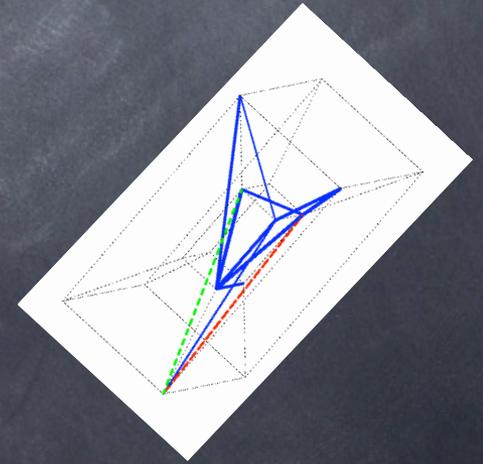




Emergence of complex structure through co-evolution: The Tangled Nature model of evolutionary ecology

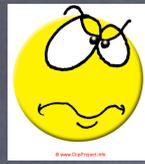
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Domininc Jones, Simon Laird, Daniel Lawson, Paolo Sibani

What are we after ?



>> Connecting micro to macro

Micro level:

- stochastic individual based dynamics always running at clock speed one

Collective
adaptation

Macro level:

- intermittent dynamics
- networks, structure

List of content:

- Motivation:
- The Tangled Nature Model
- Co-evolution and the evolved networks

Phenomenology: ❄ intermittency

❄ emergent networks

❄ connectance

❄ evolving correlations

Explanation

Simple mean field

Fokker-Planck equation

Motivation:

- 😊 How far can a minimal model go?
- 😊 Input: mutation prone reproduction at level of **interacting** individuals.
- 😊 Output: Species formation, macro dynamics, decreasing extinction rate + SAD, SAR, etc.
- 😊 Check: Trend in broad range of data.

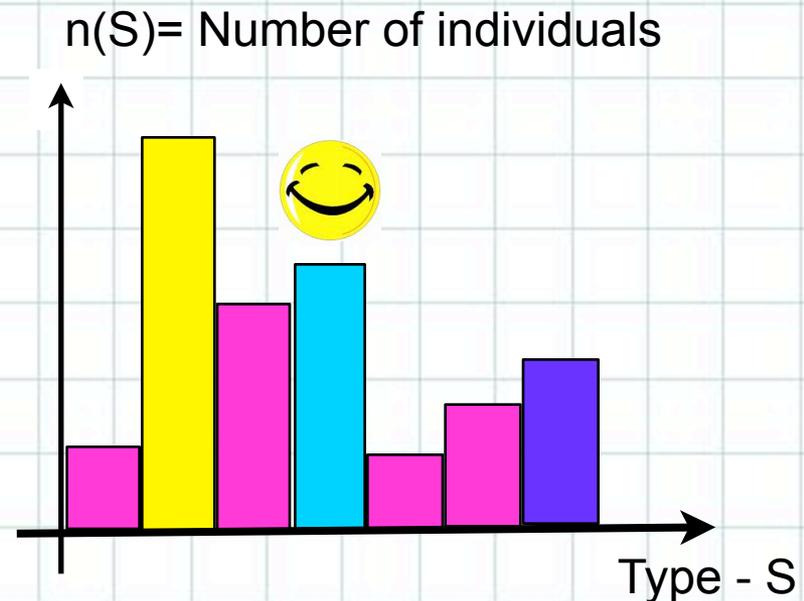
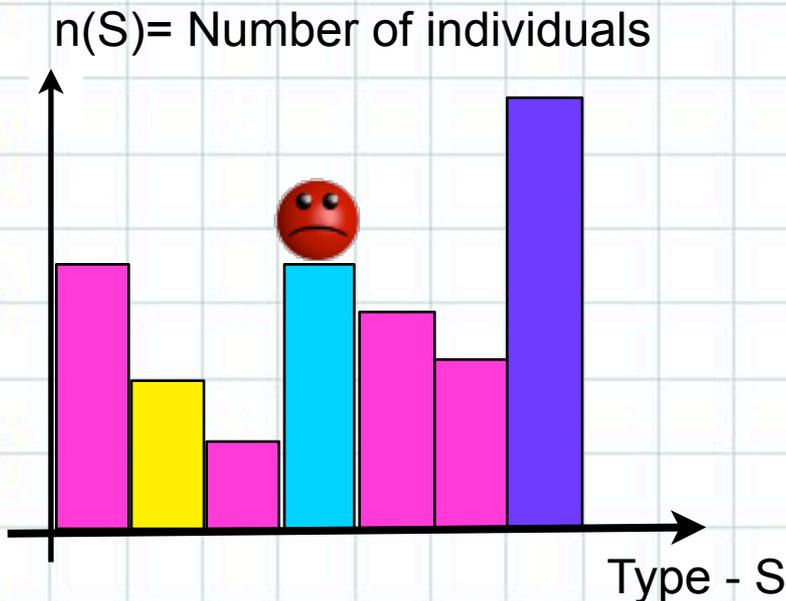


Phenomenology

Interaction and co-evolution

The Tangled Nature model

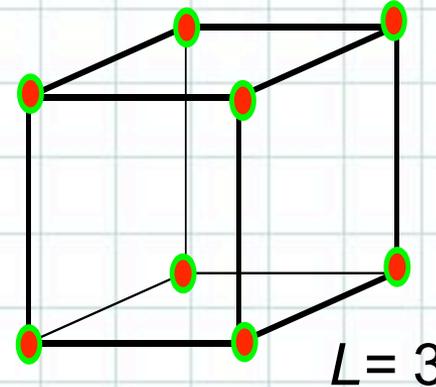
- Individuals reproducing in type space
- Your success depends on who you are amongst



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

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

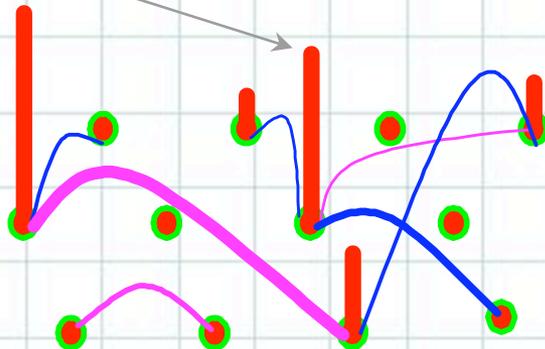


Reproduction:

- ▶ 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}

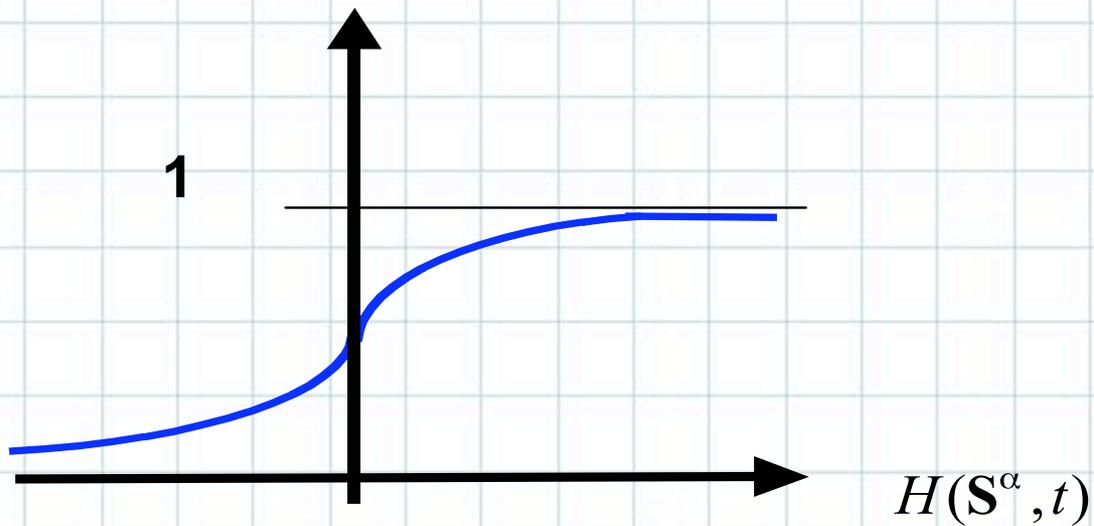


The coupling matrix $J(S, S')$

- Either consider $J(S, S')$ to be uncorrelated
- or to vary smoothly through type space.

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

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





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

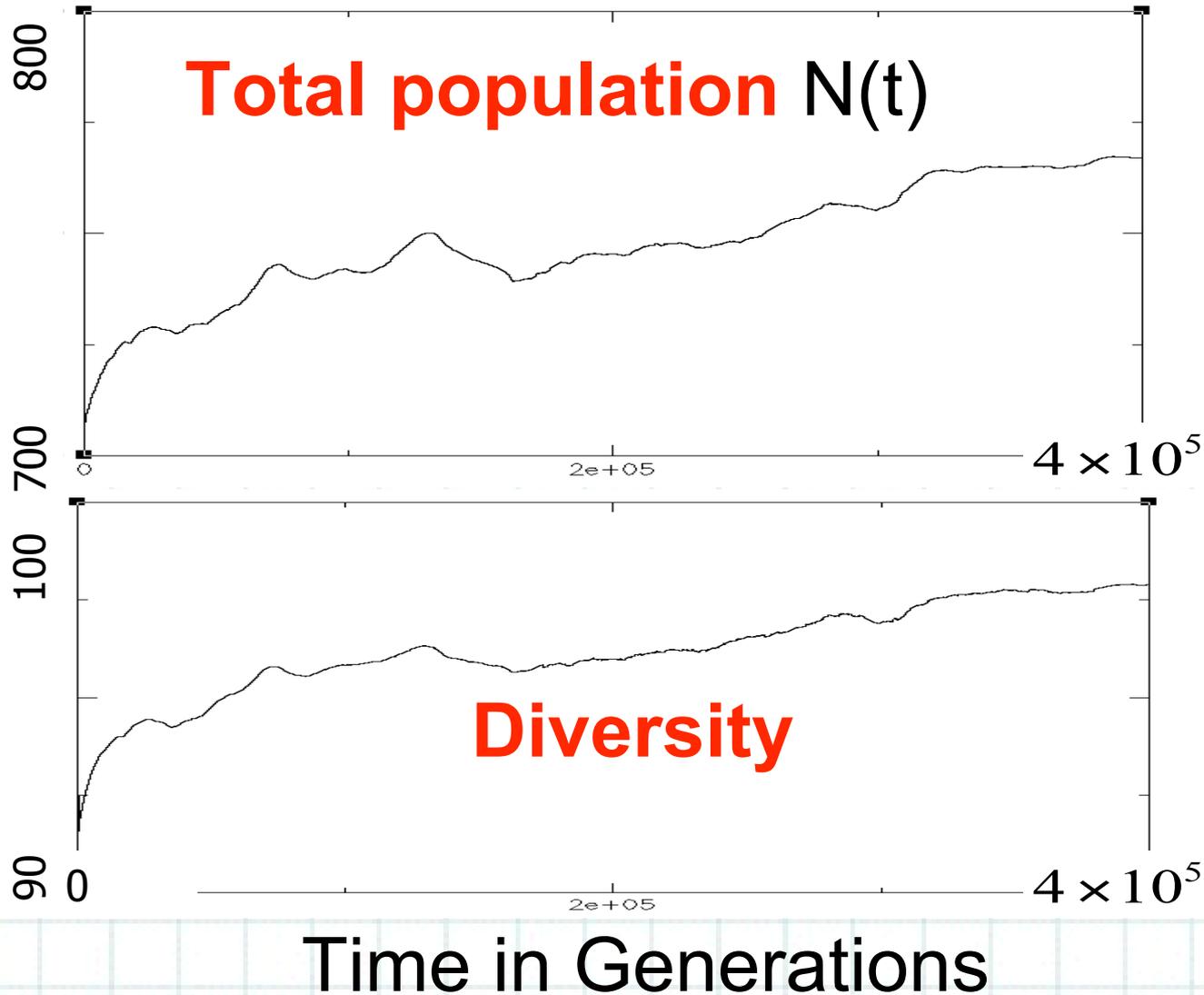
P_{mut} , i.e.

$$S_i^\gamma \mapsto -S_i^\gamma$$



Time dependence

(Average behaviour)





Origin of drift?

Effect of mutation

Let

$$H = \tilde{J} - \mu N, \quad \text{then the effect of a mutation is}$$

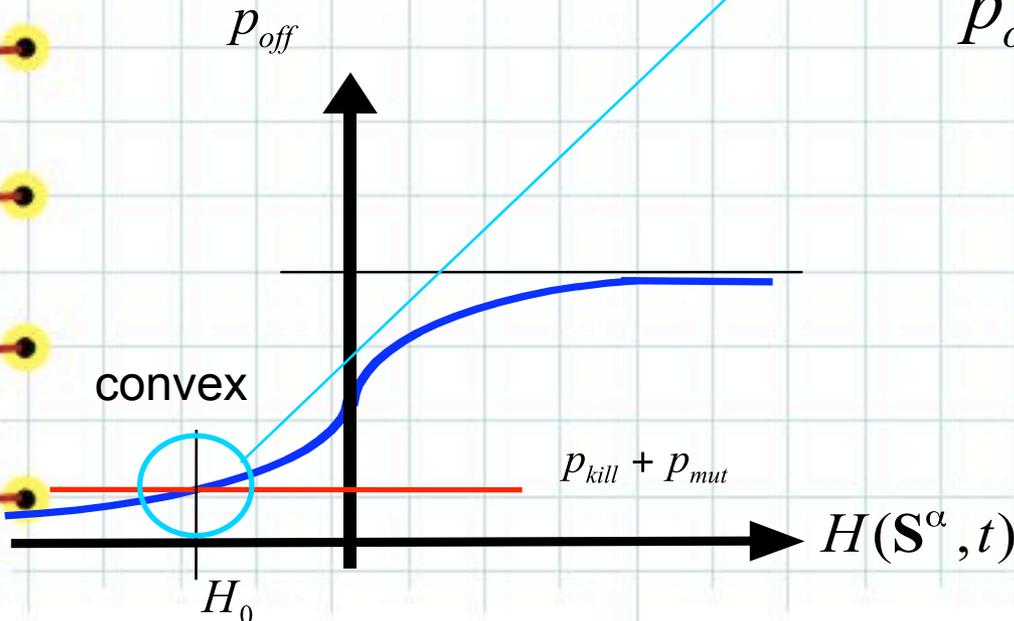
$$H \mapsto H + \delta \tilde{J}.$$

→ Symmetric fluctuations $prob(\delta \tilde{J}) = prob(-\delta \tilde{J})$

leads to asymmetri

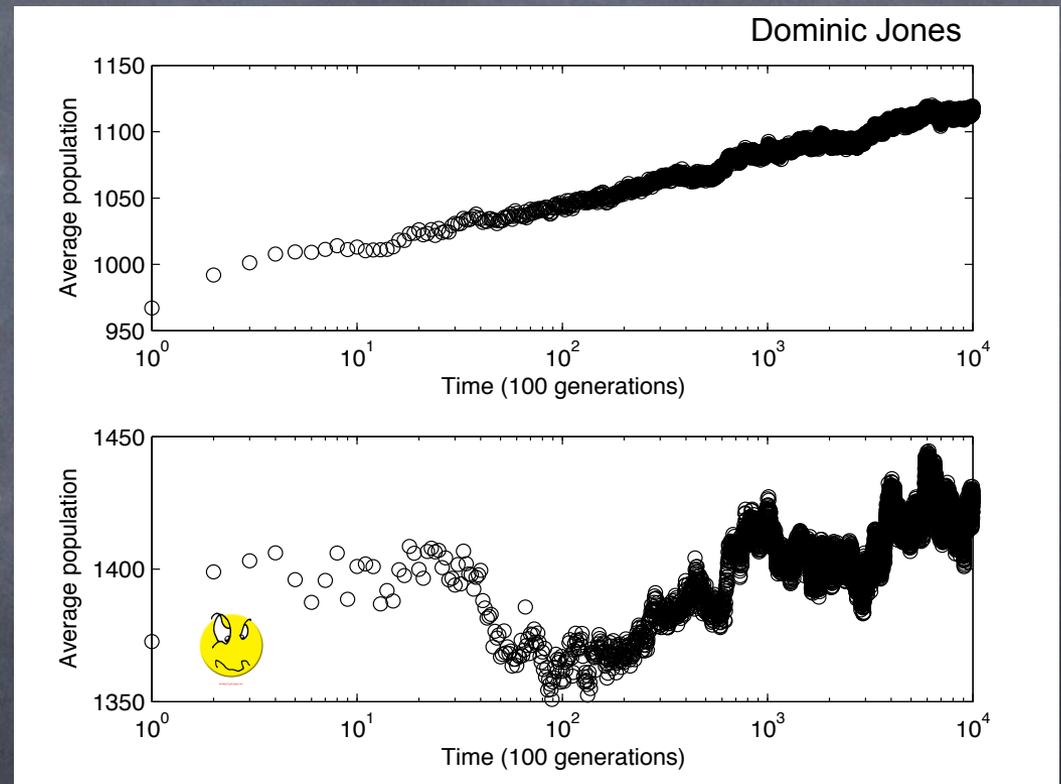
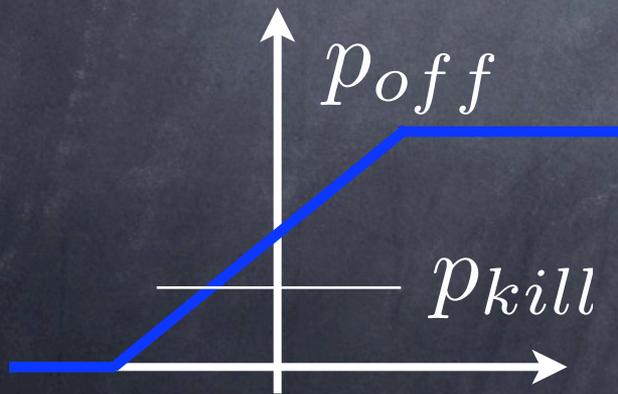
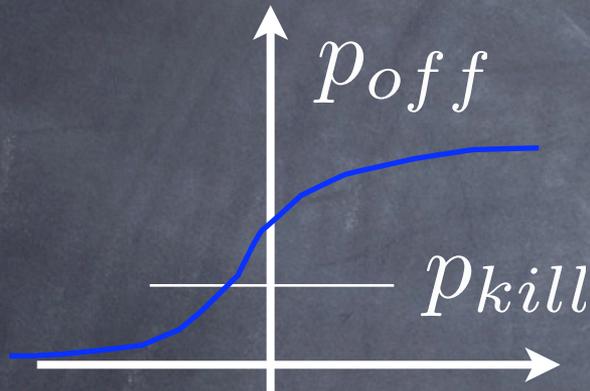
$$p_{off}(H_0 + \delta \tilde{J}) - p_{kill} >$$

$$p_{kill} - p_{off}(H_0 - \delta \tilde{J})$$



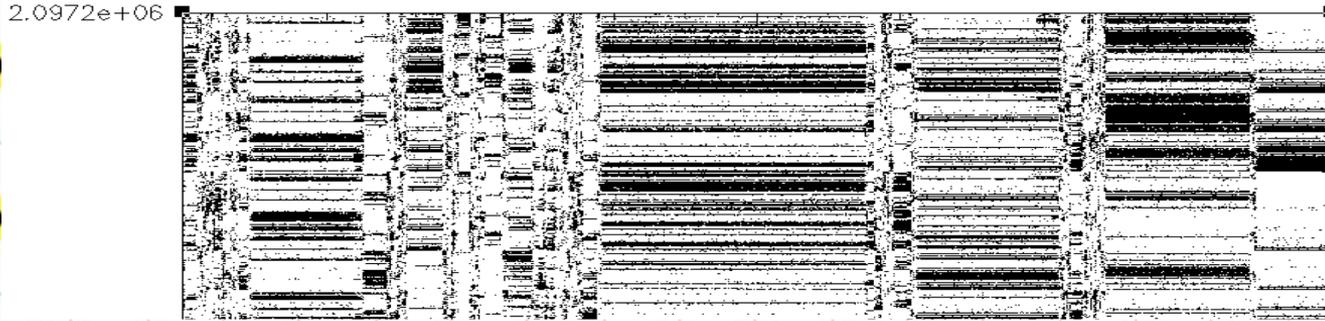
Dynamics:

The functional form of reproduction probability



Intermittency:

Non Correlated

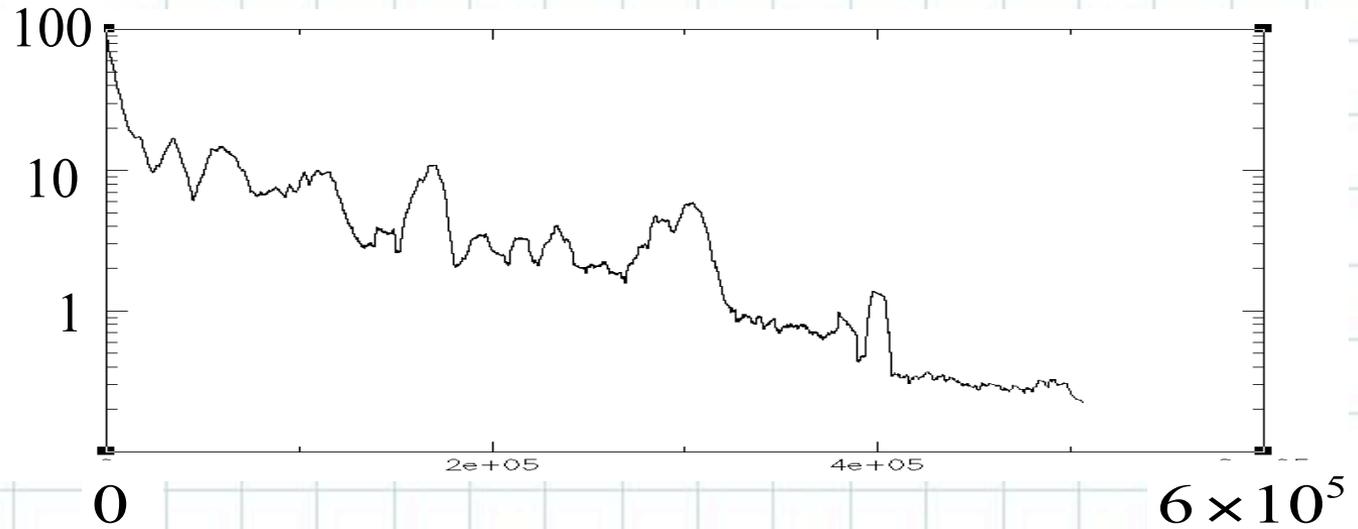


of transitions in window

Matt Hall

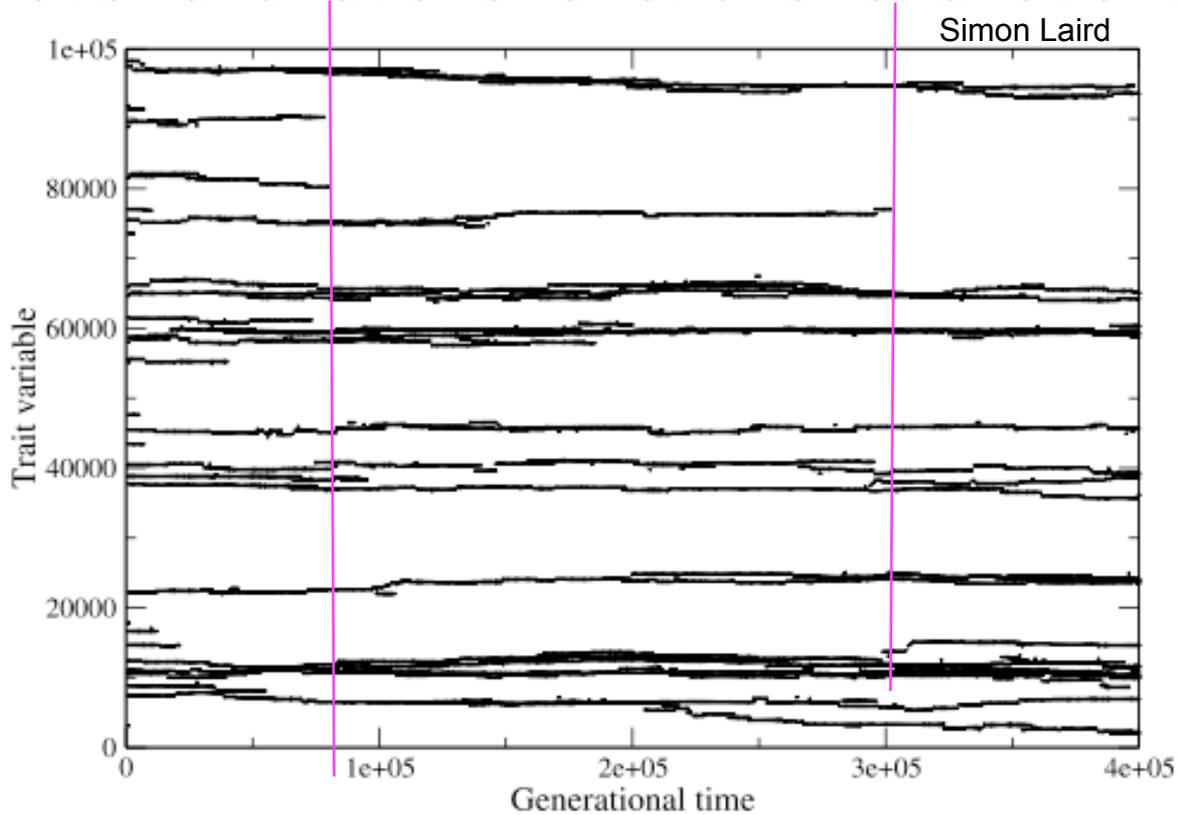
1 generation =

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



Intermittency at systems level:

Correlated



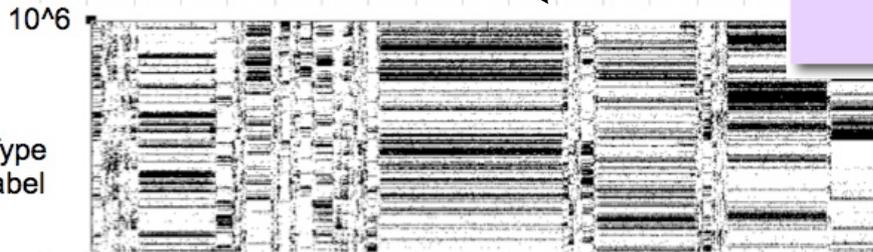
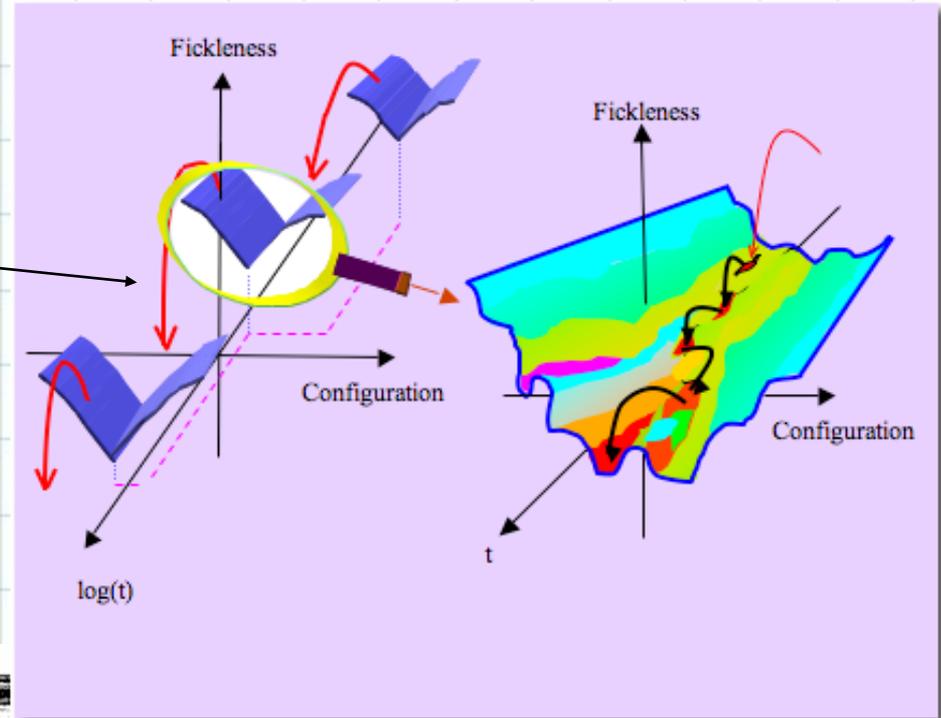
Complex dynamics:



Intermittent, non-stationary

Jumping through collective adaptation space

Transitions

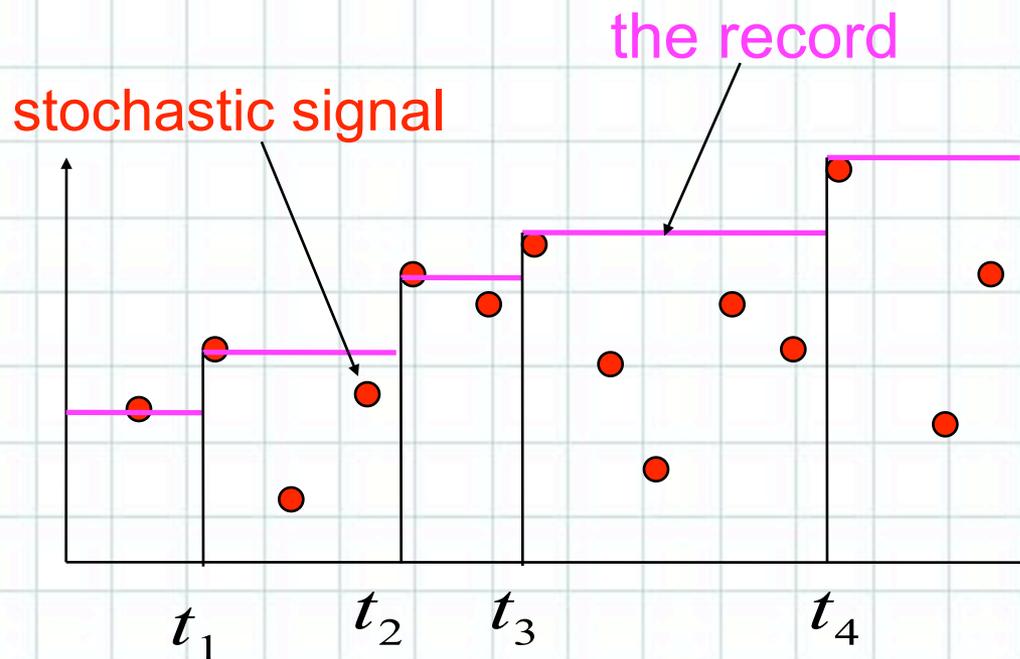


generations

Record dynamics



Record dynamics:



Paolo Sibani and Peter Littlewood:

$$\tau = \ln(t_k) - \ln(t_{k-1}) = \ln\left(\frac{t_k}{t_{k-1}}\right) \text{ exponentially distributed}$$

Record dynamics:

$$\tau = \ln(t_k) - \ln(t_{k-1}) = \ln\left(\frac{t_k}{t_{k-1}}\right) \quad \text{exponentially distributed}$$

- ▶ Poisson process in logarithmic time
- ▶ Mean and variance

$$\langle Q \rangle \propto \ln(t) \quad \text{and} \quad \langle (Q - \langle Q \rangle)^2 \rangle \propto \ln(t)$$

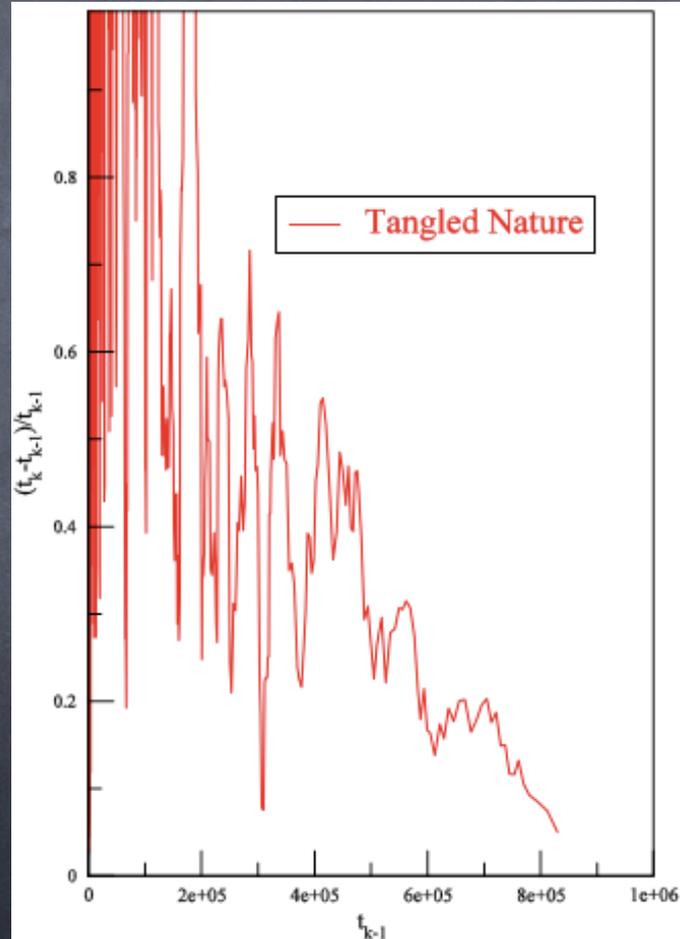
- ▶ Rate of records constant as function of $\ln(t)$
- ▶ Rate decreases

$$\propto \frac{1}{t}$$

Record dynamics:

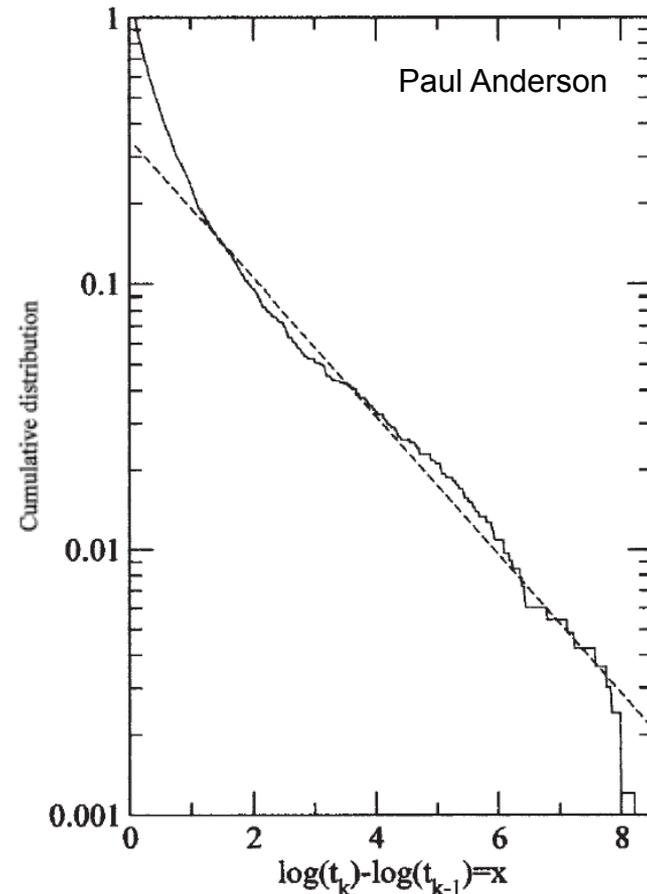
Ratio $(t_k - t_{k-1})/t_{k-1}$

remains non-zero



Cumulative Distribution

Tangled Nature



Consequences of record dynamics.

Statistics of transition times independent of underlying “noise mechanism”.

Evolution:

same intermittent dynamics in micro- as in macro-evolution.



Decreasing extinction rate.

Other systems

- Ants:

exit times

- Earthquakes:

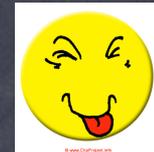
After shocks – Omori law (?)

- Magnetic relaxation:

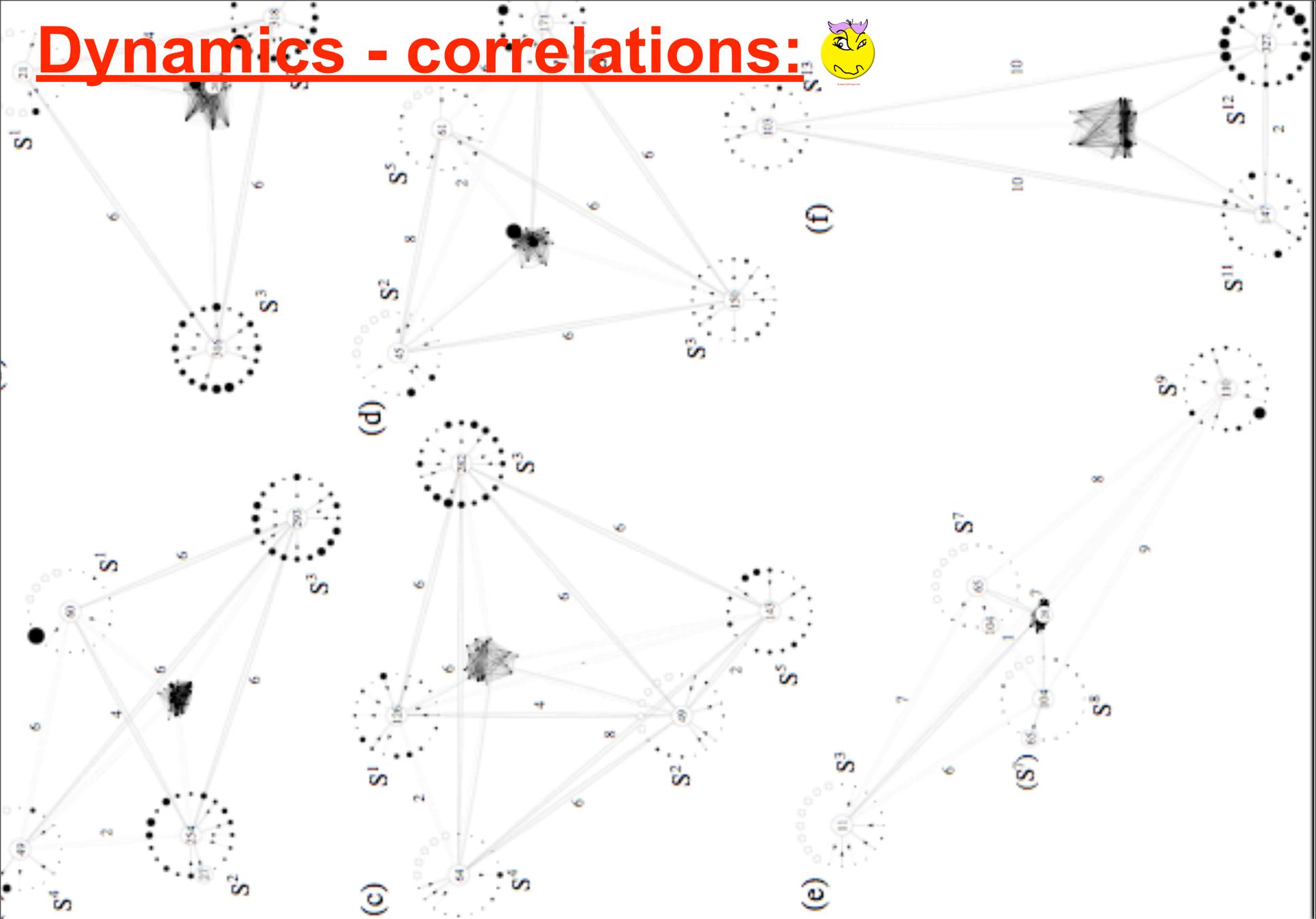
temperature independent creep rate

- Spin glass:

exponential tails



Dynamics - correlations: 🤔

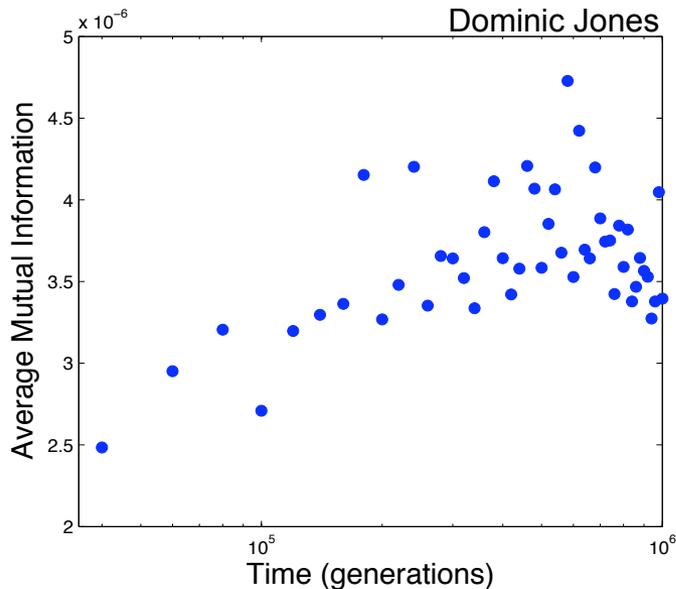




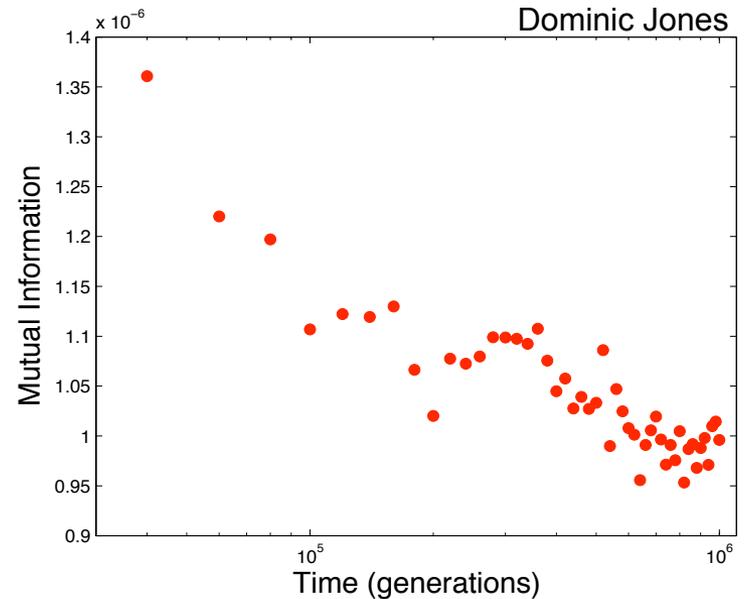
Dynamics - correlations:

The evolution of the correlations

$$I = \sum_{J_1, J_2} P(J_1, J_2) \log \left[\frac{P(J_1, J_2)}{P(J_1)P(J_2)} \right]$$



Mutual information of core



Mutual information of all

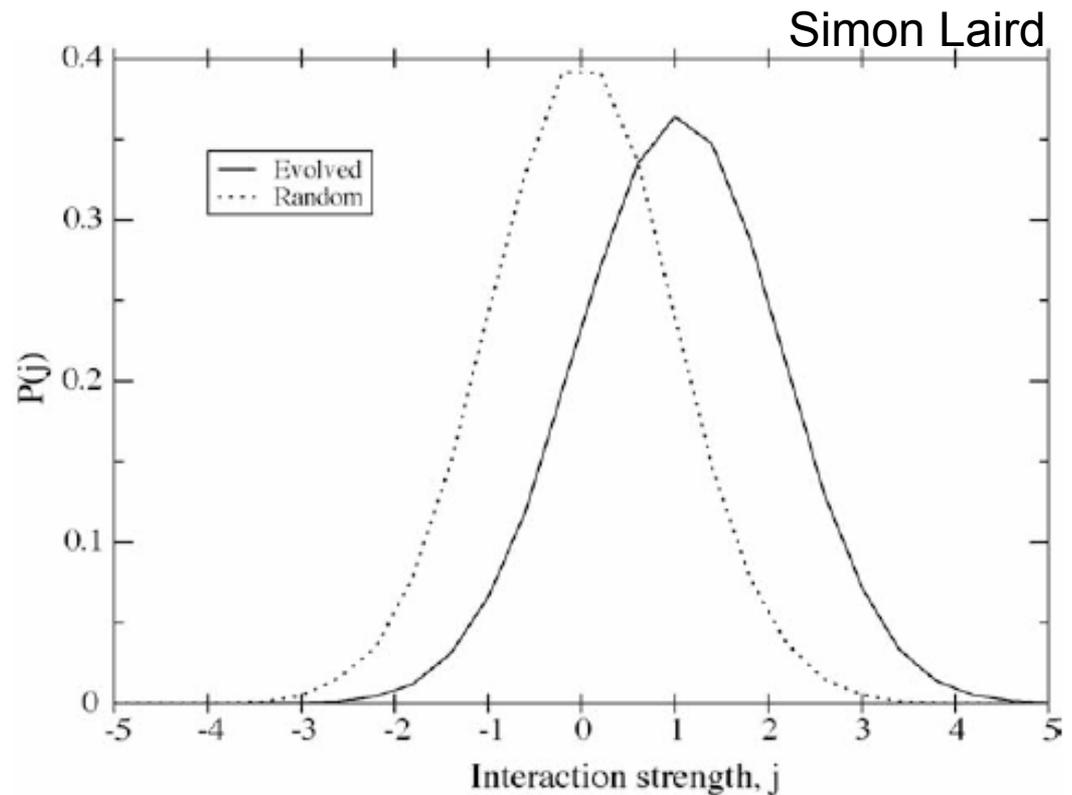


Networks emerge

Time evolution of

Distribution of active coupling strengths

Correlated



The evolved degree distribution

Correlated

Simon Laird

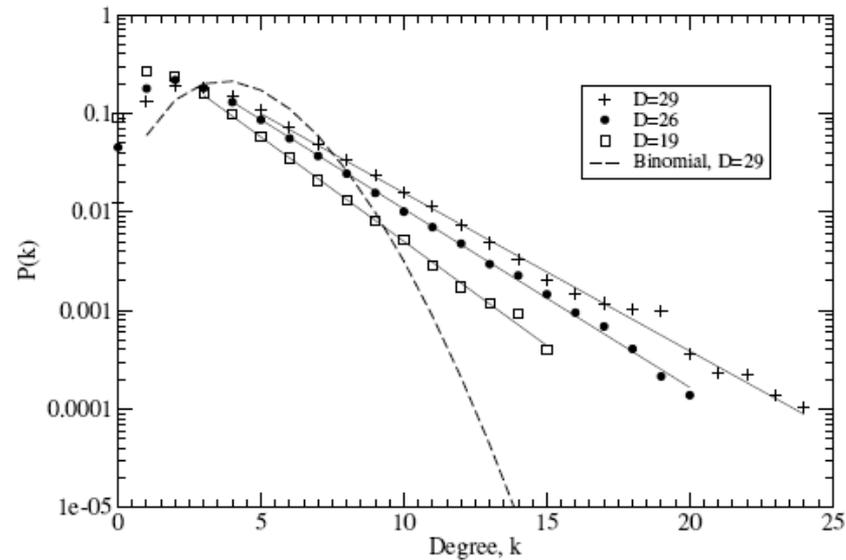
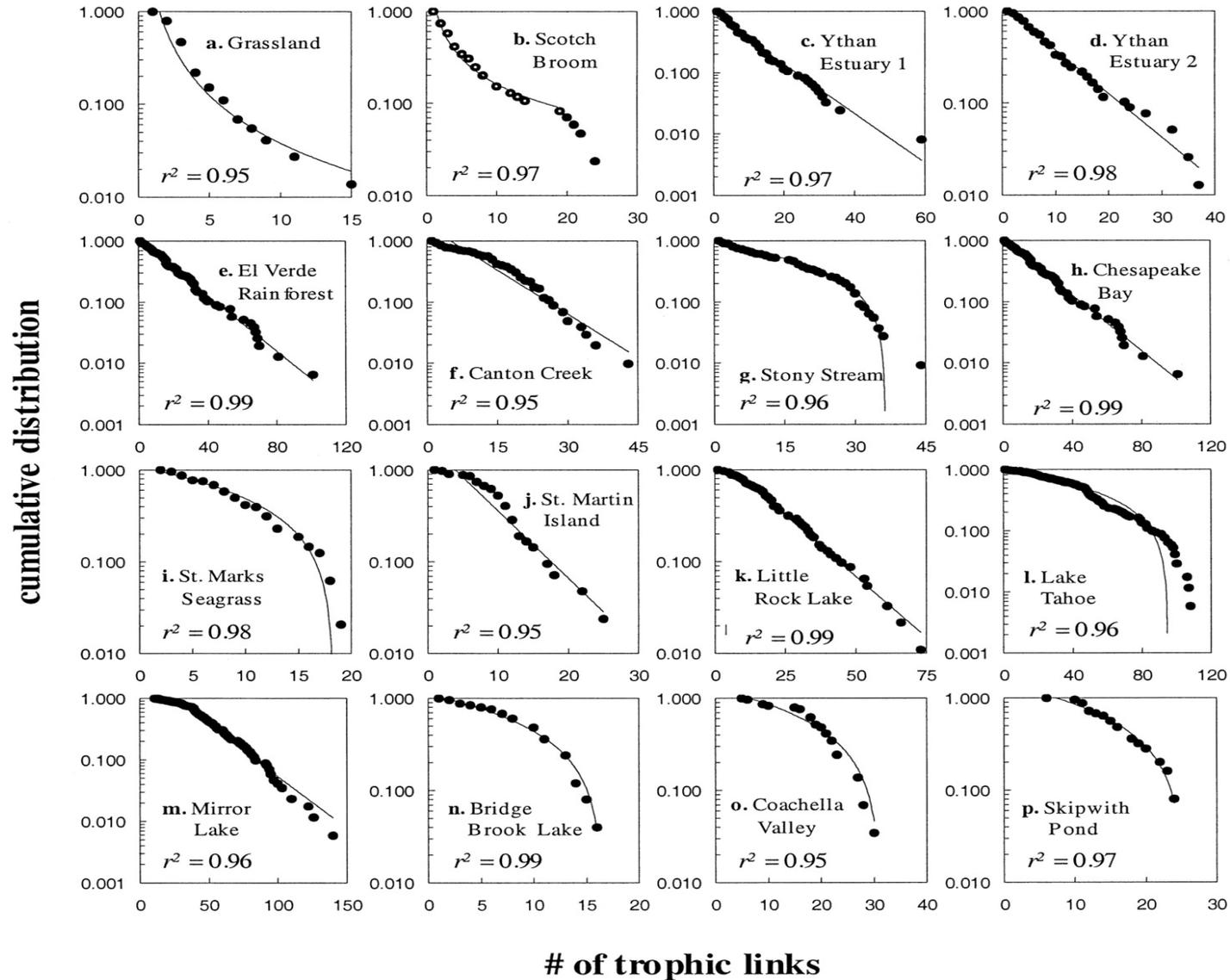


Figure 1: Degree distributions for the Tangled Nature model simulations. Shown are ensemble averaged data taken from all networks with diversity, $D = \{19, 26, 29\}$ over 50 simulation runs of 10^6 generations each. The exponential forms are highlighted by comparison with a binomial distribution of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



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



Dunne, Jennifer A. et al. (2002) Proc. Natl. Acad. Sci. USA 99, 12917-12922

The evolved connectance

$$\frac{\#edges}{D(D-1)}$$

Correlated

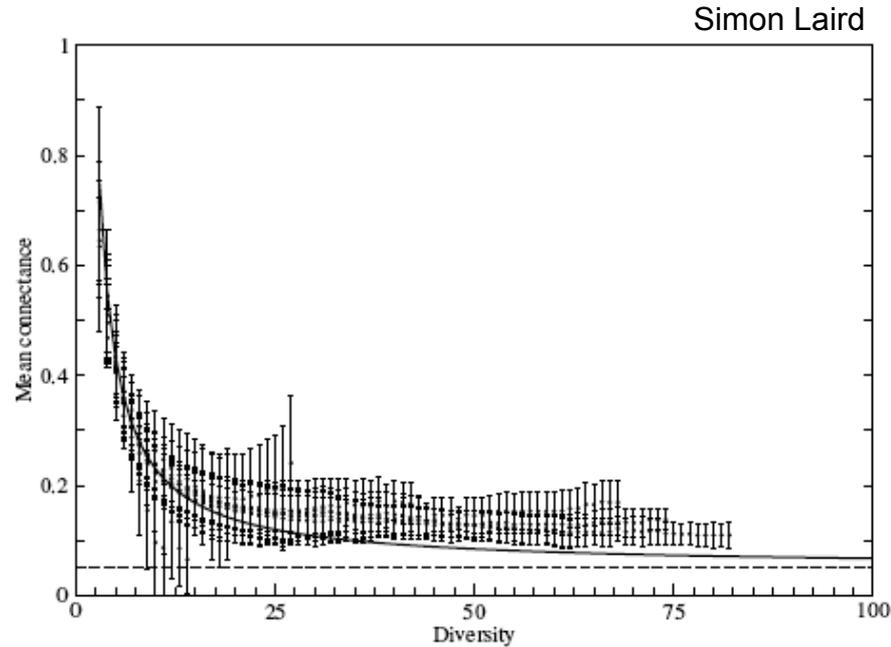
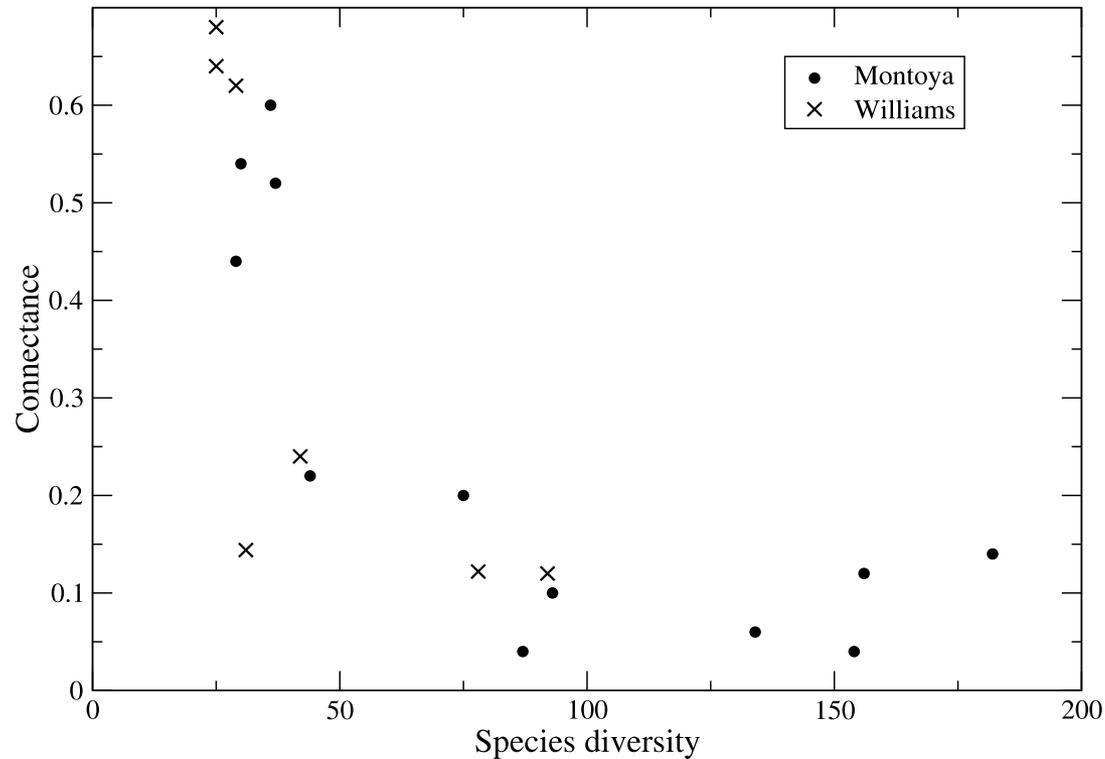


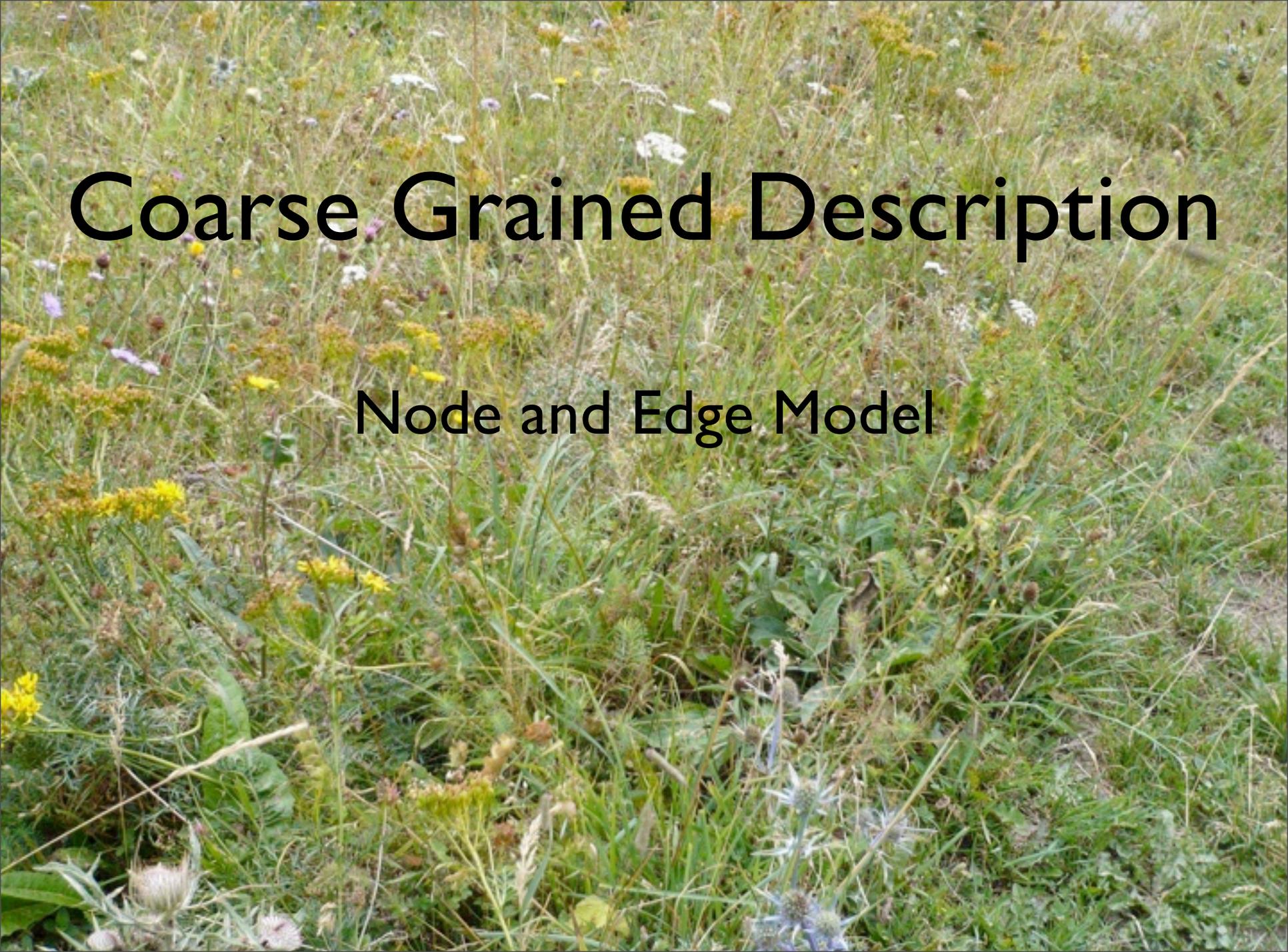
Figure 4: Plot of ensemble-averaged mean connectances, $\langle C \rangle$ against species diversity. Error bars represent the standard error. The lower dotted line marks the null system connectance, $C_J = 0.05$, which the evolved systems clearly surpass. The overlaid functional form is that given by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

Connectance



Montoya JM, Sole RV *Topological properties of food webs: from real data to community assembly models*, OIKOS **102**, 614-622 (2003)

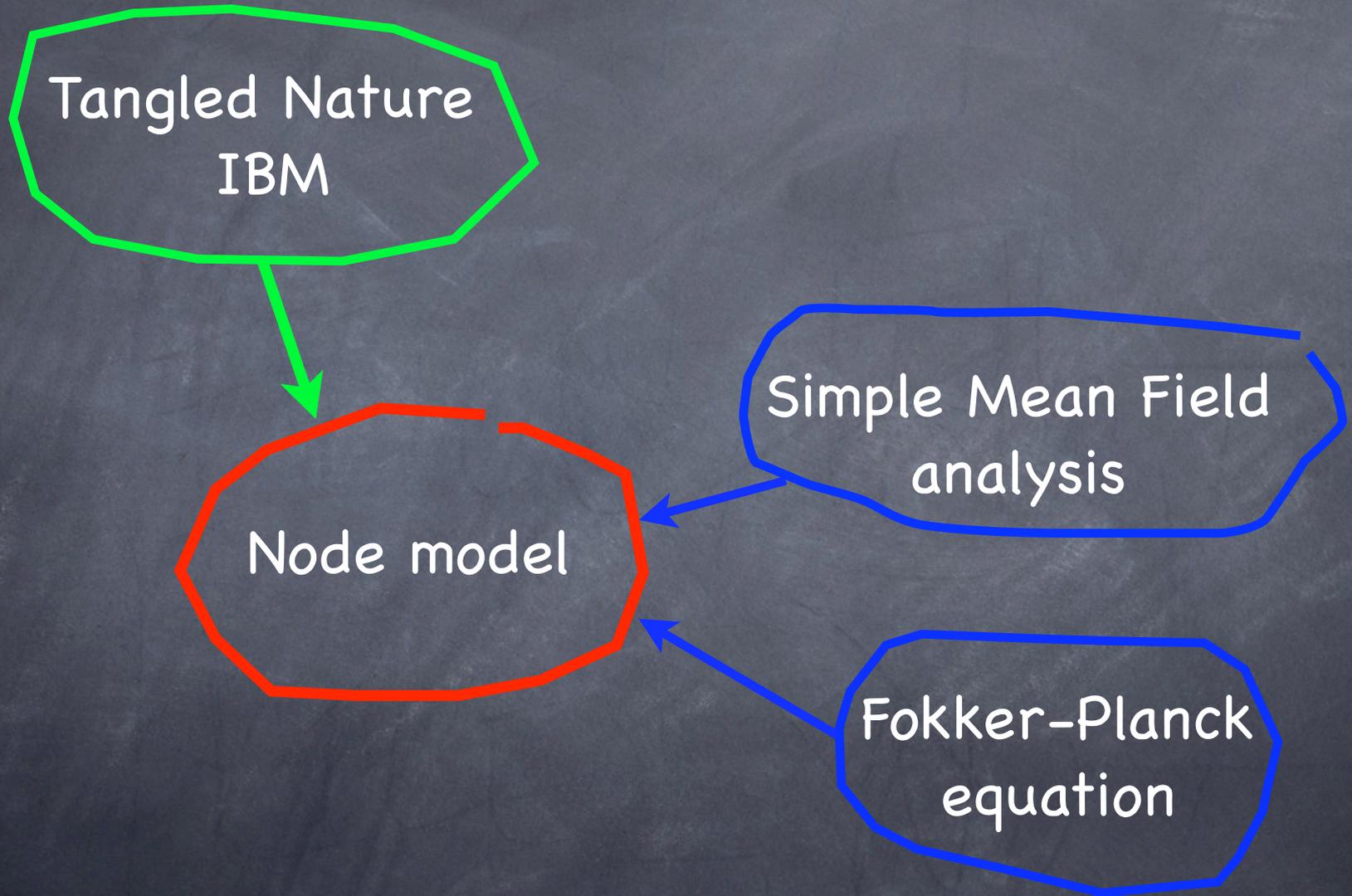
Williams RJ, Berlow EL, Dunne JA, Barabasi AL, Martinez ND *Two degrees of separation in complex food webs*, PNAS **99**, 12913-12916 (2002)



Coarse Grained Description

Node and Edge Model

Analysis approach:



Focus only on whether a type is occupied or not

Dynamical Rules

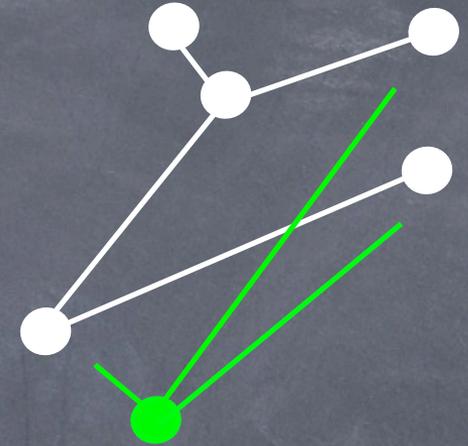
Removal: with probability $1/D$

Duplication:

place edge between parent and child P_p

copy existing edge with probability P_e

introduce new edge with probability P_n



Self-consistent Mean Field Degree Dynamics

Resulting evolution equation for degree distribution

$$\begin{aligned}
 n_k(t+1) = & n_k(t) - \frac{n_k(t)}{D} && \text{Removed node} \\
 & + \langle k \rangle \frac{n_{k+1} - n_k}{D} && \text{Adjacent node loses an edge} \\
 & + [P_e \langle k \rangle + P_n (D - 1 - \langle k \rangle)] \frac{n_{k-1} - n_k}{D} \\
 & + P_p \frac{n_{k-1}}{D} + (1 - P_p) \frac{n_k}{D} && \text{Adjacent gains an edge} \\
 & && \text{Daughter node}
 \end{aligned}$$



Mean field Degree Dynamics

Stationary solution $n(k) = n(0) \exp[-k/k_0]$

with $k_0 \rightarrow \infty$ as $P_n \rightarrow 0$

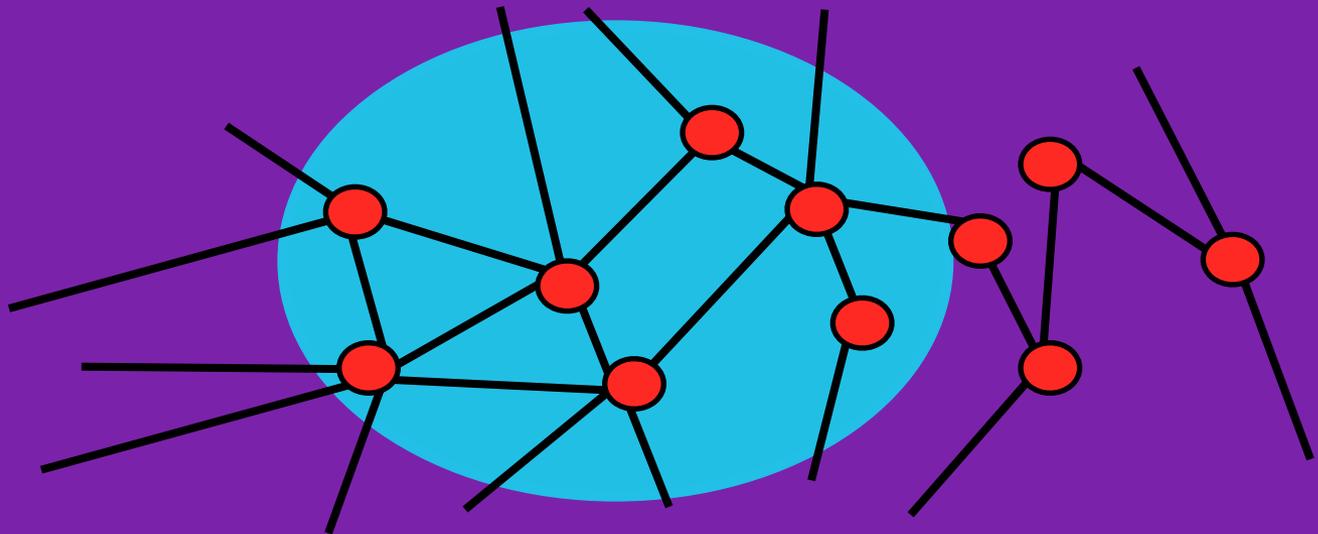
Qualitative agreement with simulations of Node
Model (and TaNa)



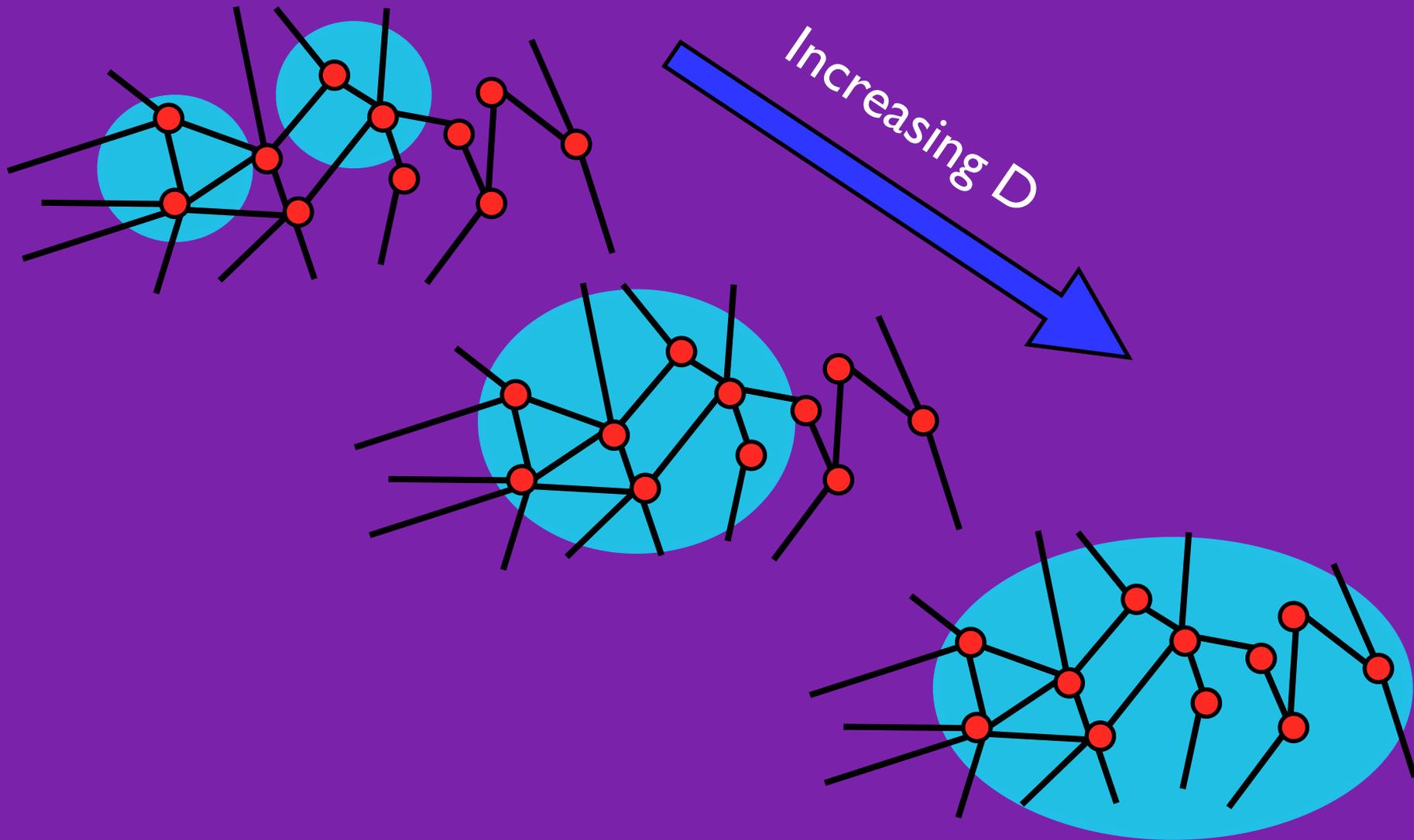
Effect of adaptation on connectance

Underlying type space is a binomial net - place a sub-net of size D

Some regions of this space will, due to fluctuations, locally have an above average connectance. It is beneficial for the evolved configurations to enter into these regions



With increasing size, D , of the adapted sub-net; it becomes increasingly difficult to confine the sub-net to within the above average regions



Effect of selection on connectance

Consider a binomial net of size D and connectance C (= edge probability).

Assume that adapted sub-net is located in a region of the master-network in which the total number of edges E is larger than the global average.

Estimate this increase as

Fraction

Fluctuations
in E

$$E = \langle E(D, C) \rangle + s\sigma(D, C)$$

$$= E_m C + s[E_m C(1 - C)]^{\frac{1}{2}}$$

Max, i.e., $E_m = D(D-1)$

Effect of selection on connectance

The resulting estimate for the connectance, E/E_m , of the adapted sub-net

$$\begin{aligned} C_{Adap} &= C + s \left[\frac{C(1 - C)}{E_m} \right]^{\frac{1}{2}} \\ &= C + s \left[\frac{2C(1 - C)}{D(D - 1)} \right]^{\frac{1}{2}} . \end{aligned}$$

Qualitative agreement with simulations of Tangled Nature model

The evolved connectance

$$\frac{\#edges}{D(D-1)}$$

Correlated

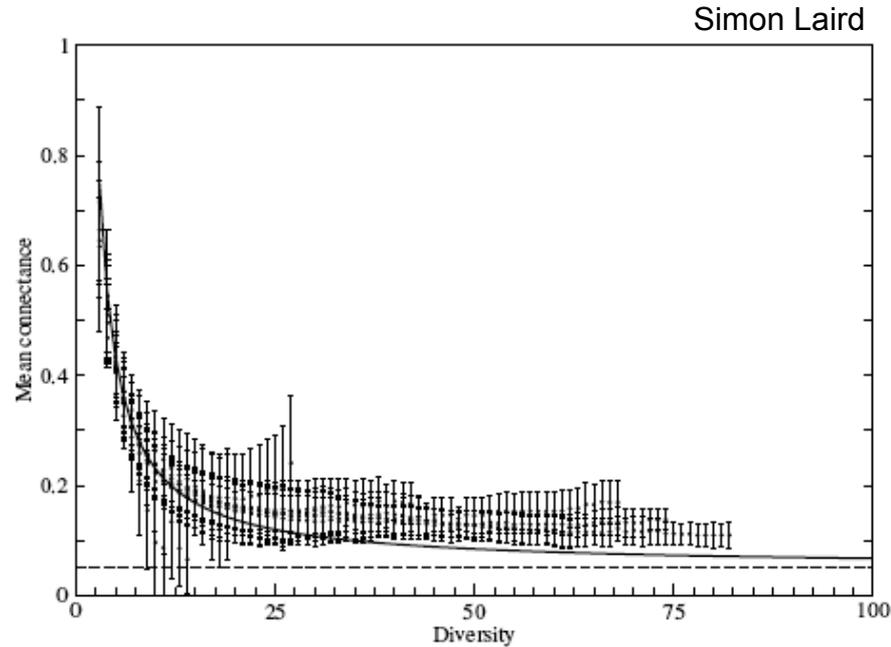


Figure 4: Plot of ensemble-averaged mean connectances, $\langle C \rangle$ against species diversity. Error bars represent the standard error. The lower dotted line marks the null system connectance, $C_J = 0.05$, which the evolved systems clearly surpass. The overlaid functional form is that given by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



Fokker-Planck equation

Analytical result

$$n_k(t+1) = n_k(t) + \Gamma_R(D, k, t) + \Gamma_{Du}(D-1, k, t).$$

$$\Gamma_R(D, k, t) = \Gamma_R^d(k) + \Gamma_R^N(k+1) - \Gamma_R^N(k).$$

$$\begin{aligned} \Gamma_{Du}(D-1, k, t) &= \Gamma_{Du}^P(k-1) - \Gamma_{Du}^P(k) + \Gamma_{Du}^C(k) \\ &\quad + \Gamma_{Du}^N(k-1) - \Gamma_{Du}^N(k). \end{aligned}$$

Fokker-Planck eq. iterated

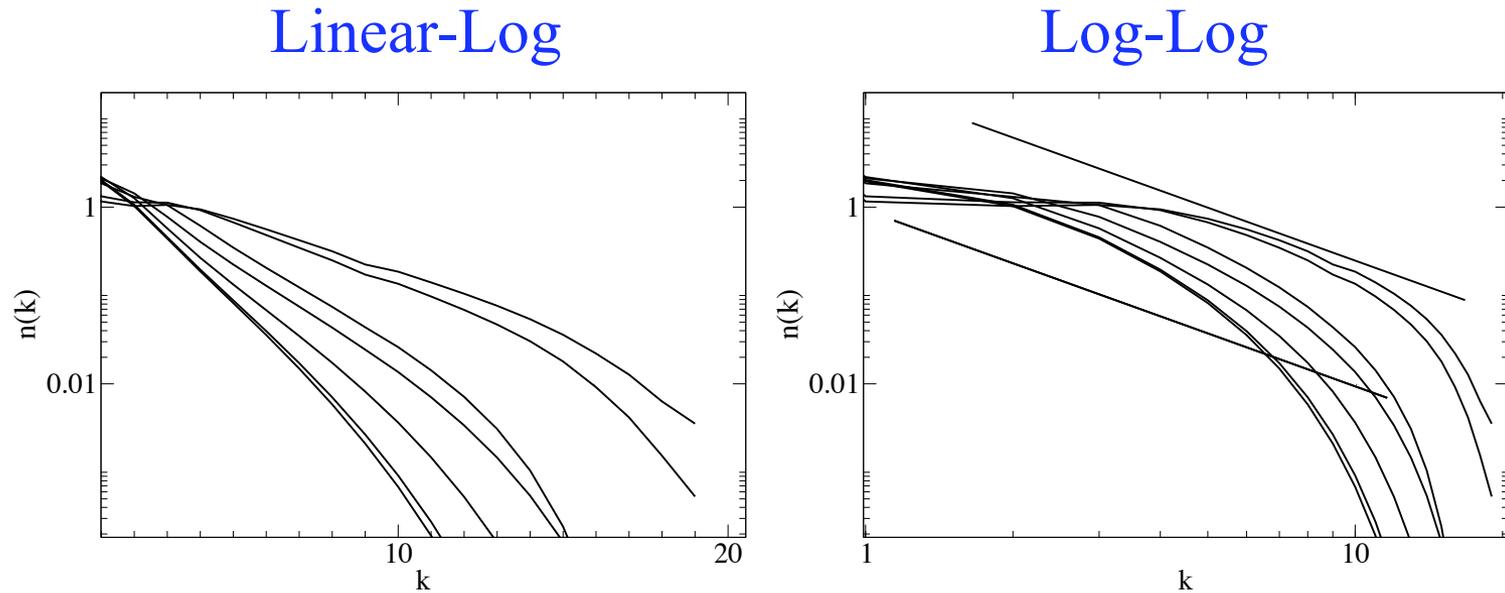


Figure 2: The degree distribution obtained by iteration of the Fokker-Planck equation (9). The exponential form is visible for a broad range of parameter values in the linear-log plot to the left. The approach towards a $1/k$ dependence in the limit of $P_e \rightarrow 1$ can be seen in the log-log plot to the right. The two straight lines have slope -1. The parameters are $D = 20$, $P_e = 0.01, 0.1, 0.3, 0.5, 0.7, 0.9, 0.95$ and $P_p = 0.01$. P_n was chosen to be $P_n = P_p(1 - P_e)/(1 - P_p)$

Limiting behaviour

In limit mutations $\longrightarrow 0$

Implies $P_e = 1$ and $P_n \rightarrow 0$

Fokker-Planck eq. reduces to

$$\begin{aligned} n_k(t+1) = & n_k(t) + n_k \left(\frac{1}{D-1} - \frac{1}{D} \right) + \frac{2P_p}{D-1} (n_{k-1} - n_k) \\ & + \sum_{k_1=1}^{D-2} \sum_{q=1}^{k_1} q n_{k_1} \left[\frac{1}{D} P_{Ed}(k_1, k+1, q) - \frac{1}{D-1} P_{Ed}(k_1, k, q) \right. \\ & \left. - \frac{1}{D} P_{Ed}(k_1, k, q) + \frac{1}{D-1} P_{Ed}(k_1, k-1, q) \right] \end{aligned}$$

Limiting behaviour

Include only leading terms from $k_1 = 1$ and $q = 1$

$$\begin{aligned}n_k(t+1) &= n_k + \frac{n_k}{D(D-1)} + \frac{2P_p}{D-1} [n_{k-1} - n_k] \\ &\quad + \frac{n_1}{M} \left[\frac{1}{D} \{ (k+1)n_{k+1} - kn_k \} \right. \\ &\quad \left. - \frac{1}{D-1} \{ kn_k - (k-1)n_{k-1} \} \right].\end{aligned}$$

Stationary solution $n_k \propto 1/k$



A photograph of a lush, green field filled with tall grasses and various wildflowers. The flowers include yellow, white, and purple blooms. The word "Summary" is written in a large, black, sans-serif font in the center of the image.

Summary

Summary and conclusion

From minimal micro-dynamics



- Collective evolution and adaptation
- Intermittent dynamics \gg record dynamics.
- Nature of the evolved networks - compares well
- Dynamics (degree of overlap with parent) determines degree distribution
- Adaptation/selection influences connectance

Thank you for the chance to speak



Papers from

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

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Paol Sibani