# Evolutionary rescue
# in structured populations

## Joachim Hermisson

## Mathematics & MFPL, University of Vienna

# Evolutionary rescue

*Imagine* …

# Evolutionary rescue

*Imagine* …



environment deteriorates

(e.g. climate change, new predator, new drug...)

population becomes maladapted
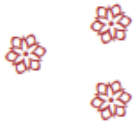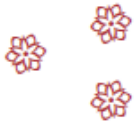
? extinction

? adaptive evolution

Can a population escape extinction
through adaptive evolution?

# Evolutionary rescue

*Imagine* …



environment deteriorates
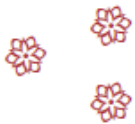
(e.g. climate change, new predator, new drug…)

↓

population becomes maladapted

? extinction

? adaptive evolution

Can a population escape extinction through adaptive evolution?

Recent work in progress

joint with:

**Hildegard Uecker**
[Vienna]
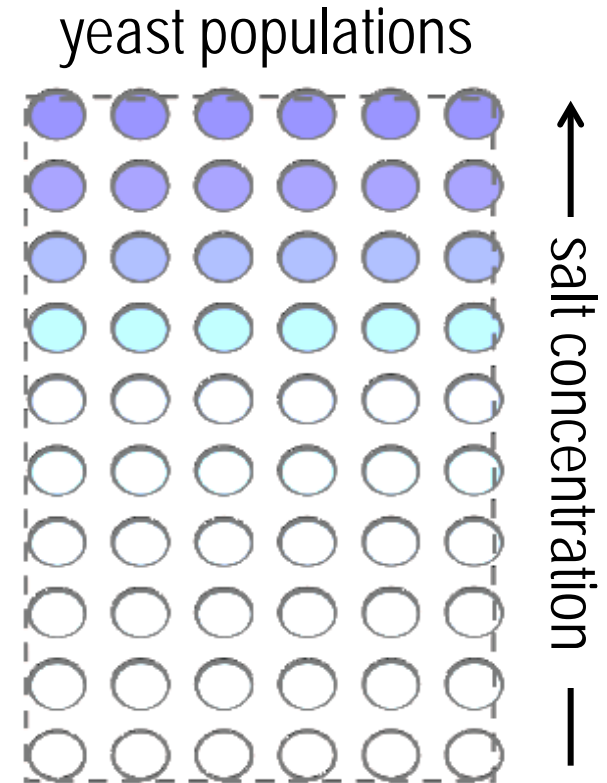
and Sally Otto
[UBC]

# Evolutionary rescue

Empirical Relevance :

- Human impact & global change
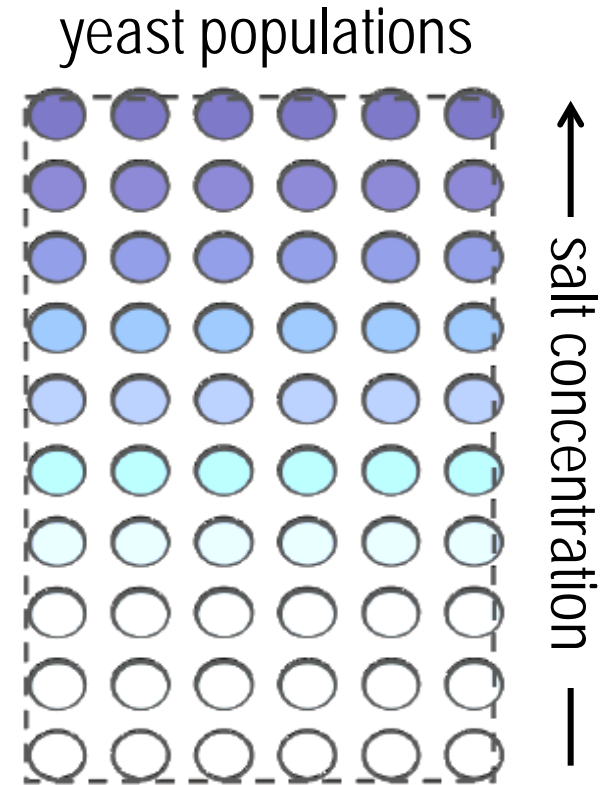- Antibiotic resistance

# Evolutionary rescue

Empirical Relevance :

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- New data from experimental evolution
  (Bell and Gonzales, Science 2011)

yeast populations



salt concentration

# Evolutionary rescue

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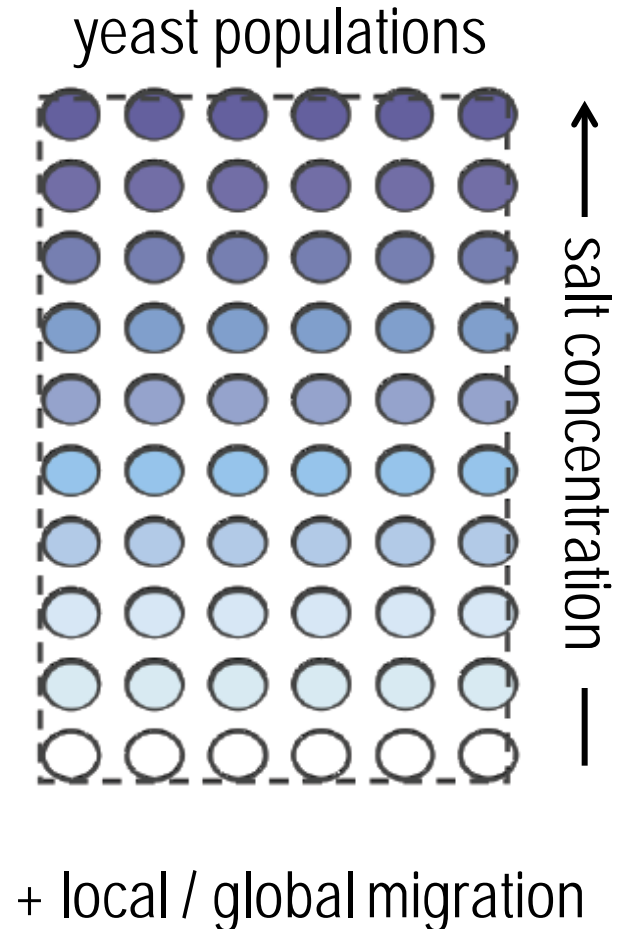


salt concentration

# Evolutionary rescue

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salt concentration

+ local / global migration
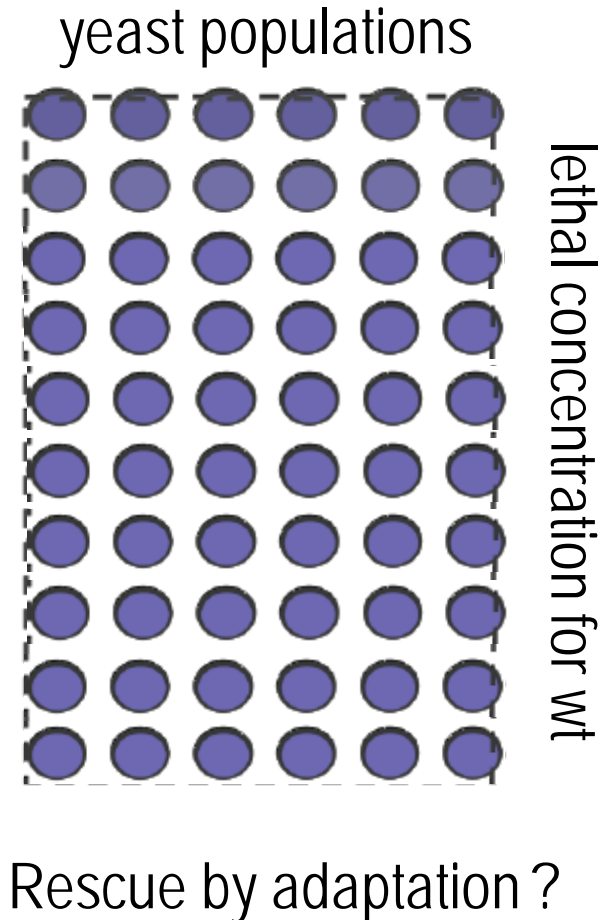
# Evolutionary rescue

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yeast populations

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lethal concentration for wt

Rescue by adaptation ?

# Evolutionary rescue

Empirical Relevance :

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  (Bell and Gonzales, Science 2011)

Theory:

- Evolution and ecology cannot be separated

yeast populations



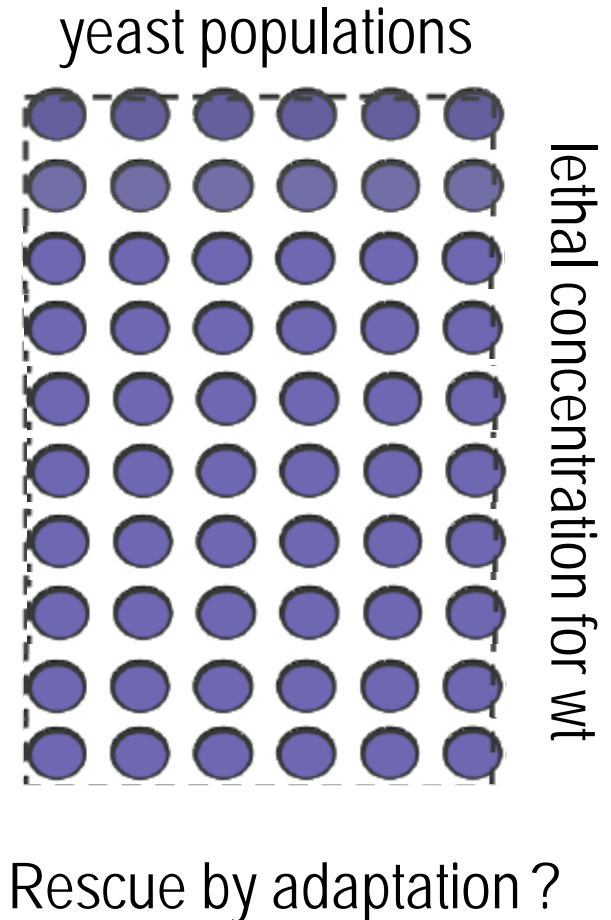lethal concentration for wt
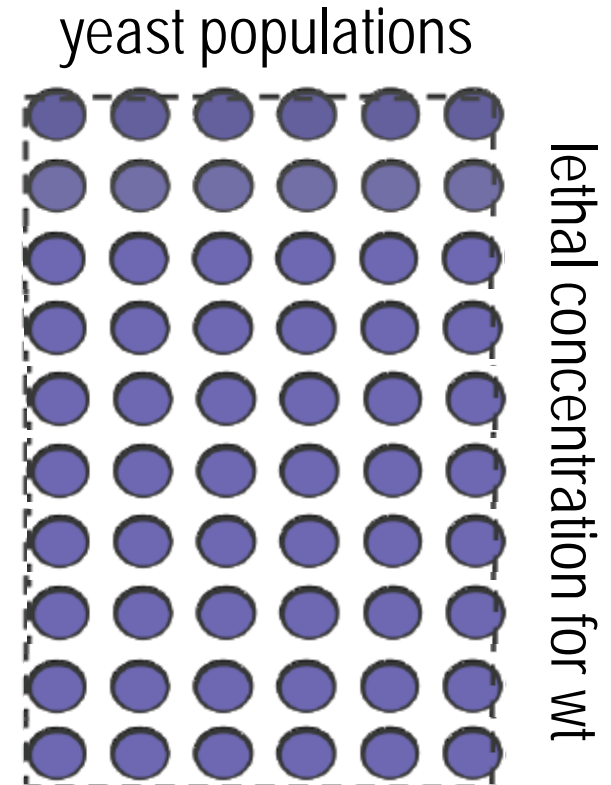
Rescue by adaptation ?

# Evolutionary rescue

Empirical Relevance :

- Human impact & global change
- Antibiotic resistance
- New data from experimental evolution
  (Bell and Gonzales, Science 2011)

Theory:

- Evolution and ecology cannot be separated
- Very little previous work
  - Holt /Gomulkiewicz 1995; Bürger /Lynch 1995: quantitative trait with fixed variance: speed of adaptation vs. speed of population decline
  - Orr /Unckless 2008; Uecker /Hermisson 2011; Pennings 2012, panmictic populations

yeast populations

lethal concentration for wt

Rescue by adaptation ?

# Island model

- $D$ islands
- migration rate $m$
- wildtype $\xrightarrow{u}$ mutant
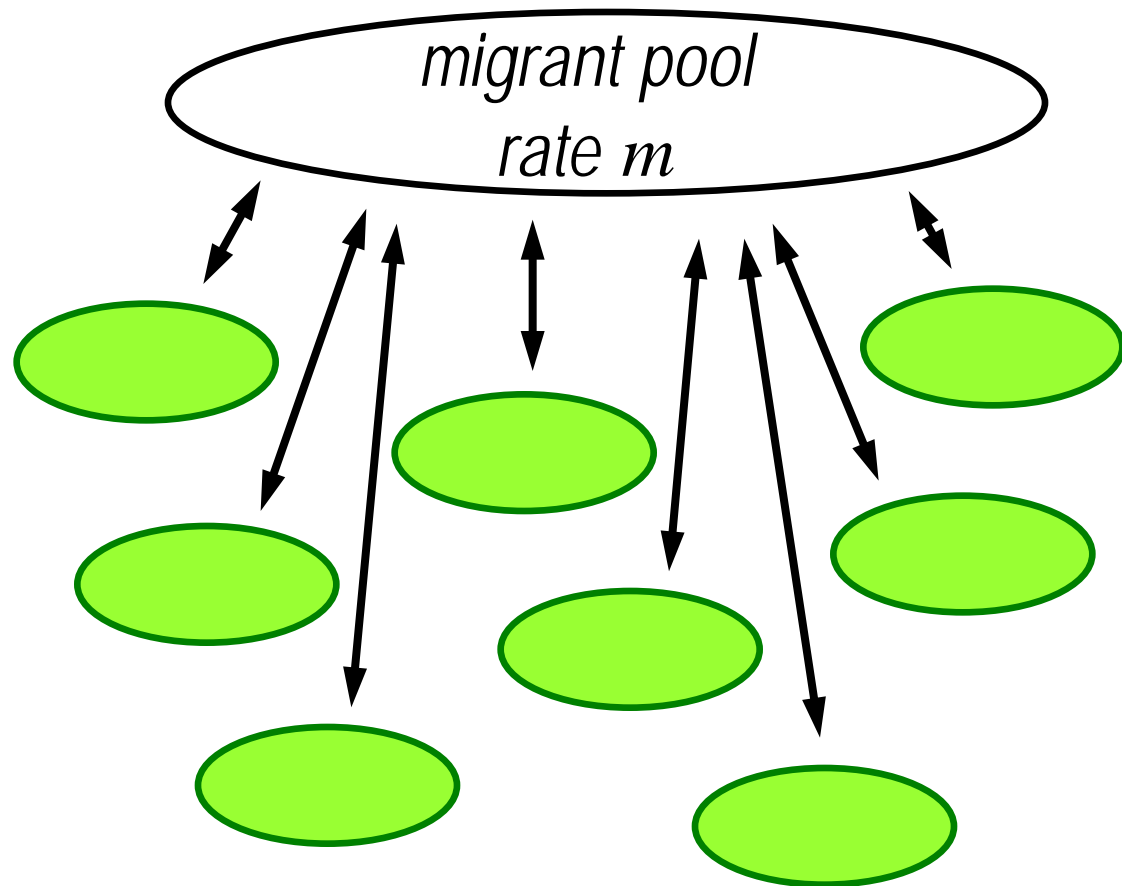
*migrant pool rate m*
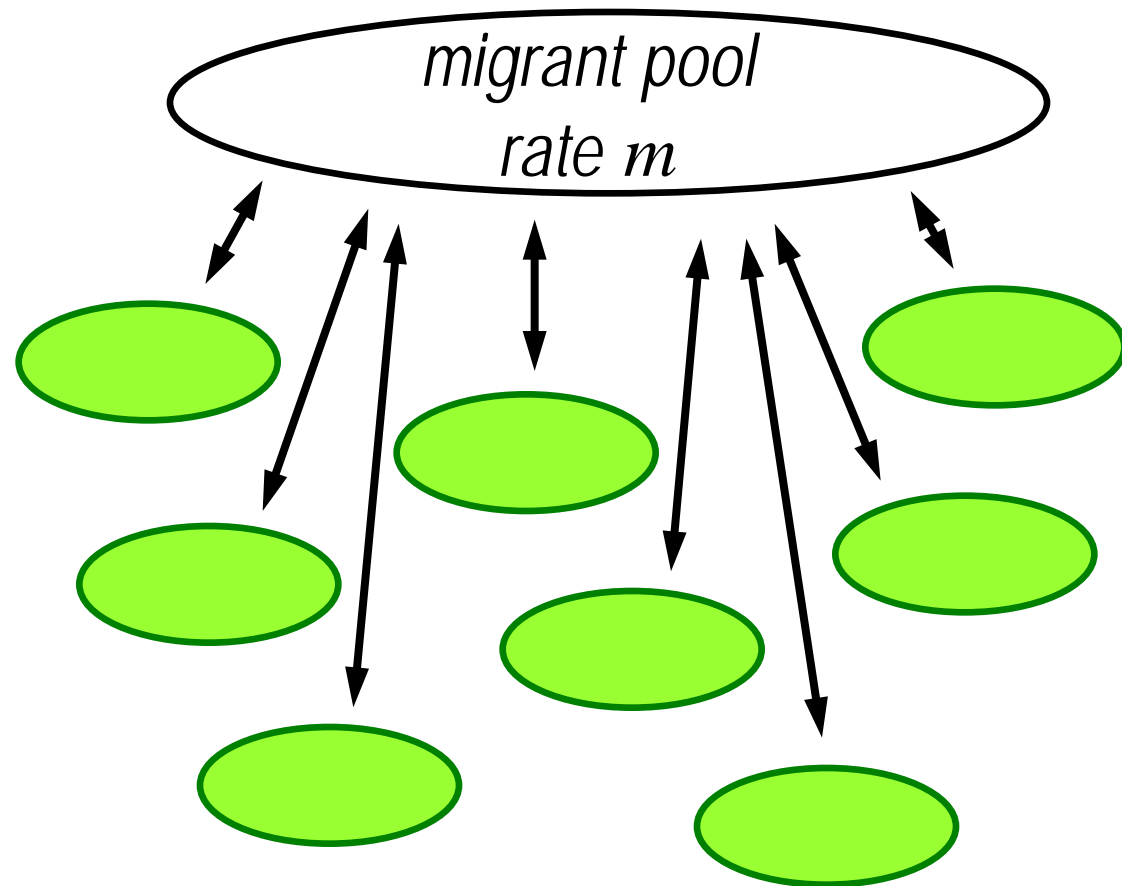
# Island model

- $D$ islands
- migration rate $m$
- wildtype $\xrightarrow{\;u\;}$ mutant

original conditions:

- population size $K = \text{const}$
- wildtype fitness 1
- mutant fitness $1 - z$
  (mutation-selection balance
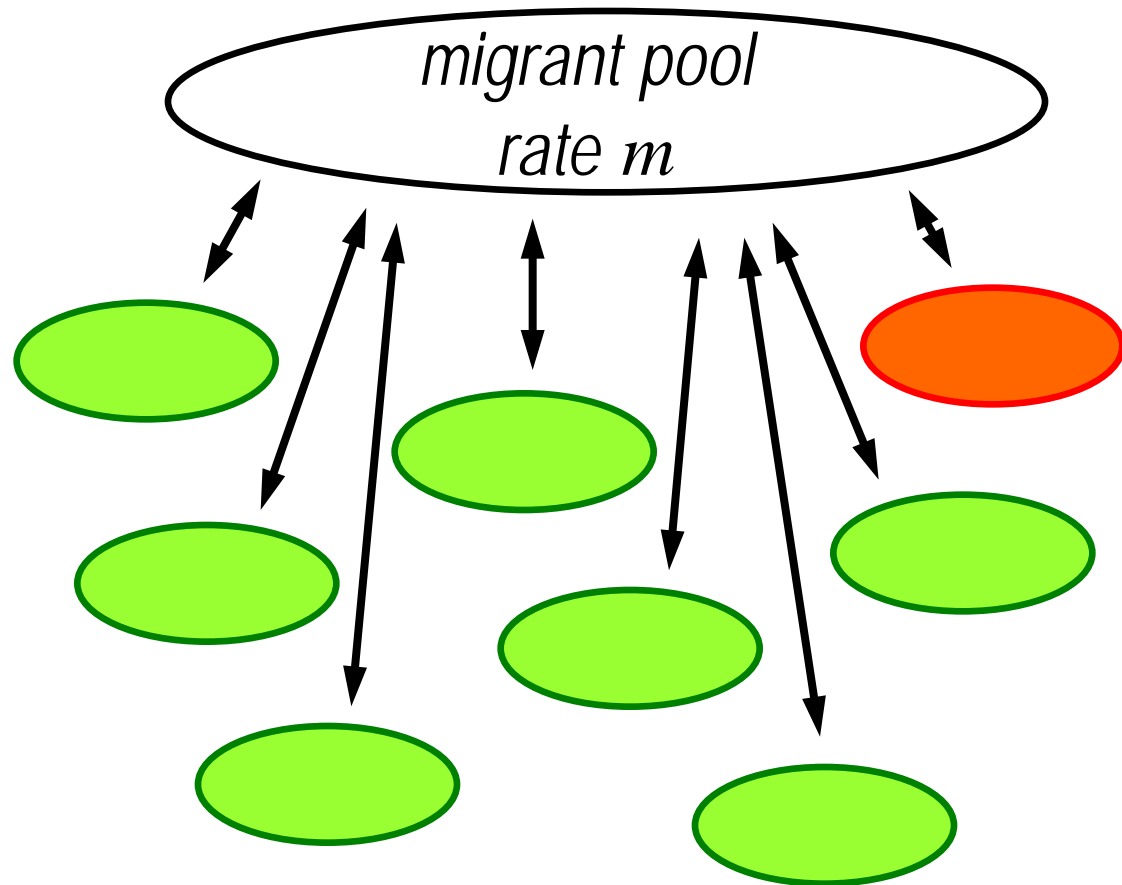  = standing genetic variation)

*migrant pool rate $m$*

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perturbation:

- conditions on islands change every $T$ generations

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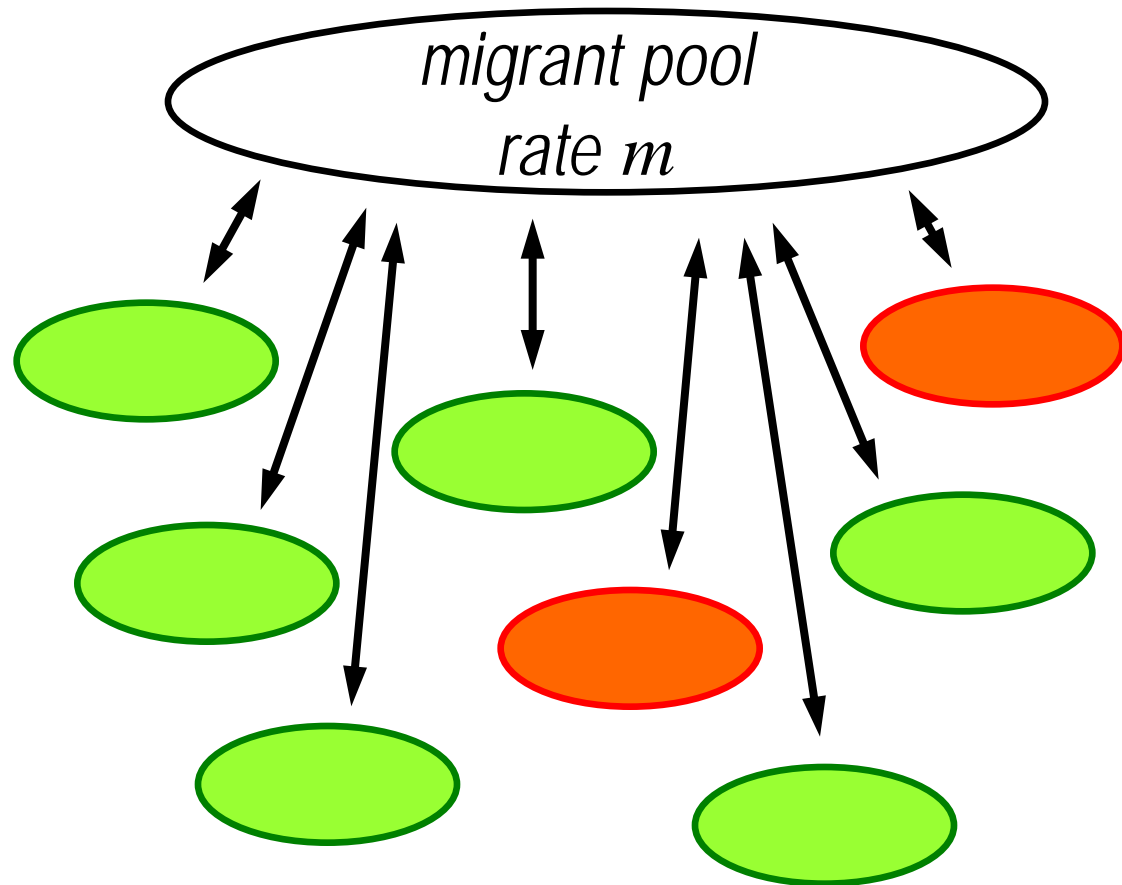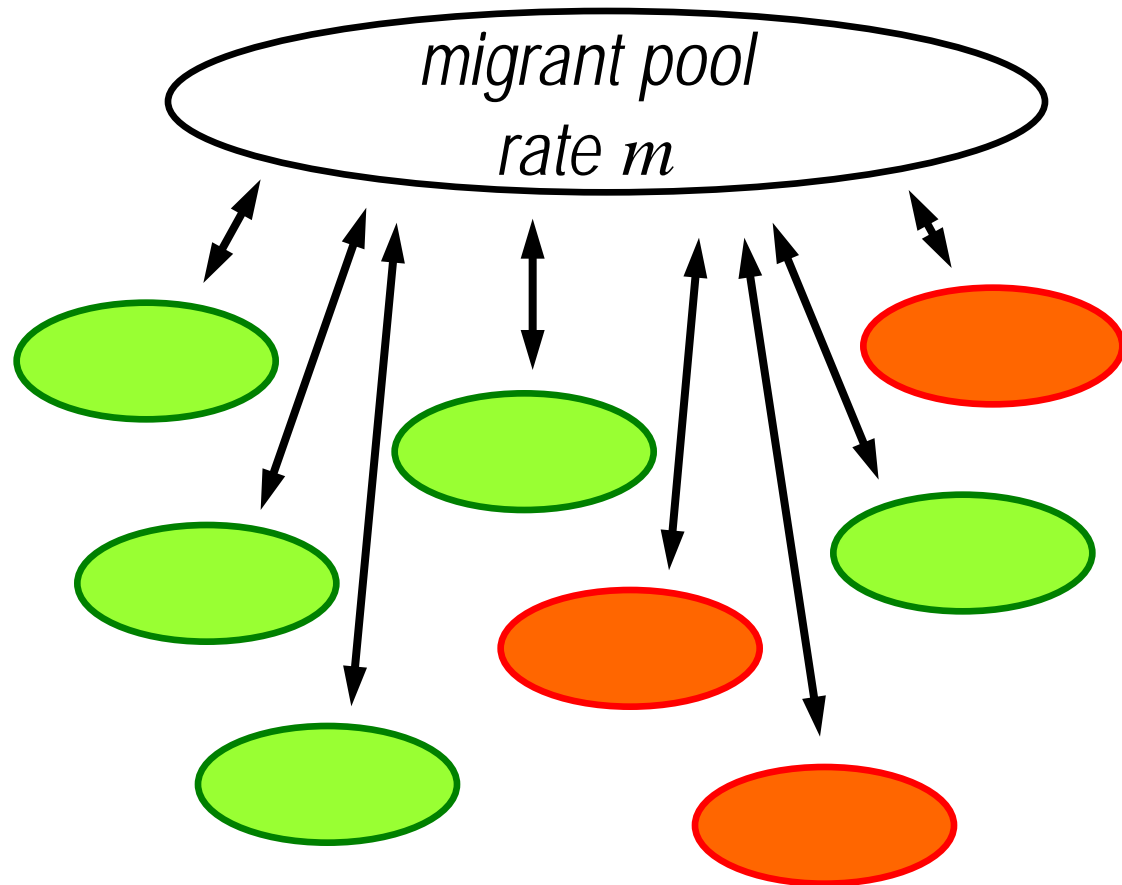- conditions on islands change every $T$ generations

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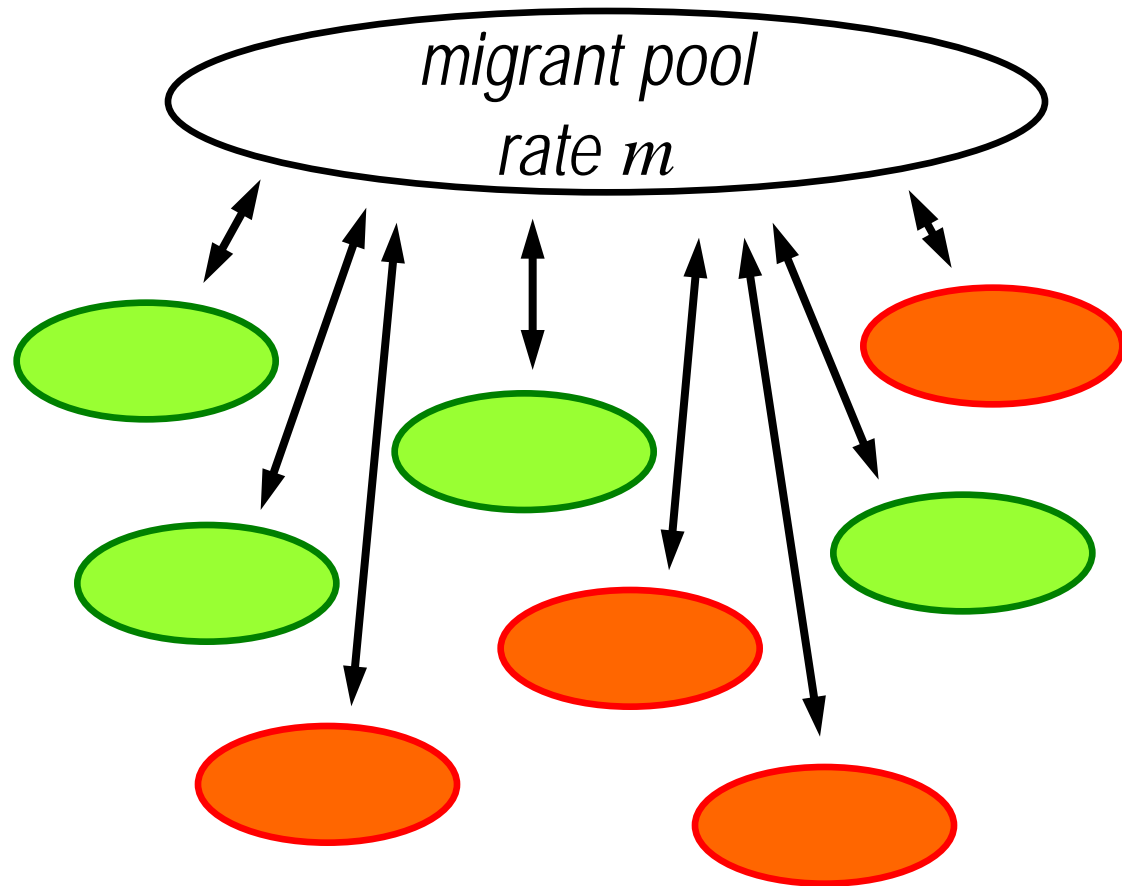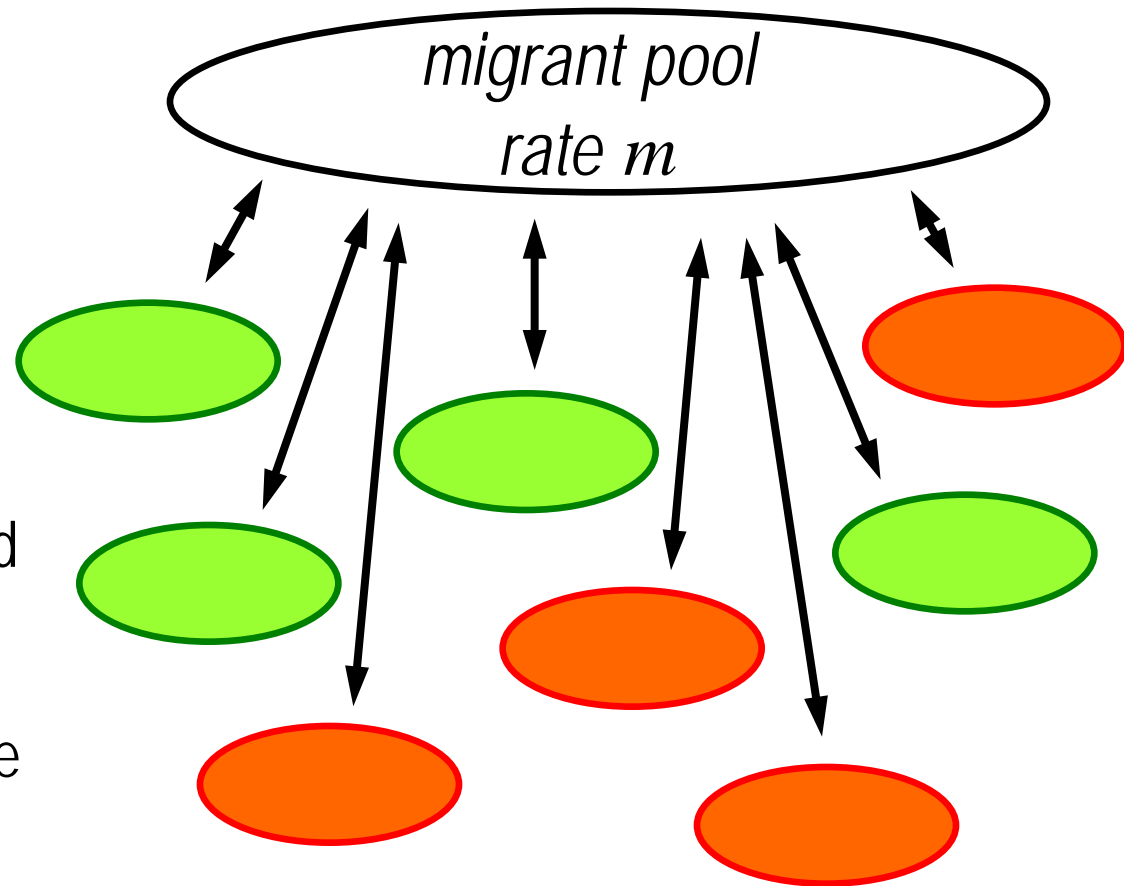
# Island model

perturbed conditions:

1.  wildtype:

- absolute fitness $1 - r$
- exponential decline plus immigration as long as original islands exist

- population size on $k$-th island

$$N_k(t) \, < \, K$$

( approaches mig-sel balance for long intervals $T$ )
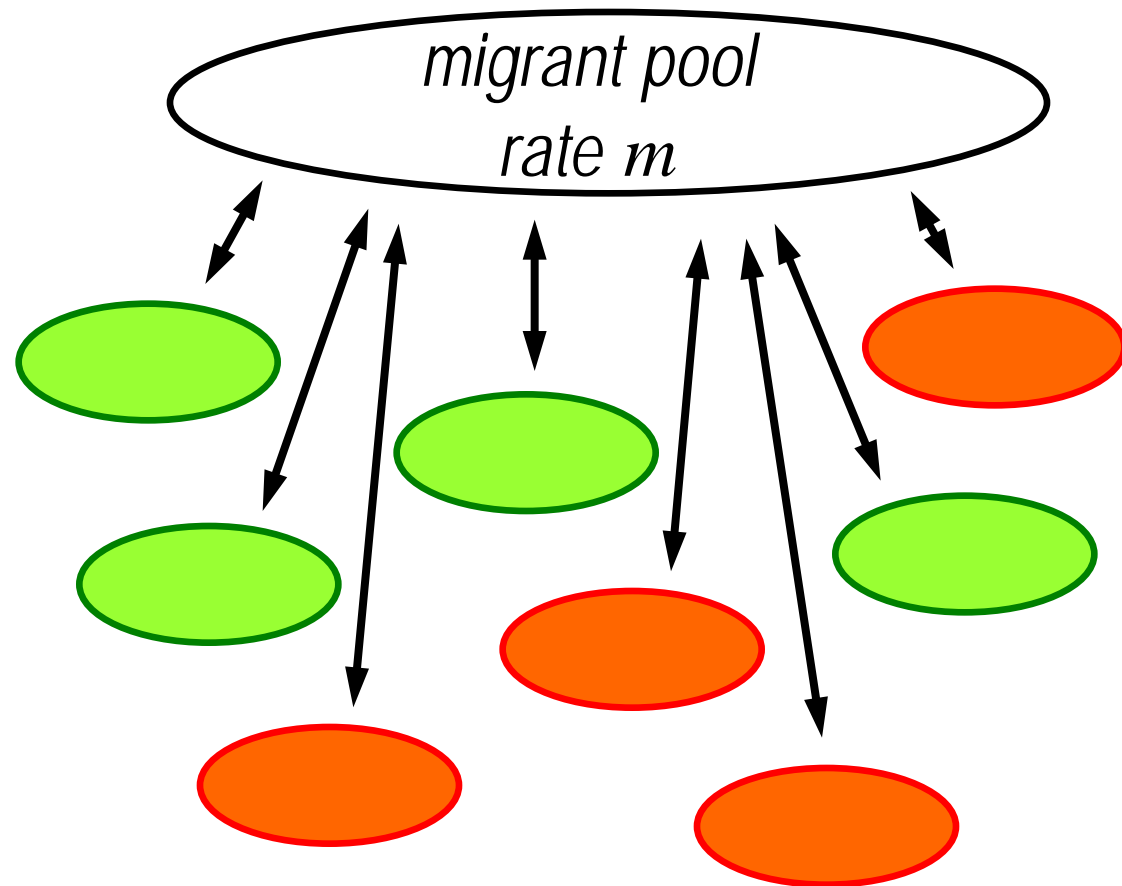


*migrant pool rate $m$*

# Island model

perturbed conditions:

2.  mutant:

· absolute fitness

$$1 + s\left(1 - \beta \, \frac{N_k(t)}{K}\right)$$

· $s > 0$ : can grow under perturbed conditions

· $\beta$ : density dependence

$\beta > 1$ : mutants can only grow at low densities
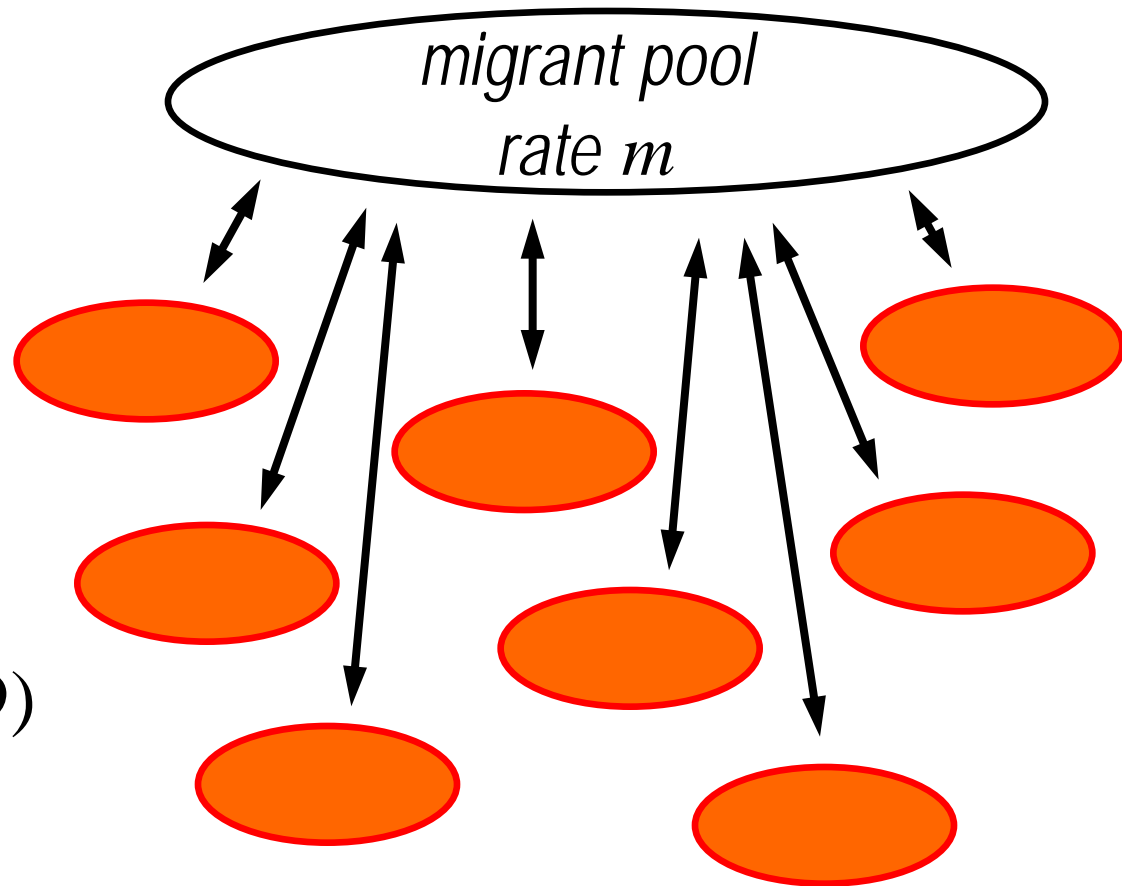


*migrant pool rate m*

# Island model

perturbed conditions:

after $TD$ generations:

- wildtype declines to extinction
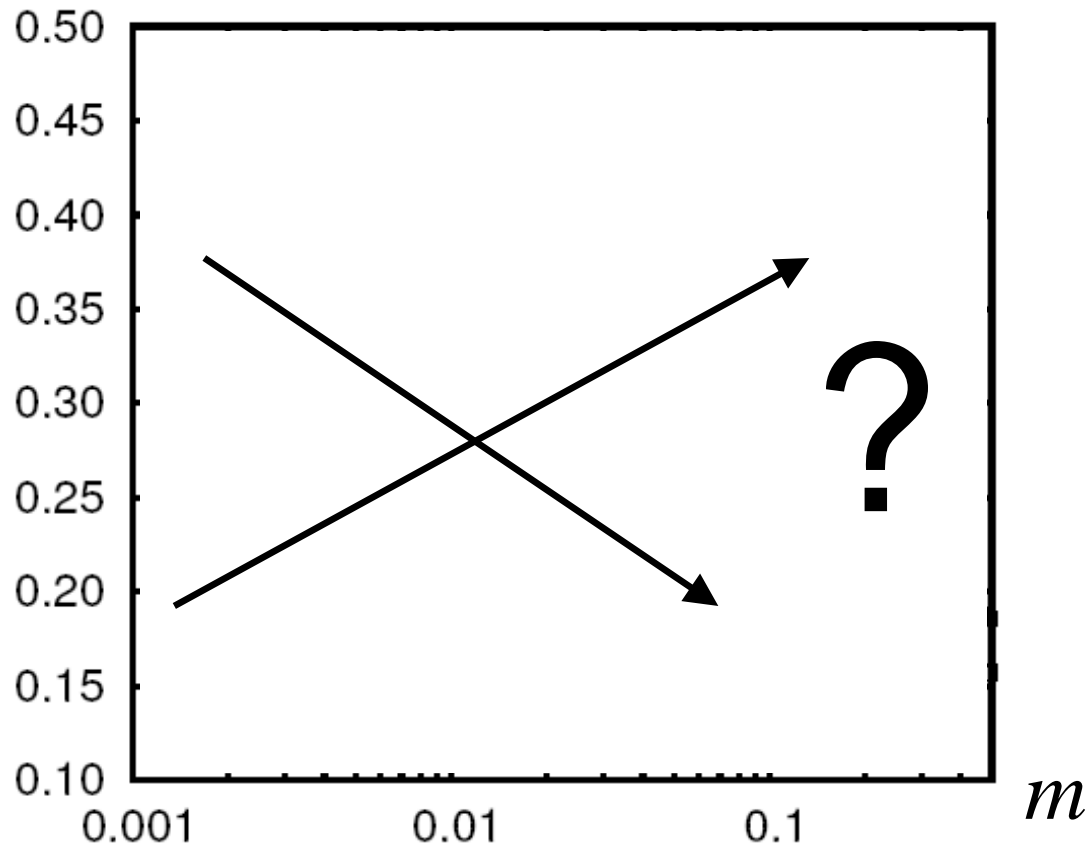
➢ can the mutant establish to rescue the population?

rescue probability:

$$P_{resc}(m, r, z, s, \beta, u, T, D)$$


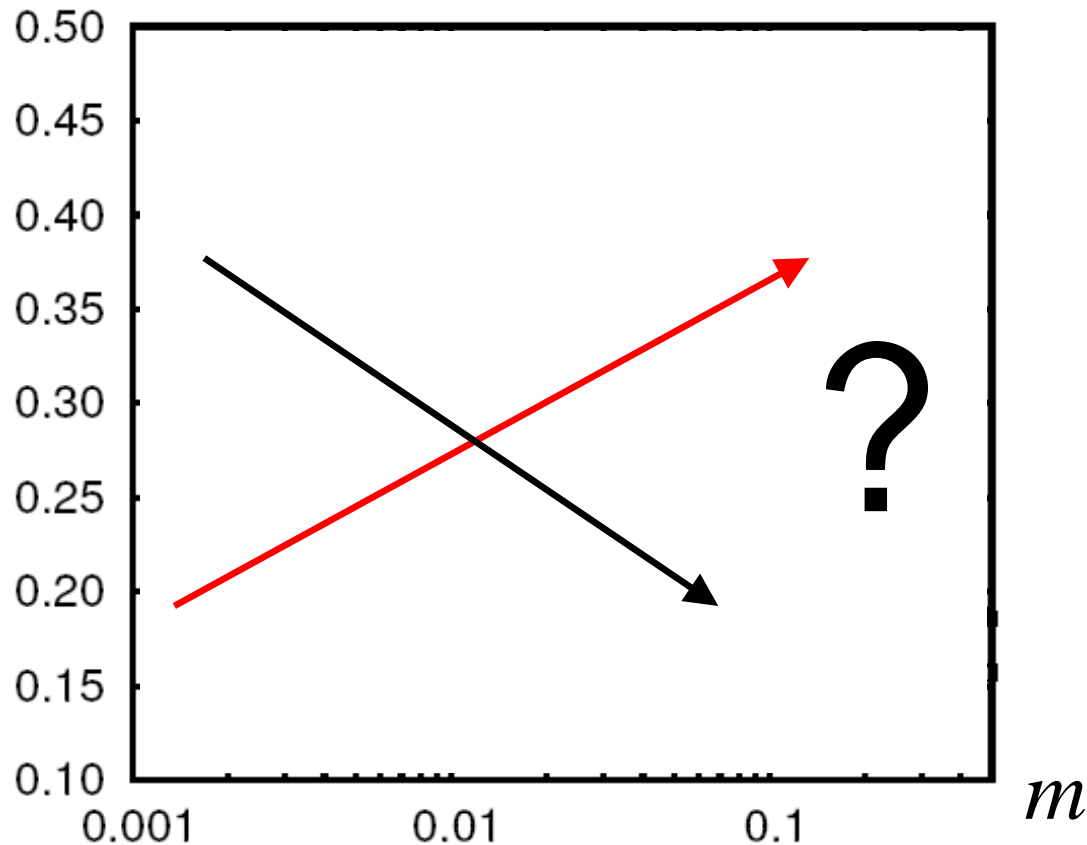
*migrant pool rate $m$*

# Level of gene-flow

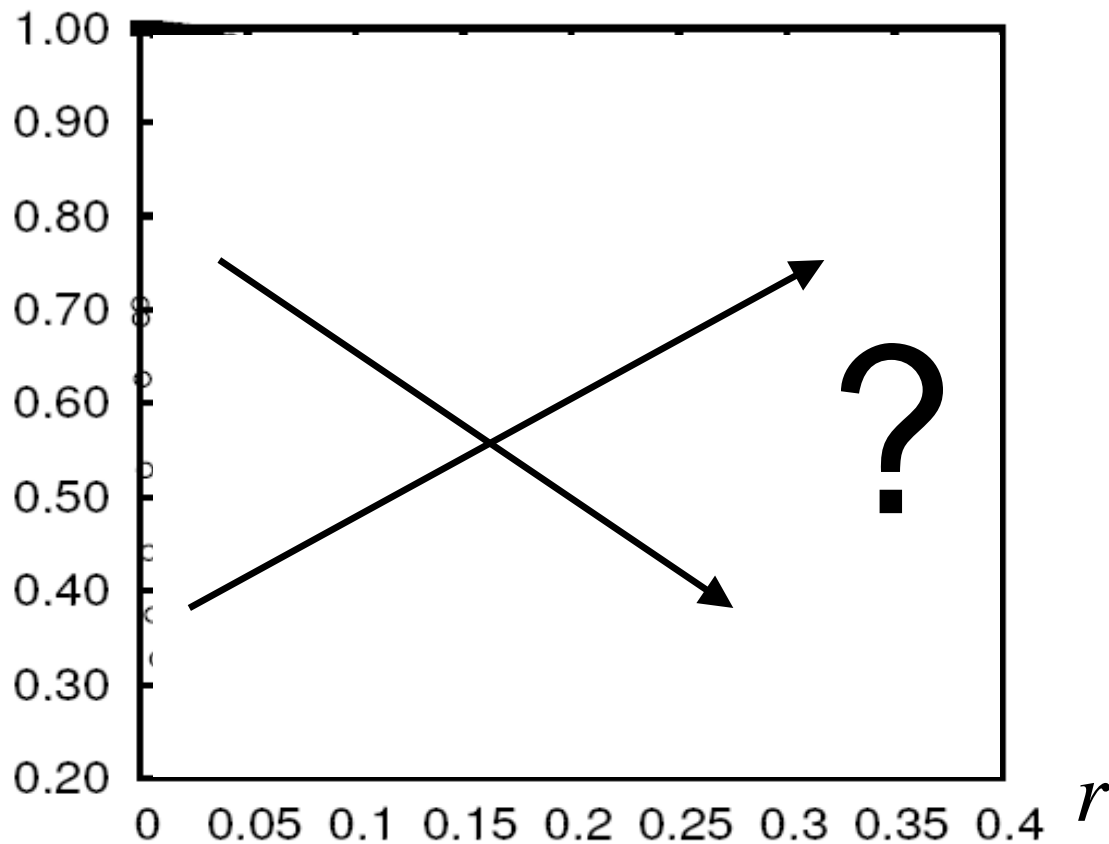$P_{resc}(m)$



$m$

# Level of gene-flow

$P_{resc}(m)$



Expectation:
"gene-flow is good
– fragmentation is bad"

(confirmed, e.g. by
Bell and Gonzales)

# Severity of the change
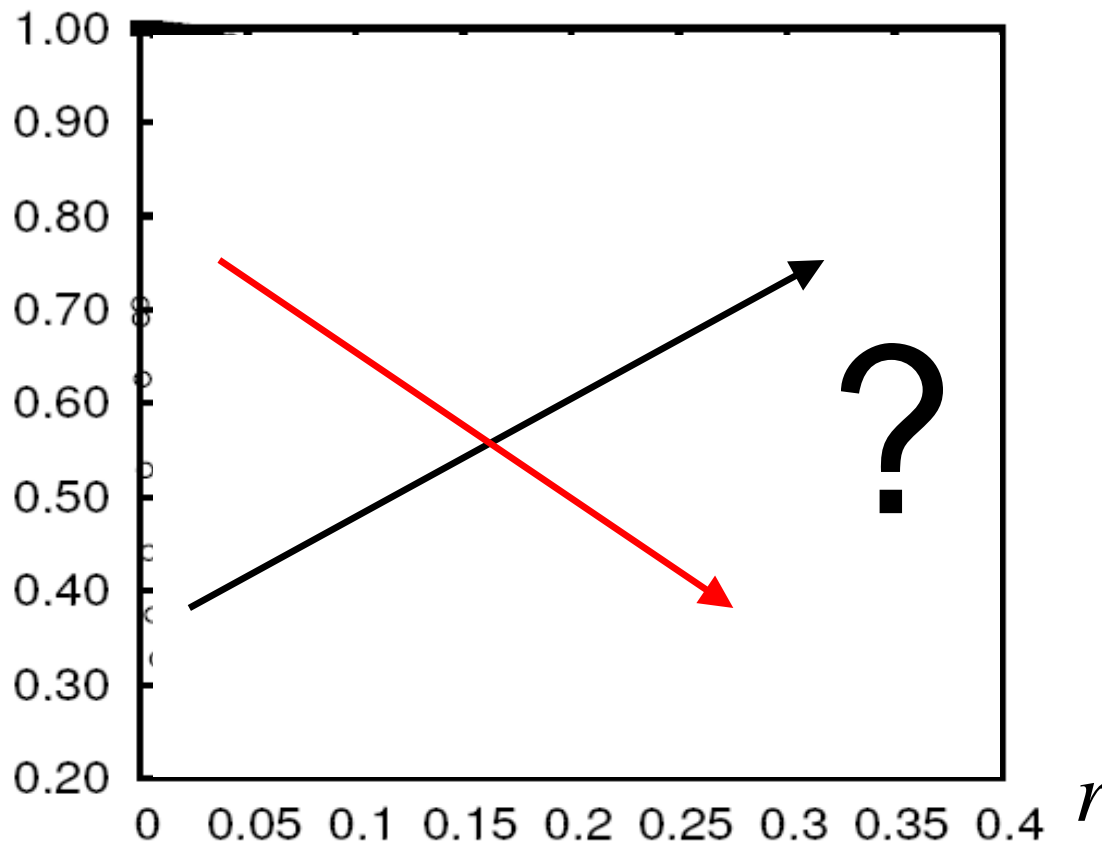
$$P_{resc}(r)$$

# Severity of the change

$$P_{resc}(r)$$



Expectation:
"severe change is bad"

(confirmed, e.g. by
Bell and Gonzales)

$r$

# Analytical approach

- Without density dependence:   two compartments



$t$    $\boxed{D - d(t)}$   $\xrightarrow{m(t)}$   $\boxed{d(t)}$

$t+T$    $\boxed{D - d(t) -1}$   $\xrightarrow{m(t+T)}$   $\boxed{d(t) +1}$

original        perturbed
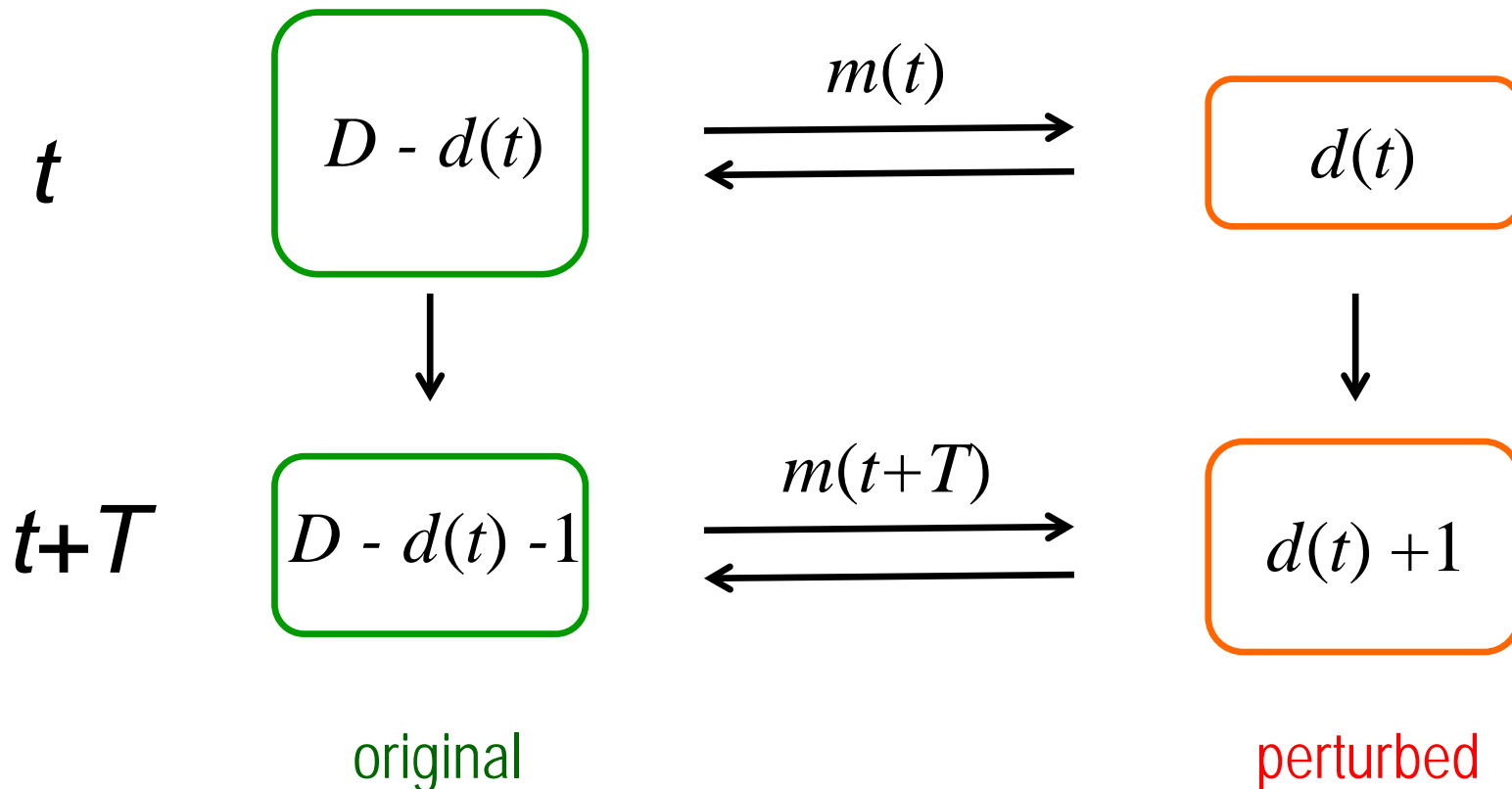
# Analytical approach
## I: No back migration of mutants

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$$\Rightarrow N_W^p(t) = \ \dots$$

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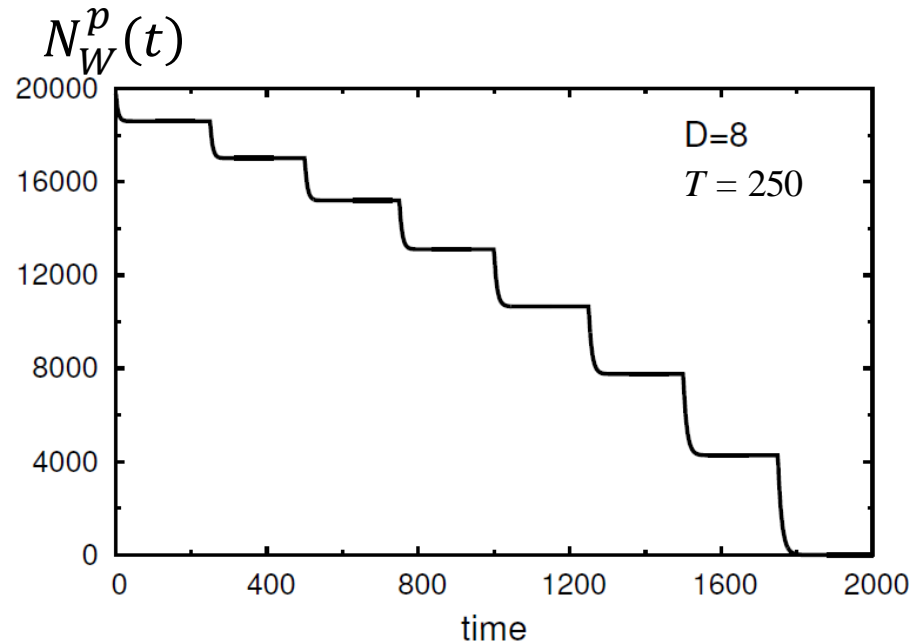$N_W^p(t)$

D=8
$T = 250$

time

# Analytical approach
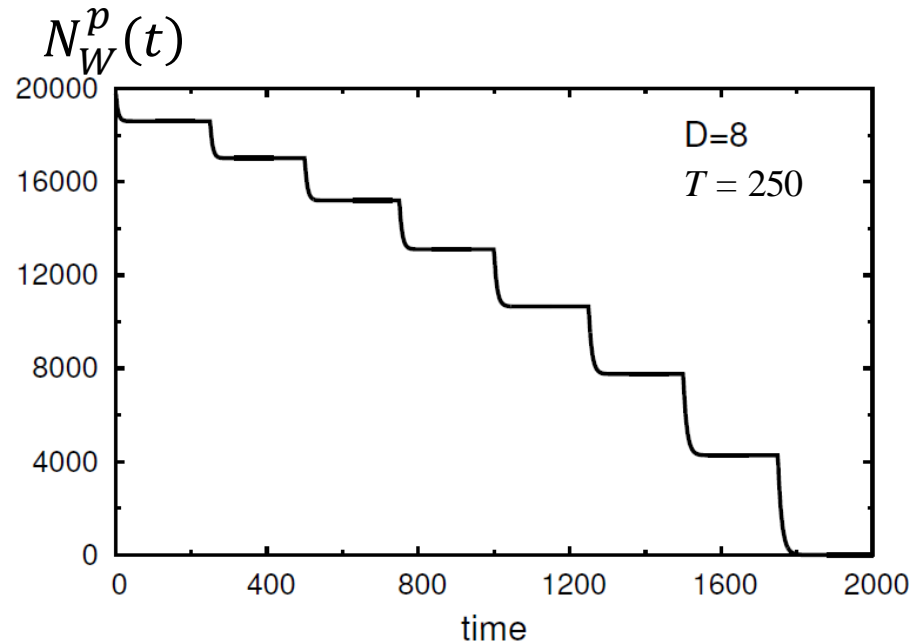## I: No back migration of mutants

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$$\Rightarrow N_W^p(t) = \ \ldots$$

- Mutants:

$$N_M^o(t) \approx \frac{Ku}{z}(D - d(t))$$
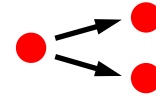
$N_W^p(t)$



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# Analytical approach
## I: No back migration of mutants

Branching process <span style="color:red">in perturbed demes</span>:

- birth rate    $\lambda = 1 + s$

- death rate    $\mu(t) = 1 + m(D - d(t))$

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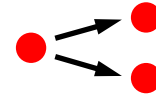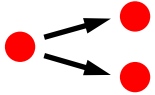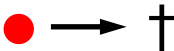
- death rate   $\mu(t) = 1 + m(D - d(t))$

- $s_{\text{eff}}(t) = \lambda - \mu(t) = s - m(D - d(t))$

➤ <span style="color:red">establishment probability</span>

$$p_{est}(t) = \frac{1}{1 + \frac{1}{2}\int_t^\infty \exp\left(-\int_t^u s_{\text{eff}}(\tau)\mathrm{d}\tau\right)\mathrm{d}u}$$

Kendall 1948, Uecker /Hermisson 2011

# Analytical approach
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$$n_{resc} = \int_0^\infty (uN_w(t) + m(t)N_m(t))p_{est}(t)dt$$

$$+ \sum_{k=1}^D \frac{k}{D} N_m(kT)p_{est}(kT)$$

# Analytical approach
## I: No back migration of mutants

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new mutants from wt
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<span style="color:red">new mutants</span> from wt in perturbed demes

<span style="color:red">migrating mutants</span> from unperturbed demes

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new mutants from wt
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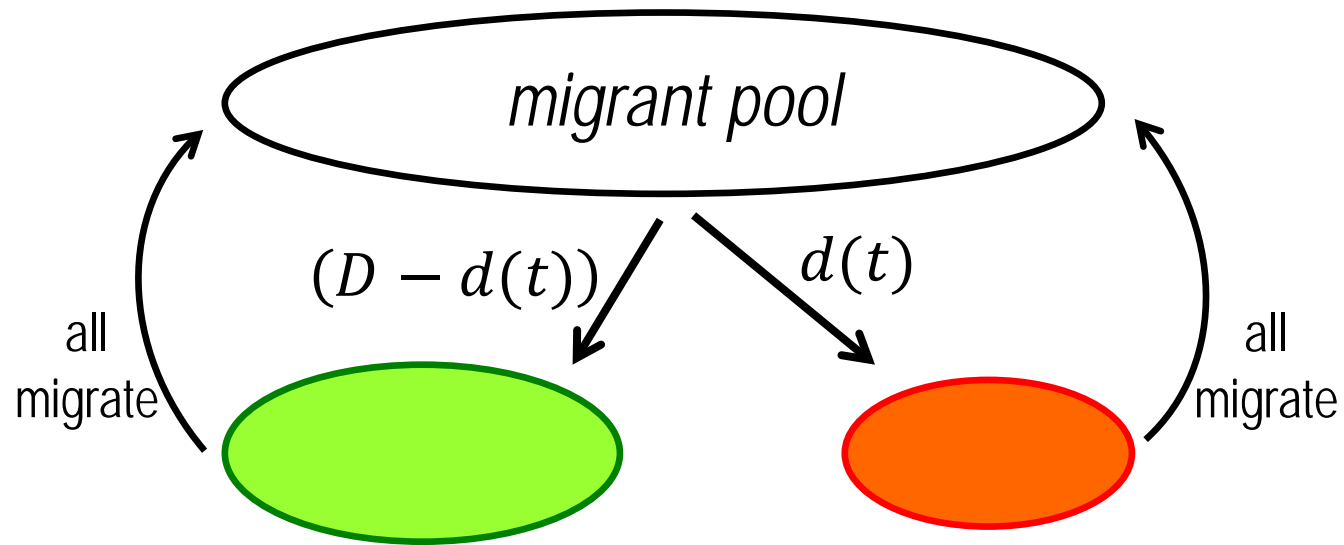migrating mutants from
unperturbed demes

$$n_{resc} = \int_0^\infty \left( u N_w(t) + m(t) N_m(t) \right) p_{est}(t) dt$$

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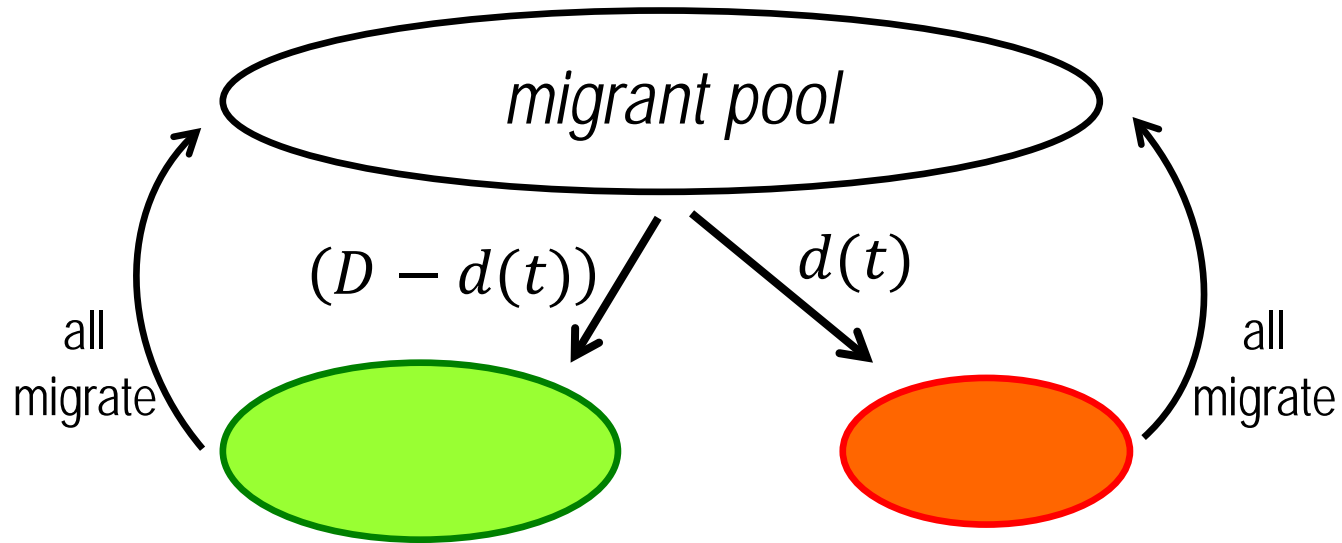
pre-existing mutants
at environmental change

# Analytical approach
## II: Levene model ($m =1$)

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*migrant pool*

$(D - d(t))$   $d(t)$

all migrate

all migrate

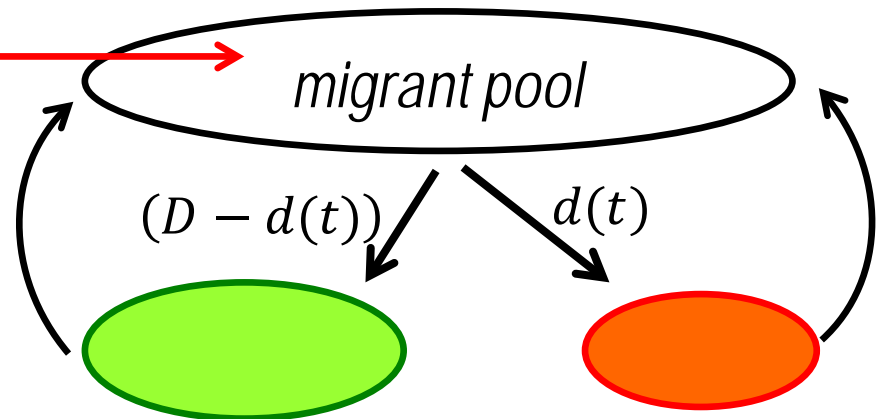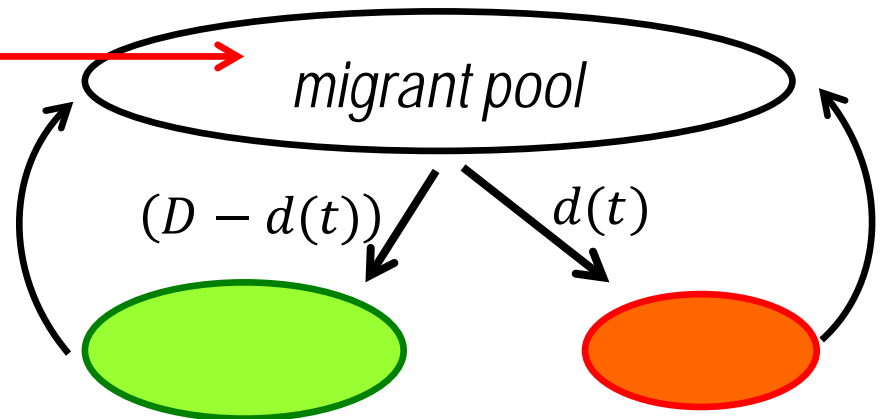$$\dot{N}_W(t) = -rN_W(t) + (D - d(t))\,(K - N_W(t)/D)$$

$$\Rightarrow N_W(t) = \ \ldots$$

# Analytical approach
## II: Levene model ($m = 1$)

Branching process
in the migrant pool:

$$s_{\text{eff}}(t) \approx \frac{d(t)}{D}(s + \boldsymbol{r}) - \frac{D - d(t)}{D}z$$

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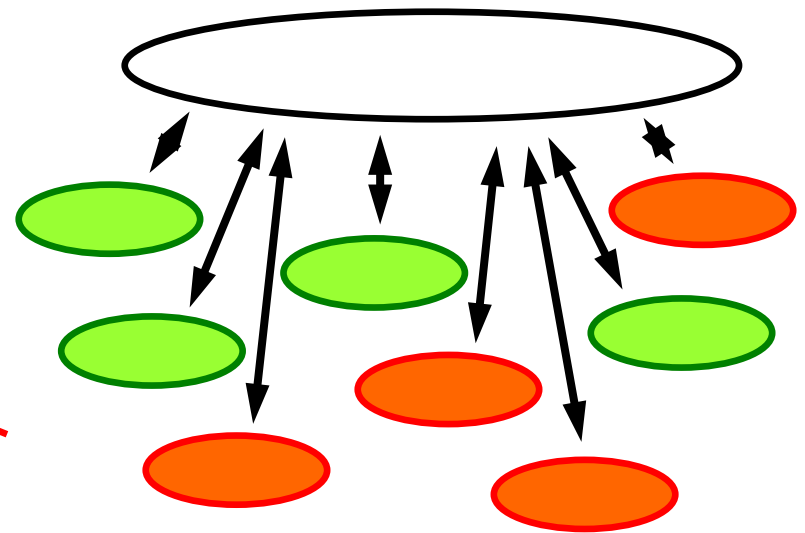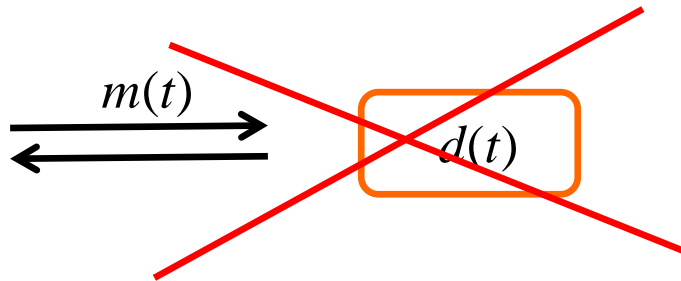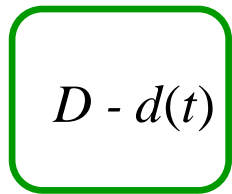
*migrant pool*

$(D - d(t))$     $d(t)$

- number of wildtypes in the migrant
  pool depends on severity of perturbation $\boldsymbol{r}$

- mutants compete with wildtypes in the
  original demes

$$\Rightarrow P_{resc} = \ \dots$$

➢ mutant growth increases with $\boldsymbol{r}$

# Analytical approach
## III: Density dependent selection ( ? )

Unequal density among
perturbed islands:
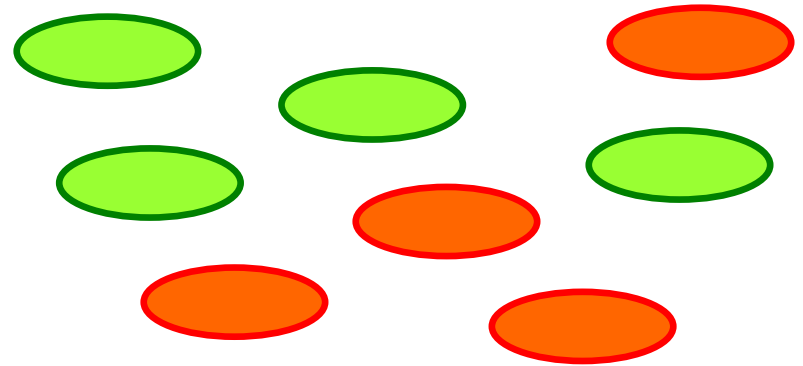
$D - d(t)$     $m(t)$     $d(t)$

# Analytical approach
## III: Density dependent selection $(m = 0)$

No gene-flow

- independent islands

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- branching process
  on a single island:

$$s_{\text{eff}}(t) = s\left(1 - \beta\frac{N_W(t)}{K}\right)$$
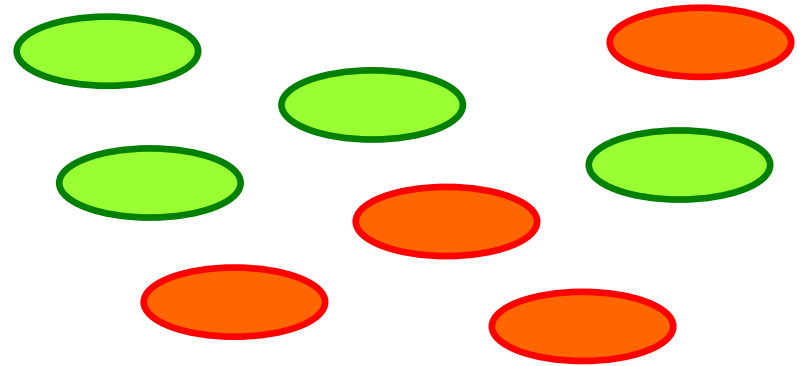
# Analytical approach
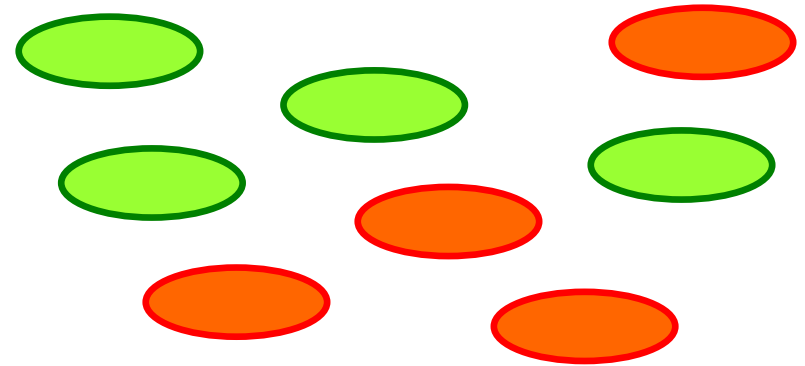## III: Density dependent selection $(m = 0)$

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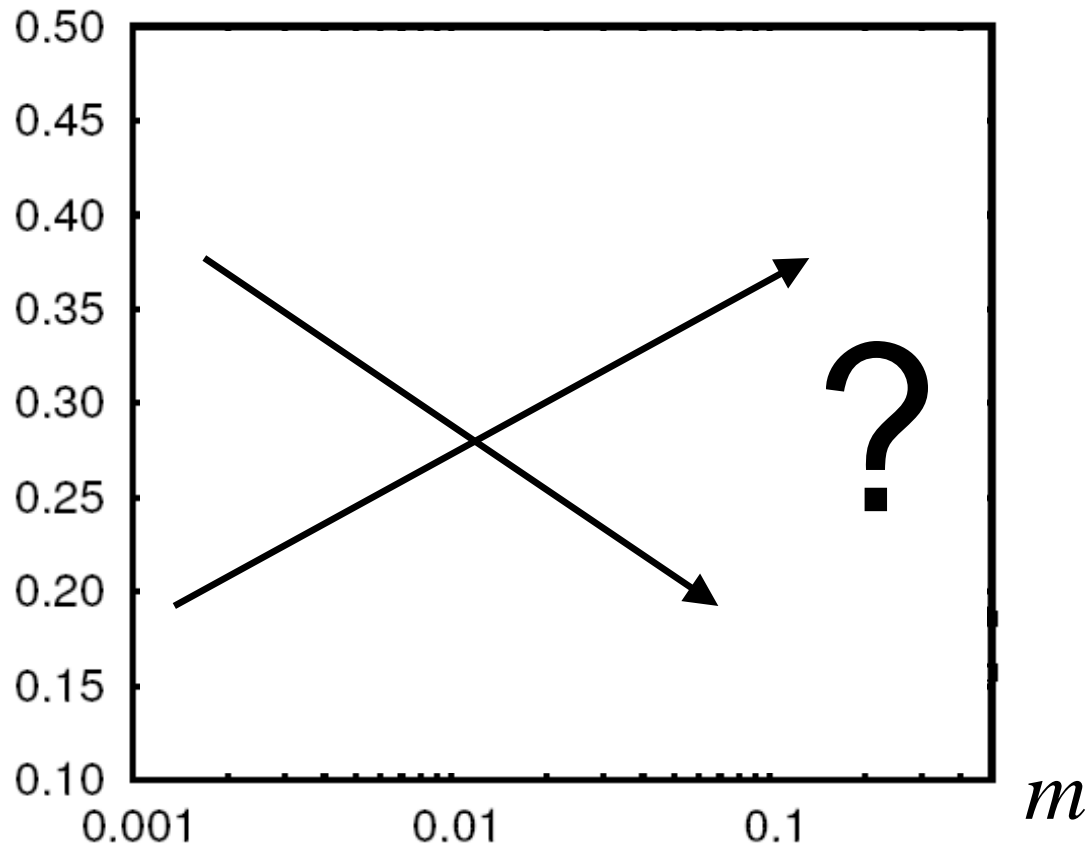
$$\text{ODE} \Rightarrow N_W(t) = \ldots$$

$$\Rightarrow P_{resc} = \ldots$$

results just depend on population size, not on the number of demes
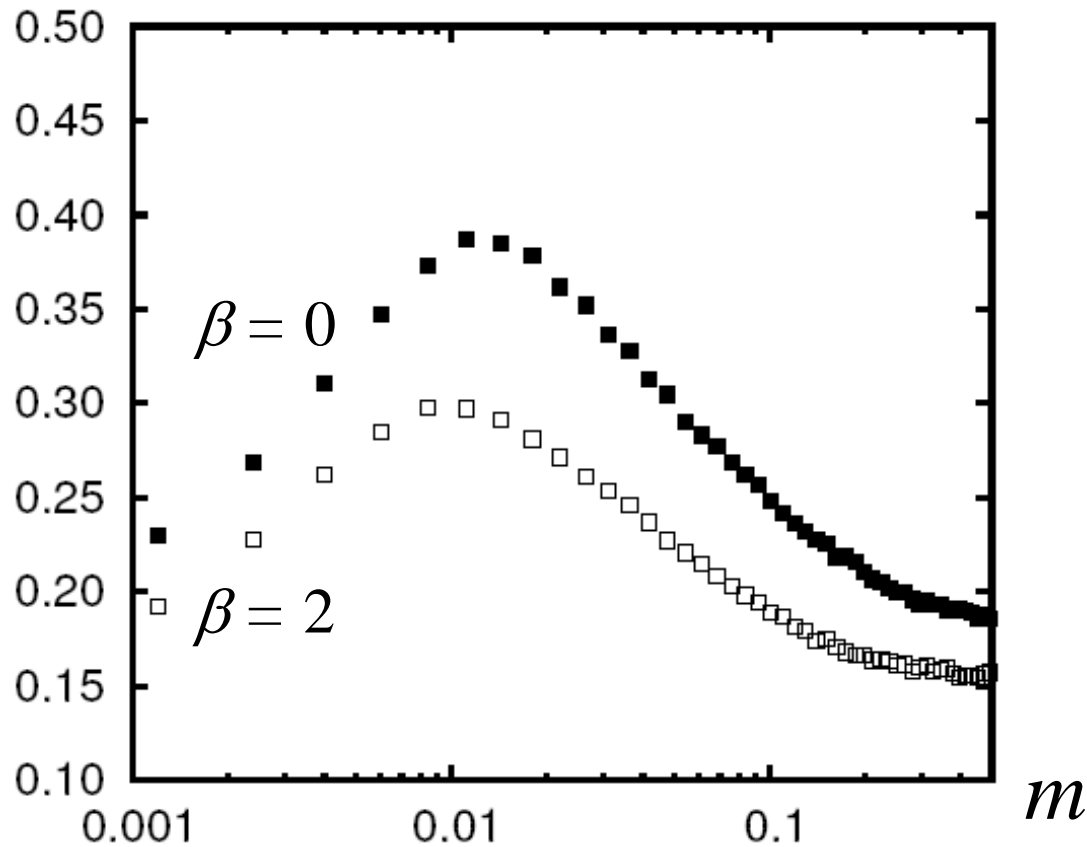$\rightarrow$ same as panmictic population

# Level of gene-flow



$P_{resc}(m)$

$m$

# Level of gene-flow

$P_{resc}(m)$



no standing
genetic variation
$(z = 1)$

$D = 8$
$N_0 = 2500$
$T = 250$
$u\,D\,N_0 = 1$
$r = 0.1$
$s = 0.01$

$\beta = 0$

$\beta = 2$

$m$

# Level of gene-flow

$$P_{resc}(m)$$
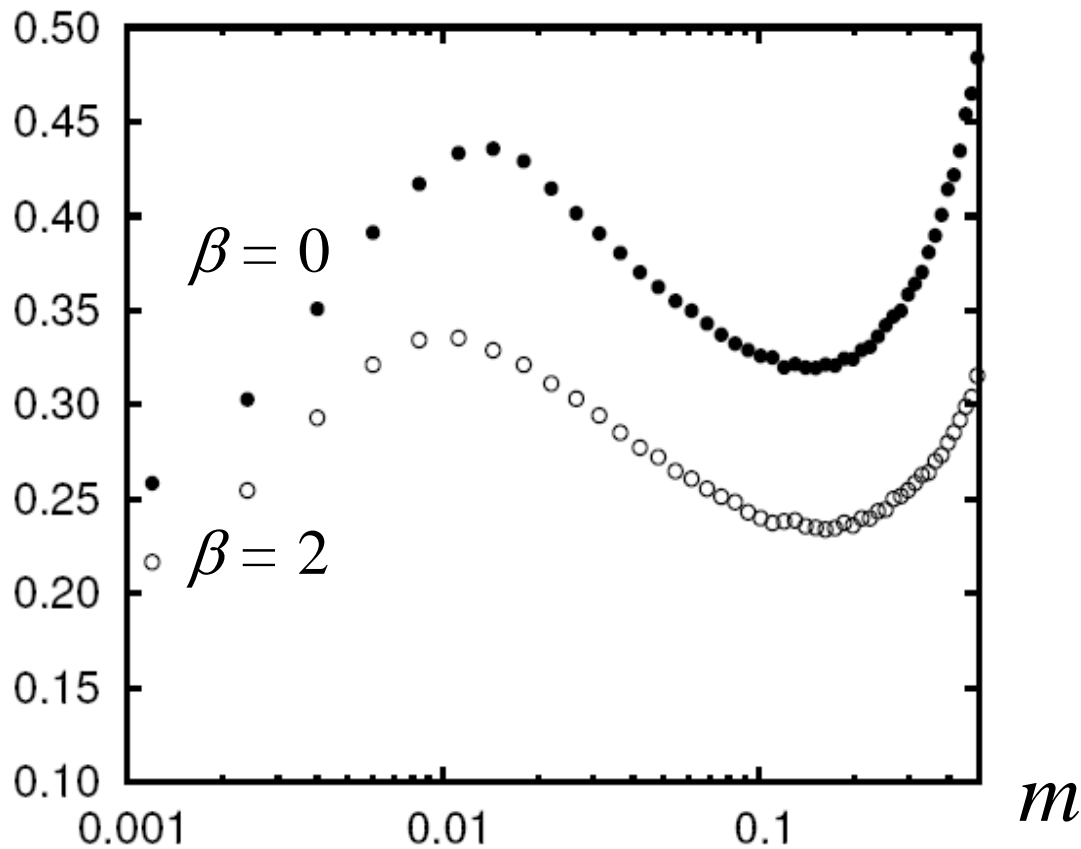


high standing
genetic variation
$(z = 0.1)$

$D = 8$
$N_0 = 2500$
$T = 250$
$uDN_0 = 1$
$r = 0.1$
$s = 0.01$
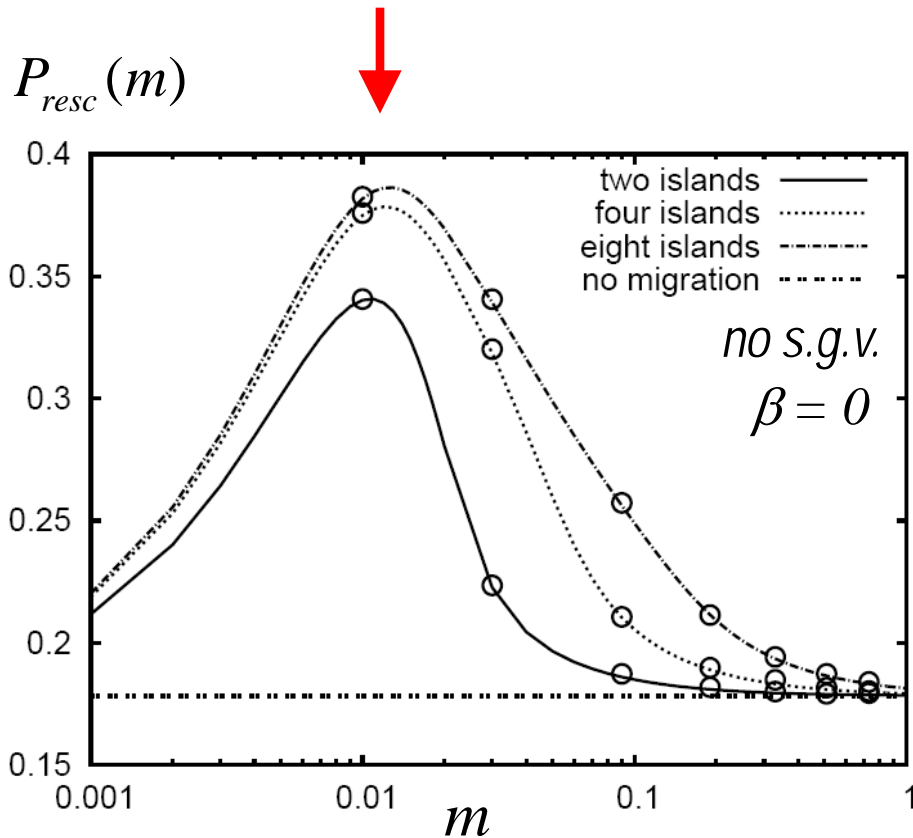
$\beta = 0$

$\beta = 2$

$m$

# Level of gene-flow

Why the intermediate
maximum?

$P_{resc}(m)$



*no s.g.v.*

$\beta = 0$

# Level of gene-flow

Why the intermediate maximum?

$P_{resc}(m)$



*no s.g.v.*

$\beta = 0$
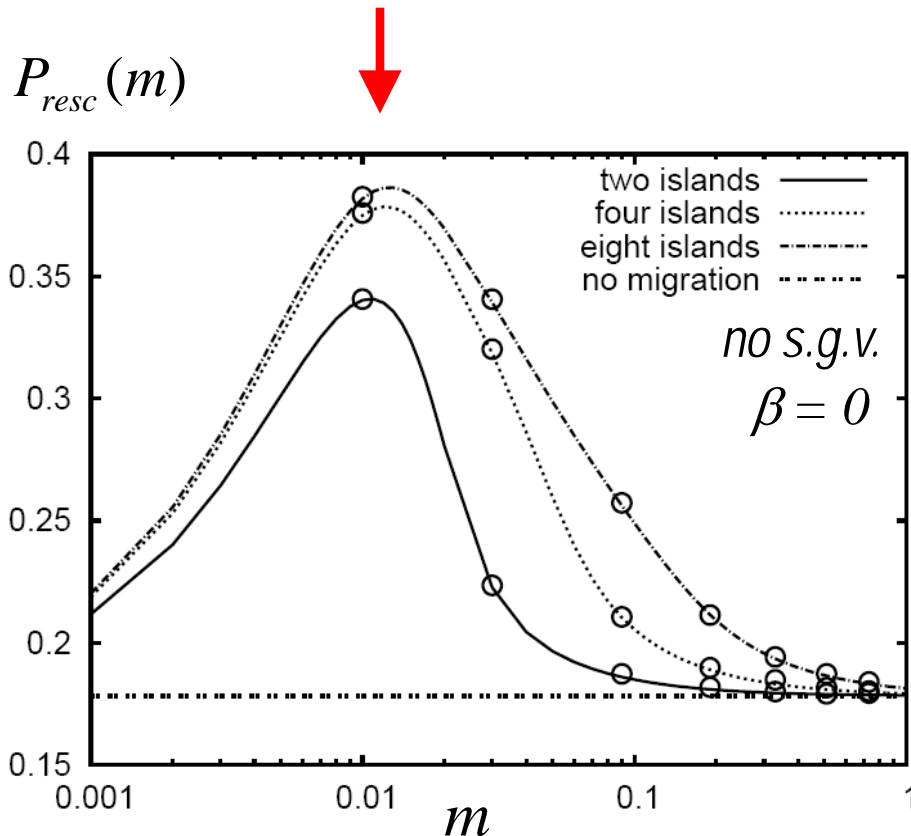
Two consequences of migration:

- wildtype migration beneficial: increases population size on perturbed islands

➢ gain proportional to $m$

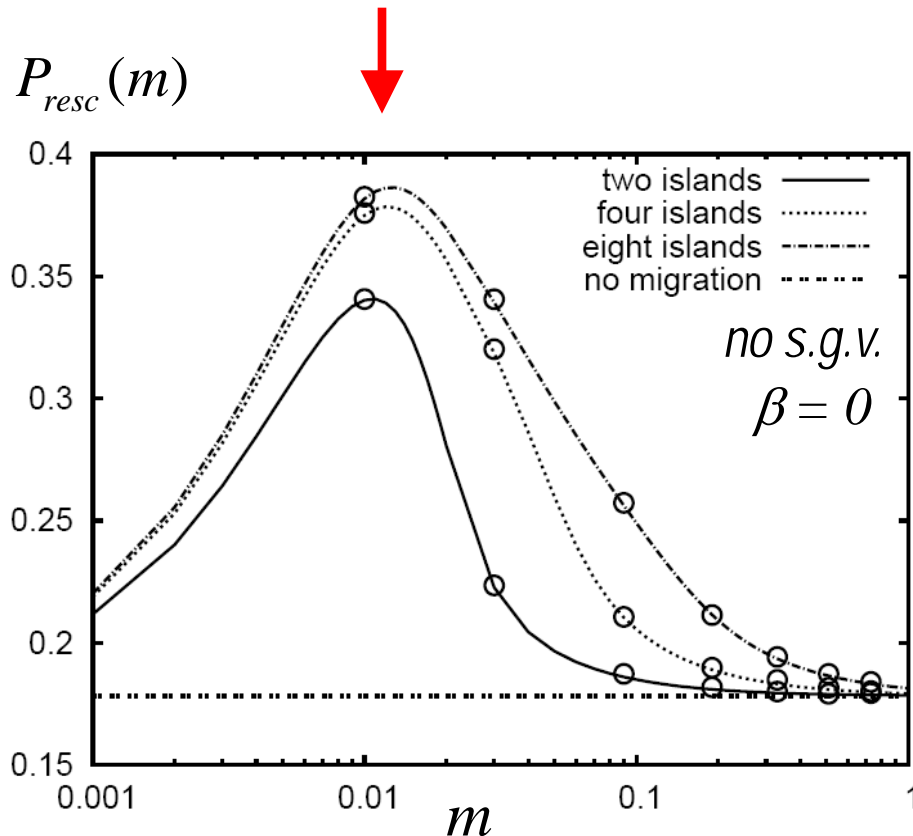# Level of gene-flow

Why the intermediate
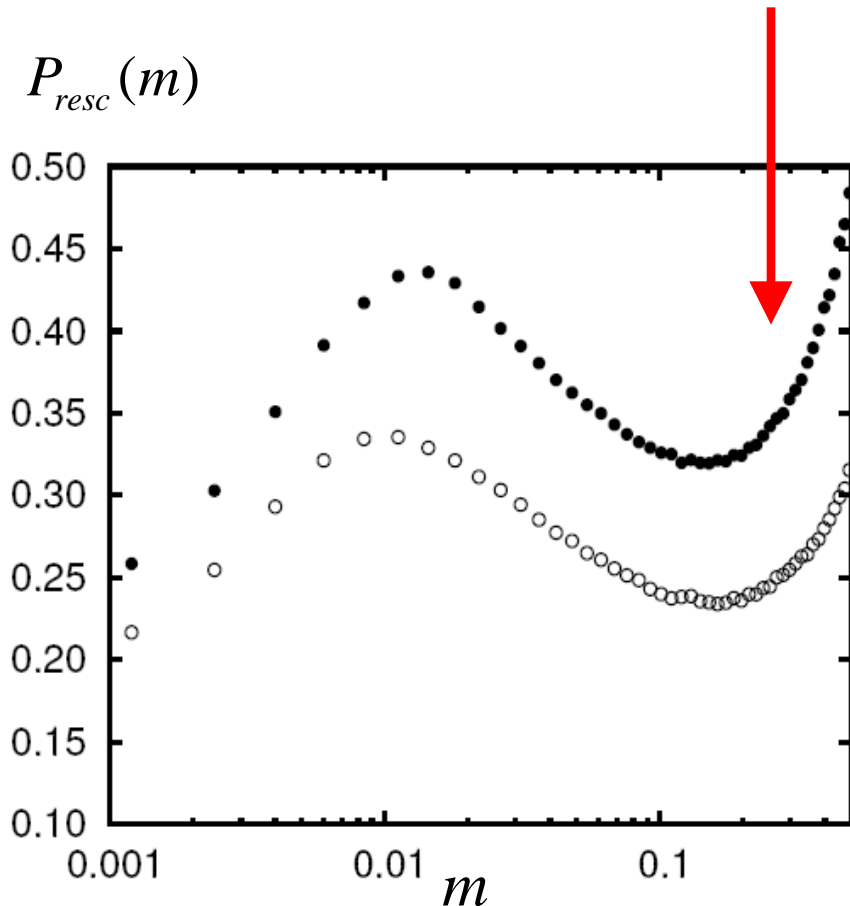maximum?

$P_{resc}(m)$



*no s.g.v.*

$\beta = 0$

Two consequences
of migration:

- wildtype migration beneficial:
  increases population size on
  perturbed islands

➢ gain proportional to $m$

- mutant migration detrimental:
  perturbed → original
  corresponds to loss of mutants

➢ loss proportional to $s - m$

# Level of gene-flow
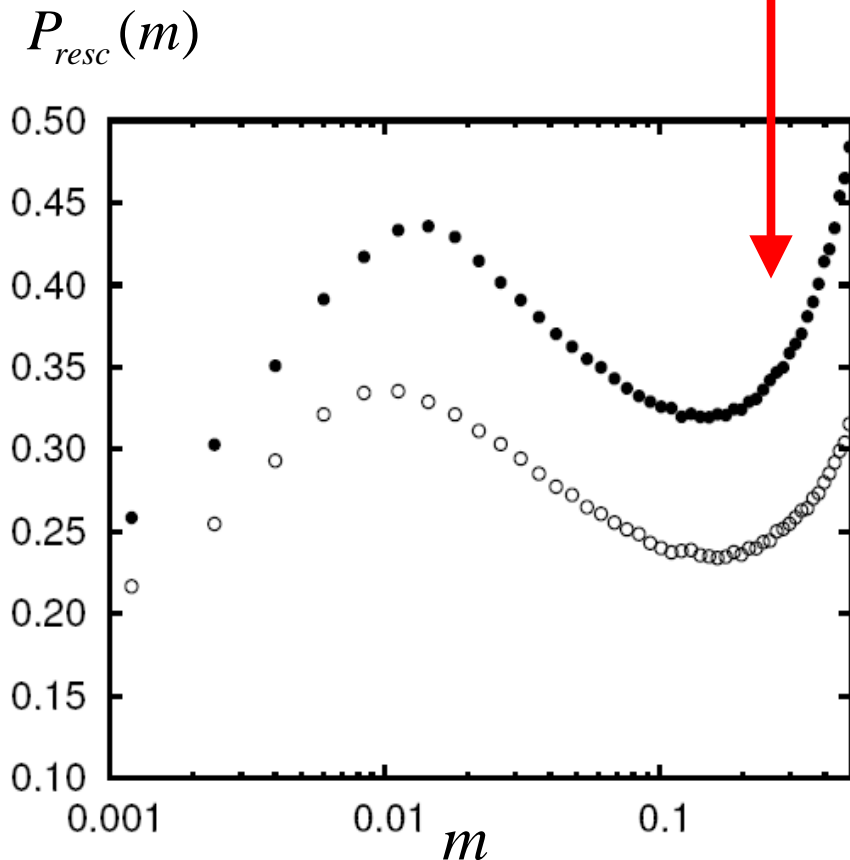
Why the increase?

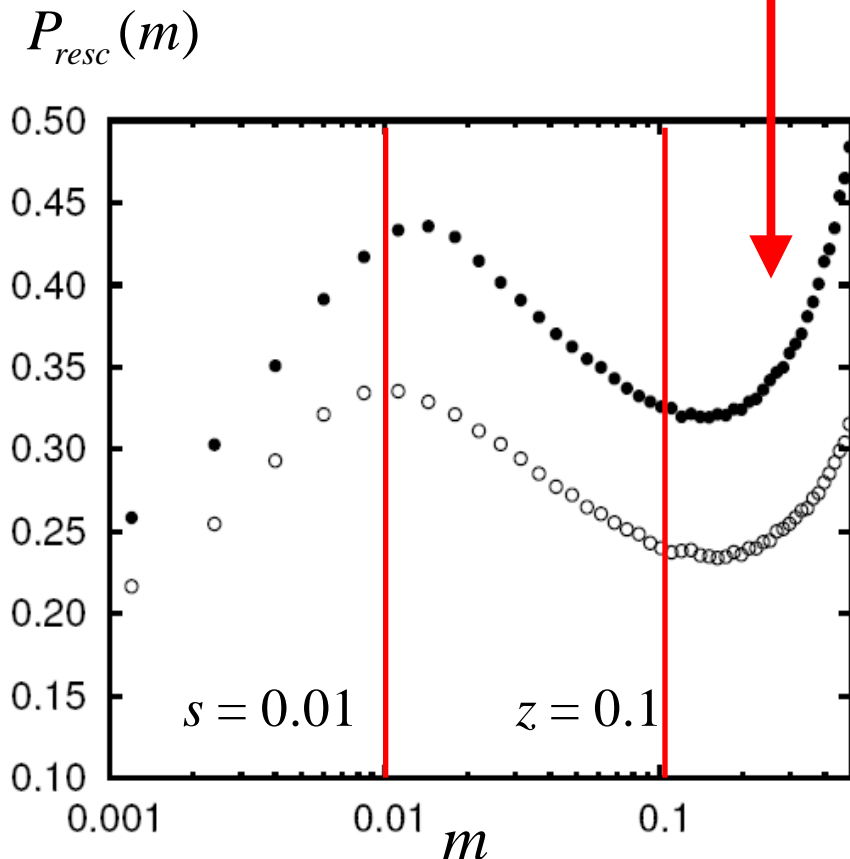$P_{resc}(m)$

# Level of gene-flow

Why the increase?

$P_{resc}(m)$



Further consequences
of migration:

- wildtype migration

➤ gain proportional to $m$

- back migration of migrants :
  – perturbed → original: loss
  – original → perturbed: recovery

➤ loss proportional to
  $s - m\,(1 - m/z)$

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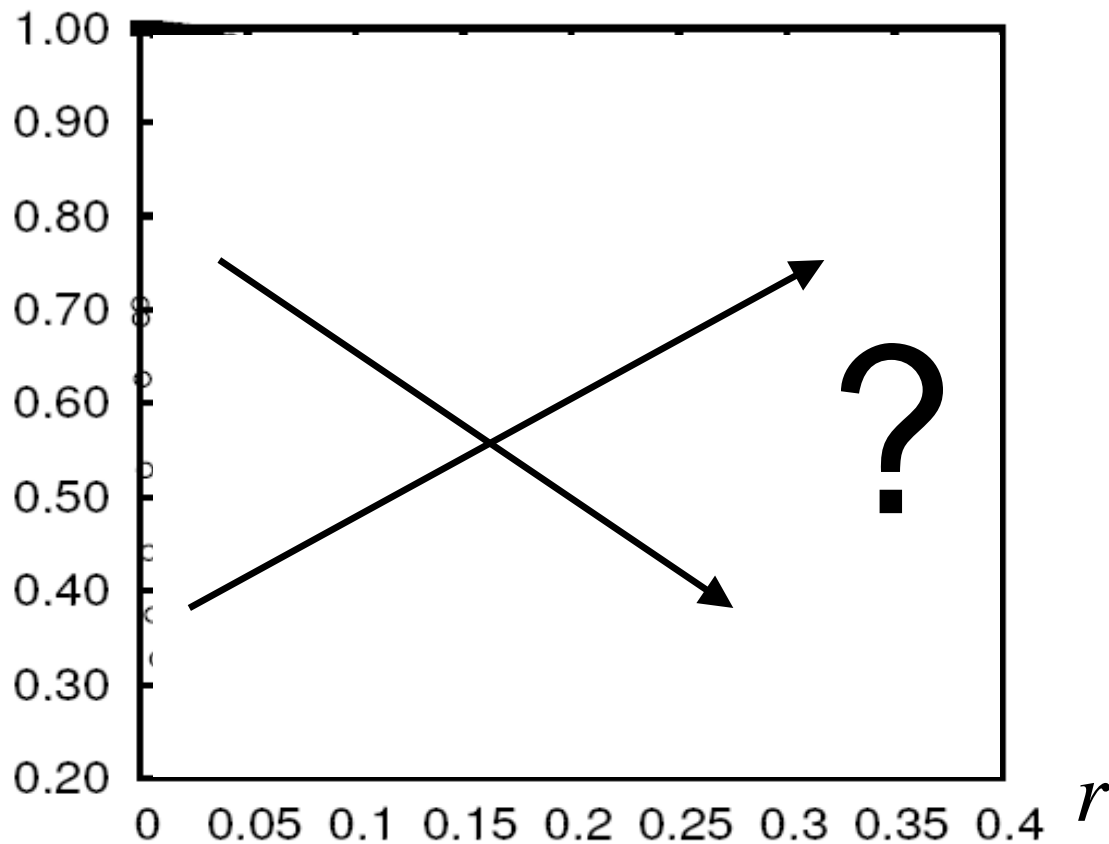
$P_{resc}(m)$



$s = 0.01$     $z = 0.1$

$m$

- wildtype migration

➢ gain proportional to $m$

- back migration of migrants :
  – perturbed $\rightarrow$ original: loss
  – original $\rightarrow$ perturbed: recovery

➢ loss proportional to
   $s - m\,(1 - m/z)$

$$P_{resc} \propto m\big(s - m\,(1 - m/z)\big)$$

# Severity of the change

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$$P_{resc}(r)$$

<span style="color:red">no density dependence</span>



high s.g.v.

no s.g.v.

$r$

<span style="color:red">$\beta = 0$</span>
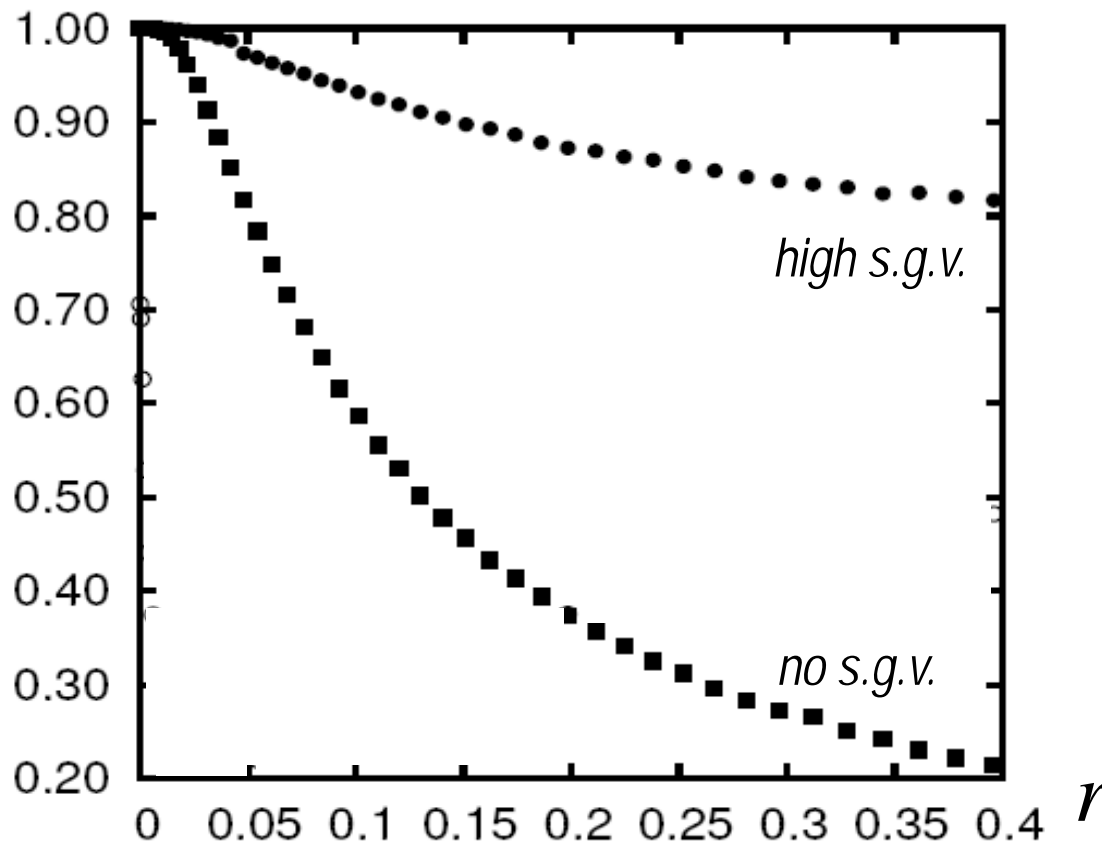
$D = 8$
$N_0 = 2500$
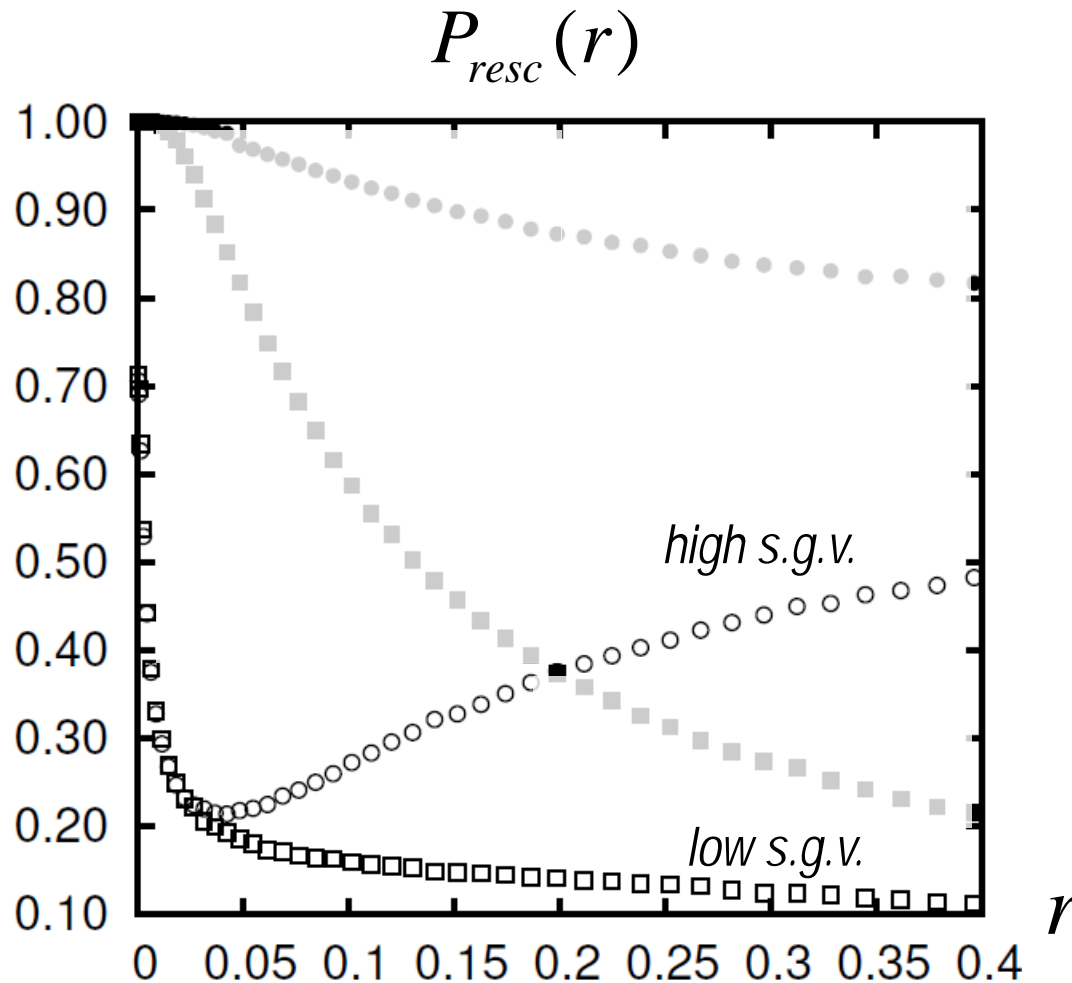$T = 250$
$uDN_0 = 1$
$m = 0.1$
$s\ = 0.02$

# Severity of the change

$P_{resc}(r)$ density dependence



$\beta = 2$

$D = 8$
$N_0 = 2500$
$T = 250$
$uDN_0 = 1$
$m = 0.1$
$s = 0.02$
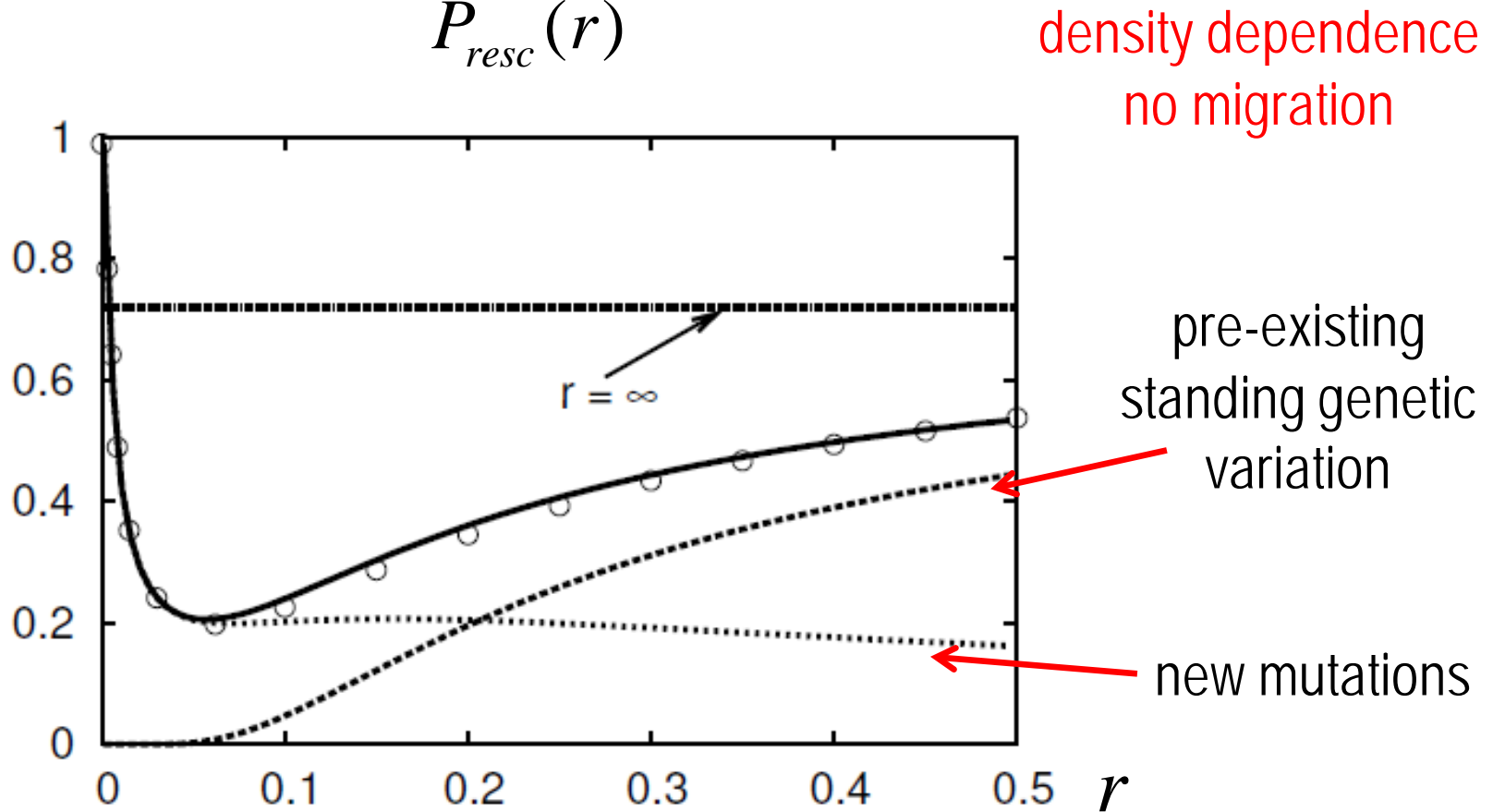
# Severity of the change

$P_{resc}(r)$



density dependence
no migration

pre-existing
standing genetic
variation

new mutations

$r = \infty$

# Severity of the change

Why increase
with $r$ ?

$P_{resc}(r)$

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Why increase
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$P_{resc}(r)$
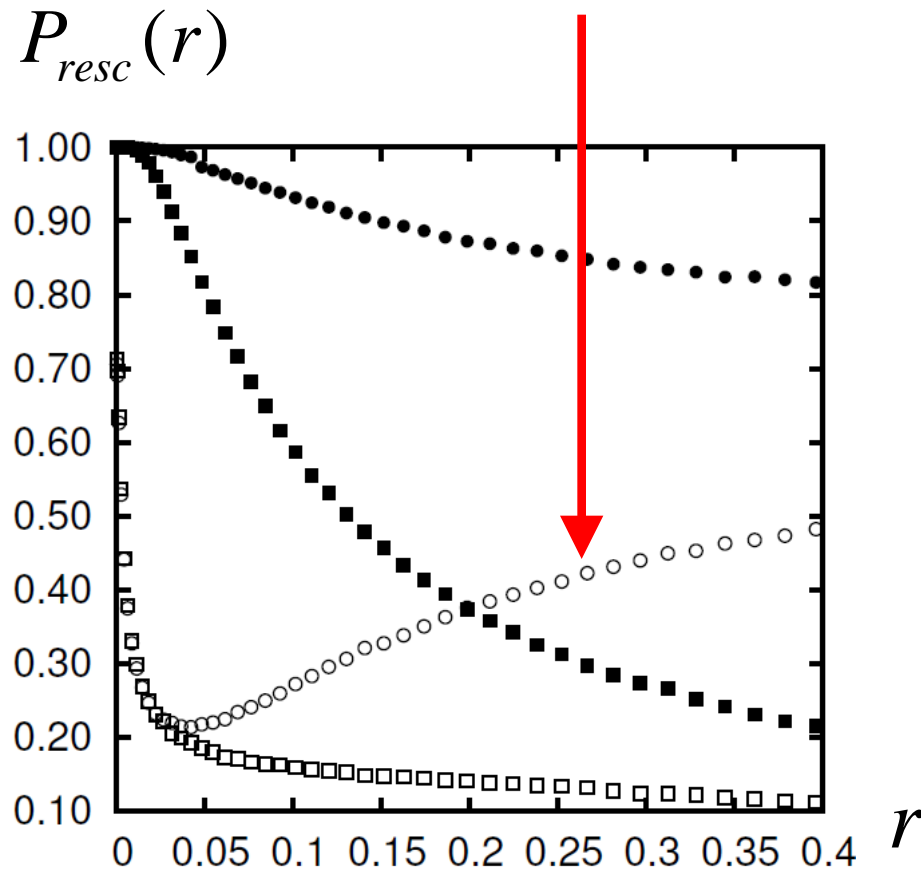


Interaction of standing variation
and density dependence:

- standing genetic variation :
  main source for mutant alleles

# Severity of the change

Why increase
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$P_{resc}(r)$



Interaction of standing variation
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- density dependence :
  adaptation only possible with
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➤ fast decline of wildtype needed
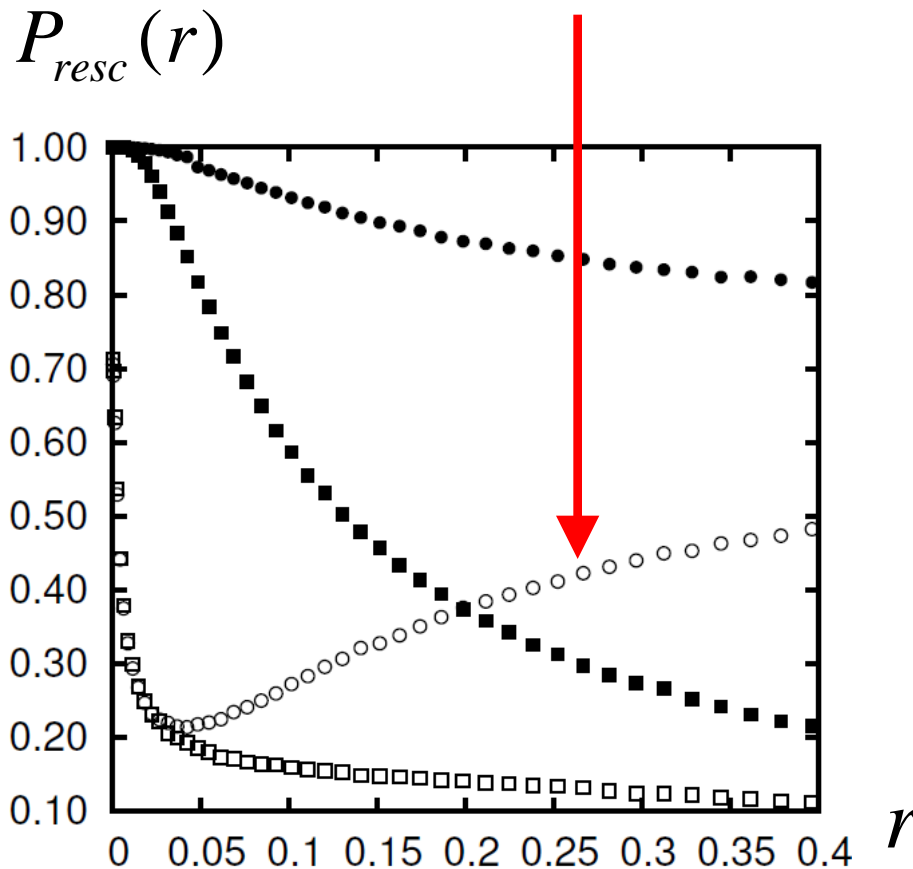  otherwise standing variation lost
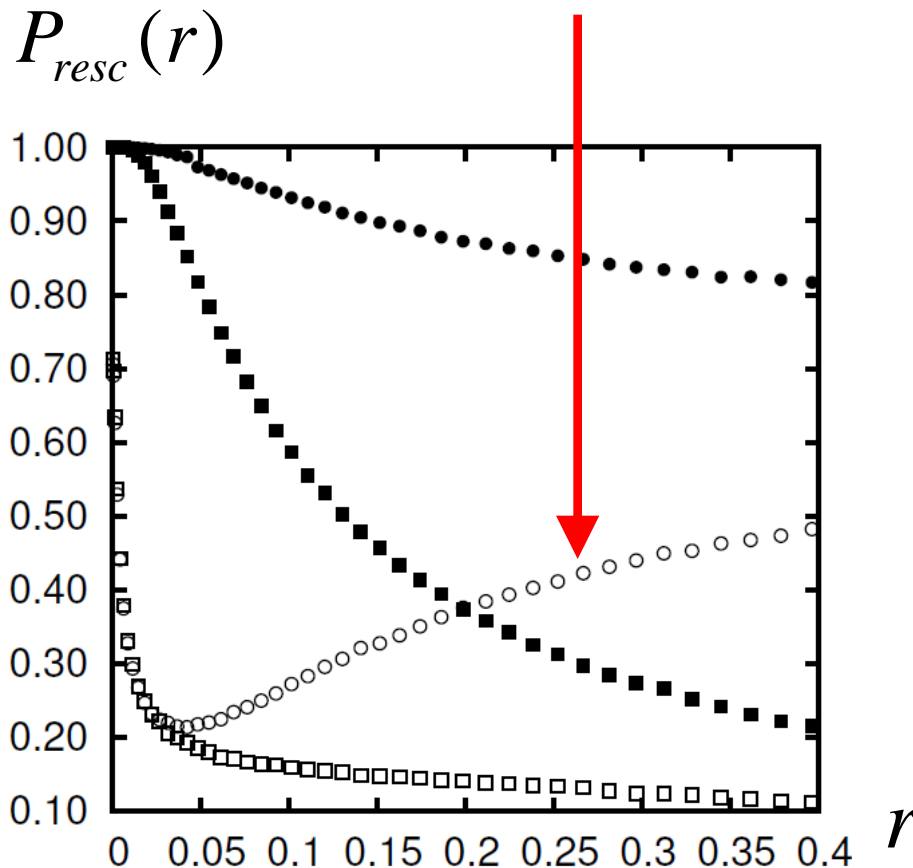
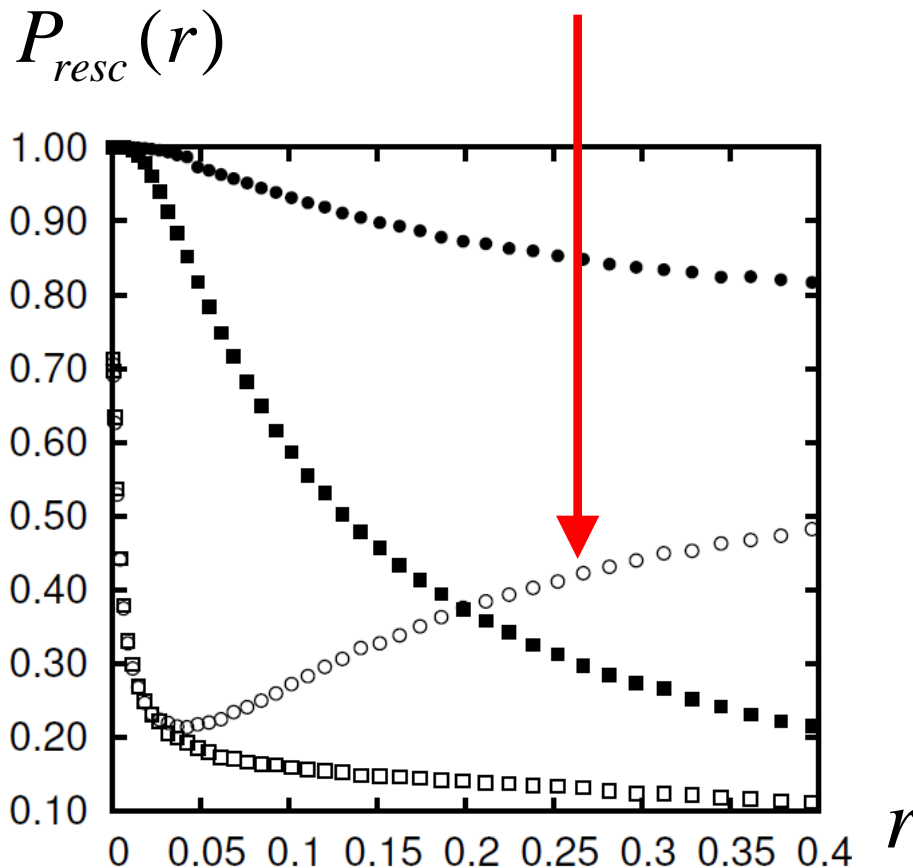# Severity of the change

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# Severity of the change

Why increase
with $r$ ?

Levene model $(m = 1)$
no density dependence !
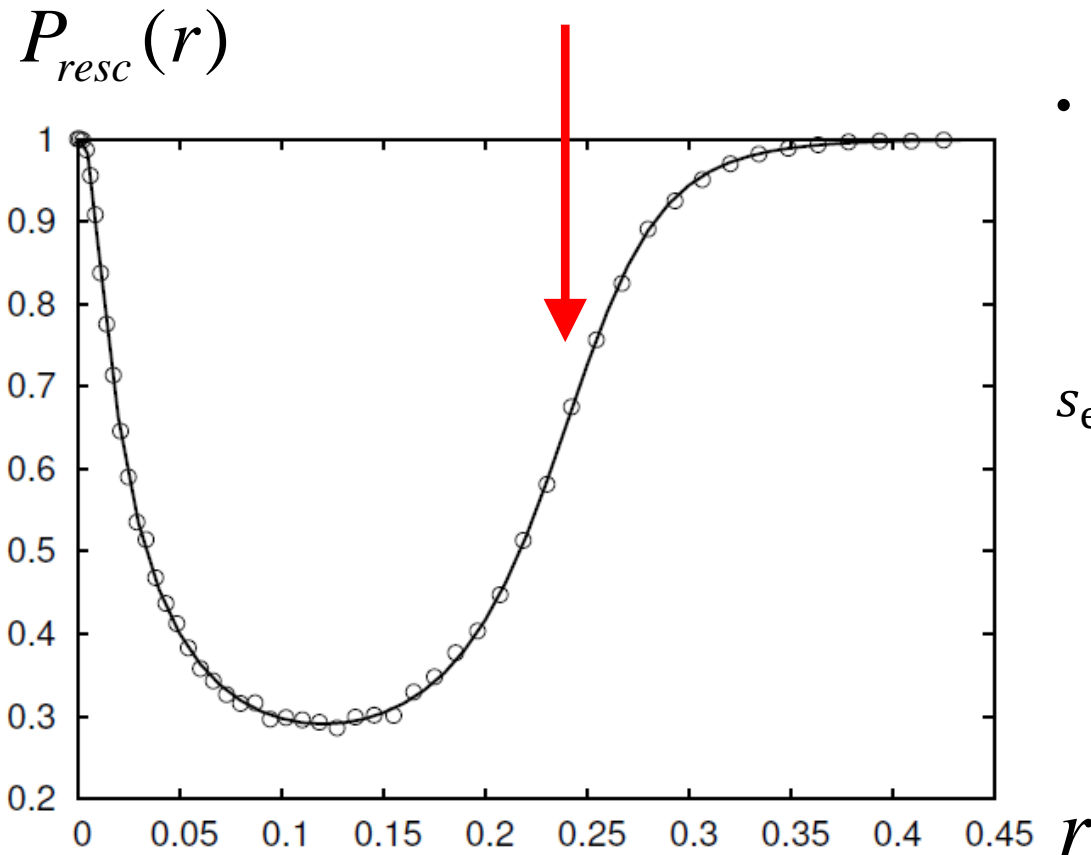
$P_{resc}(r)$

# Severity of the change

Why increase
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$P_{resc}(r)$

Levene model ($m = 1$)
no density dependence !

- for large back migration,
  mutant growth depends on
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$$s_{\text{eff}}(t) \approx \frac{d(t)}{D}(s + r) - \frac{D - d(t)}{D}z$$

# Severity of the change

Why increase
with $r$ ?

$P_{resc}(r)$



Levene model $(m = 1)$
no density dependence !

- for large back migration, mutant growth depends on wildtype decline:

$$s_{\text{eff}}(t) \approx \frac{d(t)}{D}(s + r) - \frac{D - d(t)}{D}z$$

➤ relaxed competition
➤ it can be easier to adapt to faster changes

# Summary

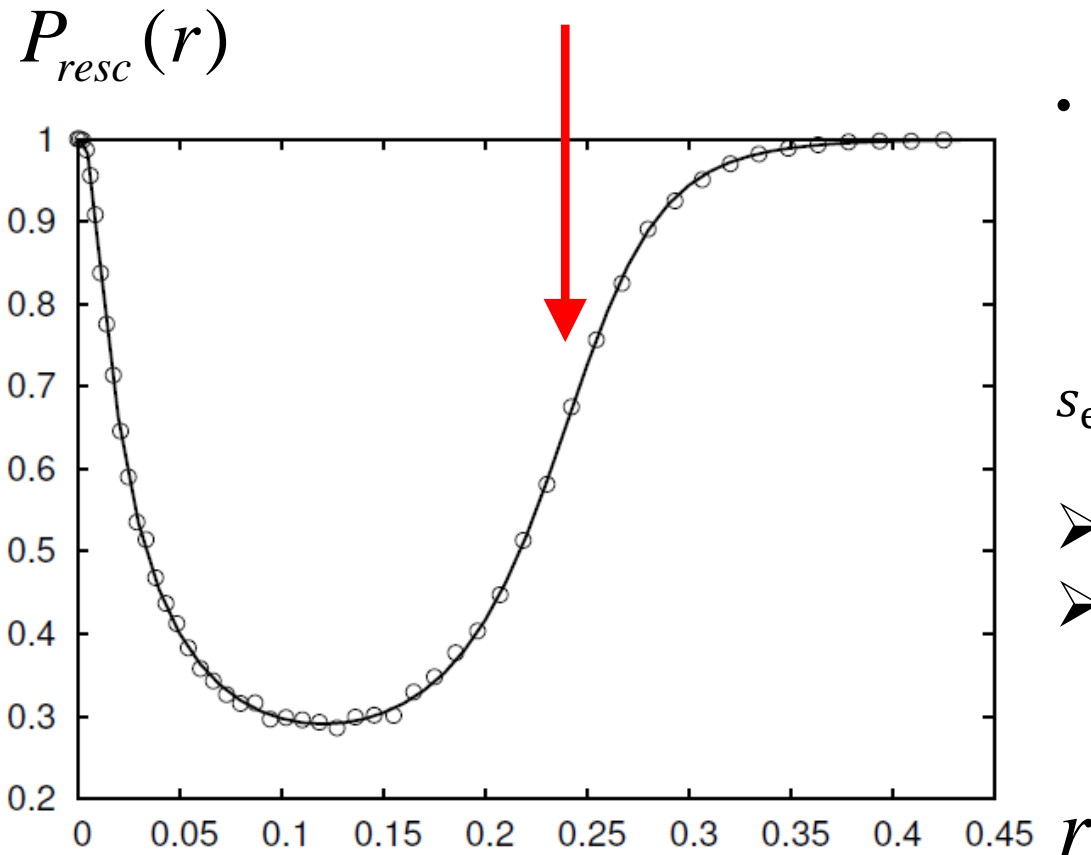Evolutionary rescue: ecology and evolution intertwined

- details & combination of many factors matters and can lead to unexpected behavior:

# Summary

Evolutionary rescue: ecology and evolution intertwined

- details & combination of many factors matters and can lead to unexpected behavior:

1. Three ways for migration to affect rescue probabilities
   - increases size of the source of wildtypes that might mutate
   - emigration decreases establishment probability for mutants
   - increases establishment probability through reduced competition

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*Ecology matters for the adaptive process !*

# Merci !

- Hildegard Uecker



- … and  **DFG**