

# Genetic Variability in the Mendelian Diploid Model

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Journée de la chaire MMB, 13 avril 2016

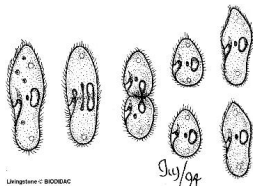


- 1 Introduction
- 2 Clonal reproduction model
  - Trait substitution sequence
- 3 Mendelian diploid model
  - Genetic variability

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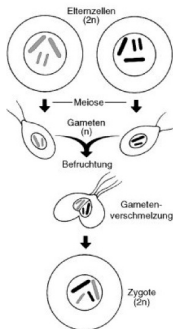
# Clonal Reproduction versus Sexual Reproduction

## Clonal Reproduction



vs.

## Sexual Reproduction



- individual reproduces out of itself
- offspring = copy of the parent
- offspring genom:
  - ▶ 100% of genes of the parent

- individual needs a partner for reproduction
- offspring genom:
  - ▶ 50% genes of mother
  - ▶ 50% genes of father

# Clonal Reproduction versus Sexual Reproduction

## Clonal Reproduction

- + fast growing populations
- + no time loss for partner selection
- genes stay constant over generations
- hard adaptation to changing environment

## Sexual Reproduction

- slowly growing population
- time cost for partner selection
- + genetic variability
- + possible adaptation to changing environment
- + correction of genetic defects
- + elimination of disadvantageous mutations

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# Clonal reproduction model

*Bolker, Pacala, Dieckmann, Law, Champagnat, Méléard,...*

$\Theta \simeq \mathbb{N}$  : Trait space

$n_i(t)$  : Number of individuals of trait  $i \in \Theta$

Dynamics of the process

$$n(t) = (n_0(t), n_1(t), \dots) \in \mathbb{N}^{\mathbb{N}} \quad :$$

Each individual of trait  $i$

- reproduces clonally with rate  $b_i(1 - \mu)$
- reproduces with mutation with rate  $b_i\mu$  according to some mutation kernel  $M(i, j)$
- dies due to age or competition with rate  $d_i + \sum_j c_{ij}n_j$

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Dynamics of the process

$$n(t) = (n_0(t), n_1(t), \dots) \in \mathbb{N}^{\mathbb{N}} \quad :$$

The population  $n_i$

- increases by 1 with rate  $b_i(1 - \mu)n_i$
- makes  $n_j$  increase by 1 with rate  $b_i\mu \cdot M(i, j) \cdot n_i$
- decreases by 1 with rate  $(d_i + \sum_j c_{ij}n_j)n_i$



# Clonal reproduction model

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$\Theta \simeq \mathbb{N}$  : Trait space

$n_i(t)$  : Number of individuals of trait  $i \in \Theta$

Dynamics of the **rescaled** process (with competition  $c_{ij}/K$ )

$$n^K(t) = \frac{1}{K}(n_0(t), n_1(t), \dots) \in (\mathbb{N}/K)^{\mathbb{N}} \quad :$$

The population  $n_i^K$

- increases by  $1/K$  with rate  $b_i(1 - \mu) \cdot Kn_i^K$
- makes  $n_j^K$  increase by  $1/K$  with rate  $b_i\mu M(i, j) \cdot Kn_i^K$
- decreases by  $1/K$  with rate  $(d_i + \sum_j c_{ij}n_j^K) \cdot Kn_i^K$

# Large populations limit

$$\mu = 0 \text{ and } K \rightarrow \infty$$

Fournier, Méléard, 2004

## Proposition

Let  $\Theta = \{1, 2\}$ , assume that the initial condition  $(n_1^K(0), n_2^K(0))$  converges to a deterministic vector  $(x_0, y_0)$  for  $K \rightarrow \infty$ . Then the process  $(n_1^K(t), n_2^K(t))$  converges in law, on bounded time intervals, to the solution of

$$\frac{d}{dt} \begin{pmatrix} x(t) \\ y(t) \end{pmatrix} = X(x(t), y(t)) = \begin{pmatrix} (b_1 - d_1 - c_{11}x - c_{12}y)x \\ (b_2 - d_2 - c_{21}x - c_{22}y)y \end{pmatrix}.$$

with initial condition  $(x(0), y(0)) = (x_0, y_0)$ .

Monomorphic equilibria :  $\bar{n}_i = \frac{b_i - d_i}{c_{ii}}$

Invasion fitness :  $f_{ij} = b_i - d_i - c_{ij}\bar{n}_j$ .

# Large populations and rare mutations limit

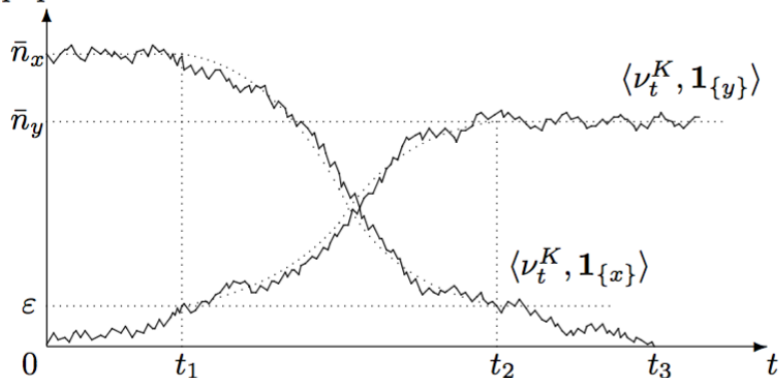
$$\mu = \mu(K) \ll (K \log K)^{-1}$$

Champagnat, 2006

Start with  $n_i^K(0) = \bar{n}_x 1_{i=x} + \frac{1}{K} 1_{i=y}$  (time of the first mutation).

If  $y$  is fitter than  $x$ , i.e.  $f_{yx} > 0$  and  $f_{xy} < 0$ , then with proba  $\rightarrow 1$ :

population size



$O(\log K)$

Supercritical BP

$O(1)$

LLN

$O(\log K)$

Subcritical BP

## Proposition

Assume

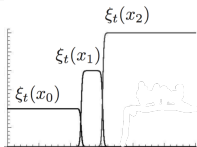
- $\log K \ll \frac{1}{K\mu} \ll \exp(cK)$
- $\forall (i, j) \in \Theta^2$ , either  $f_{ji} < 0$  or  $f_{ji} > 0$  and  $f_{ij} < 0$ .

Then the rescaled process

$$(n_{t/K\mu}^K)_{t \geq 0} \Rightarrow (\bar{n}_{X_t} \mathbf{1}_{X_t})_{t \geq 0}$$

where  $X_t$  is a Markov chain on  $\Theta$  with transition kernel

$$P(i, j) = b_i \frac{[f_{ji}]_+}{b_j} M(i, j).$$



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Let  $\mathcal{U}$  be the allelic trait space, a countable set.

For example  $\mathcal{U} = \{a, A\}$ .

- An individual  $i$  is determined by two alleles out of  $\mathcal{U}$  :

- ▶ **genotype:**  $(u_1^i, u_2^i) \in \mathcal{U}^2$

- ▶ **phenotype:**  $\phi((u_1^i, u_2^i))$ , with  $\phi : \mathcal{U}^2 \rightarrow \mathbb{R}_+$

- Rescaled population:

let  $N_t$  be the total number of individuals at time  $t$ ,

$$n_{u_1, u_2}^K(t) = \frac{1}{K} \sum_{i=1}^{N_t} 1_{(u_1^i, u_2^i)}(t)$$

# Reproduction

**Reproduction rate** of  $(u_1^i, u_2^i)$  with  $(u_1^j, u_2^j)$ :

$$\frac{f_{u_1^i u_2^i} f_{u_1^j u_2^j}}{\text{Number of potential partners of } (u_1^i, u_2^i) \times \text{their mean fertility}}$$

# Reproduction

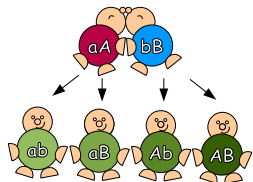
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## Reproduction without muta-

**tion:** Probability  $1 - \mu_K$

⇒ Mendelian rules: newborn getting genotype with coordinates that are sampled at random from each parent.





# Reproduction

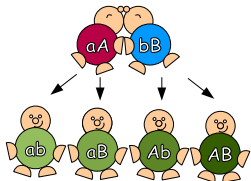
**Reproduction rate** of  $(u_1^i, u_2^i)$  with  $(u_1^j, u_2^j)$ :

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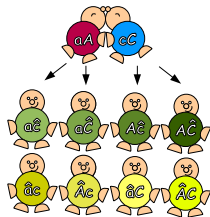
**Reproduction without mutation:** Probability  $1 - \mu_K$

$\Rightarrow$  Mendelian rules: newborn getting genotype with coordinates that are sampled at random from each parent.



**Reproduction with mutation:** Probability  $\mu_K$

$\Rightarrow$  changing one of the two allelic traits of the newborn from  $a$  to  $b$  according to the kernel  $M(a, b)$ .



# Birth and Death Rate

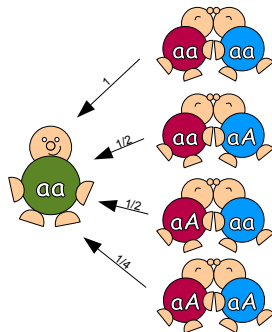
Let  $\mathcal{U} = \{a, A\}$ , and  $\mu_K = 0$ .

- The populations increase by 1 with rate

$$b_{aa} = \frac{(f_{aa}n_{aa} + \frac{1}{2}f_{aA}n_{aA})^2}{f_{aa}n_{aa} + f_{aA}n_{aA} + f_{AA}n_{AA}}$$

$$b_{aA} = 2 \frac{(f_{aa}n_{aa} + \frac{1}{2}f_{aA}n_{aA})(f_{AA}n_{AA} + \frac{1}{2}f_{aA}n_{aA})}{f_{aa}n_{aa} + f_{aA}n_{aA} + f_{AA}n_{AA}}$$

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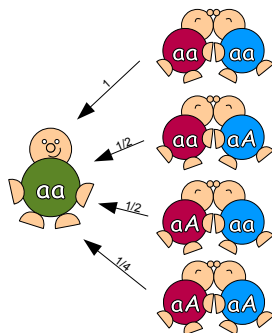
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- The populations decrease by 1 with rate

$$d_{aa} = (D_{aa} + C_{aa,aa}n_{aa} + C_{aa,aA}n_{aA} + C_{aa,AA}n_{AA})n_{aa}$$

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$$d_{AA} = (D_{AA} + C_{AA,AA}n_{AA} + C_{AA,aA}n_{aA} + C_{AA,aa}n_{aa})n_{AA}$$



## Proposition

Assume that the initial condition  $(n_{aa}^K(0), n_{aA}^K(0), n_{AA}^K(0))$  converges to a deterministic vector  $(x_0, y_0, z_0)$  for  $K \rightarrow \infty$ . Then the process  $(n_{aa}^K(t), n_{aA}^K(t), n_{AA}^K(t))$  converges in law to the solution of

$$\frac{d}{dt} \begin{pmatrix} x(t) \\ y(t) \\ z(t) \end{pmatrix} = X(x(t), y(t), z(t)) = \begin{pmatrix} b_{aa}(x, y, z) - d_{aa}(x, y, z) \\ b_{aA}(x, y, z) - d_{aA}(x, y, z) \\ b_{AA}(x, y, z) - d_{AA}(x, y, z) \end{pmatrix}.$$

- $b_{AA}(x, y, z) = \frac{(f_{AA}z + \frac{1}{2}f_{aA}y)^2}{f_{aa}x + f_{aA}y + f_{AA}z}$
- $d_{AA}(x, y, z) = (D_{AA} + C_{AA,aa}x + C_{AA,aA}y + C_{AA,AA}z)z$
- and similar expressions for the other terms

# The 3-System ( $aa, aA, AA$ )

## Phenotypic viewpoint

- allele A **dominant**
- allele a **recessive**

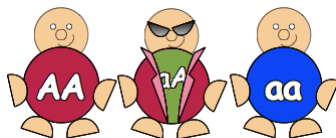


The dominant allele  $A$  defines the phenotype  $\Rightarrow \phi(aA) = \phi(AA)$

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- $c_{u_1 u_2, v_1 v_2} \equiv c, \quad \forall u_1 u_2, v_1 v_2 \in \{aa, aA, AA\}$
- $f_{AA} = f_{aA} = f_{aa} \equiv f$
- $D_{AA} = D_{aA} \equiv D$  **but**  $D_{aa} = D + \Delta$

# The 3-System ( $aa, aA, AA$ )

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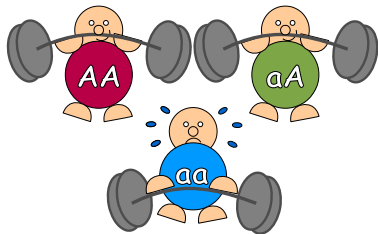
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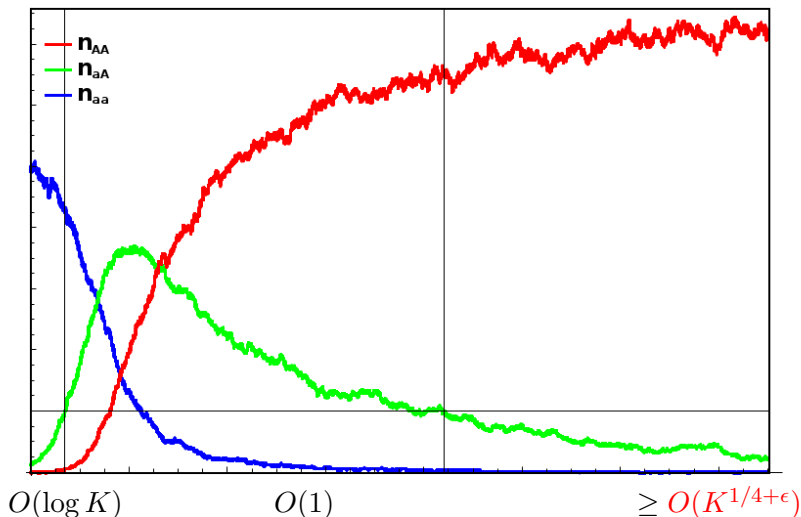
- $c_{u_1 u_2, v_1 v_2} \equiv c, \quad \forall u_1 u_2, v_1 v_2 \in \{aa, aA, AA\}$
- $f_{AA} = f_{aA} = f_{aa} \equiv f$
- $D_{AA} = D_{aA} \equiv D$  **but**  $D_{aa} = D + \Delta$

$\Rightarrow$  **type  $aA$  is as fit as  $AA$  and both are fitter than type  $aa$**



# Work of Bovier, Neukirch (2015)

Start with  $n_i^K(t) = \bar{n}_{aa}1_{i=aa} + \frac{1}{K}1_{i=aA}$  then :



The system converges to  $(0, 0, \bar{n}_{AA})$  as  $t \rightarrow \infty$  but **slowly** !



## Genetic Variability ? Polymorphism?

Suppose a new dominant mutant allele  $B$  appears before  $aA$  dies out.

Suppose that phenotypes  $a$  and  $B$  cannot reproduce.

Can the  $aa$ -population recover and coexist with the mutant population ?

We will study the deterministic system and start with initial condition

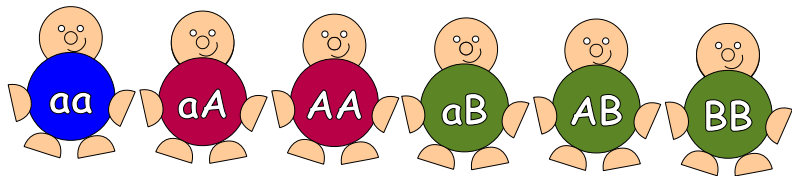
$$n_i(0) = \bar{n}_{AA}1_{i=AA} + \epsilon 1_{i=aA} + \epsilon^2 1_{i=aa} + \epsilon^3 1_{i=AB}$$

## Model with a second mutant

Mutation to allele  $B \rightarrow \mathcal{U} = \{a, A, B\}$

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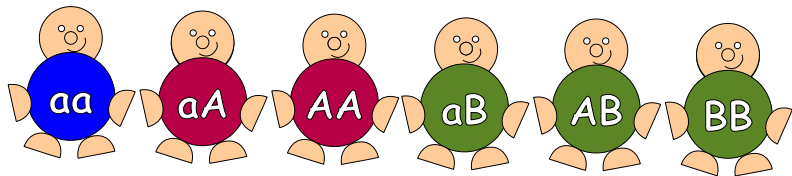


$\Rightarrow$  6 possible genotypes:  $aa$ ,  $aA$ ,  $AA$ ,  $aB$ ,  $AB$ ,  $BB$

$\Rightarrow$  Dominance of alleles  $a < A < B$

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Mutation to allele  $B \rightarrow \mathcal{U} = \{a, A, B\}$



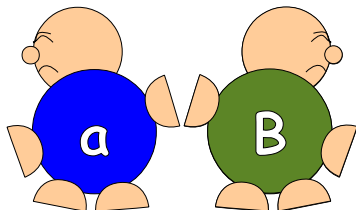
$\Rightarrow$  6 possible genotypes:  $aa, aA, AA, aB, AB, BB$

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### Differences in Fitness:

- fertility:  $f_a = f_A = f_B = f$
- natural death:  $D_a = D + \Delta > D_A = D > D_B = D - \Delta$

**No recombination** between  $a$  and  $B$

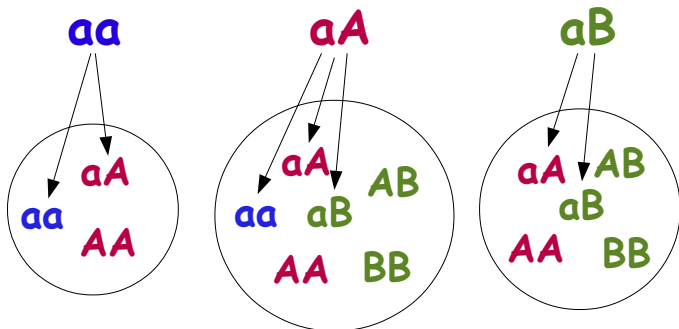


# Birth Rates

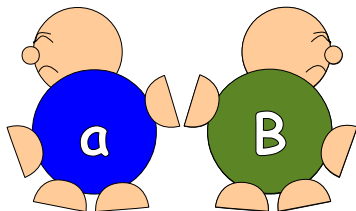
birth-rate of *aa*-individual:

$$b_{aa} = \frac{n_{aa} (n_{aa} + \frac{1}{2}n_{aA})}{\text{Pool}(aa)} + \frac{\frac{1}{2}n_{aB} (\frac{1}{2}n_{aA} + \frac{1}{2}n_{aB})}{\text{Pool}(aB)} + \frac{\frac{1}{2}n_{aA} (n_{aa} + \frac{1}{2}n_{aA} + \frac{1}{2}n_{aB})}{\text{Pool}(aA)}$$

Pools of potential partners:



**No competition** between  $a$  and  $B$

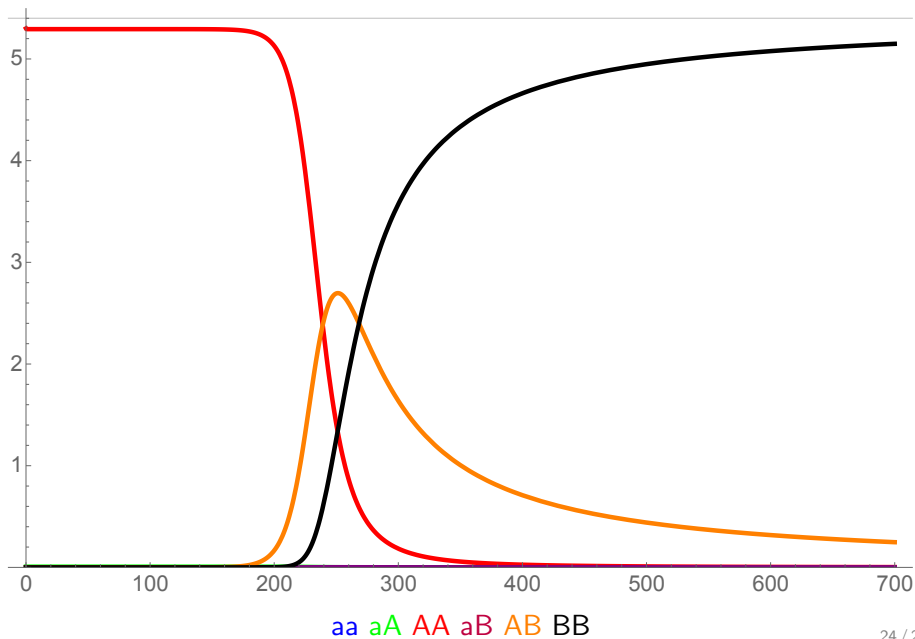


# Competition - first try

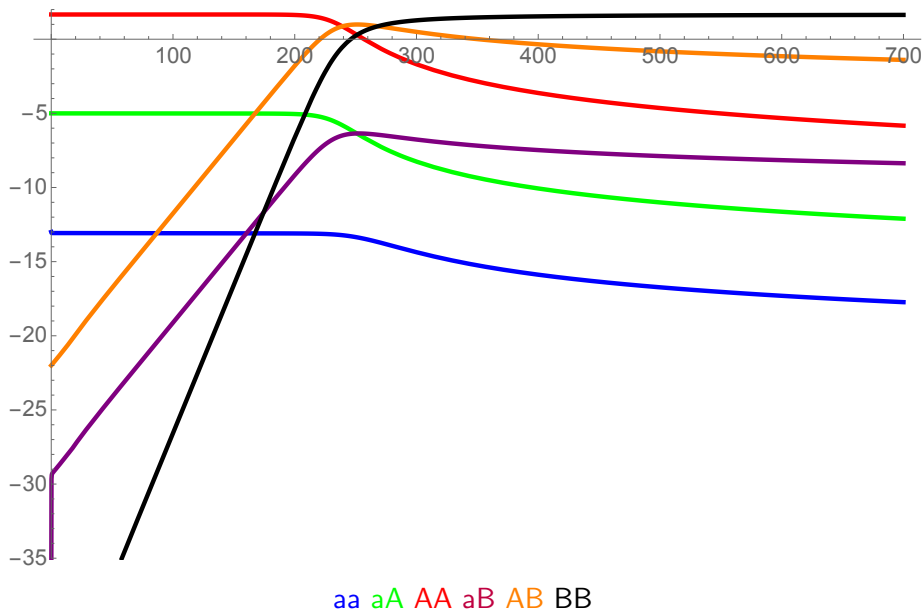
|    | aa       | aA       | AA       | aB       | AB       | BB       |
|----|----------|----------|----------|----------|----------|----------|
| aa | <i>c</i> | <i>c</i> | <i>c</i> | 0        | 0        | 0        |
| aA | <i>c</i> | <i>c</i> | <i>c</i> | <i>c</i> | <i>c</i> | <i>c</i> |
| AA | <i>c</i> | <i>c</i> | <i>c</i> | <i>c</i> | <i>c</i> | <i>c</i> |
| aB | 0        | <i>c</i> | <i>c</i> | <i>c</i> | <i>c</i> | <i>c</i> |
| AB | 0        | <i>c</i> | <i>c</i> | <i>c</i> | <i>c</i> | <i>c</i> |
| BB | 0        | <i>c</i> | <i>c</i> | <i>c</i> | <i>c</i> | <i>c</i> |



# Competition - first try

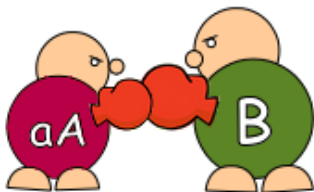


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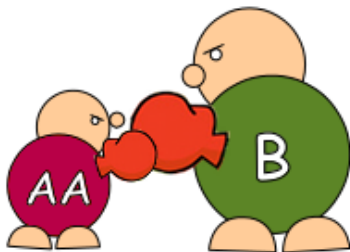
# Competition - second try

competition felt by  
 $n_{aA}$  from  $B$ -individuals



<

competition felt by  
 $n_{AA}$  from  $B$ -individuals

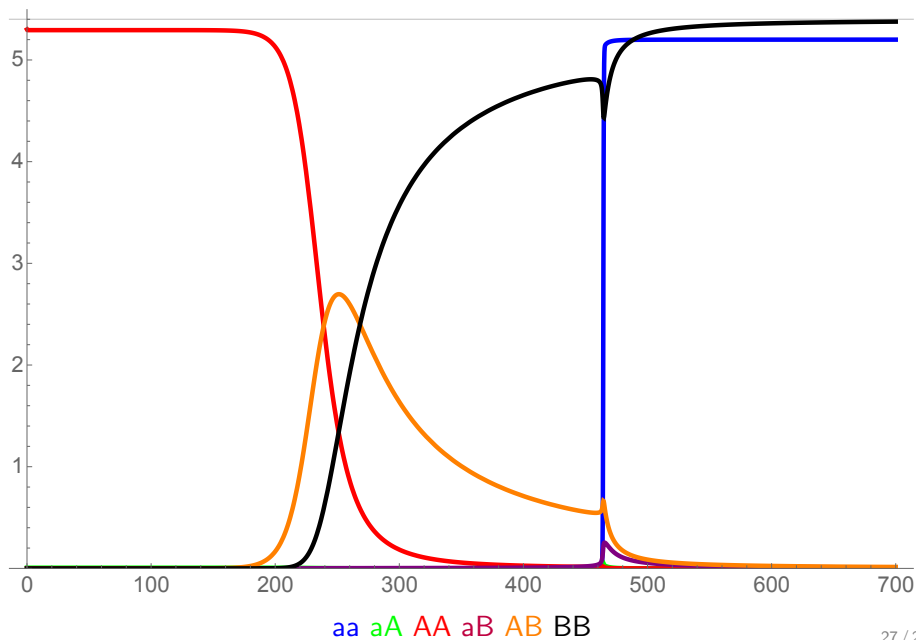


- the decay of  $aA$ -population slows down
- $aa$ -population can recover

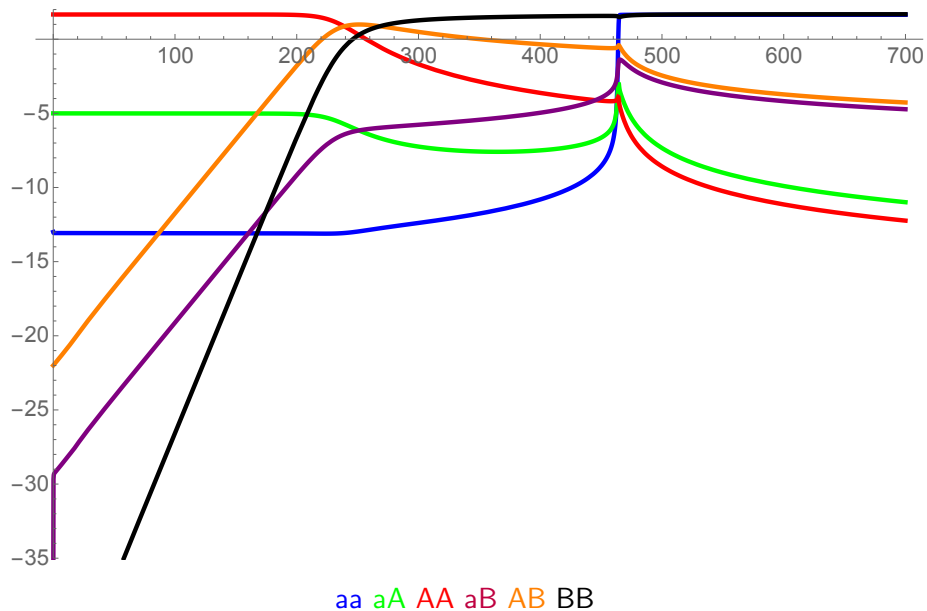
# Competition - second try

|    | aa  | aA         | AA  | aB  | AB  | BB         |
|----|-----|------------|-----|-----|-----|------------|
| aa | $c$ | $c$        | $c$ | 0   | 0   | 0          |
| aA | $c$ | $c$        | $c$ | $c$ | $c$ | $c - \eta$ |
| AA | $c$ | $c$        | $c$ | $c$ | $c$ | $c$        |
| aB | 0   | $c$        | $c$ | $c$ | $c$ | $c$        |
| AB | 0   | $c$        | $c$ | $c$ | $c$ | $c$        |
| BB | 0   | $c - \eta$ | $c$ | $c$ | $c$ | $c$        |

# Competition - second try

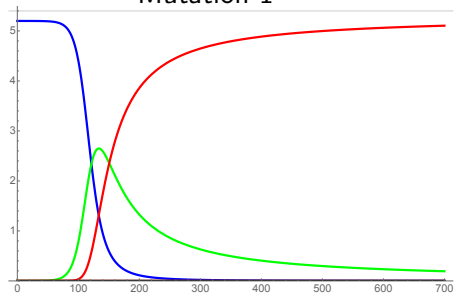


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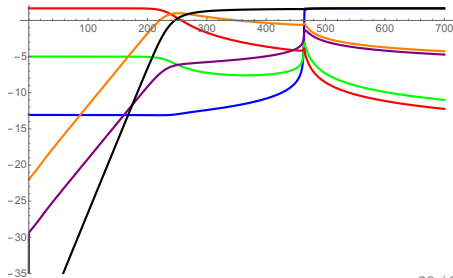
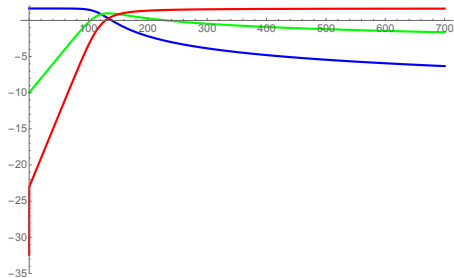
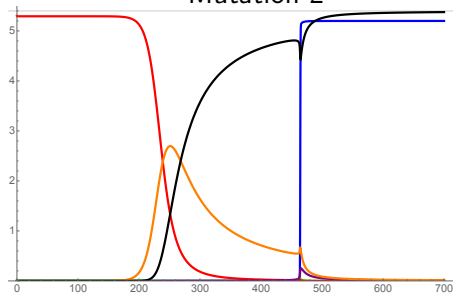


# Recap - Dimorphism in two mutations

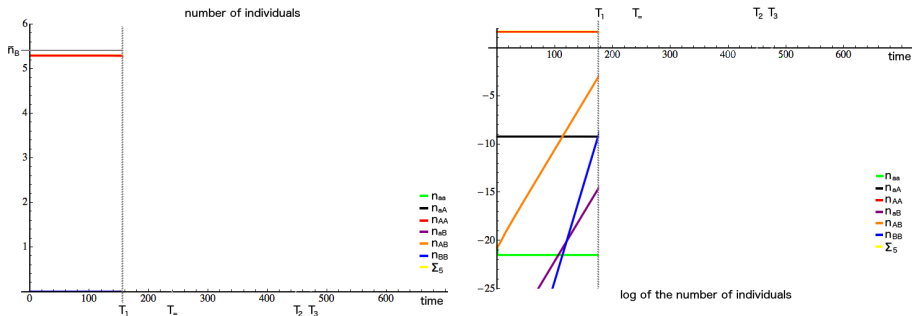
## Mutation 1



## Mutation 2



## 1.Phase: Fixation of the mutant



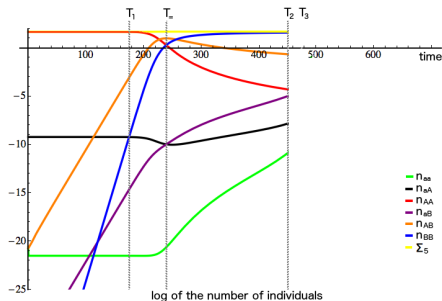
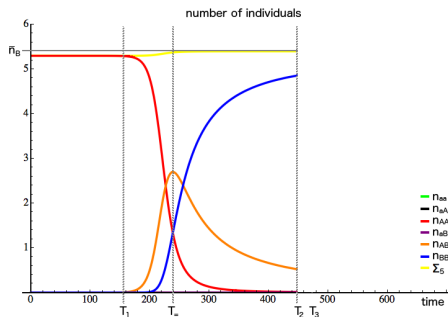
- $AB$  grows to level  $\varepsilon_0$

- $aB, BB \leq \varepsilon_0$

$\Rightarrow$  perturbation of the 3-system  $(aa, aA, AA)$  of at most  $\mathcal{O}(\varepsilon_0)$



## 2.Phase: Invasion of the mutant



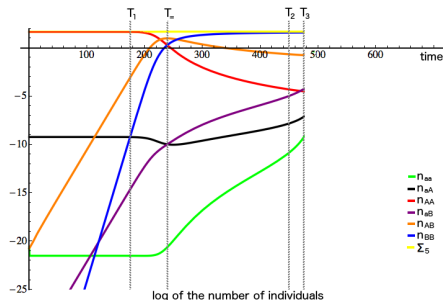
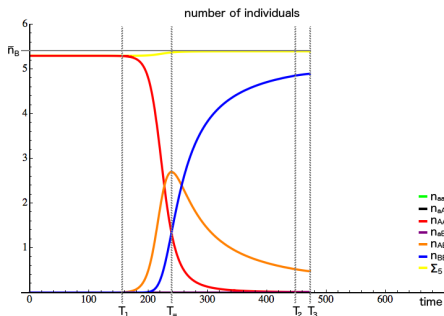
- $aa, aA, aB \leq \varepsilon_0$

$\Rightarrow$  perturbation of the new 3-system  $(AA, AB, BB)$  of at most  $\mathcal{O}(\varepsilon_0)$

$\Rightarrow$  use results of Bovier, Neukirch (2015)

- $n_{aA} + n_{aB}$  increases if  $\eta > 0$

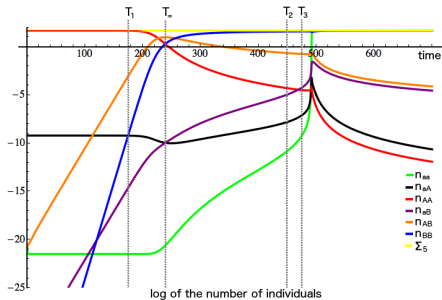
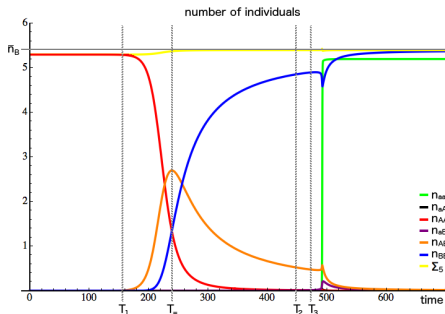
## 3. Phase: Recovery of $aa$



- $AA$  small enough
- $aA$  big enough

$\Rightarrow aa$  starts to reproduce out of itself as much as with the other partners.

## 4. Phase: Coexistence



Delicate phase :  $aa$  grows out of itself and feels no competition with  $BB$   
 $\Rightarrow$  convergence to coexistence-fixed-point  $\bar{n}_{aa, BB}$

BUT meanwhile :

due to Mendelian recombination,  $aA, aB, AB$  have a "bump" upwards,  
 and due to competition with them  $BB$  has a "bump" downwards.

