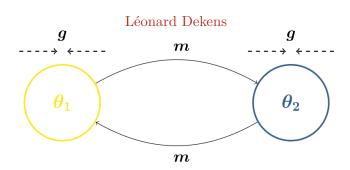
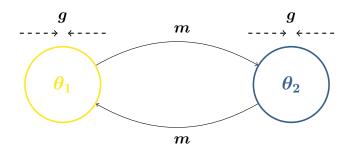
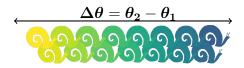


# Quantitative trait in patchy environment: beneath the Gaussian approximation

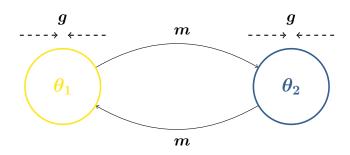


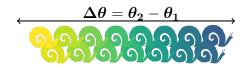
## The scenery





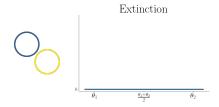
## The scenery

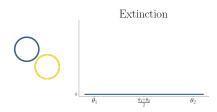


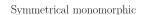


#### Main motivation

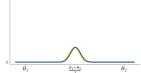
Given m (migration), g (selection),  $n_1(t=0)$ ,  $n_2(t=0)$  (initial state)  $\rightsquigarrow$  Predict long term evolutionary outcomes?

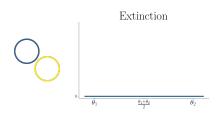


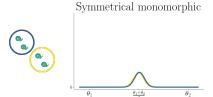


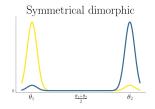




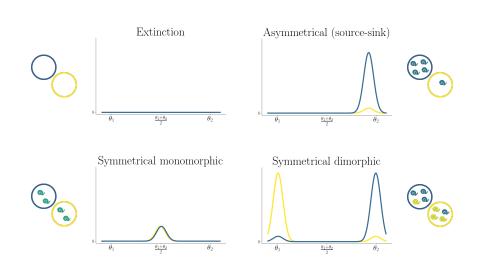


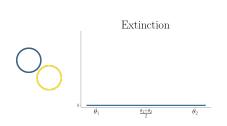




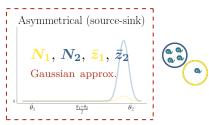


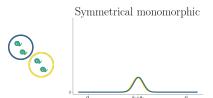


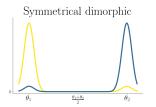




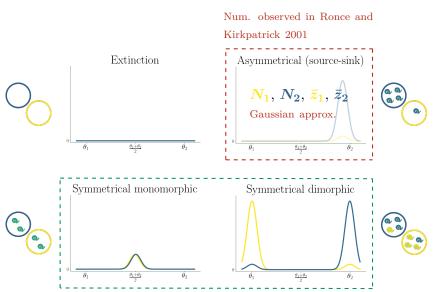
### Num. observed in Ronce and Kirkpatrick 2001



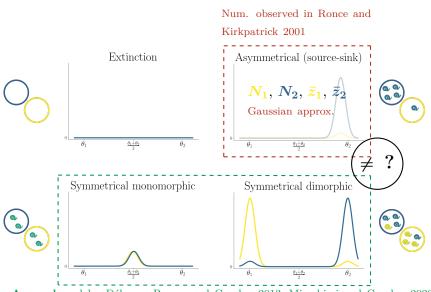








Asexual models: Débarre, Ronce, and Gandon 2013; Mirrahimi and Gandon 2020



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Deterministic model on the **trait distributions**\*  $((i, j) \in \{1, 2\})$ :

$$\frac{\partial n_i}{\partial t} = \overbrace{\mathcal{B}[n_i]}^{\text{reproduction}} - \overbrace{N_i n_i}^{\text{competition}} - \overbrace{g\left(z - \theta_i\right)^2 n_i}^{\text{selection}} + \overbrace{m\left(n_j - n_i\right)}^{\text{migration}},$$

 $<sup>^*</sup>$ Can be derived from agents-based models in large population size asymptotics.

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i Justify Gaussian approximation with the infinitesimal model of sexual reproduction.

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- ii Rigorous separation of time scales ECO/EVO.

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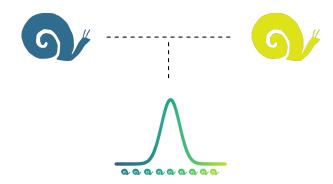
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- *i* Justify Gaussian approximation with the infinitesimal model of sexual reproduction.
- ii Rigorous separation of time scales ECO/EVO.
- *iii* Exhaustive analytical results.

 $<sup>^*\</sup>mathrm{Can}$  be derived from agents-based models in large population size asymptotics.

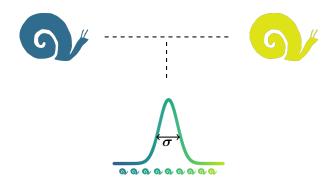
# The infinitesimal model (Fisher 1919; Barton, Etheridge, and Véber 2017)

### Within family trait distribution:



# The infinitesimal model (Fisher 1919; Barton, Etheridge, and Véber 2017)

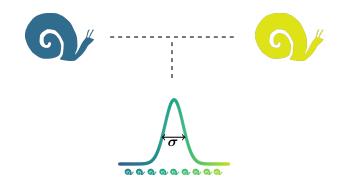
Within family trait distribution:



 $\sigma^2$ : segregational variance, parameter, constant across families

# The infinitesimal model (Fisher 1919; Barton, Etheridge, and Véber 2017)

### Within family trait distribution:

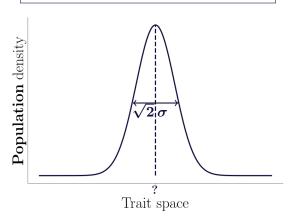


$$m{\mathcal{B}}[n](z) = \iint G_{0,\,m{\sigma}^2}\left(z - rac{z_1 + z_2}{2}
ight) n(z_1) rac{n(z_2)}{N} \, dz_1 \, dz_2$$

Justify Gaussian approximation for (large) **population** trait distributions:

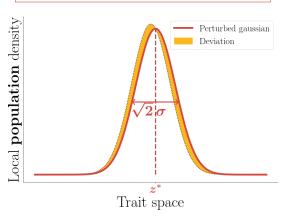
# Justify Gaussian approximation for (large) **population** trait distributions:

Homogeneous space, no selection: blending effect of sexual reproduction



Justify Gaussian approximation for (large) **population** trait distributions:  $\sigma \ll \Delta \theta$ 

> Patchy space, strong differentiation: only a perturbation, do an expansion<sup>‡</sup>



<sup>‡</sup>multiplicative: geometric optics tools adapted for concentration phenomena for quantitative genetics models in Diekmann et al. 2005

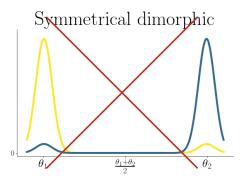
SMB 2021

Justify Gaussian approximation for (large) **population** trait distributions:  $\sigma \ll \Delta \theta$ 

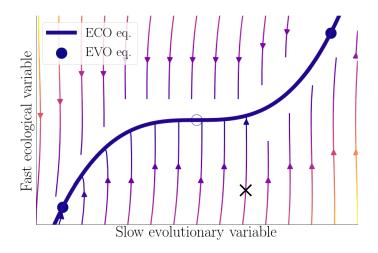
Implication: monomorphism in the meta population

 $\approx$  Gaussian trait distribution in each patch and  $\mathbf{migration}.$ 

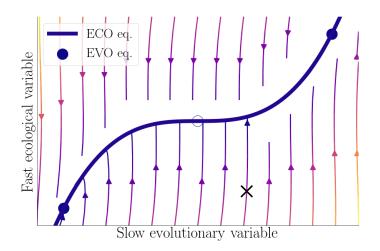
### NOT GAUSSIAN



# Separation of time scales ECO/EVO $(\sigma \ll \Delta \theta)$



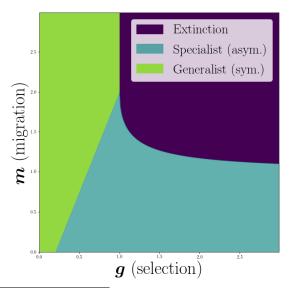
# Separation of time scales ECO/EVO ( $\sigma \ll \Delta \theta$ )



#### Reduction of complexity

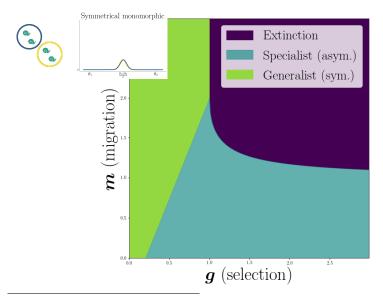
Slow dynamics (ODE) on the line (algebraic equations).

## Analytical long term evolutionary outcomes\*



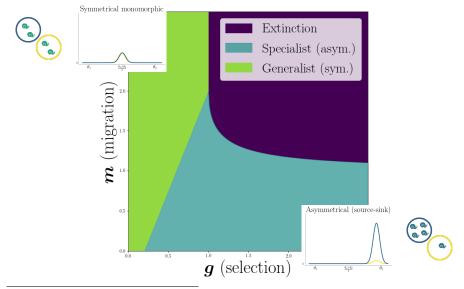
\*Dekens (2021), https://arxiv.org/pdf/2012.10115.pdf SMB 2021 dekens@math.univ-lyon1.fr

## Analytical long term evolutionary outcomes\*



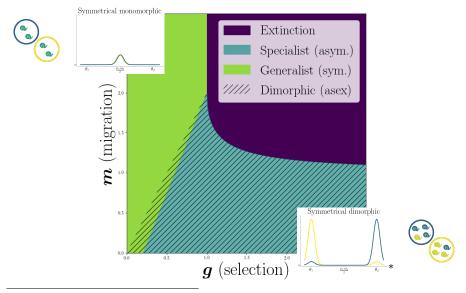
\*Dekens (2021), https://arxiv.org/pdf/2012.10115.pdf SMB 2021 dekens@math.univ-lyon1.fr

## Analytical long term evolutionary outcomes\*





## Analytical long term evolutionary outcomes



#### Conclusion

♦ Integrative framework for sexual reproduction, do not need prior assumptions on trait distributions.

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- Here, allows to describe exhaustively the outcomes.
   Substituting source-sink scenario to local adaptation by dimorphism due to combined blending by sexual reproduction (within patches) and by migration (between patches).
- Can be used for more complex genetic architecture (major locus vs infinitesimal background, forthcoming) or other biological contexts (evolution of dispersion and range expansion, ...)

## Acknowledgments



(a) Sepideh Mirrahimi<sup>†</sup>



(b) Vincent Calvez <sup>‡</sup>



(c) Sarah Otto §





<sup>†</sup>https://www.math.univ-toulouse.fr/ smirrahi/, credits: Vincent Moncorgé

<sup>&</sup>lt;sup>‡</sup>http://vcalvez.perso.math.cnrs.fr/

 $<sup>\</sup>S_{\rm https://biodiversity.ubc.ca/people/faculty/sarah-otto}$