The Renormalization Group in Genetic Dynamics

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What is the RG?

Based on the fundamental notion of coarse graining

Mapping systems with many degrees of freedom to one with fewer…

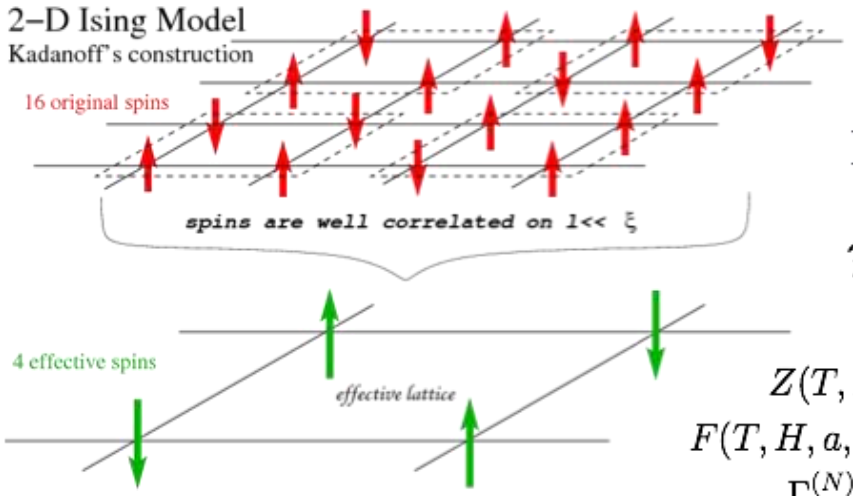
- Mechanics - e.g., rigid bodies; planetary motion,…
- Statistical mechanics - e.g., kinetic theory, thermodynamics,…
- Genetics - e.g., genotype-phenotype map; nucleotides to genes,…
- Quantum field theory - e.g., renormalisation, bound states,…
- Statistical mechanics/field theory - e.g., block spinning, majority rule,…

Single versus iterative coarse grainings…
maps from one system to "another"

Effective Theories

The Renormalization Group

Explains Scaling, Scale invariance and Universality!



$$\mathcal{H} = -(J/2T)\sum_{i,j}\sigma_i\sigma_j - (H/T)\sum_i \sigma_i + E$$

Map from one lattice to another: $\mathcal{R}_a \quad \xi \to \xi/2$

$$\mathcal{H}(T,H,E) \to \mathcal{H}(T',H',E')$$

Map is on the space of theories

No guarantee the theory will "renormalize"

$$Z(T,H,E,a,N) = Z(T',H',E',a,N/2)$$
$$F(T,H,a,N) = F(T',H',a,N/2) + G(T,H)$$
$$\Gamma^{(N)}(T,H,a,N) = \Gamma^{(N)}(T',H',a,N/2)$$

for 1D

$$\mathcal{R}_a\mathcal{R}_b = \mathcal{R}_{ab}$$ Maps form a (semi)-group

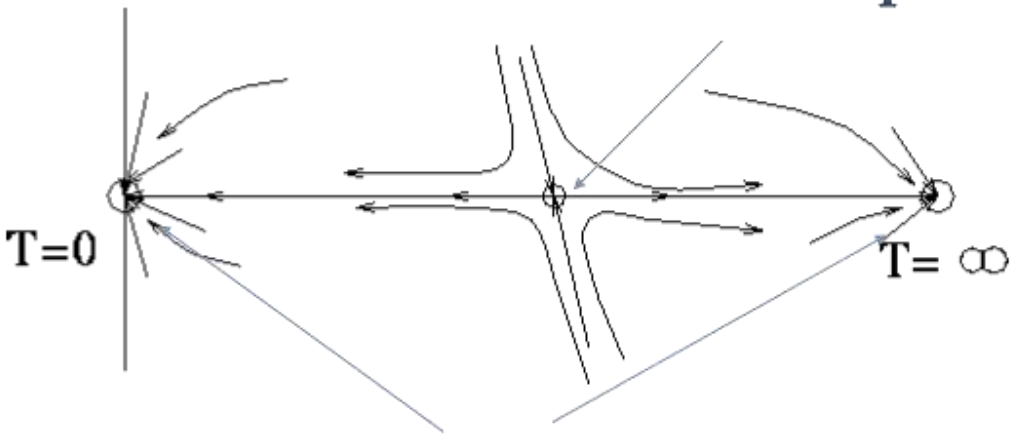
Iterate $H_n = \mathcal{R}_2^n H \quad T_n = \mathcal{R}_2^n T$ and look for fixed points: $T = T^*$ and $H = H^* \; \xi = \infty, \quad \xi = 0$

Linearize the transformation near the fixed point: $\mathcal{R}_b(T,H) \equiv (t',h') \sim (b^{y^t}t, b^{y^h}h)$

Critical exponents are related to the eigenvalues of the linearised RG transformation, e.g. $\nu = 1/y^t$

Criticality is “special” and “boring”
(phenomenologically poor)

Critical point - unstable to relevant H and T parameters, sub-manifold in the space of parameters



i.e., Other fixed points of the RG

Crossover phenomena

In the vicinity of the critical point for a ferromagnet (and many others) there are **only two scales** - a microscopic lattice scale and the correlation length. When the correlation length is much bigger than the microscopic scale then we have **universality**. But, there are **always other scales…**

Species extinctions
Electromagnetism
Animal foraging
City populations
Income distribution
Fluids
Sandpiles
Word distributions
$f(x) \sim x^{-\beta}$
Earthquakes
Ferromagnets
Gravity
Metabolic rates
Prices
Impact of scientific articles

Crossovers

For a general scaling function $\mathcal{F}(x, y, z, ...)$ where $x = g^{\phi}/t$ or $x = g\xi$ where g is a generic anisotropy parameter, then:

In the isotropic limit: $x \to 0 \quad \mathcal{F} \to x^{a}\mathcal{A}(y, z, ...)$ *The scaling function A contains a singularity*

In the anisotropic limit: $x \to x_s \quad \mathcal{F} \to (x - x_s)^{a_p - a}\mathcal{A}_p(y, z, ...)$

A richer phenomenology than standard criticality

Two different points of scale invariance

Two different fixed points of the RG!

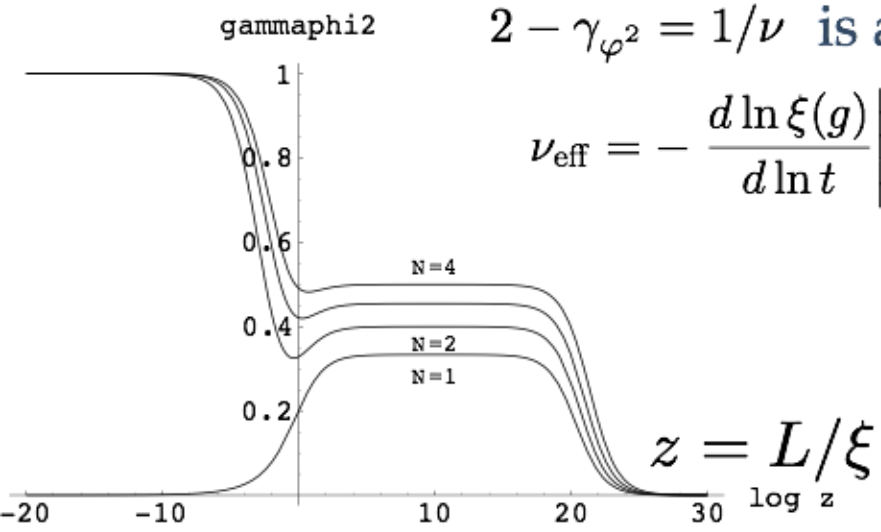
A linearisation around one fixed point cannot access the other

Some examples of g: System size L, dipolar coupling, temperature in quantum ferromagnets, distance to surface for surface/bulk (wetting), spin anisotropy, kinematic heterogeneity, etc.

Critical phenomena in a "box"
Environmentally Friendly Renormalization

Not all renormalizations capture a crossover. Need a coarse graining/RG map that captures the changing nature of the effective degrees of freedom as a function of the "environment", e.g. as 3D effective degrees of freedom transform to 2D ones in a thin film

$$\chi = At^{-\gamma} f(Lt^{\nu})$$

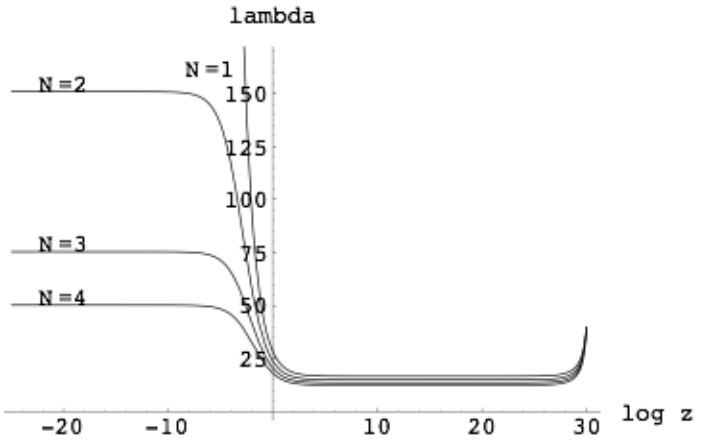


$2 - \gamma_{\varphi^2} = 1/\nu$ is a constant in the non-crossover case

$$\nu_{\text{eff}} = -\left.\frac{d\ln\xi(g)}{d\ln t}\right|_{H=0}$$

and hence γ_{φ^2} are functions in the crossover case - universal functions

$$z = L/\xi$$



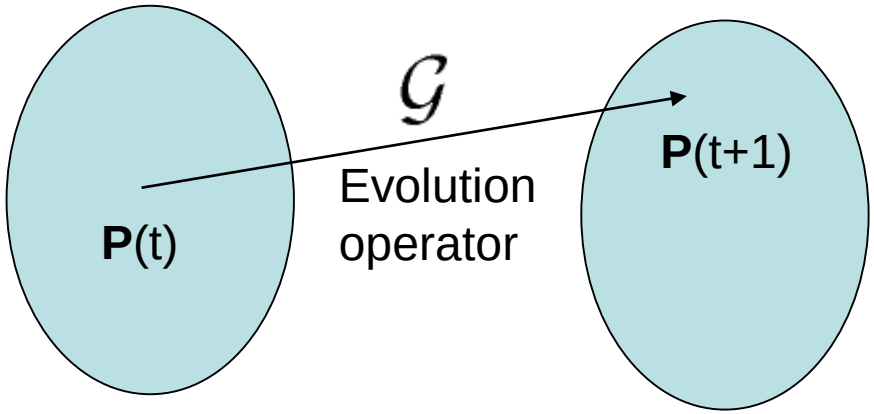
Summary of the RG

- Critical behaviour defied an appropriate quantitative description for many decades
- The RG completely solved the problem giving an accurate quantitative description of the critical region and explaining scaling and universality as associated with fixed points of the RG
- Standard criticality is “special” (not generic) in that it has to be tuned, i.e., is associated with a manifold in the space of parameters with relevant operators
- Standard criticality is “boring” (phenomenologically poor) in that there are only two length scales involved - super-universality
- In real systems there are always other scales involved
- The presence of other scales leads to crossover phenomena, with a richer phenomenology than standard critical phenomena
- There are RGs that have been used to explain and describe many crossovers – but it’s a set of measure zero!

What is Genetic Dynamics?

Population of “objects” – “genotypes”

$$\mathbf{P}(t) = (P_1(t), P_2(t), \cdots, P_\Omega(t))$$



determines the state of the population at time t; Ω is the dimension of the space of states of an “object”; for linear chromosomes with binary alleles $\Omega = 2^N$

Space of populations $\mathcal{P}$

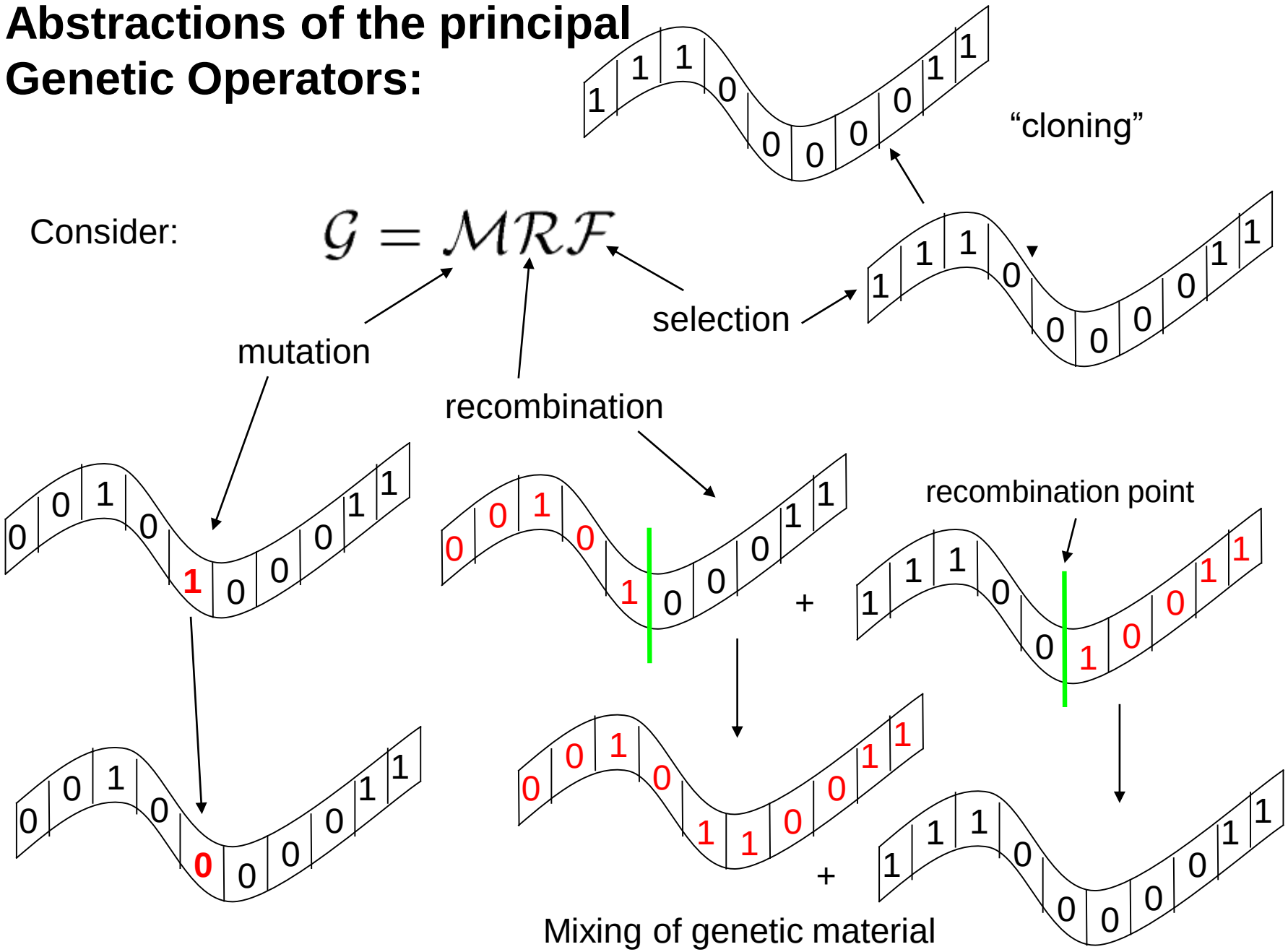
General evolution equation

$$\mathbf{P}(t+1) = \mathcal{G}(\mathbf{P}(t), \mathbf{p})$$

p represents a set of parameters associated with the evolution operator

Expected next population for finite Populations.
Describes evolution?
Fixed length strings…

Abstractions of the principal Genetic Operators:



In mathematics…

Finite population model determined by Markov chain. In the infinite population limit for haploids:

$$P_I(t+1) = M_I{}^J((1-p_c)P'_J(t) + p_c \sum_m p_c(m)\lambda_J{}^{KL}(m)P'_K(t)P'_L(t))$$

That's most of standard population genetics and evolutionary computation!

Implicit summation over repeated indices

$M_I{}^J$ Probability to mutate genotype J to genotype I

p_c Probability to implement recombination

$p_c(m)$ Probability that given recombination takes place it is implemented with mode m

$P'_I(t)$ Probability to select genotype I $P'_I(t) = \frac{f(I)}{\bar{f}(t)} P_I(t)$

$\lambda_J{}^{KL}(m)$ Conditional probability for "child" J given "parents" K and L and a mode m

Don't recombine it with another

Select an object J

Select two "parents" K and L

$$P_I(t+1) = M_I{}^J((1-p_c)P'_J(t) + p_c \sum_m p_c(m)\lambda_J{}^{KL}(m)P'_K(t)P'_L(t))$$

Mutate it to object I

Recombine them with respect to a recombination mode m applied with probability $p_c p_c(m)$ to obtain a "child" J

- **Ω coupled non-linear difference equations**
- **Population genetics has spent the last 70 years trying to deal with them**
  - Go to reduced number of loci
- **In object basis there are Ω^3 different λ_J^{KL} - that's a lot!**
  - Most of them are 0!

Two Questions…

1. Can we “solve” them?

   Put them on the computer. Not very feasible for N = 100!

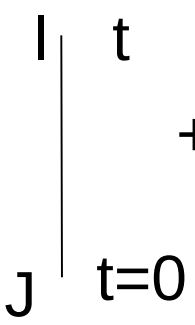
2. Can we understand anything “qualitatively” from them?

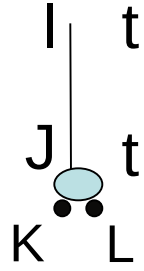
   How does genetic dynamics “work”?

   What are the effective degrees of freedom/collective modes?

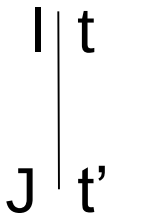
A Formal Solution…Genetic Dynamics done diagrammatically

Can iterate the equations and represent the solution graphically -

$$P_I(t) = \sum_J$$ 

$$+ \sum_{JKL} \sum_M \sum_{n=0}^{t}$$ 

Term exclusively due to constructive effect of recombination



$= G_{IJ}(t, t')$

Probability that object J propagates from t to t' and converts to I on the way


$= \frac{1}{2}\left(p(M) + p(\bar{M})\right) \lambda_J{}^{KL}(M) \frac{f_K}{\bar{f}(t)} \frac{f_L}{\bar{f}(t)}$

Measures strength of interaction between objects J, K and L

I • $= P_I(t)$

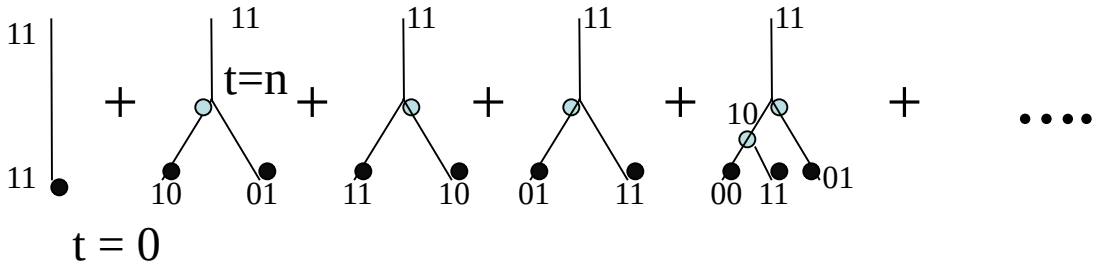
What we end up with…

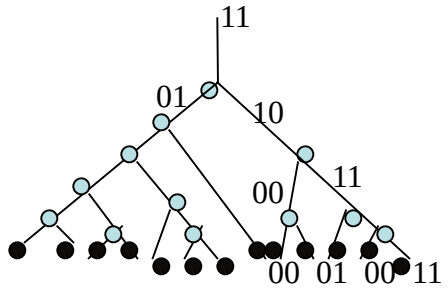
Iterate … by **recursively** substituting for • until get to t = 0

Example – 2-bits, recombination at one point

Process where 11 is formed by crossover of 10 and 01 at t = n for any n

$P_{11}(t)$ =





+ ....

Diagrams are pictorial representations of the different processes that can occur

Each tree tells us the probability of forming 11 by a given **process**. In principle can see which processes are most important. But …

tree depth bounded only by t!

COMPLICATED!

TOO MANY DIAGRAMS (PROCESSES)

Or more succinctly… using Feynman rules!

1) Draw all possible tree diagrams that contribute to creation of “object”

2) For each internal line ——— attach a propagator

$$G_{IJ}(t,t') = (1-p_c)^{t-t'} \frac{(\mathbf{FM})^{t-t'}_{IJ}}{\sum_I (\mathbf{FM})^{t-t'}_{IJ} P_J(t')}$$

3) To each vertex ⬭ attach a weight

$$\frac{1}{2}\left(p(M) + p(\bar{M})\right) \lambda_J{}^{KL}(M) \frac{f_K}{\bar{f}(t)} \frac{f_L}{\bar{f}(t)}$$

3) To each root • attach a factor $P_I(t')$

4) Carry out integration over time for all vertices

These rules generate the algebraic expressions that describe the different probabilistic processes that can occur in the dynamics of an EA

So where have we got?

- Can we really solve the equations
  - NO!
- Can we get any qualitative insight
  - Yes, objects are obtained by selecting other objects and recombining and mutating them!
  - Actually, NO!

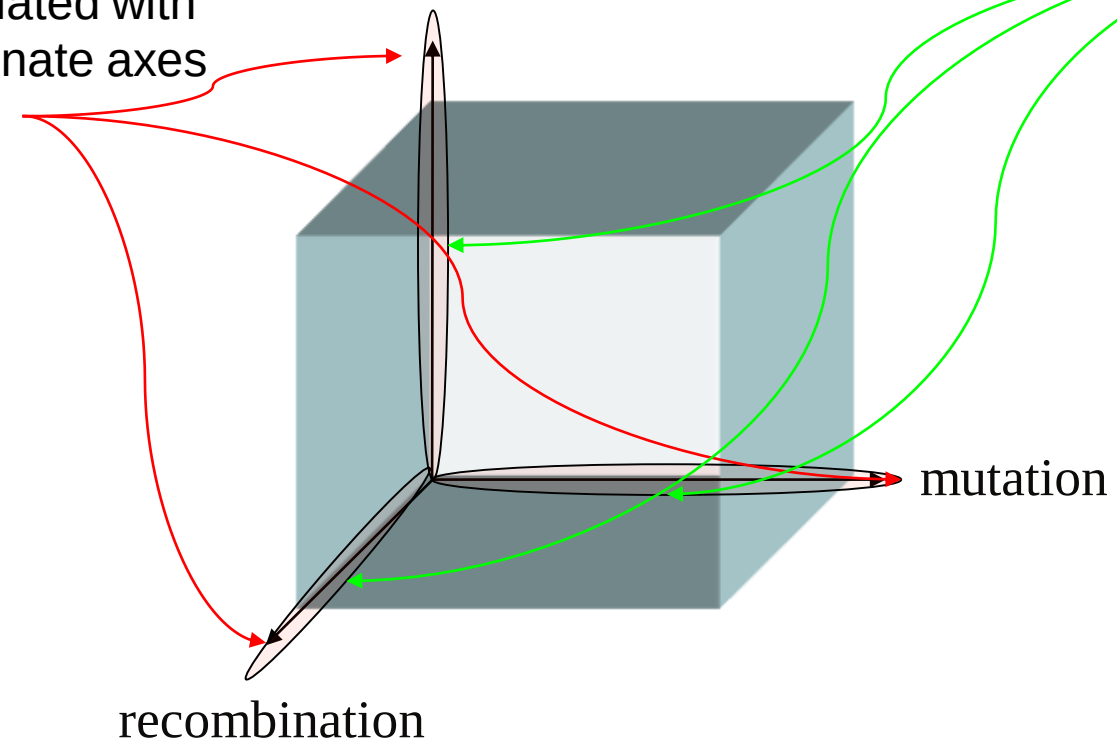
Can we make things simpler?

1. Selection only – can get exact solution in terms of “objects”, e.g. strings (microscopic degrees of freedom)
2. Mutation only – can get exact solution by Fourier transforming; Diagonalizes the mutation matrix - solutions are “normal modes” (collective/effective degrees of freedom)
3. Recombination only – can get exact solution in continuous time limit in terms of “Building Blocks” (collective/effective degrees of freedom)

Beyond the exact solutions

Exact solutions associated with coordinate axes

Can we find approximate solutions “close” to the exact ones? Or maybe even further away?

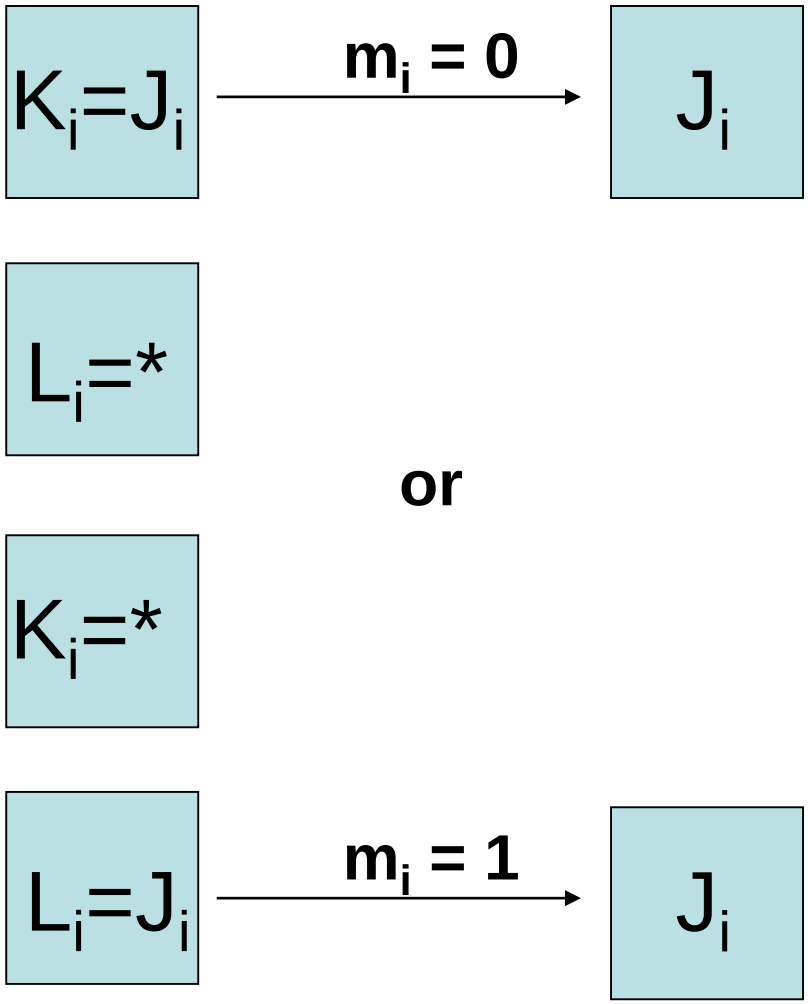


More importantly, exact solutions are associated with completely different effective degrees of freedom

So, where does the RG come in?

1. Recombinative dynamics
2. Selection-Mutation dynamics – the coarse-graining approach
3. Selection-Mutation dynamics – the reparametrization approach

Recombinative Dynamics



In recombination, at every locus, one of the parental alleles is ***always*** coarse-grained

Every m defines a particular coarse-graining

Here its “homologous” recombination which means that the ith locus of the child string comes from the ith locus of a parent string. This formalism generalises to the case where the ith locus of the child comes from ANY locus of the parent

Recombinative Dynamics

$$\lambda_J{}^{KL}(m) = \prod_{i=1}^{N} \lambda_{J_i}{}^{K_i L_i}(m_i) = \prod_{i=1}^{N}((1-m_i)\delta_{J_i}{}^{K_i} + m_i \delta_{J_i}{}^{L_i})$$

Product of locus-wise projection operators

$$\sum_{K_i} \sum_{L_i} ((1-m_i)\delta_{J_i}{}^{K_i} + m_i \delta_{J_i}{}^{L_i})$$

If $m_i = 0$ (take allele for first locus of "child" from first locus of first parent) then

$$\sum_{K_i} \sum_{L_i} ((1-m_i)\delta_{J_i}{}^{K_i} + m_i \delta_{J_i}{}^{L_i}) P_{K_1 \cdots K_i \cdots K_N}(t) P_{L_1 \cdots L_i \cdots L_N}(t)$$

$$= P_{K_1 \cdots J_i \cdots K_N}(t) P_{L_1 \cdots *_i \cdots L_N}(t)$$

where $*_i$ means we have marginalized the probability at the ith locus

Similarly, for $m_i = 1$

$$= P_{K_1 \cdots *_i \cdots K_N}(t) P_{L_1 \cdots J_i \cdots L_N}(t)$$

Recombinative Dynamics

$$P_I(t+1) = M_I{}^J((1-p_c)P'_J(t) + p_c \sum_m p_c(m) P'_{J_m}(t) P'_{J_{\bar{m}}}(t))$$

So?!

Where's λ_J^{KL} gone?

Every m, i.e., coarse-graining mode, for given target object J defines a "Building Block" J_m. At the same time this uniquely defines a conjugate Building Block $J_{\bar{m}}$ that is the set complement of J in J_m.

This coarse-graining can also be implemented as a coordinate transformation using a transformation matrix

$$\Lambda = \begin{pmatrix} 0 & 1 \\ 1 & 1 \end{pmatrix}^{\otimes N}$$

In this basis $\lambda_J^{KL}(m)$ for a given m has only one non-zero entry and it's on the skew diagonal

Recombinative Dynamics

- Thus we see how recombination “works” by taking BBs and recombining them into strings
- If $\Delta_I(m) = P'_I - P'_{I_m} P'_{I_{\bar{m}}}$ (Selection Weighted Linkage Disequilibrium Coefficient) > 0 then recombination is bad for the formation of that string and good if < 0 (more construction then destruction.
- But if we want to “solve” the dynamics have to know what happens to the BBs! E.g. what´s the equation for I_m? Need to coarse grain the string equation

Recombinative Dynamics

$$P_{I_m}(t) = \sum_{\{i:m_i=1\}} P_{I_1 I_2 \cdots I_i \cdots I_N}$$

Projection operator $\mathcal{R}(\eta, \eta')$

$$\mathcal{R}(\eta, \eta'') = \mathcal{R}(\eta, \eta')\mathcal{R}(\eta', \eta'')$$

Renormalization (semi)-group

$$P_{I_m}(t+1) = M_{I_m}^{\ J_m}((1-p_c)P'_{J_m}(t) + p_c \sum_{m'} p_c(m') P'_{J_{m m'}}(t) P'_{J_{m \bar{m}'}}(t))$$

BBs of the BB J_m

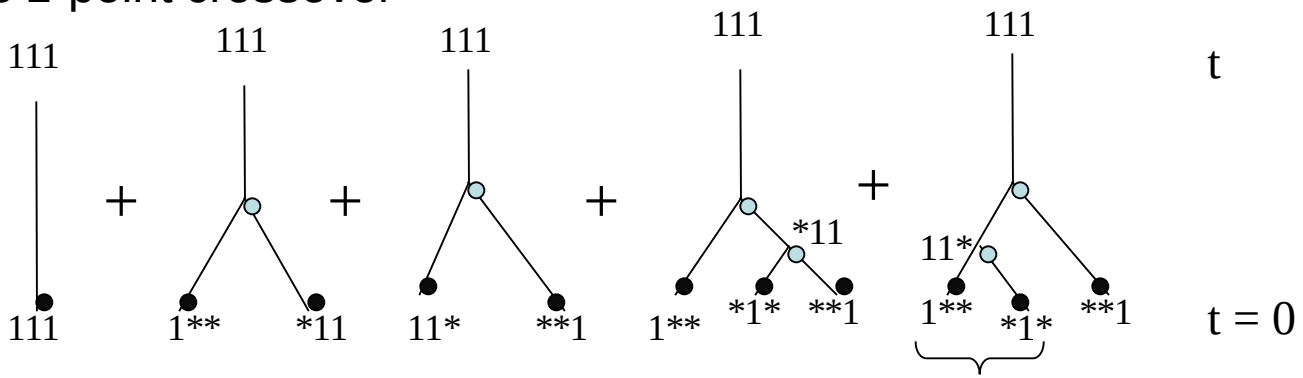
Note the form invariance under the coarse graining
Strings are built up from BBs which in turn have their BBs
which … the hierarchy ends at BBs with only one locus, e.g. ***1*****

Recombinative Dynamics

Go back to the recursive solution attempted when examining the dynamics in the string basis. i.e. Iterate … by recursively substituting for • until get to t = 0

Example – 3-bits 1-point crossover

$P_{111}(t) =$



m = 100 m = 110 m = 110 + 111

I | t
= $G_{II}(t,t')$ Probability that "Building Block" I propagates from t to t'
I | t'

 = $\frac{1}{2}\left(p(M)+p(\bar{M})\right)\lambda_J{}^{KL}(M)\,\frac{f_K}{\bar{f}(t)}\,\frac{f_L}{\bar{f}(t)}$ Measures strength of interaction between "Building Blocks" J, K and L

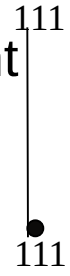
K • = $P_I(t)$

Skew-diagonal – only conjugate "Building Blocks" interact!

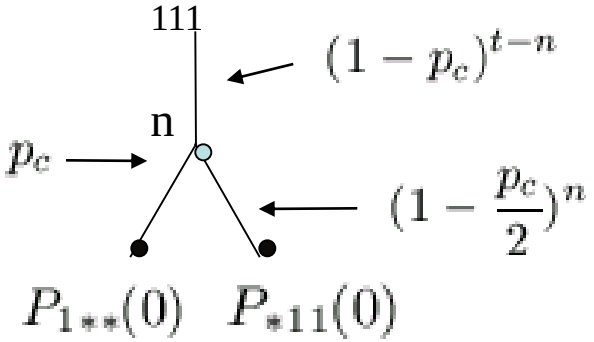
Recombinative Dynamics

Each tree tells us the probability of forming 111 by a given process. In principle can see which processes are most important. Tree depth bounded by N or t – whichever is smaller. MUCH SIMPLER THAN STRING ("OBJECT") BASIS! MUCH FEWER DIAGRAMS (PROCESSES) TO CONSIDER.

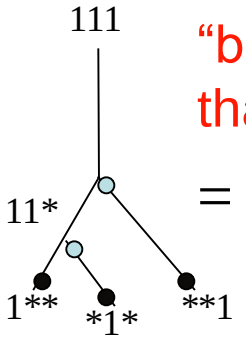
Example: 1-point crossover, no selection or mutation



$$= (1-p_c)^t P_{111}(0)$$



Moral: No point putting in "building blocks" of higher order than one!



$$= 2(1-p_c)\left((1-\frac{p_c}{2})^t - (1-p_c)^t\right)$$

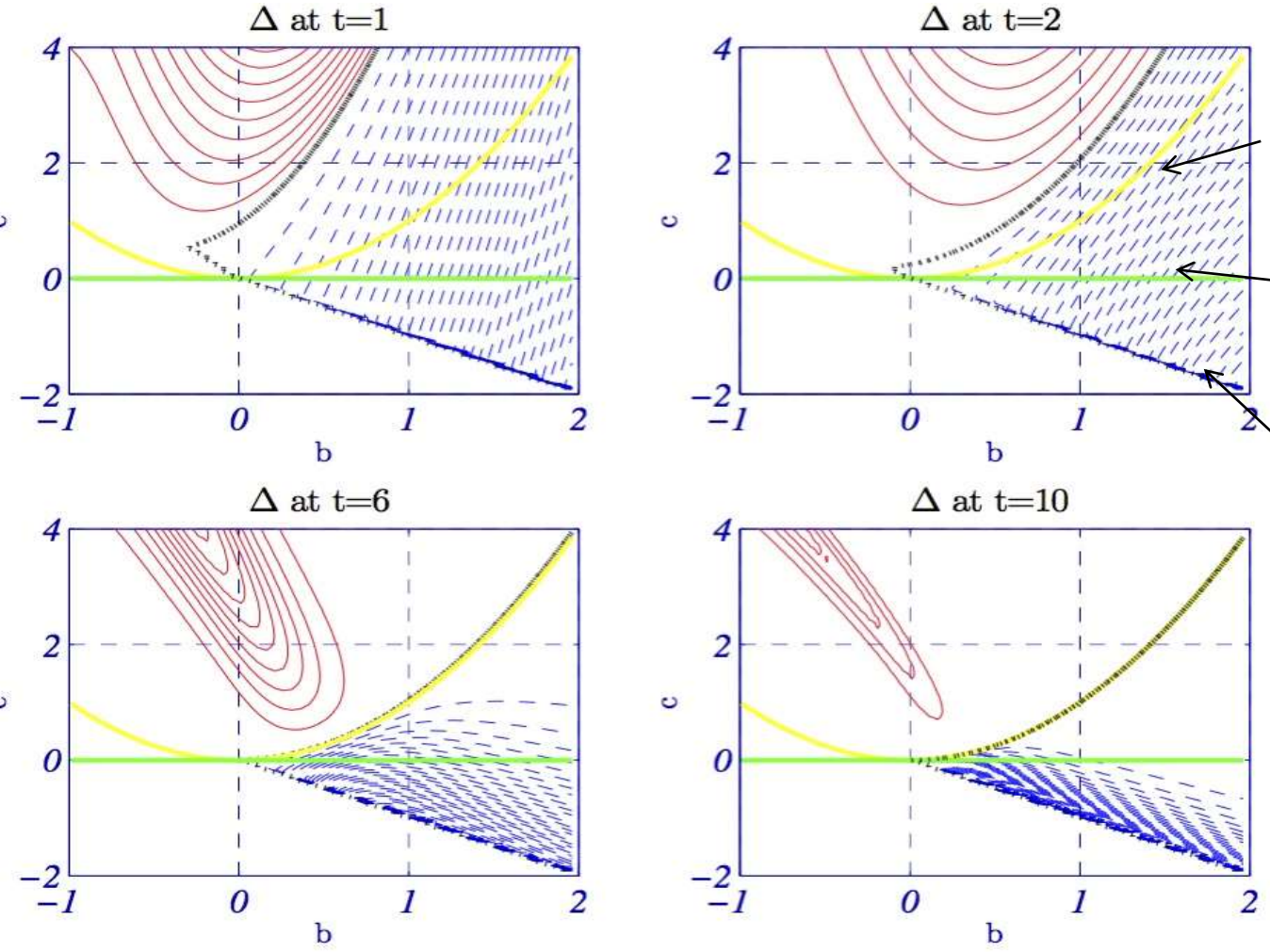
$$= 2(1-p_c)\left((1-p_c)^t - 2(1-\frac{p_c}{2})^t + 1\right) P_{1**}(0)P_{*1*}(0)P_{**1}(0)$$

Dominates in long time limit – Geiringer's theorem

Recombinative Dynamics

- Why recombination?
- Recombination itself imposes the idea of a Building Block as the appropriate effective degree of freedom
- A recombination mode/mask determines what the Building Block is
- The fitness landscape when “modular” imposes the idea of a “modular” block of loci
- Recombination evolves the recombination distribution ($p_c(m)$) so that Building Blocks and landscape blocks are compatible, i.e. recombination respects the landscape blocks

Recombination and Epistasis



Multiplicative landscapes

Additive landscapes

Negative epistasis

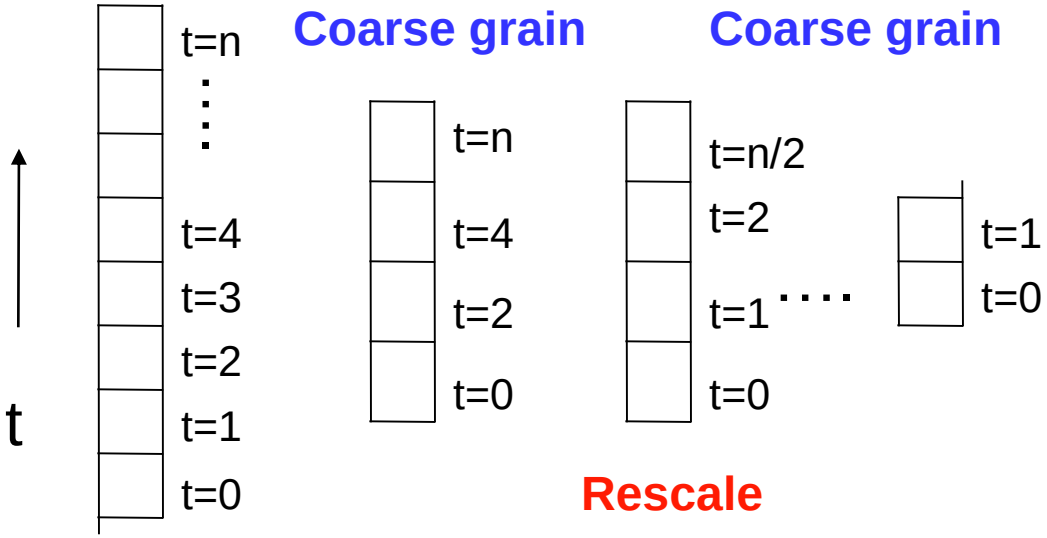
Full parameter space for two-locus system explored

Recombination is advantageous only for modular or redunant landscapes – just like we find in nature!

Fig. 1. Value of Δ at different generations for two-locus two-allele system as a function of fitness landscape, characterized by b and c. The initial population is $P_{00}(0) = 0.8999$, $P_{01}(0) = 0.05$, $P_{10}(0) = 0.05$, $P_{11}(0) = 0.0001$. The $\Delta = 0$ plane has been marked to distinguish between conditions in which recombination is favorable ($\Delta < 0$) or not. The curve on the plane is $c = b^2$, the condition for a multiplicative landscape.

Selection-Mutation dynamics – the coarse-graining approach

A simple one-locus example:



Can we coarse grain an n generation problem to a one generation problem? Much easier to solve the dynamics over only one generation!

$X_1(t)$ – unnormalized incidence vector

p – mutation rate

$$\begin{pmatrix} X_1(t+2) \\ X_0(t+2) \end{pmatrix} = \begin{pmatrix} (1-p)f_1 & pf_0 \\ pf_1 & (1-p)f_0 \end{pmatrix}^2 \begin{pmatrix} X_1(t) \\ X_0(t) \end{pmatrix}$$

Evolves locus two time steps in landscape f(1), f(0) with mutation p

Selection-Mutation dynamics – the coarse-graining approach

$$\begin{pmatrix} X_1(t'+1) \\ X_0(t'+1) \end{pmatrix} = \begin{pmatrix} (1-p'_1)f'_1 & p'_0 f'_0 \\ p'_1 f'_1 & (1-p'_0)f'_0 \end{pmatrix} \begin{pmatrix} X_1(t') \\ X_0(t') \end{pmatrix}$$

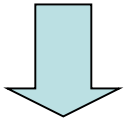
Evolves bit one time step in "renormalized" landscape f'(1), f'(0) with asymmetric mutation rates p'(1) and p'(0)

Equivalent dynamics (all we did was "change names"!, i.e. "renormalize")

$$f'_1 = (1-p_1)f_1^2 + p_1 f_0 f_1$$
$$f'_0 = (1-p_0)f_0^2 + p_0 f_0 f_1$$
$$p'_1 = p_1 \left(\frac{(1-p_1)f_1 + (1-p_0)f_0}{(1-p_1)f_1 + p_1 f_0} \right)$$
$$p'_0 = p_0 \left(\frac{(1-p_0)f_0 + (1-p_1)f_1}{(1-p_0)f_0 + p_0 f_1} \right)$$

Selection-Mutation dynamics – the coarse-graining approach

Evolution of mutation/selection dynamics over n time steps with fitness landscape f(1), f(0) and mutation rates p(2) and p(1) is same as that of a system with "renormalized" landscape and mutation rates, f'(1), f'(0), p'(2), p'(1) over n/2 time steps!



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Fixed points of Renormalization Group transformation:

|ln(f(1)/f(0))| = 0, p(1) = p(0) = 0; no selection/mutation – "FERROMAGNETIC"

|ln(f(1)/f(0))| = infinity, p(1) = p(0) = 0; strong selection – "FROZEN"

|ln(f(1)/f(0))| = constant, p(1) + p(0) = 1; neutral evolution – "PARAMAGNETIC"

Selection-Mutation dynamics – the reparametrization approach

$$\mathbf{P}(t+1) = \mathcal{M}\mathcal{F}\mathbf{P}(t)$$

Write $\mathcal{F} = (\mathbf{1} + \varepsilon\delta\mathcal{F})$ and develop perturbation expansion in ε

With zeroth order exact solution being that of the mutation only system – Fourier/Walsh modes; get solution for the Fourier transform of the unnormalized frequencies, but…e.g. for one locus

$$\hat{x}_0(t) = \left(1 + \epsilon\widehat{\mathcal{F}}_0{}^0 t\right)\hat{x}_0(0) + \epsilon\left(\frac{1-(1-2p)^t}{2p}\right)\widehat{\mathcal{F}}_0{}^1\hat{x}_1(0)$$

$$\hat{x}_1(t) = (1-2p)^t\left(1 + \epsilon\widehat{\mathcal{F}}_1{}^1 t\right)\hat{x}_1(0) + \epsilon\left(\frac{1-(1-2p)^t}{2p}\right)(1-2p)\widehat{\mathcal{F}}_1{}^0\hat{x}_0(0)$$

Secular terms that invalidate perturbation theory

Selection-Mutation dynamics – the reparametrization approach

Use the RG to resum the secular terms: $\hat{x}_I(0) = \sum_J \hat{Z}_I{}^J(\tau)\hat{x}_J(\tau)$

$$\sum_J \hat{Z}_I{}^J(\tau+1)\hat{x}_J(\tau+1) = \sum_J \hat{Z}_I{}^J(\tau)\hat{x}_J(\tau)$$

Renormalized coefficients as a function of a renormalization scale (time)

RG equation for the coefficients

$$\hat{Z}_I{}^J(\tau) = \delta_I{}^J + \sum_{n=1}^{\infty} \epsilon^n a_{IJ}^{(n)}(\tau)$$

Perturbative ansatz for the renormalization constants

Determine the coefficients a_{IJ} by demanding the removal of the secular terms

$$a_{00}^{(1)}(\tau) = a_{11}^{(1)}(\tau) = -\tau \widehat{\mathcal{F}}_0{}^0 \qquad a_{01}^{(1)}(\tau) = a_{10}^{(1)}(\tau) = 0$$

Gives exponentiated form $\hat{x}_I(\tau) = (1 + \epsilon \widehat{\mathcal{F}}_I{}^I)^\tau \hat{x}_I(0)$

Selection-Mutation dynamics – the reparametrization approach

$$\hat{P}_1(t) = \frac{1}{\sqrt{2}} \left(\frac{\frac{\epsilon(1-2p)\hat{F}_0^1}{2p} - \left(\frac{\epsilon(1-2p)\hat{F}_0^1}{2p} - \sqrt{2}\hat{P}_1(0) + \frac{\epsilon}{p}\hat{F}_0^1\hat{P}_1^2(0) \right)(1-2p)^t}{1 - \frac{\epsilon\sqrt{2}\hat{F}_0^1}{2p}\hat{P}_1(0)(1-2p)^t} \right)$$

Completely exponentiated form which agrees with exact solution to O(ε)

Note that what we are doing here is exponentiating the perturbation series to get ALL the eigenvalues of the “transfer matrix”

Conclusions

- The theory of Genetic dynamics is of interest in both a natural (as an abstract simplified representation of a “complex” systems) as well as an artificial setting
- Traditional goals for theory: “Solving” for the dynamics and/or getting “understanding” are not easily met
- A “physicsy” approach can lead to substantial progress
  - Coarse graining
  - Identify effective/collective degrees of freedom
  - Recombinative dynamics most appropriately understood in terms of “Building Blocks”
  - Diagrammatic formulation
  - RG used to relate different levels of coarse graining
  - RG can be explicitly implemented in both its coarse graining and reparametrization contexts
  - Several novel elements involved that have not been treated in statistical physics

Conclusions

- Criticality has played a miraculous role in statistical mechanics and condensed matter theory leading to huge conceptual and theoretical advances
- It appears in many different contexts in the physical, biological and social sciences.
- Power law scaling exists because there is no characteristic scale - whether it happens a surprising/unsurprising amount is somewhat subjective - like “emergence” itself.
- Maybe the puzzle is better seen by asking not why there are so many systems without a scale (statistical physics) but why there are so many systems with a scale (particle physics).
- Real systems always have multiple length scales - crossovers.

- **The RG remains out best, last hope for the mathematical modelling of such systems**