Supplemental materials for:

Age and sex influence social interactions, but not associations, within a killer whale pod

# Supplementary methods

## Estimating maximum distance captured

We use camera lens the field of view of the camera lens and the flight records stored by the UAS to estimate the maximum distance between any two points in the video. Given the drone’s vertical field of view *θ* and horizontal field of view *ϕ* (in degrees), the drone’s altitude *w* (in meters), and the camera gimbal’s pitch *p* (in degrees from a straight down view), we estimate the locations of the corners of the frame relative to the drone, which we set as the origin.

We first calculate the distance to the top of the screen *y1* and the bottom of the screen *y2*:

$y\_{1}=\tan(\left(p+ \frac{θ}{2}\right))w$

$y\_{2}=\tan(\left(p- \frac{θ}{2}\right))w$

The widths of the top of the frame (*a*) and the bottom of the frame (*b*) can then be calculated as:

$a=2∙\tan(\left(\frac{ϕ}{2}\right))\sqrt{y\_{1}^{2}+w^{2}}$

$b=2∙\tan(\left(\frac{ϕ}{2}\right))\sqrt{y\_{2}^{2}+w^{2}}$

The *x* coordinates for the top two corners of the frame are then {-*a*/2, *a*/2}, while the *x* coordinates of the bottom two corners are {*-b*/2, *b*/2}. We then have our four points *x* = {-*a*/2, *a*/2, *-b*/2, *b*/2}, *y* = {*y1*, *y1*, *y2,* *y2*}. We measure the distances between all four points, recording the maximum distance. We record this for all flight records during the study period during which the video was active, and report the median along with the 25% and 75% quantiles.

## Bout analysis

In order to test whether interactions could be broken into bouts, we measured the waiting times between observed interactions between dyads in each video clip. If interactions between dyads occurred in bouts, we would expect these waiting times to arise from a mixture of two exponential distributions, one representing the waiting time within bouts, and the other representing waiting times between bouts. In contrast, if interactions did not occur in bouts, we expect these waiting times to fit a single exponential distribution (Langton et al. 1995). We fit these two models in the flexmix package in R (Gruen & Leisch 2008). For both interaction types, we then compare these models using the Bayesian information criteria (BIC). Lower values of BIC indicate that the model is a better fit to the data, penalized for model complexity.

In both interaction types, model comparisons suggested that the mixture of two exponential distributions fit the data less well than the single exponential distribution, with differences in BIC > 10 (Table S2). We therefore analysed each interaction as an independent event, rather than measuring bouts of interaction.

**Table S2.** Model selection for exponential mixtures

|  |  |  |
| --- | --- | --- |
| Interaction type | Model | BIC |
| Synchronous surfacing | Single exponential | 6679.487 |
| Two exponentials | 6692.541 |
| Physical contact | Single exponential | 3806.613 |
| Two exponentials | 3818.561 |

## Estimating reliability of interaction networks

We assume that our observed interaction counts *x* are drawn from a Poisson distribution where the rates themselves are drawn from a gamma distribution with shape parameter *k* and scale parameter *θ*. The expected number of observed interactions is then the true rate multiplied by the sampling time (*tij*­).

$x\_{ij} \~ Poisson\left(λ\_{ij}t\_{ij}\right)$

$λ\_{ij} \~ Gamma(k,θ)$

We are interested in estimating the correlation between the true rates *λij* and the estimated interaction rates $\frac{x\_{ij}}{t\_{ij}}$*.*

We estimate the parameters of the underlying Gamma distribution by fitting a negative-binomial distribution with mean *μ* and dispersion *ф* to the observed interaction counts:

$x\_{ij} \~ NB(μt\_{ij},ϕ)$

We use our negative binomial fit to extract the estimated shape and scale parameters of the underlying Gamma distribution:

$p= \frac{ϕ}{ϕ+ μ}$

$θ= \frac{1-p}{p}$

$k= ϕ$

The mean and variance of the underlying Gamma distribution are then

$Mean(λ)=kθ$

$Var\left(λ\right)=kθ^{2}$

Therefore, the coefficient of variation of the true interaction rates (social differentiation, *S*) is:

$S= \frac{\sqrt{kθ^{2}}}{kθ}= \frac{1}{\sqrt{k}}$

Following equation 4 in Whitehead (2008), we then estimate the correlation between the observed and estimated interaction rates (*rest*) as

$r\_{est}= \sqrt{\frac{1}{1+ \frac{1}{S^{2}×G}}}$

where

$G= \frac{\sum\_{i}^{}\sum\_{j}^{}x\_{ij}}{N\left(N-1\right)}$

In order to assess whether this a reasonable estimate, we plot the empirical distribution of interaction rates against the estimated gamma distributions. For both interaction rates, the fitted Gamma distributions appear to be reasonable approximations of the empirical interaction rates, allowing for sampling noise (Figure S1).



**Figure S1.** Empirical distributions of interaction rates compared to fitted gamma distributions. Grey histograms indicate the observed distribution of estimated interaction rates, and the red lines are the estimated density of the Gamma distribution fit using maximum likelihood.

## Permutation analysis for centrality in mixed effect models.

We adopt a double-semi-partialling approach for testing the fixed effects in our mixed effect models of social centrality. For each fixed predictor *X*, we partial out the covariance between *X* and all other fixed predictors *Z* by fitting the linear model

$X= βZ+ ε$

and extracting the residuals *ε*. We then replace *X* with *ε* in the original model, and carry out 10000 permutations of these residuals. To account for matriline membership, we permute these residuals within matriline. We repeat this procedure for each predictor, using the *t*-value as the test statistic to derive *p*-values for all fixed predictors.

# Supplementary results

**Table S1** Summary of attributes and observation effort for each individual in J pod in the summer of 2019.

|  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- |
| **Matriline** | **ID** | **Birth Year** | **Sex** | **Observation time (min)** | **Sync. surfacings** | **Contacts** |
| J11 | J27 | 1991 | M | 85 | 63 | 4 |
| J31 | 1995 | F | 206 | 315 | 91 |
| J39 | 2003 | M | 121 | 77 | 45 |
| J56 | 2019 | F | 203 | 302 | 141 |
| J14 | J37 | 2001 | F | 137 | 232 | 119 |
| J40 | 2004 | F | 173 | 218 | 114 |
| J45 | 2009 | M | 134 | 134 | 58 |
| J49 | 2012 | M | 163 | 195 | 95 |
| J16 | J16 | 1972 | F | 28 | 18 | 9 |
| J26 | 1991 | M | 46 | 14 | 17 |
| J36 | 1999 | F | 37 | 29 | 28 |
| J42 | 2007 | F | 34 | 20 | 20 |
| J17 | J35 | 1998 | F | 166 | 227 | 105 |
| J44 | 2009 | M | 159 | 139 | 75 |
| J46 | 2009 | F | 219 | 259 | 190 |
| J47 | 2010 | M | 145 | 163 | 99 |
| J53 | 2015 | F | 181 | 223 | 190 |
| J19 | J19 | 1979 | F | 86 | 50 | 15 |
| J41 | 2005 | F | 131 | 219 | 120 |
| J51 | 2015 | M | 140 | 176 | 78 |
| J22 | J22 | 1985 | F | 77 | 93 | 30 |
| J38 | 2003 | M | 99 | 68 | 32 |

**Table S3.** GLMQAP results for each response network.

|  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- |
| Response | Family | Predictor | Estimate | Std. Error | *Z* | *p\** |
| Association | Beta | Kinship | 3.54 | 0.48 | 7.38 | **<0.001** |
| Age similarity | 0.02 | 0.01 | 4.00 | 0.071 |
| Sex similarity | 0.14 | 0.11 | 1.33 | 0.188 |
| Synchronous surfacing | Negative binomial | Kinship | 6.40 | 0.46 | 13.91 | **<0.001** |
| Age similarity | 0.06 | 0.01 | 5.32 | **0.005** |
| Sex similarity | 0.60 | 0.20 | 2.98 | **0.020** |
| Physical contact | Negative binomial | Kinship | 8.91 | 1.12 | 7.97 | **<0.001** |
| Age similarity | 0.12 | 0.02 | 6.82 | **<0.001** |
| Sex similarity | 1.27 | 0.28 | 4.58 | **0.002** |

\**p-*values derived from 10,000 permutations of predictor residuals

**Table S4.** Regression analysis of eigenvector centrality.

|  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- |
| Network | Predictor | Estimate | Std. Error | *t* | *p\** |
| Association | Sampling | 0.44 | 0.14 | 3.15 | **0.038** |
| Age | 0.00 | 0.003 | 0.09 | 0.965 |
| Sex | -0.01 | 0.06 | -0.11 | 0.808 |
| Synchronous surfacing | Sampling | 1.68 | 0.21 | 7.89 | **0.011** |
| Age | -0.01 | 0.01 | -0.94 | 0.300 |
| Sex | -0.34 | 0.17 | -2.01 | 0.066 |
| Physical contact | Sampling | 1.88 | 0.35 | 5.40 | **< 0.001** |
| Age | -0.03 | 0.01 | -3.30 | **0.006** |
| Sex | -0.58 | 0.16 | -3.59 | **0.004** |

\**p-*values derived from 10,000 permutations of predictor residuals within matrilines

# References

Bettina Gruen and Friedrich Leisch. FlexMix Version 2: Finite mixtures with concomitant variables and varying and constant parameters*. Journal of Statistical Software, 28*(4), pp. 1-35. <https://doi:10.18637/jss.v028.i04>

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