

Supplementary Material:

Social and genetic connectivity despite ecological variation in a killer whale social network

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Journal: Proceedings B

Article DOI: 10.1098/rspb

Paper ID: 10.1098/rspb.2016.0049

Supplementary Methods

○ Field methods

Killer whale photographs were collected onboard boat-based research surveys conducted in northern Norway: in all seasons off Andøya, in Nordland (69°16'29.47"N, 16°25'2.29"E) from 2014 to 2021; in November at herring wintering grounds off Vengsøya-Kvaløya (69°48'52.06"N, 18°38'54.31"E) in 2015-2016 and in Kvænangen (70°4'36.22"N, 21°11'29.13"E) in Troms from 2017 to 2020. Surveys were carried out daily when killer whale presence peaked in relation with seasonally abundant prey resources (Jourdain et al., 2020a; Jourdain et al., 2021) or in response to sighting reports obtained from other vessels in the area. When killer whales were found, the GPS position was noted and individuals were photographed, regardless of individuals' size, behavior or distinctiveness. In addition, killer whale photographs collected by members of the public between 2008 and 2021 along the Norwegian coast were available. Photographs, regardless of their origins, were collected using digital reflex cameras with mounted tele lenses of various focal lengths.

○ Attributes on individuals' diet

Photo-identified killer whales were assigned a dietary group based on a decade of individuals' predation records, seasonal occurrence patterns and skin stable isotopic values. Specifically, individuals that had been observed killing and consuming mammalian prey in addition to feeding on fish (Jourdain et al. 2017), were assigned the group *mixed diet*. For some of these whales that could be biopsy sampled in 2017-2020, distinctively higher isotopic nitrogen ($^{15}\text{N}/^{14}\text{N}$) ratios compared to (putative) exclusive fish-eating individuals from the same region supported persistent feeding at higher trophic level for these whales (Jourdain et al., 2020b). Individuals with no such evidence of predation on marine mammals and photo-identified at seasonal grounds of herring and/or lumpfish prey were assigned the group (exclusive) *fish diet* (Jourdain et al., 2020a, 2021).

○ Data selection criteria for network analysis

Encounters that involved large killer whale aggregations likely promoted by temporary food enhancement (e.g., around herring fisheries) rather than true associations were not included in the analysis. Encounters for which it was uncertain whether all individuals had been photographed (i.e., more individuals may have been present but missed) were also discarded. To reduce potential demographic effects related to high calf mortality in killer whales, only juveniles thought to be ~5 years or older at first sighting and bearing permanent markings that led to multiple re-identifications in at least four later years were included in the analysis. Only fair-to-excellent quality photo-identifications were retained for analysis (see Jourdain et al. 2021 for scoring details).

○ Measuring associations

A group-by-individual matrix was the initial data format, in which columns were individuals and rows were unique encounters. Individuals were assigned 1 or 0 depending on whether

they were seen or not, respectively, in each encounter. We used this matrix of who co-occurred with whom to calculate the simple ratio index (SRI) as a measure of association for each pair of whales (dyad) with: $SRI = x / (y_a + y_b + y_{ab} + x)$ - where y_a and y_b are the number of encounters in which only a or b , respectively, were photographed; y_{ab} is the number of encounters in which a and b were photographed but not associated; and x is the number of occasions in which a and b were photographed in the same encounter (Cairns & Schwager, 1987). SRI values varied between 0 (two individuals never seen together) and 1 (individuals always seen together).

- Community detection

To identify significant social units nested within the network, we applied Louvain's community detection algorithm (Blondel et al., 2008) to the modularity matrix of the association indices in the R package igraph (Csardi & Nepusz, 2006). The algorithm divides the network into communities of densely associated dyads, whilst assigning individuals that are only loosely associated to different clusters. Maximum modularity coefficient Q indicated the most parsimonious split of the network into an optimal number of communities i.e., highest average association index within clusters while maintaining lower association values between them (Newman, 2004). $Q=0$ indicated randomly assigned communities and $Q=1$ indicated a perfect split into communities with no associations between members of different clusters. Initially, each individual was assigned a community. Then, for each pair of individuals, potential gain in modularity by placing them both in the same community, as opposed to leaving them on their own, was assessed. The algorithm proceeded with individuals' relocation as long as it increased Q and until modularity could not be improved any further.

Supplementary Tables

Table S1. Summary of the sampling effort between 2008 and 2021, from which the photo-identification and genetic data were generated. Specifically, total number of identifications (including re-sightings) and of unique individuals identified in each year are given, in addition to total number of good quality photographs, number of observation days and killer whale encounters they were collected from. Total number of biopsies sampled from unique individuals in each year is also given. Due to low annual number of identifications for the period 2008-2013, these years were pooled together.

Year	Days	Encounters	Identifications	Individuals	Biopsies
2008-2013	28	26	123	70	0
2014	7	7	20	17	0
2015	28	46	222	129	0
2016	78	131	862	312	0
2017	53	68	451	253	27
2018	52	75	411	201	11
2019	36	81	539	248	9
2020	35	61	389	212	22
2021	40	53	295	159	37*
Total	357	548	3,312	-	106

*This number includes 36 biopsy sampled live individuals and an additional skin sample collected from one photo-identified dead stranded specimen

Table S2. Monthly distribution of the encounters with the 46 killer whales known to adopt a mixed diet, showcasing that individuals were repeatedly seen in various ecological contexts (i.e., characterized by variable seasonally available food sources) between 2011 and 2021.

	2011	2012	2013	2014	2015	2016	2017	2018	2019	2020	2021	Total
Jan						1						1
Feb						1						1
Mar										1	2	3
Apr									1	3	5	9
May			2	2			1		1		1	7
Jun			2	1	1	1			1	1	1	8
Jul			3		1		6		3	3	1	17
Aug		1		1	3	3	5		2	2	1	18
Sep	1					2	1					4
Oct						1					2	3
Nov							3		1	5		9
Dec							1					1
Total	1	1	7	4	5	9	17	0	9	15	13	81

Table S3. Mean (pairwise) biparental genetic relatedness measured for the population (all), and for mixed diet, fish diet, male and female individuals separately. For each estimate, sample size is given as number of whales (w) and number of whale pairs/dyads (d).

	All	Males	Females
All	0.030 ± 0.050 (n=106 w, 5565 d)	0.029 ± 0.044 (n=69 w, 2346 d)	0.030 ± 0.052 (n=21 w, 210 d)
Mixed diet	0.067 ± 0.117 (n= 17 w, 136 d)	0.049 ± 0.073 (n=8 w, 28 d)	0.051 ± 0.114 (n=7 w, 21 d)
Fish diet	0.030 ± 0.048 (n=89 w, 3916 d)	0.029 ± 0.045 (n= 61 w, 1830 d)	0.032 ± 0.046 (n=14 w, 91 d)

Table S4. Summary of pairwise association indices (nonzero simple ratio index SRI) measured over the entire network, by diet group, by sex, and within and between diet/sex groups. Sample size is given as number of whales (w) and number of whale pairs/dyads (d).

	Mean ± SD	Range
Network (n=457 w, 4768 d)	0.19 ± 0.19	0.03 - 1.00
Mammal-eaters (n=46 w, 133 d)	0.38 ± 0.25	0.05 - 1.00
Fish-eaters (n=411 w, 4330 d)	0.19 ± 0.19	0.03 - 1.00
Within dietary groups (n= 457 w, 4463 d)	0.19 ± 0.20	0.03 - 1.00
Between dietary groups (n= 457 w, 305 d)	0.09 ± 0.03	0.03 - 0.2
Females (n=186 w, 721 d)	0.20 ± 0.20	0.04 - 1.00
Males (n=215 w, 1170 d)	0.17 ± 0.19	0.03 - 1.00
Within sexes (n= 401 w, 1891 d)	0.18 ± 0.19	0.03 - 1.00
Between sexes (n= 401 w, 1878 d)	0.18 ± 0.19	0.03 - 1.00

Table S5. Summary of the 27 communities identified using Louvain’s community detection algorithm (for overall modularity $Q = 0.68$): community ID (Community), total number of whales assigned to each (Whales), whether it includes mixed-diet individuals or not (Diet), modularity coefficient Q and number of subclusters (subcl), mean nonzero association values (simple ratio index SRI), percentage of null SRIs and number of individuals biopsy sampled i.e., with genetic data available (Biopsies).

Community	Whales	Diet	Q (subcl)	SRI (mean \pm SD)	% Null SRIs	Biopsies
1	14	Mixed	0.4 (3)	0.25 \pm 0.19	42	3
2	9	Mixed	0.22 (2)	0.28 \pm 0.24	3	5
3	16	Fish only	0.22 (2)	0.37 \pm 0.18	42	0
4	34	Fish only	0.34 (4)	0.18 \pm 0.19	20	8
5	22	Mixed	0.54 (4)	0.30 \pm 0.24	71	8
6	11	Fish only	0.21 (2)	0.26 \pm 0.15	22	0
7	23	Fish only	0.3 (5)	0.22 \pm 0.19	45	2
8	26	Mixed	0.3 (4)	0.24 \pm 0.20	41	9
9	30	Fish only	0.43 (3)	0.27 \pm 0.23	48	6
10	20	Fish only	0.48 (3)	0.35 \pm 0.28	63	3
11	37	Mixed	0.48 (5)	0.19 \pm 0.20	60	2
12	21	Fish only	0.36 (2)	0.30 \pm 0.18	52	3
13	10	Fish only	0.26 (3)	0.30 \pm 0.21	31	0
14	20	Fish only	0.46 (4)	0.25 \pm 0.22	49	1
15	11	Fish only	0.085 (2)	0.40 \pm 0.30	5	0
16	14	Fish only	0.41 (3)	0.32 \pm 0.28	29	2
17	7	Fish only	1 (0)	0.47 \pm 0.33	5	0
18	25	Fish only	0.34 (3)	0.26 \pm 0.21	48	1
19	25	Fish only	0.24 (3)	0.27 \pm 0.18	27	10
20	10	Fish only	0.2 (2)	0.34 \pm 0.24	0	1
21	4	Fish only	1 (0)	0.71 \pm 0.18	0	2
22	15	Mixed	0.52 (3)	0.32 \pm 0.28	67	1
23	19	Mixed	0.51 (3)	0.29 \pm 0.22	55	1
24	10	Fish only	0.33 (2)	0.43 \pm 0.32	13	1
25	10	Fish only	0.09 (2)	0.41 \pm 0.30	9	2
26	7	Fish only	1 (0)	0.60 \pm 0.30	5	0
27	7	Mixed	1 (0)	0.51 \pm 0.19	0	2
Total	457	-	0.68 (27)	0.19 \pm 0.19	95	73

Table S6. Relatedness calculated for clusters/subclusters for which there were at least three individuals with genetic data available.

	Mean	SD	N whales	N dyads
Population	0.030	0.050	106	5,565
Network	0.030	0.051	73	2,628
Cluster				
1	0.114	0.225	3	3
2	0.242	0.193	5	10
4	0.047	0.078	8	28
5	0.045	0.061	8	28
8	0.064	0.118	9	36
9	0.050	0.063	6	15
10	0.020	0.032	3	3
12	0.020	0.025	3	3
19	0.075	0.120	10	45
Average Cluster	0.075	0.069	55	171
Subcluster				
2.1	0.306	0.246	3	3
4.1	0.132	0.123	3	3
4.1	0.105	0.111	3	3
5.3	0.071	0.077	3	3
8.4	0.128	0.154	6	15
9.1	0.070	0.073	3	3
19.1	0.061	0.067	4	6
19.3	0.208	0.217	4	6
Average Subcluster	0.135	0.084	29	42

Supplementary Figures

Figure S1. Overview of the key steps in the data collection, compiled datasets and completed analyses that made up our investigation of social/population structure of killer whales in Norway (2008-2021): a) Killer whales were photo-identified between 2008 and 2021. Considering that individuals recorded in the same photographic encounter were 'in association', we used the resulting mark-recapture data to calculate association indices (Simple Ratio Index SRI) between pairs of whales to generate the social network; b) biopsy sampling allowed building a genetic dataset for a subset of photo-identified individuals; c) predation history was used to assign photo-identified individuals a diet group (exclusive *fish diet* or *mixed diet* when known to feed on both fish and mammalian prey). The network analysis aimed at quantifying patterns of associations between pairs of whales and at the network level, taking photographic identifications (associations) as main data, and testing sex and diet group as potential correlates. Based on a minimum of three photographic encounters, 457 whales were included in the Bayesian analysis (Dataset 1). Genetic data were available for 73 of these, which allowed for including kinship as another potential correlate of association (Dataset 2). All uniquely sampled killer whales (n=106), regardless of times seen, were included in the admixture analysis to identify the number of populations in our dataset (Dataset 3).

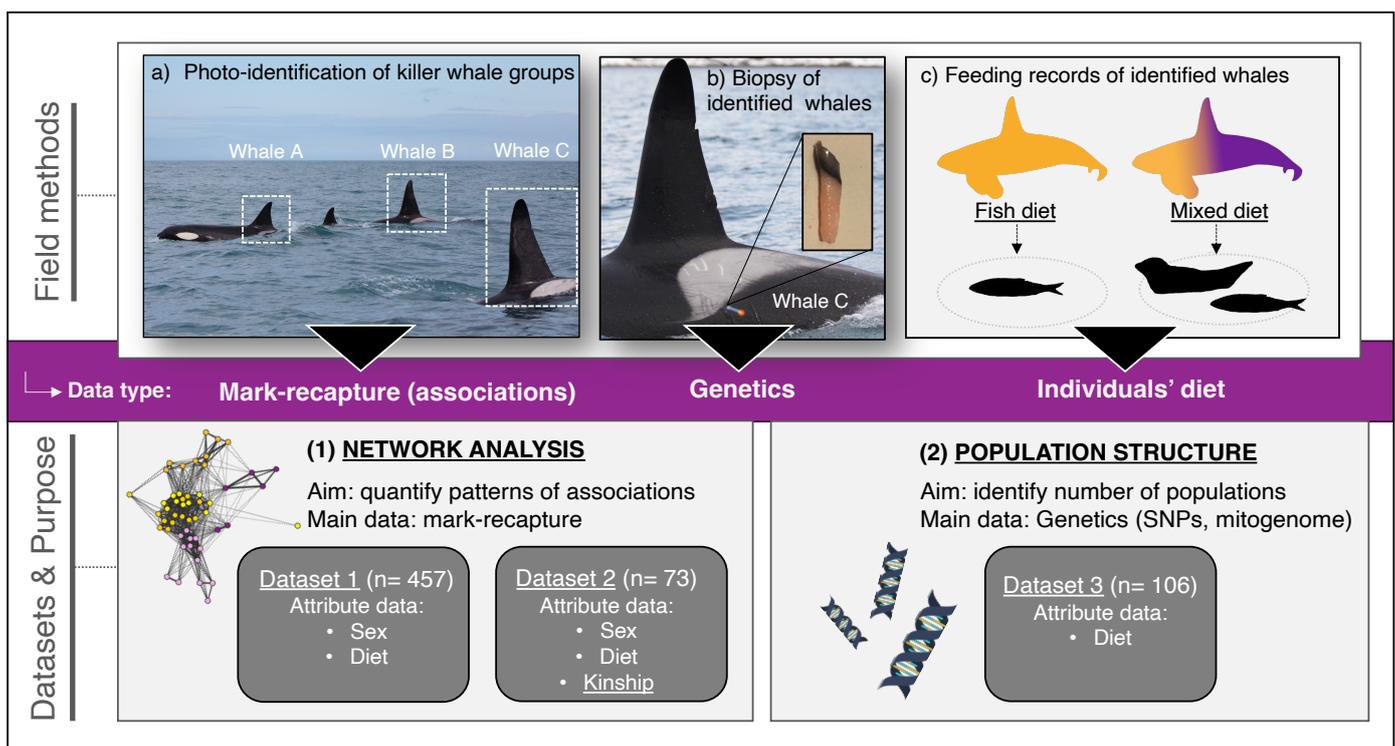


Figure S2. Pedigree chart of the killer whales from managed-care for which DNA was extracted from blood samples (bright colored whales i.e., *Katina*, *Makaio* and *Trua*) and for further validation of downstream relatedness estimates of Norwegian killer whales. The matrix in the bottom left corner indicates resulting pairwise relatedness values for all three sequenced individuals (measured as r_{xy} , as per (Hedrick & Lacy, 2015)). For completeness, individuals relevant to the pedigree but not sampled for this study are also shown (faded whales i.e., *Tilikum*, *Taku* and *Takara*).

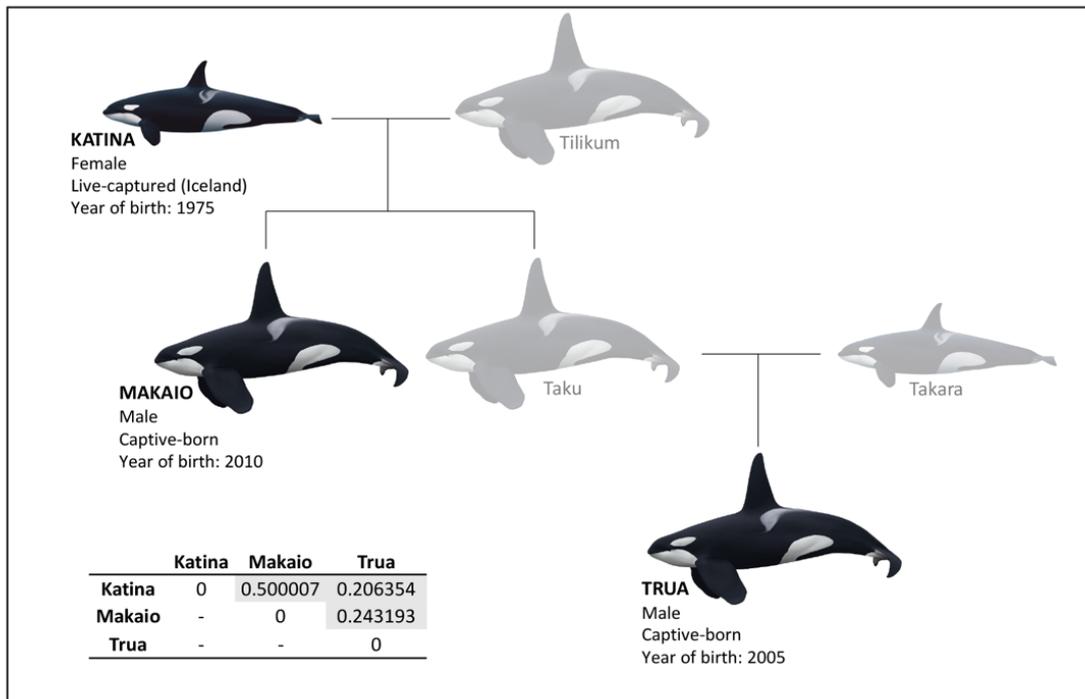


Figure S3. Mean depth of coverage and standard deviation on the logarithmic scale for each of the sequenced killer whales for this study. These include the 106 uniquely sampled individuals from Norway and the three individuals from managed care.

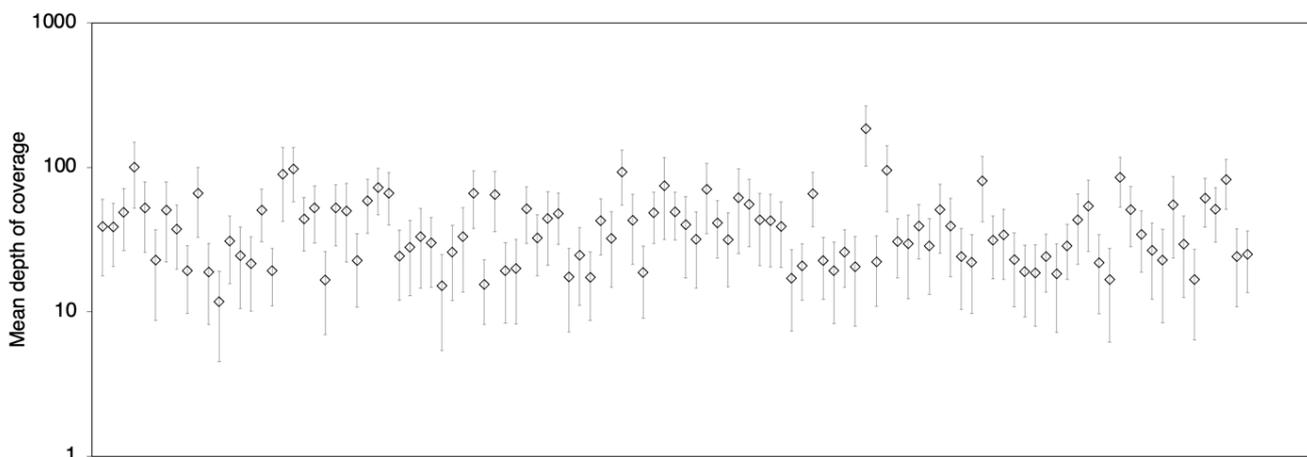


Figure S4. Distribution of a) biparental genetic relatedness values (Dataset 3, n= 106 individuals) and of b) nonzero association indices (simple ratio index SRI, Dataset 1, n= 457 individuals) for pairs of whales. Violins indicate densities, dots indicate individual data points and purple squares represent means. Sample size (n) is given in number of whale pairs (dyads).

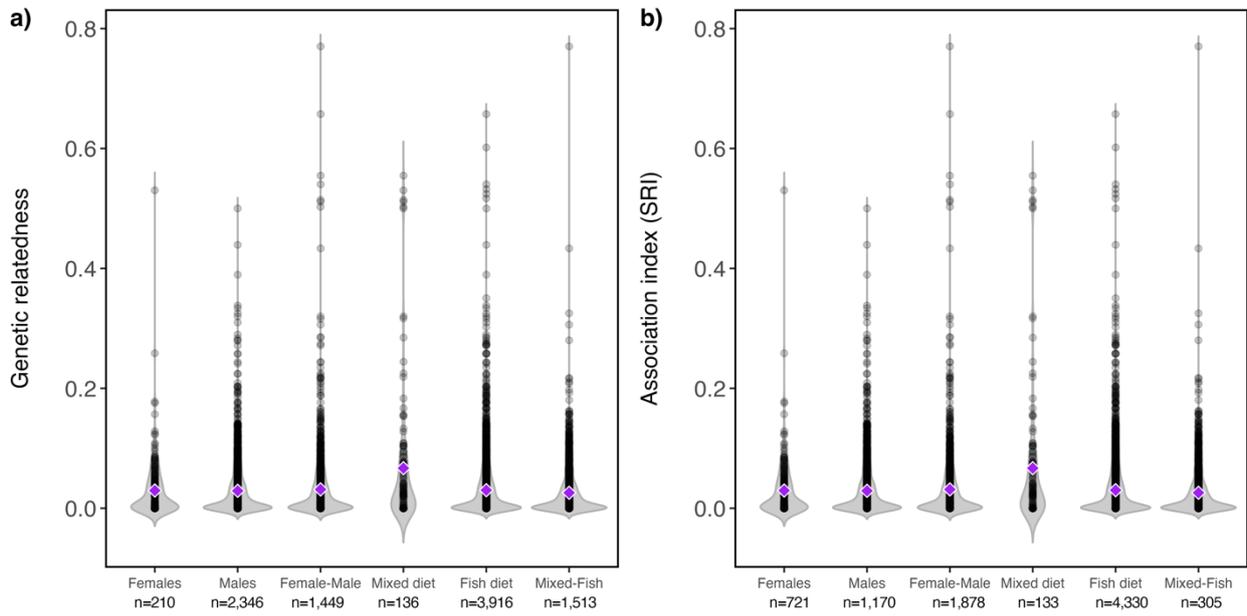


Figure S5. a) Density plots, b) trace plots and c) posterior predictive check plots used to assess convergence and fit of the Bayesian model fitted to Dataset 1 (n= 457 killer whales) on the logit scale. Trace plots (a) show number of iterations post-warmup on the x-axis and all values of the mean of the posterior distribution explored by the model on the y-axis. The latter can also be visualized on the density plots (b) on the x-axis against the number of times the model identified each value - i.e., plots a) show the probability distributions of the most likely correct mean values. Plot c) assesses whether the model predicts the data accurately. Light blue lines represent 10 random draws i.e., data distributions created by the model using the estimates. Because the distribution of these look similar to that of the posterior distribution (dark blue line), we can use the model to confidently generate new data and make realistic predictions.

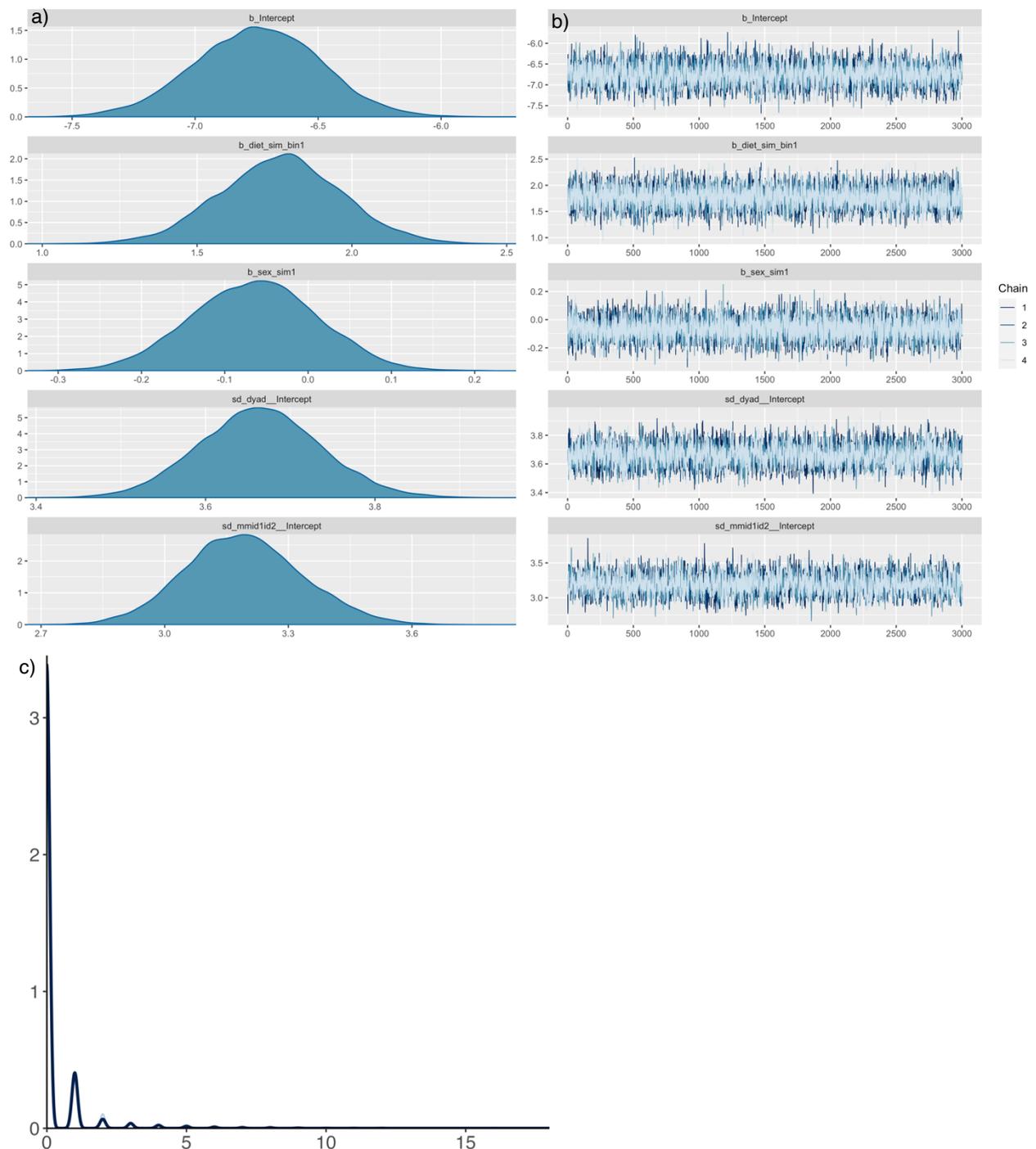


Figure S6. a) Density plots, b) trace plots and c) posterior predictive check plots used to assess convergence and fit of the Bayesian model fitted to Dataset 2 (n= 73 killer whales with genetic data). Trace plots (a) show number of iterations post-warmup on the x-axis and all values of the mean of the posterior distribution explored by the model. The latter can also be visualized on the density plots (b) on the x-axis against the number of times the model identified each value. On c), the light blue lines represent 10 random draws i.e., distributions created by the model, whilst dark blue lines depict the posterior distribution.

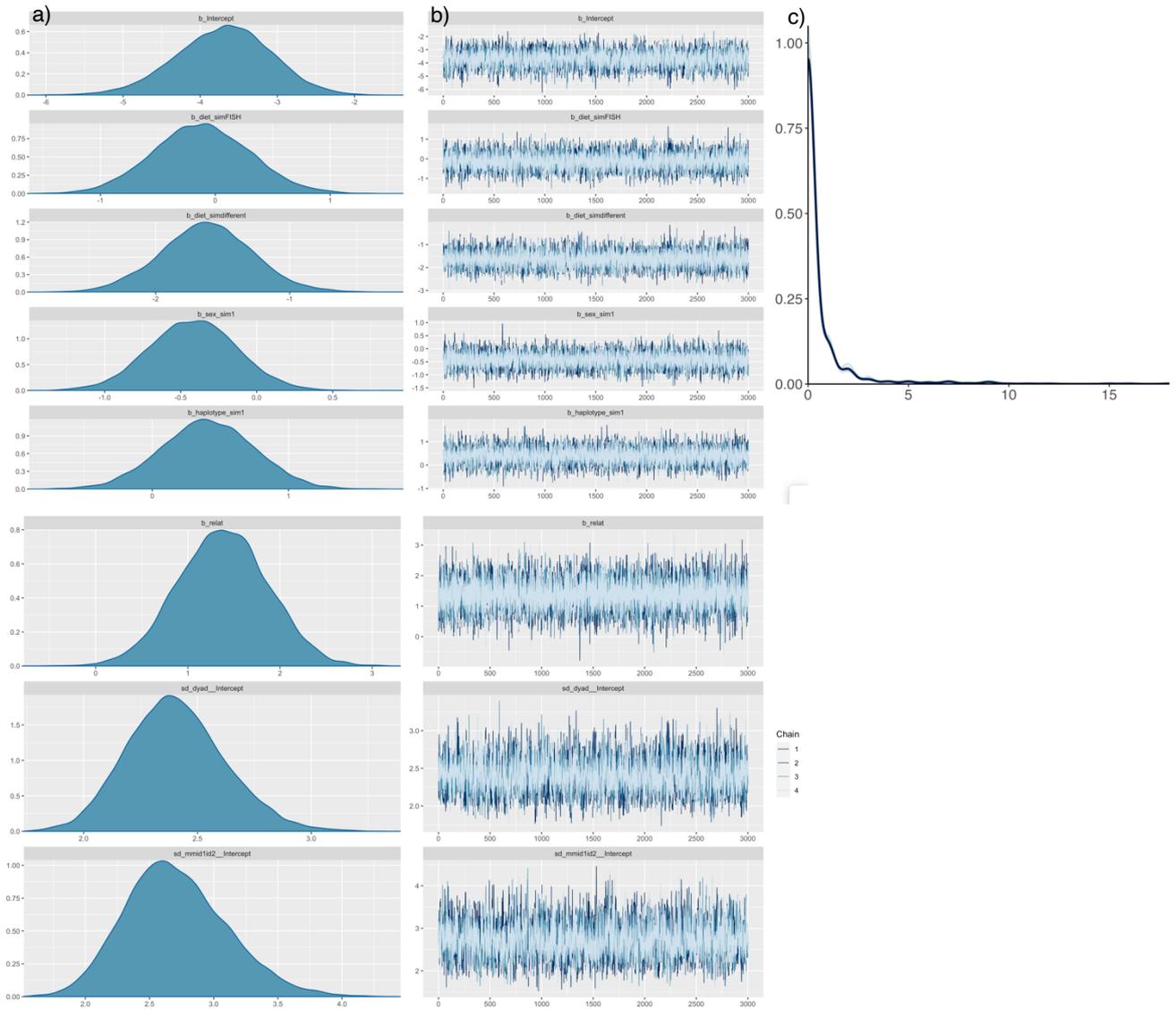


Figure S7. Estimated effect size for diet and sex, as evaluated from the posterior distributions of parameter estimates, when applying a more restrictive data selection criteria of five minimum sightings for inclusion of individuals (without genetics) in the Bayesian analysis (n= 263 individuals). The model (R^2_{Bayesian} : mean= 0.897, 95% CI= 0.889 – 0.905) identified diet similarity as correlate of association at the dyadic level (odds ratio= 3.710, 95% CI = 2.384 – 5.801), but not sex (odds ratio= 0.922, 95% CI = 0.759 – 1.123). Error bars indicate 95% credible intervals.

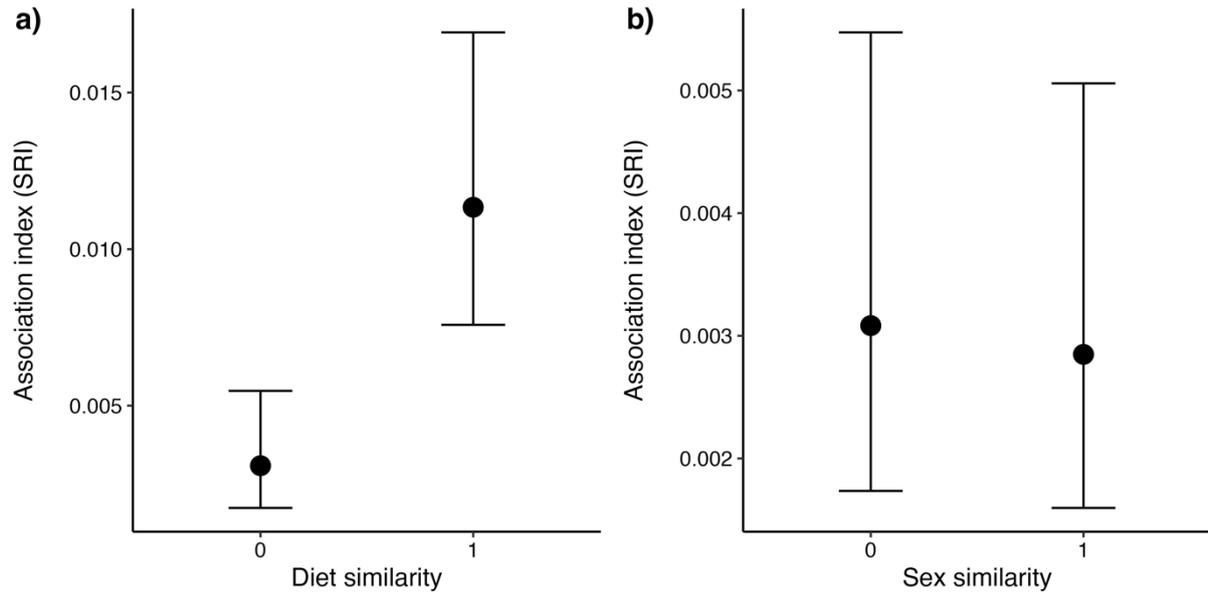
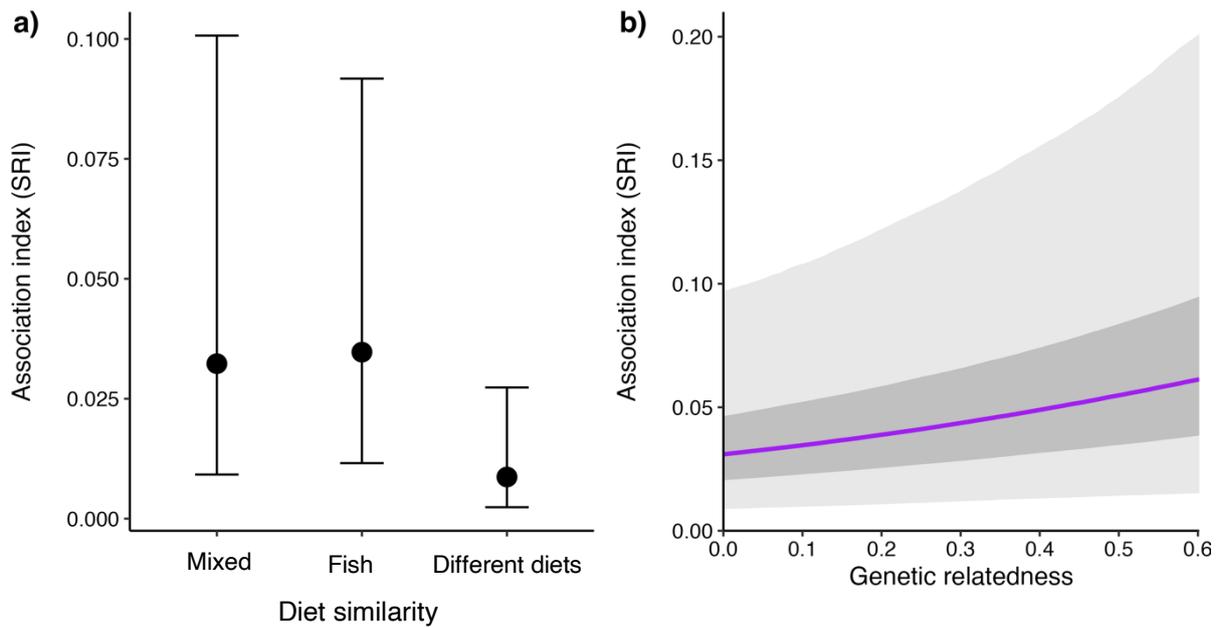


Figure S8. Estimated effect size of a) diet similarity and b) biparental genetic relatedness, as evaluated from the posterior distributions of parameter estimates, when including individuals (n= 55) with genetic data that were photo-identified in at least five (instead of three) encounters as selection criteria. The model (R^2_{Bayesian} : mean= 0.927, 95% CI= 0.904 – 0.945) revealed that pairs of whales with similar diets i.e., pairs fish diet / fish diet (odds ratio = 4.12, 95% CI= 1.37 - 8.62) and pairs mixed diet / mixed diet (odds ratio = 3.84, 95% CI = 1.60 - 7.07) were more likely than fish diet / mixed diet pairs. The odds of finding pairs fish diet / fish diet or pairs mixed diet / mixed diet did not differ (odds ratio= 0.93, 95% CI = 0.31 - 1.90). Social bond also increased with increasing biparental genetic relatedness (odds ratio= 3.24, 95% CI= 1.26 – 8.42). Error bars indicate 95% credible intervals (plot a) and dark and grey shaded areas depict 50% and 95% credible intervals, respectively.



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