Nonequilibrium Phase Transitions and Spatial Population Genetics

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Outline

□ Nonequilibrium phase transitions and connection to evolutionary dynamics
□ Directed percolation with inflation and radial range expansions
□ Scaling at the phase transition
□ Spherical range expansions
□ Models of range expansions with mutualism
□ Mutualism with rough fronts
Directed Percolation (DP)

Avalanche Flows  Phase Nucleation  Range Expansions

H. Hinrichsen  K. A. Takeuchi et al.  O. Hallatschek and D. R. Nelson

Typical Initial Conditions

single seed:  uniform:

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Range expansions and evolution

There is an interplay between (spatial) population dynamics and evolutionary dynamics:

Well mixed:

Spatially distributed:


experiment photos from: O Hallatshek and DR Nelson, Physics Today July 2009 p. 44
Quasispecies theory

Set of sequences \( \{\sigma\} \) with \( \sigma = (s_1, s_2, \ldots, s_N) \) where \( s_i = 1, 2, \ldots, \ell \)

DNA sequences: \[\text{ATCGATCGTACGTAACTGACATGACTGTACTGTACGTGACCTT} \]

\( \ell = 4 \)

- Green circle: cell with master seq. \( \sigma_0 \)
- Red circle: cell without master seq.

Cross error threshold

\( \mu < \mu_c \) for \( \mu \) below the threshold.

\( \mu > \mu_c \) for \( \mu \) above the threshold.

Sequence space \( \sigma \)
Quasispecies theory: fitness functions

sharply peaked

\[ W = \delta_{d(\sigma, \sigma_0)} + W_0 [1 - \delta_{d(\sigma, \sigma_0)}] \]

distance from master sequence: \( d(\sigma, \sigma_0) \)

multiplicative

\[ W = (1 - s)^{d(\sigma, \sigma_0)} \]

directed percolation

\( d(\sigma, \sigma_0) : 0 \quad d > 0 \)

unidirectionally coupled directed percolation

\( d(\sigma, \sigma_0) : 0 \quad 1 \quad 2 \ldots \quad K - 1 \)
The Domany-Kinzel model

(1) selection with parameter $s \in [0, 1]$

$$p_G = \frac{1}{1 + (1 - s)}$$

green outcompetes red

(2) mutations

Evolution of a population with 5 individuals:

$t = 0$

$t = 1$

$t = 2$

Time is measured in units of the generation time $T_g$

Model described in: H Hinrichsen, Adv. in Phys. 49(7), 815 (2000);
Radial Domany-Kinzel model

(1) selection

$$p_G = \frac{2}{2 + (1 - s)}$$

(2) mutations:

$$\mu_f = \frac{n_G}{n_G + n_R(1 - s)}$$

$$\mu_b = 0$$
Radial models exhibit lattice artifacts

Simulations with well-mixed initial conditions

hexagonal lattice:

square lattice:
The Heterozygosity

The heterozygosity is the probability two cells are different:

$$H(\delta r, t) \equiv \langle f(r, t)[1 - f(r + \delta r, t)] + f(r + \delta r, t)[1 - f(r, t)] \rangle_{\text{ensemble}},$$

fraction of green cells
Lattice artifacts (with mutations)

The heterozygosity can capture important spatial features of the dynamics

\[
\begin{aligned}
& s = 0.57 \\
& \mu_f = 0.1 \\
& \mu_b = 0 \\
& R_0 = 15 \text{ cells}
\end{aligned}
\]
An amorphous lattice fixes the artifacts

We employ a Bennett model using two cell sizes to construct an isotropic lattice:

structure factor: \( S(k) \equiv \frac{1}{N} \left| \sum_{i=1}^{N} e^{i k \cdot r_i} \right|^2 \)

The stepping-stone Langevin equation for the green cell density $f(x, t)$ in the limit $N \to 1$ is the same as coarse-grained DK model (at small $s, \mu_b, \mu_f$):

$$\partial_t f(x, t) = \frac{a^2}{\tau_g} \nabla_x f + sf(1 - f) + \frac{\mu_b}{\tau_g} (1 - f) - \frac{\mu_f}{\tau_g} f$$

$$+ \sqrt{2a\tau_g^{-1}} f(1 - f)\eta(x, t) \quad \text{genetic drift}$$

Gaussian noise: $\langle \eta \rangle = 0 \quad \langle \eta(x, t)\eta(x', t') \rangle = \delta(t - t')\delta(x' - x)$
The neutral case \((s = \mu_f = \mu_b = 0)\)

From the Langevin equation:

\[
\begin{cases}
\partial_t H(\mathbf{r}, t) = 2D \nabla^2 H(\mathbf{r}, t) \\
H(\mathbf{r} = 0, t) = 0
\end{cases}
\]

**Linear:**

\[
\partial_t H(r, t) = 2D_l \frac{\partial H}{\partial r^2} + \frac{2D_l(d - 1)}{r} \frac{\partial H}{\partial r}
\]

**Radial:**

\[
\partial_\eta H(\phi, \eta) = \frac{2D_r}{R_0^2} \frac{\partial^2 H}{\partial \phi^2} + \frac{2D_r(d - 1)}{R_0^2 \tan \phi} \frac{\partial H}{\partial \phi}
\]

**Absorbing BC:**

\[H(0, \eta) = H(0, t) = 0\]

We identify a conformal time coordinate:

\[\tau = \eta/t^* = \frac{t/t^*}{1 + t/t^*} \quad \text{with} \quad t^* = \frac{R_0}{v}\]

0 < \eta < \frac{R_0}{v}

0 < t < \infty
The neutral case \((s = \mu_f = \mu_b = 0)\)

Radial:

Linear:

Collapsed:

\[ \xi = \sqrt{\frac{R_0 + vt}{D_r R_0 t}} \phi \]

Exact solution:

\[ H(\xi) = H_0 \operatorname{erf} \left( \frac{\xi}{2\sqrt{2}} \right) \]

Effective lattice spacing:

\[ D_r \approx (2.6)^2 D_l \propto a^2 \]
Survival probability without mutations

Treating sector boundaries as random walks, we can find the probability $p(\phi, \tau)$ of observing a sector size $\phi$:

\[
\begin{align*}
\partial_\tau p(\phi, \tau) &= \left[ \Delta \partial_\phi^2 - \frac{w}{1-\tau} \partial_\phi \right] p(\phi, \tau) \\
S_r(\tau) &= 1 - \Delta \int_0^\tau d\tau' \left[ \partial_\phi p(\phi, \tau') \right]_{\phi=0}
\end{align*}
\]

\[
\begin{align*}
w &\approx \gamma \frac{a s}{v \tau_g} \\
\Delta &\approx \frac{a^2}{R_0 v \tau_g}
\end{align*}
\]

key parameter:

\[
\kappa = \frac{w}{\sqrt{2} \Delta} \approx 2.4
\]

\[
\phi_0 \approx 0.036
\]

\[
R_0 = 300 \text{ cells}
\]

\[
\kappa \approx 0.05
\]
Directed percolation phase transition

The deleterious mutation rate balances the selective advantage of the unmutated strain:

Experiment photos from: O Hallatshek and DR Nelson, Physics Today July 2009 p. 44
Absorbing phase transitions generally have four independent critical exponents.

Two typical initial conditions:
- all active (green)
- single seed

\( \xi_\perp \sim |\delta|^{-\nu_\perp} \)
\( \xi_\parallel \sim |\delta|^{-\nu_\parallel} \)

\( f(t) \) fraction of active cells
\( S(t) \) survival probability

\( t \to \infty : \)
\( f_\infty \sim \delta^{-\beta} \)
\( S_\infty \sim \delta^{-\beta'} \)
Regular versus inflationary DP

Inflation takes over after a crossover time:  \( t^* = \frac{R_0}{\nu} \)

For a fixed \( \mu_f = 0.1 \) :

\[
\begin{align*}
\text{inactive} & \quad s = 0.4 \\
\text{critical} & \quad s = 0.55 \\
\text{active} & \quad s = 0.7 
\end{align*}
\]
Inflationary single seed scaling

After inflation takes over, surviving sectors will have fixed angular sizes $\Delta \phi$ so that

$$N_G(t \gg t_*) \sim (\Delta \phi) R(t) \rho(t) \sim \Delta \phi(\nu t)t^{-\alpha}$$
Range expansions with deflation

Bacterial inoculation on Petri dish using the rim of a test tube:

(see MOL, K. Korolev, D. R. Nelson PRE 87, 012103 (2013))
Comparison of survival probabilities

$S_r(t \to \infty)$  $S_d(t \to t^*)$  $S_l(t \to \infty)$  $\phi_0$

$R_0 = 100$ cells
Population genetics in three dimensions

Linear:

Radial:
Bennett model cluster

- Logarithmic coarsening of domains $\xi(t) \sim \log t$
- Domains have no line tension ("cluster dilution")
- Boundaries are no longer simple random walks
Spherical range expansions (neutral case)

\[ \partial_t H(r, t) = 2D \nabla^2 H(r, t) \]

\[ H(|r| = a \to 0, t) = 0 \]

\[ H(\phi, t) \approx \frac{\ln(R_0 \phi / a)}{2 \ln \left( 2\sqrt{2Dt^* \tau} e^{-\gamma E / a} \right)} \]

cell size \( a \)

conformal time: \( \tau = \frac{t / t^*}{1 + t / t^*} \)
Inflationary DP in 2+1 dimensions

\[ d = 2 + 1 \text{ Phase Diagram} \]

\( (R_0 = 10) \) **active**

\( s = 0.6, \mu_f = 0.1 \)

\( t = 10 \)

\( (R_0 = 10) \) **critical**

\( s = 0.26, \mu_f = 0.1 \)

\( t = 20 \)

\( (R_0 = 10) \) **inactive**

\( s = 0.3, \mu_f = 0.2 \)

\( t = 30 \)
Single seed scaling at criticality

\[
\begin{align*}
R_0 &= 10 \text{ cells} \\
t &= 20 \text{ gen.}
\end{align*}
\]

Typical clusters:

![Graphs showing scaling behavior with different $R_0$ values and scaling exponents $2/z$ and $\theta$.]
Range Expansions With Mutualism

We are interested in range expansions of two species that grow faster when they are next to each other:
Mutualism with Flat Fronts: Update Rules

Each cell is updated based on its and its neighbor's states:

\[
p\left(\begin{array}{c}
\text{green} \to \text{red} \\
\text{red} \to \text{green} \\
\text{green} \to \text{green}
\end{array}\right) = p\left(\begin{array}{c}
\text{red} \to \text{red} \\
\text{green} \to \text{red} \\
\text{red} \to \text{green}
\end{array}\right) = p\left(\begin{array}{c}
\text{red} \to \text{green} \\
\text{green} \to \text{red} \\
\text{green} \to \text{green}
\end{array}\right) = \frac{1}{3} + \beta \\
p\left(\begin{array}{c}
\text{red} \to \text{red} \\
\text{red} \to \text{green} \\
\text{green} \to \text{green}
\end{array}\right) = \frac{1}{3} + \alpha
\]

Update rules can be implemented in two or three dimensions:

\[d = 1 + 1:\]

\[d = 2 + 1:\]

single cell update

216 sphere fcc block

Time
Flat Fronts: Phase Diagram for $d = 1 + 1$

Fluctuations locally fix red and green domains, preventing mixing even for certain $\alpha = \beta > 0$
Mutualism with Flat Fronts: Heterozygosity

For compact directed percolation, we expect:

\[ \partial_t H(x, t) = 2D_{\text{eff}} \partial^2_x H(x, t) \quad \Rightarrow \quad H(x, t) = H_0 \operatorname{erf} \left( \frac{x}{\sqrt{8D_{\text{eff}} t}} \right) \]

We test this for various \( \alpha = \beta < \alpha_{\text{crit}} \):

\[ (1/2)\operatorname{erf}(x/\sqrt{8D_{\text{eff}} t}) \]
Mutualism in three dimensions

In three dimensions, a mutualistic phase exists for all $\alpha = \beta > 0$
A Droplet Simulation

- $d = 2 + 1$
- $\alpha = \beta = -0.25$
- $\alpha = \beta = -0.05$
- $\alpha = \beta = -0.005$
- $t = 500$
- $t = 10000$
The interface density for an initially well-mixed population decays:

\[ \rho(t) \sim t^{-\delta(t)} \text{ with effective exponent } \delta(t) \equiv -\ln \left[ \frac{\rho(t + \Delta t)/\rho(t)}{(t + \Delta t)/t} \right] \]

The voter model result:

\[ \rho_A \approx A \left[ \frac{1}{\ln(\kappa t)} - \frac{\gamma E}{[\ln(\kappa t)]^2} \right] \]
Mutualism with Rough Fronts: Model

Each cell with an empty nearest or next nearest neighbor can reproduce with a certain rate. We pick one cell to reproduce at each time step.

A cell has a reproduction rate:

\[ b(i) = \Gamma_g + \alpha N_r(i) \]

- \( \Gamma_g \): base growth rate
- \( \alpha \): mutualistic advantage
- \( N_r(i) \): number of neighbors of opposite color
Mutualism with Rough Fronts

Rough fronts preserve the mutualistic phase. However, the dynamics and shape of the phase boundary are different.
We can track the average size of the interface fluctuations. They peak at the phase boundaries and are larger in the mutualistic regime.
Thank you!

- This is work with K. S. Korolev and D. R. Nelson
Power law range expansions (neutral case)

Range expansions can inflate with an arbitrary power law:

\[ R(t) = R_0 \left[ 1 + \left( \frac{t}{t^*} \right)^\Theta \right] \]

\(\Theta = 1/2\)  \(\Theta = 1\)  \(\Theta = 2\)

Results for neutral evolution:

\[ N_{\text{surv}} = \begin{cases} 
0 & \Theta \leq 1/2 \\
R_0 H_0 \sqrt{\frac{2\Theta^2 \sin(\pi/\Theta)}{D_r (\Theta-1)t^*}} & \Theta > 1/2 
\end{cases} \]
Multiplicative Fitness (Well-mixed)

Class fitness:

\[ W = (1 - s)^k \]

Evolution of classes:

\[ \frac{df_k}{dt} = s(k - k)f_k - \mu f_k + \mu f_{k-1} \]

Steady state:

\[ f_k = \frac{(\mu/s)^k e^{-\mu/s}}{k!} \]

Figure from LE Nicolaisen (LEN and M. Desai Mol Biol Evol 2012)
Mutation-Selection Balance

\[ f_k \]

\[ k = 0 \quad 1 \quad 2 \quad 3 \quad \ldots \quad K - 1 \]

\[ \mu \]

\[ s = 0.1 \]

\[ \mu = 0.1 \]

\[ \mu = 0.3 \]

\[ \mu = 0.5 \]

\[ \mu f_k \]

\[ (1 - s)^k f_k \]

death

mutation

division
Spatial Mutation-Selection Balance

unidirectionally coupled directed percolation

\[ \sigma_0 \rightarrow \mu_f \rightarrow \sigma_1 \rightarrow \ldots \rightarrow \sigma_{K-1} \]

\[
\begin{align*}
\mathcal{P}_k &= \frac{N_k g_k}{\sum_{k'} N_{k'} g_{k'}} \\
g_k &= (1 - s)^k
\end{align*}
\]
Muller’s ratchet

velocity

\[ v \sim (1 - f_0)^N \quad f_0 \approx e^{-\mu/s} \]

width

\[ W \sim \sqrt{\frac{\mu}{s}} \]

UCDP ratchet

velocity

\[ v \sim (\mu - \mu_c)^{\nu_{||}} \quad \nu_{||} \approx 1.7 \]

width

\[ W \sim (\ln t)^\gamma \quad \gamma \approx 0.24 \]

For bond percolation: $\langle f(t) \rangle = \langle S(t) \rangle$

In general for DP: $\langle f(t \gg t_{tr}) \rangle \simeq \langle S(t \gg t_{tr}) \rangle$

Three exponents characterize DP: $\beta = \beta'$, $\nu_\perp$, $\nu_\parallel$
Rapidity reversal violation

Inflation breaks rapidity reversal in both dimensions:

\[ d = 1 + 1 \]

\[ \propto \langle S_r(t) \rangle (t^*)^\alpha \]

\[ \propto \langle f(t) \rangle (t^*)^\alpha \]

\[ d = 2 + 1 \]

\[ \propto \langle S_r(t) \rangle (t^*)^\alpha \]

\[ \propto \langle f(t) \rangle (t^*)^\alpha \]
Stochastic Differential Equations

\[ \partial_t p(f, t) = -\partial_f [v(f)p] + \partial^2_f [D(f)p] \]

Fokker-Planck Equation

\[ \partial_t f = v(f) + \sqrt{2D(f)} \eta(t) \]
\[ \langle \eta(t)\eta(t') \rangle = \delta(t - t') \quad \langle \eta(t) \rangle = 0 \]

\[ \tau_i = \begin{cases} t_{i-1} & \text{Ito} \\ (t_i + t_{i-1})/2 & \text{Stratonovich} \end{cases} \]

\[ t_{i-1} \quad \tau_i \quad t_i \]
Stationary Distributions

\[ p_*(f) = C e^{s f \tau_{gen}^N} f^{\mu_{RG} \tau_{gen}^N - 1} (1 - f)^{\mu_{GR} \tau_{gen}^N - 1} \]

\[ \mu_{GR} = \mu_{RG} = 0.3 \]

\[ s = 2 \]

\[ \mu_{RG} = 0.3 \]

\[ s = 2 \]

\[ \mu_{GR} = 0.9 \]

\[ s = 0.05 \]
In the active state, linear and radial range expansions have the same steady state.
Regular DP occurs at short times

The early time dynamics are the same in linear and radial range expansions:

\[ R_0 = 2500 \text{ cells} \]

\[ \langle f(t) \rangle t^\alpha \]

\[
\begin{align*}
\mu_f &= 0.1 \\
\delta s &= s - s_c
\end{align*}
\]

The collapse is consistent with the DP critical exponents:

\[
\begin{align*}
\alpha &= \frac{\beta}{\nu_\parallel} \approx 0.159 \\
\nu_\parallel &\approx 1.73
\end{align*}
\]
Stepping-Stone Model

- Spatially Distributed Populations (Demes)
- Exchange of Individuals

\[ M \text{ demes} \]

\[ \ell^{th} \text{ deme} \]

\[ x = \ell a \]

\[ N \rightarrow 1 \]

\[ \tilde{m}N \quad \tilde{m}N \]

\[ N \text{ cells} \]

\[ \partial_t f(x, t) = ma^2 \nabla_x^2 f + sf(1-f) + \mu_{RG}(1-f) - \mu_{GR}f + \sqrt{2(N\tau_{gen})^{-1}f(1-f)\eta(x, t)} \]

Noise correlations:
\[ \langle \eta(x, t)\eta(x', t') \rangle = \delta(x - x')\delta(t - t') \]
The Critical Phase

**UCDP ratchet**

velocity
\[ v \sim (\mu - \mu_c)^{\nu_\parallel} \quad \nu_\parallel \approx 1.7 \]

width
\[ W \to K^{1/2} \quad W_c \sim (\ln t)^\gamma \]
\[ \gamma \approx 0.24 \]

**Muller’s ratchet**

velocity
\[ v \sim (1 - f_0)^N \quad f_0 \approx e^{-\mu/s} \]

width
\[ W \sim \sqrt{\frac{\mu}{s}} \]
The Voter Model (no selection)

- Consider a lattice of "voters"

\[ \sigma_i = \begin{cases} 1 & \text{green} \\ -1 & \text{red} \end{cases} \]

- Flip spin \( i \) with rate

\[
\omega(\{\sigma\} \to \{\sigma\}_i) = \frac{1}{2} \left[ 1 - \frac{\sigma_i}{z} \sum_{k \text{ n.n. of } i} \sigma_k \right] + \frac{\mu_{GR}(1 + \sigma_i)}{2} + \frac{\mu_{RG}(1 - \sigma_i)}{2}
\]

- Continuous time Master Equation

\[
\partial_t P(\{\sigma\}, t) = \sum_{\{\sigma'\}} \left[ \omega(\{\sigma'\} \to \{\sigma\}) P(\{\sigma'\}, t) - \omega(\{\sigma\} \to \{\sigma'\}) P(\{\sigma\}, t) \right]
\]
Inflationary scaling (all green homeland)

- We treat crossover time $t^*$ as a new variable in all scaling functions.
- We find that $t^*$ scales the same way as a finite time variable.

![Graph showing scaling behavior](image)

- $\langle f(t) \rangle \propto t^{\alpha}$
- $\text{slope} \approx -0.16$
- $\text{slope} \approx -0.26$

Legend:
- $R_0$ values include 8, 16, 32, 64, 128, 256, 512, 1024, 2048.
Directed Percolation Phase Transition

The control parameter: \[ \tau = p_G - p^*_G \]

- \( \tau < 0 \) absorbing phase
- \( \tau = 0 \) phase transition
- \( \tau > 0 \) active phase

no mutations, CDP

\( p_{GR} \)

\( \xi_{||} \)

\( \xi_{\perp} \)

Active Phase

Inactive Phase

\( 2R(t) \)
Initial Conditions are Important

1) Isolated seed initial condition:

\[ N_G \sim t^\Theta \]
\[ P_{\text{surv}} \sim t^{-\delta} \]
\[ R \sim t^{1/\gamma} \]

2) Fully occupied initial condition:

\[ P_{\text{perc}} = \lim_{t \to \infty} P_t(\text{active}) \]
\[ \rho = \lim_{t \to \infty} P_t(\text{occupied}) \]

Near critical point:

\[ P_{\text{perc}} \sim \tau^{\beta'} \]
\[ \rho \sim \tau^\beta \]
Interface width scaling:

\[ \delta h \sim t^{\eta} F_h(L t^{-1/z}) \]

\[ \sim \begin{cases} 
L^{\gamma} & L \ll t^{1/z} \\
 t^{\eta} & L \gg t^{1/z} 
\end{cases} \]

Mixed phase density scaling:

\[ \rho_A \sim t^{-\alpha} \]
Effective Potentials

\[ V(f) \approx -\frac{\beta}{2}(1 - f)^2 \]
Correlation Lengths

\[ \xi_\perp \sim |\tau|^{-\nu_\perp} \]
\[ \xi_\parallel \sim |\tau|^{-\nu_\parallel} \]
Lattice Effects (no mutations)
Bennett Model Simulations

$p_G = 0.5 \quad p_{GR} = 0$

Compact Directed Percolation:

$p_G = 0.7 \quad p_{GR} = 0.1$

Directed Percolation:

Corrected heterozygosity:
$R_0 = 15 \quad p_G = 0.7 \quad p_{GR} = 0.1$
Neutral with Mutations

Linear:

$$H(x, t) = \frac{2\mu_{RG} \mu_{GR}}{(\mu_{GR} + \mu_{RG})^2} \left[ 1 - e^{-|x| \sqrt{\frac{2(\mu_{GR} + \mu_{RG})}{D}}} \right] + e^{-2t(\mu_{GR} + \mu_{RG})} f(x, t)$$

Radial: Approaches the same stationary distribution and exhibits a cross-over time:

$$t_* = \frac{R_0}{\nu}$$

$$\mu_{GR} = \mu_{RG} = 0.01$$

$\begin{align*}
R_0 &= 5 \\
\nu &= 1
\end{align*}$
One-way Mutations and Selection

Linear:

\[ \ln \langle f(t) \rangle \]
\[ p_{GR} \approx 0.13 \]
\[ p_G = 0.8 \]
\[ \text{slope} \approx -0.16 \]

Radial:

\[ \ln \langle f(t) \rangle \]
\[ p_{GR} \approx 0.13 \]
\[ p_G = 0.8 \]
\[ 0.75 \]
\[ 0.74 \]
\[ 0.725 \]
One-way Mutations and Selection

It is easier to connect the linear and radial model on the same lattice:

Linear:

\[ \ln \langle f(t) \rangle \]

- \( p_{GR} \approx 0.13 \)
- \( p_G = 0.8 \)
- \( p_G = 0.75 \)
- \( p_G = 0.74 \)
- \( 0.7 \) slope \( \approx -0.16 \)
- \( 0.64 \)
- \( 0.725 \)

Radial (hexagonal lattice):

\[ \ln \langle f(t) \rangle \]

- \( p_{GR} \approx 0.13 \)
- \( p_G = 0.74 \)
- slope \( \approx -0.16 \)

\( R_0 = 40 \)

\( t_* \)


K. Korolev et al. *Genetic demixing and evolution in linear stepping stone models*, Reviews of Modern Physics, **82** (2), 2010, pp. 1691-1718

N. G. Van Kampen *Stochastic Processes in Physics and Chemistry* (Elsevier 2007)