

The Tangled Nature Model of Evolutionary Ecology:
(Is the approach of Statistical Mechanics relevant to
the New Ecology Systems Perspective project.)

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Evolutionary ecology:

- 👁 Interacting organisms + Evolution → Evolving bio-net
- 👁 Each type will see an ever changing environment

Focus on system level properties

- ✓ stability
- ✓ mode of evolution
- ✓ nature of the adaptation
- ✓ ecological characteristics: SAD, SAR, Connectance,...

Interaction and co-evolution

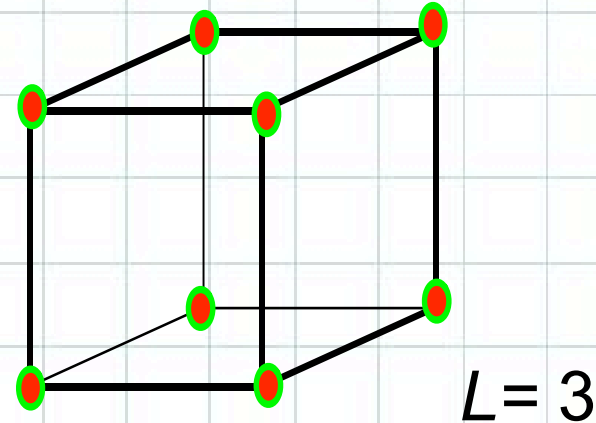
The Tangled Nature model

- Individuals reproducing in type space
- Different types influence the livelihood of each other

Definition

Individuals $\mathbf{S}^\alpha = (S_1^\alpha, S_2^\alpha, \dots, S_L^\alpha)$, where $S_i^\alpha = \pm 1$

and $\alpha = 1, 2, \dots, N(t)$



Dynamics – a time step



Annihilation

Choose indiv. at random, remove with probability

$$p_{kill} = \text{const}$$

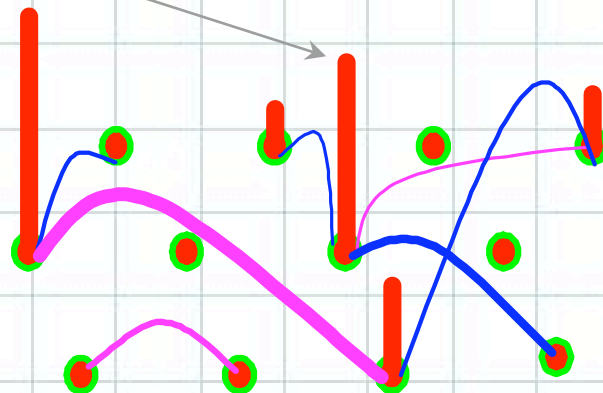


Reproduction:

- ▶ Choose indiv. at random
- ▶ Determine

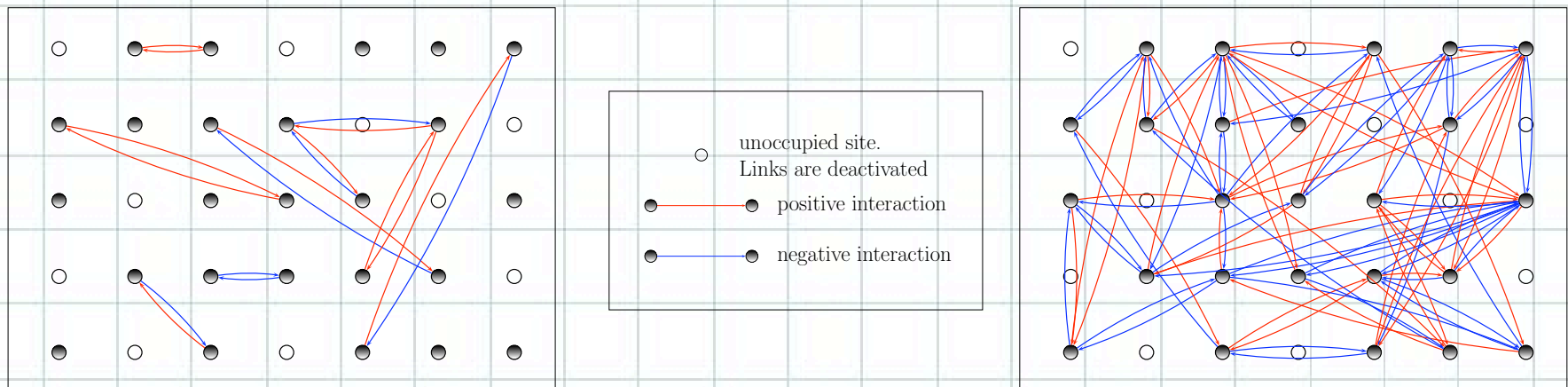
$$H(\mathbf{S}^\alpha, t) = \frac{k}{N(t)} \sum_{\mathbf{S}} J(\mathbf{S}^\alpha, \mathbf{S}) n(\mathbf{S}, t) - \mu N(t)$$

$n(\mathbf{S}, t) =$ occupancy at the location \mathbf{S}



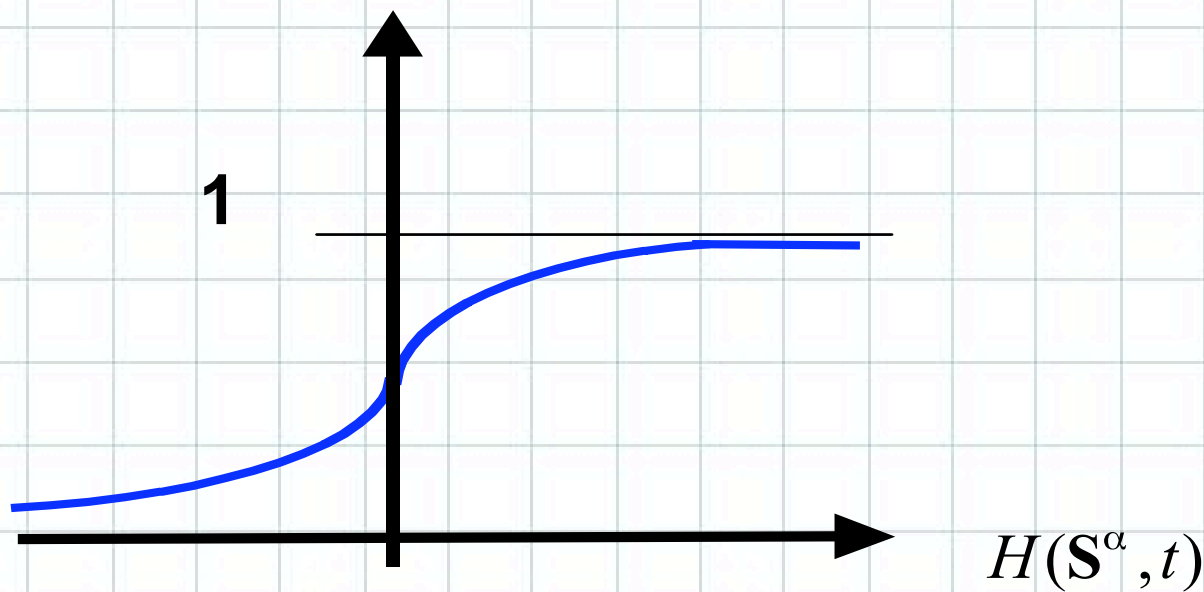
The coupling matrix $J(S, S')$

- ✓ Either consider $J(S, S')$ to be uncorrelated
- ✓ or to vary smoothly through type space
- ✓ and sparse or dense



from $H(S^\alpha, t)$ reproduction probability

$$p_{off}(S^\alpha, t) = \frac{\exp[H(S^\alpha, t)]}{1 + \exp[H(S^\alpha, t)]} \in [0, 1]$$





Asexual reproduction:

Replace

S^α

by two copies

S_1^α

S_2^α

with probability

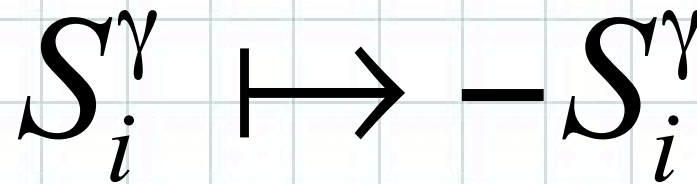
$p_{off}(S^\alpha, t)$

Mutations



Mutations occur with probability

P_{mut} , i.e.



See also work on similar models by Rikvold et al.

RESULTS



😊 Segregation in genotype space

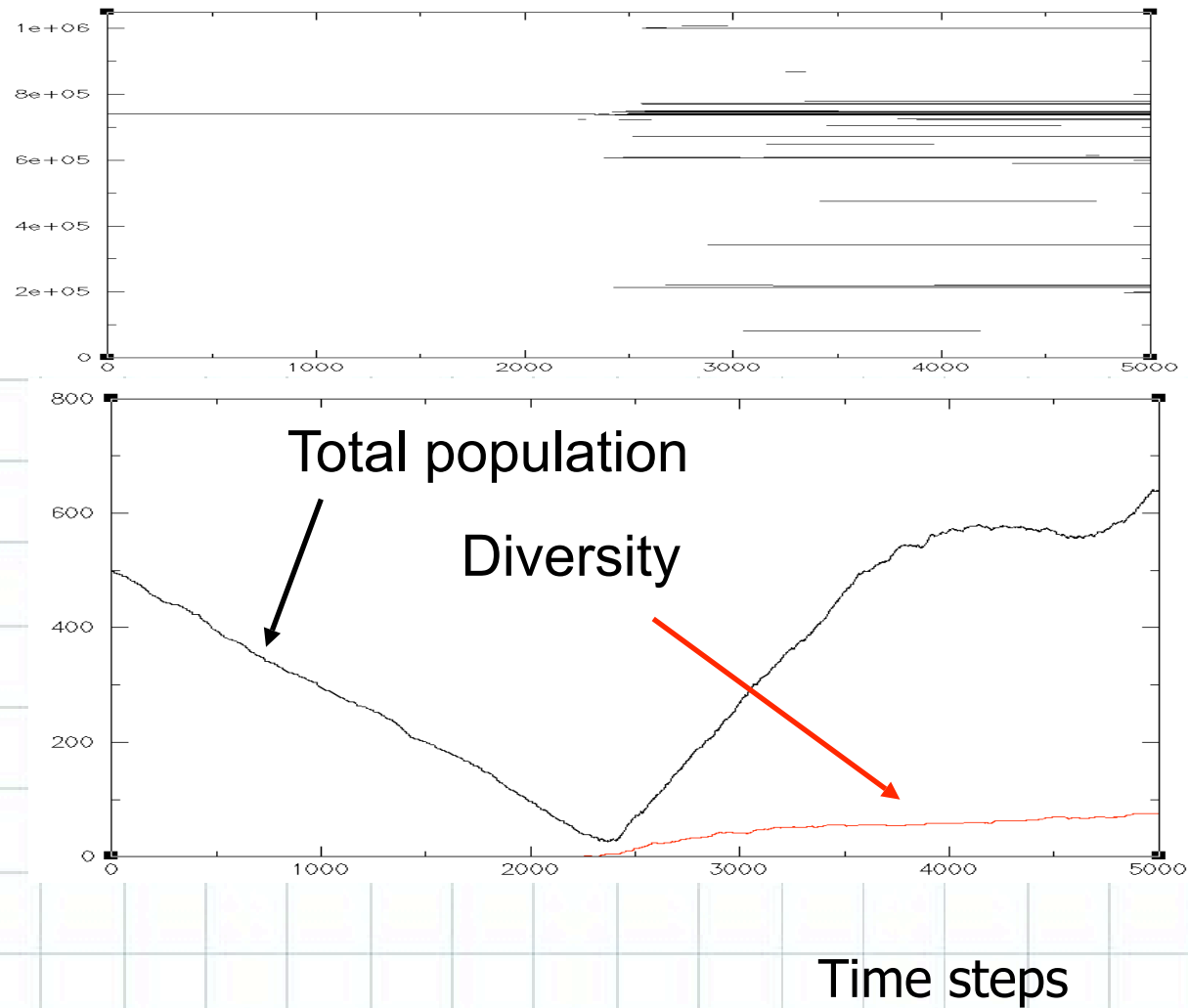
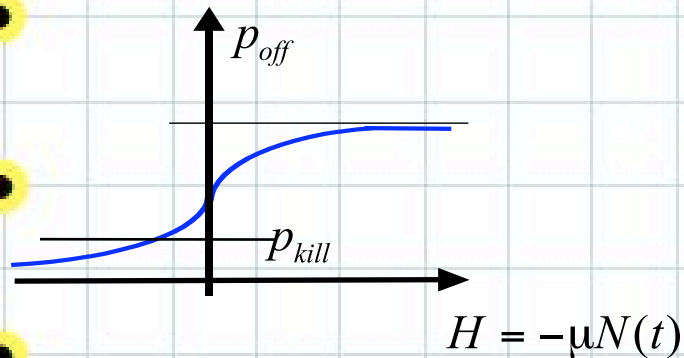
Initiation

Only one genotype

J_n term = 0

$$H = \frac{k}{N(t)} \sum_s J_n - \mu N(t)$$

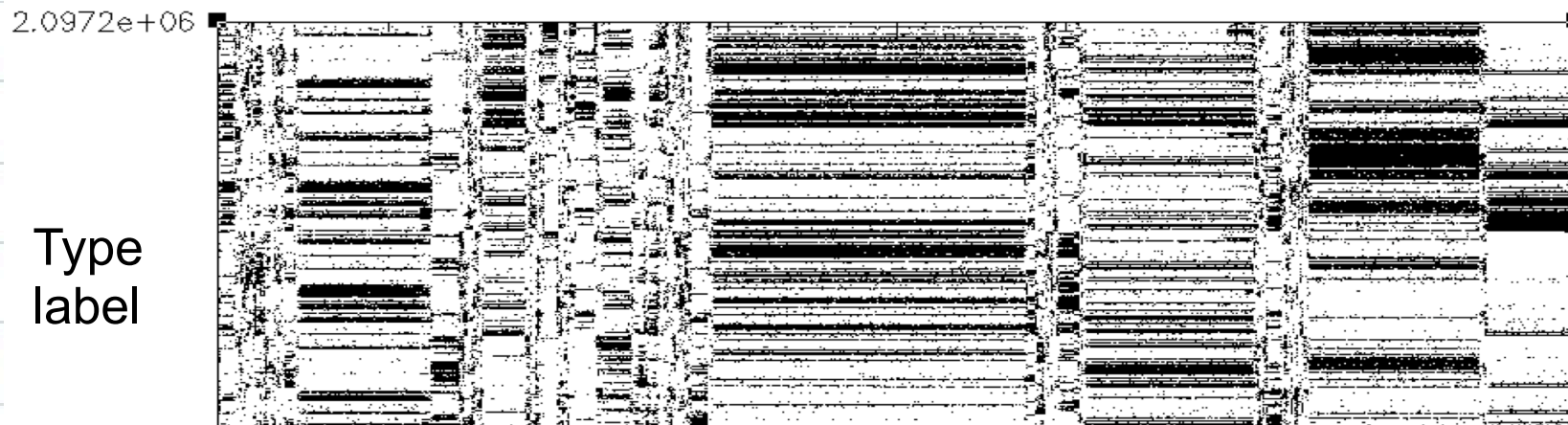
$N(t)$ adjusts



Macro dynamics:

Non correlated

Graph courtesy to
Matt Hall



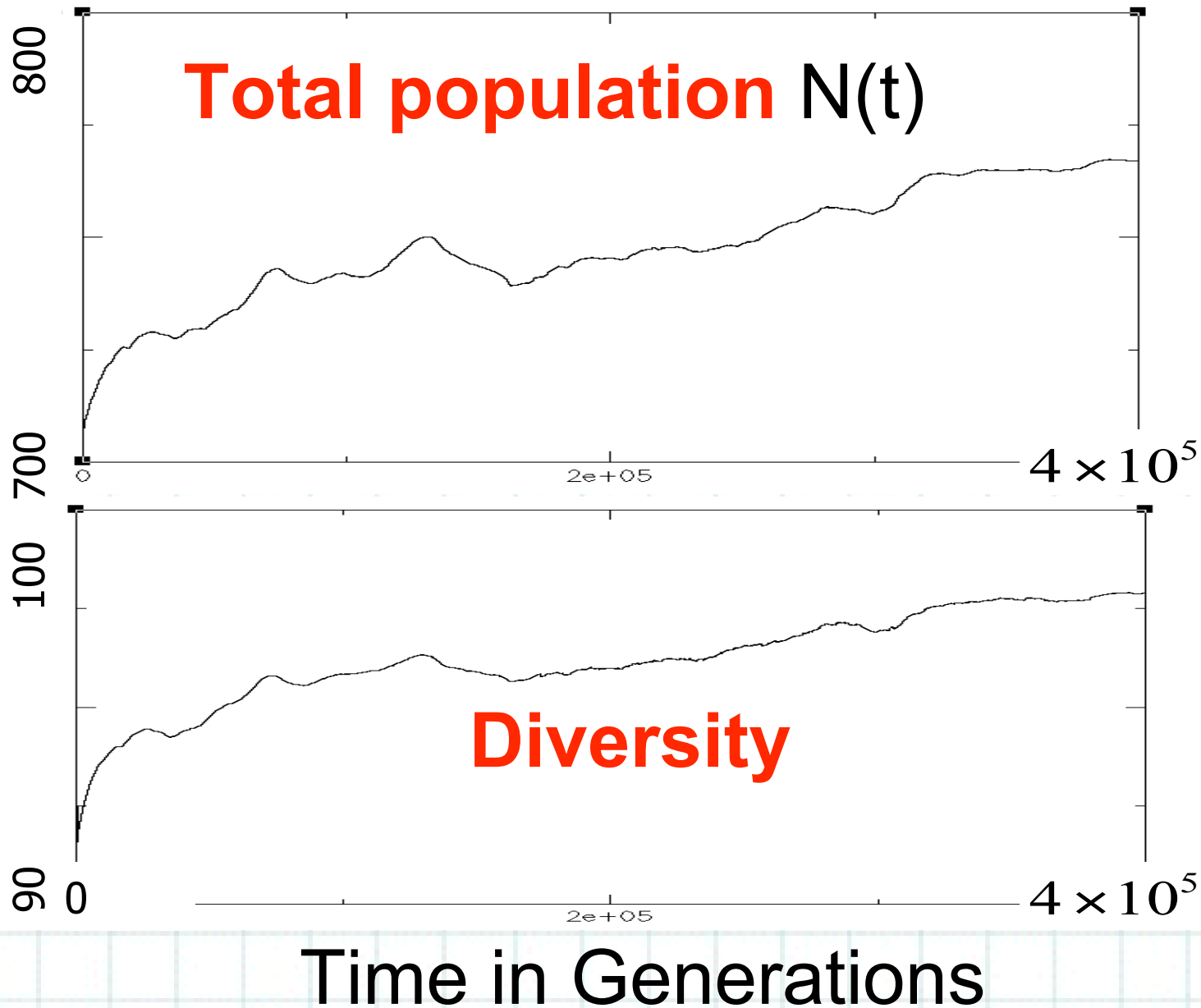
generations

1 generation

$$= N(t) / p_{kill}$$

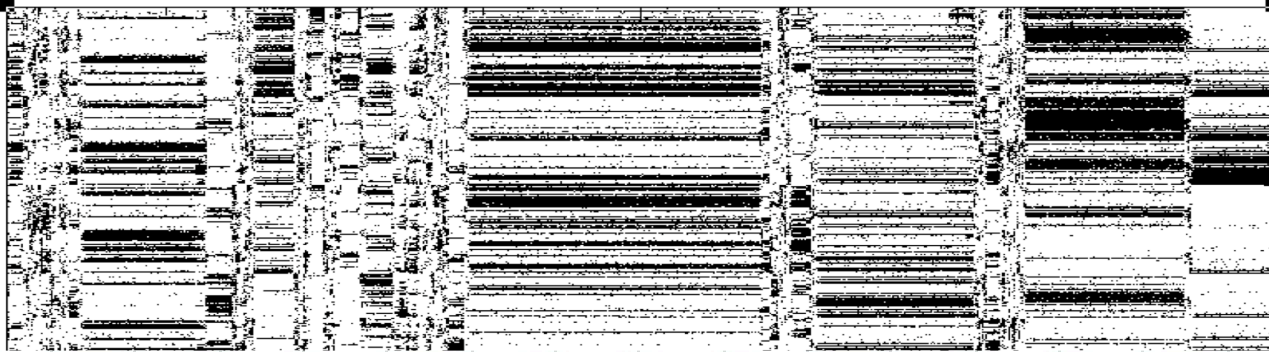


Time dependence (Average behaviour)



Intermittency:

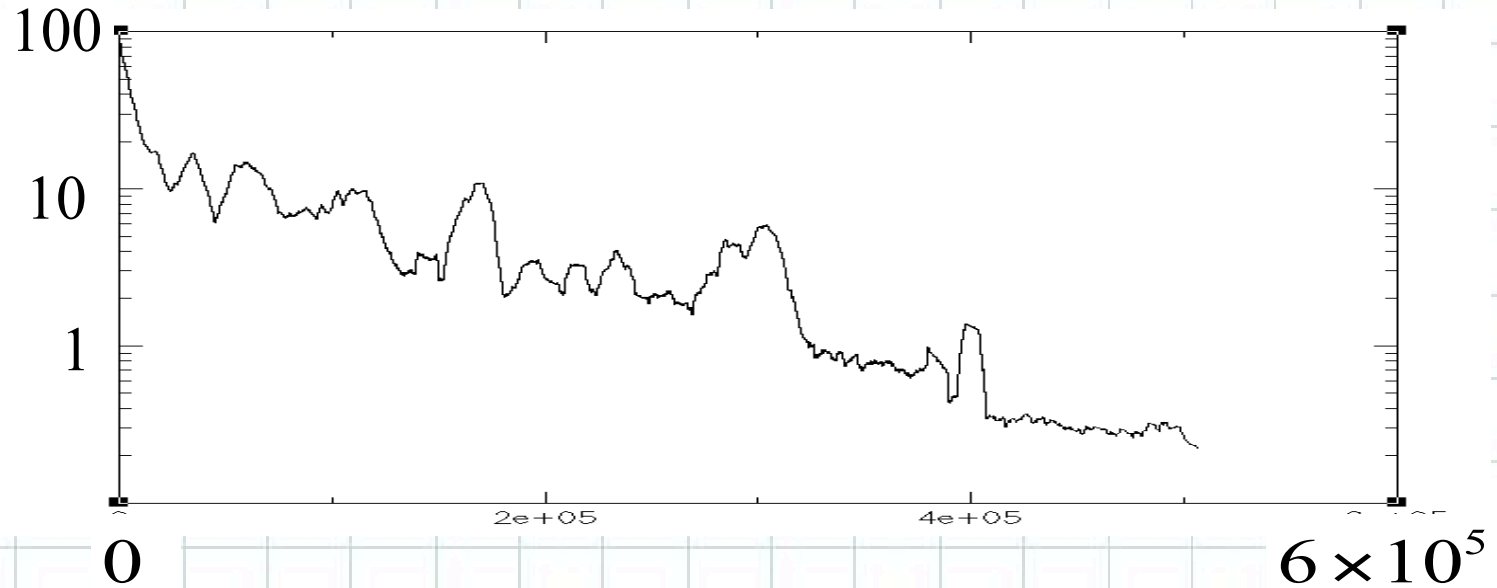
2.0972e+06



of transitions in window



Matt Hall



1 generation
 $= N(t) / p_{kill}$

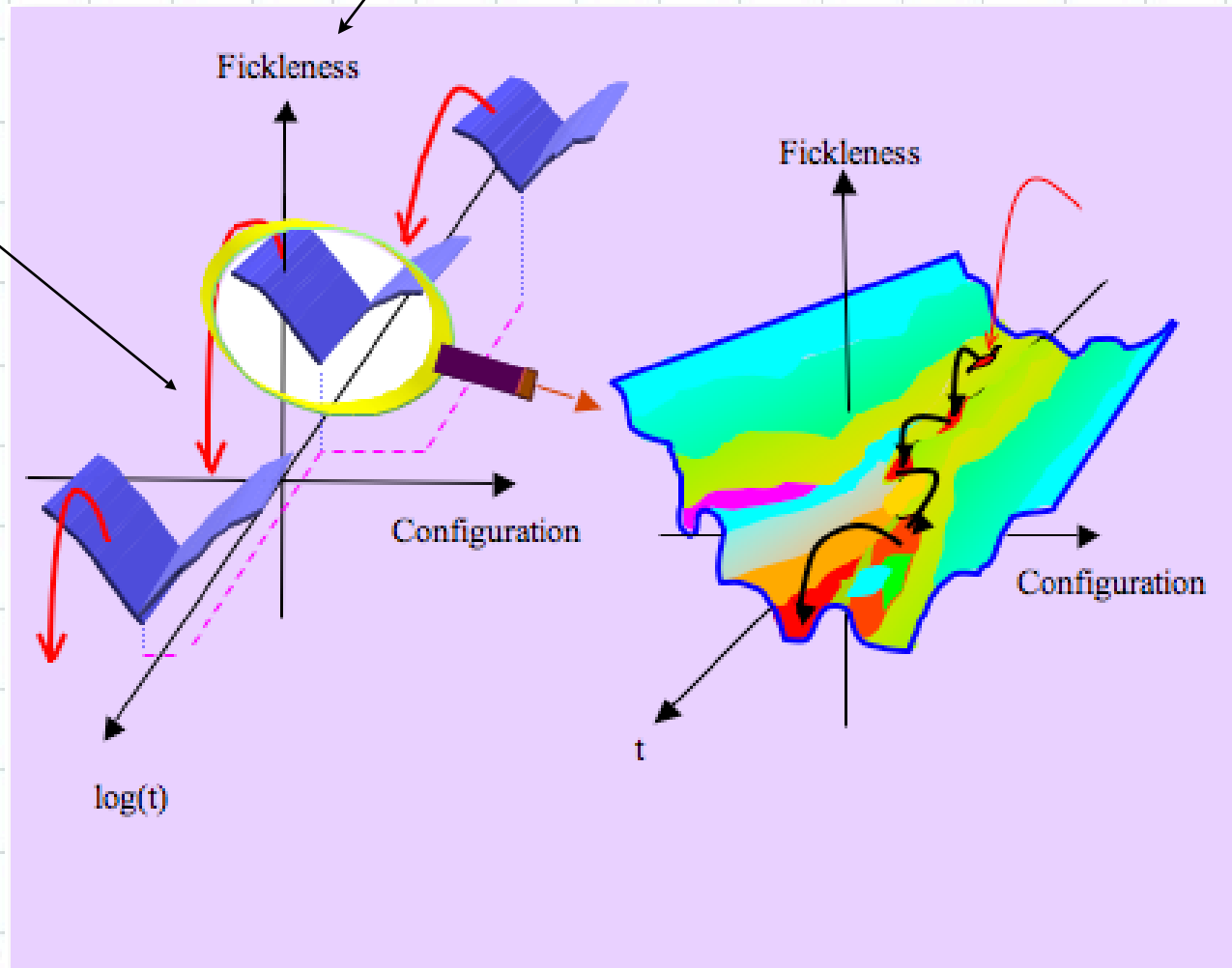
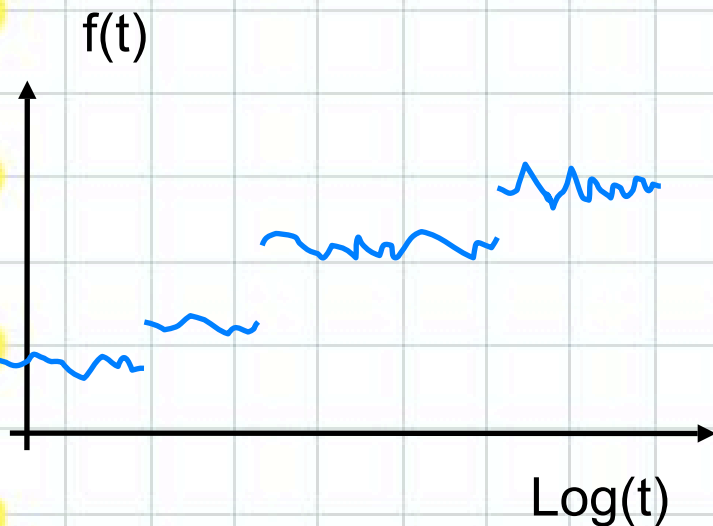
Complex dynamics:

Exergy ??

Intermittent, non-stationary

Jumping through collective adaptation space: quake driven

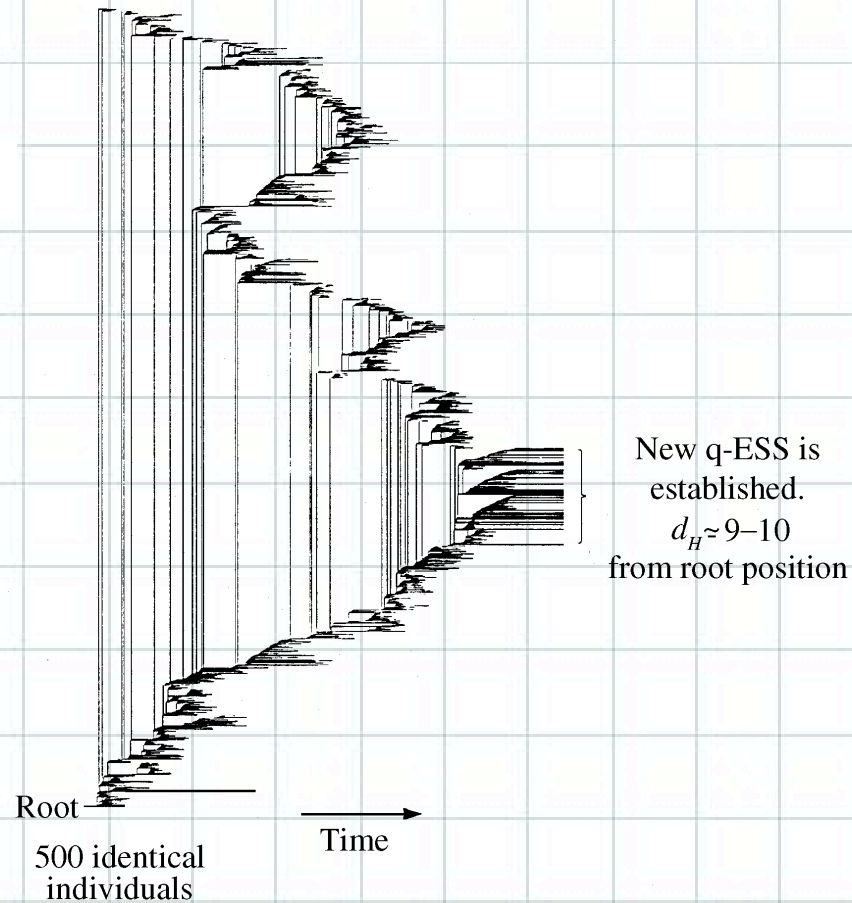
Transitions



Macro dynamics - the transitions

Non correlated

Graph courtesy to
Matt Hall



Stability of the q-ESS:

Consider simple adiabatic approximation.

Stability of genotype S assuming: $n(S', t)$ independent of t for $S' \neq S$

Consider
$$\frac{\partial n(S, t)}{\partial t} = [p_{off}(n(S, t), t) - p_{kill} - p_{mut}] \frac{n(S, t)}{N(t)}$$

Stationary solution $n_0(S)$ corresponds to $p_{off}(n_0(S)) - p_{kill} - p_{mut} = 0$

Fluctuation $\delta = n(S, t) - n_0(S)$

Fulfil
$$\dot{\delta} = A \frac{n_0}{N_0} \delta$$

with
$$A = -(1 - p_{mut})(p_{off})^2 e^{-H_0} \left(\frac{J}{N_0^2} + \mu \right) < 0$$

i.e. stability



Transitions between q-ESS caused by co-evolutionary collective fluctuations

$n(S', t)$ needs to be considered

dependent of t for $S' \neq S$

Macro dynamics:

Correlated

Simon Laird

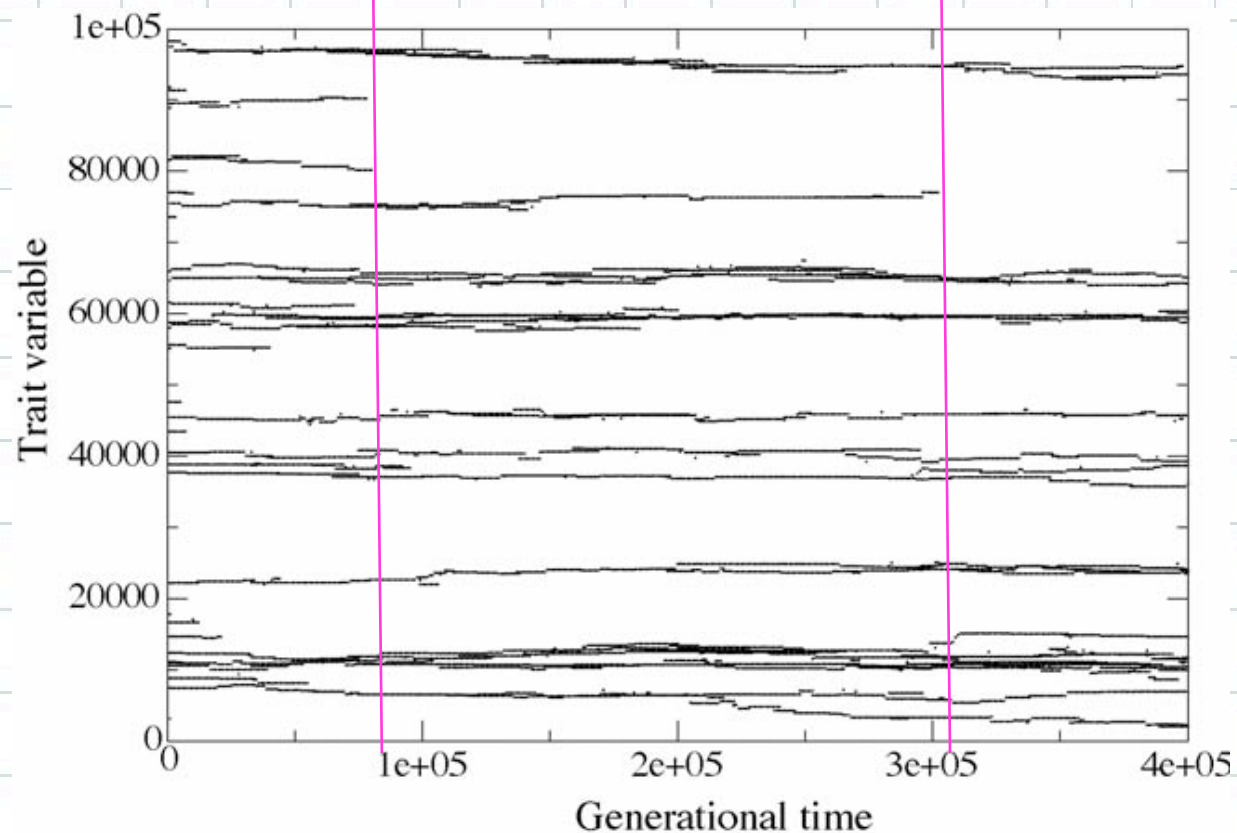


Fig. 1 – An occupation plot of a single run for a system with $R = 10,000$. For each timeslice a point appears where a phenotype is in existence but as the full space is in 16 dimensions a projection onto a single trait is used.

Time evolution of

Distribution of active coupling strengths

Non correlated

Low connectivity

High connectivity

From Anderson & Jensen
J Theor Biol. **232**, 551 (2005)

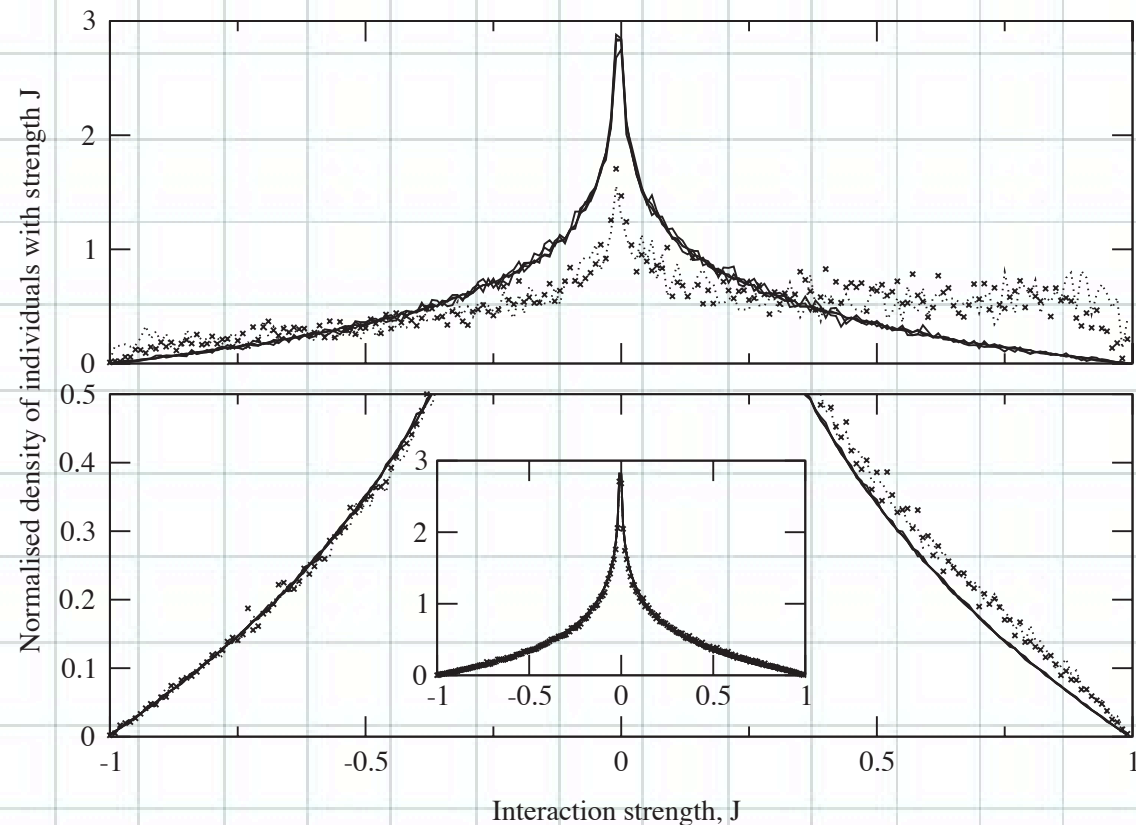


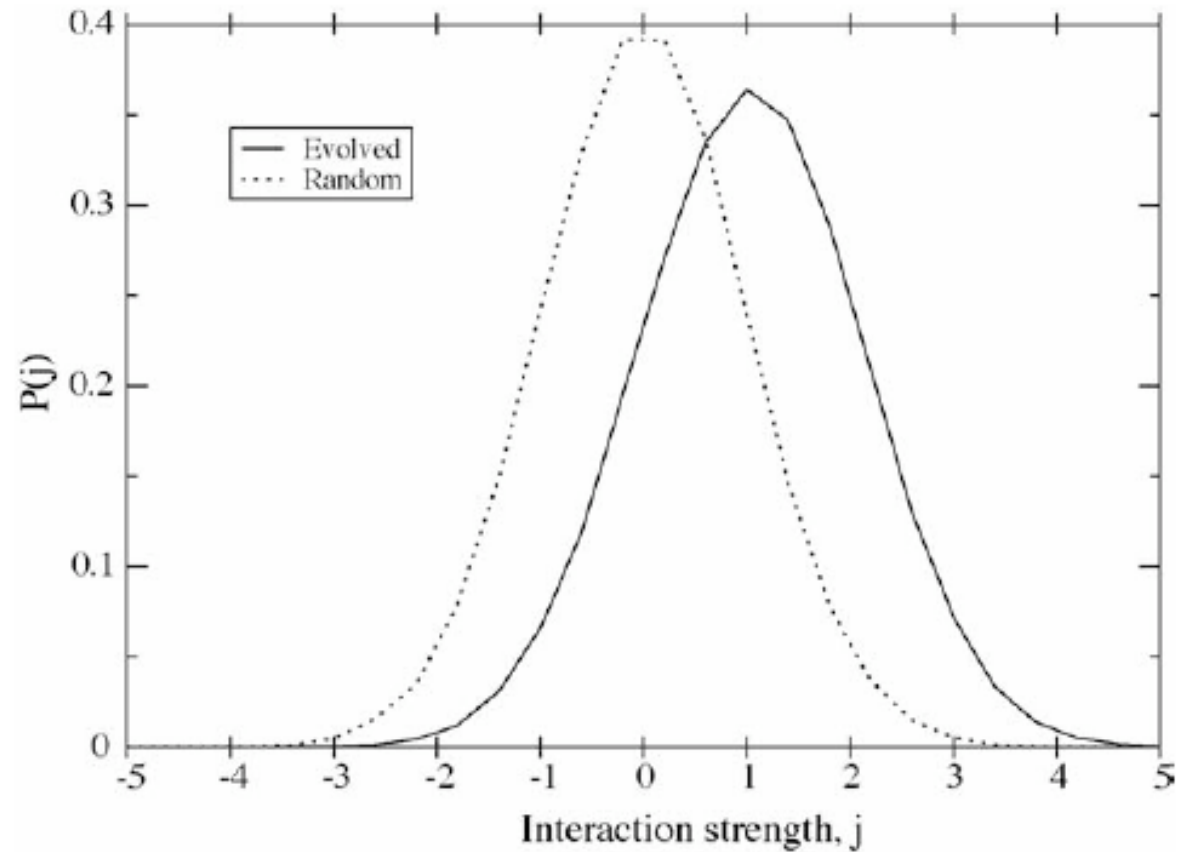
Fig. 3. Interaction distributions. Top: Distribution of interaction strengths between individuals for $\theta = 0.005$. Bottom: $\theta = 0.25$. Inset: Entire distribution. Solid lines, random; crosses, simulation at $t = 500$; dotted lines, simulation at $t = 500,000$. All plots are normalized so that their area is one. For high θ , a significant increase in positive interactions is seen. For low θ , a change is seen but for trivial reasons.

Time evolution of

Distribution of active coupling strengths

Correlated

High connectivity

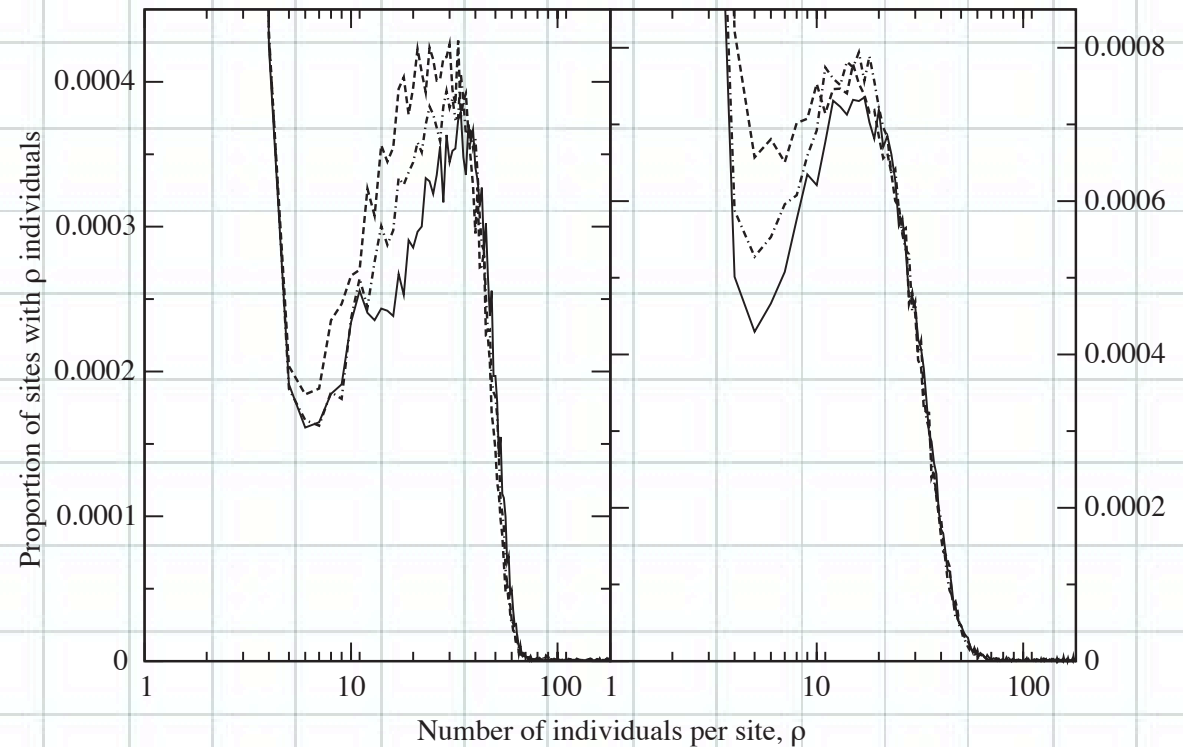


From Laird & Jensen, Ecol Compl. **3**, 253 (2006)

Time evolution of

Species abundance distribution

Non Correlated



From Anderson & Jensen
J Theor Biol. **232**, 551 (2005)

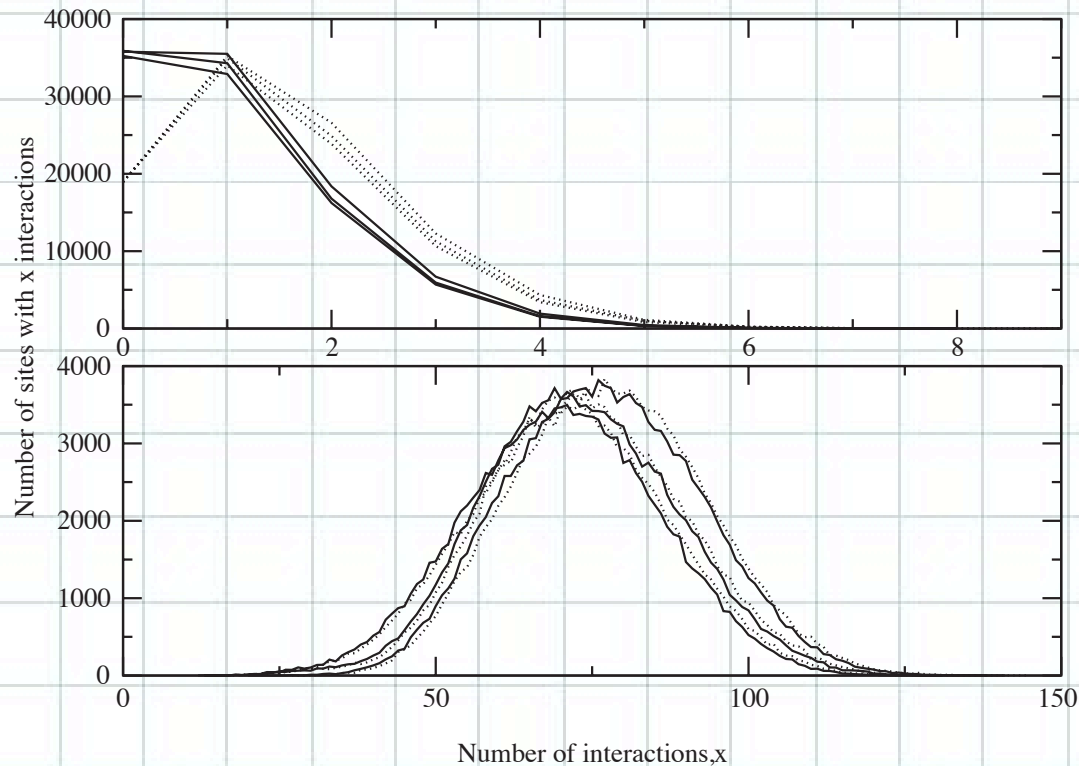
Fig. 5. Species abundance distributions. Species abundance distributions for the simulations only. Dashed line, $t = 500$; dashed-dotted line, $t = 5000$; solid line, $t = 500,000$. Low θ on the left, high θ on the right. The ecologically realistic log-normal form is only seen for high θ .

Low connectivity

High connectivity

Time evolution of Degree distribution

Non Correlated



Low connectivity

High connectivity

Fig. 2. Degree histograms. Top: Degree histogram for $\theta = 0.005$. Bottom: $\theta = 0.25$. Solid lines, random; dotted lines, simulation. From the left, the pairs of curves are for $t = 500, 5000$ and $500,000$. At later times, the number of active links increases for both the simulation and random data.

From Anderson & Jensen
J Theor Biol. **232**, 551 (2005)

The evolved degree distribution

Correlated

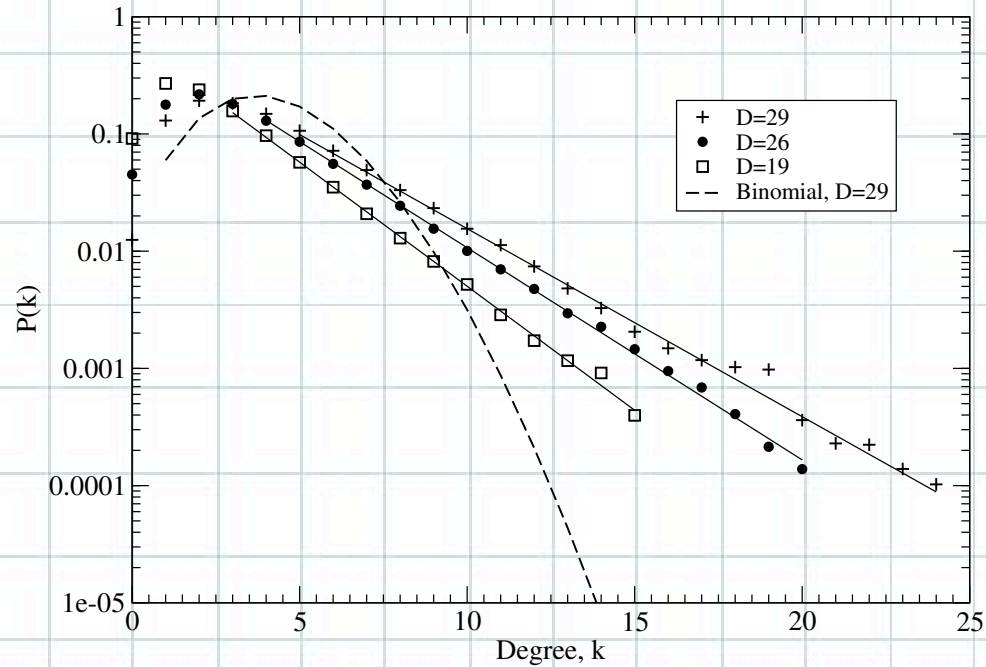


Figure 1: Degree distributions for the Tangled Nature model simulations. Shown are ensemble averaged data taken from all networks with diversity, $D = \{19, 26, 29\}$ over 50 simulation runs of 10^6 generations each. The exponential forms are highlighted by comparison with a binomial distribution of $D = 29$ and equivalent connectance, $C \simeq 0.145$ to the simulation data of the same diversity.

Exponential becomes $1/k$ in limit of vanishing mutation rate

From Laird & Jensen, Ecol. Model. In Press

See also Laird & Jensen, EPL, **76**, 710 (2006)

Diversity and interaction

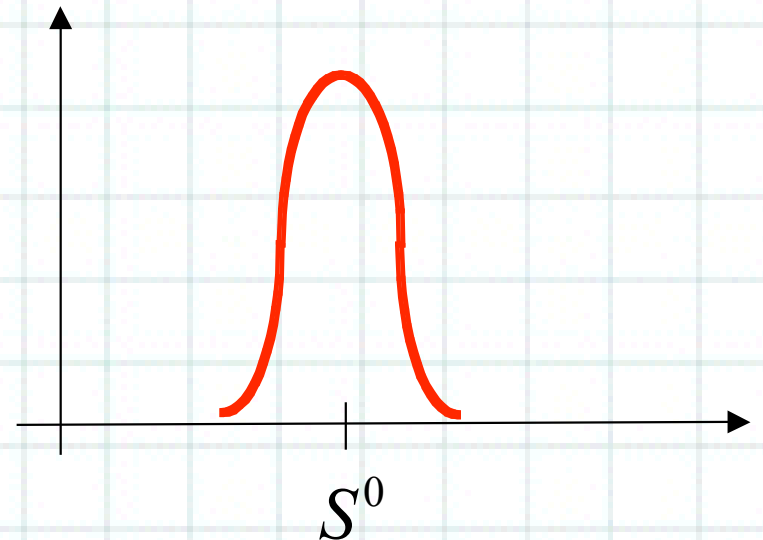
Weight function $H_0(\mathbf{S}^\alpha, t) = \frac{k}{N(t)} \sum_{\mathbf{S}} J(\mathbf{S}^\alpha, \mathbf{S}) n(\mathbf{S}, t) - \mu N(t)$

$$H(S^\alpha) = H_0 + \left\{ \begin{array}{l} \varepsilon E(S^\alpha) \frac{n(S^\alpha, t)}{N(t)} \\ \varepsilon E(S^\alpha) \end{array} \right.$$

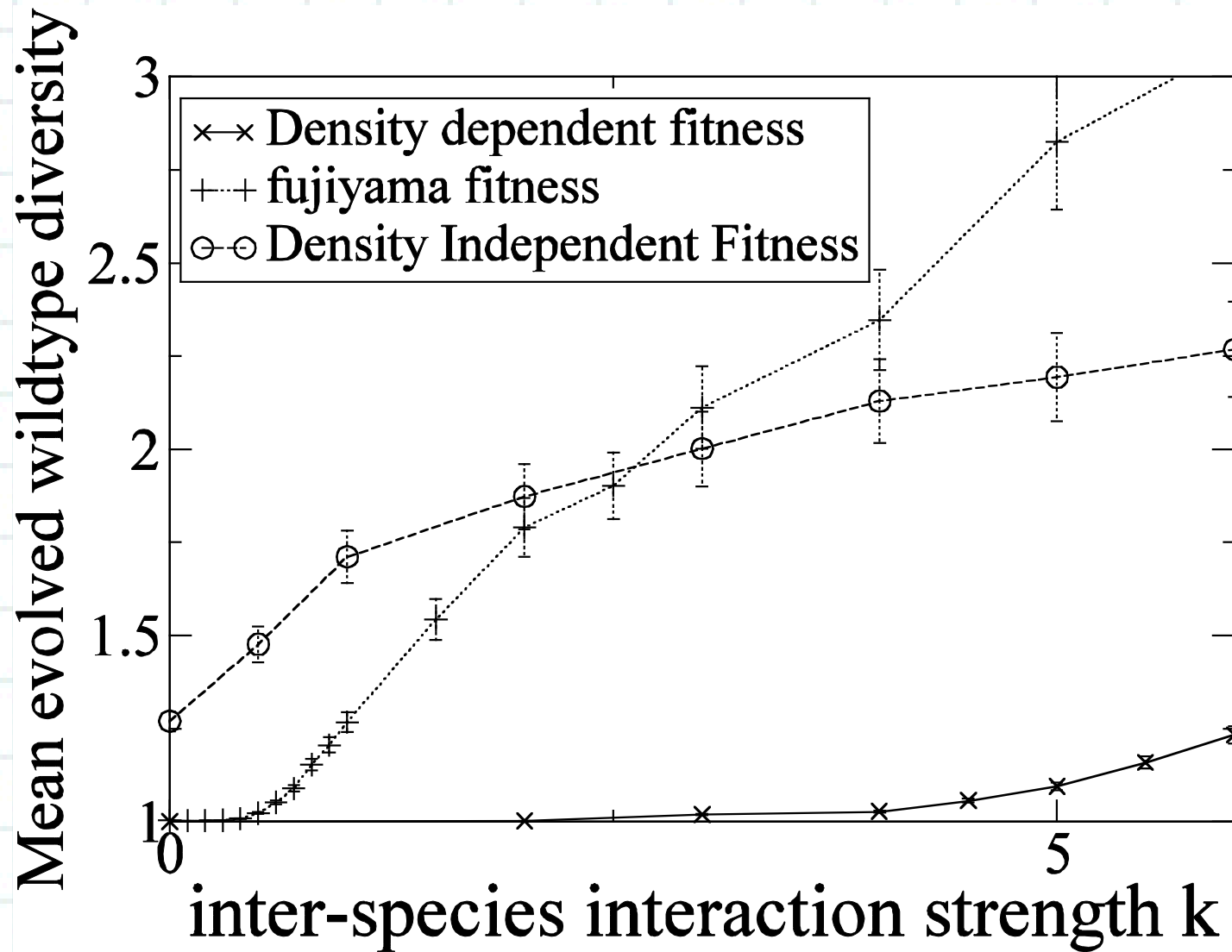
Density dependent

Density independent
Fujiyama lanscape

with $E \in [0,1]$ and ε a scale parameter



Diversity and interaction



Origin of threshold in k:

A balance between inter-species and intra-species Interaction.

$$H = H_0 + \varepsilon E(S^\alpha, t) \frac{n(S^\alpha, t)}{N(t)},$$

where $E \in [0,1]$ and

$$\bar{H}(S^\alpha, t) = \frac{k}{N(t)} \sum_{\mathbf{S}} J(S^\alpha, \mathbf{S}) n(\mathbf{S}, t) - \mu N(t)$$

Mean field sketch

Weight function for $D = 1$: $H_1 = \varepsilon E - \mu N_1$

Weight function for $D = 2$: $H_2 = \frac{k}{N_2} J n_2 + \varepsilon E - \mu N_2$

Assume $n_2 = \frac{1}{2} N_2$ and $N_1 \approx N_2$ then

$$H_1 > H_2 \Rightarrow k > \frac{\varepsilon E}{J}$$

The evolved connectance

Correlated

$$\langle C \rangle = \frac{\# \text{ Edges}}{\# \text{ Possible Edges}}$$

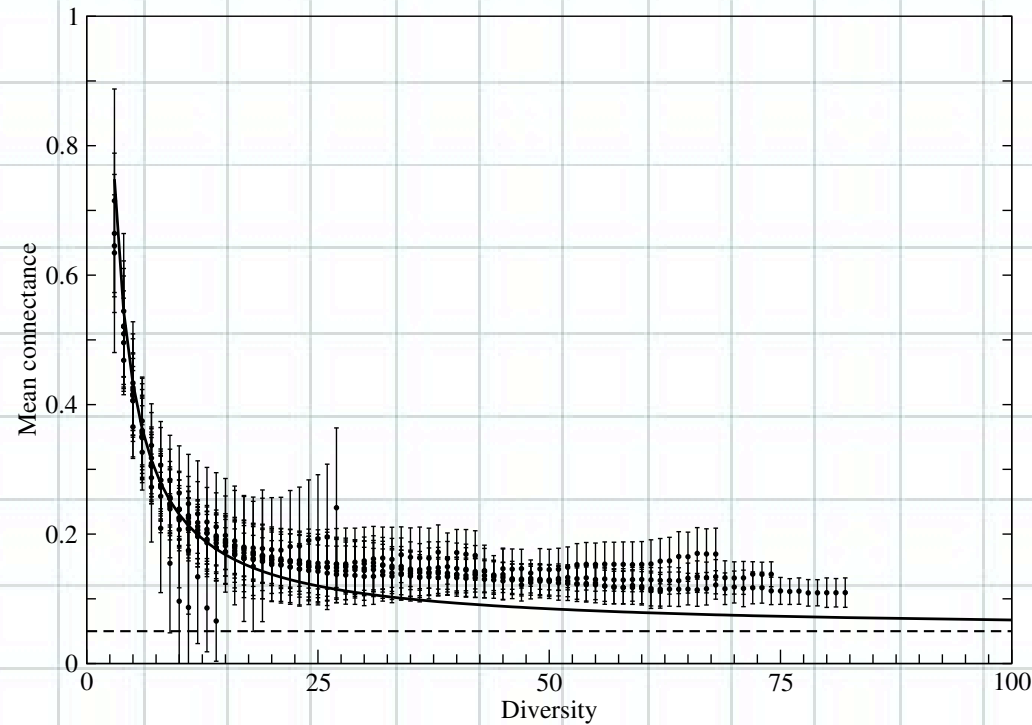
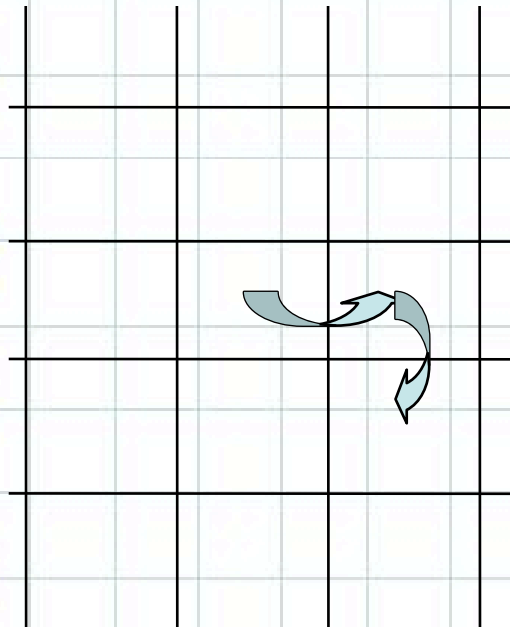


Figure 4: Plot of ensemble-averaged mean connectances, $\langle C \rangle$ against species diversity. Error bars represent the standard error. The lower dotted line marks the null system connectance, $C_J = 0.05$, which the evolved systems clearly surpass. The overlaid functional form is that given by Eq.(8) using the correct background connectance, $C_J = 0.05$ and with a value of, $s = 5.5$ for the selection parameter.

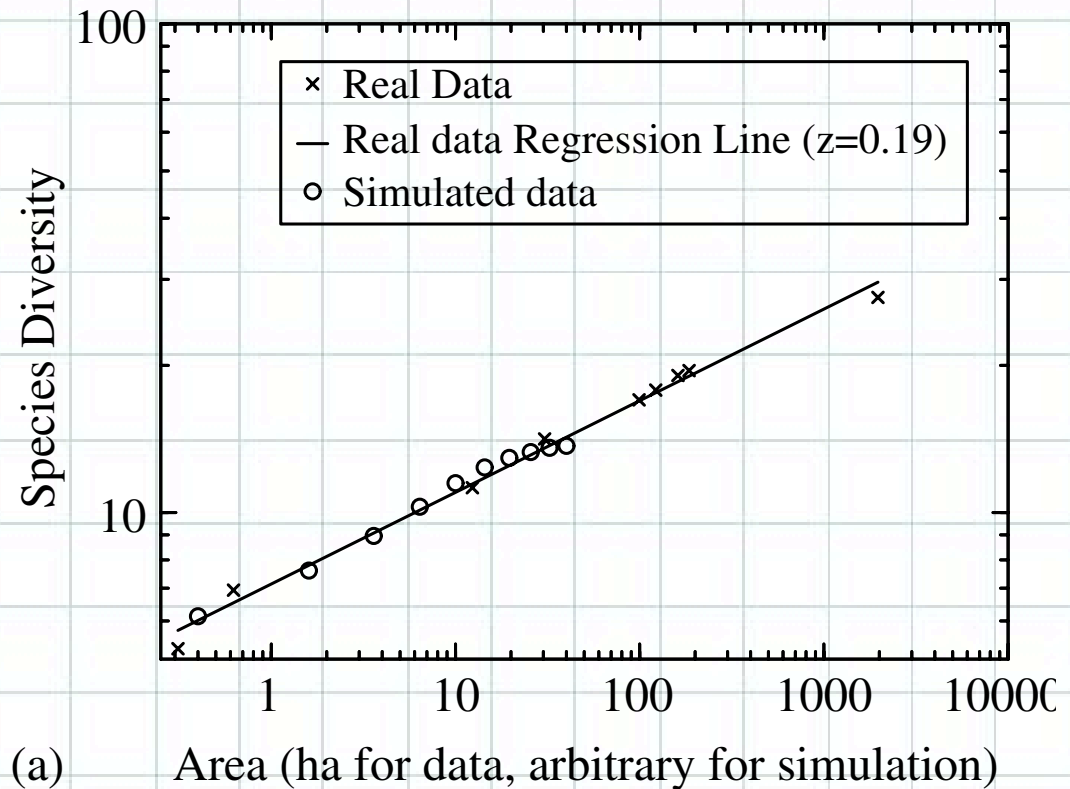
From Laird & Jensen, Ecol Compl. **3**, 253 (2006)

Species area relation:

$$\# S \propto A^z$$



Dispersion by
random walk



X plant data from Hertfordshire, see
ML Rosenzweig, Species Diversity in Space and Time,
Cambridge University Press, 1995

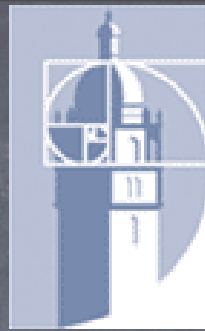
From Lawson & Jensen, J Theo. Biol. **241**, 590 (2006)

The individual in ever evolving surroundings:

- ① Collective system level adaptation towards mutualistic biased webs of interactions
- ① Macro-Evolution through intermittent transitions

Download papers from:

www.ma.imperial.ac.uk/~hjjens



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