

Supplementary material

Article title: Safari, I., Goymann, W. & Kokko, H. Male-only care and cuckoldry in black coucals: does parenting hamper sex life?

Computational details

Each model (Fig. 1) uses a specific assumption structure, where the size of the vignets varies independently or non-independently across male stages.

All models scale propensities such that the social father has propensity 1 for his 1st egg. A ‘nonlinear’ model will allow this propensity to change with egg number n such that the n th egg laid in a focal nest has propensity $1-a(n-1)^b$ (e.g. red and blue lines in Fig. S1), a ‘linear’ model behaves assumes that b takes the value 1 (orange line in Fig. S1), and a ‘flat’ model assumes that a social father’s propensity stays at 1 throughout the egg-laying period (black line).

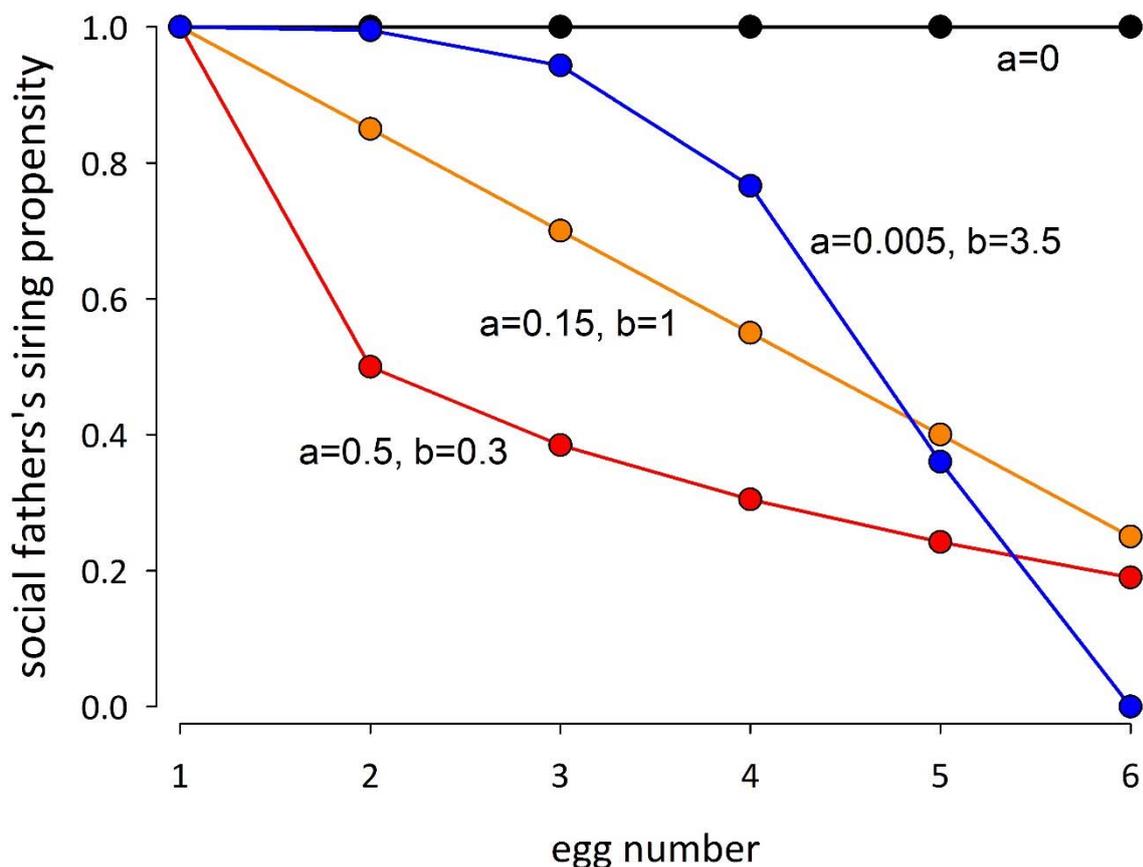


Fig. S1. Four examples (two nonlinear, and two linear) of potential shapes for the social father’s propensity decline; the maximum likelihood search will look for the shape that best predicts the observed patterns of paternity, including no decline at all (achieved by setting $a = 0$).

All other males have their propensities determined by two factors: a baseline that is estimated separately (p_W and p_E) for within-group and extra-group males, and three modifiers that multiply the baseline in case the male is incubating (multiplier p_{inc}), feeding nestlings (multiplier p_m), or feeding fledglings (multiplier p_{ff}).

To exemplify the procedure, we will present the calculation in detail for the 100th egg in our dataset, before generalizing. This egg comes with the following data structure:

Egg number: 5 (i.e. nest already had 4 eggs before this one was laid)

Known sire: 3rd row of the data, i.e. the 2nd potential extra-pair sire in the list below (in bold)

1	Social father:	not the sire	
2	1 st potential extra-pair sire:	a within-group male	activities 0 → 0 → 0
3	2nd potential extra-pair sire:	a within-group male	activities 0 → 0 → 0
4	3 rd potential extra-pair sire:	an extra-group male	activities 2 → 3 → 3
5	4 th potential extra-pair sire:	an extra-group male	activities 0 → 0 → 0
6	5 th potential extra-pair sire:	an extra-group male	activities 2 → 2 → 3
7	6 th potential extra-pair sire:	an extra-group male	activities 0 → 0 → 0
8	7 th potential extra-pair sire:	an extra-group male	activities 1 → 1 → 1
9	8 th potential extra-pair sire:	an extra-group male	activities 0 → 0 → 0
10	9 th potential extra-pair sire:	an extra-group male	activities 0 → 0 → 0
11	10 th potential extra-pair sire:	an extra-group male	activities 2 → 2 → 3
12	11 th potential extra-pair sire:	an extra-group male	activities 2 → 3 → 3
13	12 th potential extra-pair sire:	an extra-group male	activities 0 → 0 → 0
14	13 th potential extra-pair sire:	an extra-group male	activities 0 → 0 → 0
15	14 th potential extra-pair sire:	an extra-group male	activities 3 → 3 → 3
16	15 th potential extra-pair sire:	an extra-group male	activities 2 → 2 → 2
17	16 th potential extra-pair sire:	an extra-group male	activities 2 → 2 → 2
18	17 th potential extra-pair sire:	an extra-group male	activities 1 → 1 → 1
19	18 th potential extra-pair sire:	an extra-group male	activities 1 → 1 → 1
20	19 th potential extra-pair sire:	an extra-group male	activities 1 → 1 → 1

Here, activities are 0 = free, 1 = incubating, 2 = feeding nestlings, 3 = feeding fledglings, and the arrows denote changes over time from day 0 (nest ready but without any eggs) to day 1 (egg 1 was laid) to the day the focal egg was laid.

Each of the 20 different models (A to N, Fig. 1), at every point during the iteration that searches for the best parameter values given each model's constraint structure, makes assumptions about the relative propensities (biologically 'availability') of each male. The initial values do not matter (though better initial guesses make the solution converge faster). For example, the 'guesses' of propensities in model A could begin with $a = 0.005$, $b = 3.5$ (one of the functions in Fig. S1 above), $p_W = 0.5$, $p_E = 0.5$, $p_{inc} = 0.5$, $p_{fn} = 0.5$, $p_{ff} = 0.5$. In that case, the model with its current parameter guesses produces a likelihood that the 2nd within-group male, who was free at the time, indeed sired the egg:

$$L_{100} = \frac{P_W}{((1 - a(5 - 1)^b) + p_W + p_W + p_E p_{ff} + p_E p_{ff} + p_E + p_E p_{ff} + p_E + \dots + p_E p_{inc})}$$

$$= \frac{0.5}{(0.36 + 0.5 + 0.5 + 0.25 + \dots + 0.25)} = \frac{0.5}{7.11} = 0.0703$$

Here, each term in the denominator is one male's assumed propensity in the current circumstances, which for model A is based on the current day's activity (e.g. feeding fledglings for the 5th potential extra-pair male, who is also extra-group, hence the 5th term is $p_E p_{ff}$). The subscript 100 indicates that this is the 100th egg in the dataset.

The 0.0703 is only one ‘guess’, i.e. the result of assuming $a = 0.005$, $b = 3.5$ and all p values being set to 0.5. If egg number 100 was the only egg in the entire dataset, the likelihood would be maximized (L_{100} as high is possible) if all p values except p_w were made zero, and a and b were modified such that the social father’s propensity becomes zero (any high enough a value will achieve this for a 5th egg). This makes most terms disappear, and L_{100} simplifies to $p_w/2p_w = 0.5$, much higher than the initial guess that lead to 0.0703. In other words, this particular egg suggests that free within-group males sire eggs and other males do not (and since there were two within-group males in this category, each has a chance of 0.5 to be the sire).

However, the choices for parameter values that maximize L_{100} do not produce adequate likelihoods for other eggs whose sires were not within-group males. L_{100} is only one example out of 560 likelihoods (information provided by 560 eggs) that need to be computed for each set of parameter values. The log likelihood of the entire set is $\sum_{i=1}^{560} \ln(L_i)$. The optimization procedure (Matlab’s `fminsearch`) computes the values of a , b , p_w , p_E , p_{inc} , p_{fn} , and p_{ff} that collectively produce the best log likelihood for $\sum_{i=1}^{560} \ln(L_i)$.

This procedure is repeated separately for all models listed in Fig. 1. Each model differs from the others in terms of constraints that are imposed on the estimation procedure. For example, model D replaces the independent estimation of p_{fn} and p_{ff} with the assumption that both stages of parenting lead to the same propensity reduction, thus the optimization follows the constraint $p_{fn} = p_{ff}$, and the estimated values are identical in Table 1 whenever such constraints have been assumed. Model N (the null model) is the extreme choice, where every male is assumed equally likely to be the father; the likelihood for e.g. L_{100} is $1/20$ (social father + 19 competitors) and no parameters need to be estimated.

Each model thereafter has its AIC score computed as

$$AIC = -2 \sum_{i=1}^{560} \ln(L_i) + 2k$$

where k is the model-specific number of parameters that have been estimated.