 2021). Analysing the variation in
- social organisation across a population's geographic range enables us to compare social and
- 107 environmental mechanisms driving the varying patterns of sociality exhibited in such species
- 108 (Lusseau *et al.*, 2003).

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Social structure within bottlenose dolphin societies

- Social networks within bottlenose dolphin societies are governed by fission-fusion dynamics (Connor
- 2000). Fission-fusion societies are defined as those where population group size and composition are
- changeable and adaptable (Connor et al., 2000). Associations between individuals are partly driven
- by the voluntary presence or absence of group members, forming communities of individuals which
- frequently change pods, resulting in complex social relationships (Gero et al., 2005; Pesante et al.,
- 115 2008b). Management of these social networks is thought to be facilitated by highly developed
- cognitive abilities (due to large brain to body size ratio) used for communication, information transfer,
- social learning, and anticipation of other individuals' behaviour, evolved as a result of sociality and
- synchronous behaviours (Mann *et al.*, 2000; Gero *et al.*, 2005). However, as cetaceans live primarily
- underwater, few studies have analysed levels of social complexity and type of social interaction
- involved in maintaining sophisticated social network structures, as well as possible drivers of change.
- Therefore, it is important to explore the crucial factors influencing bottlenose dolphin group
- 122 composition, formation, and individual identity when understanding bottlenose dolphin social
- network structure (Pesante *et al.*, 2008a; Whitehead 2009).

Associations within bottlenose dolphin social networks

- Hammerschmidt and Fischer (2019) demonstrated how 'social bonds' between preferred associates,
- where individuals display consistent affiliative preferences, are formed to increase an individual's
- reproductive success. This is achieved through enhanced breeding opportunities, reduced predation
- and aggression, efficient information exchange, as well as decreased infanticide. Associations vary
- by social position, ecological conditions, age, and sex (Pesante *et al.*, 2008a; Whitehead 2009).
- 130 Records show that males form strong long-term associations between one or two preferred
- individuals. Small groups of male companions are classified as alliances and are typically established

to consort females (Krützen et al., 2003). Bottlenose dolphin male-male alliances can potentially last many years. For example *T.truncatus* populations inhabiting Sarasota Bay, Florida, are recorded to have alliances lasting 20 years, whilst populations of *T.aduncus* within Shark Bay, Australia, are known to have alliances of at least 12 years (Parsons et al., 2003). Association strength has been compared to that of mother-calf relationships, signifying the stability and consistency of male bonds (Sim 2015) Complicated male alliances have also been observed within certain populations, such as Shark Bay, in which males form second order alliances to mitigate attack and defend against rival male alliances (Sim 2015). Overall, male-male associations are fundamental in increasing the reproductive success of affiliated individuals.

Evidence of strong associations such as male-male alliances have not been recorded among female bottlenose dolphins. Most females have no or very limited associations, maintaining a large network of weak or moderate bonds which fluctuate regularly (Möller and Beheregaray 2004). Studies on female *T.aduncus* within Port Stephens, Australia, suggest that the majority of closely associated female bottlenose dolphins are genetically related. On the other hand, many populations have non-related female associations, indicating biological and environmental factors may also determine social bonds (Möller *et al.*, 2006). One significant factor driving female associations and grouping is their reproductive state (Parsons *et al.*, 2003; Möller *et al.*, 2006). Preferential bonds with fellow maternal kin are highly valuable, facilitating protection from predators and cooperative defence mechanisms of resources (Pesante *et al.*, 2008a.b). Alloparental care may also bond females, as observed in several odontocete species (Connor *et al.*, 1998; Wiszniewski *et al.*, 2009).

Calf association is the strongest bond that a female develops (Feingold and Evans 2014). Although, social behaviour develops rapidly, calves have a prolonged foraging dependence on their mother during the first 3-6 years (Feingold and Evans 2014). Association strength declines before the mothers next gestation period. However, juveniles can associate with their peers after leaving their mother (Pesante *et al.*, 2008a.b). Despite the length of juvenile postweaning and pre-reproductive stages, limited data exists on how they develop or influence the structure of social networks through behaviours such as play, sexual behaviours, and displays (Connor *et al.*, 2000).

160 Male-female associations are generally through reproductive courtships, with interactions increasing in the frequency when a female is cycling (Connor 2007). Typical patterns are: (A) solitary males defend an area used by a female, with male pairs covering a larger area, and do not stay with the female, or (B) male pairs and trios form courtships with individual females for a month (Connor *et al.*, 1999). Although male-female associations are not strong, mixed sex groups are not uncommon especially if they use the same natal range (Connor *et al.*, 2000).

Drivers of change

Although previous studies have reported the type and strength of associations within bottlenose dolphin social networks, how social networks change over time due to community divisions such as sex, behavioural state, age, and geographical location has not been fully examined (Connor 2007; Feingold and Evans 2014). For instance, male and female associations are restricted by their reproductive state and effort, whilst juveniles group together based on various behavioural characteristics as they are less constrained by reproductive effort (Connor 2007). Relationship uncertainty, where certain individuals are more closely associated compared to others due to overlapping geographical ranges, can cause change within social networks (Connor 2007). Thus, to establish how association patterns have changed over time and whether this can be related to observed changes in the status of the population, studying bottlenose dolphins within spatiotemporal groups is considered a suitable proxy as associates can be easily identified (Whitehead 2009)

Over the past decade, numerous studies have determined the gender of an increasing number of individuals, as well as establishing the nature of associations between individuals from the data collected during each individual encounter. However, few studies have undertaken a full analysis of social networks, establishing how association patterns have evolved over time and the drivers of such change. The purpose of this study was to establish whether members of the Cardigan Bay bottlenose dolphin population exhibit differences in the strength of associations shared between individuals due to their gender, social group, and geographical location. This study aimed to determine how trends in social networks and association patterns have changed over time between 2001 and 2017, and whether this can be related to environmental factors (such as changing levels of recreational disturbance), observed changes in population status, or changes in geographic location due to movements between Cardigan Bay and other parts of the Irish Sea (North Wales and the Isle of Man).

To analyse patterns of association, data were collected by extracting identification features (such as the unique patterns of nicks and the appearance of epidermal lesions located on the dorsal fin) from high resolution photographic images of groups of individuals which had been photo-identified in the Sea Watch Foundation (SWF) annual monitoring database, consisting of observational data from 1990 to the present in the waters around Wales, but particularly within Cardigan Bay. A social network analysis using an integrated set of programs in SOCPROG (Whitehead 2009) was undertaken to establish which individuals expressed preferential associations with certain individuals, and whether these social bonds were maintained in the long-term. Levels of association were determined for all pairwise combinations of non-calf males, females, and those of undetermined gender using the

Half-Weight Index (HWI) in SOCPROG. These can be established for different years, geographical areas, and even seasons.

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METHODS

Study site

Cardigan Bay is situated on the west coast of Wales (52°28'N, 4°09'W), extending from St David's 204 head in the south to the tip of the Lŷn Peninsula at Bardsey Island (Figure 1). Encompassing over 205 100km of open coastline, Cardigan Bay is nationally recognised as one of the largest embayment's 206 207 in the British Isles (Vergara-Peña, 2020). Across the bay mean annual temperatures seldom exceed 11°C, although higher temperatures (20°C) are recorded in shallower near-shore regions between 208 August-September. Lower temperatures of 5°C or less are reported from February-March (Barne 209 1995). The large inlet is relatively shallow, with average depths failing to exceed 60m off the Lŷn 210 Peninsula and west Pembrokeshire coasts (Evans 1995). Current speeds reach up to 1.8kn, whilst the 211 most prevalent tidal movements are usually observed around estuaries, headlands, and within St 212 Georges Channel (Magileviciute et al., 2007). Regular influxes of freshwater from three major rivers, 213 Aeron, Ina, and Teifi, significantly influence salinity levels (33.3% in winter to 34.2% in summer, 214 with lower salinities closer to the coast), local water temperatures, and water quality within the region 215 (Magileviciute et al., 2007). The bay's biological and physical characteristics are heavily influenced 216 by semi-diurnal tides entering the inlet from St Georges Channel. Tidal current speed determines 217 sediment distribution and substrate composition. Regions of strong currents, where tidal current speed 218 and energy are high, are characterised by sandy or gravel-type substrate; the habitat most favoured 219 220 by bottlenose dolphins. In comparison, areas where current speed and water energy are low, sediment composition is usually mud (Barne 1995; Evans 1995). 221

The study was primarily conducted within the Cardigan Bay SAC and Pen Llŷn a'r Sarnau SACs (Figure 2). The southern Cardigan Bay SAC is situated between Aberath and Ceibwr, encompassing approximately 1039km² and extends 19.3km offshore (Barnes 2010; Vergara-Peña, 2020). The exact geographical coordinates of the study areas are shown in Table 1. SAC site selection was based upon regular sightings of semi-resident bottlenose dolphins since at least the early 1920s.

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Figure 1: Cardigan Bay. Rectangle shows the Cardigan Bay SAC. The hatched polygon shows Pen Lyn a'r Sarnau SAC, with the diagonal line showing the edge of Cardigan Bay (*Sourced: Pesante, et al., 2008b*).

Pen Llyn a'r Sarnau cSAC

Cardigan Bay / Bae Ceredigion SAC

New Ouay

Cardigan Bay

Cardigan

Cardigan Bay

Cardigan

Figure 2: Location of the Cardigan Bay SAC, the main study area. (Sourced: Ceredigan County Council, Cardigan Bay cSAC Management Plan, 2001).

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Data collection

Encounter data were primarily collected aboard various motorised vessels within the perimeter of the two SACs in Cardigan Bay, particularly the southernmost SAC (Table 1). Boat-based surveys were only conducted at a Beaufort scale of three or less, and only when observation conditions were suitable. Survey trips were terminated if visibility levels significantly diminished because of heavy rain or dense cloud cover, due to potential unreliable sightings and inadequate digital images for dorsal fin photo-identification.

Table 1: The coordinates defining the geographical boundary of the Cardigan Bay SAC study site. The boundaries of the three study regions are expressed in decimal degrees.

Study area code	Region	Study area boundaries in	
		decimal degrees	
A	Southern Cardigan Bay	<52.5 decimal degrees	
В	Northern Cardigan Bay	52.5-53.0 decimal degrees	
\mathbf{C}	North Wales/northern Irish Sea	>53.0 decimal degrees	

Survey effort was recorded whenever effort status fluctuated, vessel direction adjusted, every sighting event, and otherwise periodically at 15-minute intervals. Effort entries included: survey approach (methodical line-transect, casual search, dedicated search, or photo-identification), time of effort entry (hh.mm, GMT/BST), position effort entries were recorded (start and end longitude and latitude in degrees and decimal minutes), vessel speed (knots) and course of travel (degrees), angle subtended by sea surface glare obstructing the field of view, presence or absence of precipitation, level of visibility, sea state (Beaufort Scale), and height of sea swell. Every effort entry which corresponded to a sighting was assigned a unique reference number. The sighting number (encounter record ID) was transferred to a sighting survey form which correlated to an individual encounter.

Sighting surveys also recorded the species observed, group size, age group (classified as either newborn, calf, juvenile, or adult) and number of each sighted. Qualitative age categories were based on swimming pattern, body size, proximity to an adult, and skin colour variations. Noteworthy behavioural characteristics (or reaction to watercraft) included swim speed, breaching, bow-riding, feeding or foraging, socialising and resting.

Individuals, or groups of bottlenose dolphin were approached following the regulations outlined in the license to disturb granted by Natural Resources Wales regardless of group size. Suitable photo-

identification images were captured following Wursig and Jefferson (1990). A single encounter was defined as the total time spent photographing every individual, irrespective of how distinctive 256 markings (dorsal nicks or skin lesions) appeared. An encounter was terminated once all individuals had been photo-identified, lost from view, or displayed avoidance behaviour.

Individuals belonging to the same group were classed as all the bottlenose dolphins photographed during a single encounter. Total group size was the number of associated individuals observed in a sighting, in which individuals within a spatial area of 100m were affiliated in the same behavioural activity. If multiple groups were sighted, each group was surveyed independently and recorded as a separate encounter.

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Data analysis

Photo-ID matching

Photo-IDs from each encounter were analysed using ACDSee 5.0.1 following specific matching procedures developed by the Sea Watch Foundation. Only high-quality photographs were used to identify associated individuals, determined by dorsal fin shape and patterns of lesions, nicks and scars, as they are the most stable feature to use for this species (Wilson et al., 2000; Bearzi et al., 2009). Photographs of distinctive body features were also used if they correlated to a known individual through dorsal fin identification. Group size and age (new-born, calf, juvenile, adult) were also confirmed through photo analysis procedures. After matching to the master photo-ID database, each individual was assigned an alpha numerical code. Accurately identified individuals were used to statistically analyse social networks and spatial distribution patterns of bottlenose dolphin groups.

Social analysis

Association patterns

- Associated dolphins were classed as all those identified within the same group during an encounter, 278
- with a one-day sampling interval to minimise potential demographic effects (Whitehead & Dufault 279
- 280 1999). Individuals were included in social analyses regardless of how many times they were sampled
- and group photo-ID coverage. 281
- In SOCPROG, a one-day sampling interval was used to calculate mean associations per individuals 282
- and per dvad (g'), social differentiation (S), and correlation coefficient (r), by conducting Whitehead 283
- (2008a, b) likelihood approximation techniques. Accuracy of association measures utilised in 284

constructing social structure models is represented by r. Variability within the social network is defined by S, ranging from homogenous to highly differentiated (Whitehead 2008b). Combined r and S values provides reassurance that the results and social network can be analysed accurately (Bertulli $et\ al.$, 2018). A high S value signifies less association data is required to achieve an r value closest to 1, with 1 being the highest degree of accuracy the dataset processes in representing true associations, and to demonstrate the occurrence of preferred associations (Whitehead 2008a). Bootstrap methods were conducted to calculate standard errors around estimates using 10,000 replicates to increase the accuracy when working with a large dataset (Whitehead 2008b). $S \times \acute{g}$, where \acute{g} is the mean association per individual, was calculated to see whether the association data could detect preferred associations, acknowledging that if $S \times \acute{g} > 5$ it is likely that individuals show tendencies to form preferred companions (Whitehead 2008a).

The Half weight index (HWI) was used to quantify the amount of time dolphins within a pair spend together, to accurately measure the level of association between individuals belonging to the same group on a scale from 0-1. This procedure was chosen as it significantly reduces observer bias during photo-identification and boat-based surveys (Wells 1991; Fortuna 2007). It also allows results to be compared against association patterns recorded in other bottlenose dolphin studies (Wells 1987). The HWI was cited as HWIG, as it was modified to accommodate biases induced by differences in sociality; to distinguish between associations occurring by chance during aggregations and preferred companionships (Lusseau *et al.*, 2006). A HWIG lower than 1 suggests individuals are more likely to evade each other, while a HWIG greater than 1 indicates two individuals are interacting more frequently than what would be predicted (Godde et al. 2013). To test whether associations where significantly higher. The Mantel test (Mantel 1967) to test whether individuals within the same region had significantly high levels of association, compared to individuals from different regions, was also run in SOCRPORG. The null hypothesis was that the rate of association between and within regions were similar.

Test for preferred and avoided companionship: long-term (between-) associations and short-term (within-sampling) associations

Patterns of preferred and avoided associations were tested for in SOCPROG using a variation of the Bejder et al., (1998) permutation test created by Whitehead et al., 2005. The routine chosen was to "permute groups within samples" as bottlenose dolphins are known to move across the different study regions (Table 1), and as a consequence some identified individuals do not appear in each sampling period across the duration of the study. This tested the null hypotheses that individuals do not preferentially associate or avoid one another given the number of groups each individual was seen in during each sampling period (Whitehead 2008a). Associations were permuted with 10,000 trial per permutation to avoid the test being too conservative and to

stabilise the p-values, with association index equal to HWIG (Pearson *et al.*, 2017). If individuals develop long-term (between-sampling periods) preferential associations with other individuals the SD and CV values of the real data should be higher than the random datasets. The SD and CV real values should be lower than the random datasets if individuals preferentially associate short-term (within-sampling periods). Individuals demonstrating avoided companionship is indicated by the proportion of non-zero values being lower for the real data compared to the random (Whitehead and Dufault 1999; Blasi and Boitani 2014).

Temporal analysis

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Lagged association rates

Standardised lagged association rates (SLAR) were calculated to analyse how a dyadic association changes over time, using all identified individuals (n = 505) and a moving average of 400 associations (Whitehead 1995). The sampling restrictions on the number of individuals was relaxed from those sampled >5 times to all marked individuals, as SLAR generates an integration of all the available data. The expected SLAR values of individuals associating randomly was illustrated by the null association rate (no preferred associations; Whitehead 2009). The lagged association rate represented an estimate of the probability that if two or more individuals are associated at any time, then, after the specified time lag, the second individual is a randomly chosen associate of the first (Whitehead 2019). The intercept on the y-axis (with lag 0) is an estimate of the inverse of the mean typical group size (number of associated individuals including itself) minus one (Whitehead 1995; Whitehead 2015). Null and lagged association rates were standardised since during the present study it was not realistic to precisely photo-identify all social group members during an encounter (Gowans and Whitehead 2001). To corroborate whether lagged association rates were calculated with accuracy, the temporal jackknife method (Gowans and Whitehead 2001) was implemented in SOCPROG to calculate standard errors. Mathematical models were fitted to the SLAR utilising maximum likelihood procedures (Whitehead 1995) such as: (i) "preferred companions", some pairs of individuals preferentially associate over time creating long-lasting social bonds; (ii) "casual acquaintances", pairs who associate for some time, disassociate, and may reassociate over time forming non-permanent associations, (iii) "constant companions and casual acquaintances", pairs with preferred and casual associations, and (iiii) "two levels of casual acquaintances" pairs with fluctuating association and dissociation stability over short and long period of time (Whitehead 2015). The best fitting model for the association data was selected by the lowest quasi Akaike Information Criterion value (QAIC; Whitehead 2015, 2019).

Movement analysis

Lagged identification rate

To analyse how individuals move into and out of the three different study regions (A, B, and C: Table 1), the Lagged Identification Rate (LIR) was calculated. LIR is the probability that if an individual is identified within an area at any time, it is identified some time lag later in the same area during any single encounter (Whitehead 2001). If the LIR is the inverse of the population size, the population is closed. The LIR typically falls with time lag if there is mortality or emigration. LIR that rise and fall with time lag signify cyclical movements within the population. The LIR was used to determine bottlenose dolphin mean residency time "within and between" study areas, indicating the general probabilities that individuals are in the same study area or in a different area after particular time lags. The mean residency time generated by the LIR helped determine the threshold of the sampling period to classify short-term and long-term associations (see test for preferred and avoided companionship).

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RESULTS

Survey effort and group composition

- From 2001 to 2017 a total of 505 reliably marked bottlenose dolphins were photo-identified from
- each individual sighting (8420) across 1113 sampling days comprising 28858 hours of survey effort.
- The year with the most encounters was 2012 (1081), whilst the year with the least was 2002 (81). The
- highest number of encounters (69) was recorded on the 28th January 2012. A total of 2345 groups
- were encountered, in which photo-identification images were successfully taken of each group
- member. The total number of individuals photo-identified one or more times in southern Cardigan
- Bay (A) was 6238, whilst the number of sightings in northern Cardigan Bay (B) and North Wales and
- northern Irish Sea (C) was 1180 and 1002 respectively.
- Of the 505 identified dolphins, 200 were excluded from the social analysis as they were associating
- with others less than 5 times (Numsamp>=5). A total of 305 individuals were therefore used in this
- social analysis (sampled \geq 5 times) as associations were sufficiently strong to represent social bonds
- accurately and reliably (Table 2). Individuals were sighted across 1106 different days from 2001 to
- 380 2017. The mean number of identifications per day was 7, whereas the mean number of individuals
- identified per day was 6 (Table 2). Of the 305 individuals, 84 were classed as female and 23 were
- classed as male (Table 3).

Table 2: Mean number of identifications and individuals per sampling period (day) calculated from the number of individual bottlenose dolphins chosen for social analysis (sampled ≥5 times) and the frequency of sightings across the sampling period.

Number of individuals	Number of sampling periods (Day)	Number of identifications	Mean identifications per sampling period	Mean individuals identified per sampling period	Proportion of individuals identified per sampling period
305	1106	8019	7.25	6.46	0.02117

Table 3: Sex of the 305 individuals selected for social analysis sampled ≥5 times. F: Female; M: Male; Probable Female: PF; Probable Male: PM; Unknown: U.

F	M	PF	PM	U
84	23	15	22	161

The discovery curve of the number of individual bottlenose dolphins identified against the cumulative number of identifications rose progressively across the study period before plateauing in 2014 (Figure 3, A). This indicates that part of the population within the study area remained to be sampled prior to 2014 as demonstrated by previous studies conducted in the region (Pesante *et al.*, 2008a, b; Feingold

and Evans 2014, Lohrengel *et al.*, 2017)

The average group size across the 17-year period was six. Although 2002 had the lowest number of sightings, 2017 had the lowest average group size (3). The year with the highest average group size was 2012 (9).

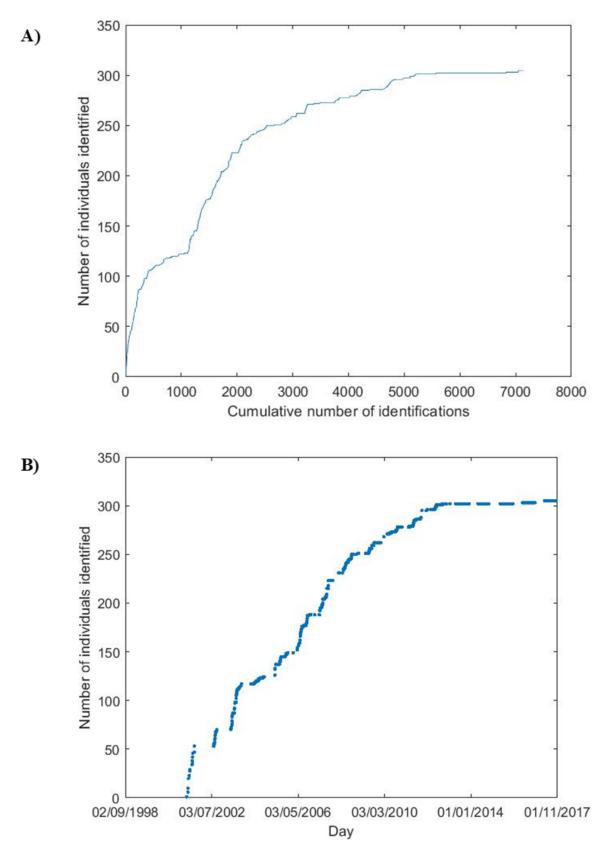


Figure 3: (A) Discovery curve of number of individual bottlenose dolphins identified versus cumulative number of identifications, with year of sampling between 2001 and 2017 (n = 305). **(B)** Discovery curve of number of individual bottlenose dolphins identified versus sampling period (days), with year of sampling between 2001 and 2017 (n=305). A and B SE of social differentiation are calculated using 10,000 bootstrap replicates for greater accuracy.

Social analysis

Association patterns

Mean association per dyad was ± 0.64 and per individual was ± 193.40 . The letter ' \acute{g} ' (1.30) represents the mean association per individual and was used to test whether association data detected preferred associations. The estimate of social differentiation (S) using the Poisson method was 2.026 (SE=0.169), indicating that the society is differentiated. The correlation estimate between true and estimated association indices (r) using the Poisson method was 0.850 (SE=0.007). This suggests the power to resolve these relationships is acceptable, although limited, despite time consuming efforts in the field spanning over a decade. Standard errors were calculated from bootstrapping with 10,000 replications for greater bootstrapping accuracy when analysing such an immense data set.

Hierarchical cluster analysis

A hierarchical agglomerative cluster analysis of the association data calculated the modularity, the difference between the proportion of the total association, for the division of the population into clusters, and the expected proportion (Newman 2004; Whitehead 2008b). Modularity 1 demonstrated the expected proportion of association indices given the summed associations (from standardised gregariousness). Maximum modularity was 0.44572 and the value of the association index at this modularity (AI) was 1.2775. The cophenetic correlation coefficient (clustering using average linkage) was 0.98493 (Figure 4). Modularity 2 used the expected proportions from the number of permutations (10000 trials per permutation) of associations within samples in preferred/avoided association module routines. This controlled for gregariousness and the structure of the data (Whitehead 2019). The maximum modularity was 0.063591 at AI = 2.6474. This suggested that clusters formed had mutual association preferences as opposed to being identified together. The cophenetic correlation coefficient was 0.98493 (Figure 4). Maximum modularity of both types were greater than 0.3, suggesting useful divisions of the data (Newman 2004). The cophenetic correlation was lower than 0.8 indicating that graphing in relation to the data was reliable.

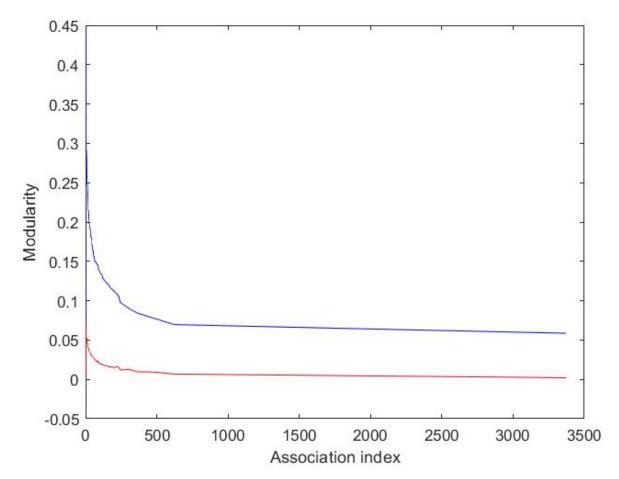


Figure 4: Hierarchical agglomerative cluster analysis of the association data. Modularity demonstrates the difference between the proportion of the total of the association indices, or interaction rates, within clusters and the expected proportion. Blue line (modularity 1): the expected proportions given the summed associations of the different individuals. Red line (modularity 2): the expected proportions are from the permutation (10,000) of associations within samples in the preferred/avoided association module routines.

Community division by modularity

Modularity was used to assess whether the population could be usefully divided into clusters, to evaluate whether association indices were generally higher among individuals within the same cluster and lower with individuals from different clusters. Assignment of individuals to clusters was done using the eigenvector-based method (Newman 2006) and modularity 1, as it was the most efficient delineation (highest modularity) and worked the best for this procedure. All 305 individuals were arranged into 1 of 11 individual clusters. The 6th cluster had the highest average eigenvector (0.7013) corresponding to the final bifurcation involving that individual, which therefore had the most uncertainty in the assignment of the individual. The cluster with the lowest average was 7 (-0.34848). The modularity of this arrangement was 0.450. A modularity greater than 0.3 suggests there was a useful and clear divisions of the population data.

Network analysis statistics

Several measures treating the matrix of symmetric association indices as a weighted network were calculated (Table 4). The average sum of association indices of any individual with all other individuals (strength) was 364.11 (Table 4). This high strength signifies how strong associations exist between an individual and other dolphins within the network. The eigenvector centrality measured the degree to which an individual is associated with others and how closely they are associated. Although the average value was low (0.01), a highly associated individual does not necessarily have a high eigenvector of centrality (Table 4). It could potentially mean that all associates have relatively low or null eigenvector centrality. It is not guaranteed that an individual with a high value is greatly linked, the individual may have few but important associates. The reach is a useful tool when measuring a society containing behavioural contagion. A high reach (218341.34) reflected how an individual was strongly connected indirectly (Table 4). The affinity measured the strength of an individual's associates weighted by the association index between them. The high affinity score (385.08) indicates an individual on average has relatively high associations with other individuals with a high strength (Table 4). The correlation coefficients, over individuals, of strength by clustering coefficient was 0.2376, and strength by affinity was 0.8972.

Table 4: Variety of measures treating the matrix of association indices. Strength: sum of association indices of any individual with all other individuals. Eigenvector centrality: a measure of how well an individual is associated to other individuals, and how well they are associated. Reach: a measure of indirect connectedness. Clustering coefficient: a measure of how well the associates of an individual are themselves associated. Clustering coefficient: a measure of how well the associates of an individual are themselves associated. Measures are calculated for each individual. Each measure presents the average and standard deviation (SD) for the whole population.

	Strength	Eigenvector centrality	Reach	Clustering coefficient	Affinity
Overall	364.11	0.01	218341.34	0.00	385.08
means	(293.34)	(0.06)	(1015017.34)	(0.00)	(297.83)

Distribution of association indices

For each individual, the mean half-weight index (HWIG) value was 1.20 ± 0.96 (mean association index with all other individuals excluding itself \pm SD). This shows there are preferred associations among individuals (Table 5). The sum of all associations (which for association indices is similar, but not identical, to the group size) was 364.11. Maximum association rate (excluding individuals with themselves) was 69.00 (Table 5). Table 5 also gives the standard deviation of such measures over all individuals and by the class variable 'sex' (each sex with all individuals, between pairs of the same sex, and within- and between- individuals of the same or different sex).

A Mantel test for analytical approximation was carried out on the null hypothesis that associations between study region are similar (Schnell *et al.* 1985). The t-value (with infinite degrees of freedom) was 2.876. A positive t-value indicates associations between individuals within the same region is higher. The p-value (2-sided test) was 0.0040. A p-value ≤ 0.05 suggests the results were statistically significant and provides strong evidence against the null hypotheses. A mantel test with 1000 permutations p-value was 0.0000. As bootstrapping accuracy was increased, this result has an even greater statistical significance and supports rejecting the null hypothesis. The matrix correlation coefficient was 0.0133. Therefore, bottlenose dolphins ranging within area A, B or C (Table 1) associated significantly more with other dolphins within their geographic region than between regions.

Table 5: For each individual, the mean association index with all other individuals, the sum of all associations, and the maximum association rate. Standard deviations of these measures over all individuals and by sex (each sex with all individuals, between pairs of different sex, and overall within- and between pairs of different sex).

	Mean of assoc. (±SD)	Sum of assocs. (±SD)	Max. Assoc (±SD)
Overall	1.20 (0.96)	364.11 (293.34)	69.00 (281.15)

Standard deviation in brackets

478 Test for preferred and avoided companionship: long-term (between-) associations and short-term 479 (within-sampling) associations

The routine chosen to permute the association data randomly in different ways was to "permute groups within samples" to determine whether individuals associate with the same probability with all other individuals (or among some set of them) given their availability. This tested the null hypotheses that individuals do not preferentially group together or avoid one another (preferred or avoided associations) given the number of groups in which each individual was seen during each sampling period (day). The number of trials per permutation was 10,000 to avoid the test being too conservative and an unstablised p-value.

Results showed the real value, the mean of the values for the random data sets, and the number of times the test statistic from the random data was less than the real value (Table 6). The mean of the real association indices is not significantly lower than the random data (real = 1.19773, random = 1.15525, P = 0.9600). As the simulation used half-weight (standardized for gregariousness), this suggests few random short-term (within-sampling period) preferred companions. The standard deviation (SD) and coefficient of variation (CV) values of the real association indices were higher (SDo = 16.96985, CVo = 14.16834) compared to those of random datasets (SDr = 13.17329, CVr = 11.30411). This implies there is a strong presence of long-term (between-sampling period) preferred associations between individuals over several sampling periods. The proportion of non-zero association indices for real data (0.31844) was significantly lower than the random data (0.35442, P = 0.0010), representing how some individuals preferentially avoid others (Table 6). The null hypothesis was therefore rejected as the distribution of association indices from the real data was different from the distribution of association indices from many permuted data sets.

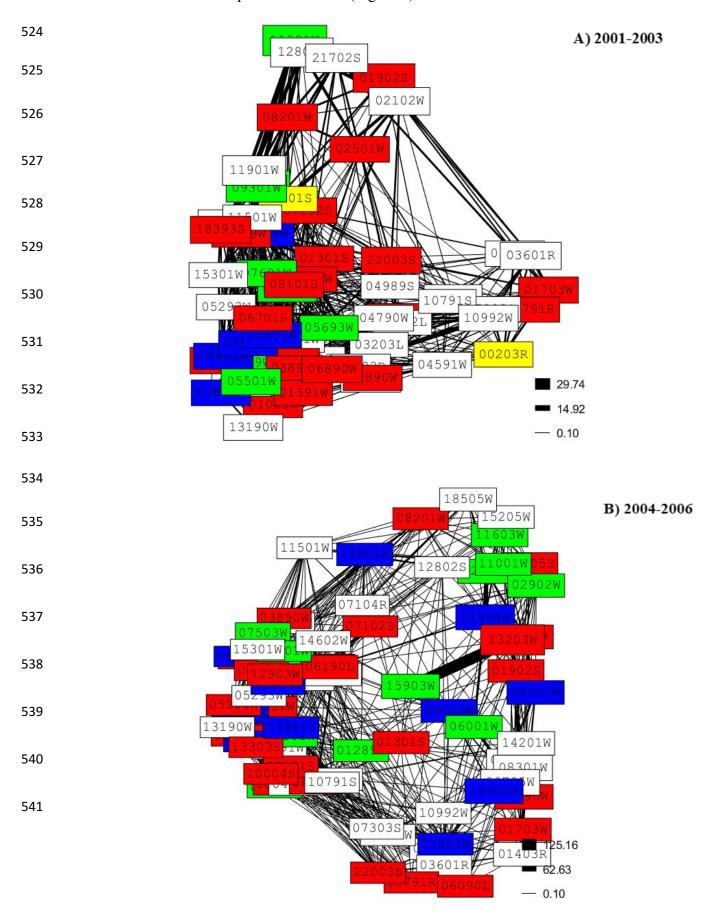
Table 6: Random permutations of association data via the 'permute groups within samples routine'. Number of trials per permutation: 10,000. Results of the tests are presented in the table giving, for each of these test statistics, the real value, the mean of the values for the random data sets, and the number of times the statistic from the random data was less than the real value. These values are translated into the p-value of a one-sided test.

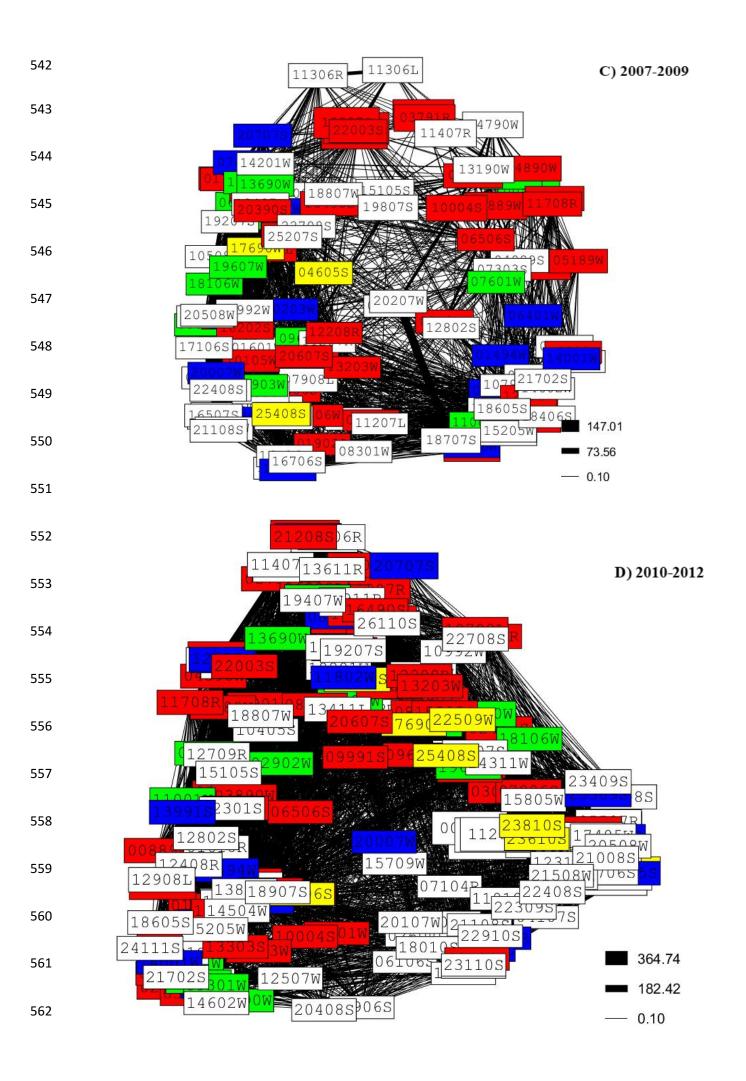
	Real	Mean (random)	(Real>Random)	P(1-sided)
Mean	1.19773	1.15525	(922/ 1000)	P = 0.9600
SD	16.96985	13.17329	(752/1000)	P = 0.1490
CV	14.16834	11.30411	(728/ 1000)	P = 0.1650
Proportion of non-zero elements	0.31844	0.35442	(1/1000)	P = 0.0010
Mean non-zero elements	3.76121	3.28084	(996/1000)	P = 0.0040
SD non-zero elements	29.91162	22.01858	(779/1000)	P = 0.1240
CV non-zero elements	7.95265	6.65207	(685/1000)	P = 0.2050
SD (typical group size)	5.10738	4.90884	(998/1000)	P = 0.0010

Network diagram: principal coordinates arrangement

The network diagram (sociogram) of the matrix of association indices shows the arrangement of individuals (nodes) in two-dimensions (Figure 5). The arrangement of nodes displayed is the "principal coordinates analysis" (Whitehead 2008b). Each point represents an individual in which the unique alpha-numeric code and sex is presented. The distance between individuals is inversely proportional to their association. Therefore, the distance between each node is proportional to 1 minus the squareroot of their association index (Whitehead 2019). Strongly associated individuals are plotted together, whilst weakly associated individuals are plotted apart (Figure 5). The width of the links between pairs of nodes represents the strength of their relationship (value of association index between individuals) (Whitehead 2019). The period with the maximum level of association (364.74) was between 2010-2012 (Figure 5, D), whilst the period with the second largest (147.01) was 2007-2009 (Figure 5, C). The highest median level of association (182.42) was also seen between 2010-

2012. The greatest range of maximum and minimum association index indices was between 2004-2006 (125.06), 2007-2009 (146.91), 2010-2012 (364.64) (Figure 5, B, C, D). The lowest minimum level of association for all periods was 0.10 (Figure 5).





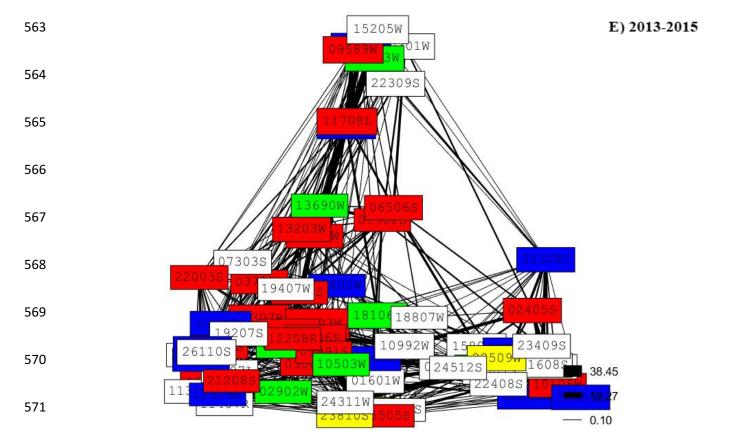


Figure 5: Network diagram displaying the principal coordinates arrangement of individuals between 2001-2015, in which the distance between the arrangement of nodes is inversely proportional to their association. Node size is proportional to the gregariousness of the individual (the sum of its associations). Node color represents the sex of the individual. Red: female, blue: male, probable female: yellow, probable male: green, and unknown is white. A) 2001-2003, B) 2004-2006, C) 2007-2009, D) 2010-2012, and E) 2013-2015).

Network diagram: circular arrangement

The most appropriate network diagram to represent the most recent association indices calculated for the past two years (2016-207) was to arrange nodes in a "circular arrangement" (Figure 6). This shows the most strongly linked individuals which are usually close to one another. Similar to the principal coordinates analysis, the thickness of links between pairs of individuals demonstrates the strength of their relationship (value of association index) (Whitehead 2019). The maximum level of association was 18.29 (median = 9.19, minimum = 0.10), with an association index range of 18.19. The most closely associated individuals were 07006S (F) - 11101S (PF), 16005W (U) - 00301W (U), and 26316S (U) - 14117R (U) (Figure 6).

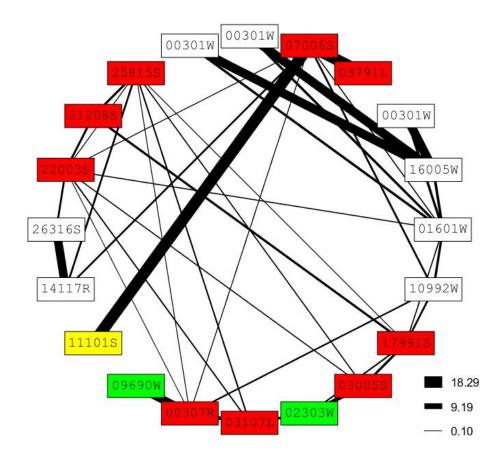


Figure 6: Network diagram displaying the circular arrangement of individuals between 2016-2017, visually representing strongly linked individuals close to one another. Node size is proportional to the gregariousness of the individual (the sum of associations).

Temporal analysis

Lagged association rates

The best fitting mathematical model for the association data, and best interpretation of bottlenose dolphins in the study area, was "preferred companions and casual acquaintances" (QAIC = 74290.0489, Table 7; Figure 7). The standardized lagged association rate (SLAR) showed an immediate rapid decrease, followed by a short and steady increase at approximately 10 days, before an immediate sharp decrease at around 50 days to below 0.01. This pattern was repeated; the SLAR peaked again at approximately 475 days before a second sharp drop, peaking again at 600 days. The error bar fell below the null association rate approaching around 850 days, after which the general trend is a decline in SLAR despite numerous fluctuations (SLAR, Figure 7). Although no other curve was similar or fitted the first 100 days, the "two levels of casual acquaintances" was the next closet fit (QAIC = 74361.5338; Table 7). This demonstrates that the majority of associations among bottlenose dolphins are between particular pairs of individuals which have a preference for associating (and which is constant over time), and between individuals who associate for some time,

dissociate, and then may reassociate (Whitehead 2019). The inverse of the intercept of the SLAR with a lag of 0 also shows how from each day to the next, bottlenose dolphins have a mean of approximately 6 associates.

Table 7: Model types fit to the standardized lagged association rates (SLAR) for all identified bottlenose dolphins sighted ≥ 1 times.

Model	Number of parameters	Goodness of fit chi- squared	Maximum- likelihood for parameters	AIC	QAIC
Preferred companions	1	50840.055	a1 = 0.011748	1050667.9000	75044.8115
Casual acquaintances	2	36328.482	a1 = 0.00036317 a2 = 0.016728	1041833.2244	74415.6436
Preferred companions + casual acquaintances	3	36277.846	a1 = 0.026444 $a2 = 0.010546$ $a3 = 0.038752$	1040048.8327	74290.0489
Two levels of casual acquaintances	4	35295.295	a1 = 2.5134 $a2 = 0.00035441$ $a3 = 0.55434$ $a4 = 0.016502$	1041023.6573	74361.5338

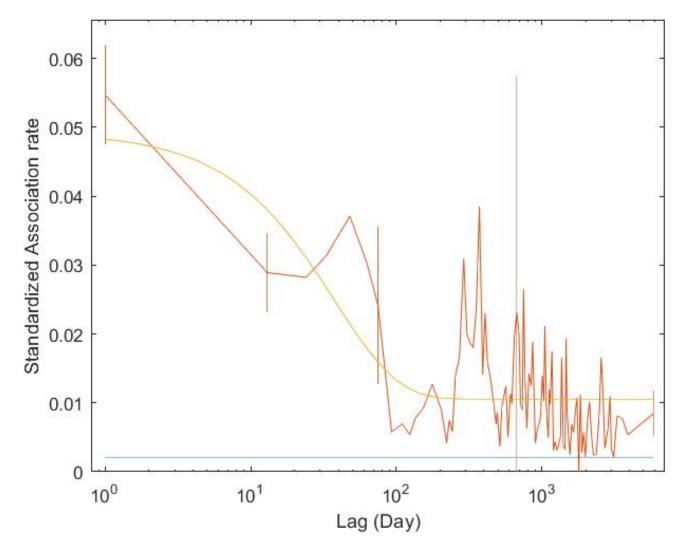


Figure 8: Standardized lagged association rates (red line) for all marked bottlenose dolphins sighted within Cardigan Bay (n = 505) with a moving average of 400 associations. Vertical bars indicate approximate standard errors calculating using the temporal jackknife method (jackknife grouping factor (in sampling units): 1, number of jackknife groupings: 1113). The best fitting model was "preferred companions and casual acquaintances". The null association rate (orange line) is the lagged association rate expected if individuals were associating at random.

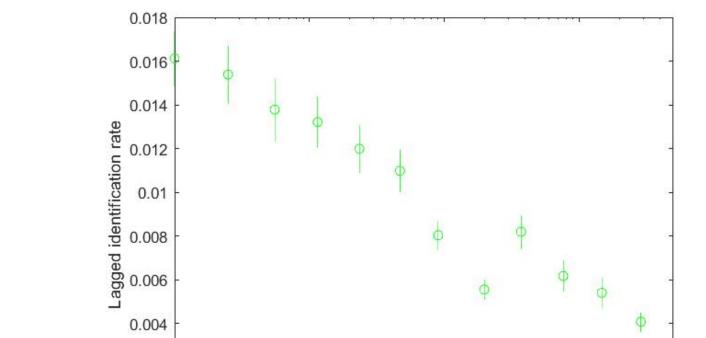
Movement analysis

Lagged identification rate

As data were collected in more than one area, a movement analysis in order to analyse the movement of individuals into and out of, and perhaps back into, the specific study areas (Table 1) were conducted. This was examined using the 'lagged identification rate' (LIR). The LIR is the probability that if an individual is identified in the area at any time, it is identified during any single identification made in the area some time lag later (Whitehead 2001). All sampling restrictions were removed to investigate all identified individuals. "Log x-axis" logged the x-axis (time lag) of the lagged

identification rate plots which was useful when considering the study's large range of time lags. 10,000 bootstrap replications were used to get more precise bootstrap-estimated standard errors of the lagged identification rates, and parameter estimates for fitted models of lagged identification rates and movement parameters. Two different forms of analysis were implemented "whole study" and "among all areas". Each analysis gave a plot of lagged identification rate against time lag (in days).

The "whole study" LIR analysis demonstrated the lagged identification rates for the whole study area (Figure 9). Emigration and mortality were clear within the Cardigan Bay population for the whole study area as the LIR typically fell with time lag. However, the population also exhibits cyclical movements as the LIR rose and fell with time lag (Figure 9).



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Figure 9: Lagged identification rates (LIR) against time lag (day) for individual movements of all individual bottlenose dolphins (n = 505) within (empty circles) areas of the three study regions: A) southern Cardigan Bay (<52.5 decimal degrees), B) northern Cardigan Bay (52.5 – 53.0 decimal degrees), and C) north Wales/northern Irish Sea >53.0 decimal degrees). Bootstrap-estimated standard errors (bars) are calculated from 10,000 bootstrap replications.

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Time lag (Day)

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The "among all areas" LIR analysis was chosen as the study area was divided into multiple areas (Table 1). Lagged identification rates were calculated and plotted for each area alone and between each pair of areas (Figure 10). Each graph visually illustrates the movement of individuals into and out of each study region, as well as the movement of individuals between each region. It demonstrates the probability that if an individual is identified within a particular study region at any time during the study period, it is identified in a later encounter either in the same area or moving between the two areas of comparison (Figure 10). The data shows that bottlenose dolphins spend time in each study region and then leave, to re-enter at a later point.

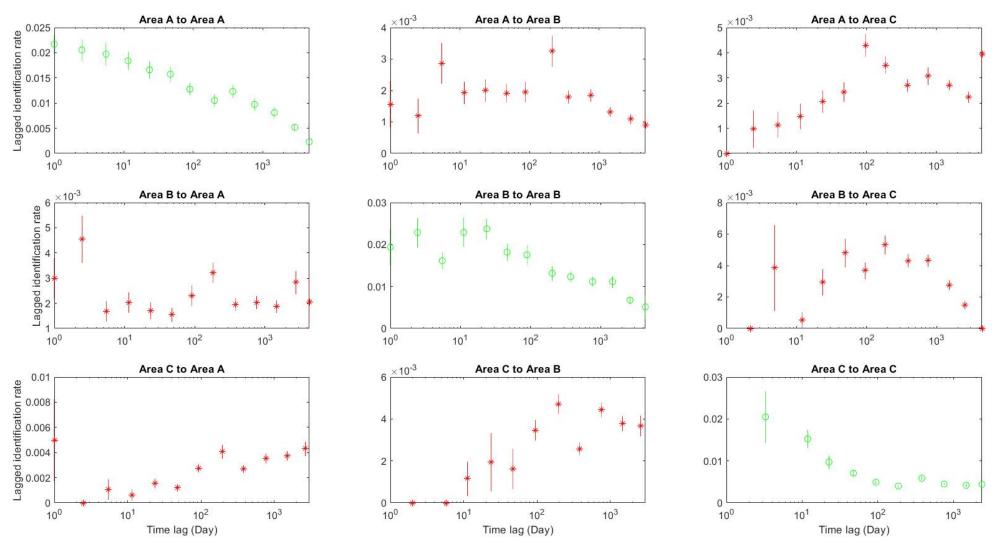


Figure 10: Lagged identification rates (LIR) against time lag (day) for individual movements of all individual bottlenose dolphins (n = 505) within (empty circles) and between (asterisks) areas of the three study regions: A) southern Cardigan Bay (<52.5 decimal degrees), B) northern Cardigan Bay (52.5 – 53.0 decimal degrees), and C) north Wales/northern Irish Sea >53.0 decimal degrees). Bootstrap-estimated standard errors (bars) are calculated from 10,000 bootstrap replications.

DISCUSSION

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This study utilised a 17-year dataset to provide concurrent empirical evidence of how social networks and association patterns of bottlenose dolphins in Cardigan Bay have changed over time (2001-2017) due to changes in population status as well as movements between Cardigan Bay and other parts of the Irish Sea (North Wales and the Isle of Man). The present study examined differences in association strength between individuals as a result of their gender, social group, and geographical location, by applying various network analytical techniques. Whilst the power of this study is limited to resolving the social ecology of this species, partially because of the impracticalities of analysing a mobile pelagic species that moves in and out of the study area, results demonstrate that the semiresident bottlenose dolphins live in a society governed by fission-fusion dynamics with remarkably differentiated non-random relationships consisting of intermittent short-term and preferential longterm associations. This is similar to social networks observed in several other dolphin species ranging within temperate, sub-tropical, and cold waters including from other genera such as dusky and Commerson's dolphins (Würsig and Pearson 2014; Weir et al., 2018). This may indicate potential universality in the drivers of change in social patterns within networks across latitude, especially in relation to trade-offs in prey availability, group size, and predation risk (Gero et al., 2005; Gowans et al., 2007; Bertulli et al., 2021). The results of this comprehensive research spanning almost two decades indicated that there were numerous social groups of bottlenose dolphins, and that specific regions within the study area encompass part of their home range. In general, individuals spend the majority of their time within a particular geographic range (Table 1), and then leave, to re-enter at a later point. Individuals belonging to different social groups on average associate more with other dolphins within the same group forming long-term preferential associations (HWIG between sampling period SDo = 16.96985, CVo = 14.16834), although, interconnectivity between various groups still exists following fission-fusion dynamics. The cohesion and continuity of social bonds between individuals across the total sampling period (1106 days) is comparable to association patterns in other delphinid studies, such as Atlantic spotted dolphins (Herzing and Elliser 2013), Indo-Pacific bottlenose dolphins (Gero et al., 2005), and, more recently, in white-beaked dolphins (Bertulli et al., 2021), where individuals displayed consistent affiliative association preferences with others belonging to the same cluster than between clusters (Hammerschmidt and Fischer 2019) Identification of central individuals within the social network, as well determining the strength of social associations within and between social groups, varied with group size. This is a particular pattern within bottlenose dolphin populations as average group size can range between 3 to >100

individuals. The calculated mean group size of the Cardigan Bay network recorded in this study was

690 similar to those reported in other coastal populations of *Tursiops truncatus*. However, there is a certain level of ambiguity surrounding group classification which should be considered (Connor et 691 al., 2000). The average group size was comparable with group sizes for this species in the Morray 692 Firth off the east coast of Scotland (mean = 4.50; Wilson 1995; Wilson et al., 1997, 1999), along the 693 694 north-eastern coast of Sardinia, Italy (mean = 4.94, ±SD = 0.30; Díaz López 2006), and in the northern Adriatic Sea (mean = 7.40, \pm SD 0.06; Bearzi *et al.*, 1997). On the other hand, mean group sizes were 695 larger compared to those recorded in Turneffe Atoll, Belize (mean = 3.8, \pm SD = 3.55; Campbell et 696 al., 2002), and near Isla del Coco, Costa Rica (mean = 3.00, ±SD = 2.58; Acevedo-Gutiérrez and 697 Stienessen 2004), but smaller than those estimated in the Shannon Estuary, Ireland (mean = 9.71, 698 $\pm SD = 0.12$; Barker and Berrow 2016). This variation in how a society is demographically structured, 699 as a result of group size, influencing the sex ratio and spatial cohesion of social groups, determines 700 the social organisation within a network and could therefore explain the differences in type and level 701 of social interaction observed between individuals (Whitehead 2008a). 702 Across the literature it is considered that the risk of predation, resource availability, inter- and intra-703 specific competition, and areas of suitable habitat are the major factors determining grouping and 704 705 therefore the type of- and strength of association associations in cetacean fission-fusion societies (Connor et al., 1998; Gowans et al., 2007). It is suggested that in warm waters at least, shark predation 706 707 is the primary factor influencing delphinid group size (Connor et al., 2000). The rate of predation is

reduced by dilution and confusion tactics through synchronised swimming of grouped individuals, as 708 709 well as increased vigilance amongst certain group members (Krause and Godin, 1996; Couzin et al., 2005). Strong associations within relatively large group sizes could therefore reflect a high predation 710 risk, as grouping and strong social bonds can increase survival chances through enhanced predator 711 detection, whilst allowing other individuals to reduce their own vigilance to prioritise other activities 712 such as foraging for their survival (Wilson 2000; Davies et al., 2012). However, since Cardigan Bay 713 has no major resident bottlenose dolphin predators, previous studies have proposed the most likely 714 factor determining group size, and consequently, association patterns and geographic range of coastal 715 bottlenose dolphins is sources of prey, their dispersion and ecology (Pesante et al., 2008a; Feingold 716 and Evans 2014; Lohrengel et al., 2017). 717

Abundance of bottlenose dolphins within Cardigan Bay increases between April and August, correlating with the seasonal appearance of migratory fish such as mackerel (*Scomber scombrus*), which may form a significant part of the population's diet at certain times of the year. In contrast, their distribution disperses over wider geographic ranges towards October as they migrate further north, occurring in significantly larger group sizes and feed on shoals of whiting (*Merlangius merlangius*) and herring (*Clupea harengus*) (Feingold *et al.*, 2010; Feingold and Evans, 2014). Patchy

or altered prey distribution is likely to dictate variations in bottlenose dolphin distribution between 2001 and 2017 as well as changes in social association, which may partly explain the results of the social analysis (as well as being an important factor for their conservation). For instance, fission-fusion societies favour group formation during cooperative feeding when resources are scarce, as information transfer is better facilitated within one large well connected group in areas of patchy prey distribution (Shane *et al.*, 1986; Mann 1999; Mann *et al.*, 2000). Thus, areas of more abundant resources can result in highly clustered social networks which consist of either short-term intra-group associations, long-term preferential associations, or both. (Daura-Jorge *et al.*, 2012). Nevertheless, concluding that prey availability is a direct cause of bottlenose dolphin spatio-temporal distribution, and therefore association strength, is difficult to prove due to the realities faced in prey sampling (Mann 1999; Mann *et al.*, 2000). An alternative strategy is to relate group size and association strength to environmental factors, which in turn may determine prey distributions.

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Recent studies conducted in Cardigan Bay used Generalised Additive Models to demonstrate how abiotic environmental variables such as bathymetry significantly influence the demographic structure of bottlenose dolphin groups over time, which could potentially explain changes in social associations (Feingold et al., 2010; Lopes 2017; Nuuttila et al., 2017). Bathymetry is shown to predict distribution patterns in Cardigan Bay where bottlenose dolphin presence is higher in shallow waters. Group size, however, increases with increasing distance from shore (depth). Distribution and social organisation is heavily dependent on hydrodynamic characteristics (Dinis et al., 2016). Aggregations of bottlenose dolphins in Cardigan Bay are typically recorded around regions of high tidal stream energy (headlands, islands, and channels) defined by shear-lines caused by fast laminar flows and diminished eddies (Pierpoint et al., 2009; Lohrengel et al., 2017). Upwelling-driven nutrients (high productivity) cause dense accumulations of prey items within a concentrated area, generating an obtainable source of food for individuals or groups (Dinis et al., 2016). Studies suggest differences in social organisation and association strength between shallow- and deep-water regions is a foraging strategy developed to adapt to prey distribution (La Manna et al., 2016). Large deep-water groups in Cardigan Bay are observed when there are large patches of prey or during cooperative feeding. Small shallowwater groups occur prey densities are smaller as hunting alone or in limited numbers is more efficient (Cañadas and Vazquez 2017). Therefore, association strength may be influenced by the social organisation of bottlenose dolphin groups in response to prey availability. Bathymetry can be used as a proxy for prey availability and indirectly linked to spatio-temporal bottlenose dolphin distribution, thus, influencing the structure of social networks and association strength within small or large groups by determining foraging behaviour within groups of different size (Dinis et al., 2016; Cañadas and Vazquez 2017).

The probability that two individuals are associated and will remain associated various time lags later, was relatively low for around 10 days. These patterns suggest that groups observed in Cardigan Bay are initially transient structures composed of casual acquaintances which associate for some time. then dissociate, and re-associate some time later as the standardised lagged association rate (SLAR) falls below the null association >1000 days. Subsequently, some individuals form preferred companionships in which they preferentially associate, and these are constant over time. This is best supported by the model of "preferred companions and casual acquaintances", and loosely fits the "two levels of casual acquaintances" model. This decline in SLAR (\$850 days) could potentially be a result of emigration and re-immigration, as some identified individuals occupy certain study areas while others sporadically transition out (Bertulli et al., 2015, 2018). Long-term reassociations across the sampling period may be due to moving into seasons when prey availability is greater causing larger bottlenose dolphin aggregations, thereby reducing intraspecific competition within the large semi-resident social network (Bertulli et al., 2015, 2018), although, the relatively large error bars on the SLAR should be taken into consideration. Results should be interpreted as a general trend and are not able to determine association strength and patterns for all social groups. The seasonality (largely April-October) of the data should also be considered since this likely impacts the extent of the drop between 50-100 days.

Potential biases, limitations, and future research

There is much published literature recording the use of commercial cetacean-watching vessels, recreational watercraft, and other platforms of opportunity to facilitate research analysing cetacean association patterns to reduce expenditure (Dinis *et al.*, 2017; Baker *et al.*, 2018). However, it is acknowledged that such methods introduce their own limitations which could biase the results and interpretations. The total duration of the present study's sampling period, as well as the size and geographic distribution of the population sampled needs to be evaluated. A potential bias was apparent in the social structure analysis by the restricted sampling area of all three regions, particularly prior to 2006 as previous years' survey effort was largely concentrated in the Cardigan Bay SAC, considering the wider geographic distribution of bottlenose dolphins. In relation to this bias, the social network assessed in the present study relates to the photo-identified individuals where survey effort was conducted and does not strictly apply to the entire population of bottlenose dolphins in Welsh waters. The disparate coverage of the survey area could potentially be a reason for the relatively few bottlenose dolphins associating ≥5 times around North Wales and in the northern Irish Sea (>53.0° N) where much less time was spent undertaking surveys.

Regarding the analysis of social structure, other factors such as seasonality, irregular photoidentification of social groups, variable behaviour of identified individuals or response to watercraft, and social geography could also negatively bias results. This study relied on observational effort and sighting data in which collection in Cardigan Bay has been concentrated in the summer months (April-October), due to environmental factors such as sea states higher than Beaufort Scale 3 in winter months resulting in unsuitable survey conditions as well as low availability of survey vessels in Cardigan Bay during winter. Consequently, the ability to interpret complete annual cycles of social dynamics has been limited (Hobson *et al.*, 2013; Davis *et al.*, 2018). Occasionally, some individuals within an encounter were not identified due to a lack of reliable dorsal fin markings, challenges of accurately calculating group size in the field, and avoidance behaviour in the presence of vessels. Group size and association indices of the social network could on occasions be higher than those calculated in this study.

Movement within and between the three study areas indicates how the development of associations and association strength within each region could be influenced by hydrodynamic characteristics and geographical topography of each location, as well as partial spatial segregation. More detailed research comparing the frequency of bottlenose dolphin encounters to surrounding environmental conditions such as bathymetry, productivity, and water temperature could be conducted to investigate bottlenose dolphin habitat use, movement, and ultimately social patterns. Additionally, identification of prey species and their movements could be key to correlating dolphin spatio-temporal distribution and centres of activity, both of which have been discussed previously. An examination of mother-calf sighting data could also reveal different patterns in social network dynamics.

CONCLUSIONS

In this first study to analyse one of the largest UK bottlenose dolphin social structure dataset collected over almost two decades, the data collected in Cardigan Bay forms a good archetype analysing how association strength and patterns within a social network have changed over time due to sex, social group, and movement of individuals between Cardigan Bay and other parts of the Irish Sea (North Wales and the Isle of Man). The results have shown that the Cardigan Bay dolphin population lives in a society governed by fission-fusion dynamics with separated social groups in which association is non-random, as individuals express preferential association. Initially, short-term intra-group associations were generally random before developing preferential long-term social bonds which are constant over time. Most bottlenose dolphin associations were between pairs of individuals which preferentially associate long-term, and between pairs of individuals who associate for some time, then dissociate, but may re-associate some time later. The present study demonstrates that long-term associations are more favored over non-permanent companionships. These social patterns are similar

to that of many pelagic delphinids from temperate to tropical waters. This represents a good start in understanding population structure and identifying drivers of change in social networks of bottlenose dolphins in the region. To allow a more comprehensive view of differences in association patterns and how those patterns have changed over time within social networks, incorporation of techniques that evaluate several parameters (such as environmental and physical factors) may advance our knowledge towards a more complete picture of bottlenose dolphin social interactions and variable environment. Establishing kinship, sex ratio, and diet could also progress our understanding of the parameters determining bottlenose dolphin social structure. Such an approach may also be beneficial in devising management strategies contributing towards the conservation of this species and other small cetaceans.

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