

Neutral evolution in a type space

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Work with

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Neutrality as a null model

- Neutrality is a “null model” for evolution...
- But provides a rich behaviour of its own.
- Accurate description requires description at individual level...
- Because a “**species**” is not always well defined.
- A distribution of types is a better representation.

The Neutral Model

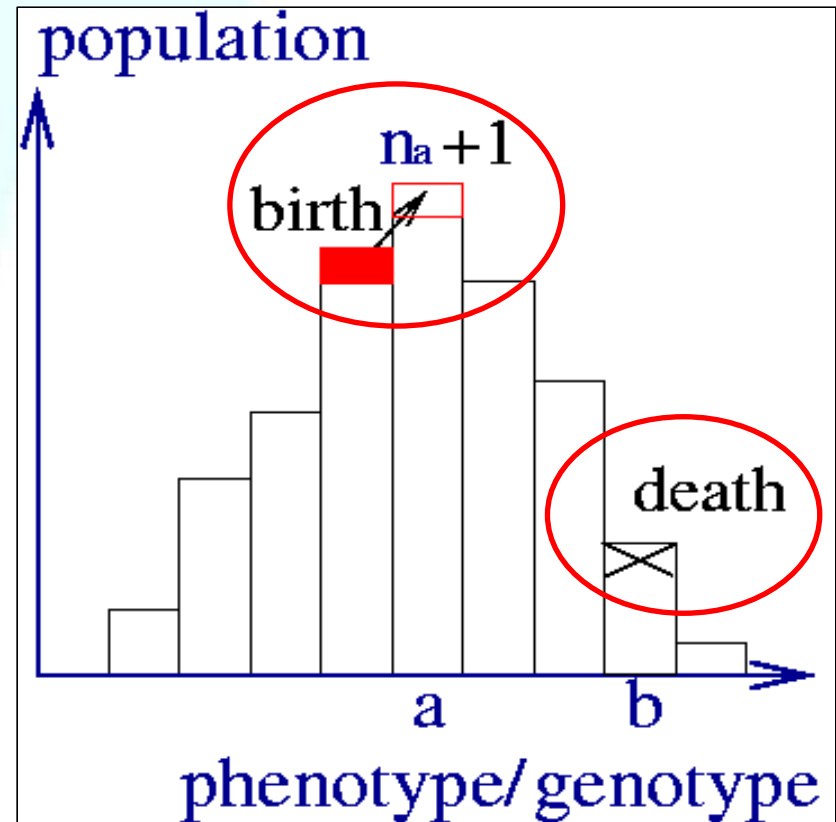
- Assume that all individuals are 'equal'
 - Valid for Phenotypes that do not have function
 - Genotype not coding for protein synthesis (**12% of Human DNA is variable!** *Redon et al. Nature. doi:10.1038/nature05329*)
- Each individual has the same probability to die (p_k), or give birth (p_b), in a time step
 - For simplicity, assume the total population (N) has reached equilibrium ($p_k = p_b$)
- Reproduction is asexual and imperfect – small changes can occur

A neutral evolution model

- Consider N individuals each labeled by a type position:

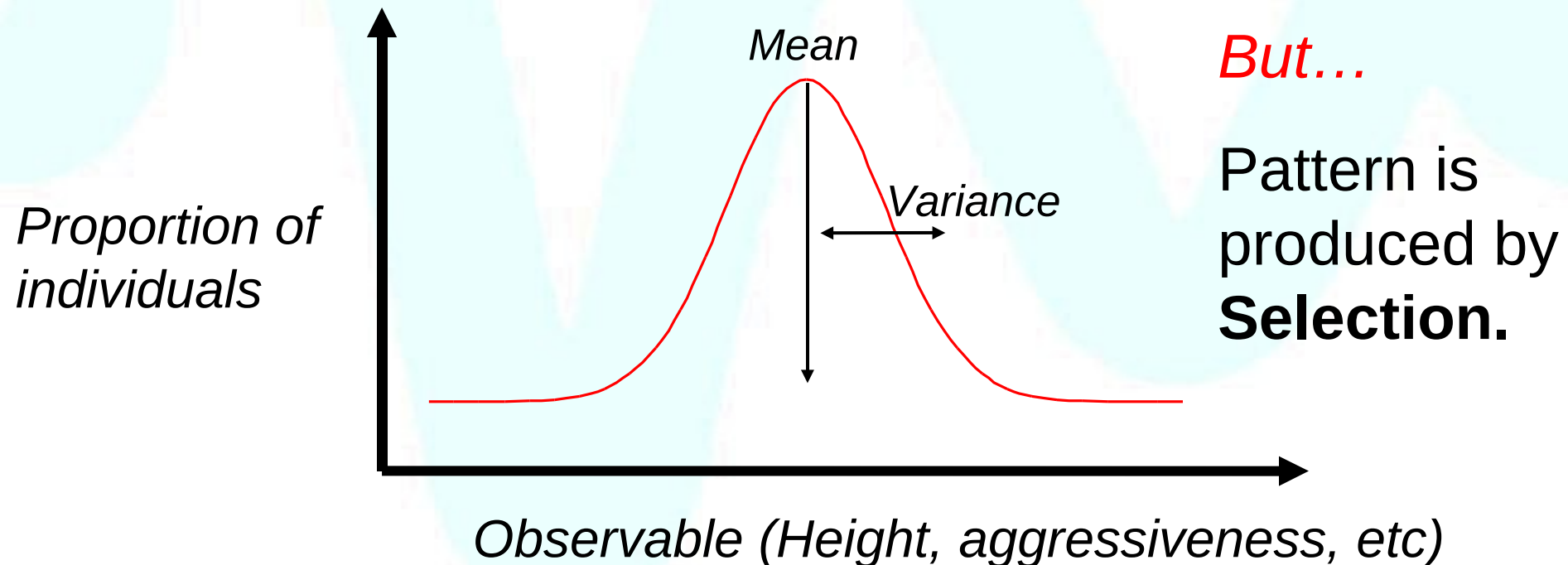
TIMESTEP:

- Pick an individual (from N) and mark it to die.
- Pick an individual (from N) and copy it. With probability p_m **Mutate to a similar type.**
- Kill the marked individual.



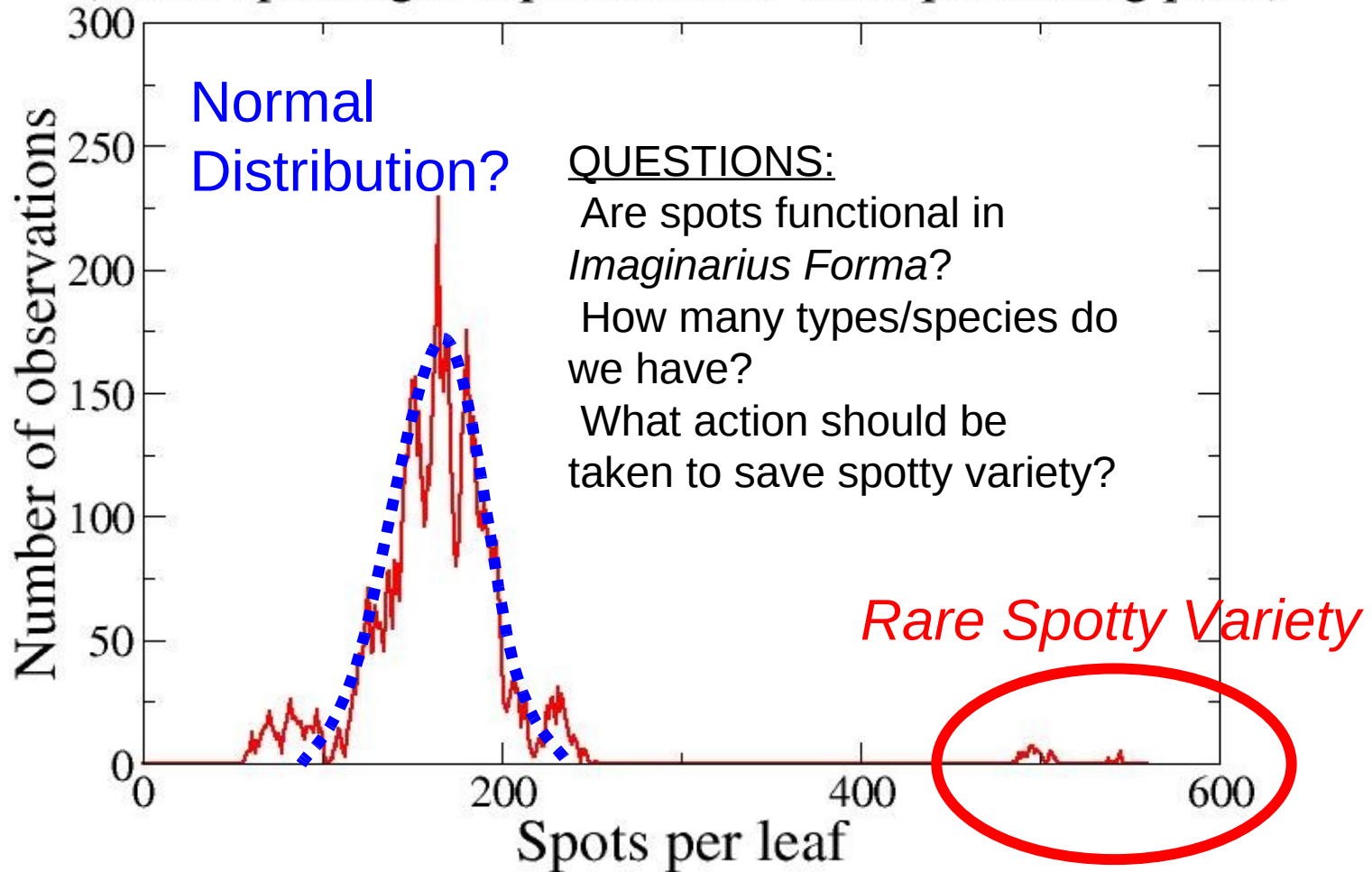
Phenotype Distribution

- Consider 1 dimensional case: mutations can be either to the left or to the right.
- Expected pattern is a Normal Distribution:



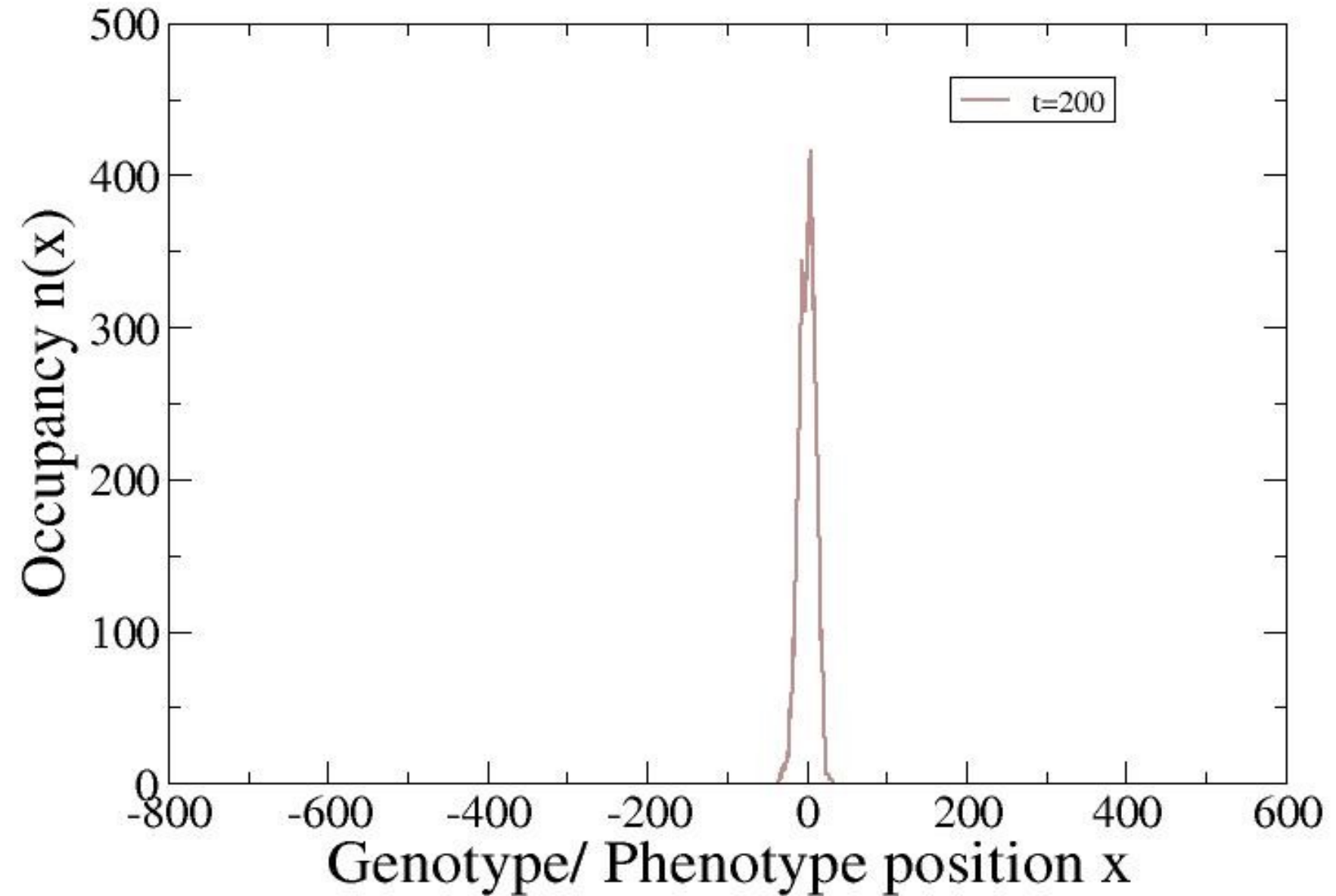
Test Problem

Observations of number of spots per leaf of *Imaginarium Forma*
(Made up thought experiment for a self pollinating plant)

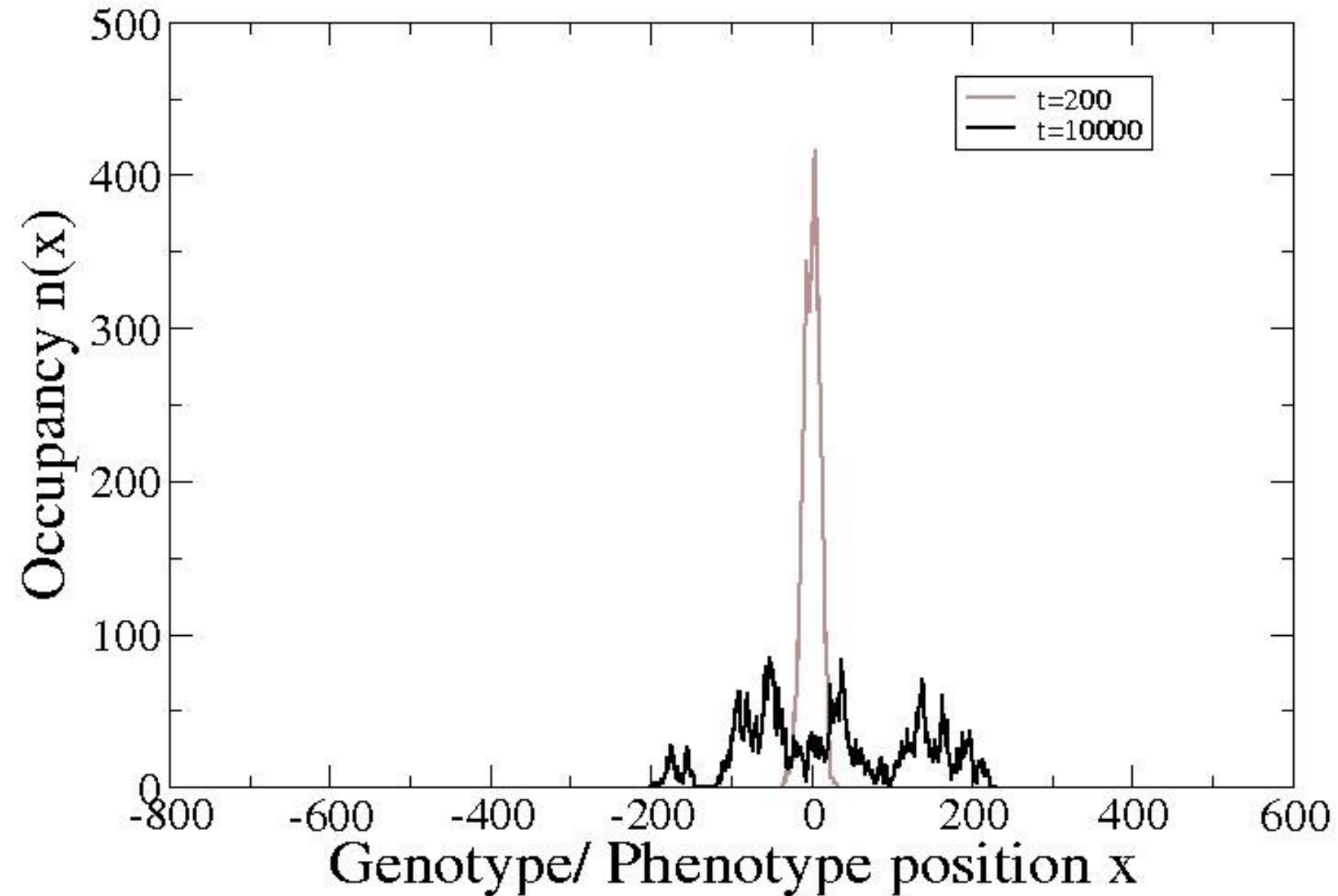


The behaviour of the neutral phenotype model

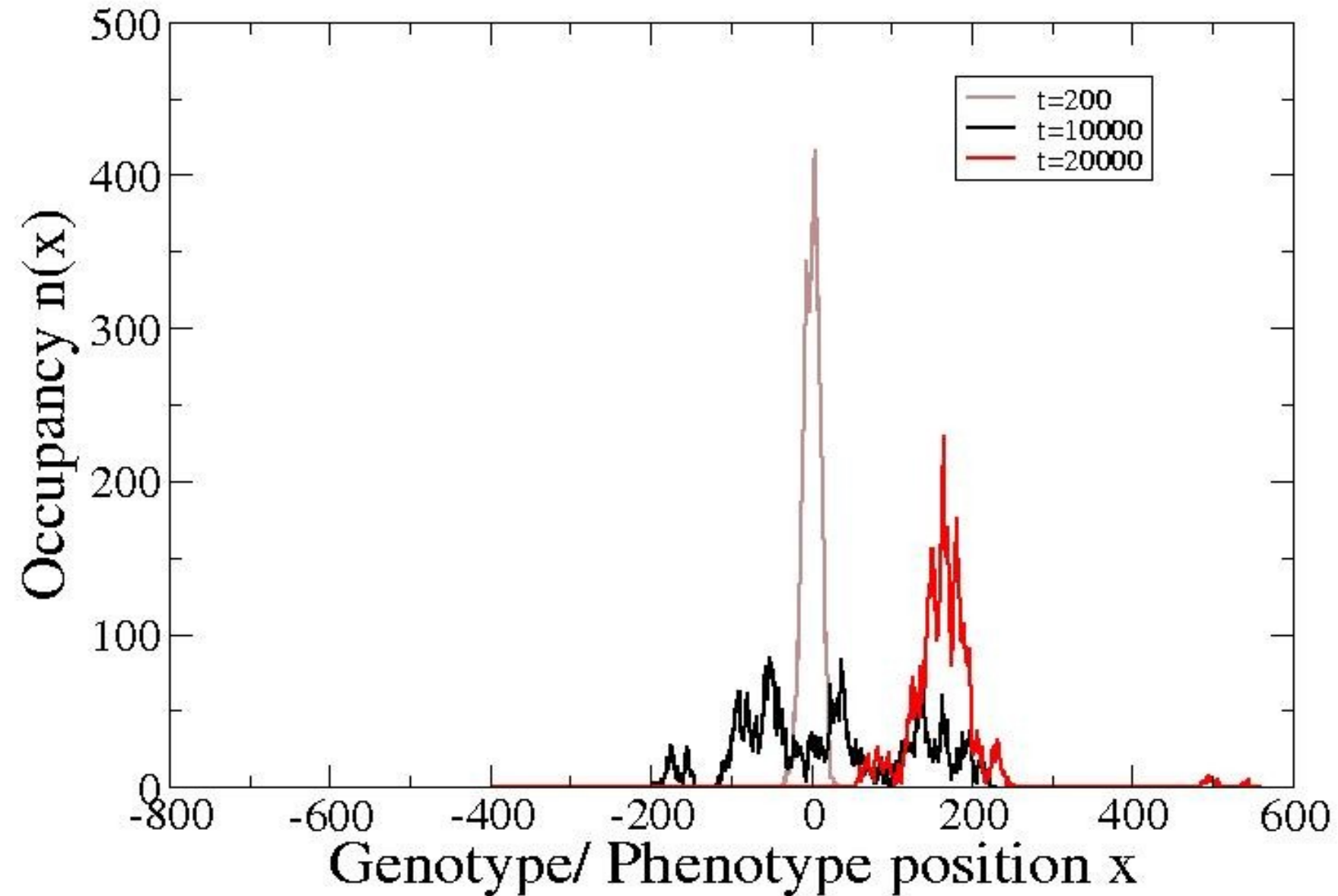
Evolution of 10000 individuals



Evolution of 10000 individuals

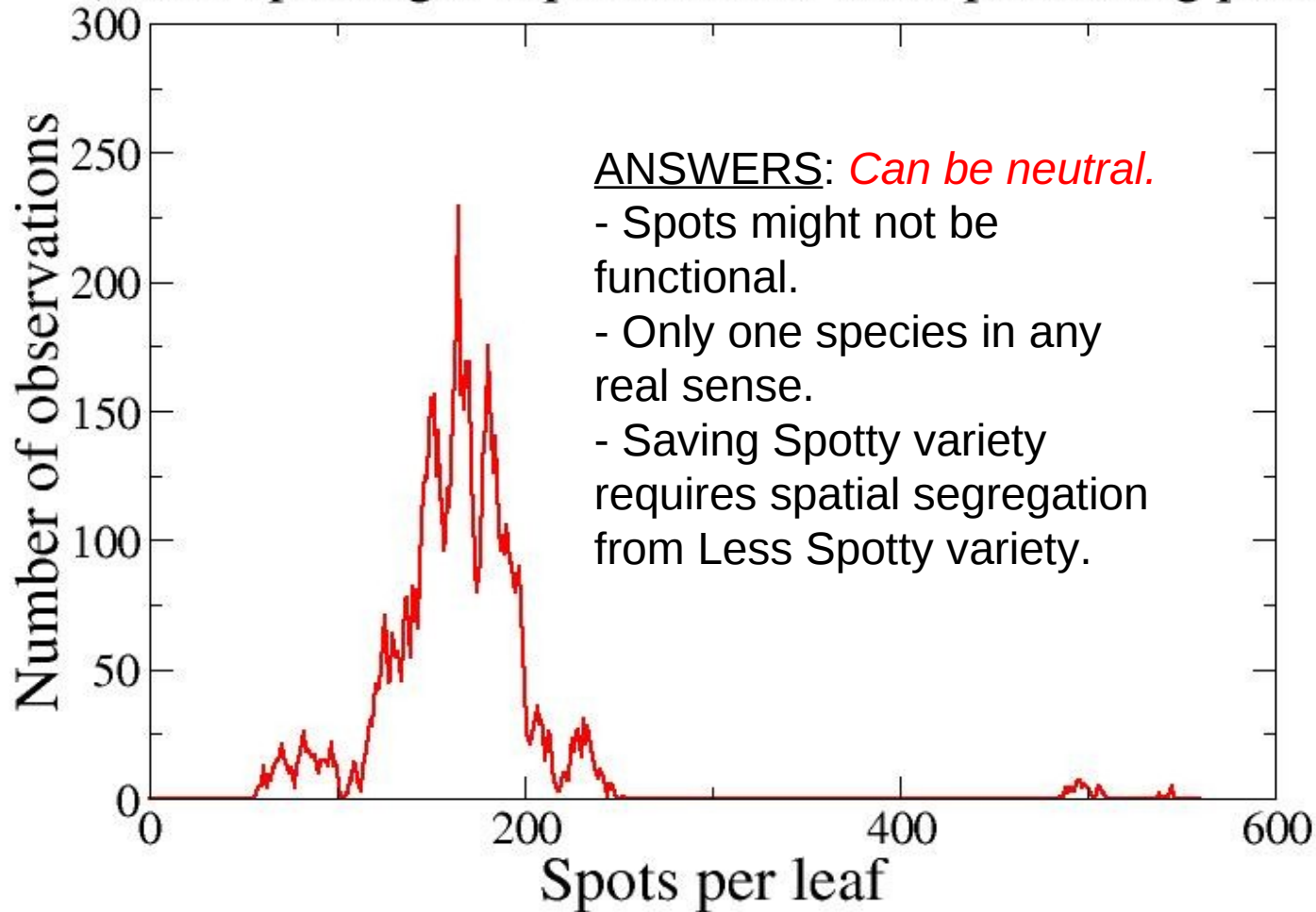


Evolution of 10000 individuals



Test Problem

Observations of number of spots per leaf of *Imaginarium Forma*
(Made up thought experiment for a self pollinating plant)



Solution

- Instead of a “species”, use a conceptual model of a “peak”:
- A Normal Distribution with dynamic mean μ and width w .

- Select death location x
- Select birth location y , mutated by 1 with probability P_m
- Remove individual from death location and place at birth location
- Update μ and w

Solution method

- Write down equations for:
 - Changes to the mean, $\langle d\mu \rangle$, $\langle (d\mu)^2 \rangle$, ...
 - Changes to the width, $\langle dw \rangle$, $\langle (dw)^2 \rangle$, ...
- Moment closure (rigorous in large N limit)
- Take continuous limit to obtain Stochastic Differential Equations
- Solve!

Solving for the width

$$d(w^2) = \left(p^* - \frac{2w^2}{N} \right) dT + \frac{2w^2}{\sqrt{N}} dW$$

Mutation distance
Generation time

dW is Random, mean 0

Change in variance (in a timestep)

Deterministic part

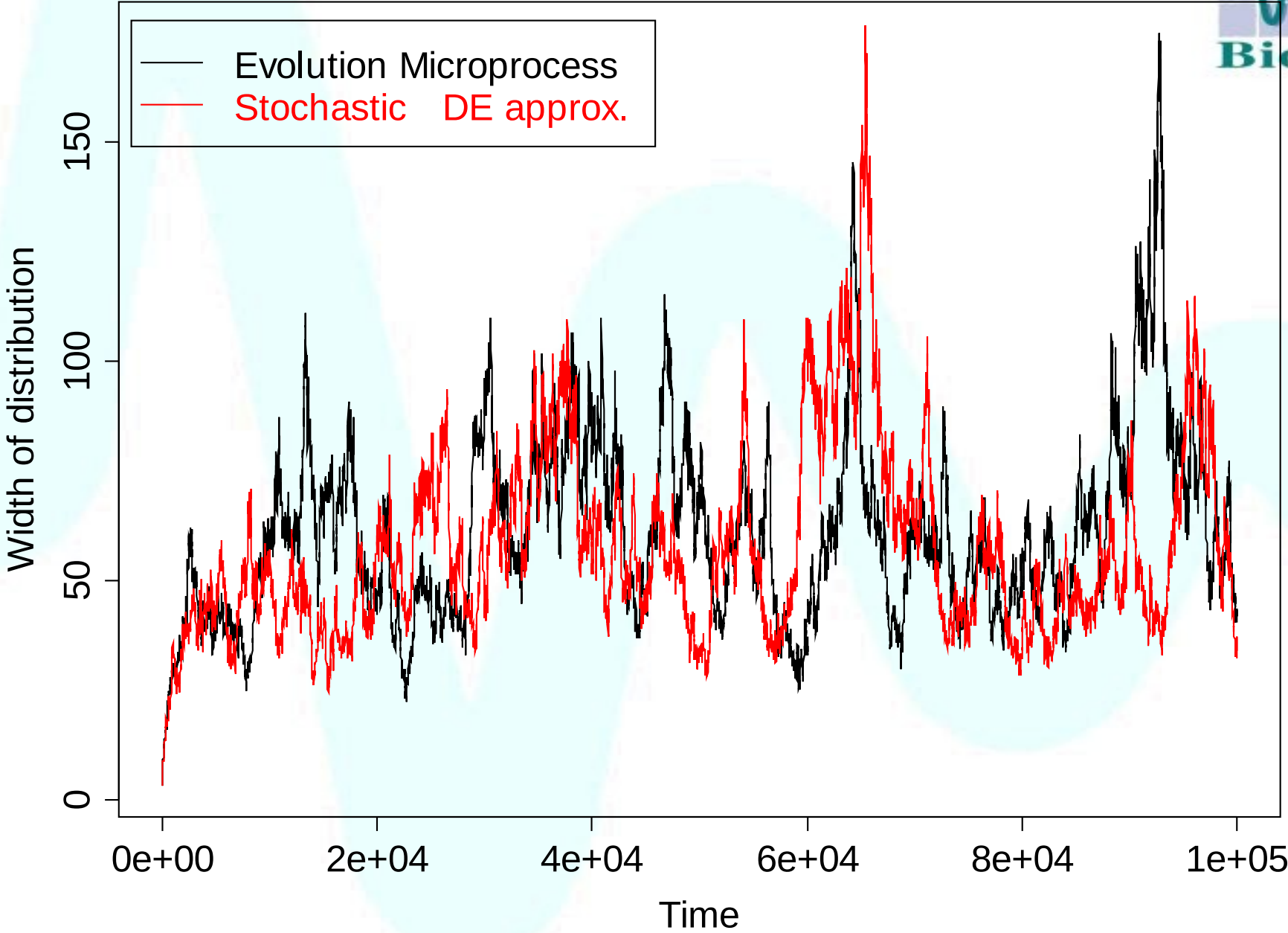
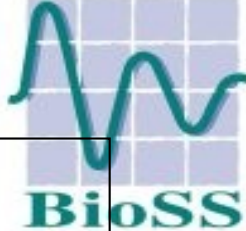
+ Noise part

Solution at steady state:

$$p(w)dw = \frac{(Np_m)^2}{2w^5} e^{-\frac{Np_m}{2w^2}} dw$$

Power-law decay at large w

Evolution in a 1D type space



The species concept

- Neutral clusters do form in type space but these are not stable in time
- Explicit distribution of types must instead be considered
- In neutrality, distribution is “effectively” a fluctuating normal distribution
- But really consists of many discrete clusters

Neutral evolution results

- Selection produces a stable peak, neutrality produces an *unstable* peak.
- Characteristic peak width, but large fluctuations (*multiple clusters*).
- Evolution speed *independent* of population size!
- *Evolution* is important for *Ecological* questions: *non-trivial* phenotype distributions are probable.
- The **Genotype** Distribution evolves similarly....
- Also relevant for **sexual** populations in explicit physical space



Reference

Lawson and Jensen:

***“Neutral Evolution as Diffusion in phenotype space:
reproduction with mutation but without selection”***

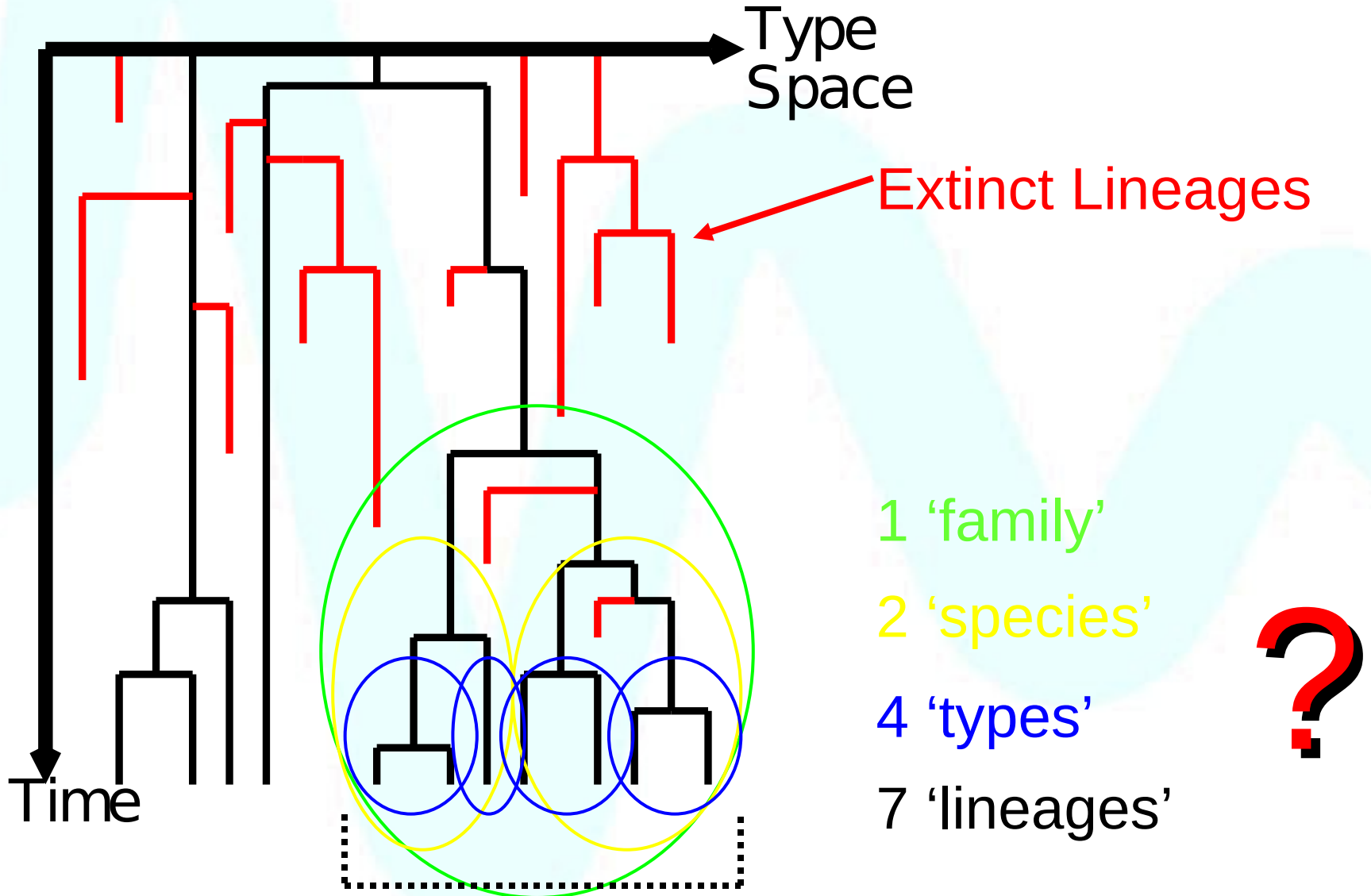
Physics Review Letters, March 07 (98, 098102)

www.arxiv.org/abs/q-bio/0609009

Thank you for your attention!

Cut material

The Lineage



The Lineage (2)

- If mutations occur at random on an “infinite length” genotype:
- All mutations are ‘away’. Equivalent to analysing the lineage.
- Reference: B. Derrida and L. Peliti, Bull. Math. Biol. **53**, 355 (1991).
- Question: Is considering a Type - *a “unit” of similar individuals* - useful for understanding diversity?

Diversity measures

- Measured diversity depends on diversity measure:

- Species Richness:

$$D_{Raw} = \sum_i 1$$

Sum over species i

- Simpson Diversity:

$$S_S = 1 - \sum_i p_i^2$$

Proportion of species i from total population N

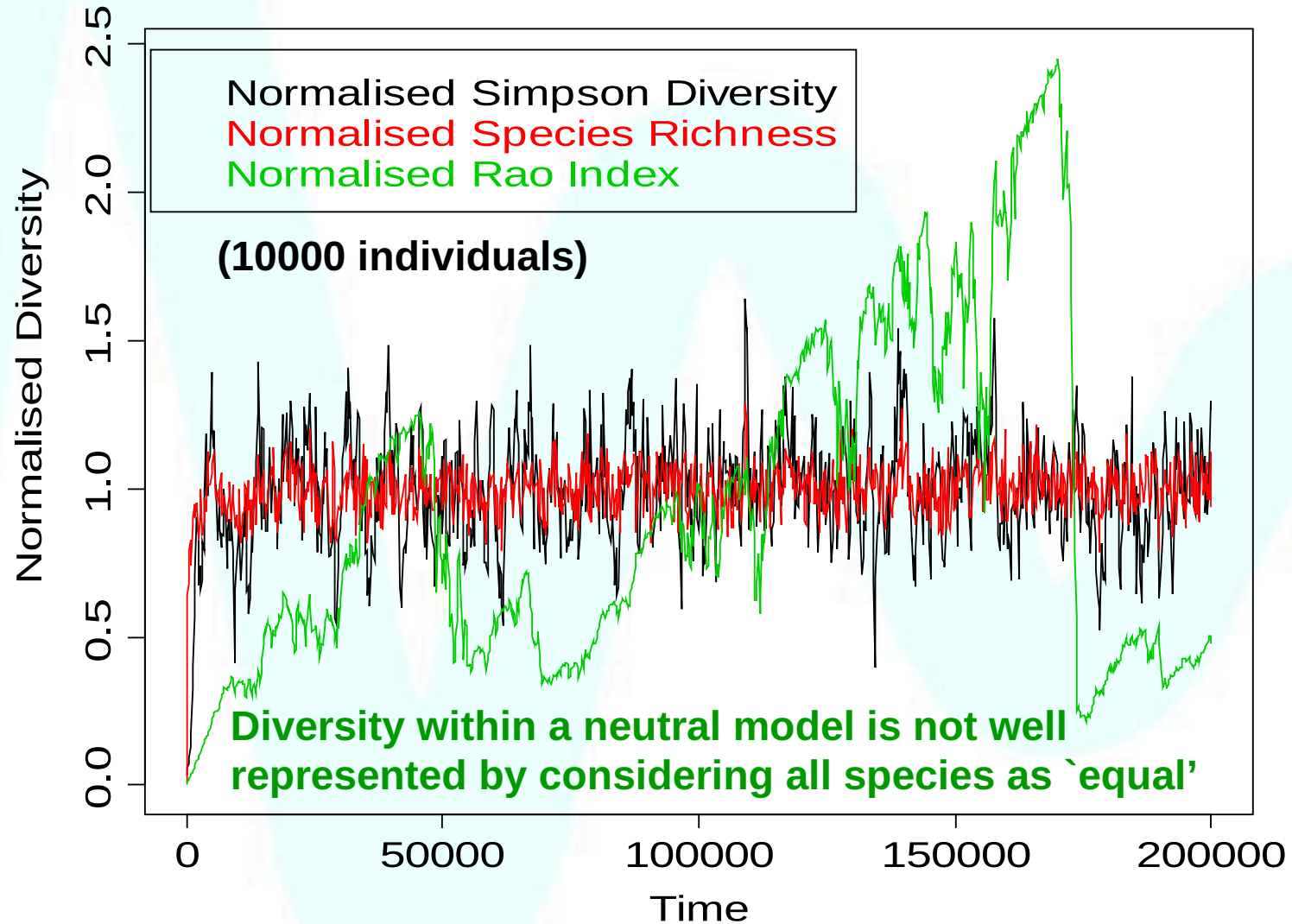
$$D_S = \frac{1}{1 - S_S}$$

- Rao Index:

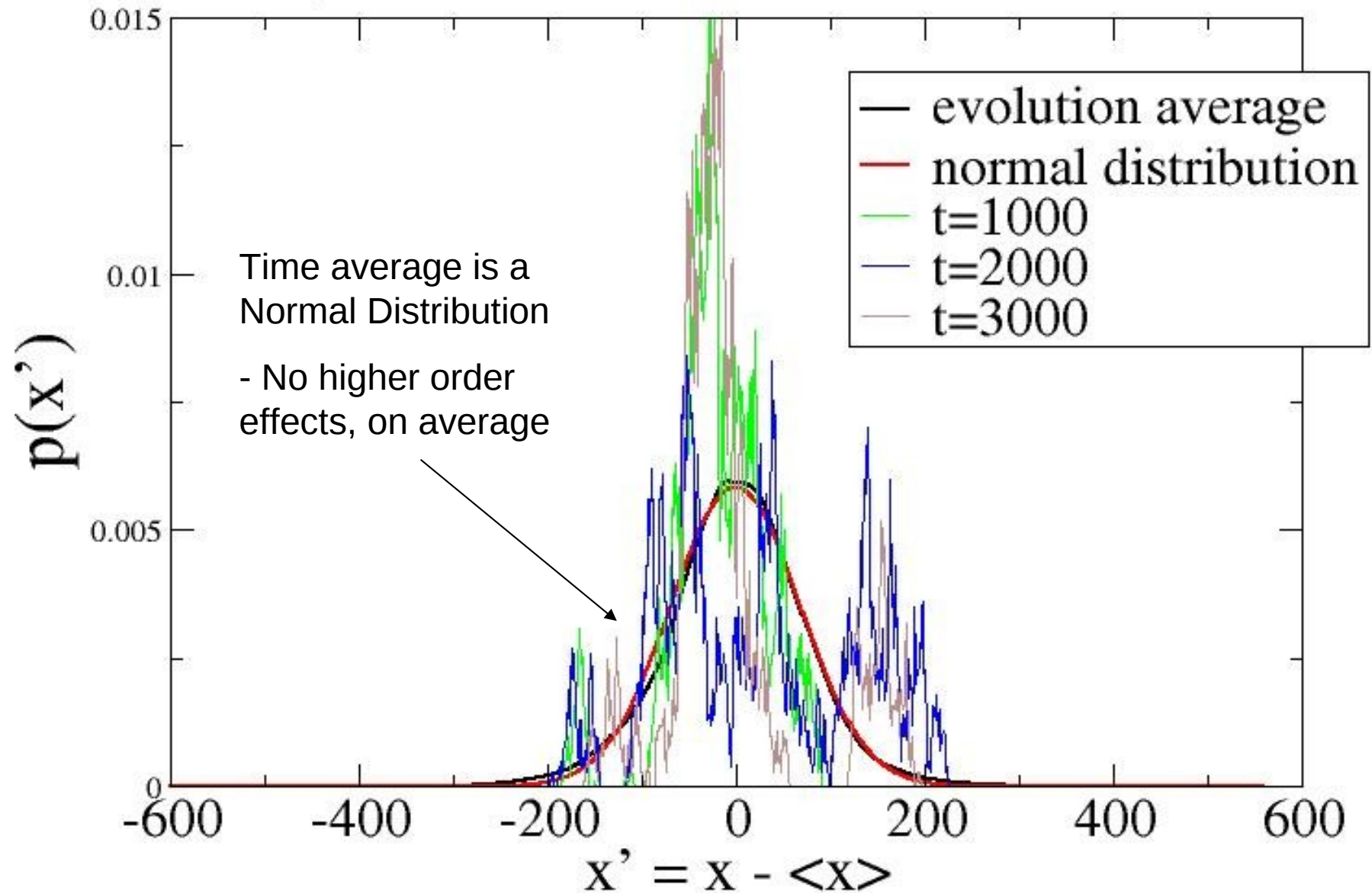
$$D_{Rau} = \sum_{i,j} d_{ij} p_i p_j$$

"Difference" between types

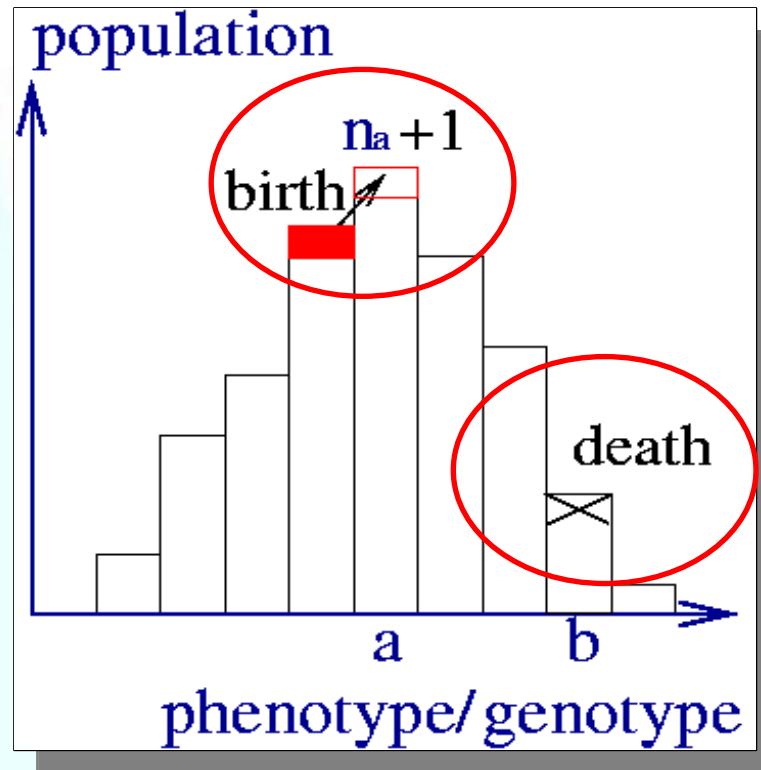
Diversity of asexual lineages



Time average distribution of evolution process around the mean compared with a normal distribution (N=10000)



Solution: first try (1)



$$p_b(a) = \frac{n_a}{N} (1 - p_m) + \frac{p_m}{2} \frac{n_{a+1} + n_{a-1}}{N}$$

$$p_k(a) = \frac{n_a}{N}$$

Solution: first try (2)

- Consider average behaviour:

$$\langle n_a(t+1) - n_a(t) \rangle = p_b(a) - p_k(a)$$

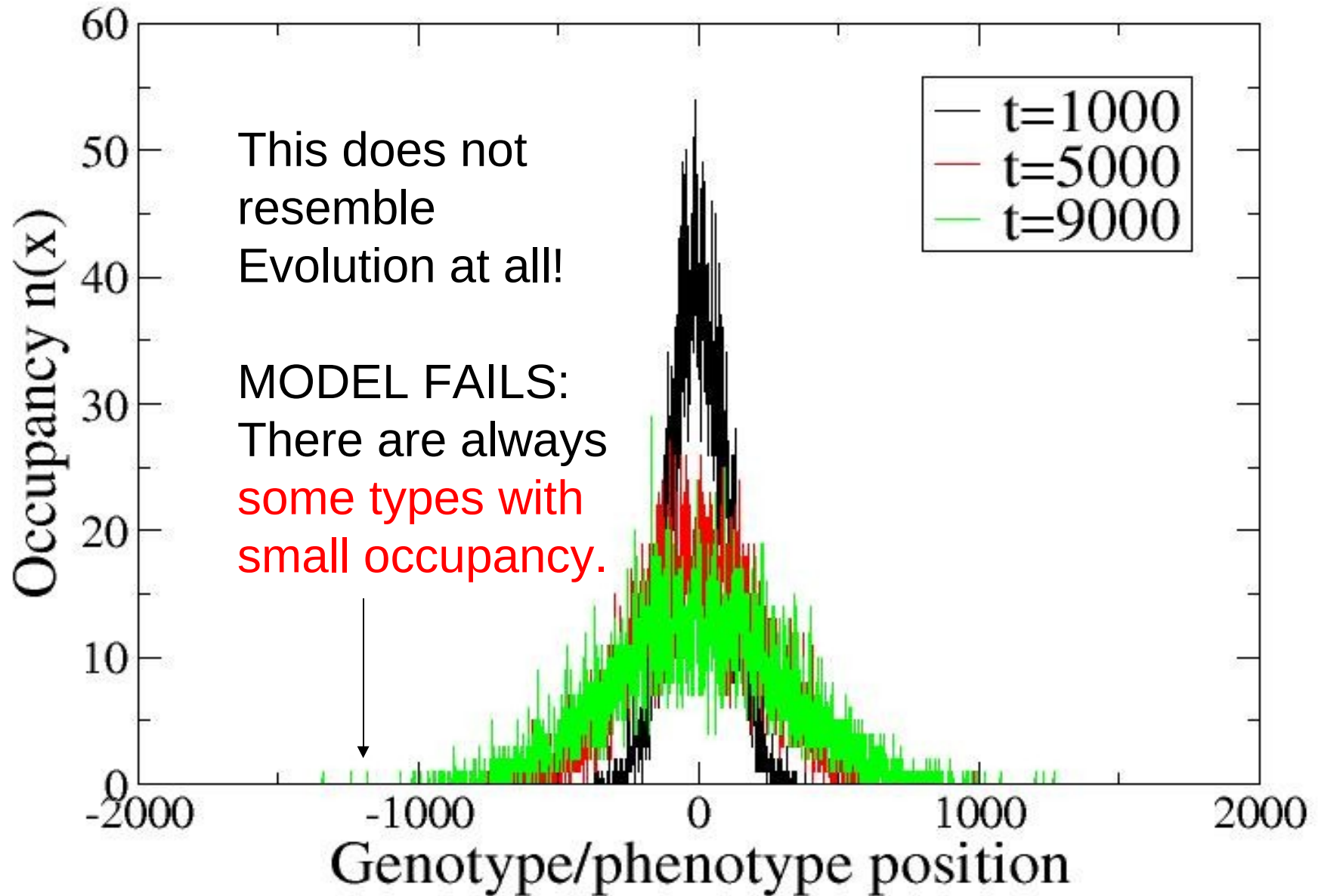
– Expect this to be valid when N large?

- This becomes:

$$\langle n_a(t+1) - n_a(t) \rangle = \frac{p_m}{2N} [n_{a+1}(t) + n_{a-1}(t) - 2n_a(t)]$$

- This is just the diffusion of N particles!

Diffusion of 10000 particles



Defining Asexual Diversity



- We want the “number” of different species or types
- Requires definition of species:
 - *Biological Species Concept?*
 - *Phenotypically distinct?*
 - *Genotypic Species Concept?*

HOWEVER:

- “Species” don't exist – though individuals cluster in type space
- Instead examine the similarity between types