Runaway demogenetic model for sexual selection

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Runaway Model

1) Objective of Runaway
2) Choices for modelling
3) Example of simulation
Runaway Model

1) Objective of Runaway
2) Choices for modelling
3) Example of simulation
To study the co-evolution of traits and genome architecture under sexual selection.
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sexual selection:
- differences in mating and reproductive success caused by competition over mate and related to the expression of traits.
- result in the evolution of this traits (it can be morphological and behavioural traits)
- distinction between sexual and other natural selection

“Sexual selection... depends, not on a struggle for existence, but on a struggle between the males for possession of females: the result is not death to the unsuccessful competitor, but few or no offspring”
Darwin 1859, p. 88
1) Objective of Runaway

To study the co-evolution of traits and genome architecture under sexual selection.

**Why this study?**

- sexual selection have a strong impact on the evolution on morphological and behavioural traits
- genetic basis of these traits : the polygeny, the pleiotropy, and the spatial location in the genome (implying possible physical linkage) affect the evolution of these traits
Runaway Model

1) Objective of Runaway
2) Choices for modelling
3) Example of simulation
When demogenetic meet behavioural ecology...

1) **Survival**
   Depend on:
   - The genetic value of R
   - The density of individuals

2) **Mating behaviour**
   Choosiness on fecundity
   Competitiveness of phenotype

3) **Reproduction**
   Offspring number depend on parent’s fecundity
   Meiosis and mutations: new genomes

Time step: 1 generation.
The age of individual is a number of generations and depend on survival.
2) Choices for modelling

b) Traits under sexual selection

When demogenetic meets behavioural ecology...

The genome of each individual is coding for 4 traits:

- R : energy invested in reproduction
- Ig : gametic investment (i.e. fecundity)
- Pr : choosiness on the Ig
- Ph : competitiveness for mating

\[ R = Ig + Pr + Ph \]

\[ S = \frac{1}{(1 + R) \times (1 + \frac{N}{C})} \]

S : survival
\( N \): nombre d'invidus
\( C \): carrying capacity
2) Choices for modelling

c) How to model mating behaviours?

1. Mate choice between individuals is mutual

2. Individuals express a choosiness on the fecondity (trait Ig) of their partner

3. Some individuals are more competitive for mating because their are more efficient at finding a partner or more conspicuous by others
2) Choices for modelling

c) How to model mating behaviours?

• Encounters between individuals

- Mating groups are done by drawing a given number of individuals (the size of the group can be chosen in the user interface)

- Mating can occur between two individuals from the same mating group

- Individuals are sorted according to their phenotypic values (decreasing order)

Ph 1 meet each individual until mutual choice
He is the first to choose his partner or the first to be presented to a potential partner
2) Choices for modelling

c) How to model mating behaviours?

• Mating between individuals

Probability that ind. 1 agrees to mate with ind. 2: logit function of Ig and Pr

\[
P_{\text{ind1} \rightarrow \text{ind2}} = \frac{\exp(pr1(a.Ig2 - b))}{1 + \exp(pr1(a.Ig2 - b))}
\]

*pr1*: choosiness value for ind 1
*Ig2*: gametic investment for ind 2
*a* and *b*: parameters to adjust the shape of the function

Mating \(\leftrightarrow\) \[
\begin{cases} 
\text{random number 1} \geq P_{\text{ind1} \rightarrow \text{ind2}} \\
\text{random number 2} \geq P_{\text{ind2} \rightarrow \text{ind1}} 
\end{cases}
\]
2) Choices for modelling

c) How to model mating behaviours?

- Mating between individuals

  The choosiness is adjusted according to mate quality distribution (Ig values) in the mating group

  $$Ig\ ind1 = \frac{Ig\ ind1 - Ig\ min}{Ig\ min - Ig\ max}$$

  $Ig\ min$: lower value of gametic investment in the mating group
  $Ig\ max$: higher value of gametic investment in the mating group
2) choices for modelisation

d) How to model genetic basis of traits?

• Genetical architecture:

Using library Genetics
- fixed number of genes
- diploid DNA
- sexual chromosomes and cytoplasmic DNA are not modeled
- recombinaison probability map can be tuned
- fixed number of potential alleles
2) Choices for modelisation

d) How to model genetic basis of traits?

• Allelic expression

Each allele can code for each of the traits (pleiotropy)

Allelic effects for each traits : random draw from beta distributions

Trait value : sum of allelic effects over all loci

\[ T_j = \sum_{l=1}^{n} a_{ij} \]

\( T = \) trait value
\( n = \) loci number
\( a_i = \) value of the allele i for the trait j at the locus l
2) Choices for modelisation

d) How to model genetic basis of traits?

- Reproduction

Number of offspring = \min (Ig \text{ ind } a, Ig \text{ ind } b) \times \alpha

New genomes are created:
- meioses and fecundation processes (library genetics)
- Mutation: random draw of a new allele from the pool of existing alleles defined by the user

\( \alpha \) demographic constant
Runaway Model

1) Objective of Runaway
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3) Example of simulation

a) interface user and choices for scenarios

- Population size
- Carrying capacity
- Number of genes
- Number of potential alleles
3) Example of simulation

a) interface user and choices for scenarios

- Mating group size
- Type of encounter
- Type of preference
3) Example of simulation
a) interface user and choices for scenarios

- Mutation rate
- Allelic effects for traits

Allelic effects for Pr, Ph and Ig: random draw from a beta (1,3) distribution

Allelic effects for R: random draw from a beta (1,1) distribution
Scenario:

- Population size and carrying capacity: 10000
- Mating group size: 30
- Encounter with competitiveness on phenotype and mate choice with choosiness on Ig
- 100 genes, 500 potential alleles per loci
- Allelic effects for traits

Allelic effects distribution for Pr, Ph and Ig

Allelic effects distribution for R
3) Instances of simulation

b) outputs: data extractor and Stand viewer

Initial stand
- Trait distribution
- genome viewer

The mean allelic effect for Pr Ph and Ig is rather low for every loci
Evolution over 1000 generations
- Mean trait values in the population

Mean value of trait R is increasing because of increasing value of phenotype while gametic investment remain constant and preference is decreasing.
3) Instances of simulation

b) outputs: data extractor and Stand viewer

Evolution over 1000 generations
- Traits distribution in the population

Unimodal distributions
Reduced variation

500 generations
1000 generations
3) Instances of simulation

b) instance of output: data extractor and Stand viewer

Evolution over 1000 generations
- Computing the correlation between traits

![Graph showing negative correlation between phenotype and preference over generations.](image)
3) Instance of simulation

b) outputs: data extractor and Stand viewer

Evolution over 1000 generations
- Demography: survival depend on resource trait value and on density

Mean survival rate in the population remain constante Because R mean value is increasing while the population size is decreasing
Evolution over 1000 generations
- Mean fitness in the population: lifetime reproductive success

Two offsprings per individual on average
3) Instance of simulation

b) outputs: data extractor and Stand viewer

Evolution over 1000 generations
- Genome structure
Number of allele
Mean allelic effect per locus

- Loss of allelic diversity
• It was just an example for a given combination of parameters.

• Several simulations are currently running in order to make a first sensitivity analysis.
  - 972 combinations of parameters
  - 30 simulations for each combination of parameters
  - evolution over 3000 generations

• To understand how the different assumption influence the course of evolution and to compare the behaviour of the model with already published analytical models
Thank you for your attention!

Any questions?