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A dynamical phase transition in a model for evolution with migration

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Migration is important in evolution of populations

animals: human migrations



T. J. Parsons et al Nature Genetics 15, 363 (1997)

Not only animals can migrate

viruses: Human influenza A virus



Migration plays an important role in evolution of pathogenic bacteria!

Migrants are usually maladapted to the new habitat

How is their evolution influenced by the rate of migration?

Model for evolution and migration



Possible mutations between genotypes \rightarrow mutation graph

Mutation graph - examples



• in general: arbitrary simple graph with weighted links



Evolution in the primary habitat



Quasispecies model (with parallel mutation and selection)

Eigen, Schuster (1977) McCaskill, Demetrius Swetina, Leuthausser M.A. Nowak,

...

• no migration term - primary habitat assumed to be very large

• fitness: i.i.d. random numbers with some distribution $P(\Phi)$

Example: binary distribution $\Phi=1$ (fit genotype) or $\Phi=0$ (unfit genotype)

How to find steady-state solution of this equation

Define rescaled abundances

$$x_i(t) = N_i(t) \exp\left(\int_0^t \sum_j N_j(t')dt'\right)$$

linear equation

$$\dot{\vec{x}} = W\vec{x}$$
 where $\begin{cases} W_{ij} = \delta_{ij}\Phi_i + \gamma\Delta_{ij} \\ \\ \Delta_{ij} = A_{ij} - \delta_{ij}\sum_k A_{ik} \end{cases}$

eigenvalues and eigenvectors of W

$$W |\Psi_i\rangle = \Lambda_i |\Psi_i\rangle$$

 $\Lambda_1 > \Lambda_2 > \dots > \Lambda_N$

• solution for $x_i(t)$:

$$\vec{x}(t) = e^{tW} \vec{x}(0) = \sum_{i} e^{t\Lambda_i} \langle \Psi_i | x(0) \rangle \vec{\Psi}_i \qquad \longrightarrow \quad \vec{x}(\infty) \propto \vec{\Psi}_1$$

steady-state solution:

$$\vec{N^*} = \frac{\Lambda_1}{(\vec{\Psi_1}^T \cdot \vec{e})} \vec{\Psi}_1$$

 $\vec{e} = (1, \ldots, 1)$

Properties of the steady state

hypercube, L=6





"quasispecies" - most populated genotype (site of the hypercube) + cloud of mutants around it





Evolution in the secondary habitat

$$\dot{n}_i = n_i(\phi_i - \sum_j n_j) + \gamma \sum_j A_{ij}(n_j - n_i) + kN_i$$

migration term - primary habitat acts as a source of genotypes

• fitness: i.i.d. random numbers with the same distribution $P(\phi)$ as in the primary habitat

• fitness ϕ_i differs from Φ_i in the primary habitat

Solution:

$$\vec{n}^* = k \sum_{\alpha=1}^{M} \frac{\vec{\psi_{\alpha}}^T \cdot \vec{N^*}}{n_{\text{tot}} - \lambda_{\alpha}} \vec{\psi_{\alpha}}$$

where $V \ket{\psi_i} = \lambda_i \ket{\psi_i}$ $\lambda_1 > \lambda_2 > \ldots > \lambda_N$

$$V_{ij} = \delta_{ij}\phi_i + \gamma \Delta_{ij}$$

n_{tot} determined from

$$n_{\text{tot}} = k \sum_{\alpha=1}^{M} \frac{(\vec{\psi}_{\alpha}^T \cdot \vec{N}^*)(\vec{\psi}_{\alpha}^T \cdot \vec{e})}{n_{\text{tot}} - \lambda_{\alpha}}$$

Properties of the steady state

1d chain of genotypes, 128 genotypes, γ=0.01 binary fitness distribution: prob(0)=0.1, prob(1)=0.9





Evidence of a dynamical phase transition





Relaxation time diverges at critical migration rate k_0

$$k_0 = \lambda_1 \left(\sum_{\alpha=2}^{M} \frac{(\vec{\psi}_{\alpha}^T \cdot \vec{N}^*)(\vec{\psi}_{\alpha}^T \cdot \vec{e})}{\lambda_1 - \lambda_{\alpha}} \right)^{-1}$$

1d chain, probability of less adapted genotypes $\epsilon <<1 \implies \langle k_0 \rangle \simeq \frac{\gamma \epsilon^2 \ln(M \epsilon)}{(\ln \ln M \epsilon)^3}$ k_0 can be very low

When is this a genuine phase transition?

transition becomes sharp if overlap between the quasispecies native to both habitats becomes zero



size of the genome space does not matter



shape of the mutation graph does not matter

1d chain, hypercube, or arbitrary graph: localized eigenvectors are sufficient enough

fitness distribution P(ϕ) does not need to be binary

Summary

simple model for evolution and migration of asexual organisms predicts a dynamical phase transition at critical migration rate

at the transition, the time to reach the steady state diverges - evolution slows down

 genetic composition of the population is diametrically different below and above the transition

 even small amount of migration can have an important effect on evolutionary dynamics

Some experiments possible...

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How to test these predictions experimentally?



Two chemostats, coupled by controlled migration Control fitness difference with antibiotics Evolution = gain of antibiotic resistance

