Evolution of disassortative mating in a mimetic polymorphic butterfly

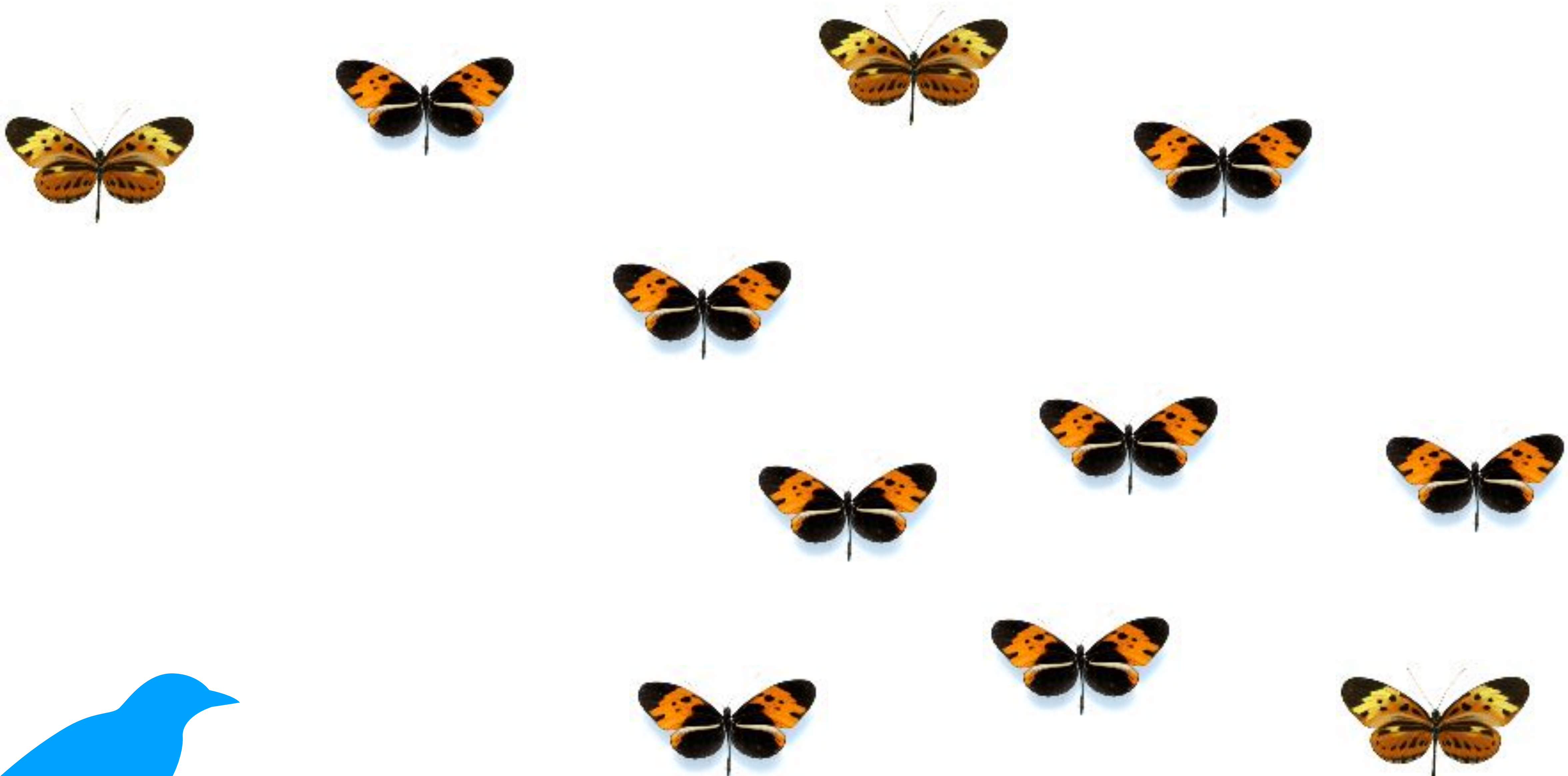
Ludovic Maisonneuve, Mathieu Chouteau, Mathieu Joron, Violaine Llaurens

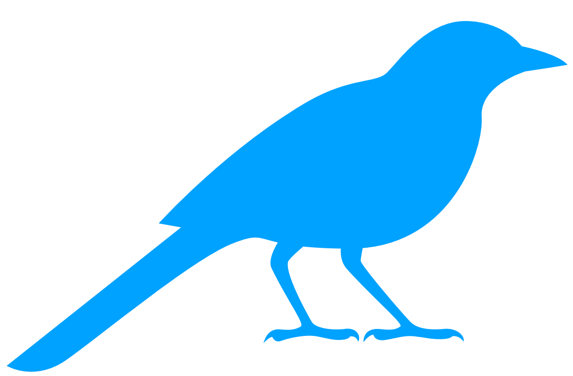
Evolution of warning signals

Predators learn to associate the signal with the unpalatability

$\lambda =$ **toxicity**

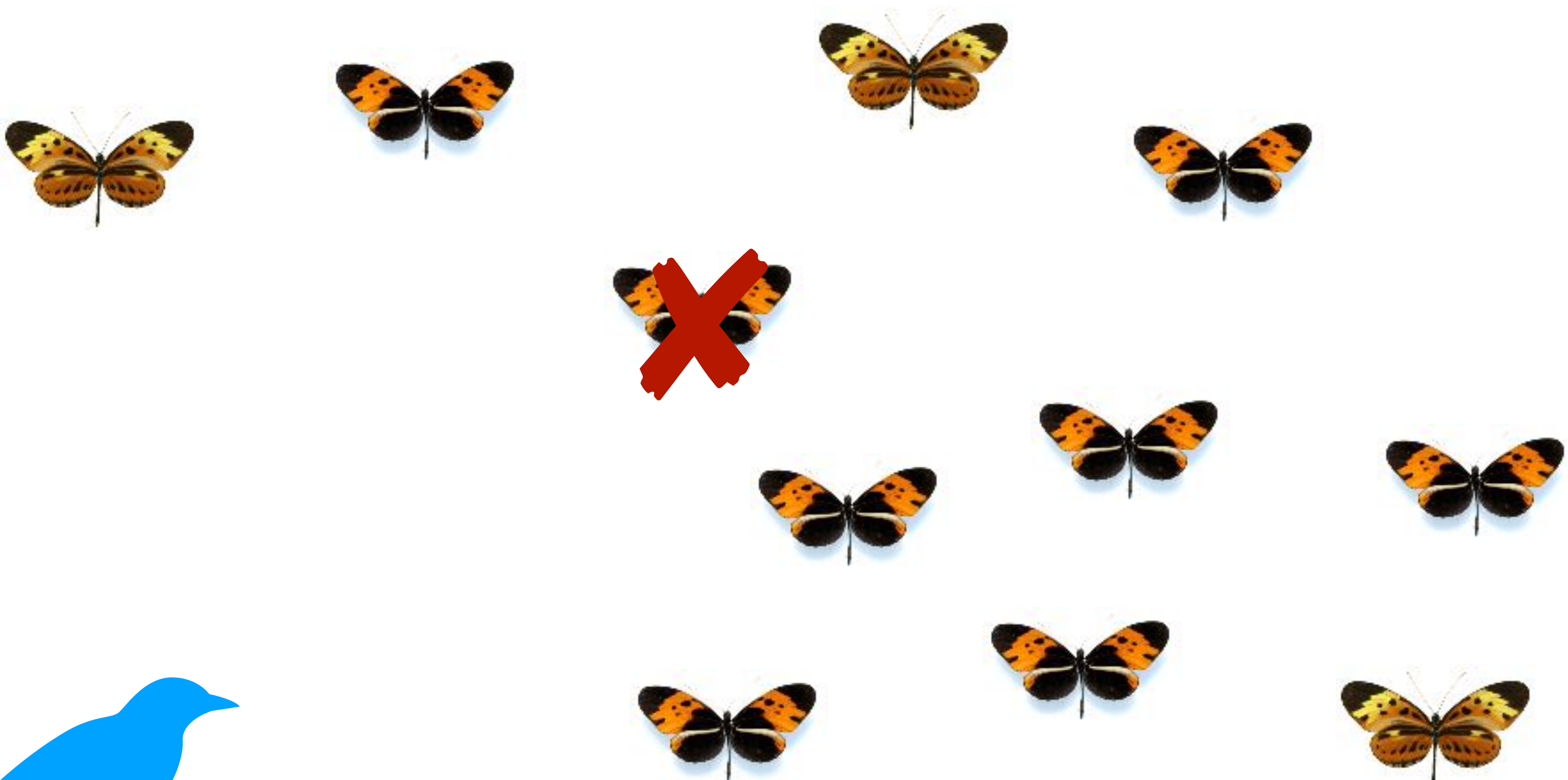
Number dependent selection on color patterns

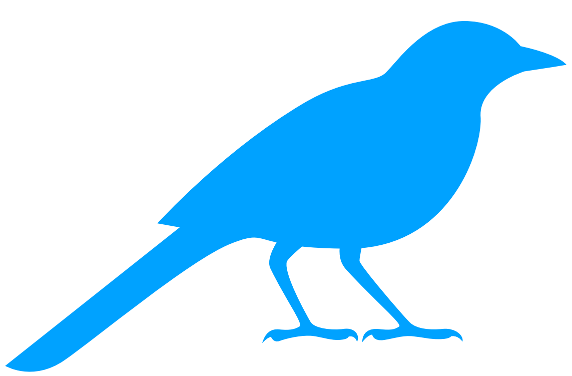




$d =$ **strength of predation**

Number dependent selection on color patterns





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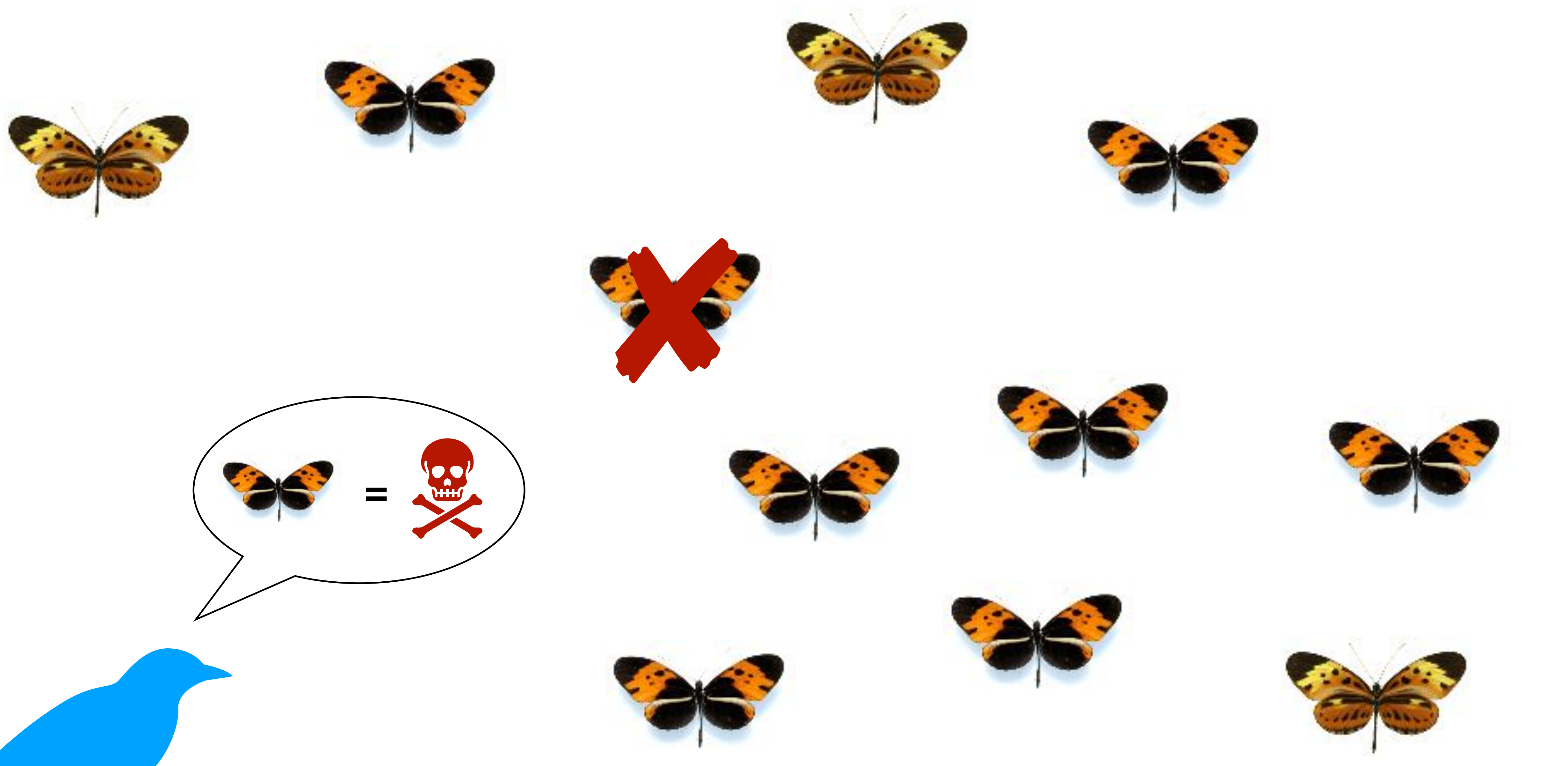

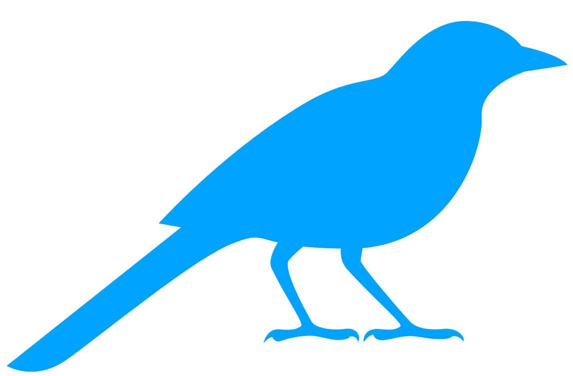

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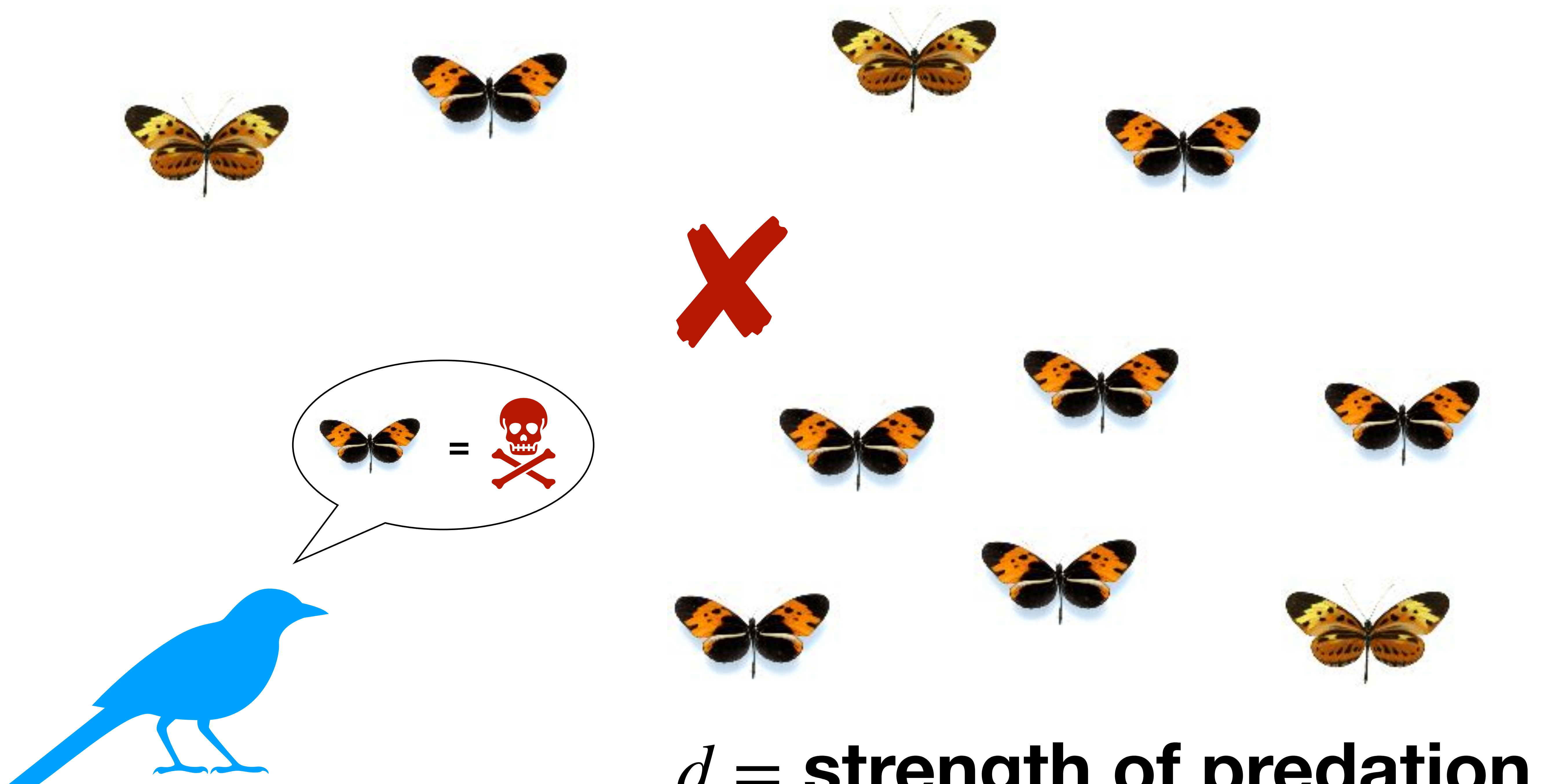

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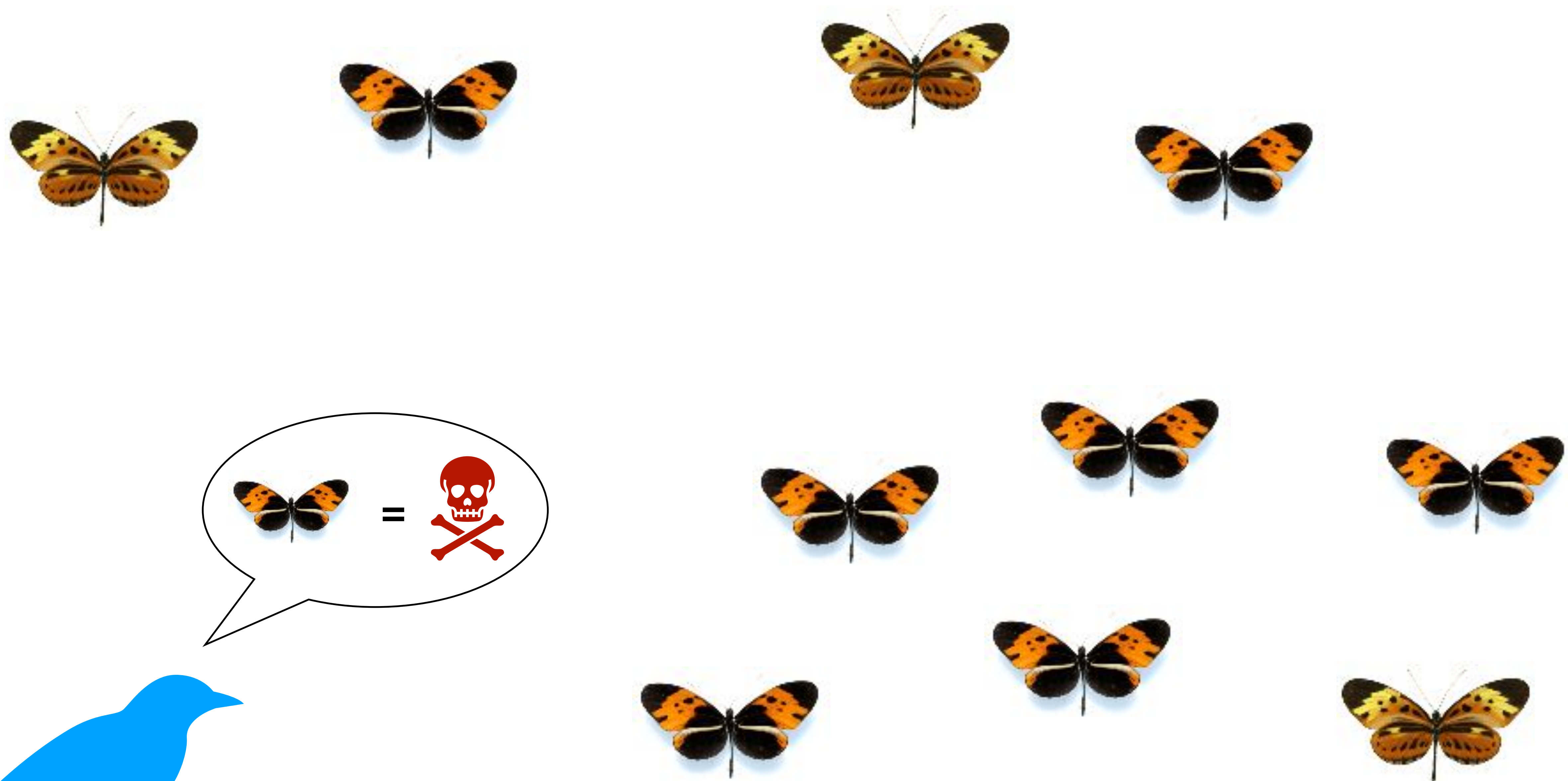

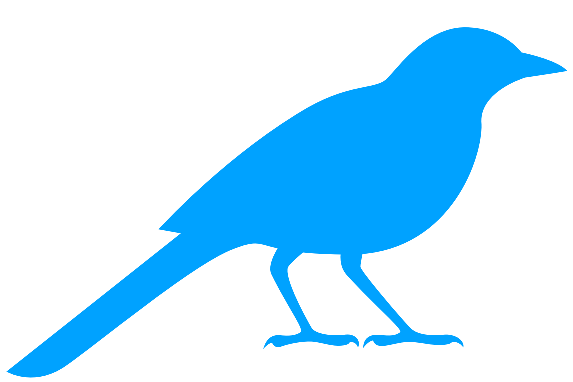

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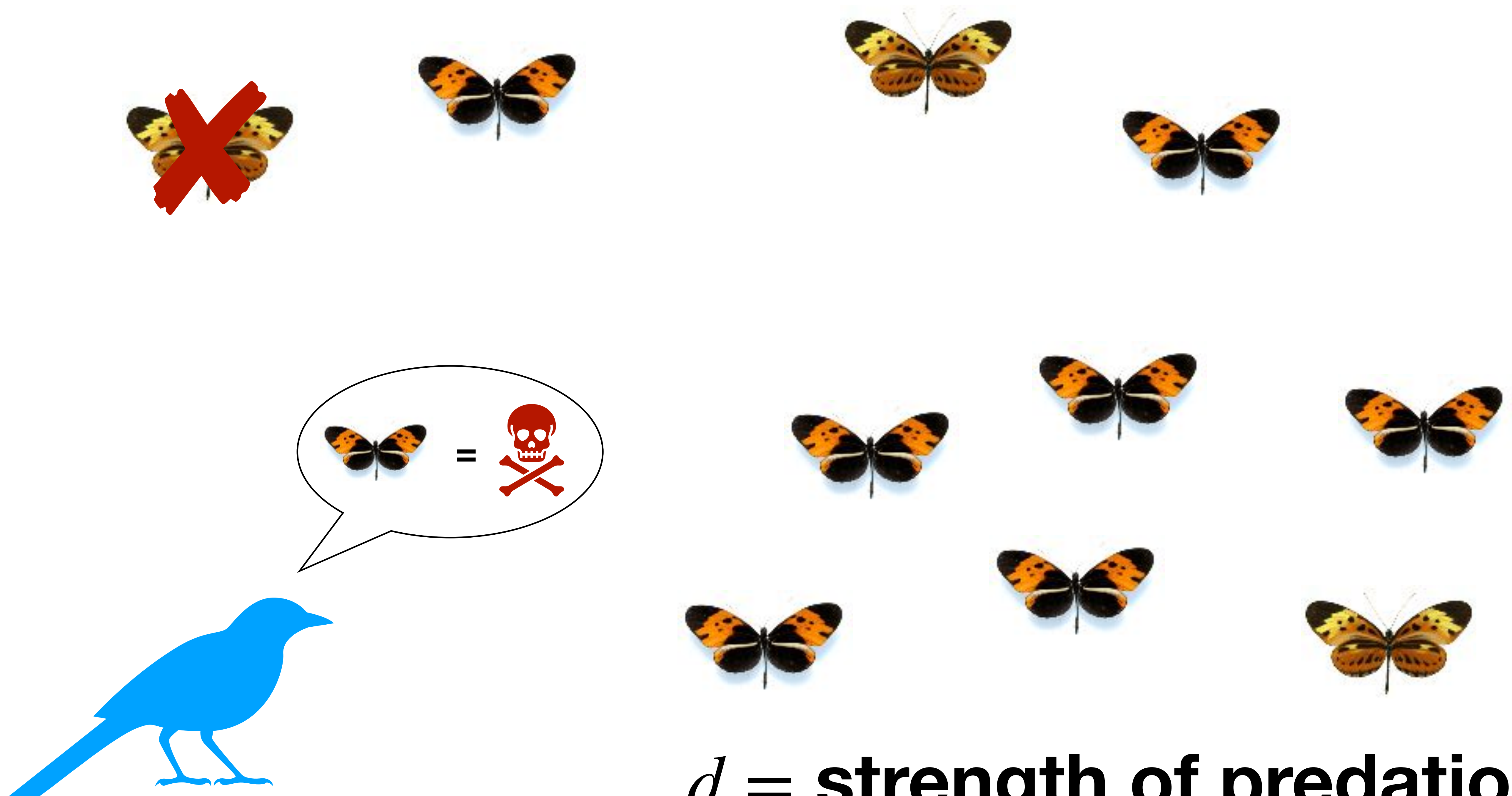
Number dependent selection on color patterns



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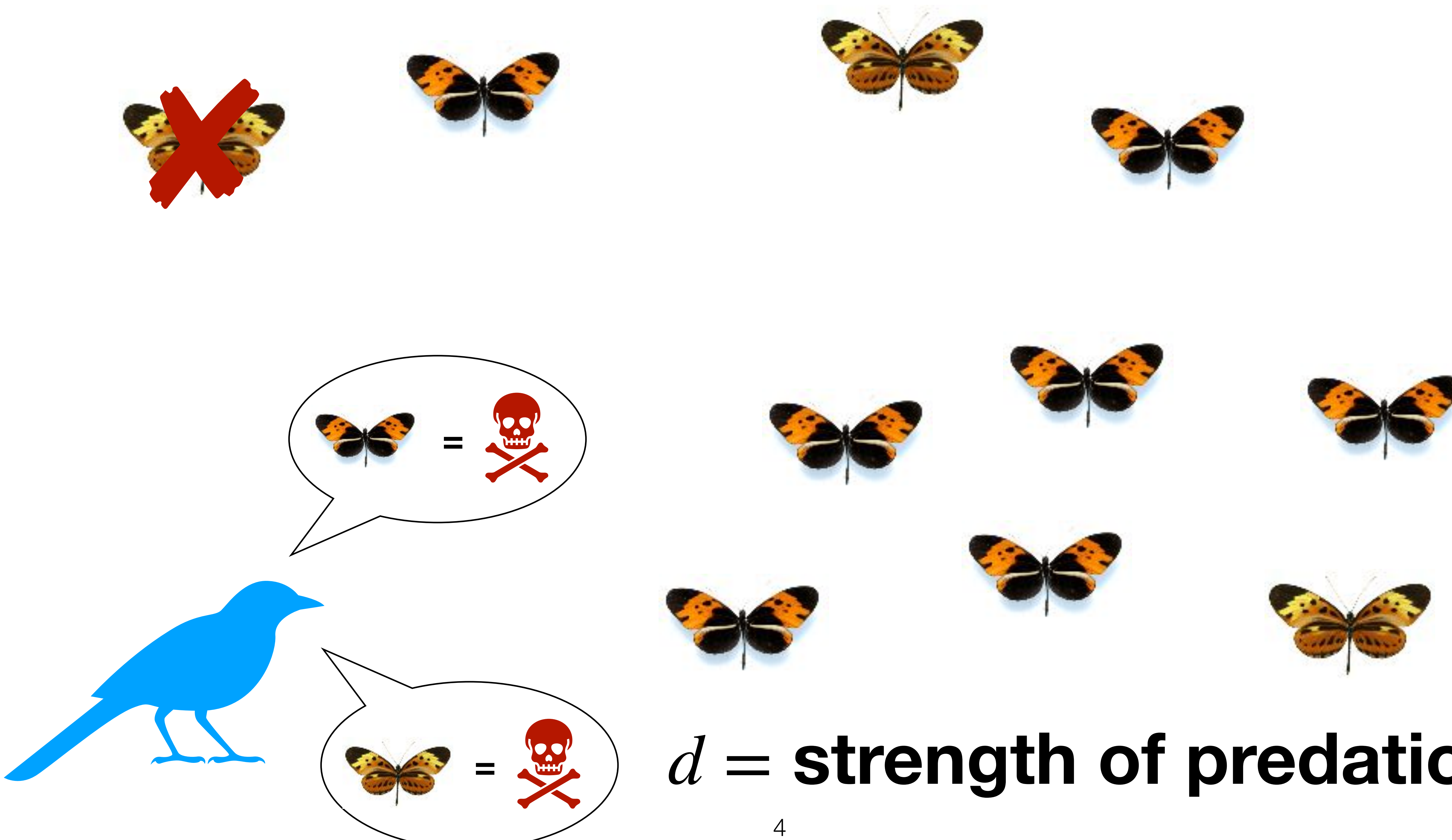
Number dependent selection on color patterns



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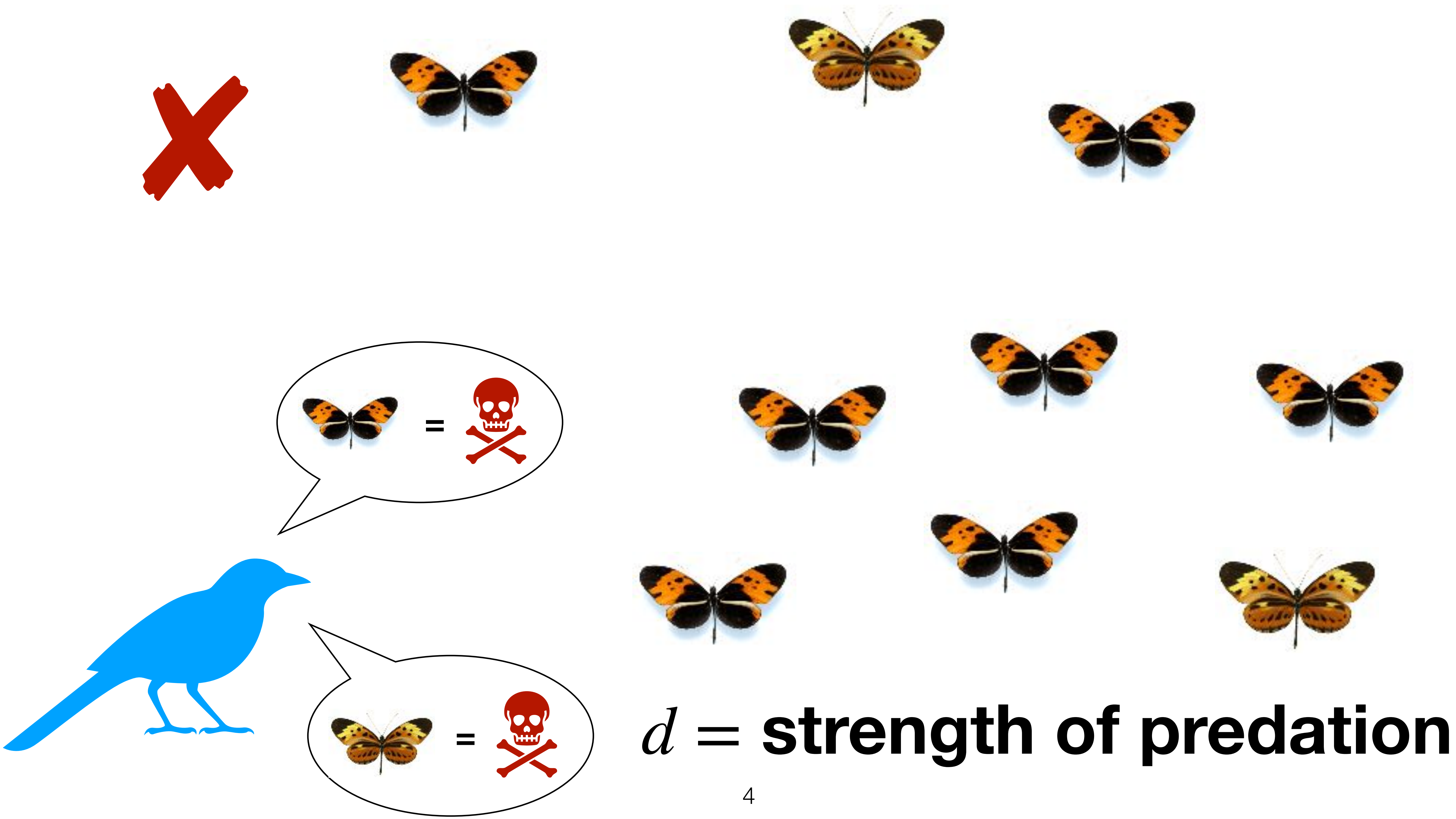
Number dependent selection on color patterns



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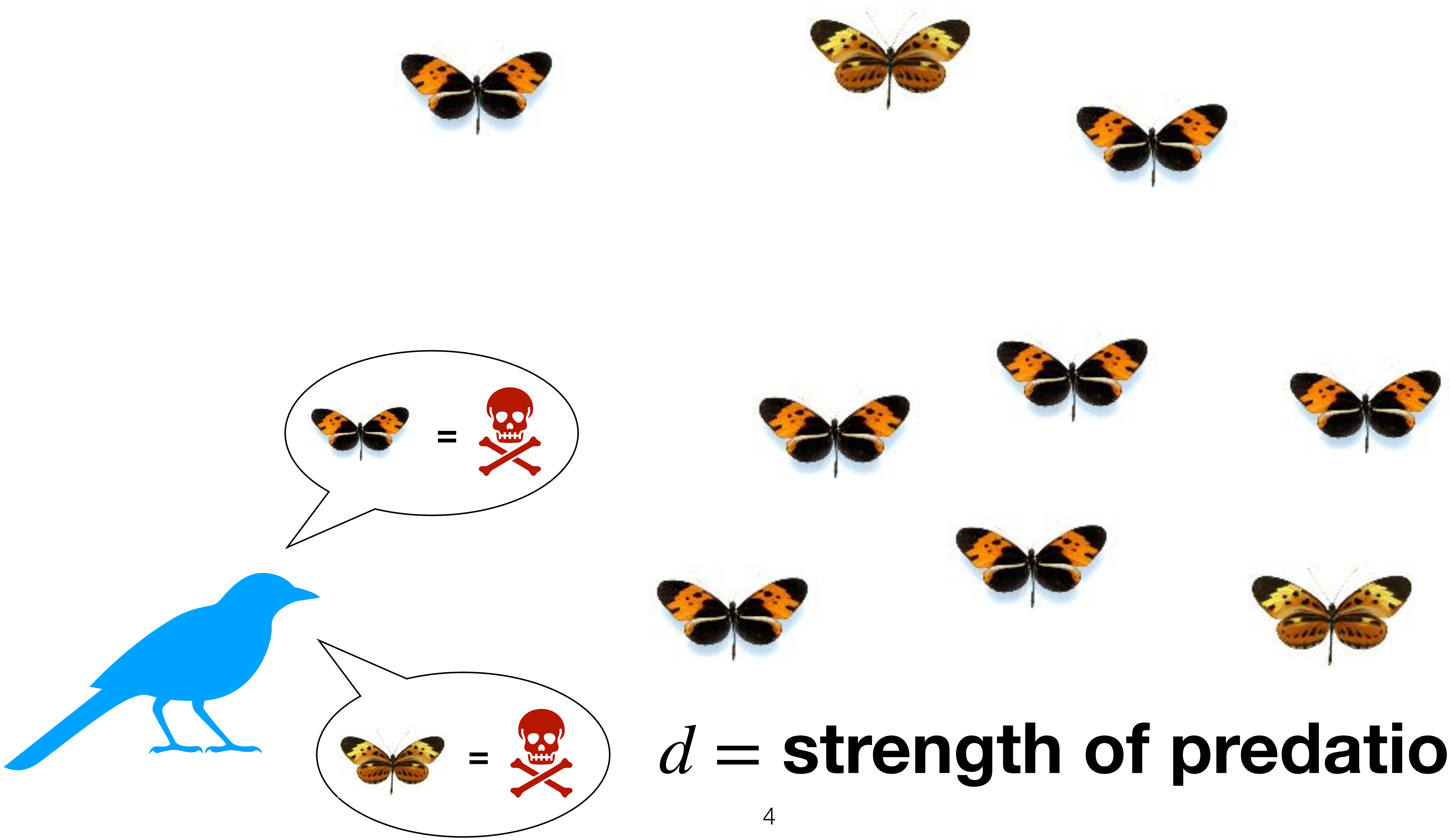
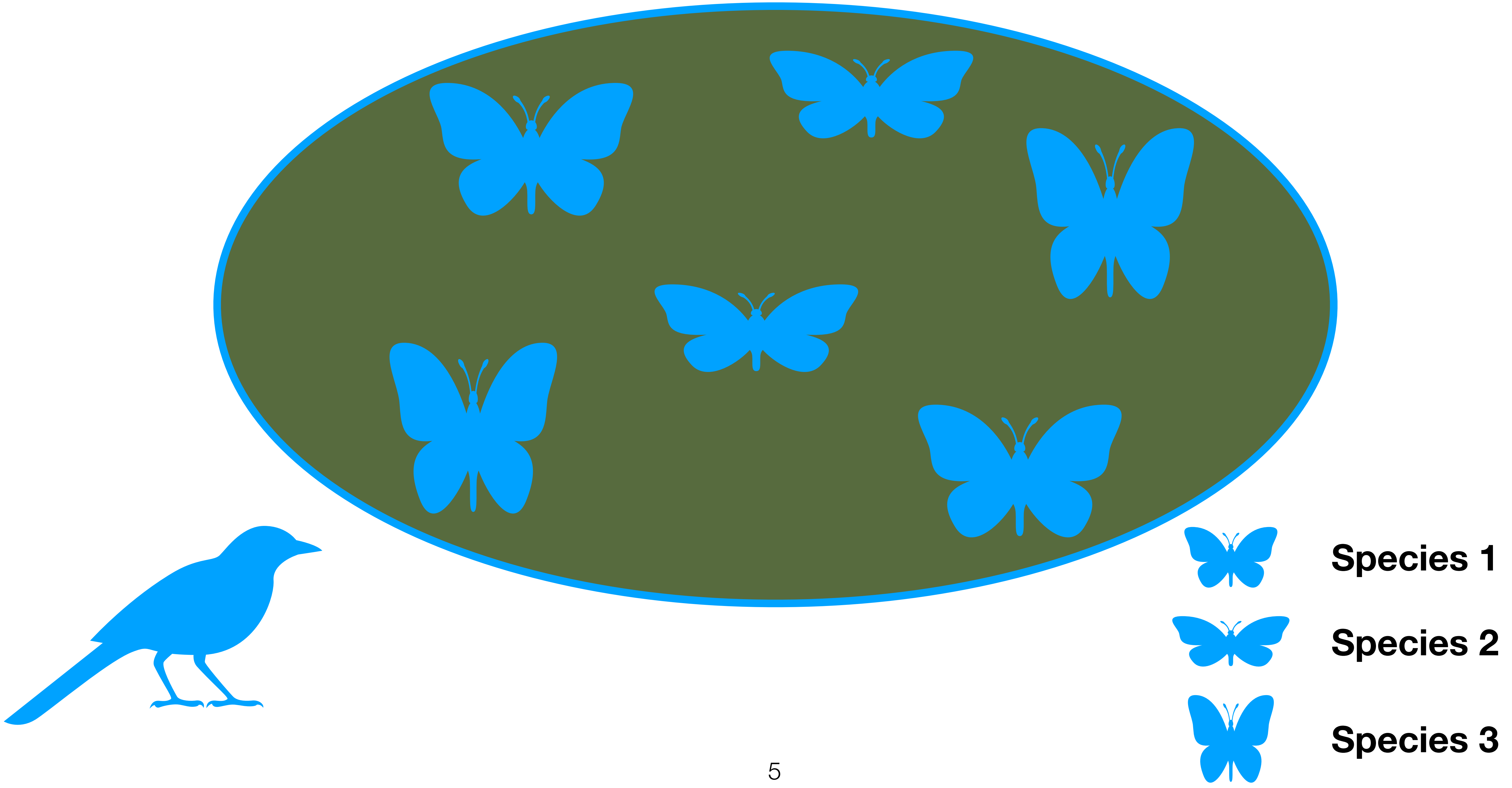
Number dependent selection on color patterns

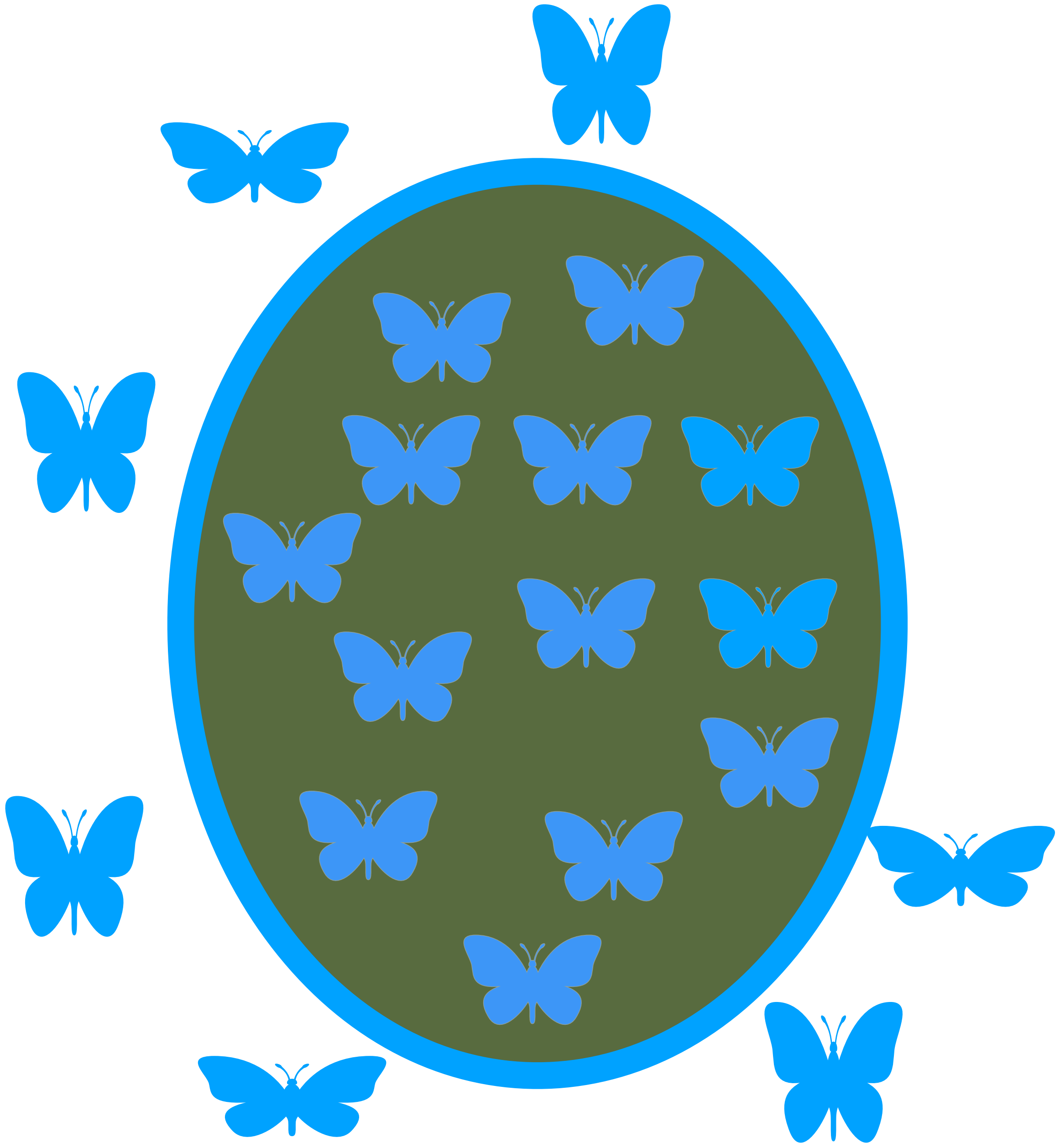


$d =$ **strength of predation**

Evolutionary convergence in mimetic patterns



Migration between mimicry rings allows light polymorphism



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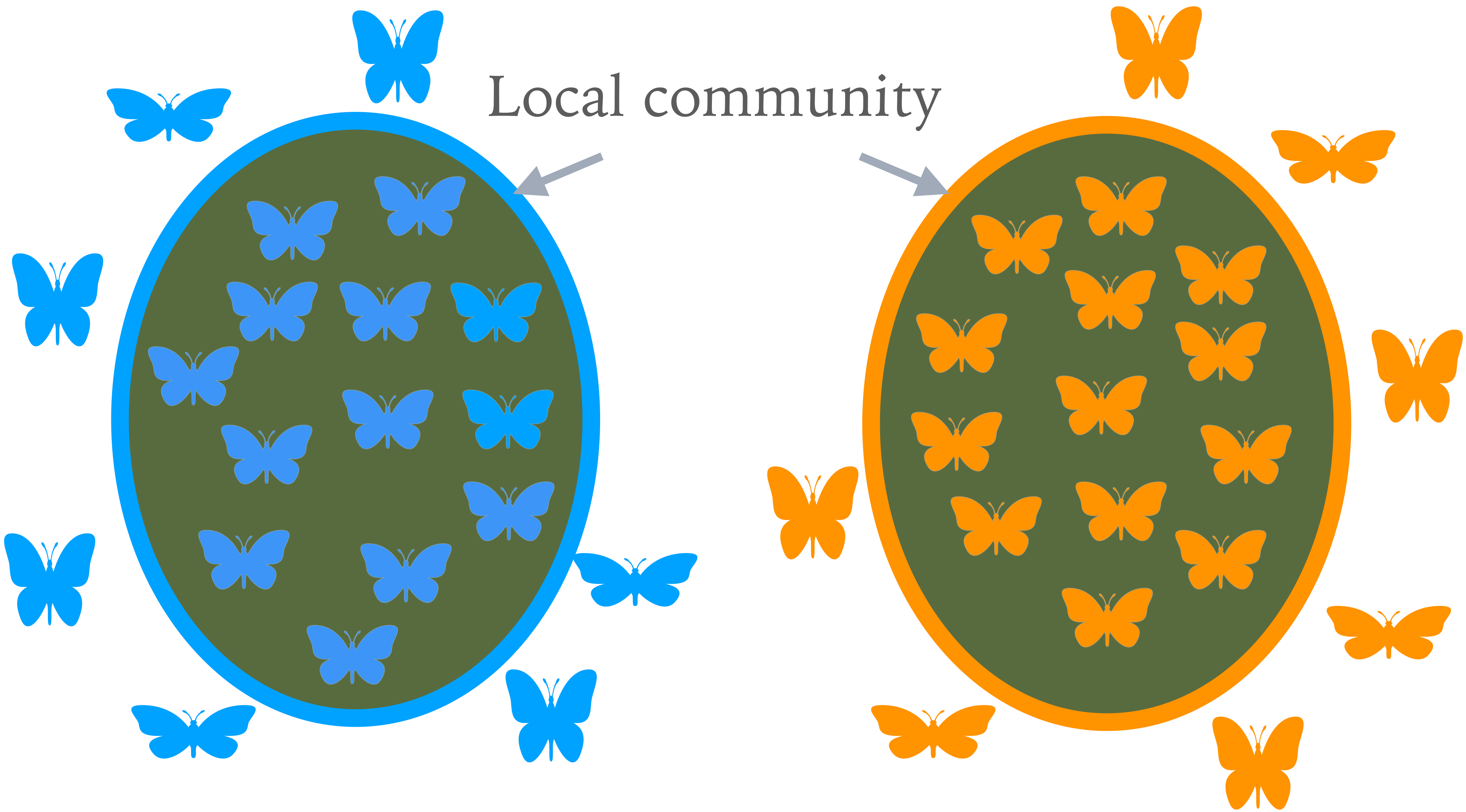

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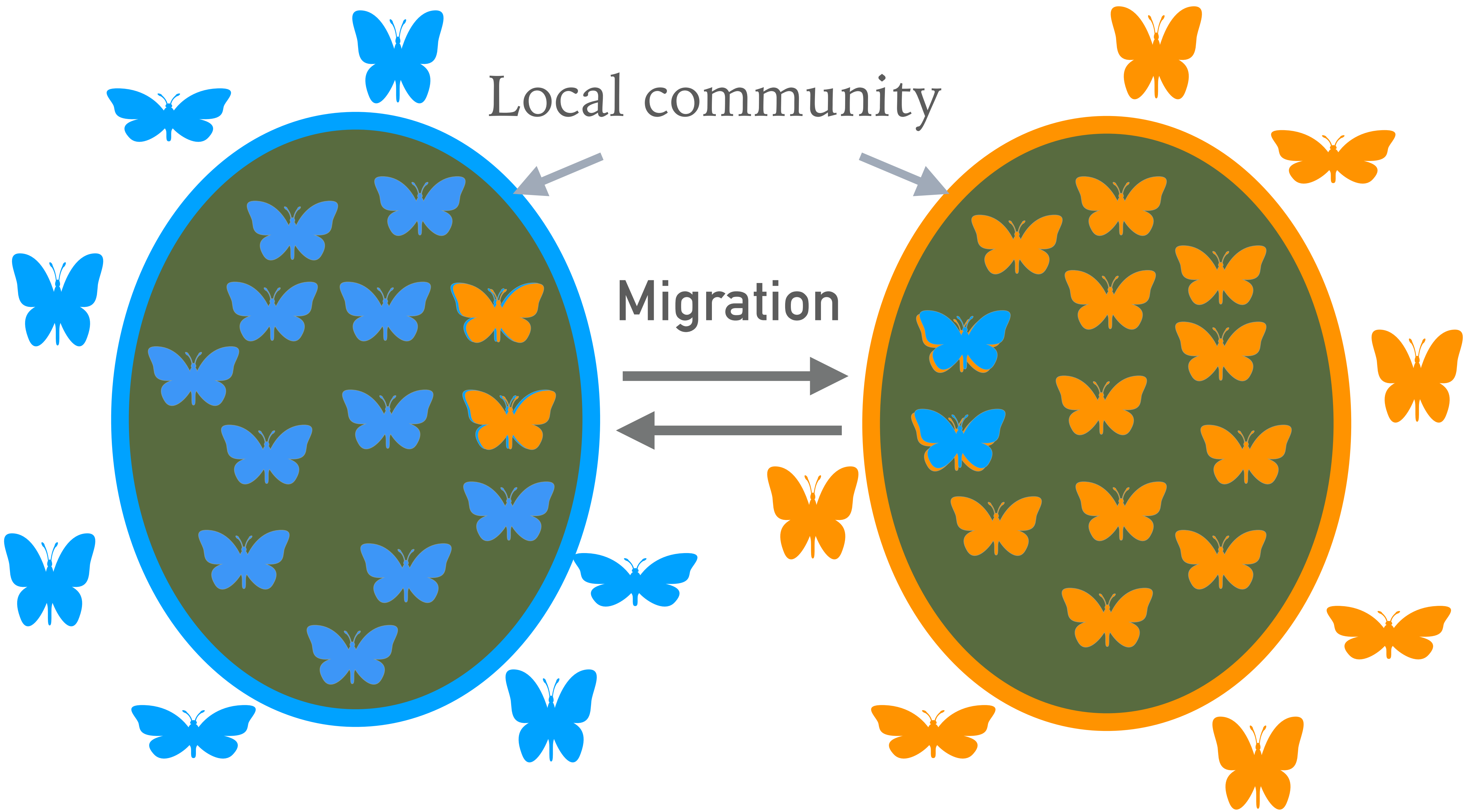

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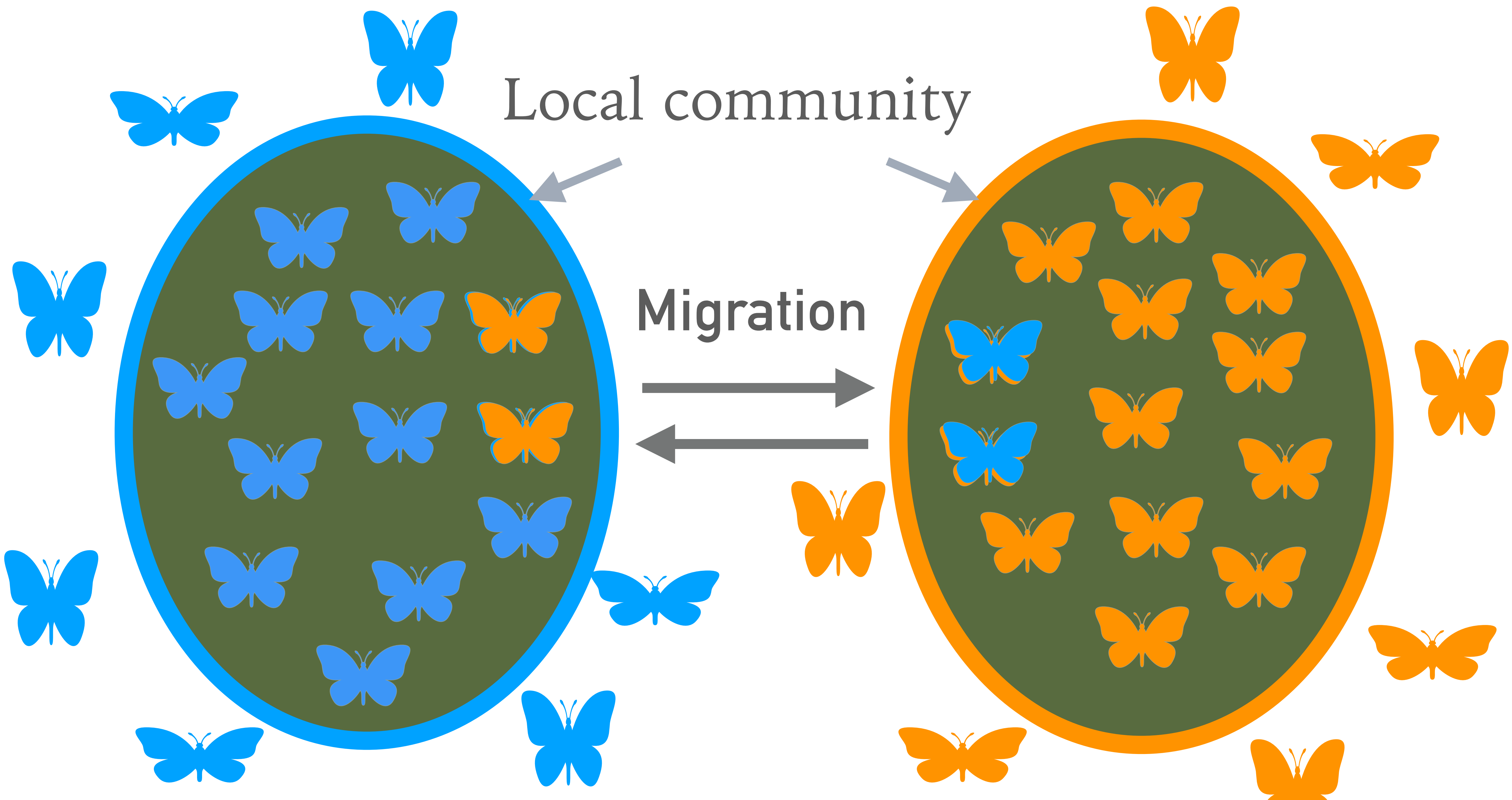
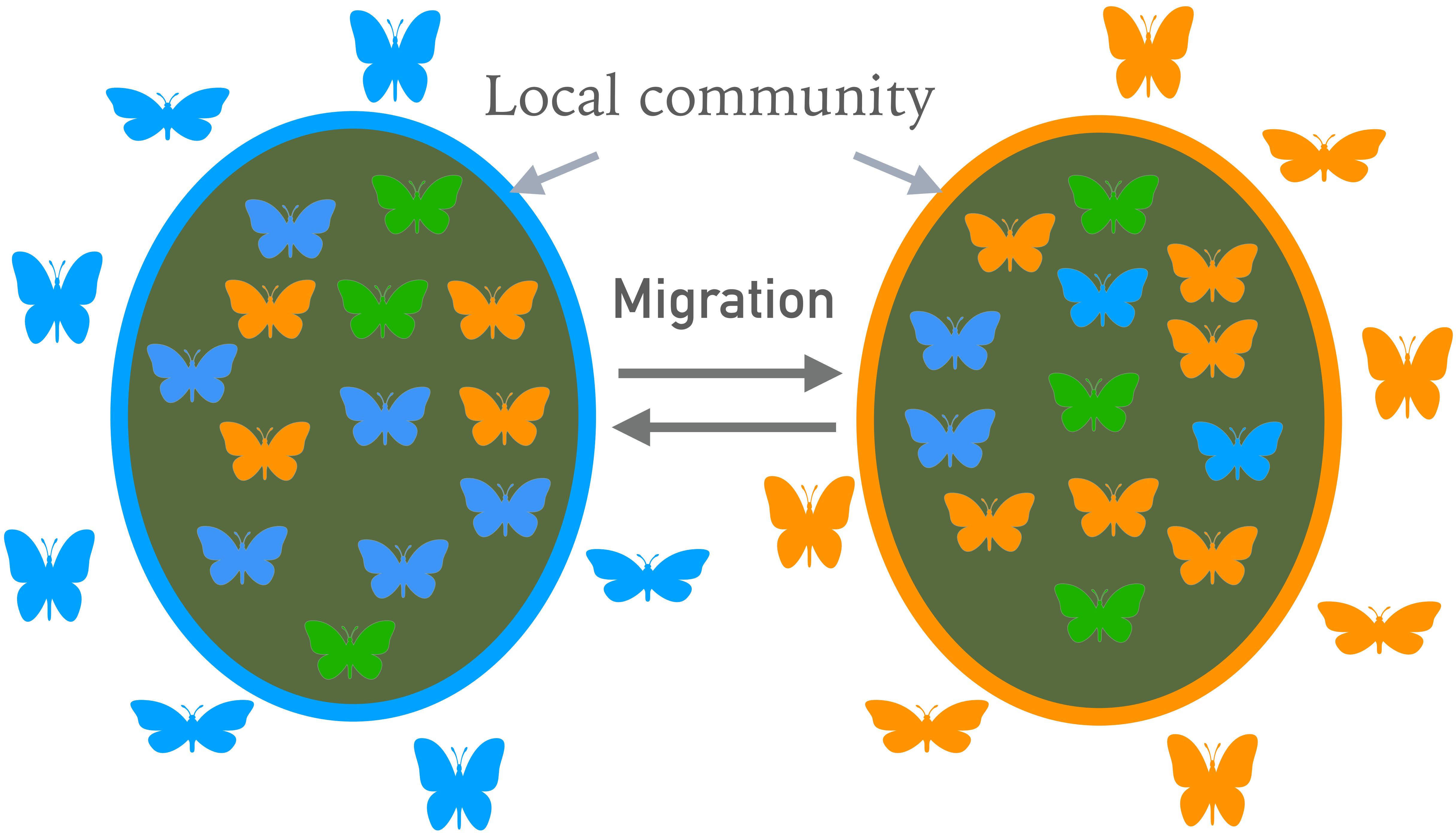
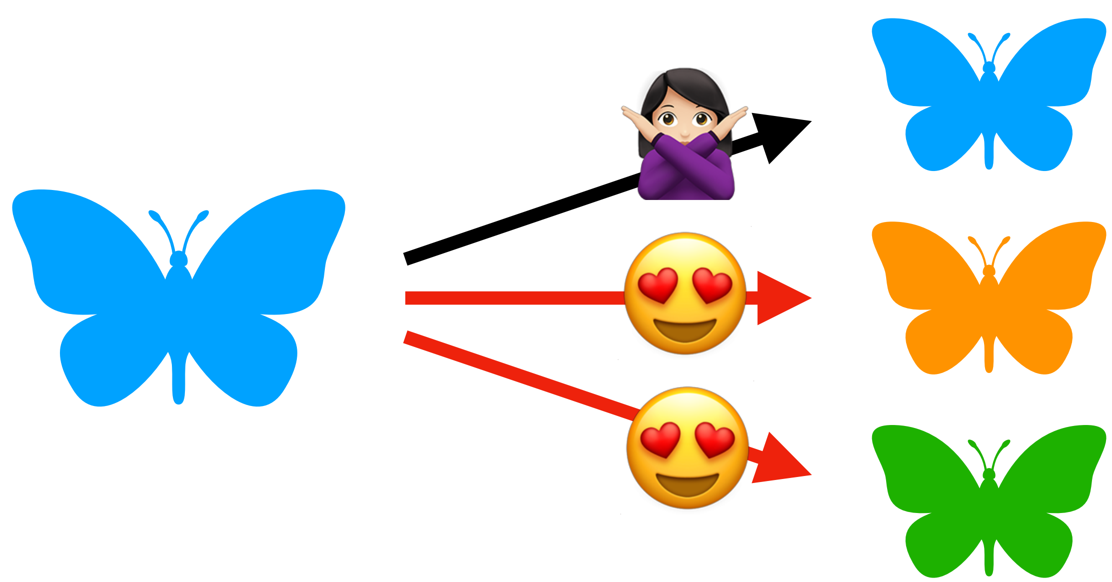


$\sigma =$ **spatial heterogeneity**

A strong polymorphism is observed in *H.numata*

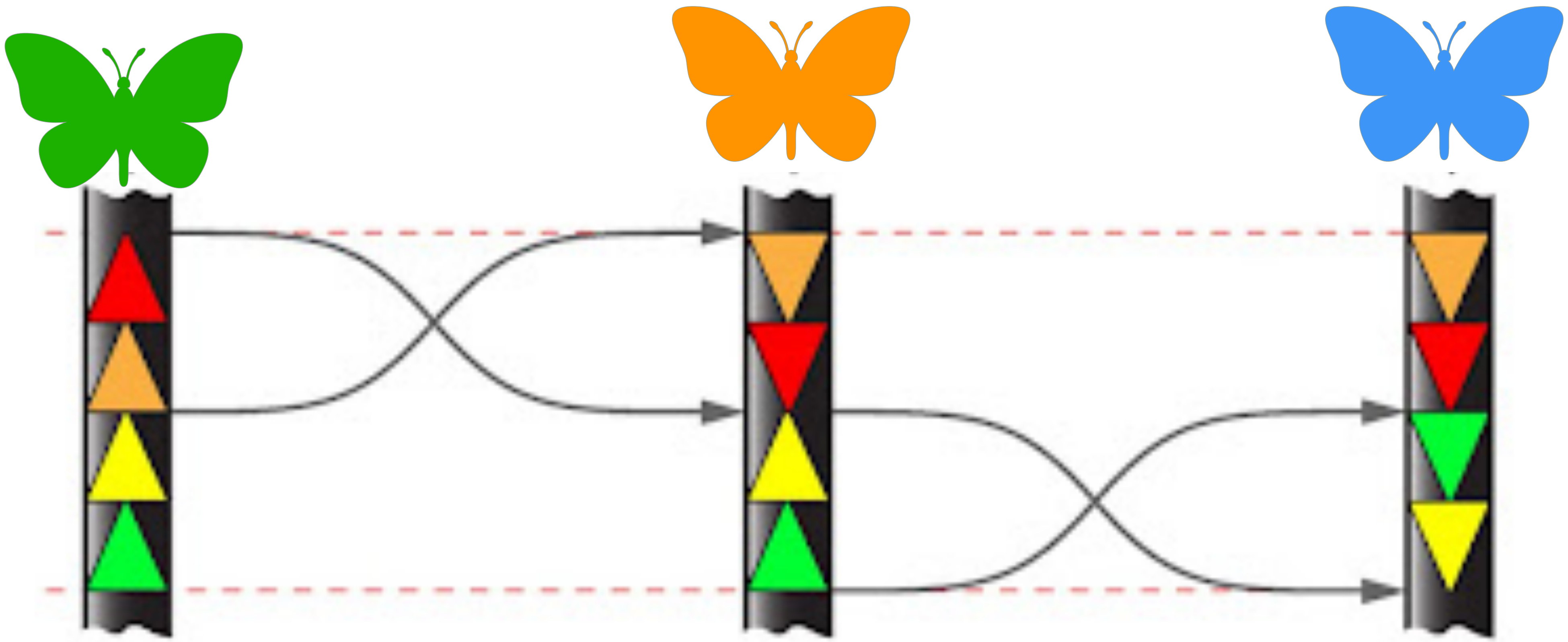


Disassortative mating in *H. Numata* favors polymorphism



- Females avoid males sharing their wing patterns => favors individuals with the rarest phenotype
- Cost of disassortative mating
- How does disassortative mating evolve in *H. numata butterflies ?*

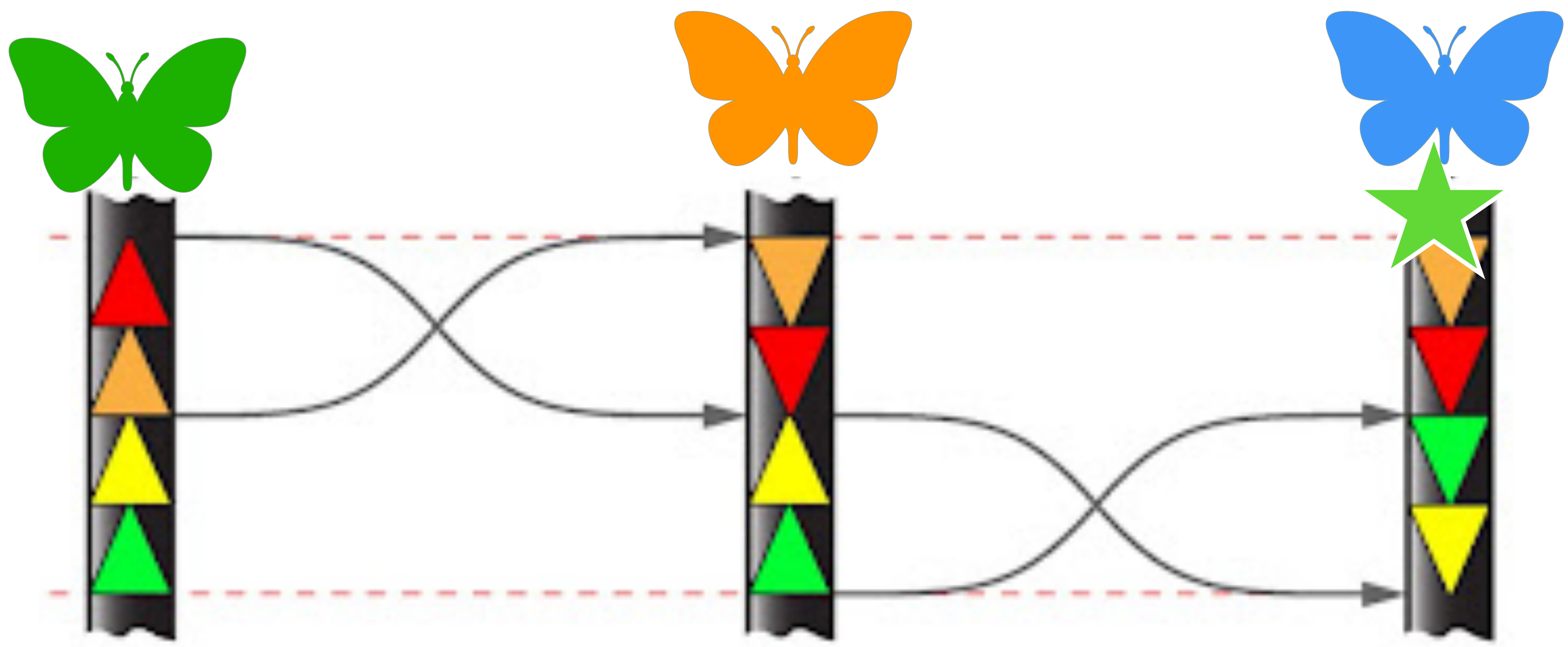
Genetic architecture of wing color pattern variations



Joron et al. 2011

- A single locus controlling wing pattern variations
- Chromosomal inversions => accumulation of deleterious mutations
- Genetic load linked to inverted haplotypes

Genetic architecture of wing color pattern variations



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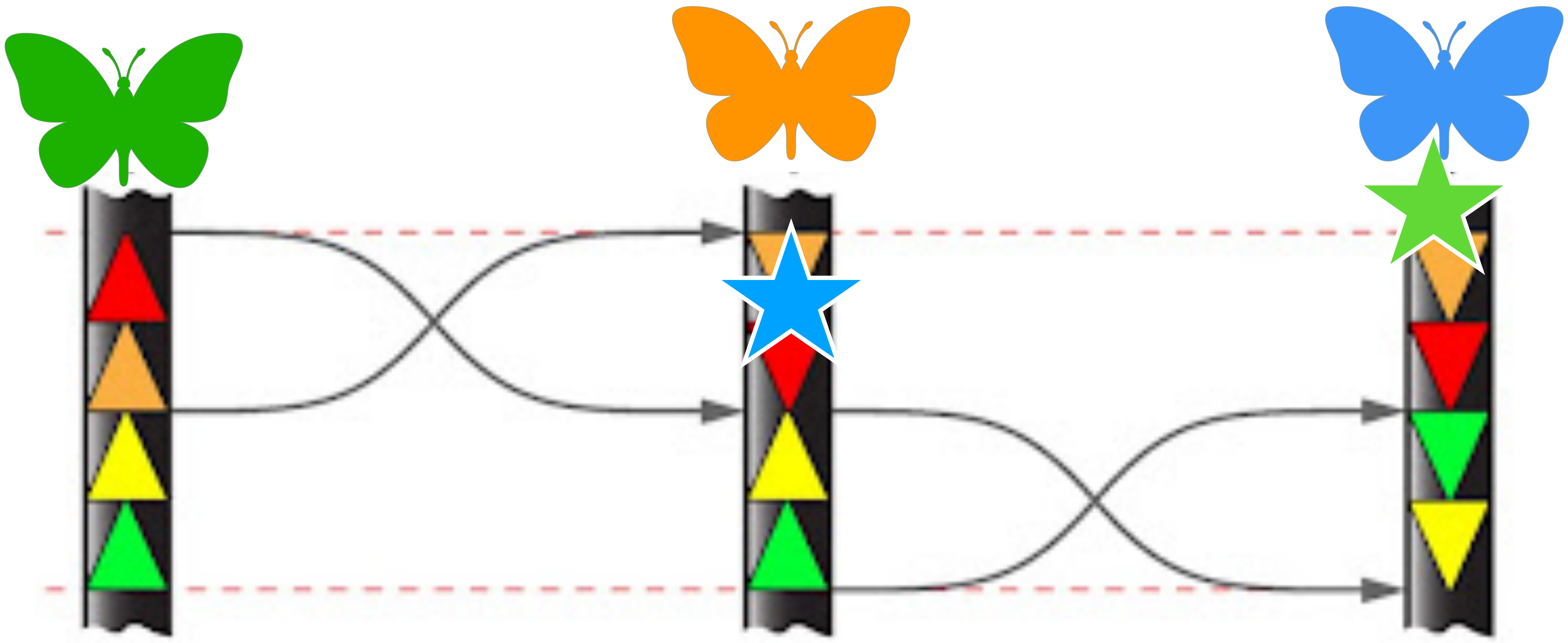

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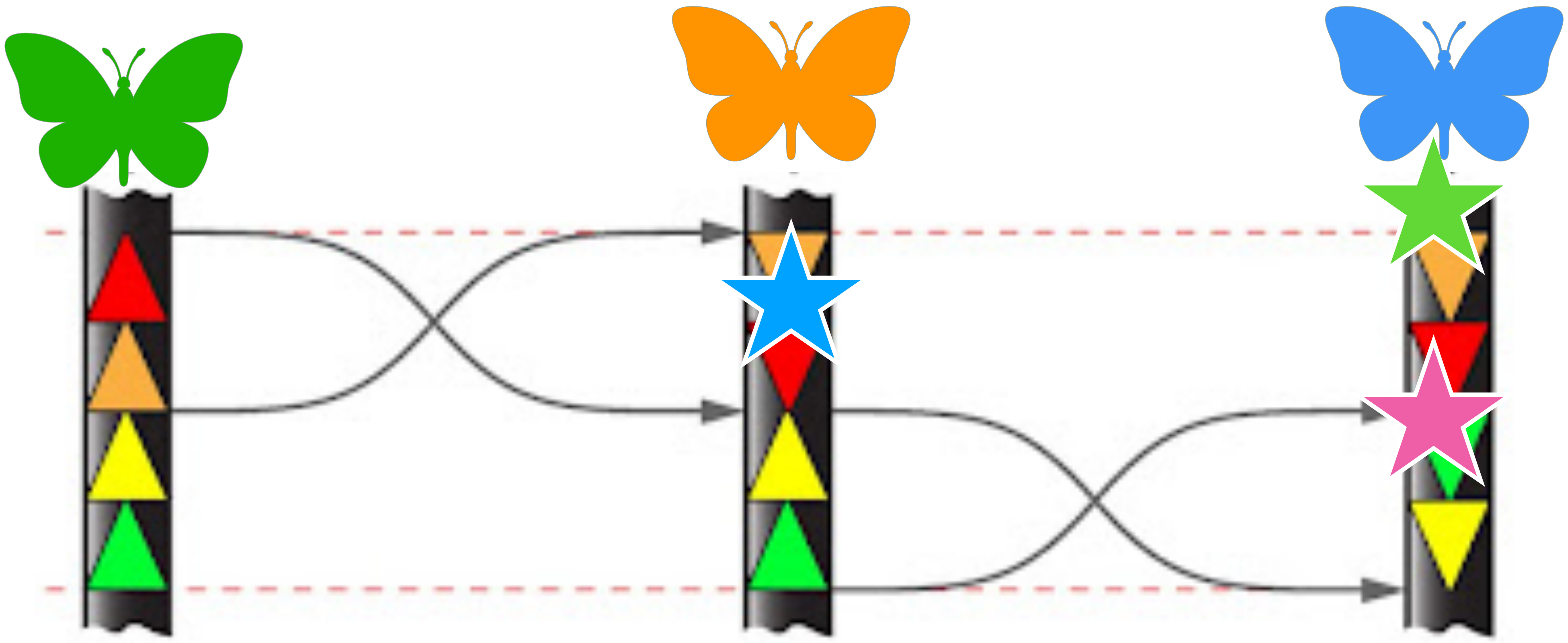

Joron et al. 2011

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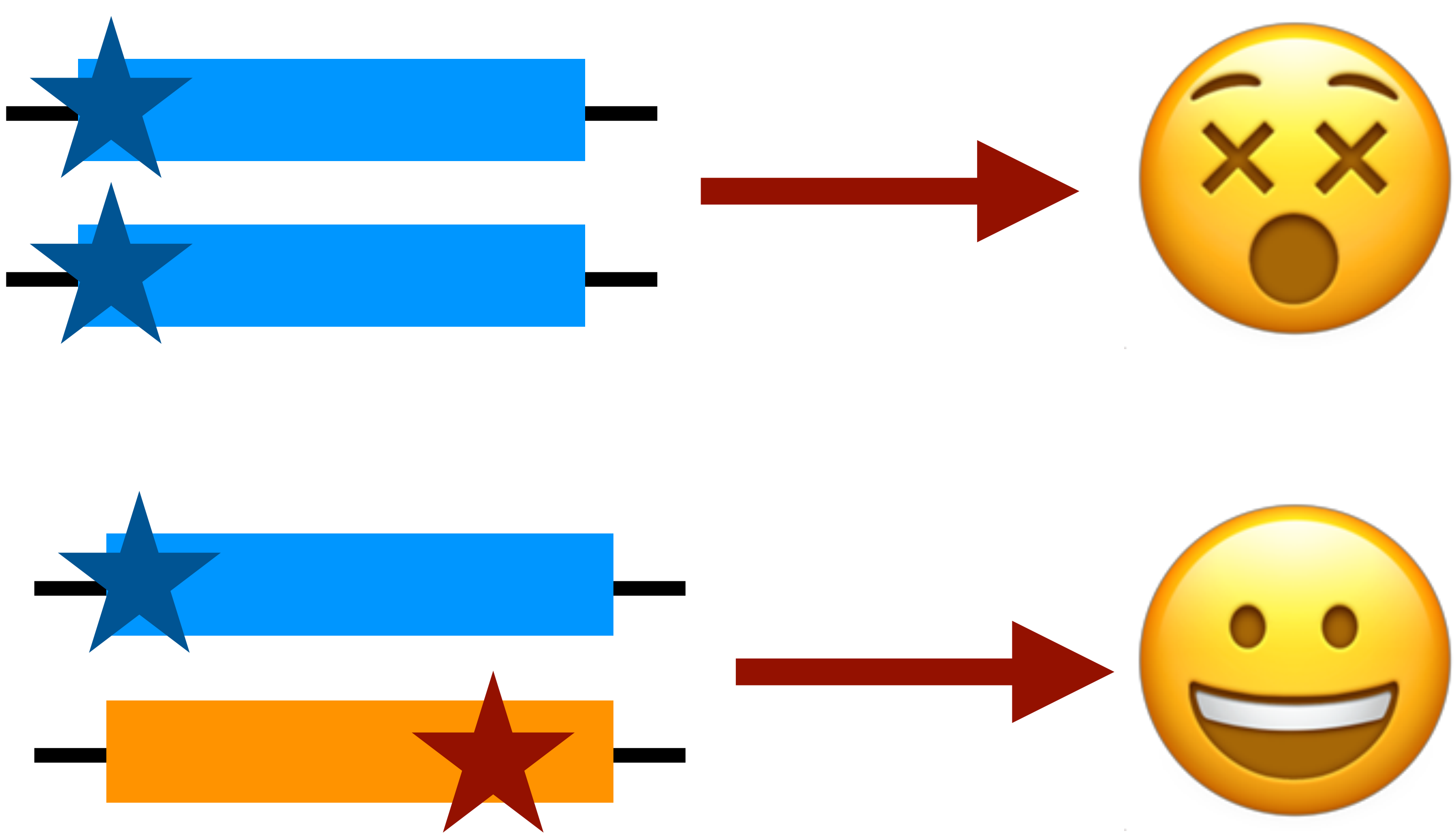
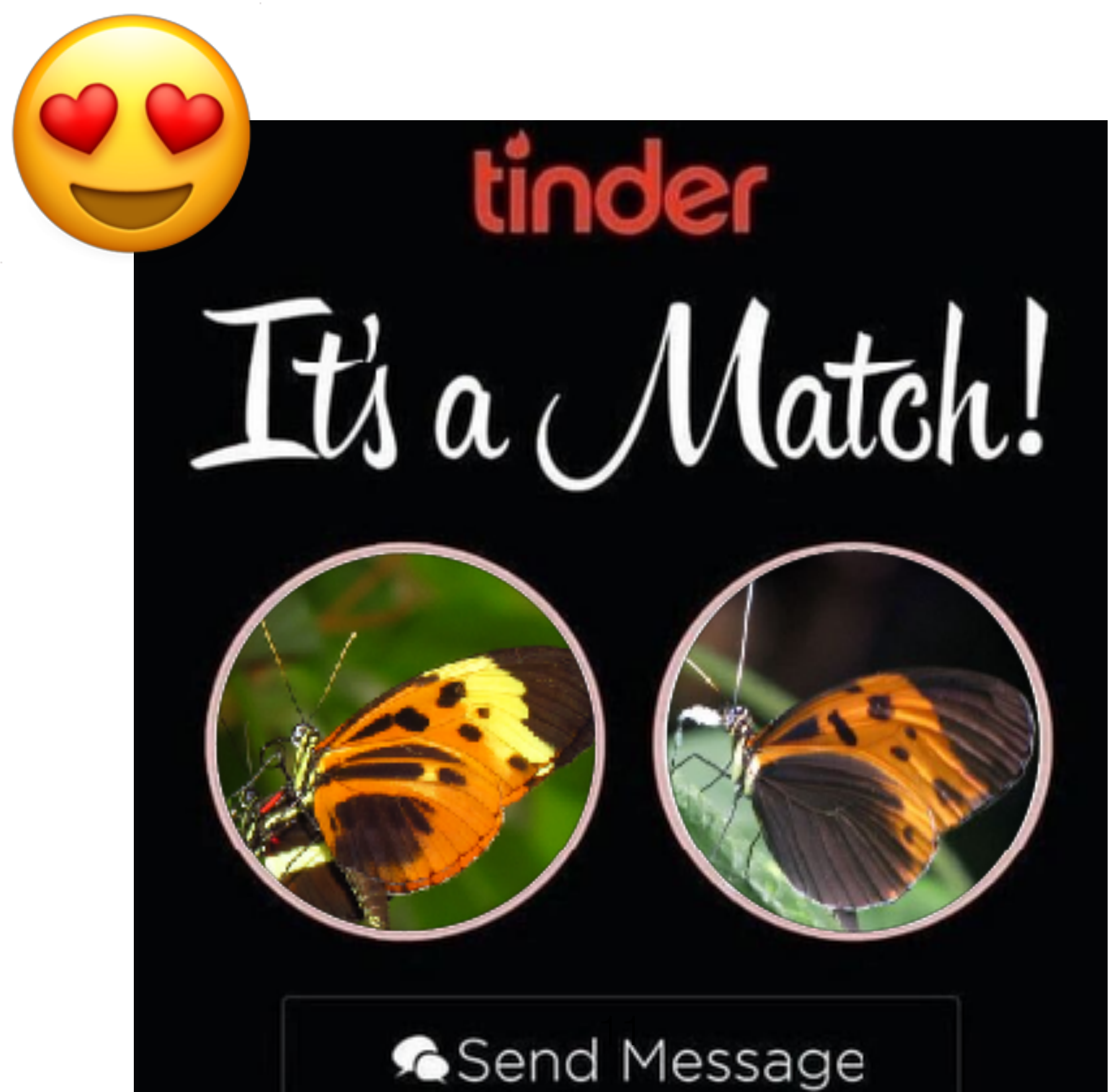
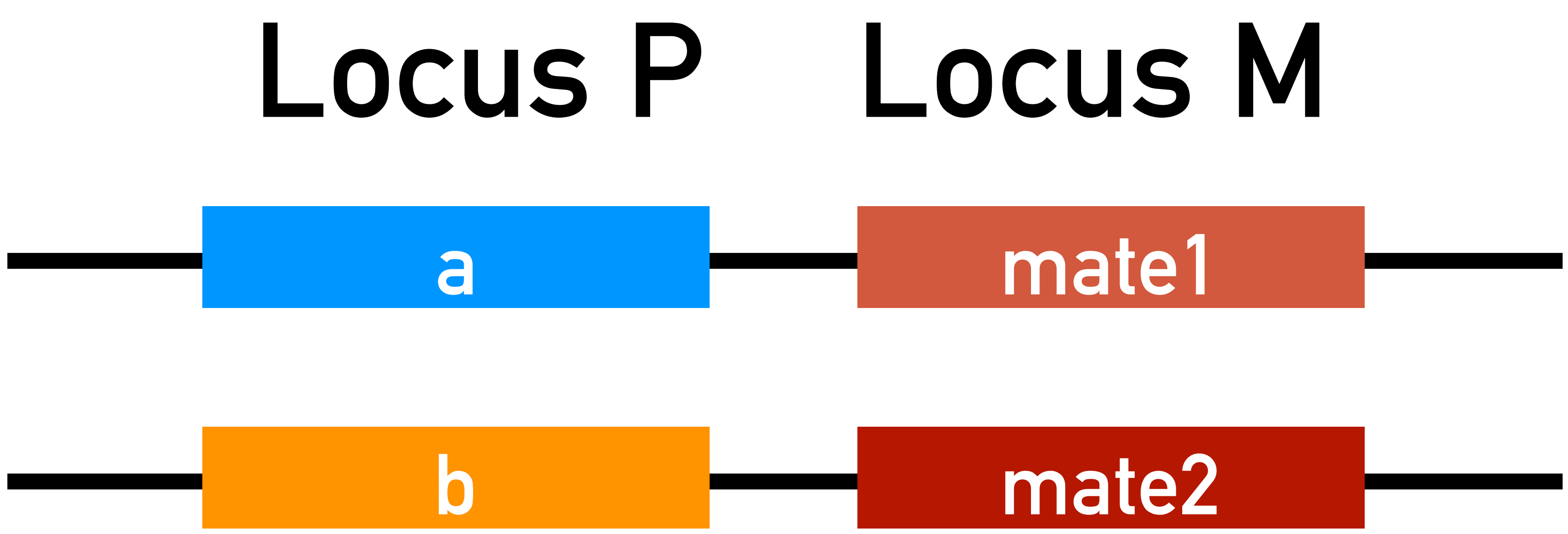
Heterozygote advantage at the color pattern supergene ?

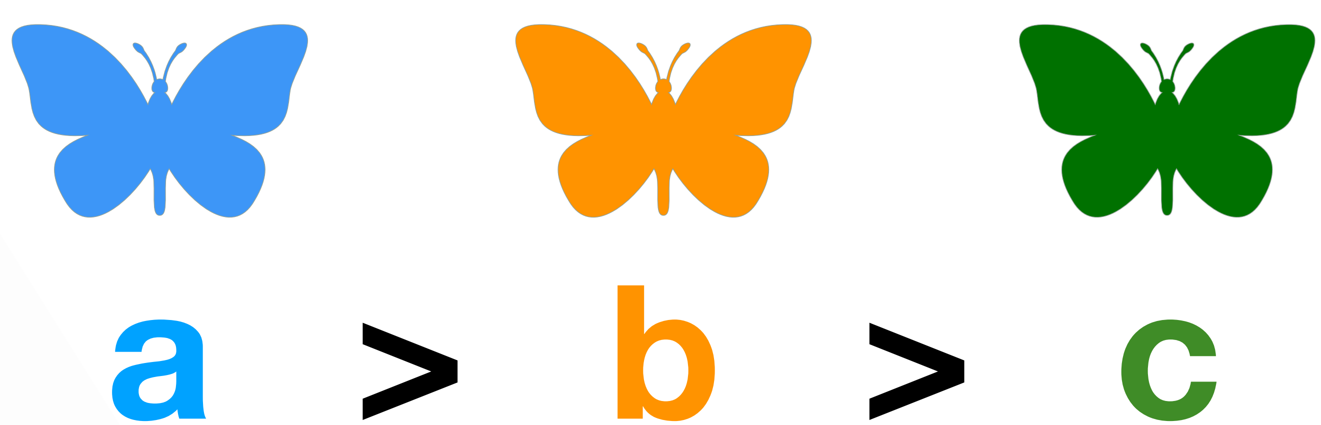


Could a genetic load linked to the locus promote disassortative mating ?

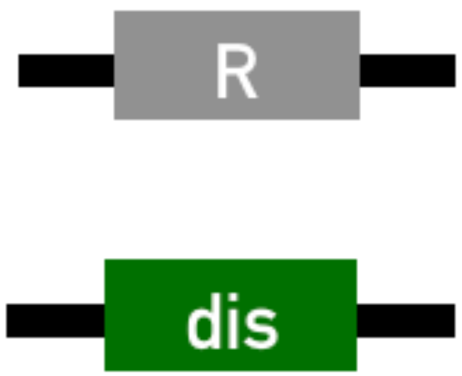


Genetic architecture





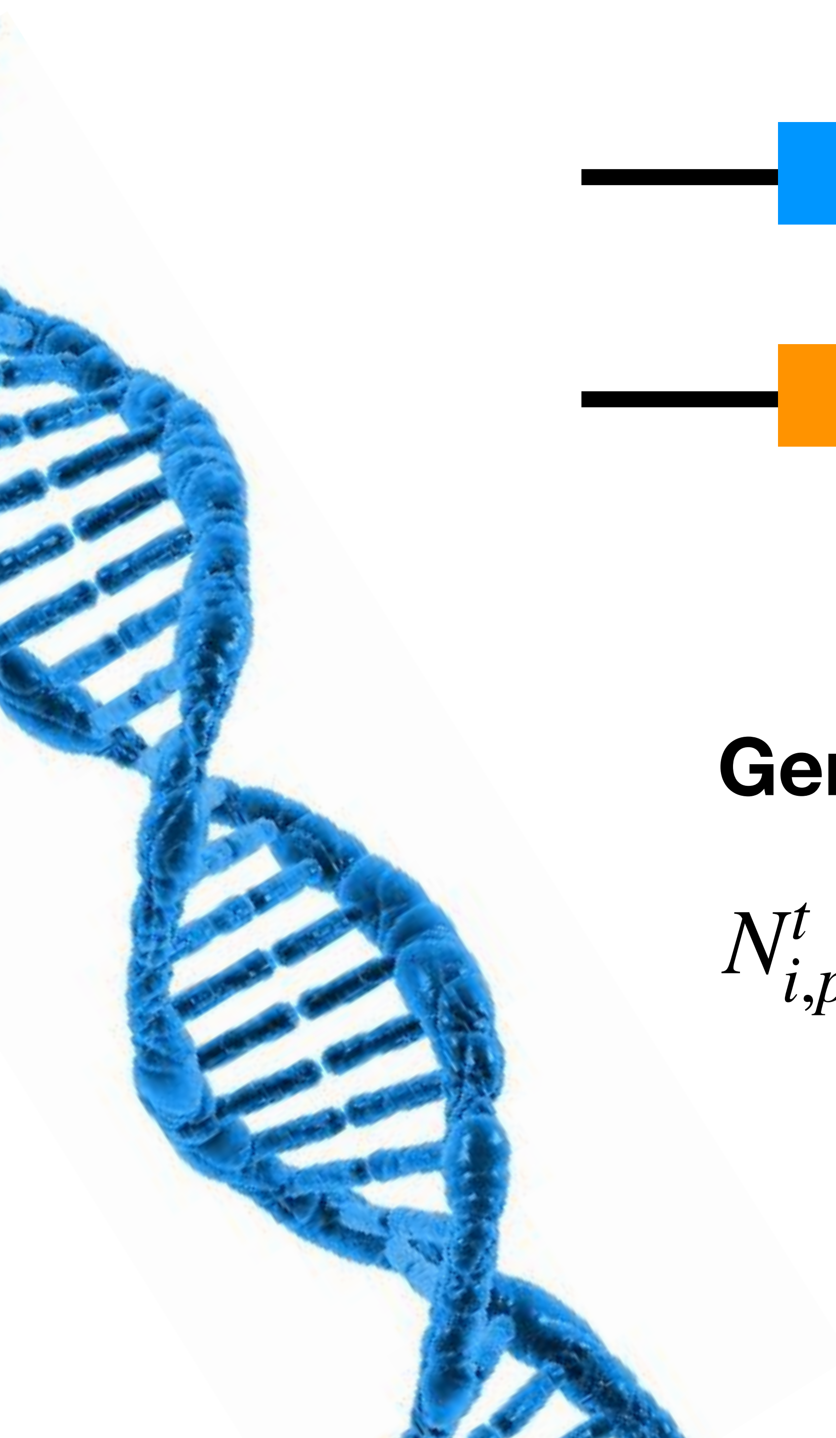
Reproduction : genetic architecture of preference

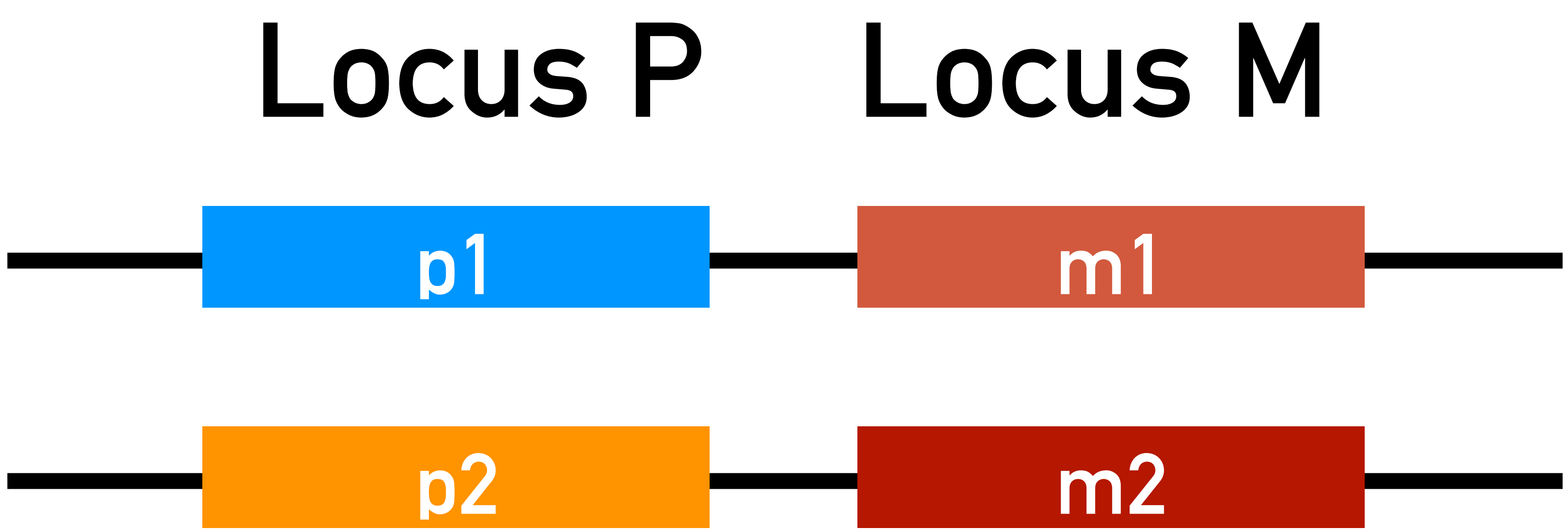


Random mating

Disassortative mating

Genetic architecture

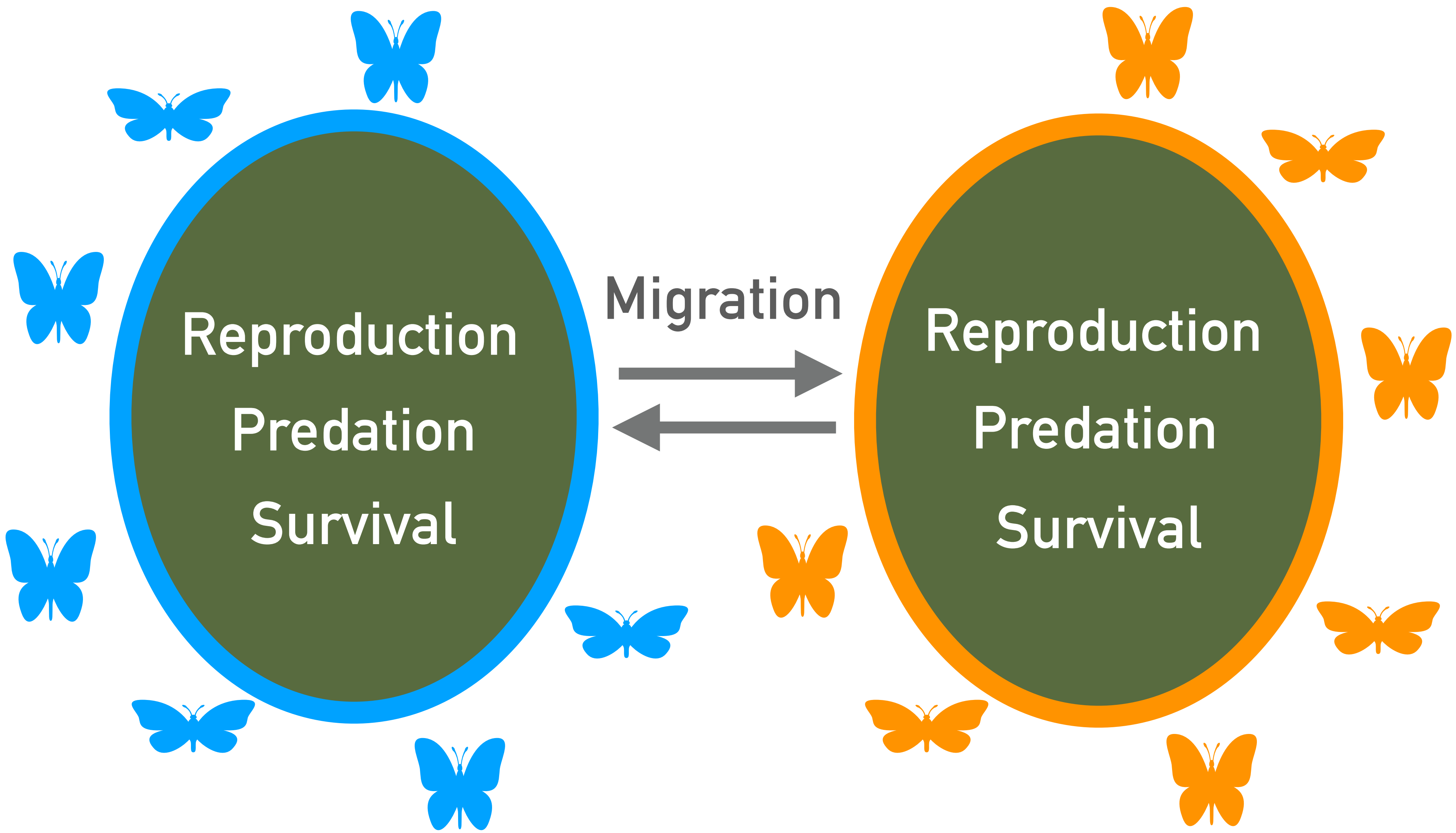




Genotype : $i = (p_1, p_2, m_1, m_2)$

$N^t_{i,pop}$ = number of individual with the genotype i in the population pop at time t

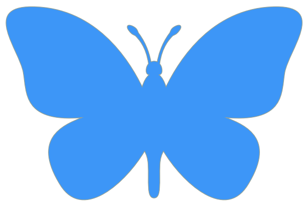
Discrete time model



$$N_{i,pop}^{t+1} = N_{i,pop}^{t} + \Delta M_{i,pop}^{t} + \Delta P_{i,pop}^{t} + \Delta R_{i,pop}^{t} + \Delta S_{i,pop}^{t}$$

Migration Predation Reproduction Survival

Predation : selection on wing color pattern

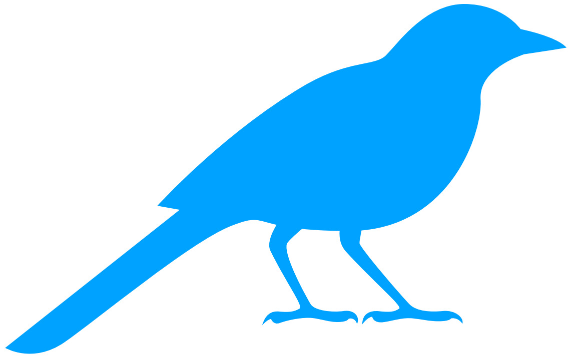


- Predation

Ressemblance to the local community

$$\Delta P^{t}_{i,pop} = -\frac{d[(1+\sigma)(1-Res_{[i],[pop]})+(1-\sigma)Res_{[i],[pop]}]}{1+\lambda(\sum_{j} Res_{[i],[j]})N^{t}_{j,pop}} N^{t}_{i,pop}$$

Number dependent selection within species



Reproduction : The cost of choosiness

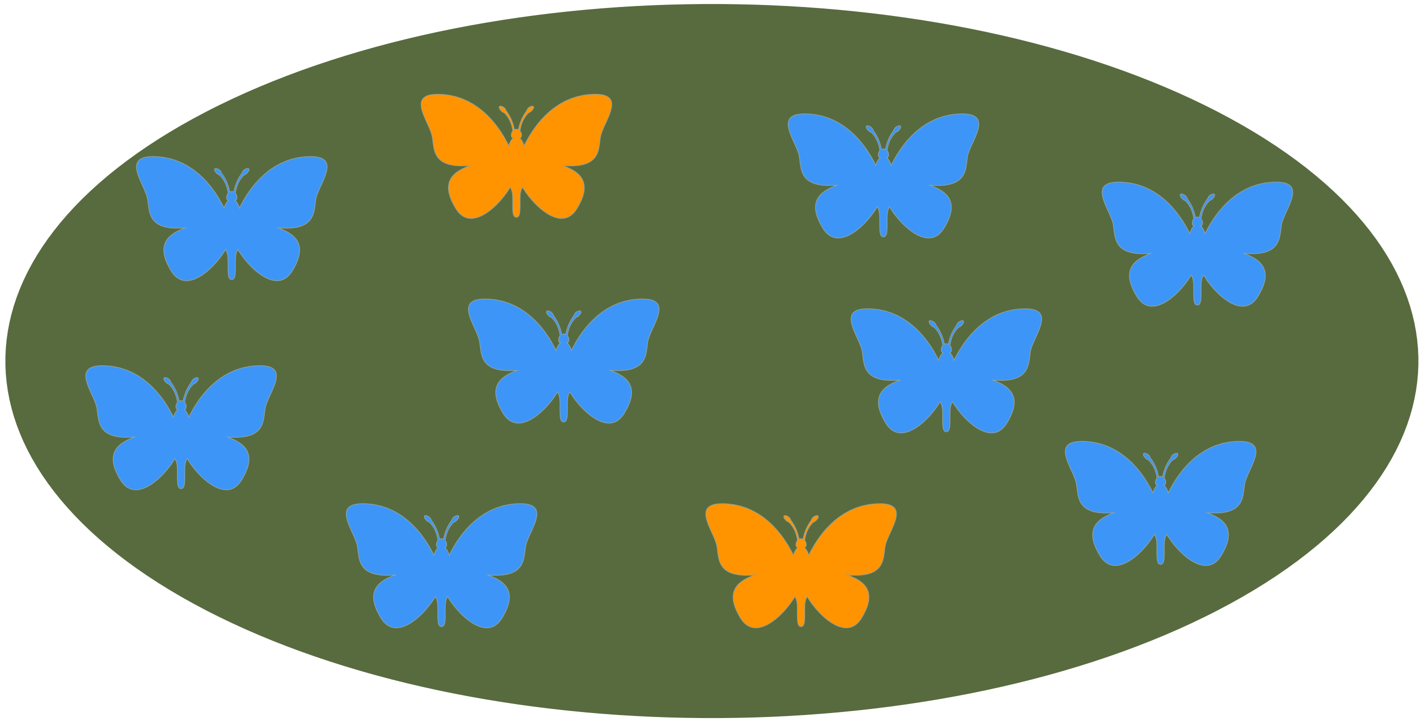
$Pref_{i,P} = 0$ If individuals with i genotype **reject** individuals displaying phenotype P as mate.

$Pref_{i,P} = 1$ If individuals with i genotype **accept** individuals displaying phenotype P as mate.

Fertility: $f_i = Pref_{i,A}P_A + Pref_{i,B}P_B + Pref_{i,C}P_C$

$$f_{b,b,dis,dis} = 0.2$$

$$f_{b,b,rand,rand} = 1$$



Reproduction : mate choice affects the number of available partners

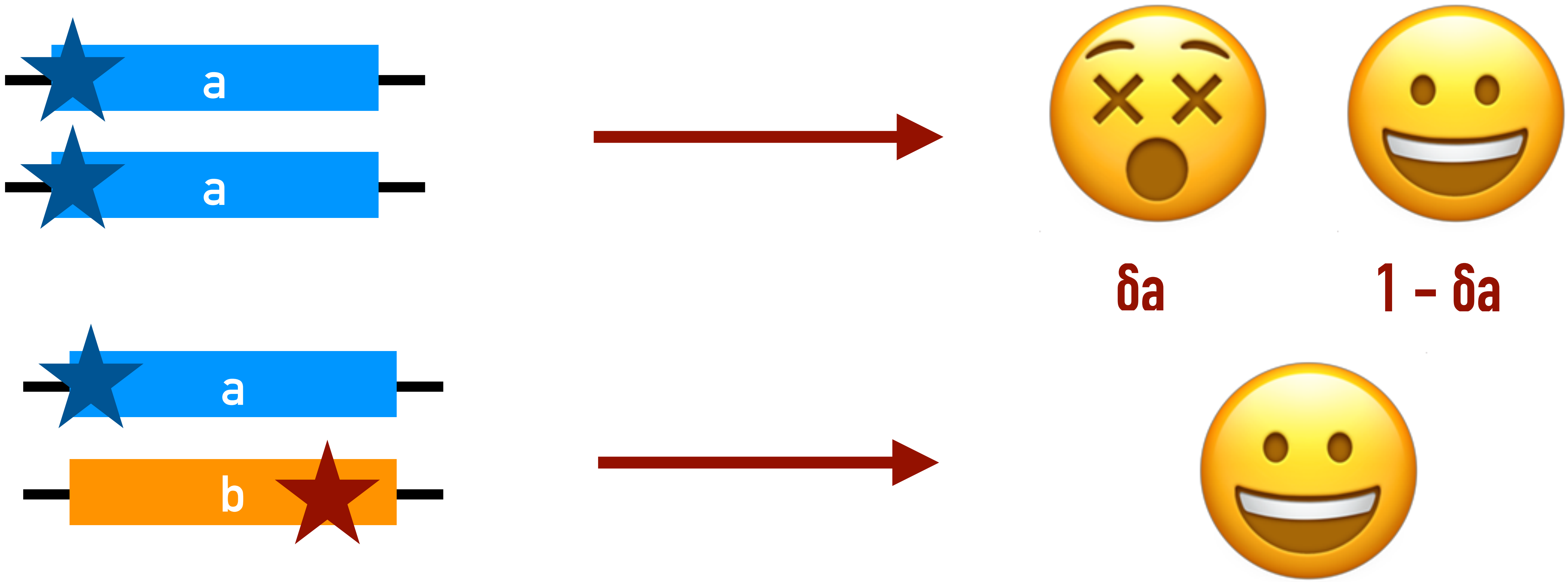
Cost of choosiness

$$F_{i,pop}^{t+1} = \sum_{j,k} coef(j,k,\rho)\frac{1 - cost + cost f_j}{f_j} Pref_{j[k]} \frac{f_{j,pop}^{t}}{2}\frac{f_{k,pop}^{t}}{2}$$

$$f_{i,pop}^{t+1} = \frac{F_{i,pop}^{t+1}}{\sum_j F_{j,pop}^{t+1}}$$ **genetic distribution among newborns.**

$$\Delta R_{i,pop}^{t} = r(1 - \frac{N_{tot,pop}^{t}}{K})N_{i,pop}^{t} f_{i,pop}^{t+1}$$

Survival : heterozygote advantage at locus P



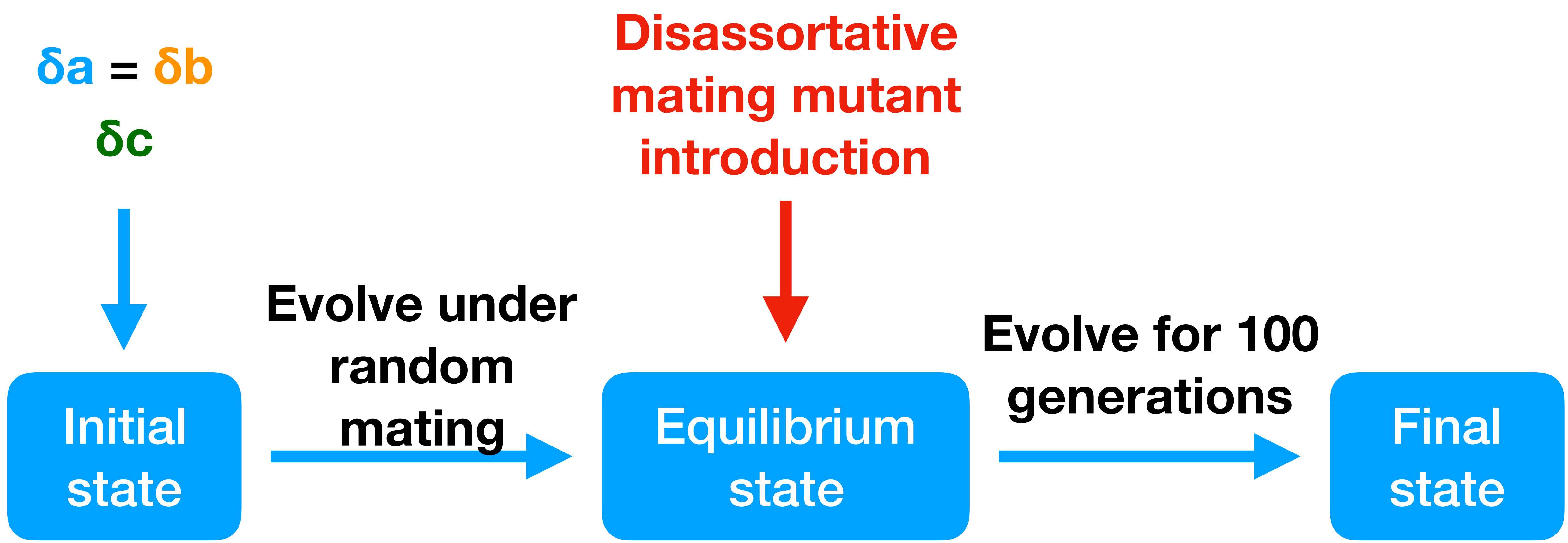
δi = strength of the genetic load for allele i

★ ★ **Recessive deleterious mutations**

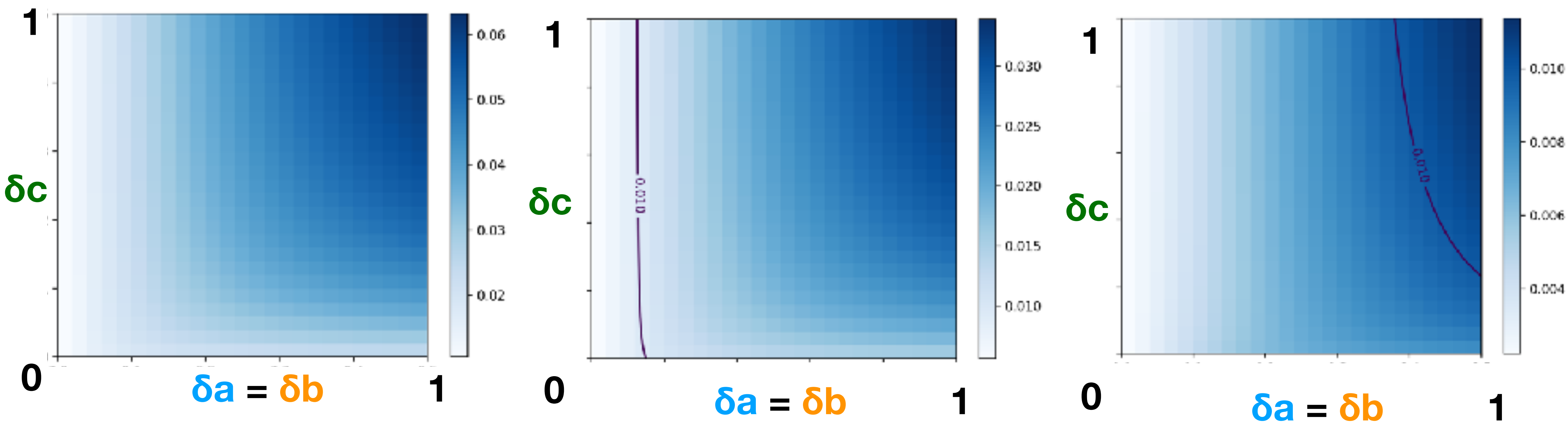
Simulations

δ cost of genetic load :

- δa and δb associated with mimetic alleles
- δc associated with non-mimetic allele



Genetic loads impact on mate choice evolution



cost = 0

cost = 0.1

cost = 0.25

δ cost of genetic load :

- **δa and δb associated with dominant alleles**
- **δc associated with recessive allele**

Literature shows no evidence for self-referencing rules

- Evidence for preference/trait mechanism in *H. melpomene*

Mr — **No preference**

Ma — **Preference for morph A**

Mb — **Preference for morph B**

Mc — **Preference for morph C**

Dominance relationship:

Mr < Ma

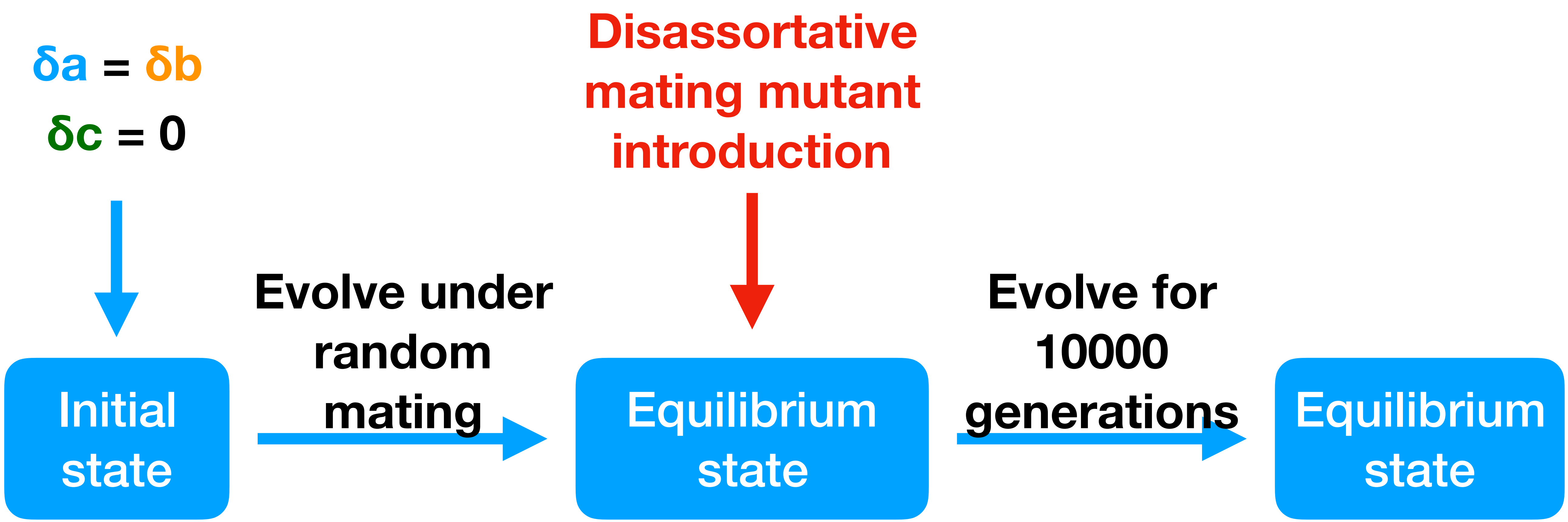
Mr < Mb

Mr < Mc

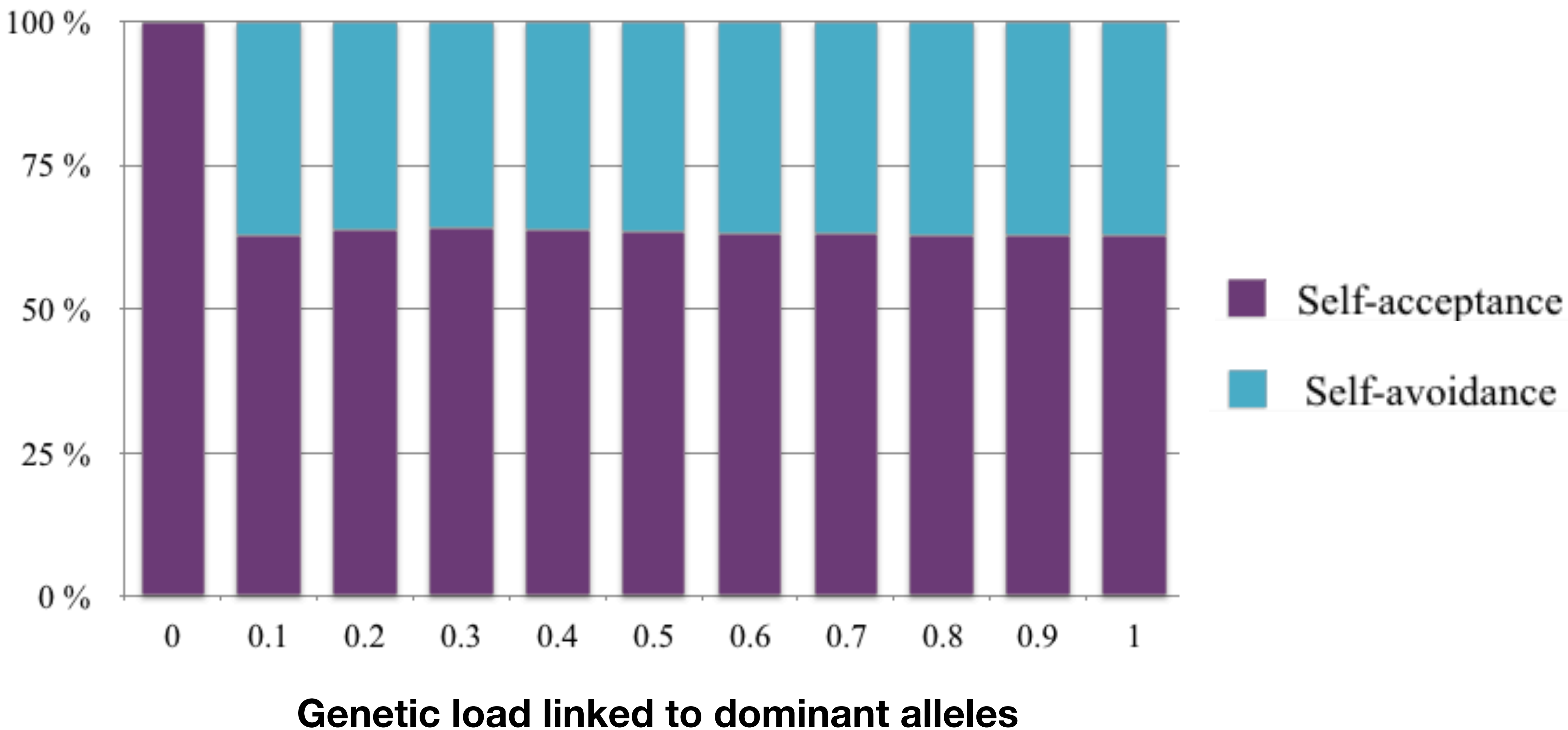
Simulations

δ cost of genetic load :

- **δa and δb associated with mimetic alleles**
- **δc associated with non-mimetic allele**



Impact of the genetic load on dominant phenotype allele on the evolution of mate choice



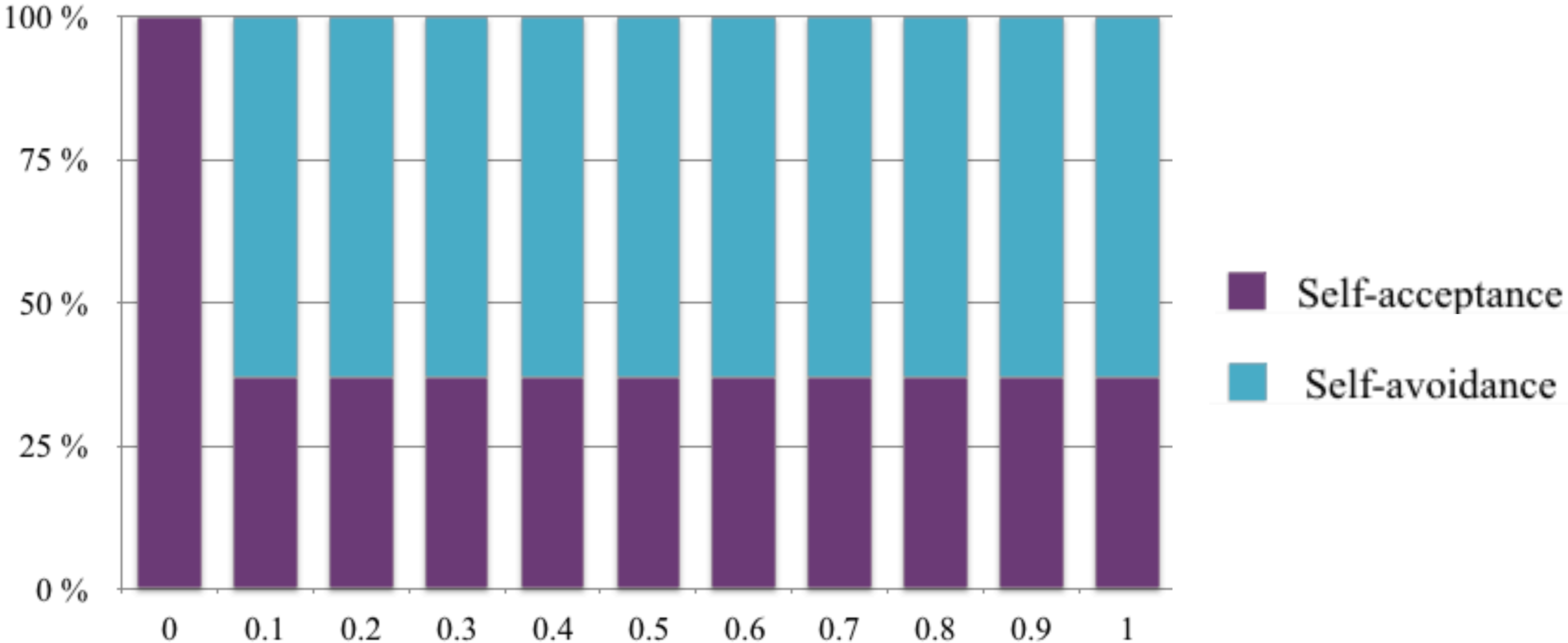
Distaste for traits

Mr	No preference
Ma	Distaste for morph A
Mb	Distaste for morph B
Mc	Distaste for morph C

Dominance relationship:

Mr	<	Ma
Mr	<	Mb
Mr	<	Mc

Impact of the genetic load on dominant phenotype allele on the evolution of mate choice



Genetic load linked to dominant alleles

Conclusion

- Genetic loads linked with the dominant phenotypic allele promote self-rejection behavior

- The genetic architecture impacts the evolution of mate choice

Thank you for your attention

Violaine Llaurens

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Mathieu Chouteau