## Methods

### Model overview

The evolutionary individual-based simulation models a population of haplodiploid organisms over 1,000,000 arbitrary time units. Each simulation starts with identical solitary breeding females (, can be appropriated as nests). Through their adult life, each individual is updated individually, wherein they perform a task choice between foraging and breeding at every update after sensing the larval population in its nest.

### Life cycle

Each simulation begins with mated, solitary foundresses. Whenever an individual is to be updated, it finishes its previous task and performs a task check between foraging and brooding for the next update time. Adult females have a survival probability and for each instance of brooding and foraging respectively.

If the individual’s current task is brooding, then a larva is added to the female’s nest at the next update. The gender of the larva is determined by a constant sex ratio (0.5 unless stated otherwise). If the current task is foraging, a random larva from the nest is chosen and is allocated resources in the next cycle. The brooding and foraging times can either be discrete and constant throughout each simulation or sampled from two separate normal distributions allowing for a more realistic scenario. Each larva is assigned a lifespan sampled from an exponential distribution, and dead larvae are periodically removed from the population. Mature males are assigned lifespans and dead males are removed similarly.

### Dispersal

Each female larva upon maturation makers the decision whether it will disperse in search for an empty nest or continue the rest of its life in the maternal nest. This decision is based on the phenotypic dispersal value, which when logistically transformed gives the dispersal probability. All simulations start with high dispersal probability 0.98 (phenotypic dispersal value ~-5). Hence, we start each simulation with solitary breeding prevalent through the individuals (unless stated otherwise). If a disperser does not find an empty nest in the existing nest instances, it dies.

### Task Choice

We assume a highly flexible natural spline function whose shape is determined by 5 gene values to model the propensity of choosing the task of foraging as a function of total larvae in the individual’s nest. This propensity is logistically transformed to obtain the foraging probability. Each simulation starts with a constant spline function with a value 0.5 unless stated otherwise, allowing for a random choice of tasks initially.

### Resource allocation and larval maturation

A foraging female that survives the task allocates a resource value sampled from a normal distribution to a random larva in the same nest. Each larva has equal probability of being chosen and matures if it’s body size is larger than maturation threshold. Females are monogamous and mate once in their life. Mature females select a male at random from the available pool; they stay unmated till males are available otherwise. Upon maturation, females check for dispersion and males are assigned a lifespan from an exponential distribution and pooled together across nests.

### Individual state update

Since individual task update is a key feature of our model, we maintain a priority queue of individuals. The topmost…..

### Genetics and mutation

Haplodiploid sex determination is implemented. Each haplotype of an individual carries 5 genes that determine the spline functions for task choice, and a singular gene for dispersal propensity. The model can be set up to allow for additive expression of genes where the phenotype values of a female is the average of the two homologous loci values, or for non-additive expression where the maternal or paternal chromosome is expressed. Recombination can occur during gene transmission to offsprings with a rate of 0.5. The model allows for complete linkage between task choice genes, or no linkage such that each locus is free to recombine.

Whenever an egg is laid, mutation can occur at each locus with a constant per-locus mutation rate. If a locus is mutated, the mutation step and direction are chosen from a normal distribution centred at 0 and gene values modified accordingly. Genes are expressed in females, with males functioning as gene carriers. Unless specified, the simulations assume an additive effect of gene values and no linkage.

### Model analysis

The model was constructed in C++ and compiled with g++ 8.5.0. Appropriate data values were calculated and stored in csv files throughout the simulations.

All data analysis and plotting were performed in R v4.2.2 using R packages *ggplot2* v3.4.2, *tidyverse* v2.0.0, *ggpubr* v0.6.0, *gridExtra* v2.3, *patchwork* v1.1.3, and *dplyr* v1.1.0.

