

# **EVOLUTIONARY DYNAMICS**

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# **Competition**

# Evolution of a population

Mean population at time  $t$ :

$$\mathbf{n}(t) = (n_1(t), \dots, n_r(t))$$

$$\mathbf{n}(t) = \mathbf{n}(0) M(t) = \mathbf{n}(0) \exp(A t)$$

$$\frac{d \mathbf{n}}{d t} = \mathbf{n} A$$

generalized Malthus law

# Population growth

$$N(t) = \mathbf{n}(t) \cdot \mathbf{1} = \sum_{i=1}^r n_i(t)$$

$$\frac{d N}{d t} = \frac{d \mathbf{n}}{d t} \cdot \mathbf{1} = \mathbf{n}' \mathbf{1}$$

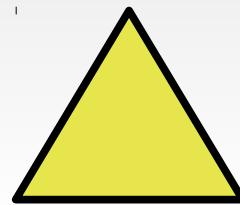
$$\frac{d N}{d t} = N \phi(\mathbf{x}) \quad \phi(\mathbf{x}) \equiv \mathbf{x}' \mathbf{1}$$

# Evolution of the composition

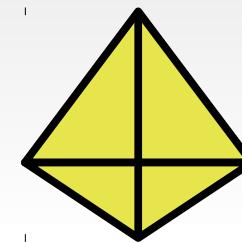
$$\boldsymbol{x}(t) = \frac{\boldsymbol{n}(t)}{N(t)} \quad \sum_{k=1}^r x_k(t) = 1 \quad x_k(t) \geq 0$$



$$r=2$$



$$r=3$$



$$r=4$$

$$\frac{d \boldsymbol{x}}{d t} = N^{-1} \frac{d \boldsymbol{n}}{d t} - \boldsymbol{n} N^{-2} \frac{d N}{d t}$$

$$\frac{d \boldsymbol{x}}{d t} = \boldsymbol{x} A - \phi(\boldsymbol{x}) \boldsymbol{x}$$

# Asymptotic growth

Steady state of composition:

$$\nu A = \phi(\nu) \nu \Rightarrow \phi(\nu) = a$$

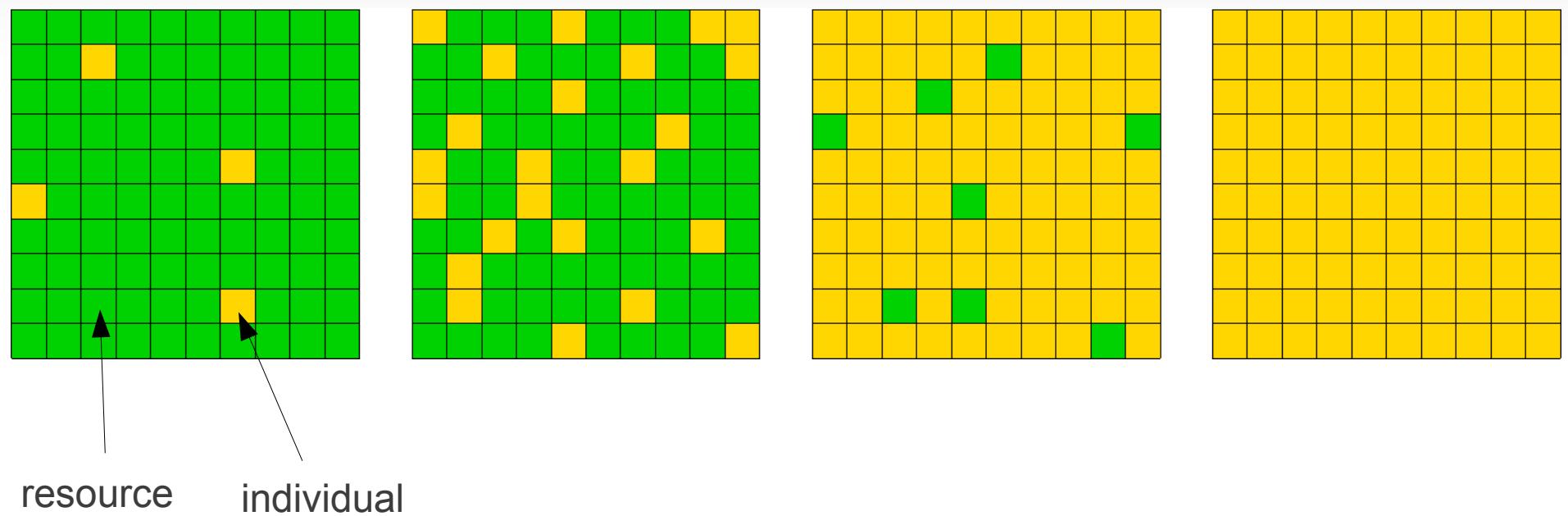
$$\lim_{t \rightarrow \infty} x(t) = \frac{\nu}{\nu \cdot 1}$$

Exponential growth of population:

$$\frac{dN}{dt} \sim N \phi(\nu) \Rightarrow N(t) \sim C e^{at}$$

# Exhaustion of resources

time



# Exhaustion of resources

$K \rightarrow$  carrying capacity of the environment ( $N(t) \leq K$ )

$$\frac{d n}{d t} = n A - \phi(x) \frac{N}{K} n$$

uniform death rate

population growth rate      fraction of “used” resources

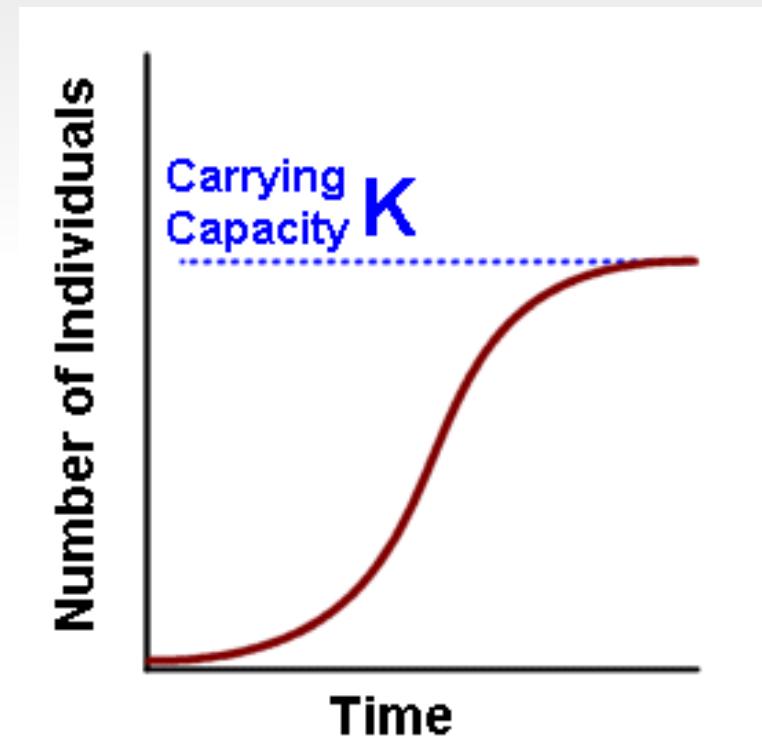
The diagram illustrates the logistic growth equation. It features a green bracket above the term  $\frac{N}{K} n$ , labeled "uniform death rate". Two green arrows point from the labels "population growth rate" and "fraction of ‘used’ resources" to the terms  $n A$  and  $\phi(x)$  respectively.

# Exhaustion of resources

$$\frac{dN}{dt} = N \phi(x) \left(1 - \frac{N}{K}\right)$$

but

$$\frac{dx}{dt} = x A - \phi(x)x$$



# Fitness and mutations

$$A = F + Q$$

$$F = \text{diag}\{f_1, \dots, f_r\} \quad f_i = \sum_{j=1}^r a_{i,j}$$

$$Q \equiv (q_{i,j}) = A - F \quad \sum_{j=1}^r q_{i,j} = 0 \quad q_{i,j} \geq 0 \quad (i \neq j)$$

$f_i \rightarrow$  average growth rate of “species”  $i$  (**fitness**)

$q_{i,j} \rightarrow$  average **mutation** rate from species  $i$  to species  $j$

# Fitness and mutations

$$\phi(\mathbf{x}) = \mathbf{x}^T \mathbf{A} \mathbf{1} = \mathbf{x}^T \mathbf{F} \mathbf{1} + \mathbf{x}^T \underbrace{\mathbf{Q} \mathbf{1}}_0 = \mathbf{x}^T \mathbf{F} \mathbf{1}$$

$$\phi(\mathbf{x}) = \sum_{k=1}^r f_k x_k$$

average fitness of the population

# Survival of the fittest



$$x_A = x$$

$$x_B = 1 - x$$

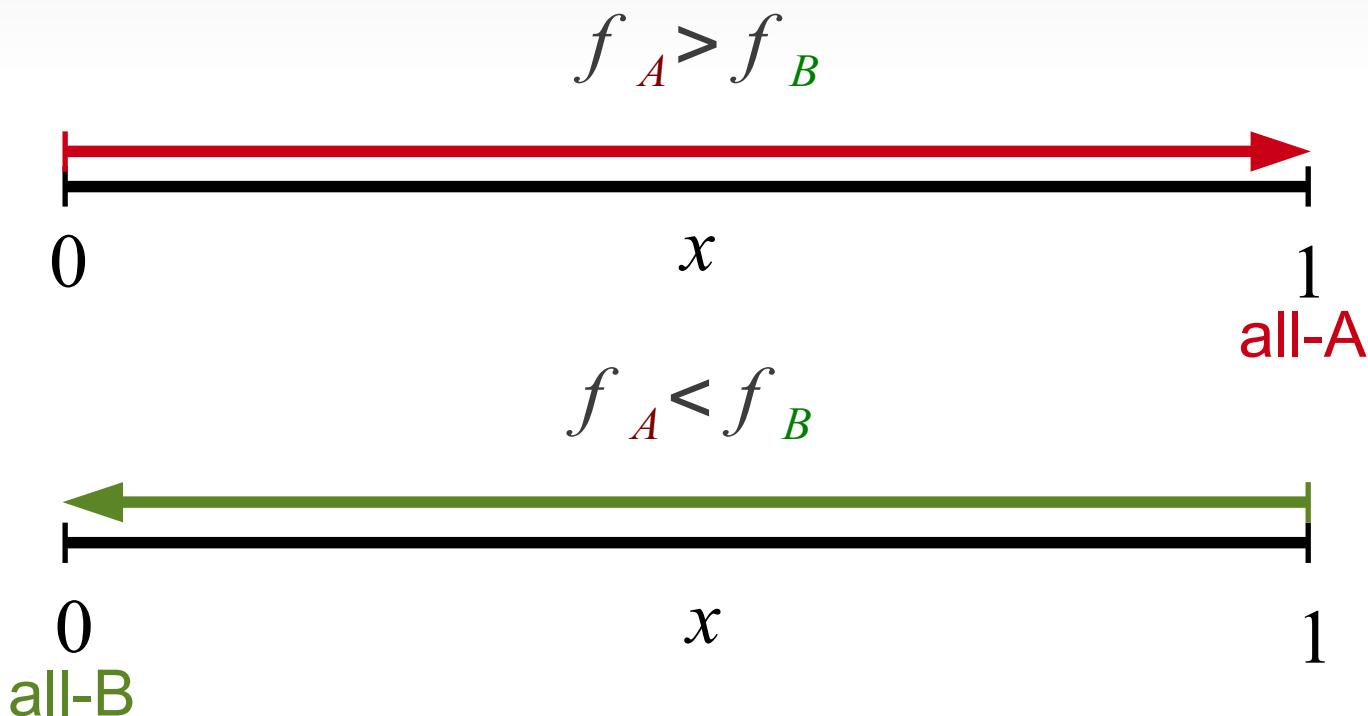
$$F = \text{diag} \{ f_A, f_B \} \quad Q = 0$$

$$\frac{d}{dt} x = x (f_A - \phi(x)) \quad \phi(x) = x f_A + (1-x) f_B$$

$$\frac{d}{dt} x = x (1-x) (f_A - f_B)$$

# Survival of the fittest

$$\frac{d x}{d t} = x(1-x)(f_A - f_B)$$



# Survival of the fittest

$$\frac{d x_k}{d t} = x_k \left( f_k - \sum_{j=1}^r x_j f_j \right) = x_k \sum_{j=1}^r x_j (f_k - f_j)$$

assume  $f_k > f_j \quad \forall j \neq k$



$$\lim_{t \rightarrow \infty} x_k(t) = 1$$

$$\lim_{t \rightarrow \infty} x_j(t) = 0 \quad (j \neq k)$$

# Fisher's fundamental theorem of natural selection

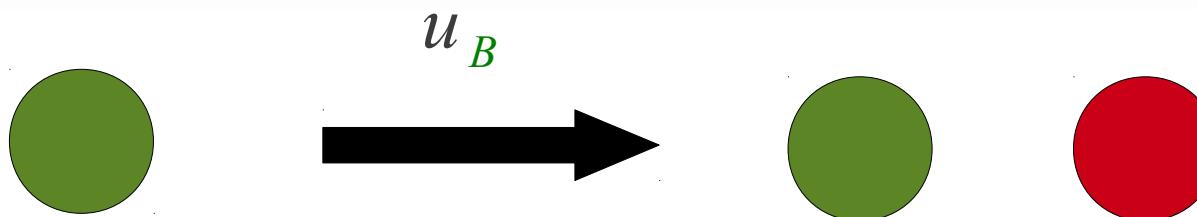
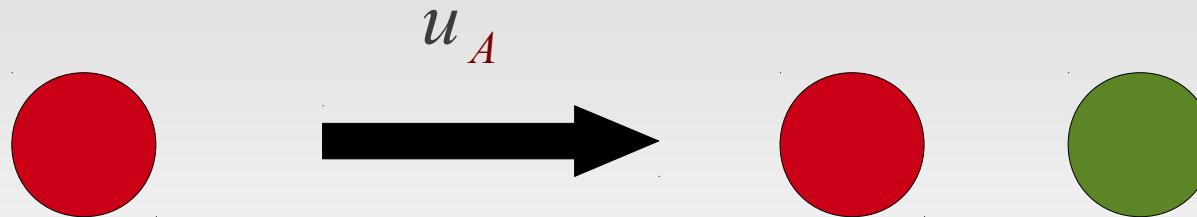
$$\frac{d\phi}{dt} = \sum_{k=1}^r f_k \frac{dx_k}{dt} = \sum_{k=1}^r f_k x_k (f_k - \phi) = \sum_{k=1}^r x_k (f_k - \phi)^2 \equiv \sigma_f^2$$

$$\frac{d\phi}{dt} = \sigma_f^2$$

- Average fitness increases as long as population is diverse
- The more diverse the population the faster it increases
- Average fitness reaches a maximum when population becomes homogeneous

# Mutation

# Replication with error



$$F = \begin{pmatrix} f_A & 0 \\ 0 & f_B \end{pmatrix} \quad Q = \begin{pmatrix} -u_A & u_A \\ u_B & -u_B \end{pmatrix}$$

# Replication with error

$$\begin{aligned}\frac{d}{dt}x &= x(f_A - u_A - \phi(x)) + (1-x)u_B \\ &= x(1-x)(f_A - f_B) + (1-x)u_B - xu_A\end{aligned}$$

$$x^* \approx 1 - \frac{u_A}{f_A - f_B} < 1 \quad f_A > f_B$$

$$x^* \approx \frac{u_B}{f_B - f_A} > 0 \quad f_A < f_B$$

$$x^* = \frac{u_B}{u_A + u_B} \quad f_A = f_B$$

mutation is the source of variability

# Mutation-selection equilibrium

$$\frac{d \mathbf{x}}{d t} = \mathbf{x} F + \mathbf{x} Q - \phi(\mathbf{x}) \mathbf{x} \quad Q\mathbf{1} = \mathbf{0} \quad \phi(\mathbf{x}) = \mathbf{x} F \mathbf{1}$$

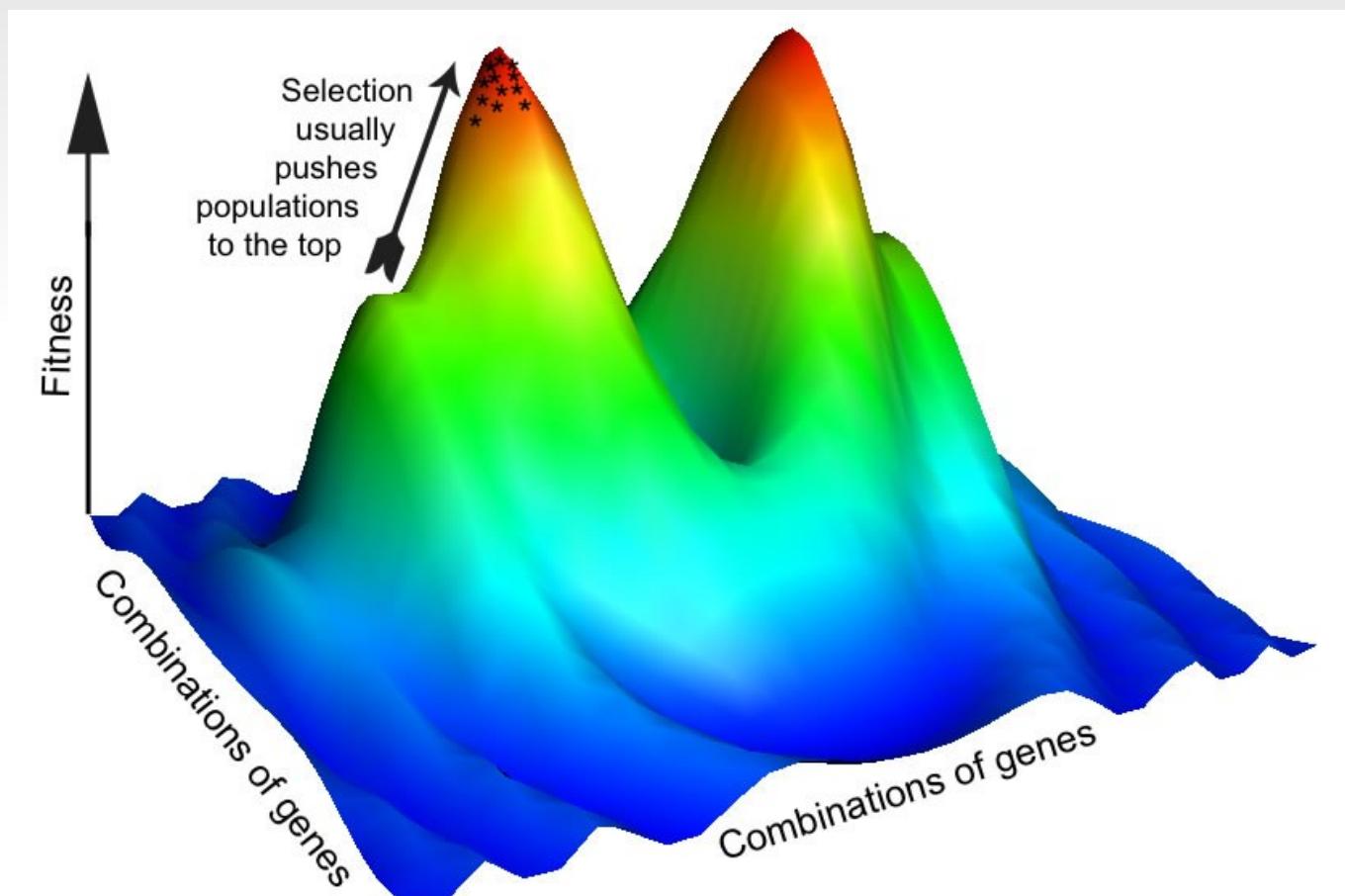
$$\text{equilibrium} \rightarrow \mathbf{x}^* (\mathbf{F} + \mathbf{Q}) = \phi(\mathbf{x}^*) \mathbf{x}^*$$

$\mathbf{Q}$  primitive  $\rightarrow \mathbf{x}^* > \mathbf{0}$  (nonhomogeneous population)

$\rightarrow \phi(\mathbf{x}^*)$  largest eigenvalue of  $\mathbf{F} + \mathbf{Q}$

$\rightarrow \phi(\mathbf{x}^*)$  is no longer a maximum ( $\sigma_f > 0$ )

# Mutation-selection equilibrium



# The quasi-species model



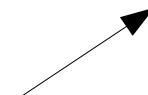
Manfred Eigen

ATTTGGAAATGCCGCAATTACGGGA  
ACTTGC~~AA~~ATTCCGCAA~~ATT~~CGGGG  
~~AG~~TTGGAACTTCCGCAATTCTCGGGGA  
ACTTGGACATTCCGATATTCTCGGGGA  
~~GG~~TTGGAAATACCCCCAATTTCGGGA  
ACTTTGAAATTCCGCAACGGTCGGGA  
ACATGGAAATTCCGCAATTTCGGGA

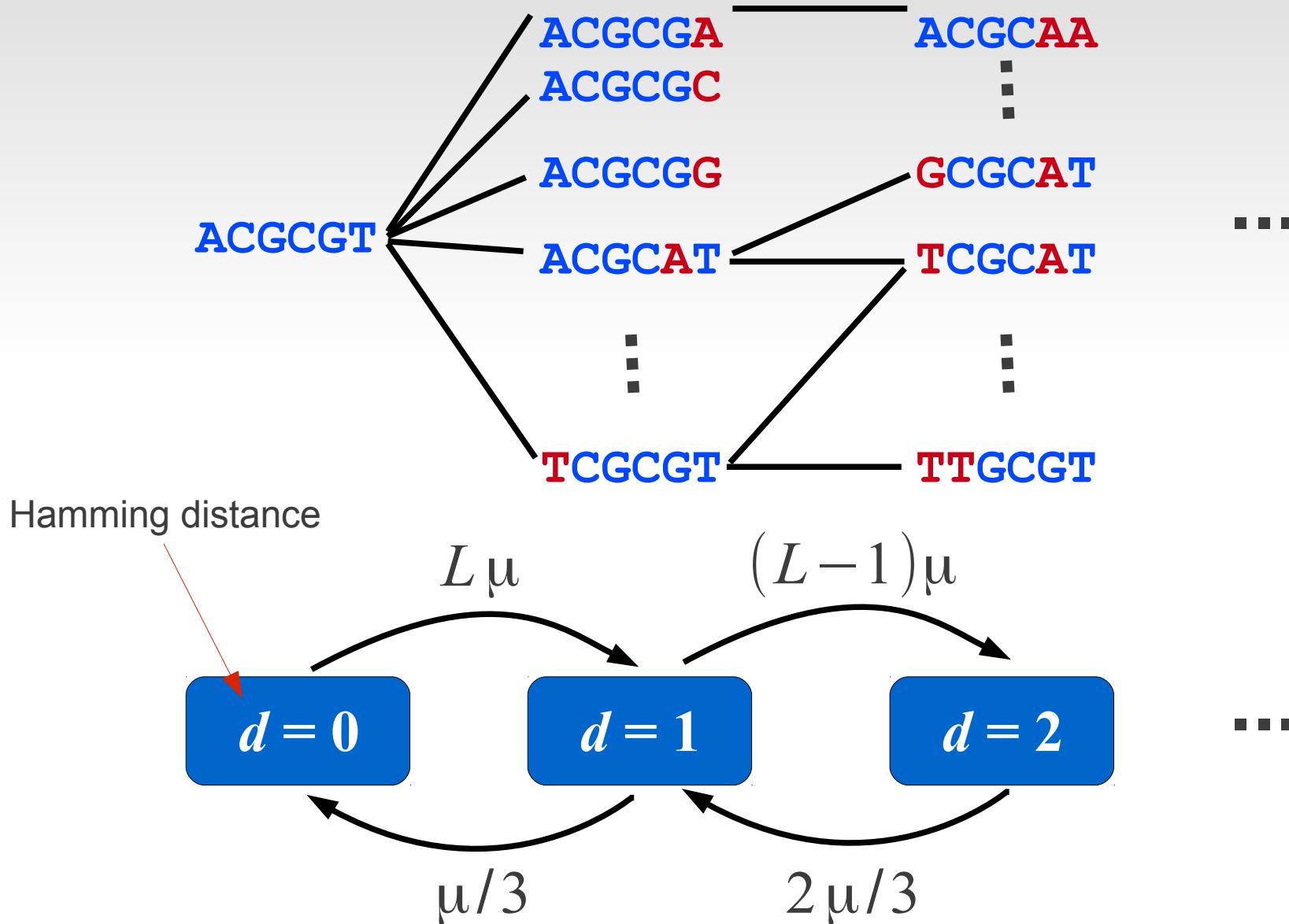
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ACTTGGAAATTCCGCAATTTCGGGA

consensus sequence  
(optimal)

A thin black arrow points from the text "consensus sequence (optimal)" upwards towards the highlighted green sequence.

# The quasi-species model



# The quasi-species model

Grouping by Hamming distance:

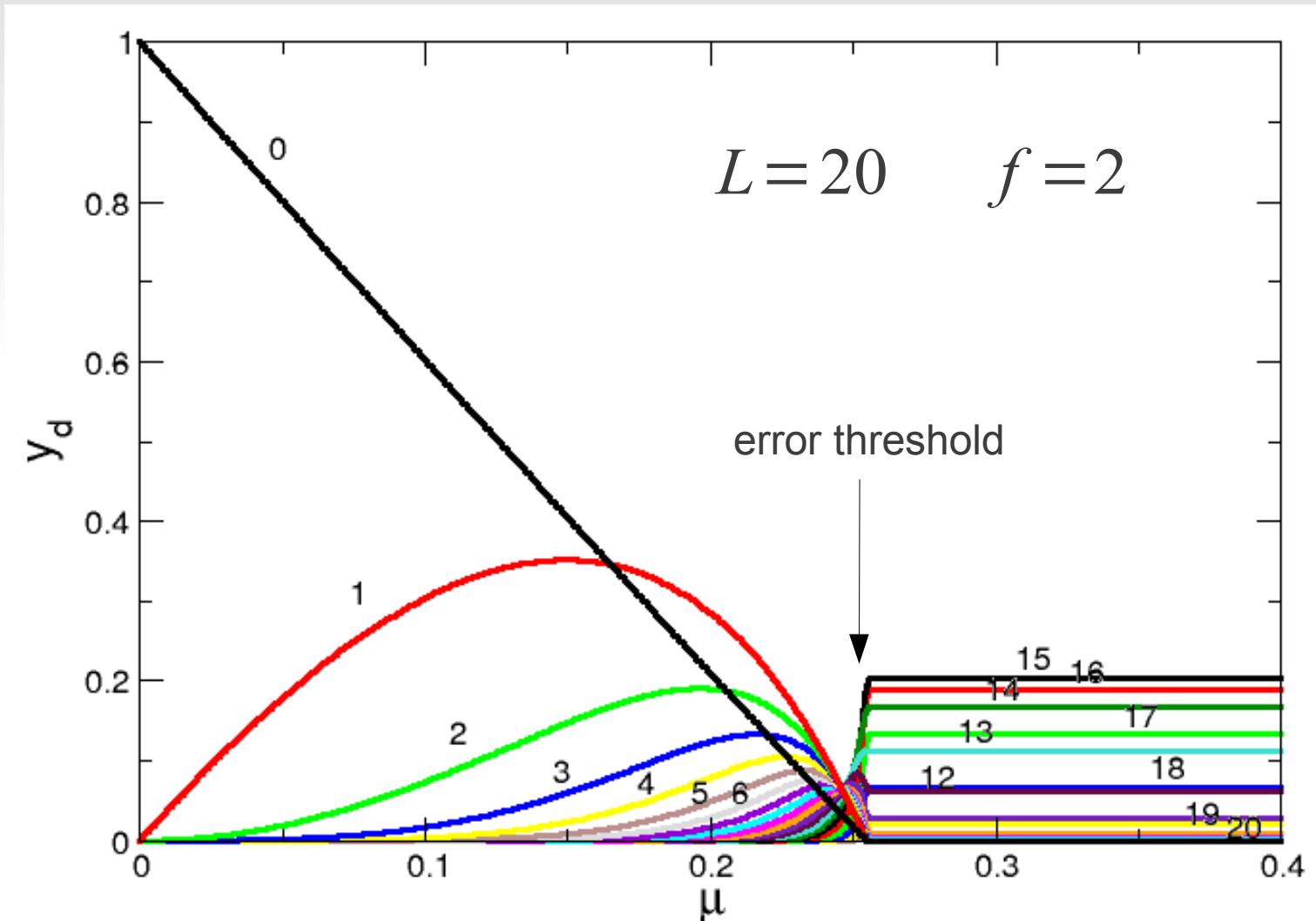
$$y_d = \sum_{i: d(i, 0) = d} x_i \quad \sum_{d=0}^L y_d = 1$$

$$f_0 = f > 1 = f_1 = \dots = f_L$$

$$q_{d,d+1} = f_d(L-d)\mu \quad q_{d,d-1} = f_d d \mu / 3$$

$$q_{d,d} = -q_{d,d-1} - q_{d,d+1}$$

# The quasi-species model



# The quasi-species model

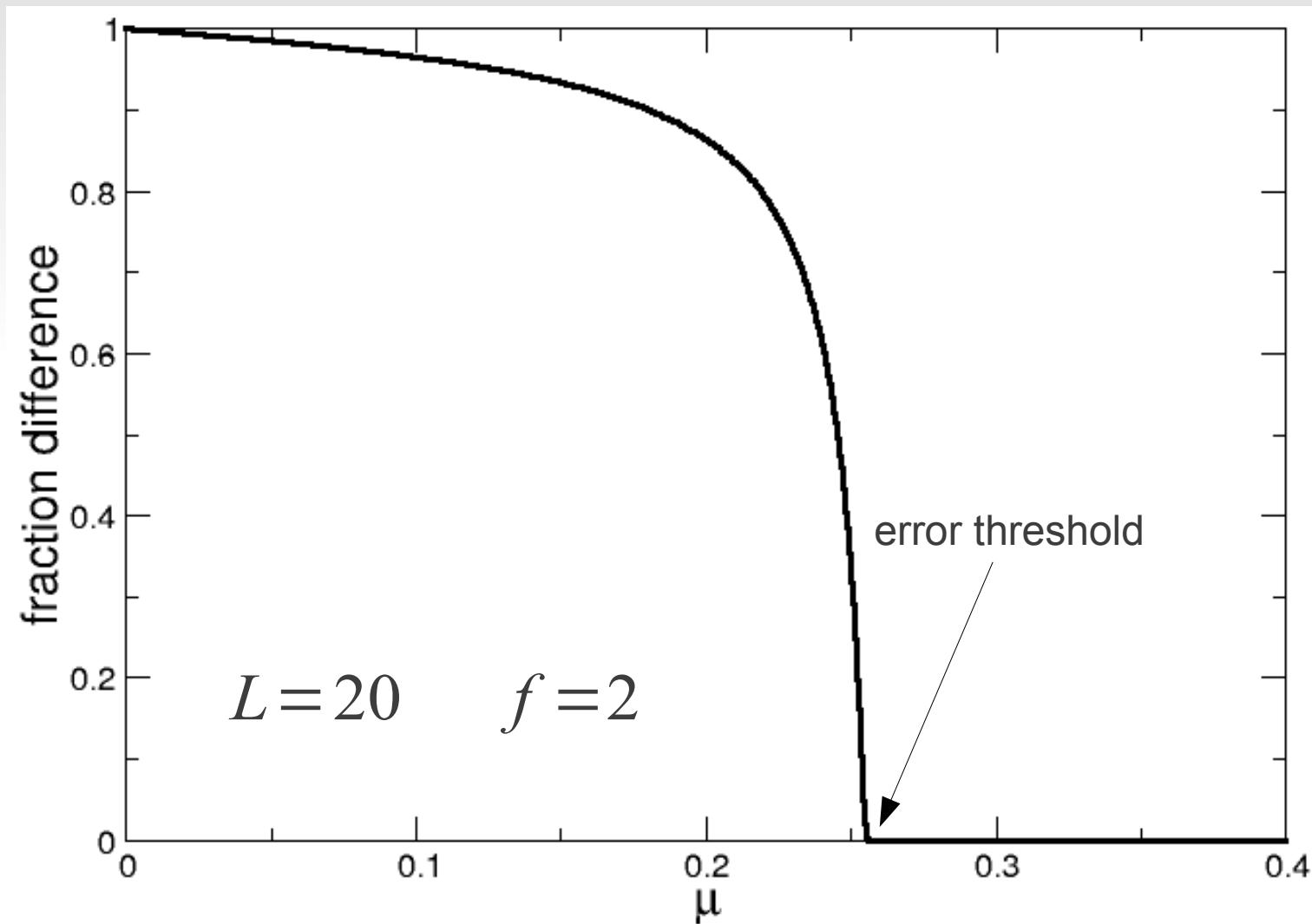
Fraction of sequences with the consensus base at a given position:

$$\sum_{d=0}^L \frac{3^d \binom{L-1}{d}}{3^d \binom{L}{d}} y_d = 1 - \sum_{d=0}^L \frac{d}{L} y_d$$

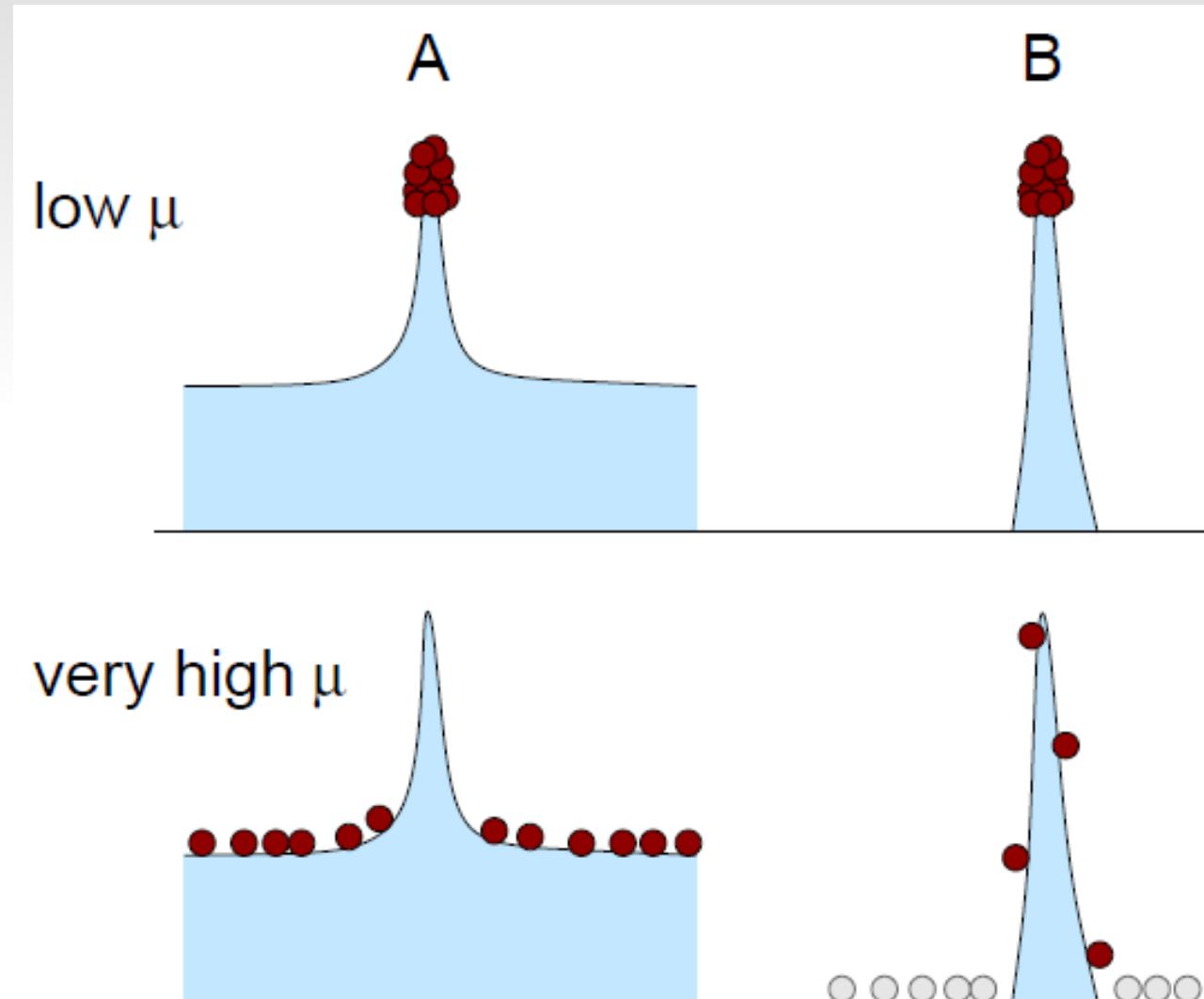
Fraction difference between sequences with the consensus base and sequences with any other base at a given position:

$$\left( 1 - \sum_{d=0}^L \frac{d}{L} y_d \right) - \frac{1}{3} \sum_{d=0}^L \frac{d}{L} y_d = 1 - \frac{4}{3} \sum_{d=0}^L \frac{d}{L} y_d$$

# The quasi-species model



# The quasi-species model



# Interaction

# Ecological fitness

The presence of other species influences the replication rate:

$$f_k = f_k(\mathbf{x})$$

Example: two species

$$f_A(x) = f + \alpha_A(1 - x)$$

$$f_B(x) = f + \alpha_B x$$

symbiosis

$$\alpha_A > 0$$

$$\alpha_B > 0$$

competition

$$\alpha_A < 0$$

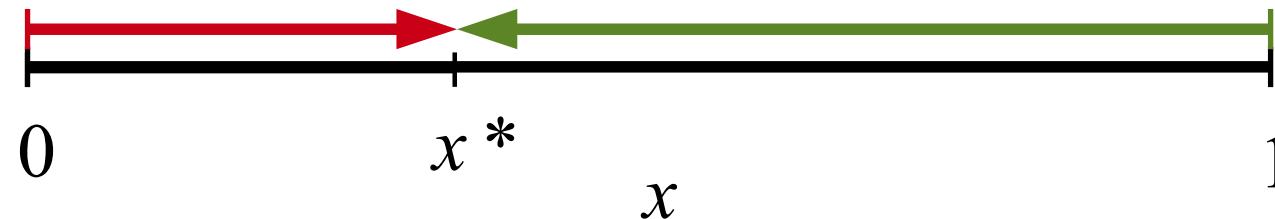
$$\alpha_B < 0$$

# Symbiotic coexistence

$$\frac{dx}{dt} = (\alpha_A + \alpha_B)x(1-x)(x^* - x) \quad x^* = \frac{\alpha_A}{\alpha_A + \alpha_B}$$

$$\alpha_A > 0$$

$$\alpha_B > 0$$

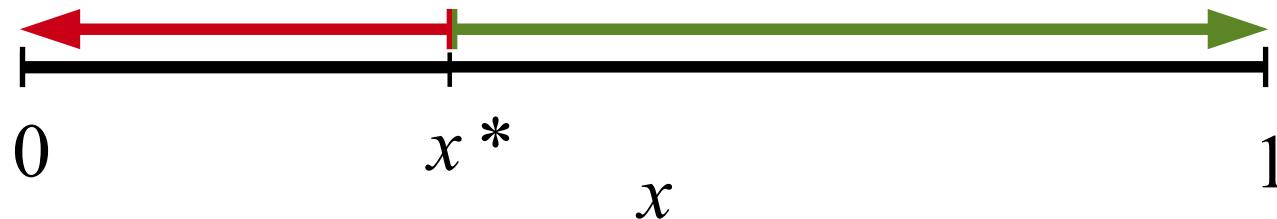


# Competitive exclusion

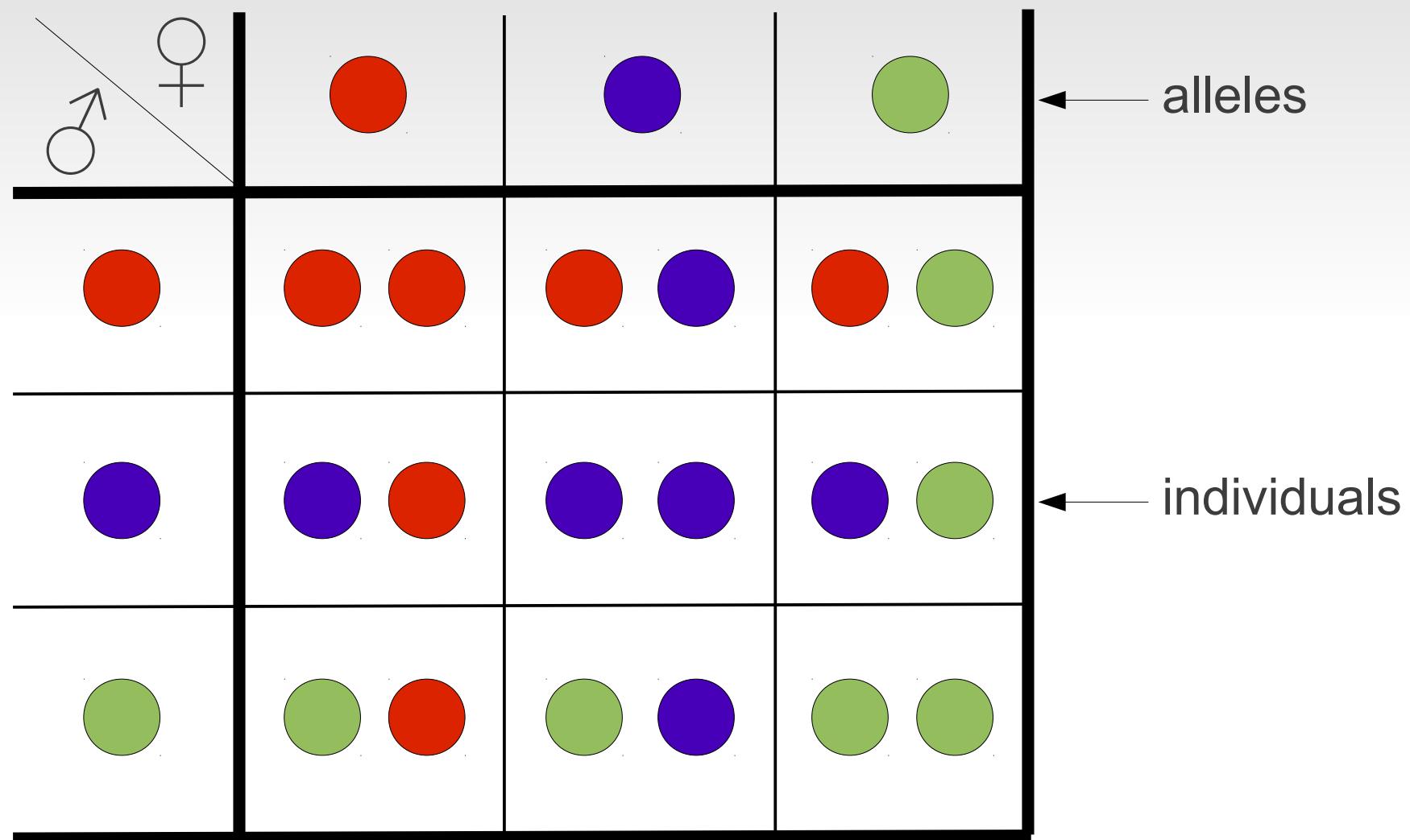
$$\frac{d x}{d t} = (\alpha_A + \alpha_B) x (1 - x) (x^* - x) \quad x^* = \frac{\alpha_A}{\alpha_A + \alpha_B}$$

$$\alpha_A < 0$$

$$\alpha_B < 0$$



# Population genetics



# Population genetics

$f_{i,j} \rightarrow$  fitness of individual  $(i, j)$  ( $f_{i,j} = f_{j,i}$ )

$$\frac{d x_{i,j}}{d t} = x_{i,j} (f_{i,j} - \phi) \quad \phi = \sum_{i,j=1}^a x_{i,j} f_{i,j}$$

$$x_i = \frac{1}{2} \sum_{j=1}^a (x_{i,j} + x_{j,i}) \quad i = 1, \dots, a$$



frequency of allele  $i$

# Population genetics

random mating  $\rightarrow x_{i,j} = x_i x_j$



$$\frac{d x_i}{d t} = \frac{1}{2} \left( \frac{d x_{i,j}}{d t} + \frac{d x_{i,j}}{d t} \right) = x_i \sum_{j=1}^a x_j (f_{i,j} - \phi(\mathbf{x}))$$

$$\frac{d x_i}{d t} = x_i (f_i(\mathbf{x}) - \phi(\mathbf{x}))$$

$$f_i(\mathbf{x}) = (\mathbf{F} \mathbf{x})_i \quad \phi(\mathbf{x}) = \mathbf{x}^\top \mathbf{F} \mathbf{x} \quad \mathbf{F} \equiv (f_{i,j})$$