nature portfolio

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Last updated by author(s): Oct 3, 2022

Reporting Summary

Nature Portfolio wishes to improve the reproducibility of the work that we publish. This form provides structure for consistency and transparency in reporting. For further information on Nature Portfolio policies, see our Editorial Policies and the Editorial Policy Checklist.

Statistics

For all statistical analyses, confirm that the following items are present in the figure legend, table legend, main text, or Methods section.

n/a	Confirmed
☐	☒ The exact sample size (*n*) for each experimental group/condition, given as a discrete number and unit of measurement
☐	☒ A statement on whether measurements were taken from distinct samples or whether the same sample was measured repeatedly
☐	☒ The statistical test(s) used AND whether they are one- or two-sided *Only common tests should be described solely by name; describe more complex techniques in the Methods section.*
☐	☒ A description of all covariates tested
☐	☒ A description of any assumptions or corrections, such as tests of normality and adjustment for multiple comparisons
☐	☒ A full description of the statistical parameters including central tendency (e.g. means) or other basic estimates (e.g. regression coefficient) AND variation (e.g. standard deviation) or associated estimates of uncertainty (e.g. confidence intervals)
☐	☒ For null hypothesis testing, the test statistic (e.g. *F*, *t*, *r*) with confidence intervals, effect sizes, degrees of freedom and *P* value noted *Give P values as exact values whenever suitable.*
☒	☐ For Bayesian analysis, information on the choice of priors and Markov chain Monte Carlo settings
☐	☒ For hierarchical and complex designs, identification of the appropriate level for tests and full reporting of outcomes
☒	☐ Estimates of effect sizes (e.g. Cohen's *d*, Pearson's *r*), indicating how they were calculated

Our web collection on statistics for biologists contains articles on many of the points above.

Software and code

Policy information about availability of computer code

Data collection	C code for 'Darwin Board' and R code used for treatment class assignment. Available from Github (see https://github.com/mkings-220920/Cornish-Jackdaws).
Data analysis	Eventnet 0.5.2 available from Github (https://github.com/juergenlerner/eventnet). R scripts used for data processing and analysis available from Github (https://github.com/mkings-220920/Cornish-Jackdaws)

For manuscripts utilizing custom algorithms or software that are central to the research but not yet described in published literature, software must be made available to editors and reviewers. We strongly encourage code deposition in a community repository (e.g. GitHub). See the Nature Portfolio guidelines for submitting code & software for further information.

Data

Policy information about availability of data

All manuscripts must include a data availability statement. This statement should provide the following information, where applicable:

- Accession codes, unique identifiers, or web links for publicly available datasets
- A description of any restrictions on data availability
- For clinical datasets or third party data, please ensure that the statement adheres to our policy

We provide the raw .csv files downloaded from the task apparatus after each session, the .csv files edited for use with the data processing script, the processed data

combined into a single .csv file, the permuted REM datasets for use in Eventnet 0.5.2. (see Supplementary Methods: REM dataset structure for details of dataset structure) and the versions of these data files output by Eventnet. Data available from GitHub (https://github.com/mkings-220920/Cornish-Jackdaws)

Human research participants

Policy information about studies involving human research participants and Sex and Gender in Research.

Reporting on sex and gender	*Use the terms sex (biological attribute) and gender (shaped by social and cultural circumstances) carefully in order to avoid confusing both terms. Indicate if findings apply to only one sex or gender; describe whether sex and gender were considered in study design whether sex and/or gender was determined based on self-reporting or assigned and methods used. Provide in the source data disaggregated sex and gender data where this information has been collected, and consent has been obtained for sharing of individual-level data; provide overall numbers in this Reporting Summary. Please state if this information has not been collected. Report sex- and gender-based analyses where performed, justify reasons for lack of sex- and gender-based analysis.*
Population characteristics	*Describe the covariate-relevant population characteristics of the human research participants (e.g. age, genotypic information, past and current diagnosis and treatment categories). If you filled out the behavioural & social sciences study design questions and have nothing to add here, write "See above."*
Recruitment	*Describe how participants were recruited. Outline any potential self-selection bias or other biases that may be present and how these are likely to impact results.*
Ethics oversight	*Identify the organization(s) that approved the study protocol.*

Note that full information on the approval of the study protocol must also be provided in the manuscript.

Field-specific reporting

Please select the one below that is the best fit for your research. If you are not sure, read the appropriate sections before making your selection.

☐ Life sciences ☐ Behavioural & social sciences ☒ Ecological, evolutionary & environmental sciences

For a reference copy of the document with all sections, see nature.com/documents/nr-reporting-summary-flat.pdf

Life sciences study design

All studies must disclose on these points even when the disclosure is negative.

Sample size	*Describe how sample size was determined, detailing any statistical methods used to predetermine sample size OR if no sample-size calculation was performed, describe how sample sizes were chosen and provide a rationale for why these sample sizes are sufficient.*
Data exclusions	*Describe any data exclusions. If no data were excluded from the analyses, state so OR if data were excluded, describe the exclusions and the rationale behind them, indicating whether exclusion criteria were pre-established.*
Replication	*Describe the measures taken to verify the reproducibility of the experimental findings. If all attempts at replication were successful, confirm this OR if there are any findings that were not replicated or cannot be reproduced, note this and describe why.*
Randomization	*Describe how samples/organisms/participants were allocated into experimental groups. If allocation was not random, describe how covariates were controlled OR if this is not relevant to your study, explain why.*
Blinding	*Describe whether the investigators were blinded to group allocation during data collection and/or analysis. If blinding was not possible, describe why OR explain why blinding was not relevant to your study.*

Behavioural & social sciences study design

All studies must disclose on these points even when the disclosure is negative.

Study description	*Briefly describe the study type including whether data are quantitative, qualitative, or mixed-methods (e.g. qualitative cross-sectional, quantitative experimental, mixed-methods case study).*
Research sample	*State the research sample (e.g. Harvard university undergraduates, villagers in rural India) and provide relevant demographic information (e.g. age, sex) and indicate whether the sample is representative. Provide a rationale for the study sample chosen. For studies involving existing datasets, please describe the dataset and source.*
Sampling strategy	*Describe the sampling procedure (e.g. random, snowball, stratified, convenience). Describe the statistical methods that were used to predetermine sample size OR if no sample-size calculation was performed, describe how sample sizes were chosen and provide a*

rationale for why these sample sizes are sufficient. For qualitative data, please indicate whether data saturation was considered, and what criteria were used to decide that no further sampling was needed.

Data collection

Provide details about the data collection procedure, including the instruments or devices used to record the data (e.g. pen and paper, computer, eye tracker, video or audio equipment) whether anyone was present besides the participant(s) and the researcher, and whether the researcher was blind to experimental condition and/or the study hypothesis during data collection.

Timing

Indicate the start and stop dates of data collection. If there is a gap between collection periods, state the dates for each sample cohort.

Data exclusions

If no data were excluded from the analyses, state so OR if data were excluded, provide the exact number of exclusions and the rationale behind them, indicating whether exclusion criteria were pre-established.

Non-participation

State how many participants dropped out/declined participation and the reason(s) given OR provide response rate OR state that no participants dropped out/declined participation.

Randomization

If participants were not allocated into experimental groups, state so OR describe how participants were allocated to groups, and if allocation was not random, describe how covariates were controlled.

Ecological, evolutionary & environmental sciences study design

All studies must disclose on these points even when the disclosure is negative.

Study description

The experiment used automated social coordination tasks, constructed using Radio-Frequency Identification (RFID) data-loggers and 'Darwin Board' microcomputers, to examine partner-choice dynamics in a group of wild jackdaws (Corvus monedula). Data-logger data enabled the determination of the identities of task participants and the timing and duration of paired foraging events. To manipulate the value of social foraging associations, participants were assigned at random to one of two experimental treatment classes, and the combination of participants' classes determined the food rewards accessible during paired foraging at the task apparatus. The study used data collected during weekday mornings across a breeding season (April - July 2019), in total comprising 3117 paired foraging events. Relational Event Models (REMs), which are designed for analysis of social network dynamics, were used to analyze how individual, dyad and network characteristics changed over time in response to the experimental treatment. The combination of treatment classes of the participants (same-class, different-class) and a categorization of the nature of a pairing's pre-existing relationship (affiliates, non-affiliates) featured in all models. In each of the models, the response term represented the rate at which an individual, dyad or grouping with given characteristics was estimated to be observed relative to an appropriate reference level (e.g. same-class versus different-class). In all models, this output was the difference between observed relative rates and expected relative rates as estimated from permuted data. Permutation procedures were utilized to produce suitable null models for hypothesis-testing.

Research sample

Jackdaws provide an ideal system to study the cognitive basis and group-level consequences of social decision-making because they live in groups featuring stable relationships between long-term affiliates as well as frequent interactions between unaffiliated individuals outside of these relationships. We used an automated social coordination task to examine partner-choice decision-making in a wild population of ringed jackdaws. The majority of individuals in the study population (approximately 90% of individuals that occupied nest-boxes at the site plus transient and non-resident individuals) were fitted with a leg ring containing a Passive-Integrated Transponder (PIT) tags. The study used data from 139 free-flying, PIT-tagged individuals that interacted with the task. Among these individuals, we recorded and analysed a total of 3117 social association events across 751 distinct dyads. Of these, 648 events involved interactions between affiliates (24 individuals across 18 dyads). The remaining 2469 events involved interactions between unaffiliated individuals (139 individuals across 733 dyads).

Sampling strategy

The task was active during the extent of a breeding season (April - July). Sampling commenced prior to the period of peak social foraging activity (post-fledging period, June - July) to maximize recruitment. Early-season sampling was essential to ensure adequate habituation to the task apparatus (to overcome neophobia). The number of birds that visited the task on a given day was stochastic. To maximize sample size, all birds that had been ringed prior to the commencement of the experiment (n=1999) were assigned a treatment class and so were able to participate in the experiment. Sample sizes for affiliate-only analyses were comparable to previous REM studies on jackdaws (Tranmer et al., 2014), whereas sample sizes for non-affiliate analyses and those including all individuals greatly exceeded this and approached sample sizes found in sociological analyses used to demonstrate typical REM applications (see Butts & Marcum, 2017).

- Butts, C.T. & Marcum, C.S. A relational event approach to modelling behavioral dynamics. In: Pilny, A. & Poole, M. (Eds) Group Processes. Computational Social Sciences. Cham: Springer (2017).
- Tranmer, M., Marcum, C.S., Morton, F.B., Croft, D.P. & de Kort, S.R. Using the relational event model (REM) to investigate the temporal dynamics of animal social networks. Anim. Behav., 101: 99-105 (2015).

Data collection

Data collection was conducted using pairs of automated feeders with Radio-Frequency Identification (RFID) data loggers connected to 'Darwin Board' microcomputers. The data-loggers and microcomputer recorded each bird's arrival and departure from feeder perches along with their unique identifier code. Time of arrival and departure was rounded to the nearest second, but changes in participant ID were detected at a resolution of 250ms. In addition, the 'Darwin Board' logged changes in task states (e.g. opening/ closing of doors) occurring in response to coordination events. Task setup, re-stocking of task rewards, maintenance of apparatus and data downloads were performed by JA. In addition, JA collected video recordings of task use for the purposes of validation of data quality.

Timing and spatial scale

Data collection commenc, UKed on 24/04/2019 and ended on 02/08/2019. The experiment was run during the breeding season as motivation to engage with novel tasks that provide food rewards is maximal during this period. Data collection was initiated prior to the egg-laying period to promote habituation of both males and females to the task apparatus and ceased once the breeding season

ended. The two tasks were placed in the vicinity of nest-boxes in different regions of fields that are home to a breeding colony in Stithians Village, Cornwall, UK.

Data exclusions

Recordings that featured the RFID codes of tags used by the experimenter to test the functionality of the task at the beginning of each sampling period (i.e. each morning) were removed. Events that contained individuals that did have a PIT-tag, but did not yet have a treatment class assigned (and so were unable to affect task state) at the time the event was recorded were filtered out of the dataset. This scenario occurred because some individuals were fitted with RFID tags during the course of the experiment (e.g. new fledglings or adults that had lost their RFID tag). For these individuals there was a lag (< 24 hours) between the time at which the tag was fitted and the time at which the text files containing treatment class information used by the task apparatus to inform changes in task state were updated. In addition, two individuals and the events in which they participated (37 events: 19 unsuccessful association events, 18 successful) were removed from the dataset as they had duplicate RFID tag codes.

Reproducibility

The experiment featured a wild population of free-flying jackdaws and all ringed members of the population could participate in the experiment. The data collected therefore represents the response of a natural, unaltered social group to an experimental manipulation of social value in a foraging context. To ensure rigour and reproducibility, our analyses feature large sample sizes and use Relational Event Models which are particularly well suited to studying fine-scale changes in social behaviour over time as they do not require any aggregation of data prior to analysis. As an additional robustness check, JA independently ran the analyses conducted by MK, obtaining the same results as those reported in the manuscript. We also ensured reproducibility of our findings by making the data and analysis scripts openly available, allowing analyses to be replicated.

Randomization

Randomization was used to determine treatment class designations. A supervised randomization procedure was used to ensure that an approximately equal number of individuals were assigned to each class and that the distribution of same- versus different-class pairings was approximately equal for key pairings (e.g. known affiliates) upon commencement of the experiment. Balanced assignment of key pairings was deemed necessary as frequency of engagement with the task could not be controlled. Individuals that had been fitted with an RFID-tag prior to the study were assigned a treatment class prior to commencement of the experiment, but individuals that were tagged during the period of the experiment (e.g., newly-fledged juveniles) were assigned a treatment class at random on the day of ringing.

Blinding

Blinding was not necessary for this study. The experiment and data collection were fully automated through RFID data loggers, so there was no scope for experimenter bias.

Did the study involve field work? ☒ Yes ☐ No

Field work, collection and transport

Field conditions

Fieldwork was conducted close to known nest-box breeding colonies near the village of Stithians in Cornwall, UK. Data was collected throughout a breeding season (April - July 2019) on weekdays between 06:00 and 10:00. Data collection was not performed on days in which there was heavy rainfall so as to minimize risk of damage to the electronics of the task apparatus.

Location

Field in the vicinity of Stithians Village, West Cornwall, UK (N 50°11'25.98'', W 5°10'49.00'').

Access & import/export

Local landowners kindly granted us permission to work on their land.

Disturbance

To minimize disturbance, the experiment was only run in the mornings. In addition, during this time the researcher (JA) only visited the task apparatus for a brief period at hourly intervals to ensure that the apparatus was not damaged and to replenish food rewards.

Reporting for specific materials, systems and methods

We require information from authors about some types of materials, experimental systems and methods used in many studies. Here, indicate whether each material, system or method listed is relevant to your study. If you are not sure if a list item applies to your research, read the appropriate section before selecting a response.

Materials & experimental systems

n/a	Involved in the study
☒	☐ Antibodies
☒	☐ Eukaryotic cell lines
☒	☐ Palaeontology and archaeology
☐	☒ Animals and other organisms
☒	☐ Clinical data
☒	☐ Dual use research of concern

Methods

n/a	Involved in the study
☒	☐ ChIP-seq
☒	☐ Flow cytometry
☒	☐ MRI-based neuroimaging

Antibodies

Antibodies used	*Describe all antibodies used in the study; as applicable, provide supplier name, catalog number, clone name, and lot number.*
Validation	*Describe the validation of each primary antibody for the species and application, noting any validation statements on the manufacturer's website, relevant citations, antibody profiles in online databases, or data provided in the manuscript.*

Eukaryotic cell lines

Policy information about cell lines and Sex and Gender in Research

Cell line source(s)	*State the source of each cell line used and the sex of all primary cell lines and cells derived from human participants or vertebrate models.*
Authentication	*Describe the authentication procedures for each cell line used OR declare that none of the cell lines used were authenticated.*
Mycoplasma contamination	*Confirm that all cell lines tested negative for mycoplasma contamination OR describe the results of the testing for mycoplasma contamination OR declare that the cell lines were not tested for mycoplasma contamination.*
Commonly misidentified lines (See ICLAC register)	*Name any commonly misidentified cell lines used in the study and provide a rationale for their use.*

Palaeontology and Archaeology

Specimen provenance	*Provide provenance information for specimens and describe permits that were obtained for the work (including the name of the issuing authority, the date of issue, and any identifying information). Permits should encompass collection and, where applicable, export.*
Specimen deposition	*Indicate where the specimens have been deposited to permit free access by other researchers.*
Dating methods	*If new dates are provided, describe how they were obtained (e.g. collection, storage, sample pretreatment and measurement), where they were obtained (i.e. lab name), the calibration program and the protocol for quality assurance OR state that no new dates are provided.*

☐ Tick this box to confirm that the raw and calibrated dates are available in the paper or in Supplementary Information.

Ethics oversight	*Identify the organization(s) that approved or provided guidance on the study protocol, OR state that no ethical approval or guidance was required and explain why not.*

Note that full information on the approval of the study protocol must also be provided in the manuscript.

Animals and other research organisms

Policy information about studies involving animals; ARRIVE guidelines recommended for reporting animal research, and Sex and Gender in Research

Laboratory animals	N/A
Wild animals	We studied free-flying jackdaws (Corvus monedula). Social foraging groups contained adult mated pairs, unpaired adults and juveniles. Ringing of adults and juveniles took place during the experimental period in accordance with established protocols (see 'Ethics oversight').
Reporting on sex	Sex was considered implicitly in study design, as breeding pairs were assigned to treatment classes in such a way as to balance the number of same-class and different-class pairings. However, the overall number of males and females in each treatment class was not identical, as other individuals (i.e., not belonging to nest-box owning pairs) were assigned (at random) to treatment classes in a fashion that did not force an equal balance of sexes. Sex was determined from blood samples via DNA fingerprinting.
Field-collected samples	Blood samples were collected during ringing for use in determination of sex.
Ethics oversight	All field protocols were approved by the Biosciences Ethics Panel of the University of Exeter ((2014/577; eCORN000406)) and adhered to the Association for the Study of Animal Behaviour Guidelines for the Treatment of Animals in Behavioural Research and Teaching. Ringing and blood sampling protocols were covered by Home Office (PPL 80/2371) and BTO (C6079, C5752, C5746) licenses.

Note that full information on the approval of the study protocol must also be provided in the manuscript.

Clinical data

Policy information about clinical studies

All manuscripts should comply with the ICMJE guidelines for publication of clinical research and a completed CONSORT checklist must be included with all submissions.

Clinical trial registration	*Provide the trial registration number from ClinicalTrials.gov or an equivalent agency.*
Study protocol	*Note where the full trial protocol can be accessed OR if not available, explain why.*
Data collection	*Describe the settings and locales of data collection, noting the time periods of recruitment and data collection.*
Outcomes	*Describe how you pre-defined primary and secondary outcome measures and how you assessed these measures.*

ChIP-seq

Data deposition

☐ Confirm that both raw and final processed data have been deposited in a public database such as GEO.

☐ Confirm that you have deposited or provided access to graph files (e.g. BED files) for the called peaks.

Data access links *May remain private before publication.*	*For "Initial submission" or "Revised version" documents, provide reviewer access links. For your "Final submission" document, provide a link to the deposited data.*
Files in database submission	*Provide a list of all files available in the database submission.*
Genome browser session (e.g. UCSC)	*Provide a link to an anonymized genome browser session for "Initial submission" and "Revised version" documents only, to enable peer review. Write "no longer applicable" for "Final submission" documents.*

Methodology

Replicates	*Describe the experimental replicates, specifying number, type and replicate agreement.*
Sequencing depth	*Describe the sequencing depth for each experiment, providing the total number of reads, uniquely mapped reads, length of reads and whether they were paired- or single-end.*
Antibodies	*Describe the antibodies used for the ChIP-seq experiments; as applicable, provide supplier name, catalog number, clone name, and lot number.*
Peak calling parameters	*Specify the command line program and parameters used for read mapping and peak calling, including the ChIP, control and index files used.*
Data quality	*Describe the methods used to ensure data quality in full detail, including how many peaks are at FDR 5% and above 5-fold enrichment.*
Software	*Describe the software used to collect and analyze the ChIP-seq data. For custom code that has been deposited into a community repository, provide accession details.*

Flow Cytometry

Plots

Confirm that:

☐ The axis labels state the marker and fluorochrome used (e.g. CD4-FITC).

☐ The axis scales are clearly visible. Include numbers along axes only for bottom left plot of group (a 'group' is an analysis of identical markers).

☐ All plots are contour plots with outliers or pseudocolor plots.

☐ A numerical value for number of cells or percentage (with statistics) is provided.

Methodology

Sample preparation	*Describe the sample preparation, detailing the biological source of the cells and any tissue processing steps used.*
Instrument	*Identify the instrument used for data collection, specifying make and model number.*
Software	*Describe the software used to collect and analyze the flow cytometry data. For custom code that has been deposited into a community repository, provide accession details.*

Cell population abundance

Describe the abundance of the relevant cell populations within post-sort fractions, providing details on the purity of the samples and how it was determined.

Gating strategy

Describe the gating strategy used for all relevant experiments, specifying the preliminary FSC/SSC gates of the starting cell population, indicating where boundaries between "positive" and "negative" staining cell populations are defined.

☐ Tick this box to confirm that a figure exemplifying the gating strategy is provided in the Supplementary Information.

Magnetic resonance imaging

Experimental design

Design type

Indicate task or resting state; event-related or block design.

Design specifications

Specify the number of blocks, trials or experimental units per session and/or subject, and specify the length of each trial or block (if trials are blocked) and interval between trials.

Behavioral performance measures

State number and/or type of variables recorded (e.g. correct button press, response time) and what statistics were used to establish that the subjects were performing the task as expected (e.g. mean, range, and/or standard deviation across subjects).

Acquisition

Imaging type(s)

Specify: functional, structural, diffusion, perfusion.

Field strength

Specify in Tesla

Sequence & imaging parameters

Specify the pulse sequence type (gradient echo, spin echo, etc.), imaging type (EPI, spiral, etc.), field of view, matrix size, slice thickness, orientation and TE/TR/flip angle.

Area of acquisition

State whether a whole brain scan was used OR define the area of acquisition, describing how the region was determined.

Diffusion MRI ☐ Used ☐ Not used

Preprocessing

Preprocessing software

Provide detail on software version and revision number and on specific parameters (model/functions, brain extraction, segmentation, smoothing kernel size, etc.).

Normalization

If data were normalized/standardized, describe the approach(es): specify linear or non-linear and define image types used for transformation OR indicate that data were not normalized and explain rationale for lack of normalization.

Normalization template

Describe the template used for normalization/transformation, specifying subject space or group standardized space (e.g. original Talairach, MNI305, ICBM152) OR indicate that the data were not normalized.

Noise and artifact removal

Describe your procedure(s) for artifact and structured noise removal, specifying motion parameters, tissue signals and physiological signals (heart rate, respiration).

Volume censoring

Define your software and/or method and criteria for volume censoring, and state the extent of such censoring.

Statistical modeling & inference

Model type and settings

Specify type (mass univariate, multivariate, RSA, predictive, etc.) and describe essential details of the model at the first and second levels (e.g. fixed, random or mixed effects; drift or auto-correlation).

Effect(s) tested

Define precise effect in terms of the task or stimulus conditions instead of psychological concepts and indicate whether ANOVA or factorial designs were used.

Specify type of analysis: ☐ Whole brain ☐ ROI-based ☐ Both

Statistic type for inference
(See Eklund et al. 2016)

Specify voxel-wise or cluster-wise and report all relevant parameters for cluster-wise methods.

Correction

Describe the type of correction and how it is obtained for multiple comparisons (e.g. FWE, FDR, permutation or Monte Carlo).

Models & analysis

n/a	Involved in the study
☐	☐ Functional and/or effective connectivity
☐	☐ Graph analysis
☐	☐ Multivariate modeling or predictive analysis

Functional and/or effective connectivity

Report the measures of dependence used and the model details (e.g. Pearson correlation, partial correlation, mutual information).

Graph analysis

Report the dependent variable and connectivity measure, specifying weighted graph or binarized graph, subject- or group-level, and the global and/or node summaries used (e.g. clustering coefficient, efficiency, etc.).

Multivariate modeling and predictive analysis

Specify independent variables, features extraction and dimension reduction, model, training and evaluation metrics.