

R code can be found here:

<https://doi.org/10.6084/m9.figshare.6072272.v2>

Datasets can be found here:

<https://doi.org/10.6084/m9.figshare.6072254.v2>

The R function “infer_power_reciprocity_kinship” uses the following arguments:

- **individuals:** a vector with unique IDs for all individuals in the study
- **observations:** a data frame with columns: actor, receiver, duration, possible.actors.list
- **possible.actors:** a matrix where each column contains a list of possible actors for each observation. The number of rows is the max number of possible actors.
- **relatedness:** a matrix of relatedness between all individuals - row and column orders must match the order of individuals
- **nreps:** number of repeated subsamples at each sample size
- **jumps:** number of observations to increment each sample size step (default = 20). First sample size is always 20.
- **simulate_data:** if set to “TRUE”, the function will simulate data. If set to “FALSE” then the function will use actual data provided by arguments above.
- **nepotism** (only used with simulated data): degree of nepotism (0 to 1)
- **N** (only used with simulated data): number of simulated individuals
- **n.events** (only used with simulated data): number of simulated helping events

Note: Depending on the number of observations and replications, this function can take several hours to run.

Table S1. Mean correlation between helping history and kinship in simulated data. Values based on 10,000 simulations. Helping history is always symmetric and determines probability and duration of observed helping events.

Nepotism	Mean Pearson’s correlation (0.025 – 0.975 quantiles)
0%	0 (-0.14—0.14)
25%	0.32 (0.19—0.44)
50%	0.71 (0.64—0.76)
75%	0.95 (0.94—0.96)
100%	1 (1—1)

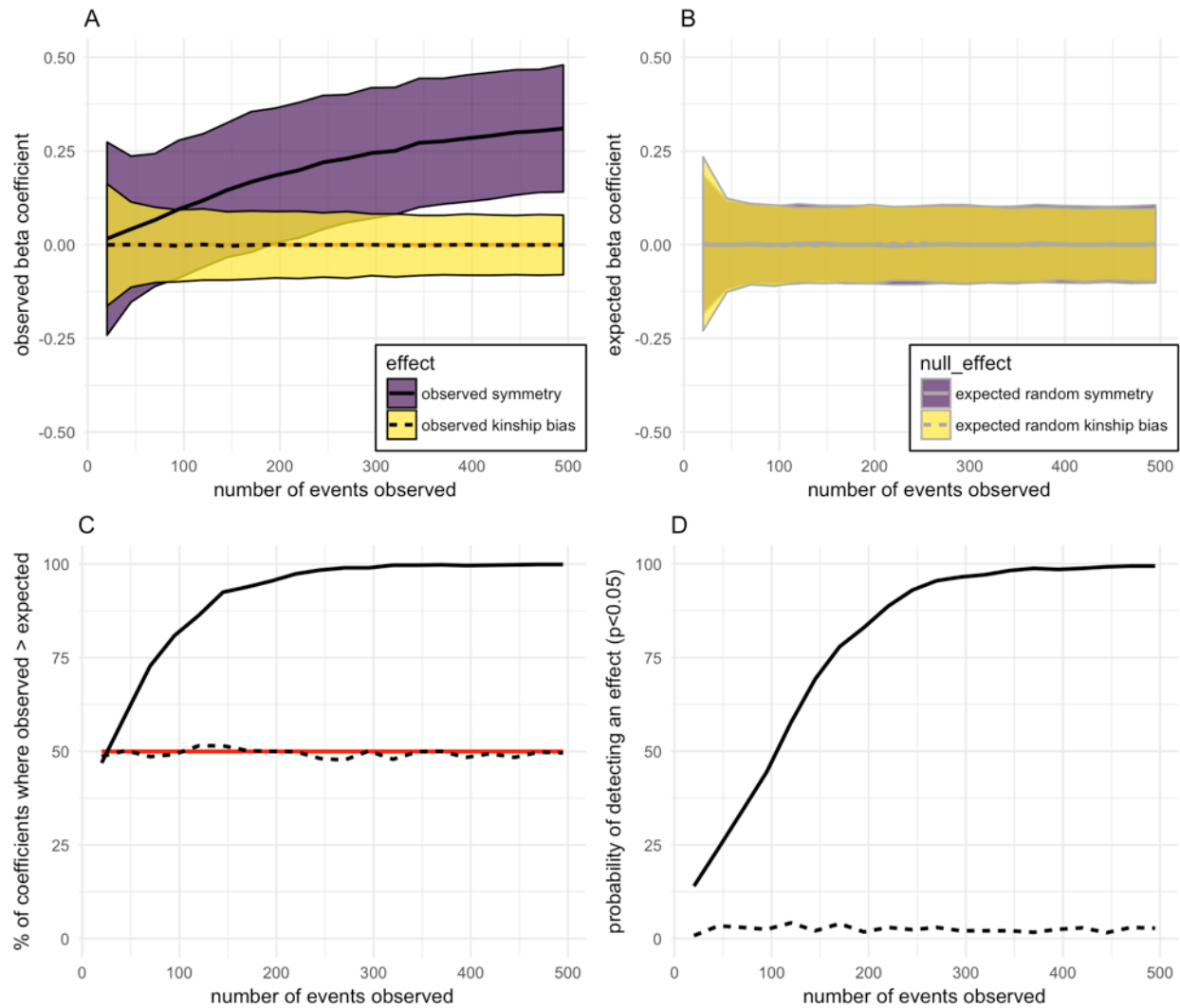


Figure S1. Power analysis for simulation of symmetrical helping with 0% nepotism. Panel A shows the mean and 95% confidence interval of the standardized slope estimates for the effects of helping rate A to B (solid line, purple shading) and kinship between A and B (dotted line, yellow shading) as predictors of helping rate B to A. Panel B shows the same for the expected null coefficients generated by permutation. Panel C shows the percentage of observed coefficients that are greater than the paired null coefficient generated from the same subsample. If effects are real, then these values should be higher than 50% (red line). Panel D shows the percentage of observed coefficients that are greater than 95% of expected null coefficients for that sample size.

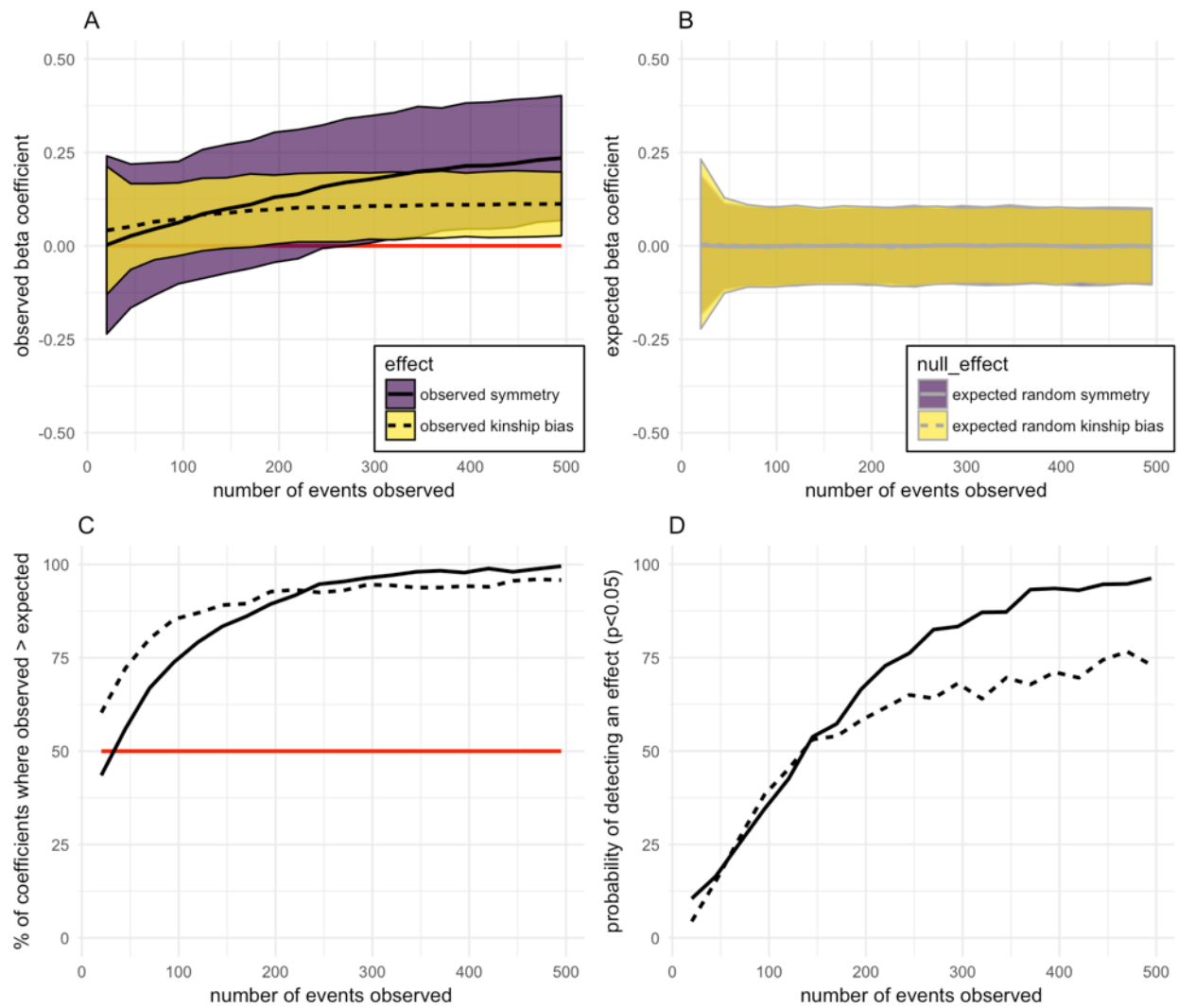


Figure S2. Power analysis for simulation of symmetrical helping with 25% nepotism. See plot Figure S2 for explanation.

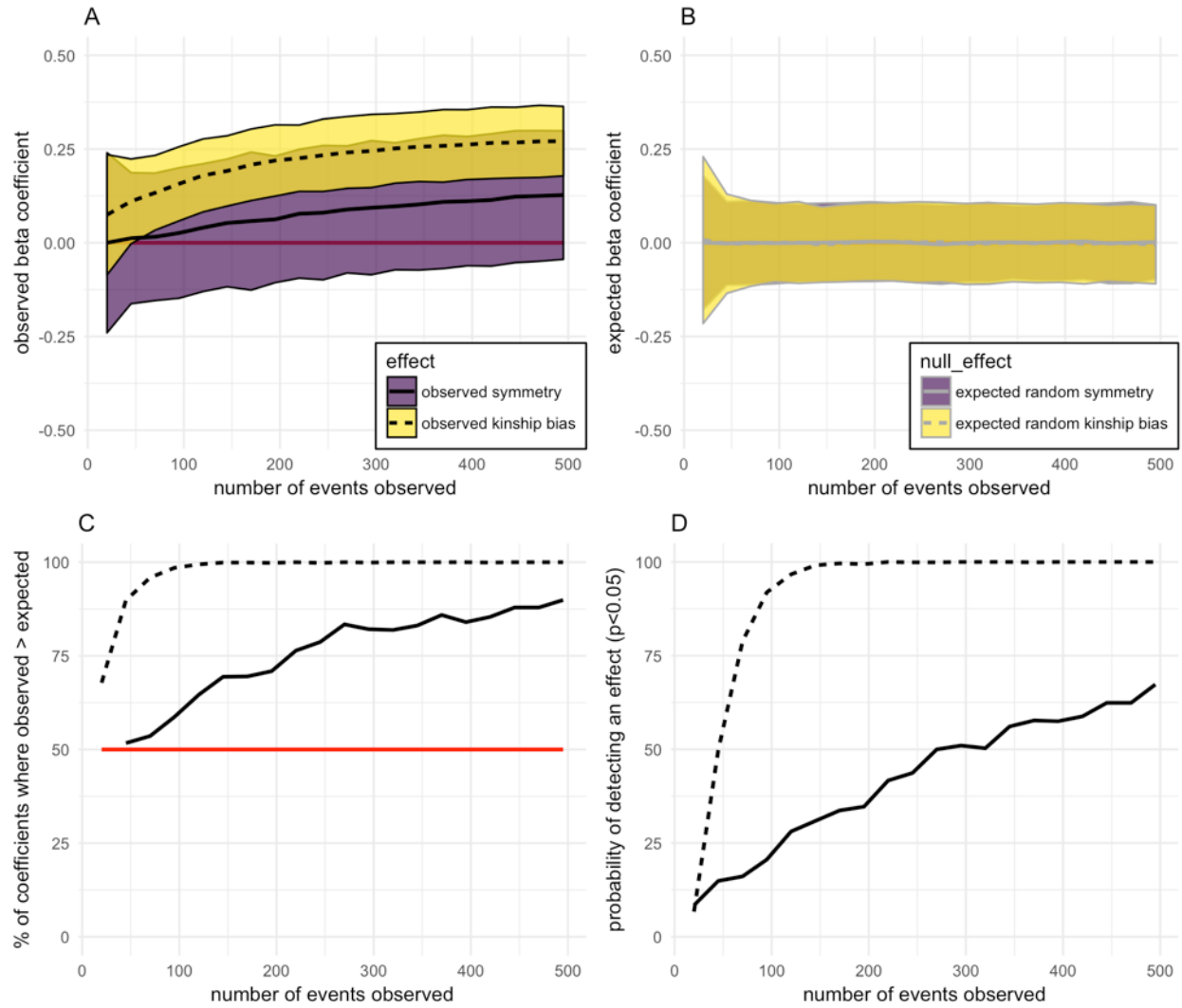


Figure S3. Power analysis for simulation of symmetrical helping with 50% nepotism. See plot Figure S3 for explanation.

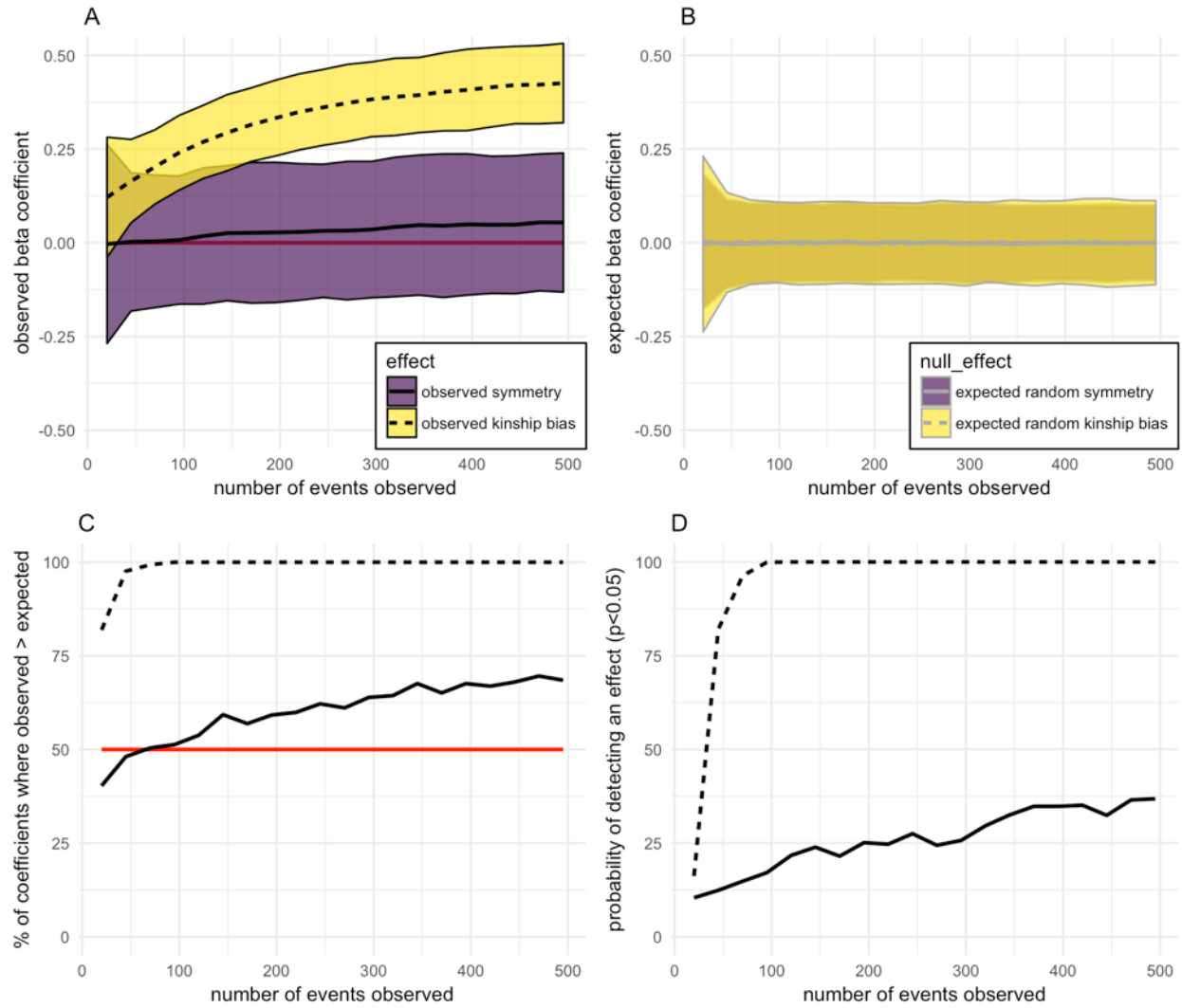


Figure S4. Power analysis for simulation of symmetrical helping with 75% nepotism. See plot Figure S4 for explanation.

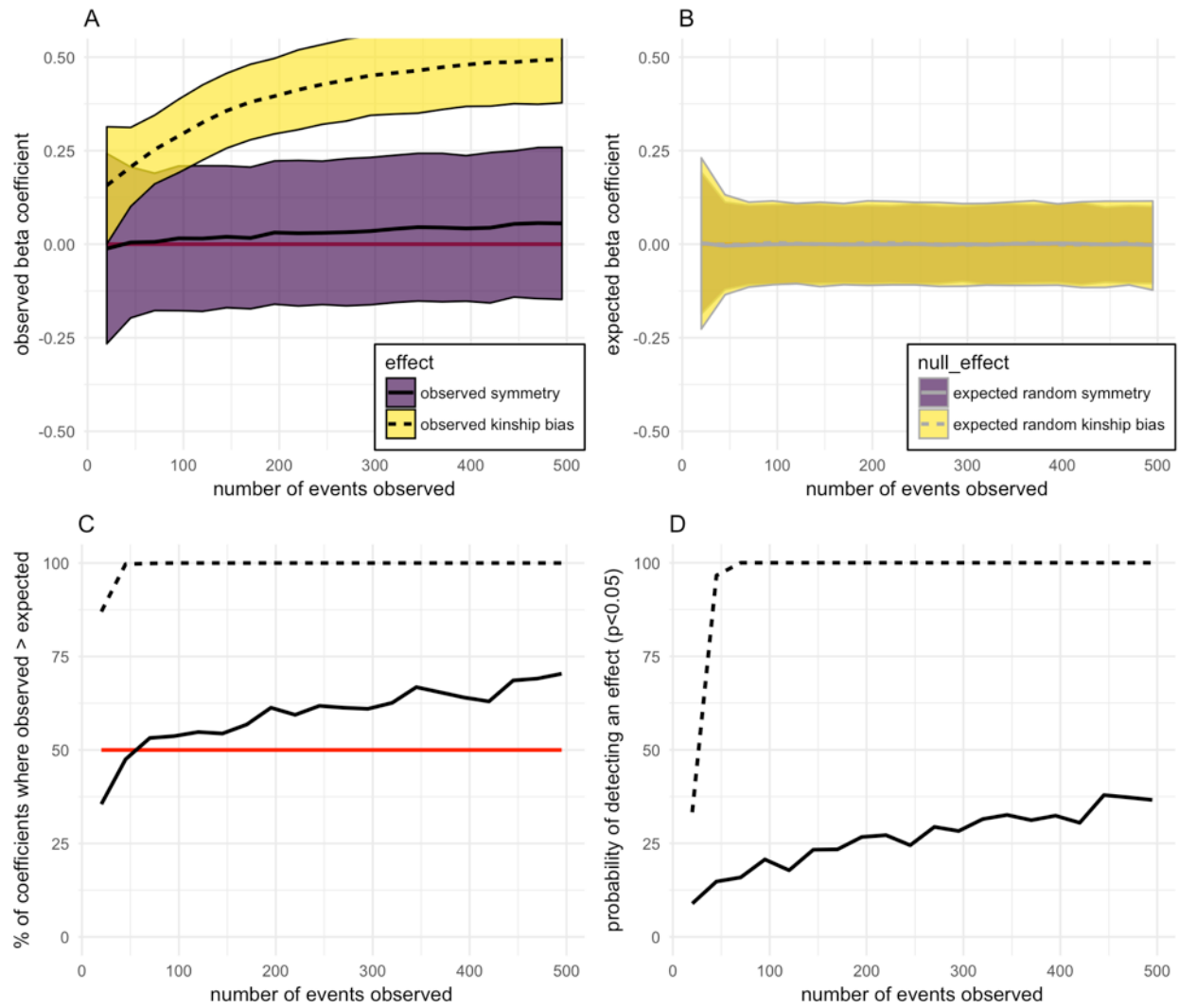


Figure S5. Power analysis for simulation of symmetrical helping with 100% nepotism. See plot Figure S5 for explanation.

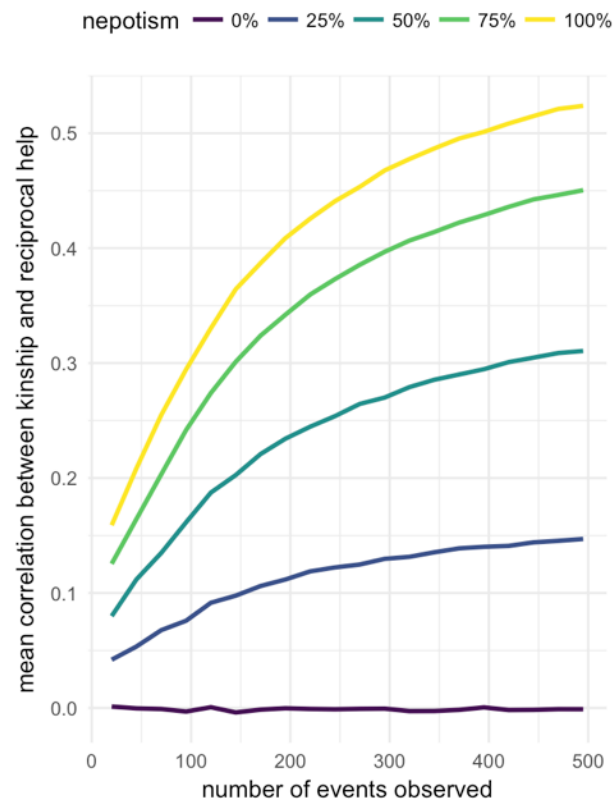


Figure S6. Collinearity. Mean Pearson's R correlation between the predictors kinship and reciprocal help for each degree of nepotism with increased sampling effort.

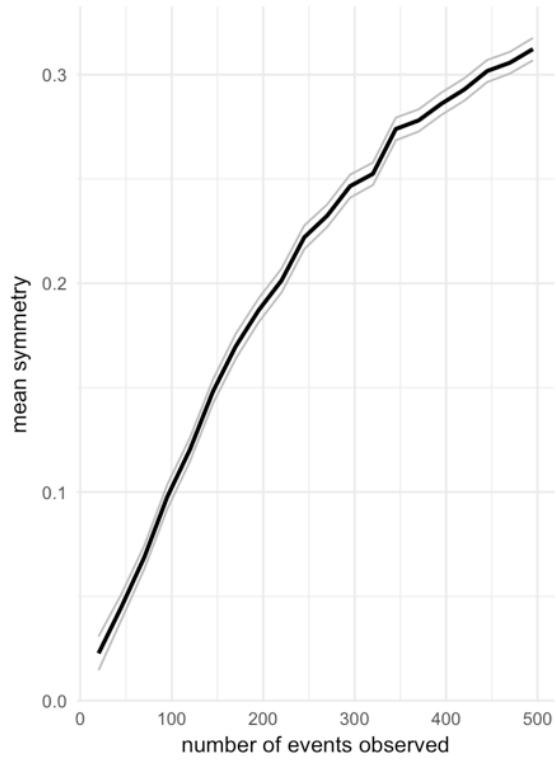


Figure S7. Symmetry under zero nepotism with increased sampling effort. Black line shows mean and grey lines show 95% confidence interval of the mean Pearson's correlation between help given and received.