

# Evolution of Phenotype as selection of Dynamical Systems

1 Phenotypic Fluctuation (Plasticity) versus Evolution

2 Phenotypic Fluctuation versus Genetic Variation  
consistency between Genetic and  
Phenotypic Levels

3 Evolution of Robustness to Developmental Noise  
and to Mutation

4 Sympatric speciation:

Fixation of Bifurcation of Phenotype to Genes

- **Underlying Motivation as Dynamical Systems**
- Dynamical Systems Model in Biology (development/gene expression,,)  
Study the behavior : OK as mathematics/physics, but
- In biology, choice of such dynamical systems itself is an essential issue
- (+) selection of dynamical systems rule through **evolution**, which is based on dynamics itself  
→ constraint in choice of rule, ‘smooth dynamics’
- (\*) Selection of ‘restricted’ low-dimensional dynamical systems from higher-dimensional space through **development**

- Mathematical Theory for Evolution and Development? (case under fixed environment, without interaction) simplified
- Development = Dynamical Systems
- Gene = Rule (parameter etc) of the DS
- Phenotype = State value at attractor of the DS
- Evolution = Selection of Phenotype  
which leads to selection of Gene  
(only gene is transferred to the next generation)  
‘Walk in the ‘Model(rule/parameter) space’  
Proposal: choice of model assimilates DS

# Starting point: Phenotypic Fluctuation → evolution ?

- Even in isogenic individuals (clones) there is large phenotypic fluctuation :recognized extensively

Exp + Model+Theory

- Relevance of this fluctuation to evolution?

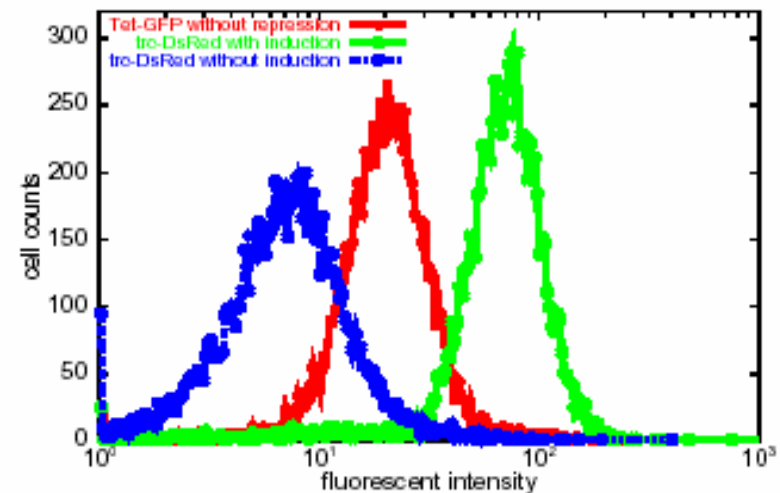
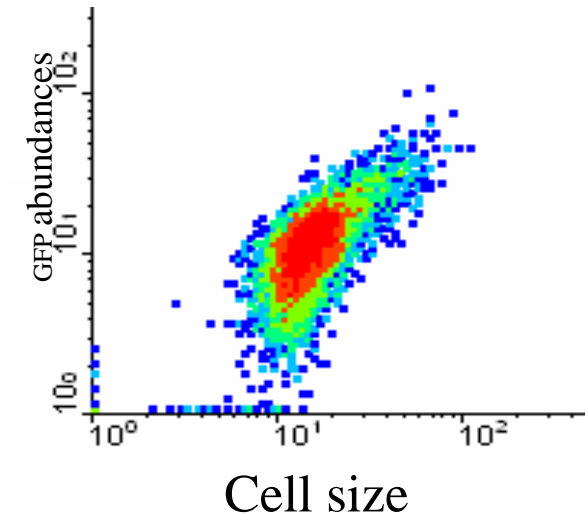
Gene ( rule for dynamics)

---(gene expression)

development dynamics ---

→ Phenotype (with fluctuation)

→ selection

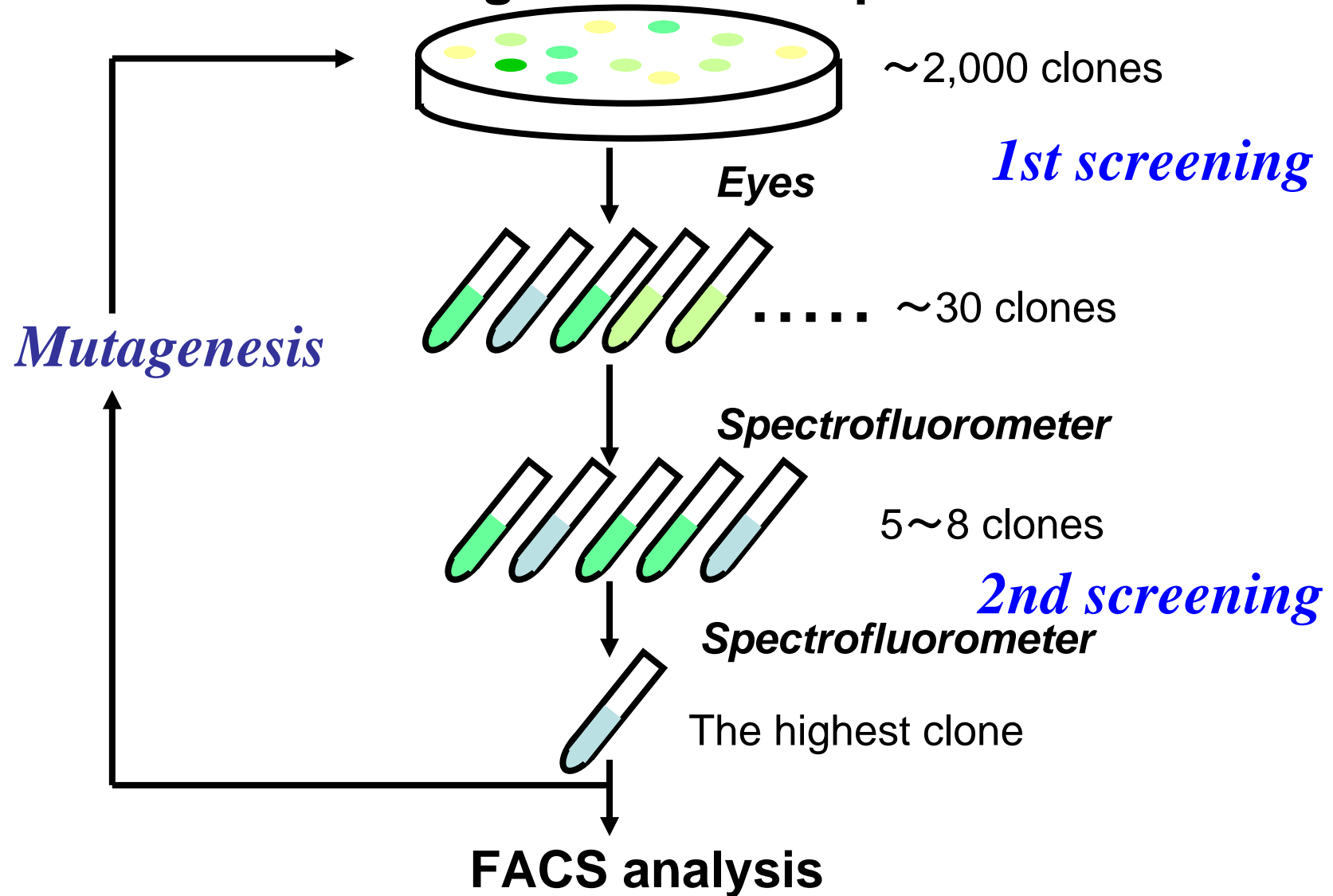


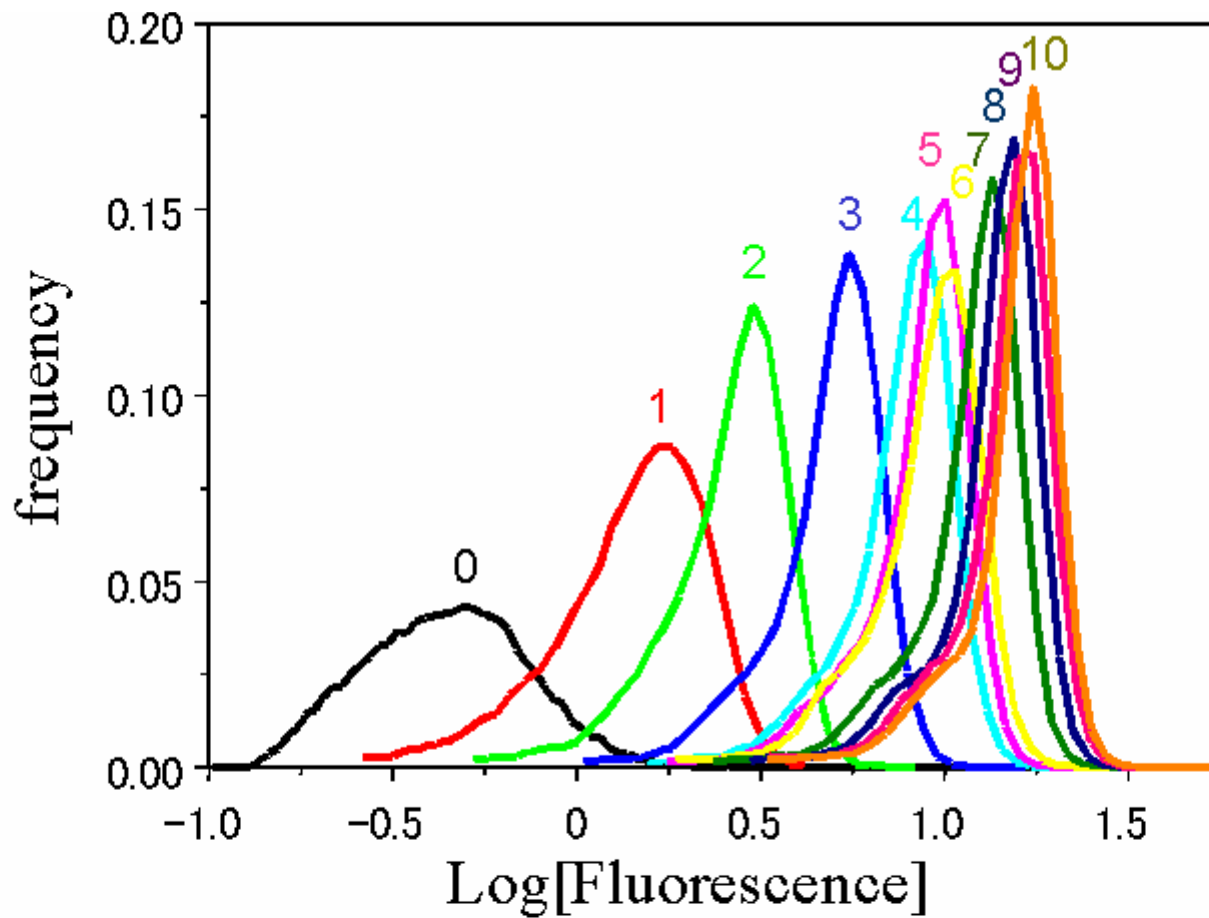
Number distribution of the proteins measured by fluorescent intensity. Three *Escherichia coli* cell populations containing different reporter plasmids.

# Artificial selection experiment with bacteria

Selection to increase the fluorescence of protein in bacteria

## Schematic drawing of selection process





Sato, Ito,  
Yomo, KK  
PNAS(2003)

Fluctuation ---- Variance of phenotype of clone  
Organisms with larger phenotypic fluctuation have  
higher evolution speed;  
Evolvability  $\leftrightarrow$  Fluctuation

Remind of fluctuation—response relation in **physics**:

Force to change a variable  $x$ ;

**response ratio** = (shift of  $x$ ) / force

**fluctuation of  $x$**  (without force)

**response ratio** proportional to **fluctuation**

originated by Einstein ...

**Generalization::(mathematical formulation)**

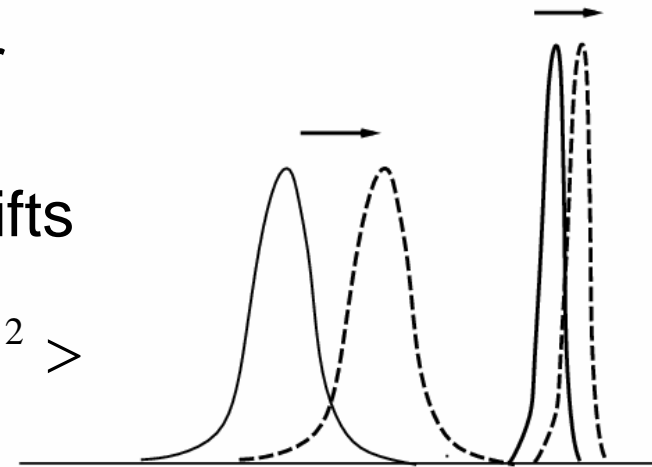
plasticity ~ **response ratio of some variable  $x$  against change of parameter  $a$**  versus **fluctuation of  $x$**

$P(x;a)$   $x$  variable,  $a$ : control parameter

change of the parameter  $a \rightarrow$

peak of  $P(x;a)$  ( i.e.,  $\langle x \rangle$  average ) shifts

$$\frac{\langle x \rangle_{a+\Delta a} - \langle x \rangle_a}{\Delta a} \propto \langle (\delta x)^2 \rangle_a = \langle (x - \langle x \rangle)^2 \rangle$$



Evolution speed per mutation rate  $\propto$  isogenic phenotype fluctuation

# Fluctuation-response relationship (generalized form)

Gaussian distribution of  $x$ ; under the parameter  $a$

$$P(x; a_0) = N_0 \exp\left(-\frac{(x - X_0)^2}{2\alpha_0}\right), \quad \text{at } a=a_0$$

Change the parameter from  $a_0$  to  $a$

$$P(x : a) = N \exp\left(-\frac{(x - X_0)^2}{2\alpha(a)} + v(x, a)\right)$$

$v(a, x) = C(a - a_0)(x - X_0) + \dots$ , with  $C$  as a constant,

$$P(x : a) = N(a) \exp\left(-\frac{(x - X_0)^2}{2\alpha(a)} + C(a - a_0)(x - X_0)\right),$$

*generalized force*  $C(a - a_0)(x - X_0)$  to shift the distribution.



$$P(x, a_0 + \Delta a) = N' \exp\left(-\frac{(x - X_0 - C\Delta a\alpha(a_0 + \Delta a))^2}{2\alpha(a_0 + \Delta a)}\right)$$

Hence, we get

$$\frac{\langle x \rangle_{a=a_0+\Delta a} - \langle x \rangle_{a=a_0}}{\Delta a} = C\alpha(a_0 + \Delta a),$$

Noting that  $\alpha = \langle (\delta x)^2 \rangle$

$$\frac{\langle x \rangle_{a=a_0+\Delta a} - \langle x \rangle_{a=a_0}}{\Delta a} = C \langle (\delta x)^2 \rangle,$$

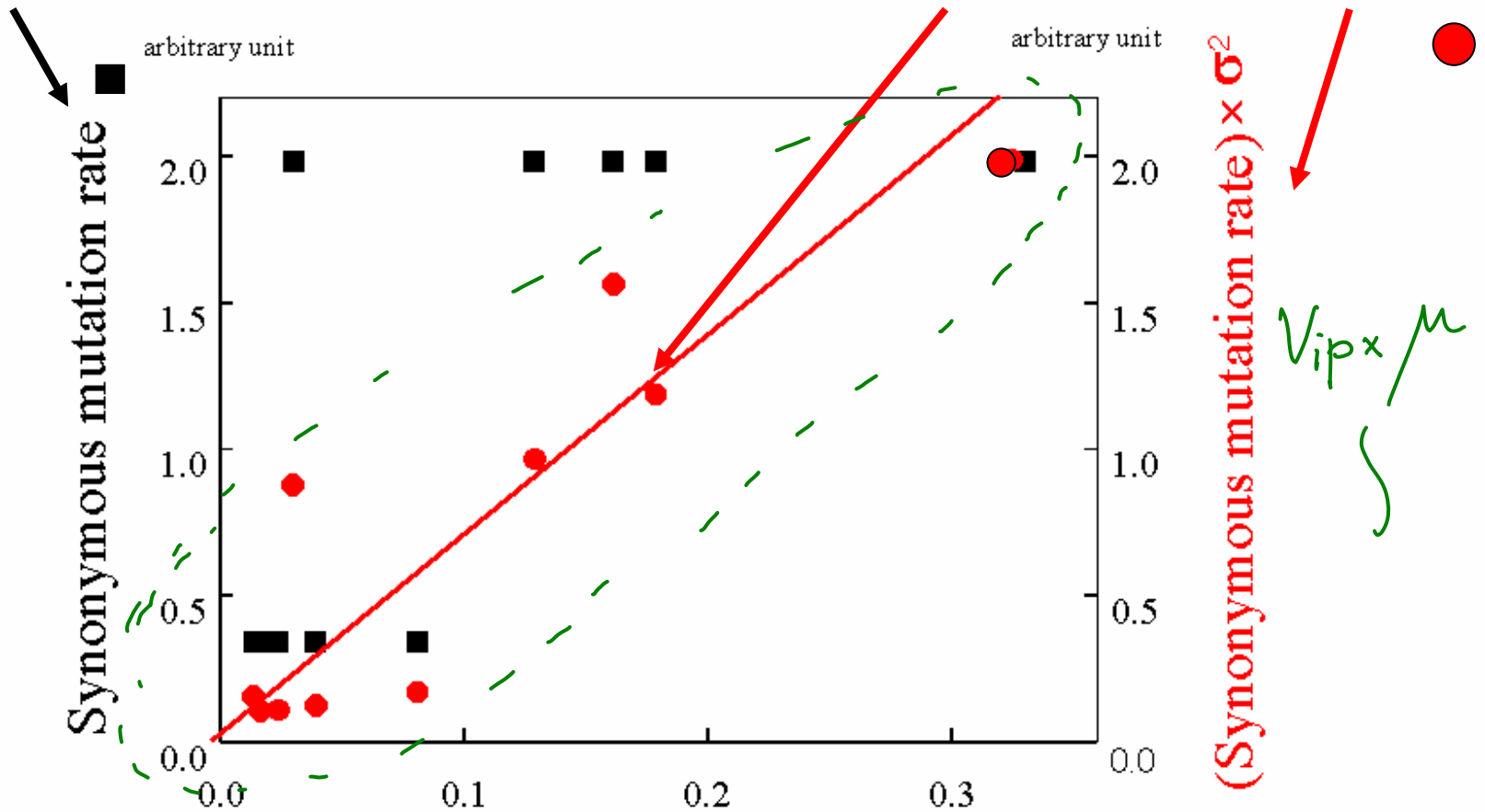
Approximate formula ; trivial by itself

Non-trivial point : representation by  $P(x;a)$

$x$  : phenotype     $a$  ; enviroment etc

Naïve expectation:  
Just prop to mutation rate

Fluctuation-response relation  
Phenotype fluct.  $\times$  mutation rate



Difference of the average value

(Evolution Speed per generation)

Sato, Ito, Yomo, KK, PNAS 2003

# Toy Cell Model with Catalytic Reaction Network

## 'Crude but whole cell model'

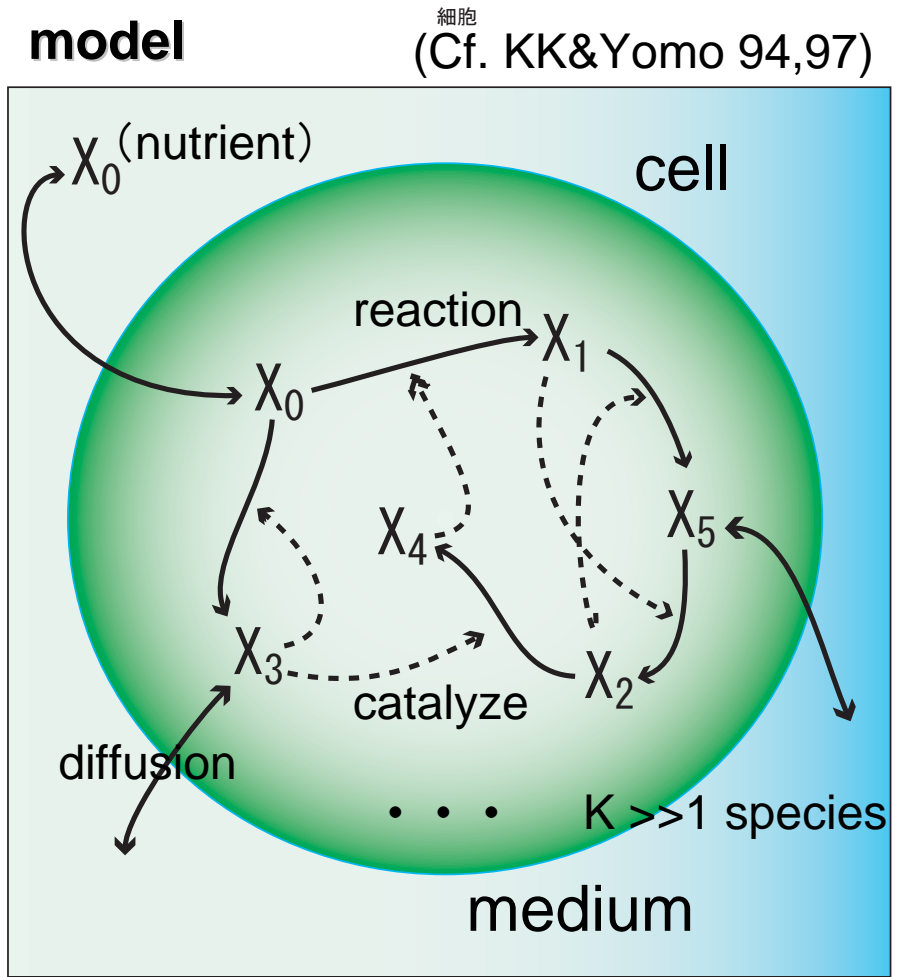
C.Furusawa & KK, PRL2003

■ **k species of chemicals** ,  $X_0 \cdots X_{k-1}$   
 number ---  $n_0, n_1 \dots n_{k-1}$

■ **random catalytic reaction network**  
 with the path rate  $p$   
 for the reaction  $X_i + X_j \rightarrow X_k + X_j$

■ some chemicals are **penetrable through the membrane with the diffusion coefficient  $D$**

■ resource chemicals are thus transformed into impenetrable chemicals, leading to the growth in  $N = \sum n_i$ , when it exceeds  $N_{\max}$   
**the cell divides into two**



$dX_1/dt \propto X_0 X_4$ ; rate equation;  
 Stochastic model here

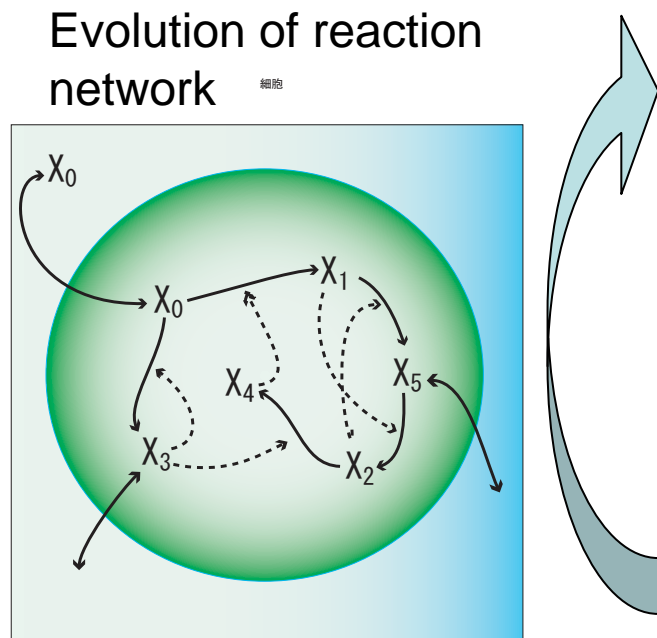
In continuum description, the following rate eqn.,  
but we mostly use stochastic simulation

$$\begin{aligned} dn_i/dt = & \sum_{j,\ell} \text{Con}(j, i, \ell) \epsilon n_j n_\ell / N^2 \\ & - \sum_{j',\ell'} \text{Con}(i, j', \ell') \epsilon n_i n_{\ell'} / N^2 \\ & + D \sigma_i (\bar{n}_i / V - n_i / N), \end{aligned}$$

where  $\text{Con}(i, j, \ell)$  is 1 if there is a reaction  $i + \ell \rightarrow j + \ell$ , and 0 otherwise, whereas  $\sigma_i$  takes 1 if the chemical  $i$  is penetrable, and 0 otherwise. The third term describes the transport of chemicals through the membrane, where  $\bar{n}_i$  is

- Confirmation by numerical evolution experiment by the reaction-net cell model

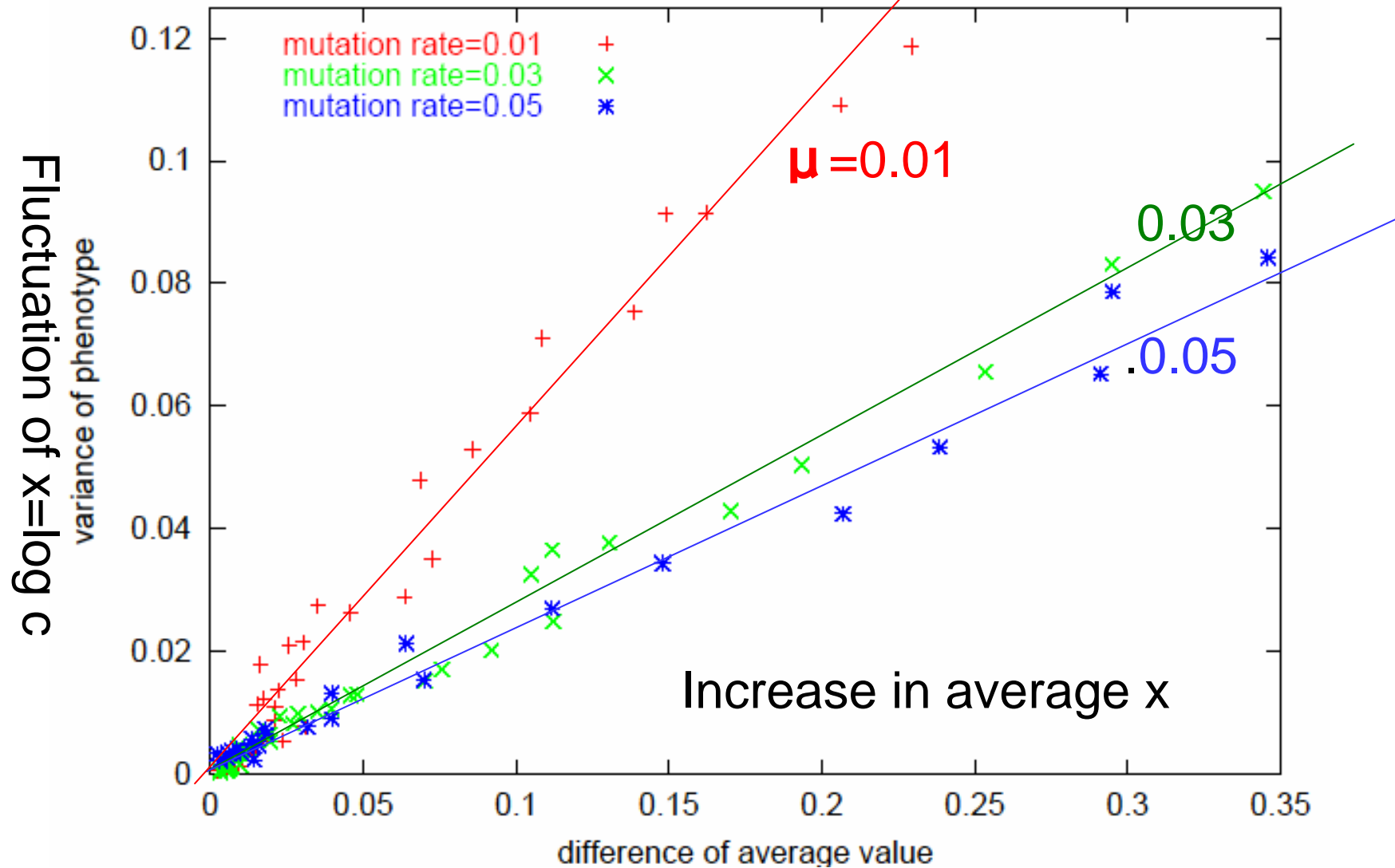
Mutate the network ('gene') with mutation rate  $\mu$ , (rewire the path of the network with the rate) and select such network having highest concentration  $c$  of a specific chemical



phenotype  $x = \log (n_s)$

1. Prepare initial mother cells.
2. From each parent cell, mutant cells are generated by randomly replacing reaction paths, with **mutation rate  $\mu$**
3. reaction dynamics of all mutants are simulated to determine phenotype  $x$
4. Top 5% cells with regard to phenotype  $x$  are selected as parent cells of next generation

# Confirmation of Fluctuation Dissipation Theorem by reaction-network cell model



..... Not yet over .....

New mystery? **phenotype fluctuation of clone**  
**vs evolution speed** in contrast to

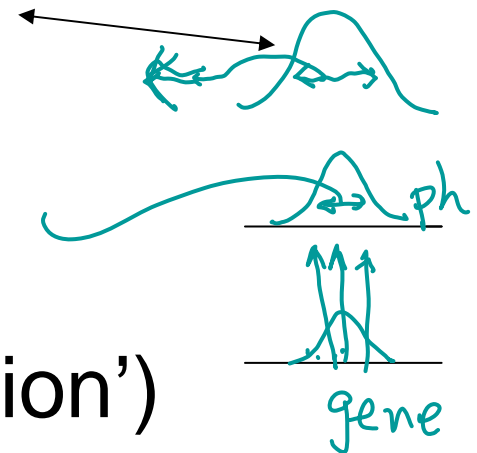
evolution speed  $\propto$  phenotypic fluctuation by  
genetic variation ( $V_g$ ): (fundamental theorem of  
natural selection; established)

isogenic phenotypic fluctuation  $V_{ip}$

$\propto$

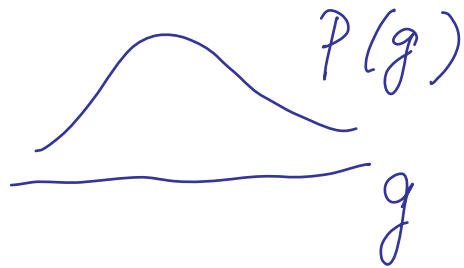
**pheno fluct by gene variation  $V_g$ ?**

(fluct by noise  $\propto$  variation in 'equation')



$V_{ip} \propto$  evolution speed (exp (?), model)

$V_g \propto$  evolution speed (Fisher) a simple derivation(?)



distribution

$P_n(g)$

(growth rate  
 $\sim$  fitness)

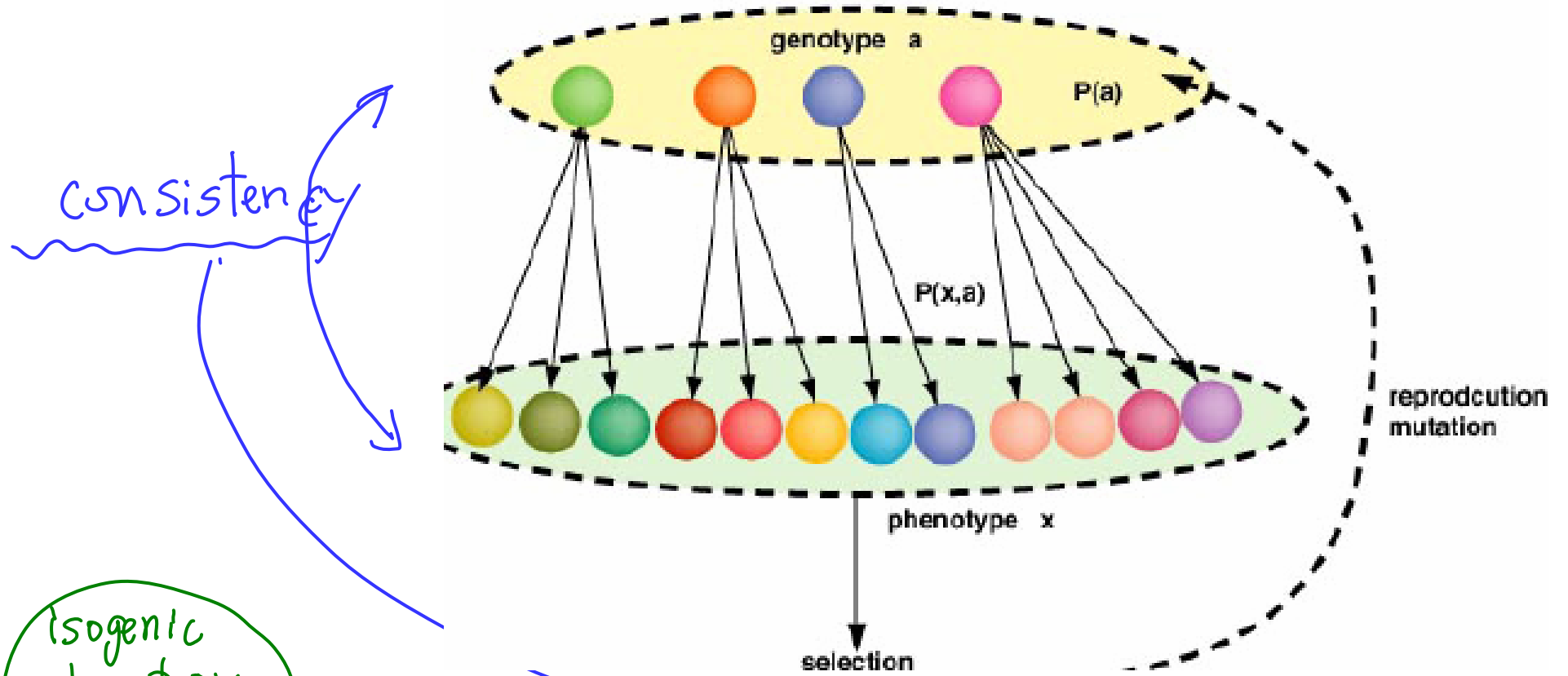
$$\bar{g}_n = \int g P_n(g) dg$$

$$P_{n+1}(g) = \frac{g P_n(g)}{\int g P_n(g) dg} = \frac{g P_n(g)}{\bar{g}_n}$$

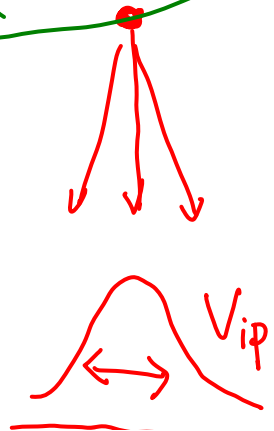
$$\begin{aligned} \bar{g}_{n+1} - \bar{g}_n &= \frac{\int g^2 P_n(g) dg}{\bar{g}_n} - \bar{g}_n = \frac{1}{\bar{g}_n} \left( \int g^2 P_n(g) dg - \left( \int g P_n(g) dg \right)^2 \right) \\ &= \frac{1}{\bar{g}_n} (\delta g_n)^2 \end{aligned}$$

(Fisher ?)



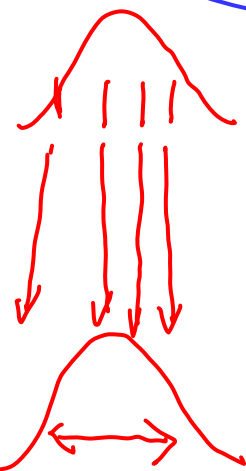


isogenic phenotypic fluct.



genotype (a)  
(same)

phenotype  $x$

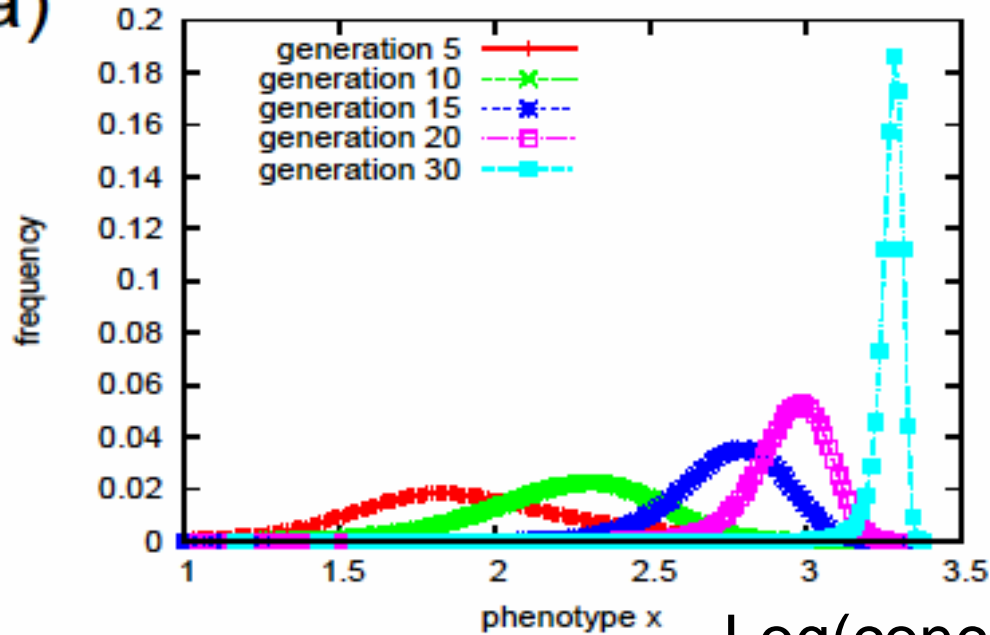


genotype (distributed)

$V_g$

evolution speed  
 $V_g \leftrightarrow$   
 $? V_{ip} ??$

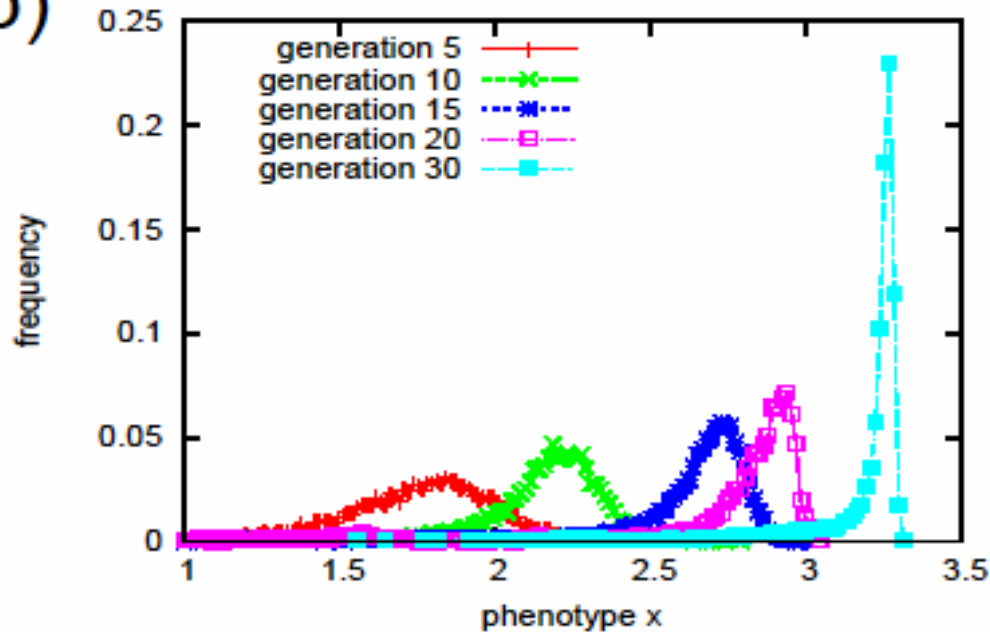
(a)



Change of distribution  
through evolution

Distribution of phenotype  
x of a clone  
→  $V_p$

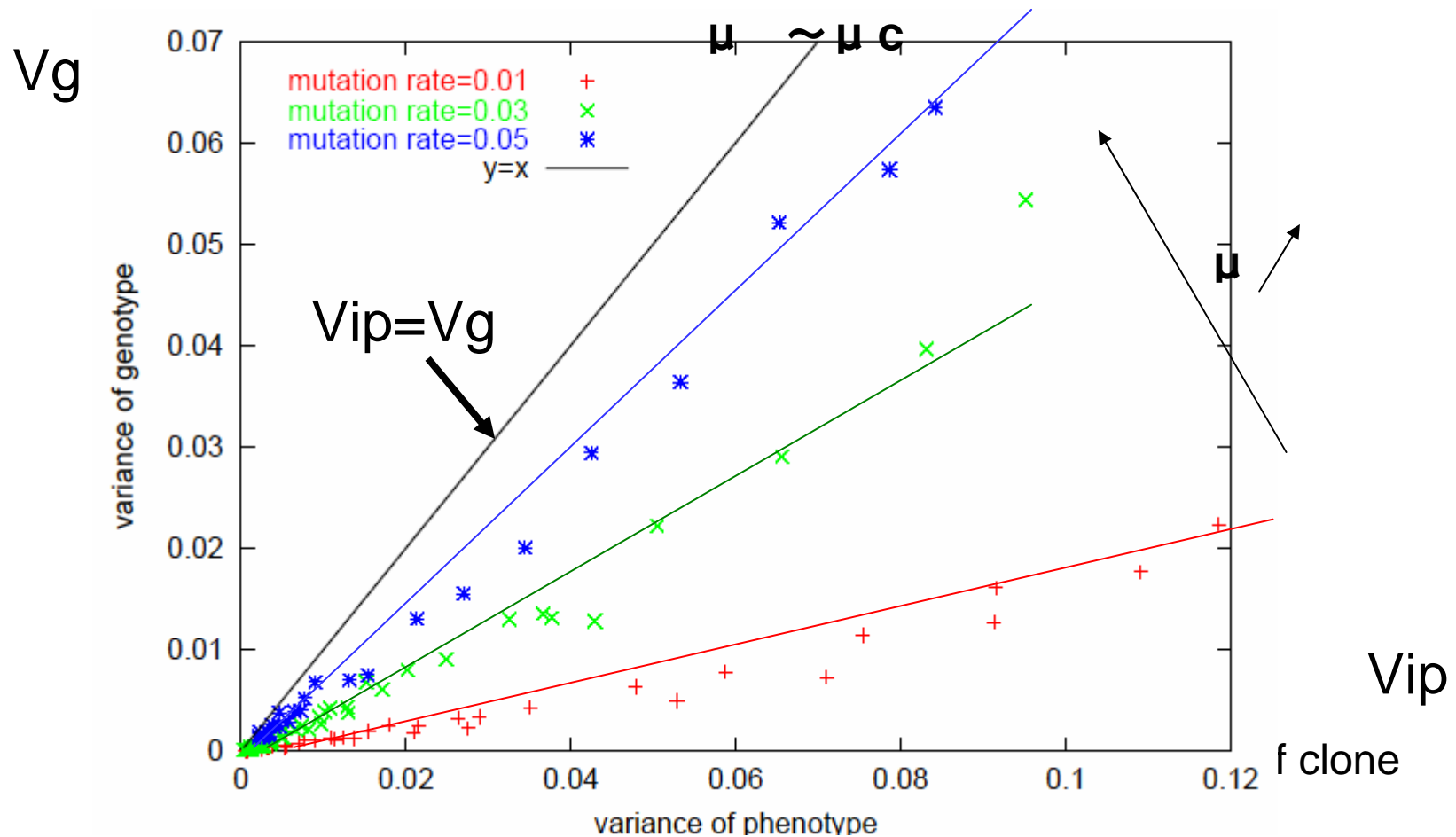
(b)



Distribution of phenotype  
x over mutants (genetic  
variation)  
→  $V_g$

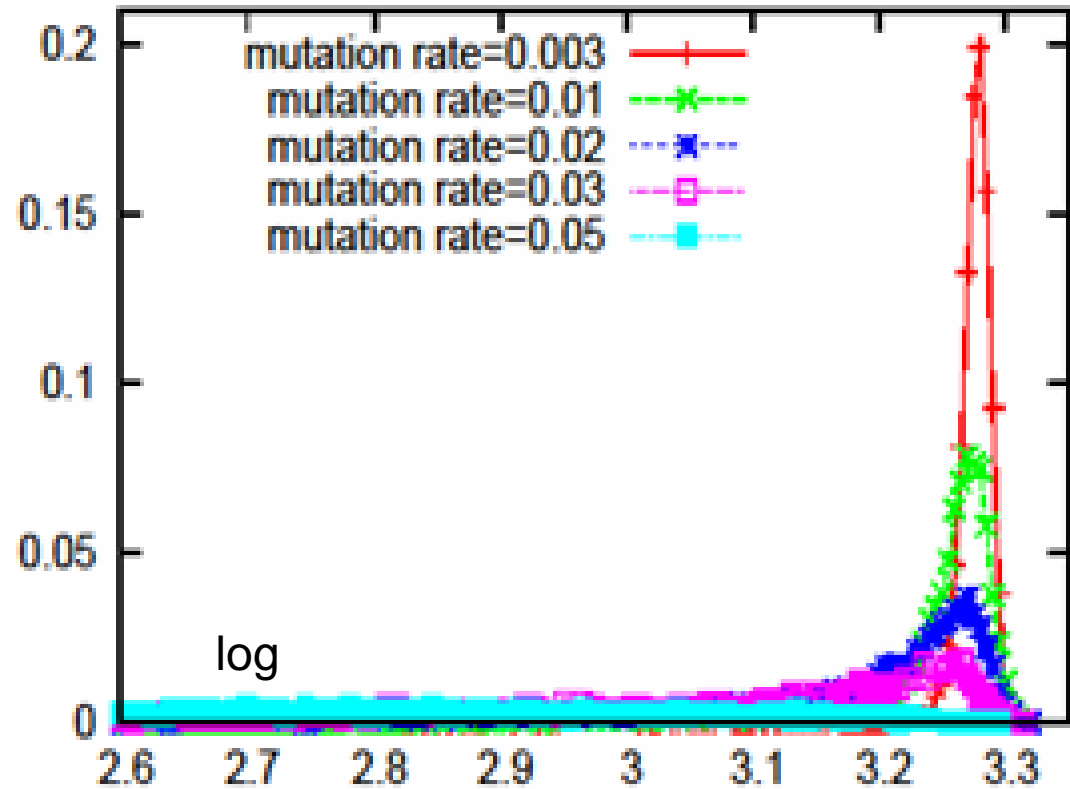
# Phenotype fluct. ( $V_p$ ) vs Gene Fluct. ( $V_g$ ) in the evolution of toy cell model

$V_p$ : fluct. for given network,  $V_g$ : fluct. by network variation



variance of  $\log(x)$ ,  $x$  is the concentration of the molecule  
 cf. also true for each molecules species (common proportional coefficient, (Furusawa, private comm.)

As mutation rate  $\mu$  is increased beyond  
 some value  $\mu_c$ ,  
 the peaked distribution collapses  $\rightarrow$  error catastrophe  
 low-fitness mutants dominate  $\rightarrow$   
 evolution does not progress  
 at  $\mu_c$   $V_{ip} \sim V_g$



Phenotype ; concentration of selected (target) chemical

Consider 2-variable distrib

$$P(x=\text{phenotype}, a=\text{genotype}) = \exp(-V(x, a))$$

Keep a single-peak (stability condition).

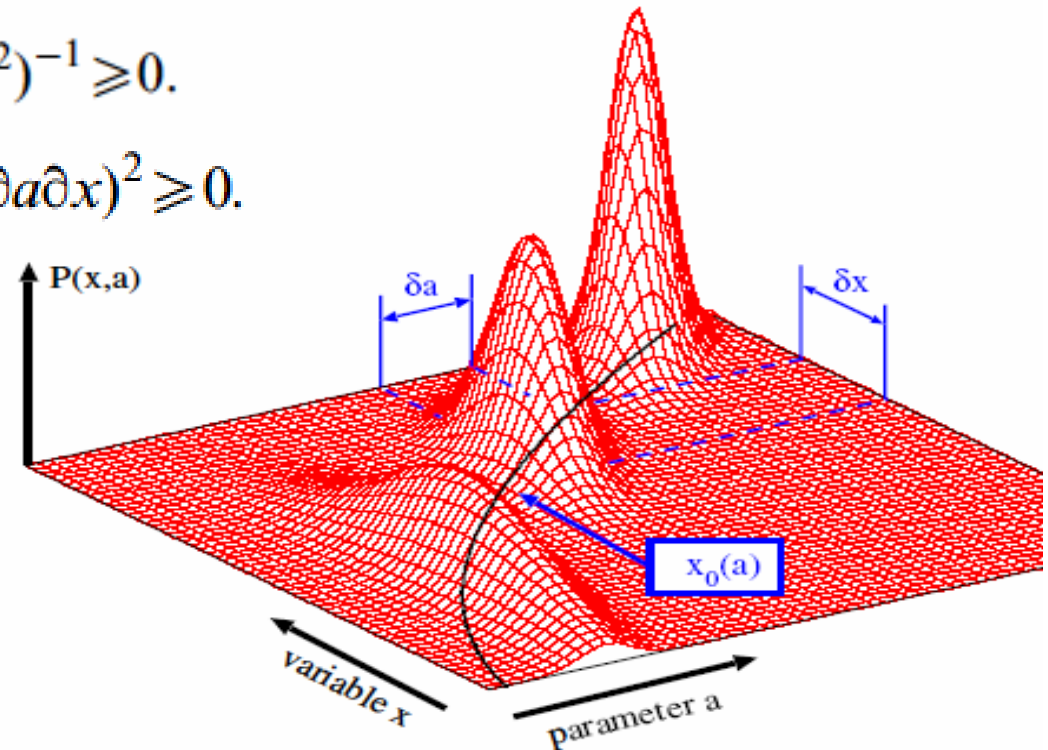
KK, Furusawa, 2006 JTB

$$(\partial^2 V / \partial a^2)^{-1} \geq 0; \quad (\partial^2 V / \partial x^2)^{-1} \geq 0.$$

$$(\partial^2 V / \partial x^2)(\partial^2 V / \partial a^2) - (\partial^2 V / \partial a \partial x)^2 \geq 0.$$

Hessian condition

Up to this point pheno (x) and geno (a) are treated in the same way. Then given a, the peak (average) phenotype is  $x_0(a)$  -- function of a --



$$\partial V / \partial x |_{x=x_0} = 0$$

Phenomenological Theory for these experimental observations?

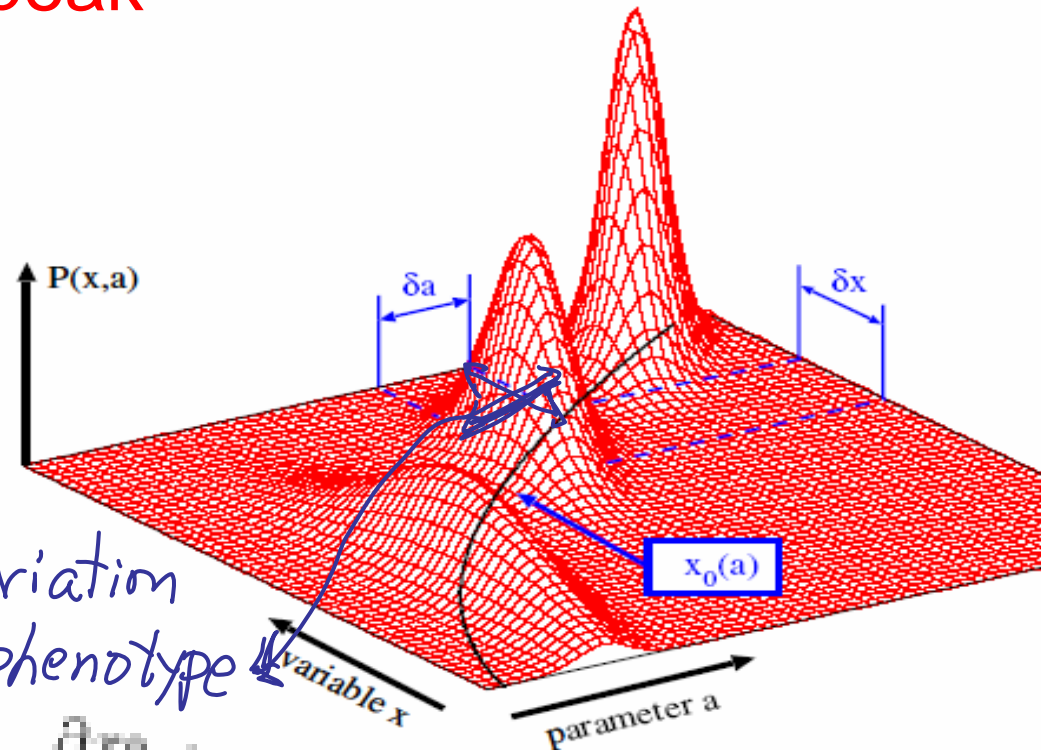
Consider P(phenotype,genotype) distribution  $P(x,a)$   
 or  $P(x,a)=\exp(-V(x,a))$

Condition to **keep single peak**  
 (evolutionary stability) .

$V_{ip}$  :  $\langle (\delta x)^2 \rangle$  of isogenic individuals

$V_{ig}$  : variance of  $x$  due to genetic variation for the identical phenotype

$$\langle (\bar{x}_a - \bar{x}_0)^2 \rangle = V_{ig} = \langle (\delta a)^2 \rangle \left( \frac{\partial x_0}{\partial a} \right)^2$$



$$P(x, a) = \widehat{N} \exp\left[-\frac{(x - X_0)^2}{2\alpha(a)} + \frac{C(a - a_0)(x - X_0)}{\alpha} - \frac{1}{2\mu}(a - a_0)^2\right]$$



$$P(x, a) = \widehat{N} \exp\left[-\frac{(x - X_0 - C(a - a_0))^2}{2\alpha(a)} + \left(\frac{C^2}{2\alpha(a)} - \frac{1}{2\mu}\right)(a - a_0)^2\right].$$

$$\mu \leq \frac{\alpha}{C^2} \equiv \mu_{max}.$$

$$\bar{x}_a \equiv \int x P(x, a) dx = X_0 + C(a - a_0).$$

$$V_g = \frac{\mu C^2}{1 - \mu C^2 / \alpha}$$

$$\overline{V_{ip}} = \frac{\alpha}{1 - \mu C^2 / \alpha}$$

$$\overline{V_{ip}} / V_g = \alpha / (\mu C^2)$$

= Ave over all populations

$$V_g \leq \overline{V_{ip}}.$$

$$V_{ig} = \frac{\mu}{\mu_{max}} \overline{V_{ip}}$$

From Stability condition  $\rightarrow$   $V_{ip} \geq V_{ig}$  is derived

$V_g$  increases with the mutation rate

if the increase continues, there is critical mutation rate

$\mu_c$  at which  $V_{ip} \sim V_{ig}$

Error catastrophe  $\rightarrow$  evolution stops

Here,  $V_{ig} \neq V_g$

$V_{ig}$  for distribution for a given phenotype

$V_g$  for all population

but for small  $\mu$

OR def  $V_p$  as average of  $V_{ip}$ ,  
Then  $V_p \geq V_g$

$$V_g \approx V_{ig} \approx \frac{\mu}{\mu_c} V_{ip}$$



$$\mu V_{ip} \propto V_g \propto \text{evolution speed}$$

consistent



• (i)  $V_{ip} \geq V_g$  (from stability condition) (\*\*)

(ii) error catastrophe at  $V_{ip} \sim V_g$  (\*\*)

(where the evolution does not progress)

(iii)  $V_g \sim (\mu / \mu_{max}) V_{ip} \propto \mu V_{ip}$

( $\propto$  evolution speed) at least for small  $\mu$

\* \* Consistent with the experiments, but,,,,,

Existence of  $P(x,a)$  assumption ??;

+ Robust Evolution assumption ?? +

Why isogenetic phenotypic fluctuation leads to robust evolution?

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(\*\*) to be precisely  $V_{ig}$ , variance those from a given phenotype  $x$ : but  $V_{ig} \sim V_g$  if  $\mu$  is small

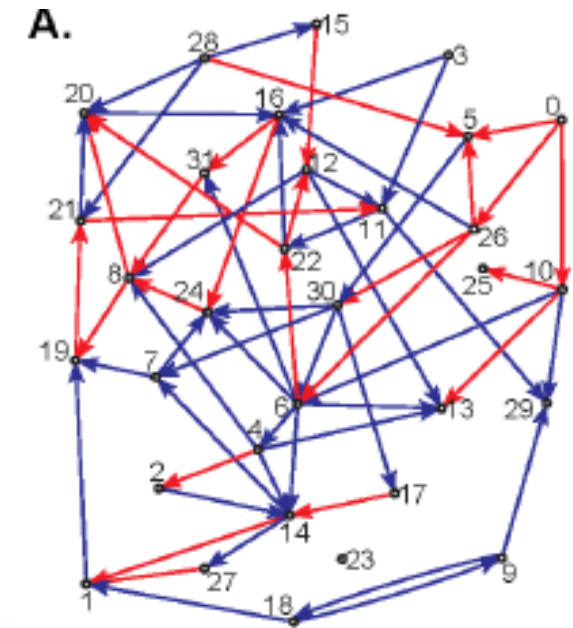
# Gene expression dynamics model: Relevance of Noise to evolution?

Simple Model: Gene-net (dynamics of stochastic gene expression)  $\rightarrow$  on/off state

$X_i$  – expression of gene  $i$  :  
on off

$$\frac{dx_i}{dt} = \tanh\left[\beta \sum_{j>k} J_{ij} x_j\right] - x_i + \sigma \eta_i(t),$$

$$\langle \eta_i(t) \eta_j(t') \rangle = \delta(t - t') \cdot \delta_{ij}$$



Activation  
Repression  
 $J_{ij} = 1, -1, 0$

**Gaussian white**

**M**; total number of genes, **k** : output genes

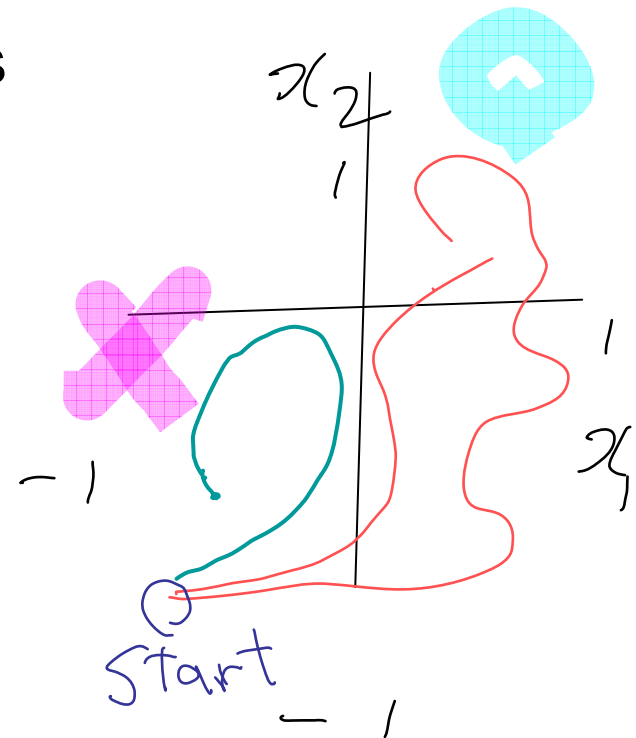
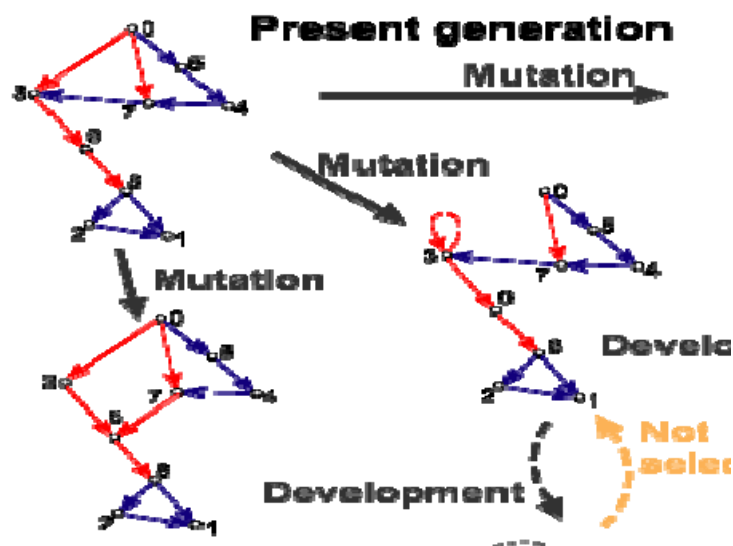
**Noise strength  $\sigma$**

- Fitness: Starting from off of all genes, after development genes  $x_i$   $i=1, 2, \dots, k$  should be on (Target Gene Pattern)

Fitness  $F = -$  (Number of off  $x_i$ )

## Genetic Algorithm

Mutate networks and Select those with higher  $\langle F \rangle$   
 Choose top  $n$  networks among total  $N$ ,  
 and mutate with rate  $\mu$  to keep  $N$  networks



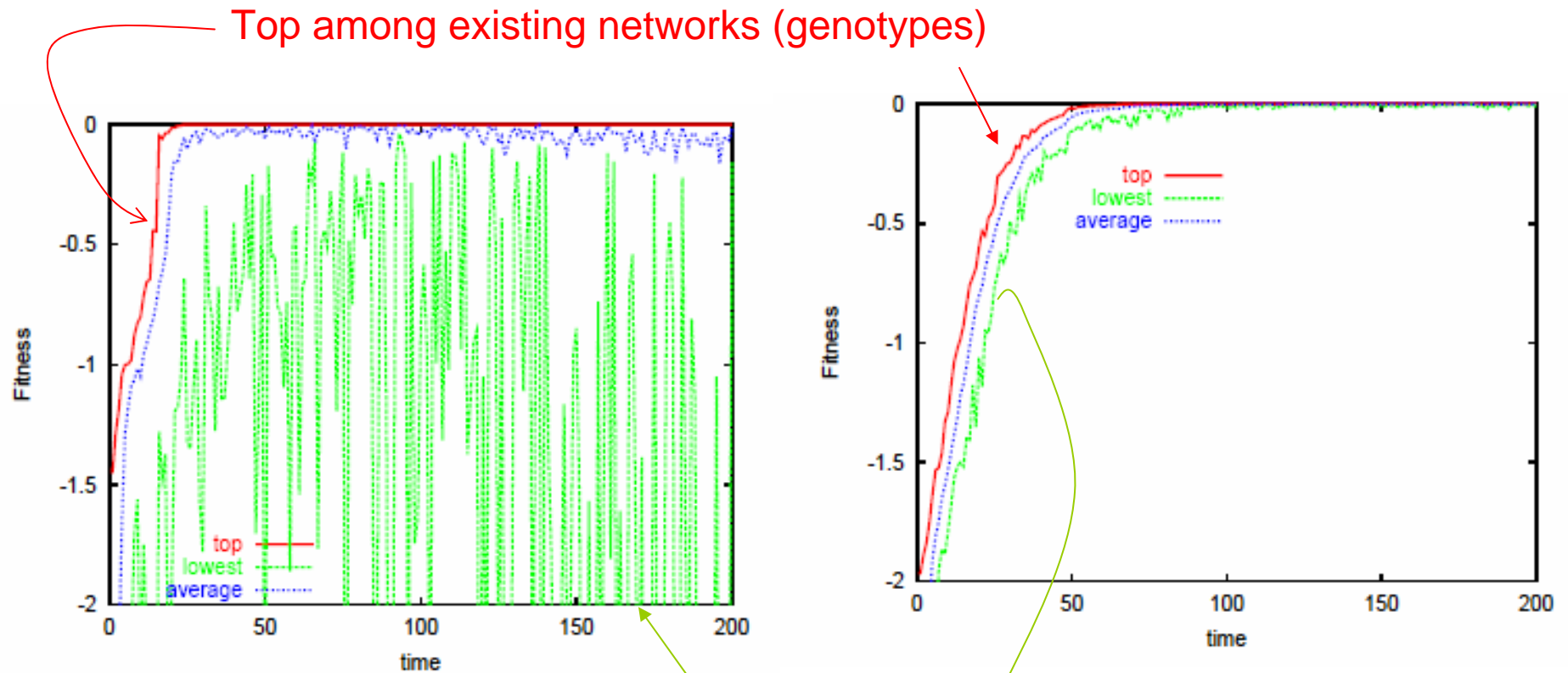
# Result of evolution

Top:reaches the fittest

faster for lower noise( $\sigma$ )

Lowest; cannot evolve

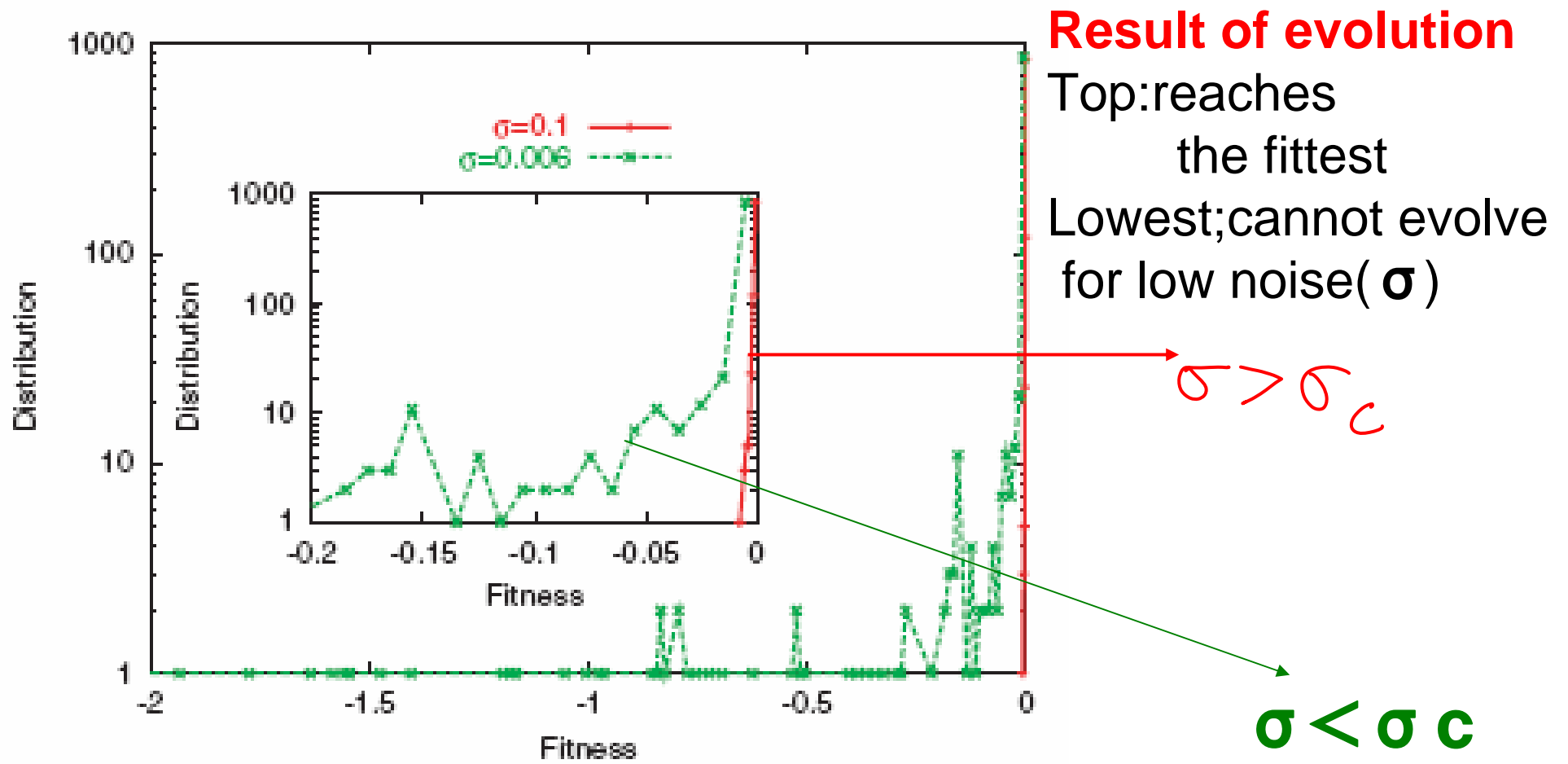
for low noise( $\sigma$ )



Low Noise case

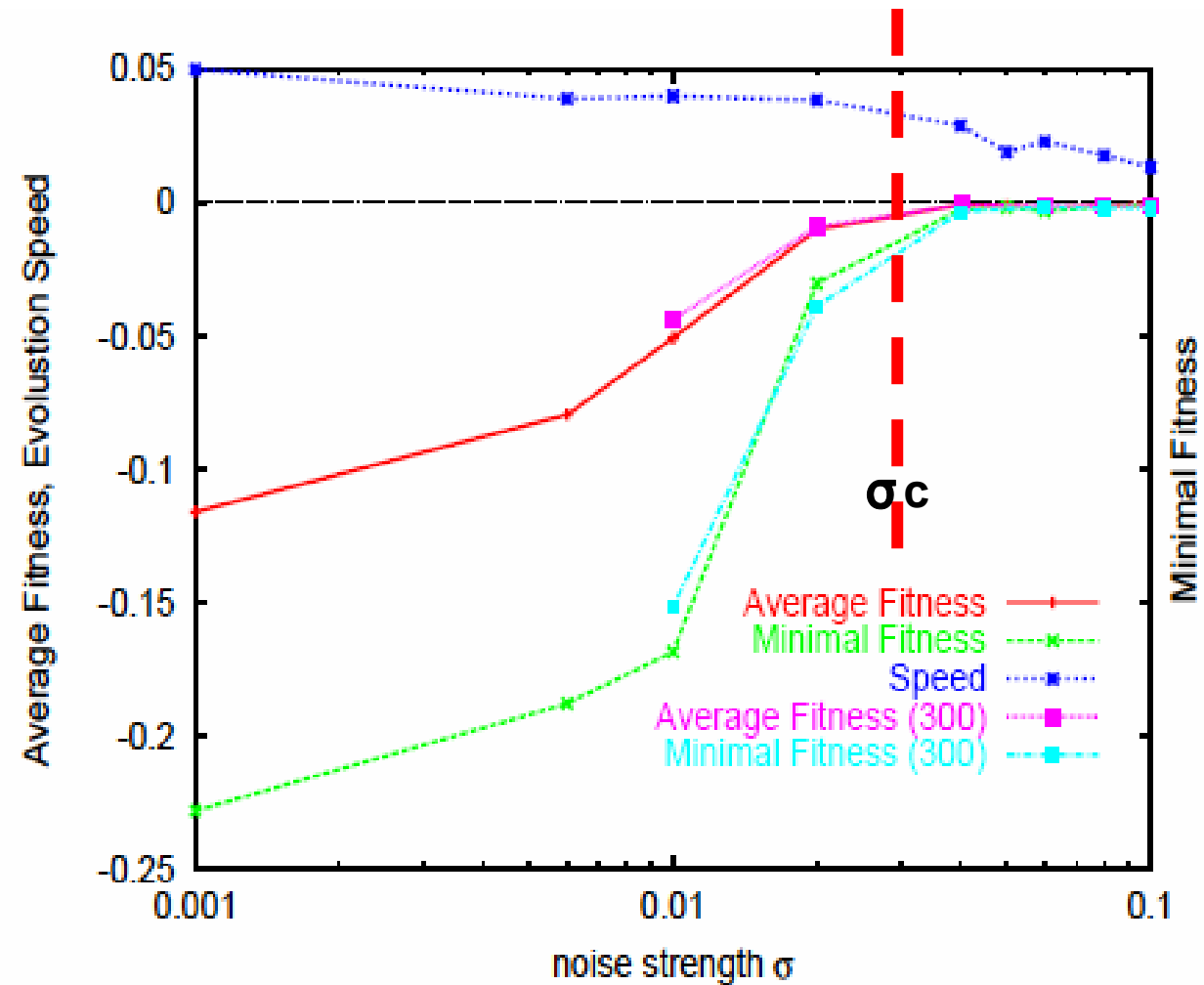
Lowest among genotypes

High Noise case



### Fitness Distribution

$\sigma < \sigma_c$  --low fitness mutants distributed  
 $\sigma > \sigma_c$  — eliminated through evolution



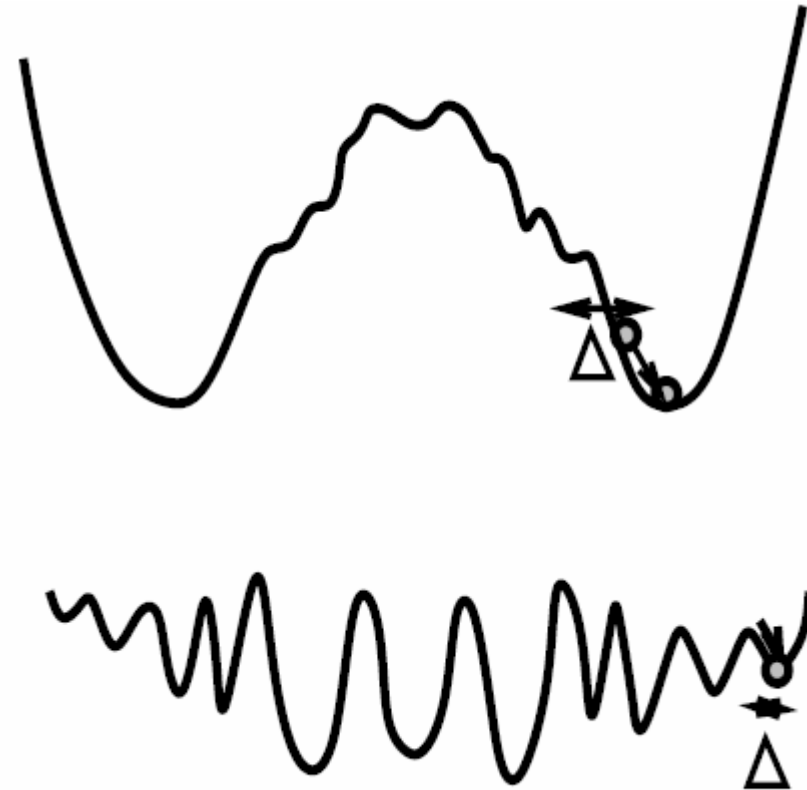
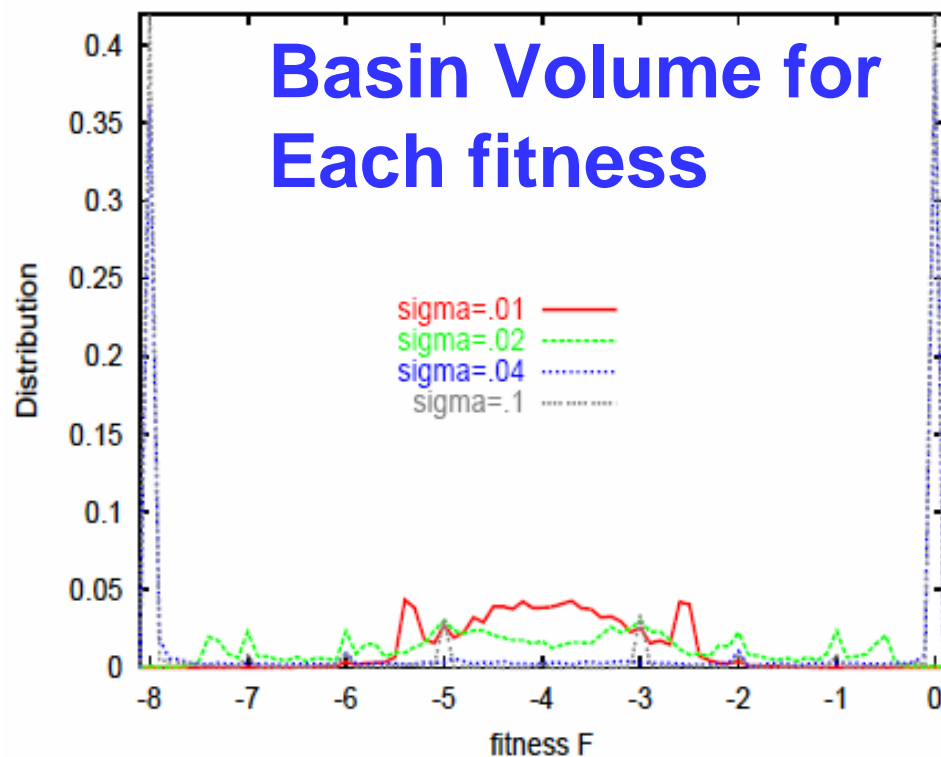
**Existence of critical noise level  $\sigma_c$   
below which low-fitness mutants accumulate  
(error catastrophe)**



Why?; difference in basin structure

$\sigma > \sigma_c \rightarrow$  large basin for target attractor  
(robust,  $\Delta$  (distance to basin boundary)  $\uparrow$ )

$\sigma < \sigma_c \rightarrow$  only tiny basin around target orbit  
 $\Delta$  remains small



$\rightarrow$  Global constraint to potential landscape (funnel?)

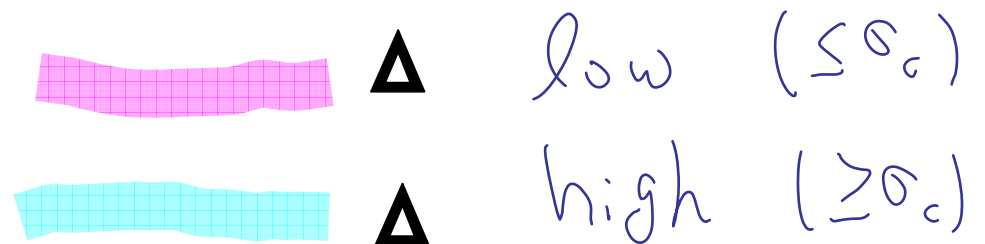
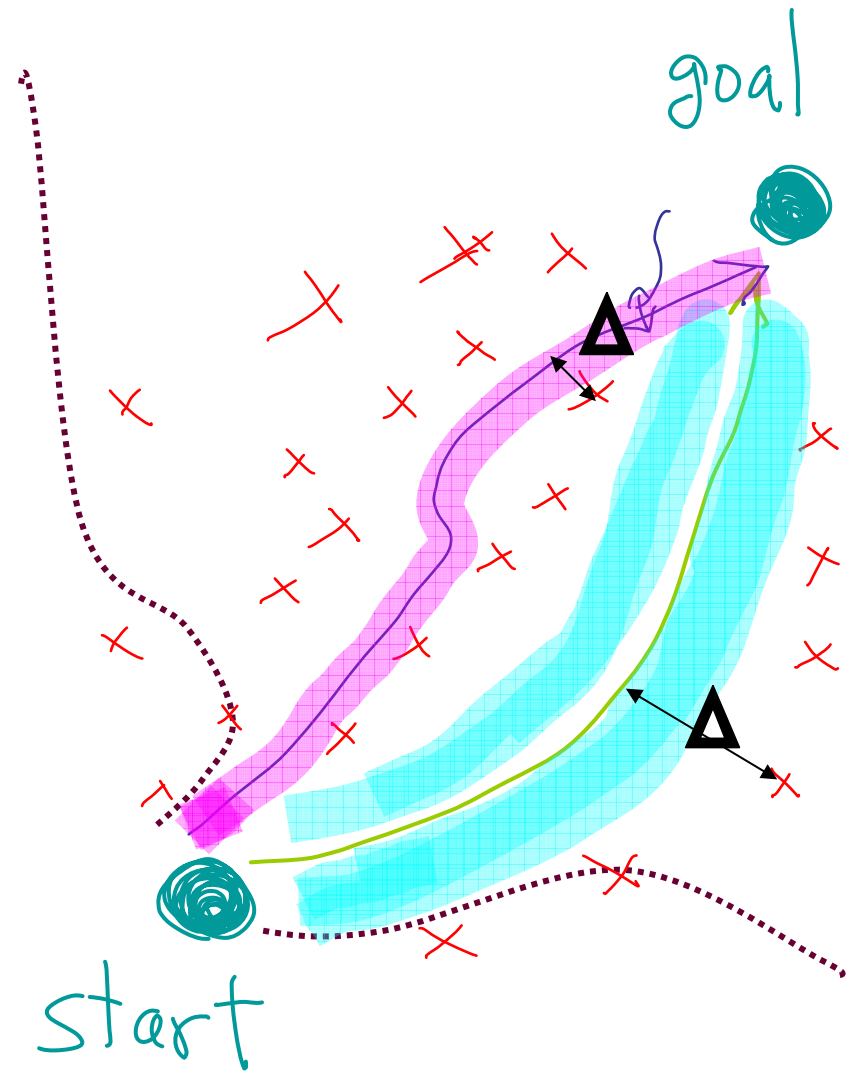


why threshold?

choose paths to avoid turning  
pts within  $\sigma$  (noise)

Mutation  $\rightarrow$  touches turning  
points within range of  $\mu$

small  $\sigma \rightarrow$   
an orbit with small  $\Delta$   
can reach the target



# Discussion: Evolution of Robustness

- Robustness ----- Insensitivity of Fitness (Phenotype) to system's change

← against noise during 'developmental process

← against parameter change by mutation

- Developmental Robustness to noise ----  $V_{ip}$
- Robustness to mutation in evolution ----  $V_g$

For  $\sigma > \sigma_c$ , both decrease, i.e., robustness ↗

Noise is necessary for evolution of robustness

$V_{ip} \propto V_g \rightarrow$  Developmental robustness and genetic (evolutionary) robustness are linked (or embedded)

WADDINGTON genetic assimilation

? Extension of Structural Stability Needed?

- Generality of our result; For a system satisfying:
  - (1) fitness is determined after developmental dynamics
  - (2) developmental dynamics is complex
  - (3) effective equivalence between mutations and noise with regards to the consequence to fitness
- under noise smooth dynamic landscape is formed ('Funnel')

# Symbiotic Sympatric Speciation

Kk, Yomo2000  
ProcRoySoc

- So far, no interaction, evolution under fixed environment -- – single-peaked distribution
- Speciation → change to double peaked distribution
- \*\* **Allopatric vs Sympatric ( S fundamental? Difficult?)**
- Our scenario for sympatric speciation (confirmed by several models):
  - (1) Isologous diversification ( **interaction-induced phenotype differentiation**);

homogeneous state is destabilized by the interaction  
e.g., by the increase in resources
  - (2) **Amplification of the difference through geno-pheno relation**

Two groups form symbiotic relationship, and coevolve
  - (3) **Genetic Fixation and Isolation of Differentiated Group**

consolidated to genotypes

## Model with Evolution :

Each unit Phenotype :: Variable  $X = (X_1, X_2, \dots, X_k)$

Gene :: Parameter in the model e.g., reaction rate  
 $(g_1, g_2, \dots, g_k)$

Parameter  Variable (dynamical systems)  
 $X(t=0) \rightarrow X(t)$

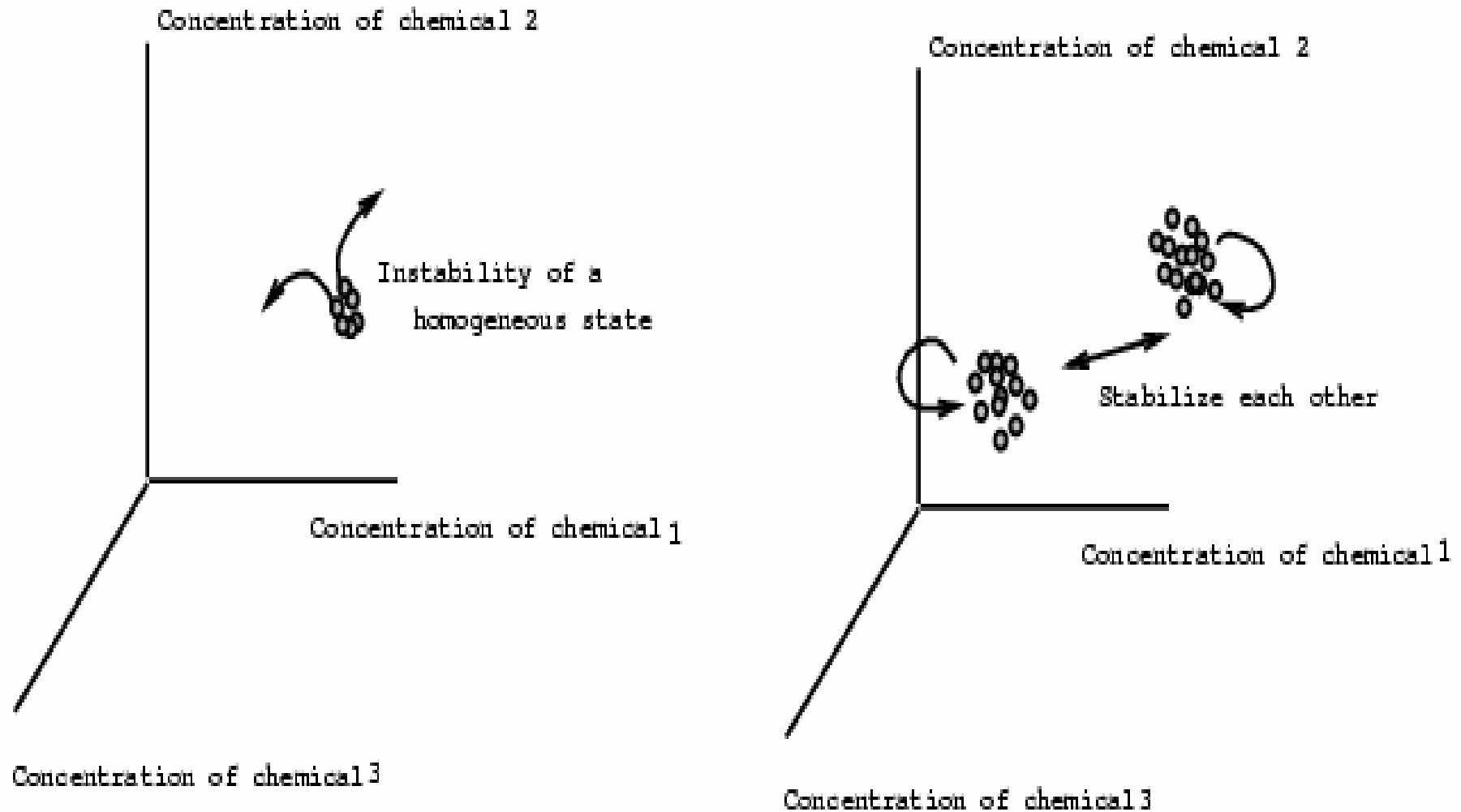
Reproduction when maturity threshold condition  
(given by  $X$ ) is satisfied

Mutation ---- small change in parameter in reproduction

Competition for survival:

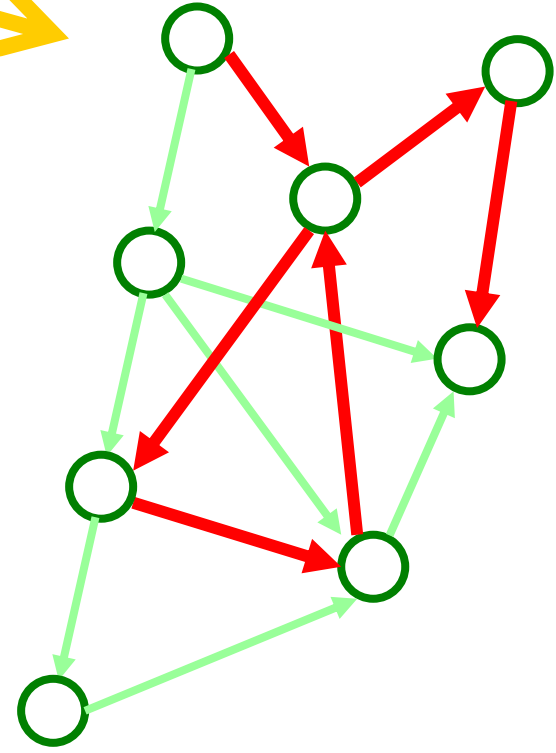
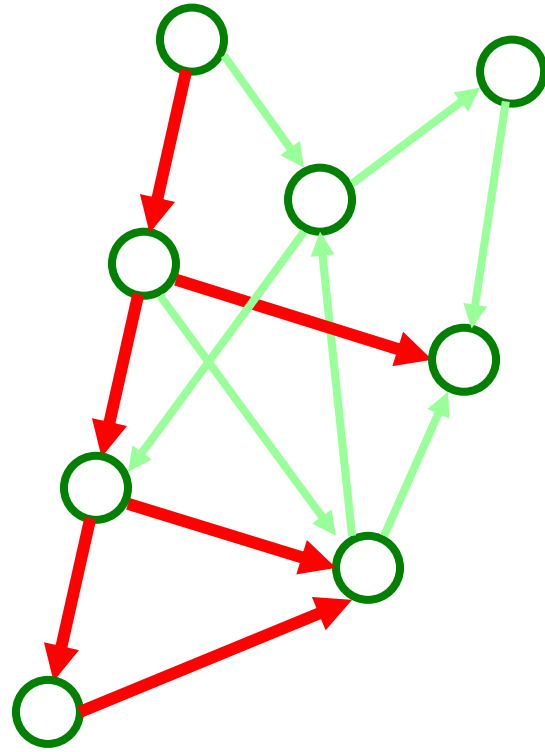
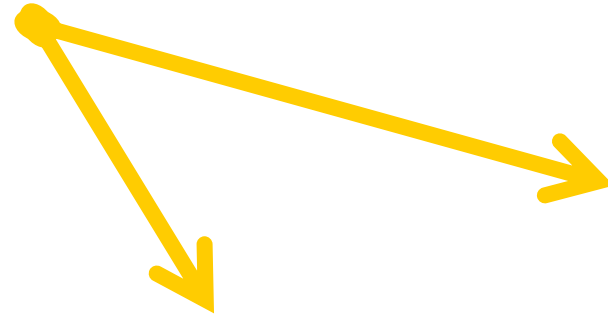
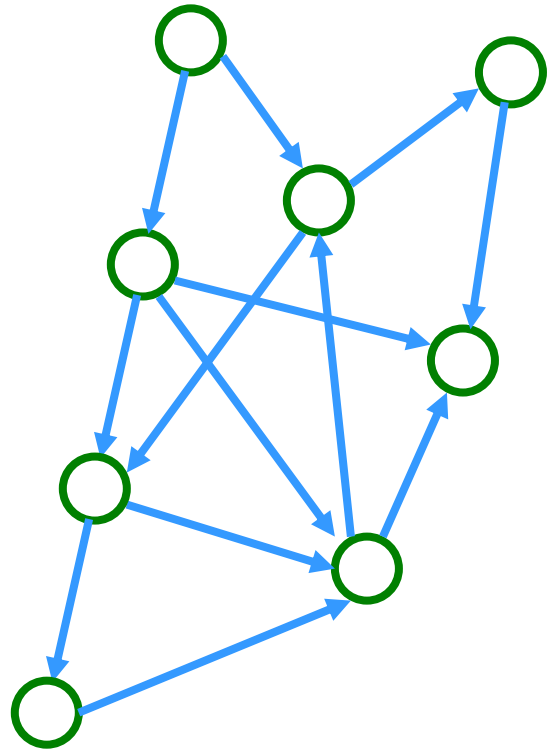
( remove some units (either randomly or under some condition))

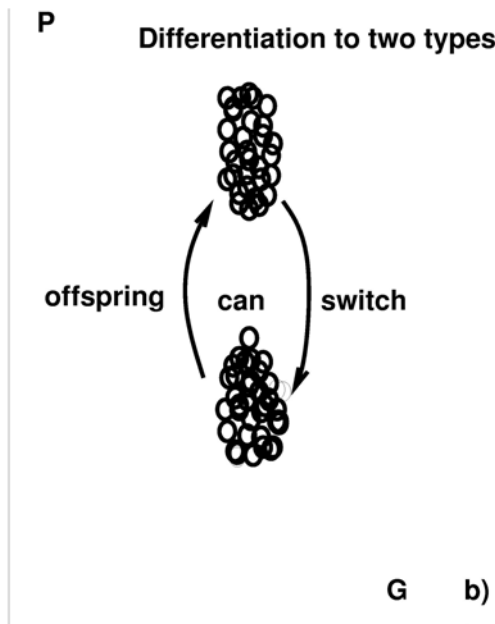
→ With the increase of the number



Distinct types are formed through instability in 'developmental dynamics' and interaction (both types are necessary)

Differentiation of role; use of different paths

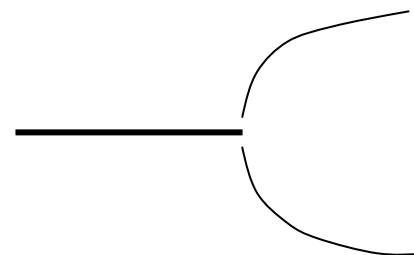
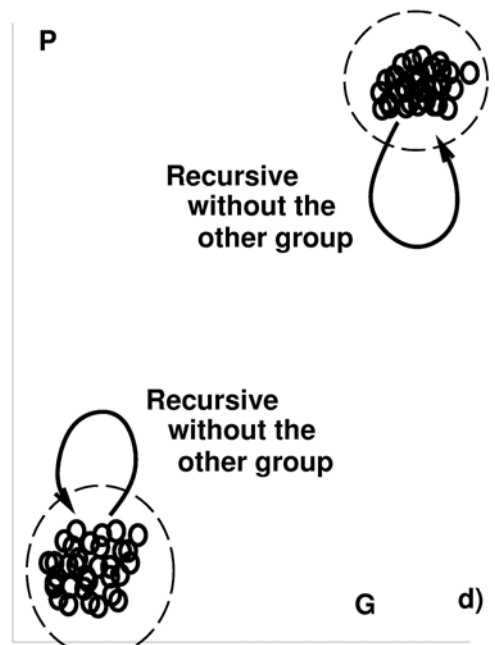
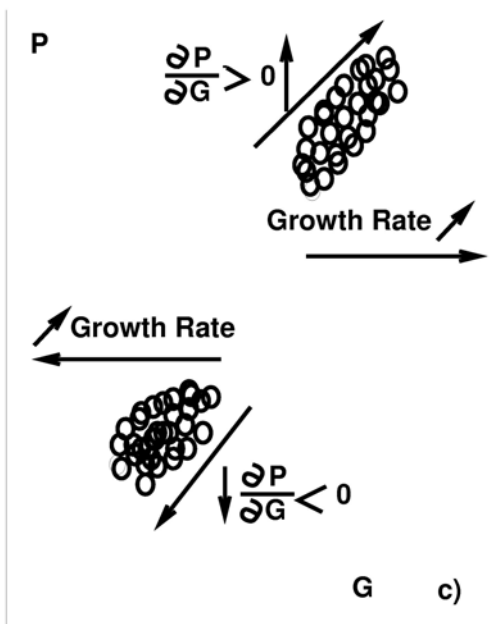




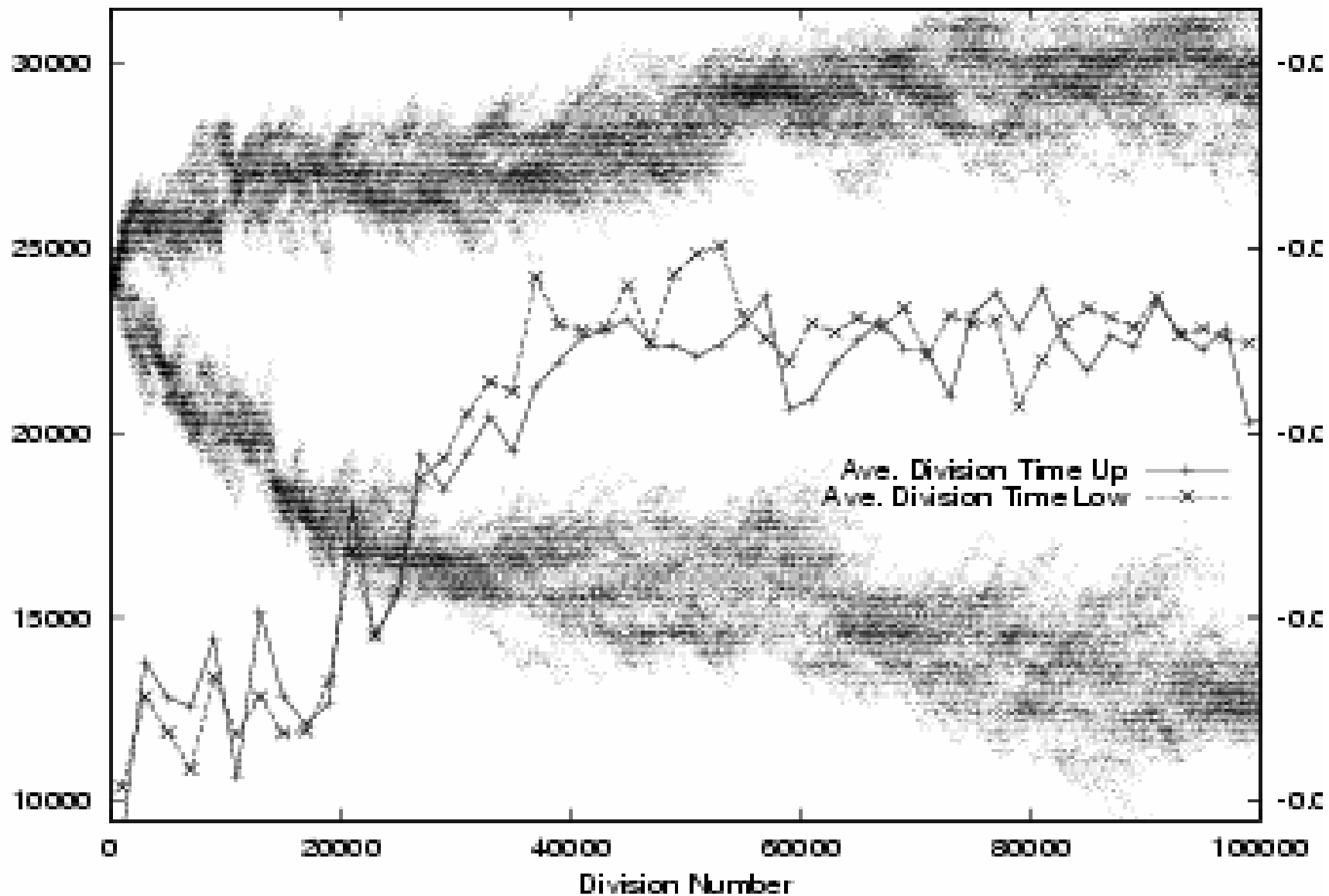
Cf: pitchfork possible

$$dX_i/dt = aX_i - X_i^3 - (\sum_j X_j)^2 X_i$$

a increases with # of units

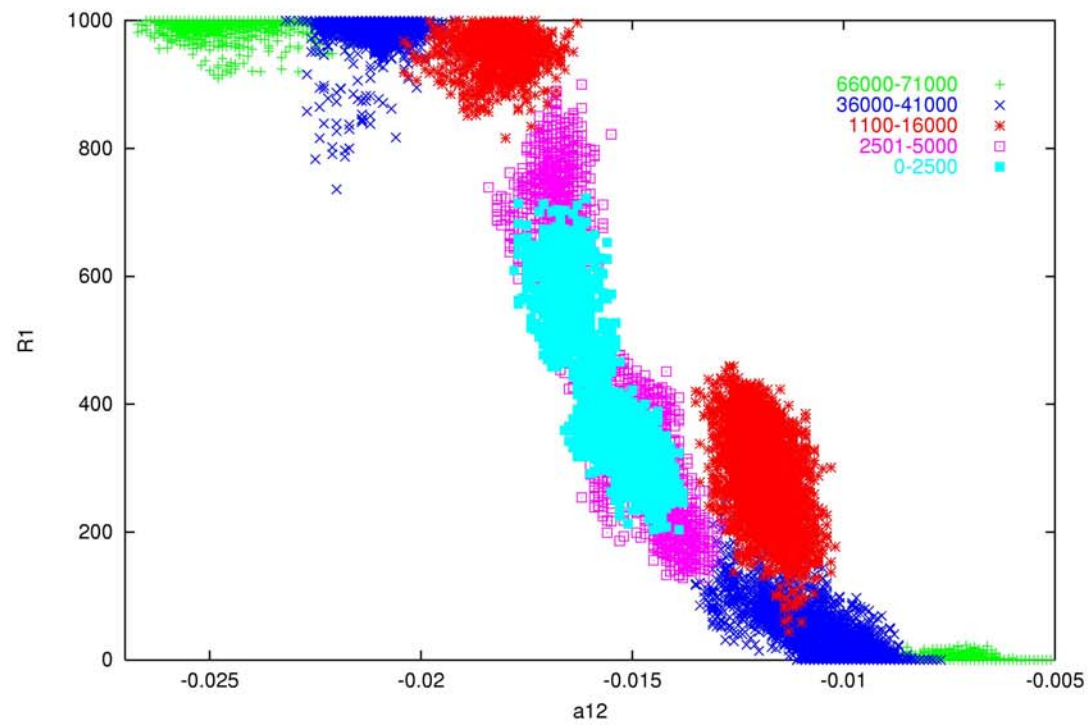






# Example of numerical simulation

Phenotype(variable)

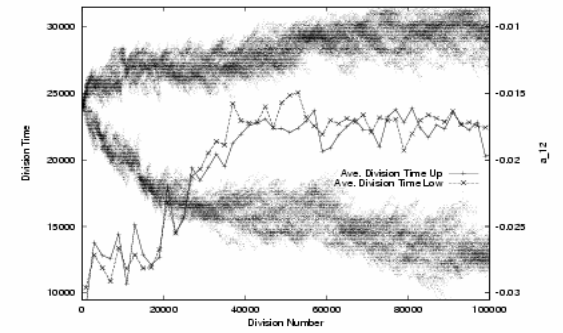
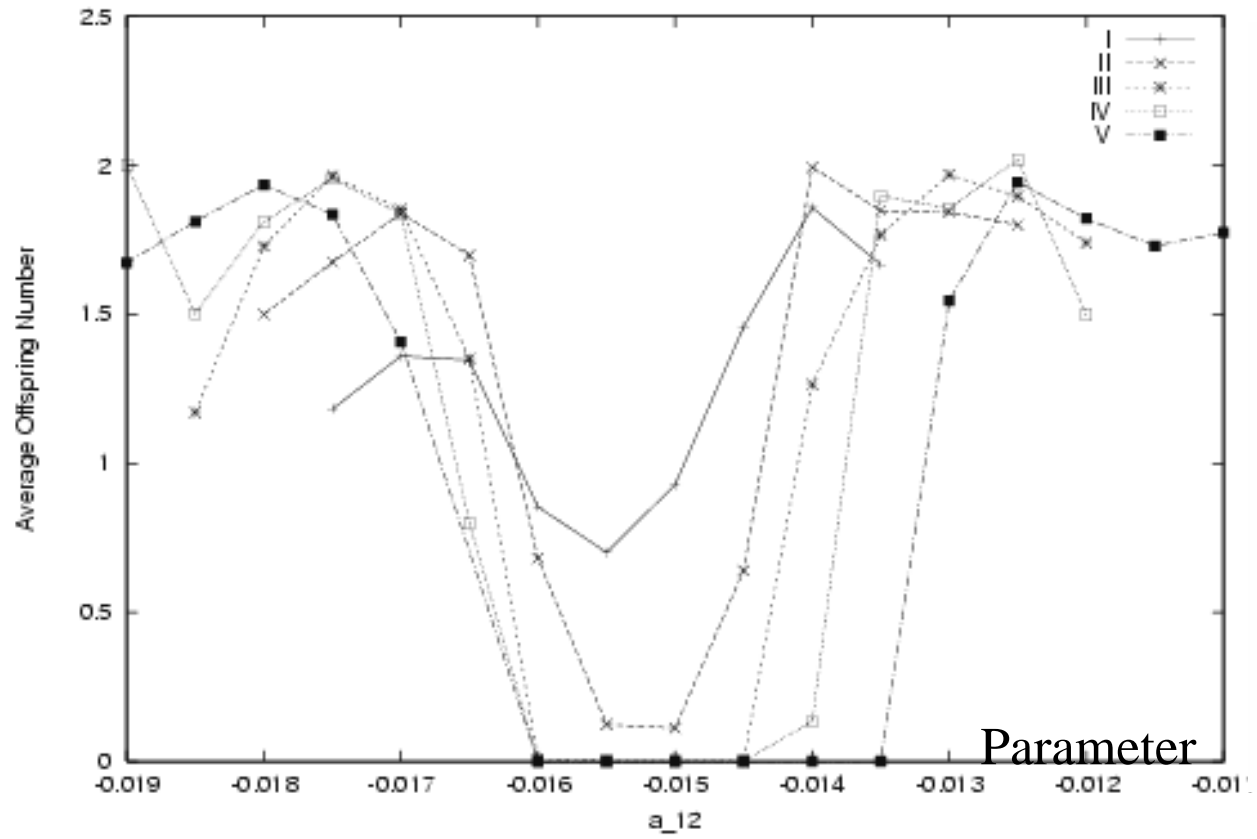


Gene (parameter)

## Characteristics of the Symbiotic Sympatric Speciation

- \*Valid (possible) in the presence of strong interaction
- \*Robust speciation; two groups coevolve; works under sexual and asexual cases as well (indeed, hybrid sterility is resulted)
- \*Genetic separation always follows if there appears interaction-induced phenotypic differentiation
- \*Relevance of the phenotypic differentiation, rather than genetic change, to genetic diversification (cf Baldwin effect or genetic assimilation)

Stage  
 I → II → III → IV → V

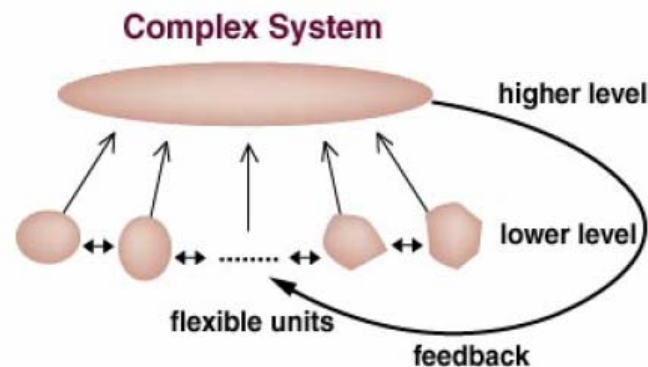


# Complex Systems Biology

Understand **Universal** features of Biological System with

--Mutual dependence between parts and whole (dynamic, flexible, and reproducible)

## Consistency between different levels



dynamic

