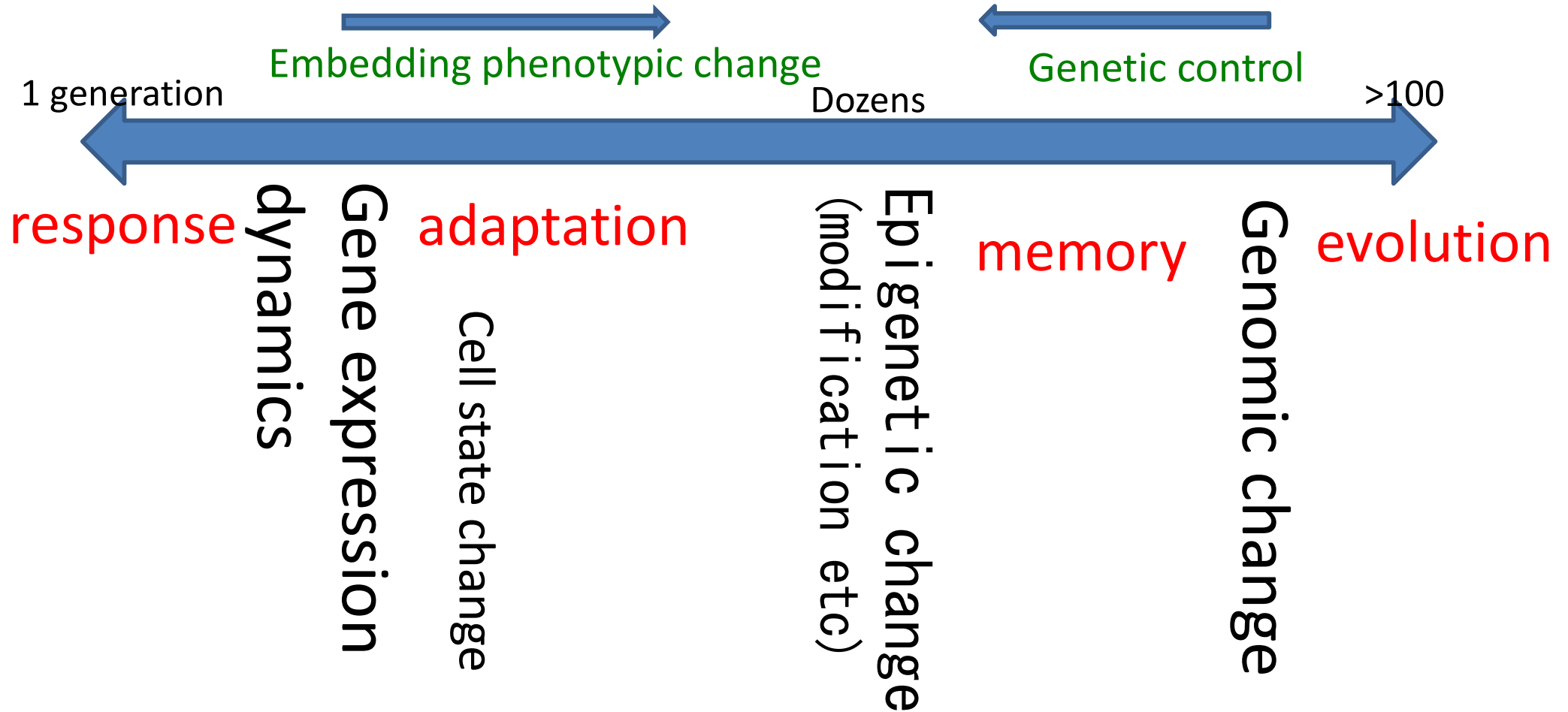


# Evolutionary Fluctuation Response Relationship, Evolution of Phenotypic Robustness

(skip some pages ,last part)

# Consistency between Developmental Process and Evolution (Evo-Devo Congruence)

Micro-Macro : Multiple-time scale dynamics



**\* Consistency between dynamics with distinct time scales**

Macroscopic relationship among plasticity,  
robustness, evolvability, and phenotypic fluctuations:  
Waddington's legacy revisited under the spirit of Einstein

Kunihiko Kaneko Univ of Tokyo+

ERATO complex systems biology

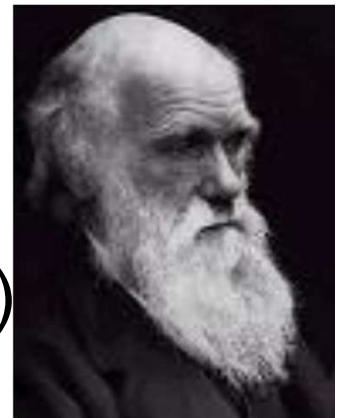
- 1 Phenotypic Fluctuation (Plasticity) vs Evolution
- 2 Phenotypic Fluctuation vs Genetic Variation**
- 3 Evolution of Robustness to Developmental Noise and to Mutation
- 4 Regaining Plasticity and Evolvability**

cf selection of dynamical systems

by dynamical systems for dynamical systems

Darwin and Lincoln

(born on the same day, Feb.12 1809)



- Evolution

1) Genotype (rule for developmental dynamical systems)

2) only genotype is transferred to offspring (in most cases,,)

3) Phenotype  $\leftarrow$  Development dynamics  
Genotype-Phenotype mapping

4) Fitness(phenotype)  $\rightarrow$   
selection process in the distribution

Now, genotype  $\rightarrow$  phenotype

$\rightarrow$  if this mapping is uniquely determined

$\rightarrow$  Fitness(Genotype) instead

- Cf;

- 1) Non-genetic inheritance is possible in principle: ( 'eigenetic memory' typical in unicellular-organism. Protein concentration. Methylation, Histone modification, Membrane..)
- 2) Just time-scale difference? ~10 generation memory is typical in bacteria?
- 3) Lamarckism would be possible, but it seems it is avoided (eg., germ-line segregation):  
If one phenotype was successful in one generation, it may not be so for the next generation, especially when all adopt the same phenotypes

Evolution= change in  
Population of geneotypes  
("Population genetics")

But gene—`development`  
→Phenotype

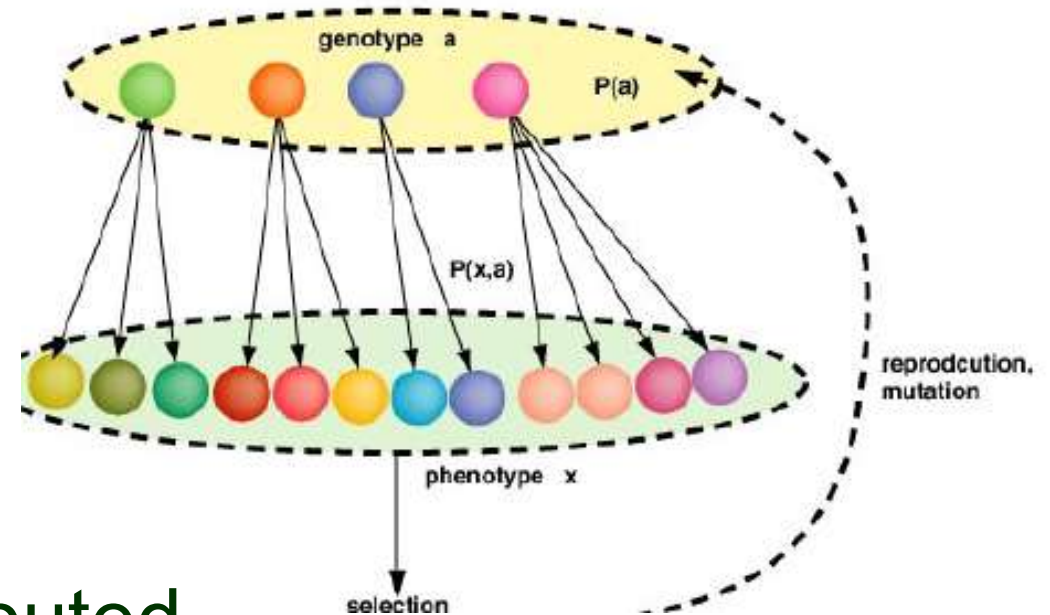
geno-pheno mapping distributed

Phenotypic fluctuation of isogenic organisms

$P(x; a)$   $x$ —phenotype,  $a$  – gene

Ensemble of dynamical Systems

Change of distribution of DS according to the  
Behavior of DS

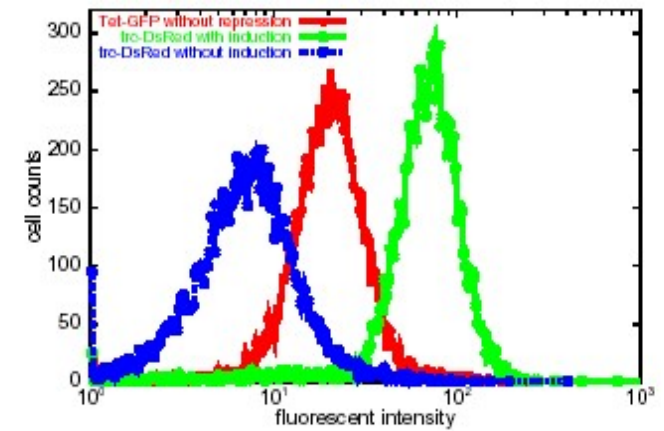


- **Motivatio1:Evolvability?** Some species are faster to evolve? -- ‘Ambiguous question’. Quantitative discussion by simplifying the issue?

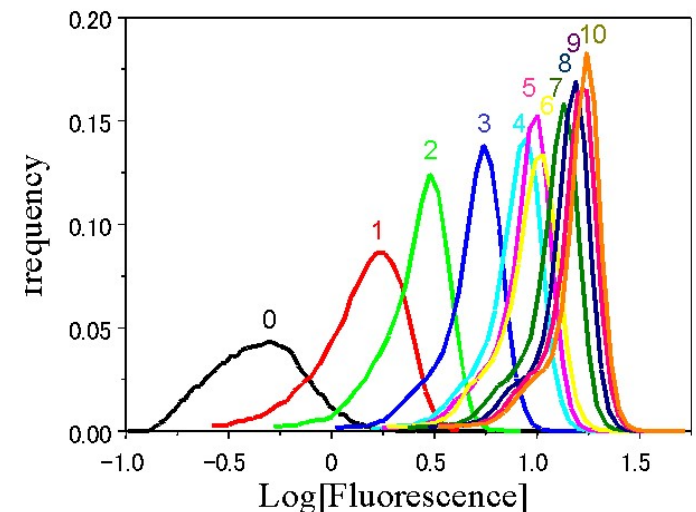
- Phenotypic Fluctuation → gives a measure for Evolution?

- Even in isogenic individuals large phenotypic fluctuation (theory, experiments)

- **Motivation1** Relevance of this fluctuation to evolution? Positive role of noise?



number distribution of the proteins measured by fluorescent intensity. from Escherichia coli cell populations containing different reporter plasmids



# Motivation2: Evolution of Robustness

- Robustness ----- Insensitivity of Fitness (Phenotype) to system's change
  - ← due to environmental change
  - ← against noise during 'developmental process
  - ← against parameter change by mutation

\*Question :

relationship among these robustness  
condition for evolution of robustness

---

Connect Motivation 1 and 2:

Study evolvability, robustness, in terms of phenotypic fluctuations

→ Insight into Geno-pheno coupling

(Waddington;;, Ancestral-Fontana.Wagner,..)



- General Viewpoint:

x: phenotype (variable)

a: genotype (parameter)

parameter → variable: condition (1)

central dogma of molecular biology

a: scalar continuous parameter showing gene (say, number of matched sequences etc.)

for given direction of specific function,

x is distributed even if gene (a) is specified

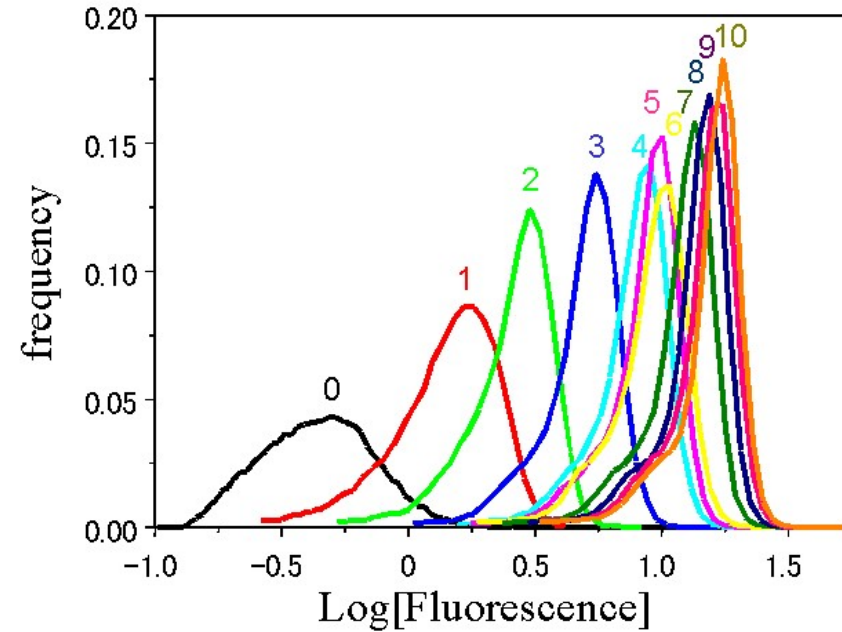
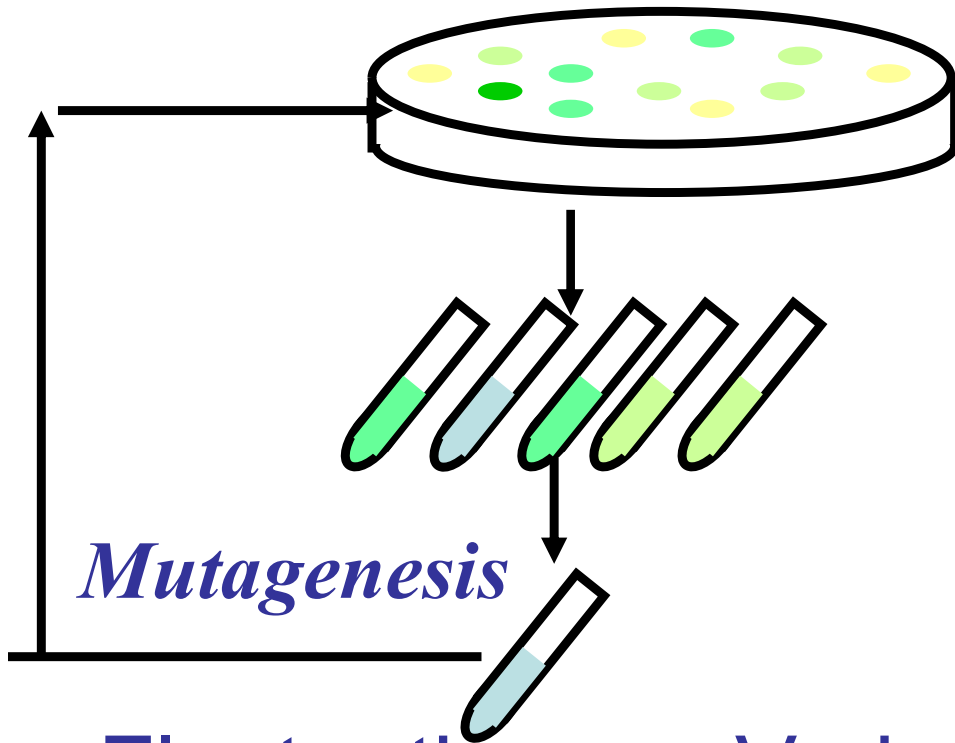
consider  $P(x;a;h)$  under given environment h

Environment h change to select 'a' value

selection : change in distribution with a

# Artificial selection experiment with bacteria

Selection to increase the fluorescence of protein in bacter



Fluctuation ---- Variance of phenotype of clone

Larger phenotypic fluctuation

---higher evolution speed ?

-

Sato, etal  
PNAS(2003)

So-called **fluctuation-response relationship** 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's paper a century ago...

**Generalization::(mathematical formulation)**

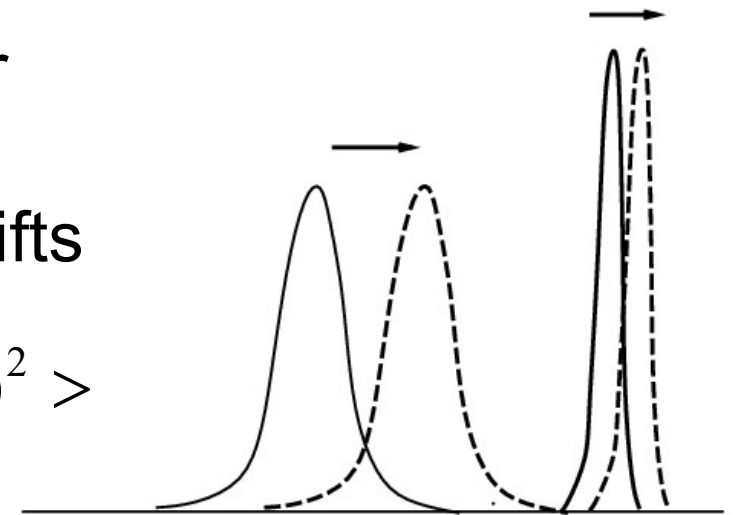
**response ratio of some variable  $x$  against the change of parameter  $a$  versus fluctuation of  $x$**

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

change of the parameter  $a \rightarrow$

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

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



-- "Response against mutation+selection" -- 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 ;

Non-trivial point

(1) Assumption of representation by  $P(x;a)$

$x$  : phenotype     $a$  ; gene (or control parameter)

(2) The coupling form  $Cxa$  is also assumption

→ Not derivation, but need to check experimentally

Artificial selection experiment with bacteria  
for enzyme with higher catalytic activity  
for some protein with higher function

Change in gene (parameter;  $a$ )  $\Rightarrow$

“Response” ----- change of phenotype  $\langle x \rangle$

(e.g., fluorescence intensity)

per generation per (synonymous) mutation rate

Fluctuation ---- Variance of phenotype  $x$  of clone

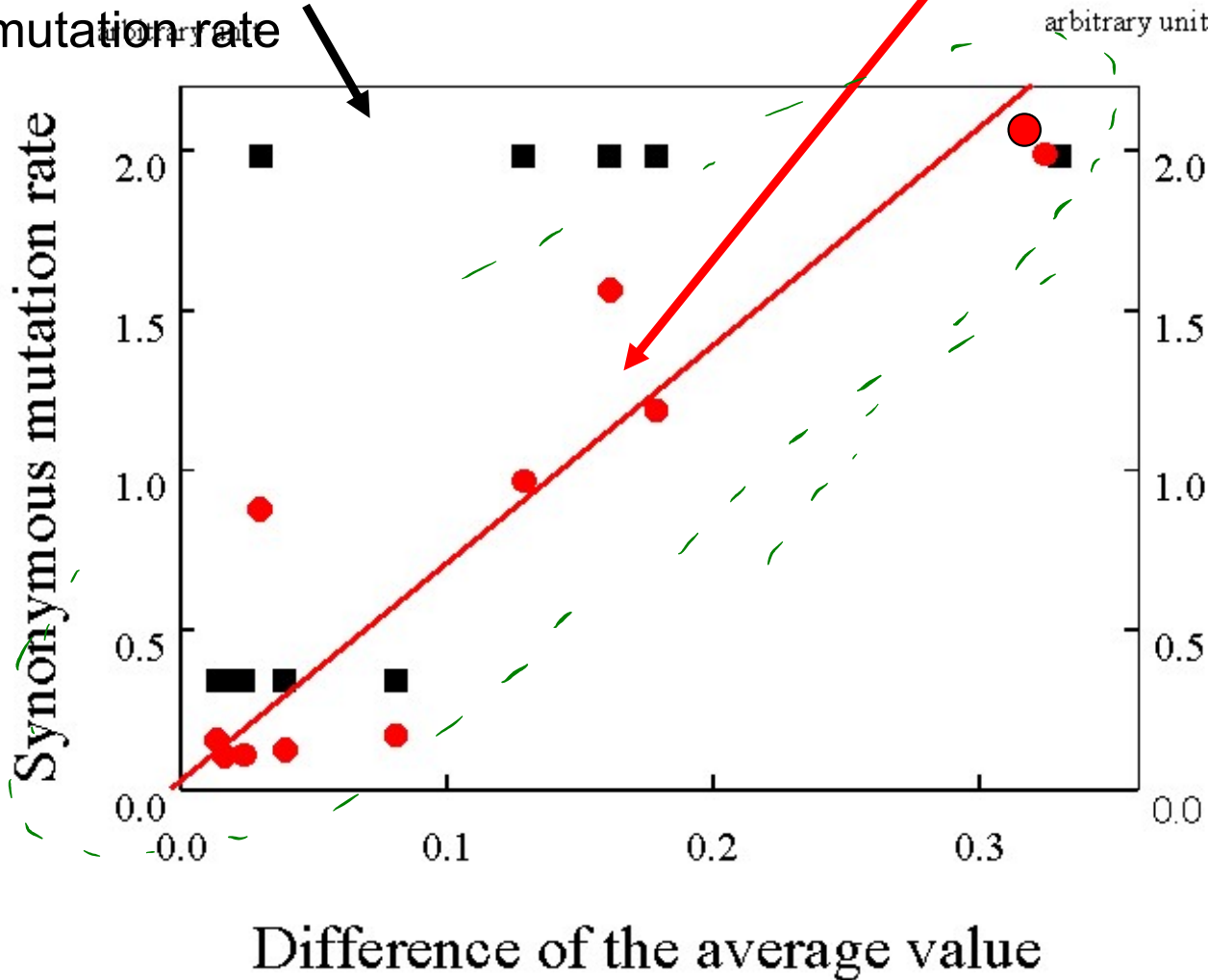
Fluctuation in the phenotype  $x$  of clone

$\Leftrightarrow$  speed of evolution to increase  $\langle x \rangle$

(proportional or correlated)

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

Naïve expectation:  
Just prop to mutation rate



(Evolution Speed per generation)

Sato, etal, PNAS 2003

# Confirmation by Toy Cell Model with Catalytic Reaction Network

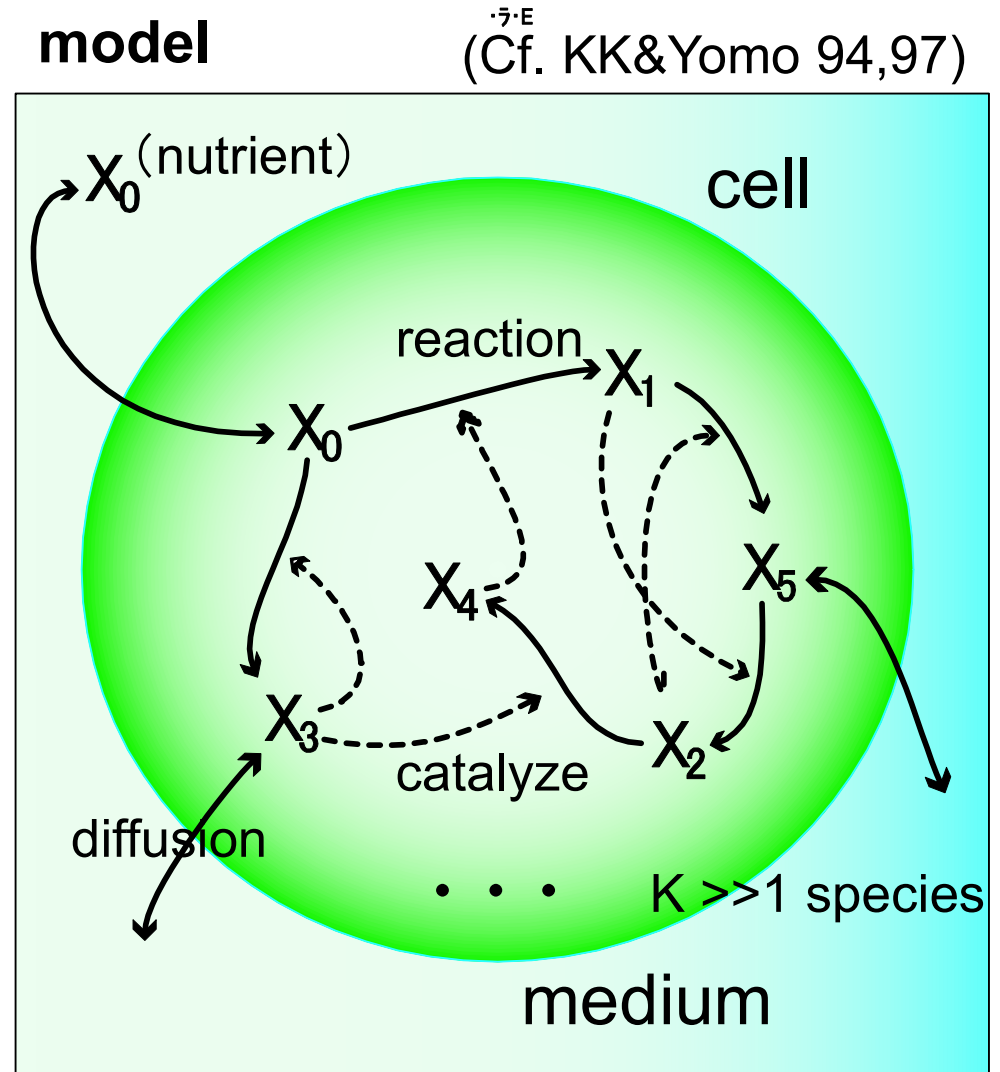
C.Furusawa & KK, PRL2003

■ **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



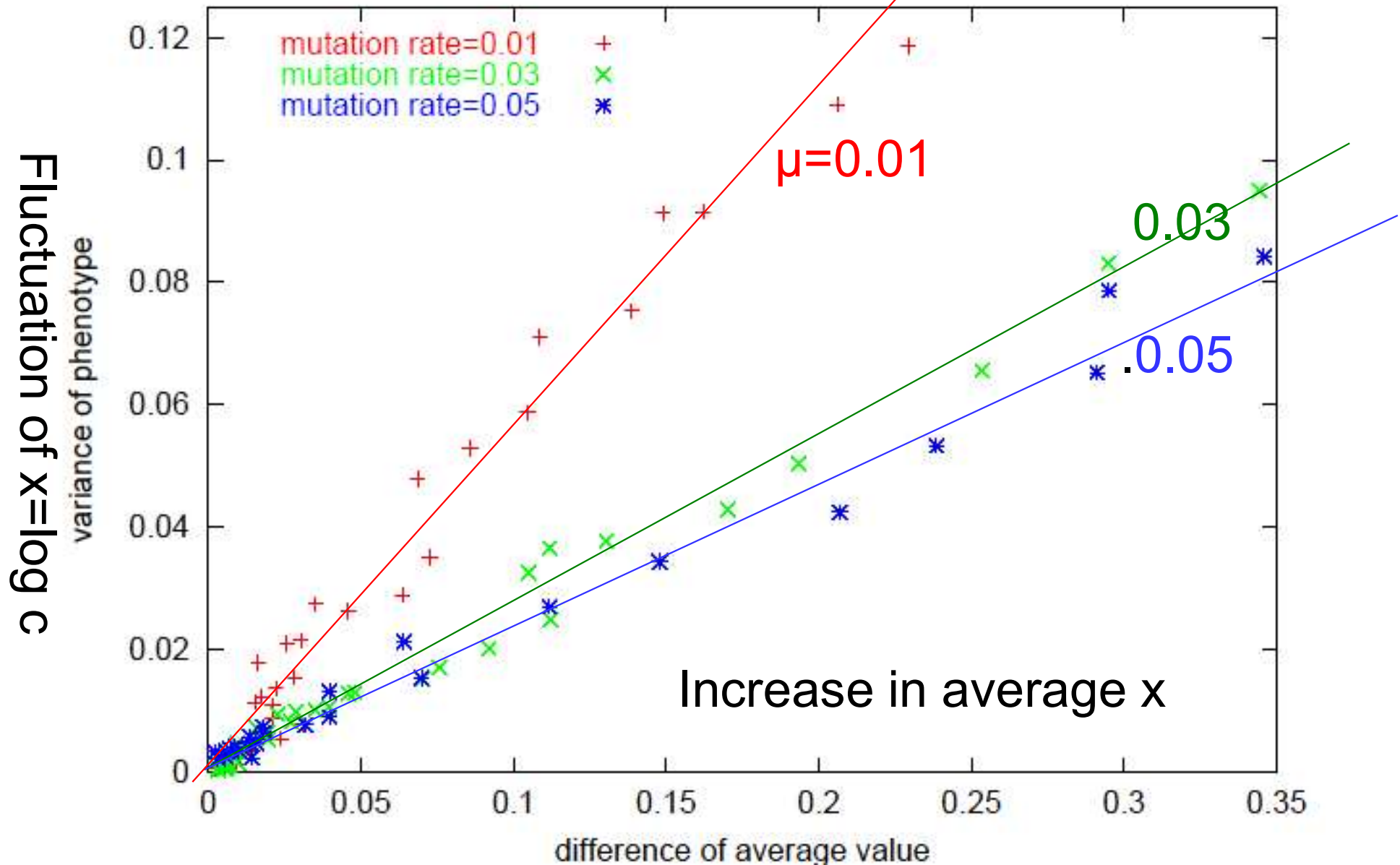
- Confirmation by numerical evolution experiment by the reaction-net cell model



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. Cells with higher  $x$  (top 5%) are selected as parent cells of next generation

**phenotype  $x = \log(n_s)$**

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

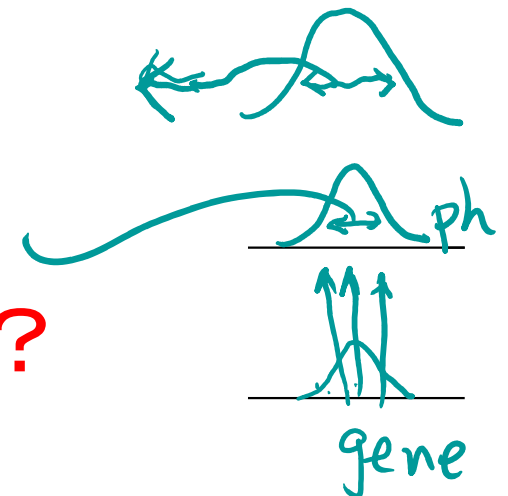


New mystery ?

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)

phenotypic fluctuation of clone  $V_{ip}$   
 $\propto$  phenotypic fluctuation  
by gene variation  $V_g$  ?



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

- Remark:

## Population Genetics

$V_{total}$  ( $V_p$ ): Total phenotypic variance consists of  
 $V_g$  (additive genetic variance)

$V_e$  (environmental)

or Fluctuating Assymetry

....

(sexual reproduction case – more complicated)

- $V_{ip}$  here due to ‘developmental noise’

(Or could be called as  $V_{noise}$ )

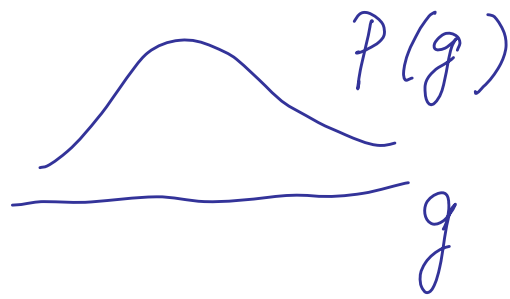
In reality, it may not be easy to distinguish  $V_{noise}$  from  $V_e$

- Anyway, relationship between  $V_{ip}$  ( $V_{noise}$ ) and  $V_g$ , if any, is non-trivial

→ check by cell model

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

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



mutation

$P_n(g)$

(growth rate  
 $\sim$  fitness)

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

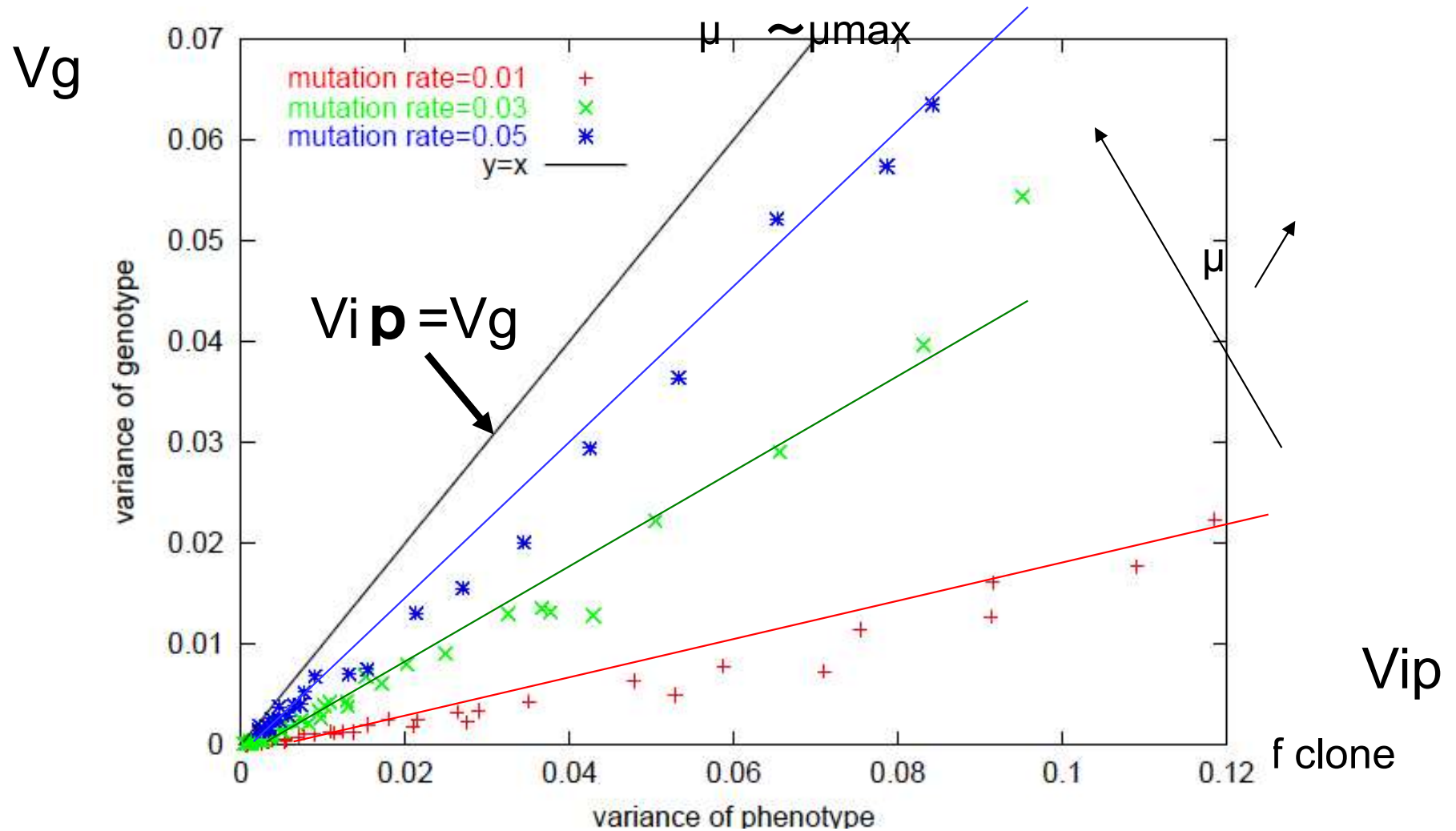
$$P_{n+1}(g) = \frac{g P_n(g)}{\int g P_n(g) dg} = \frac{g P_n(g)}{\bar{g}_n}$$

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

(Fisher?)

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

$V_{ip}$ : fluct. for given network,  $V_g$ : fluct. by network variation



variance of  $\log(x)$ ,  $x$  is the concentration of the molecule

Result of evolution;

first few generations deviated from proportionality

As  $\mu$  (mutation rate) increases to  $\mu_{max}$ ,

(1) the distribution collapses (error catastrophe)

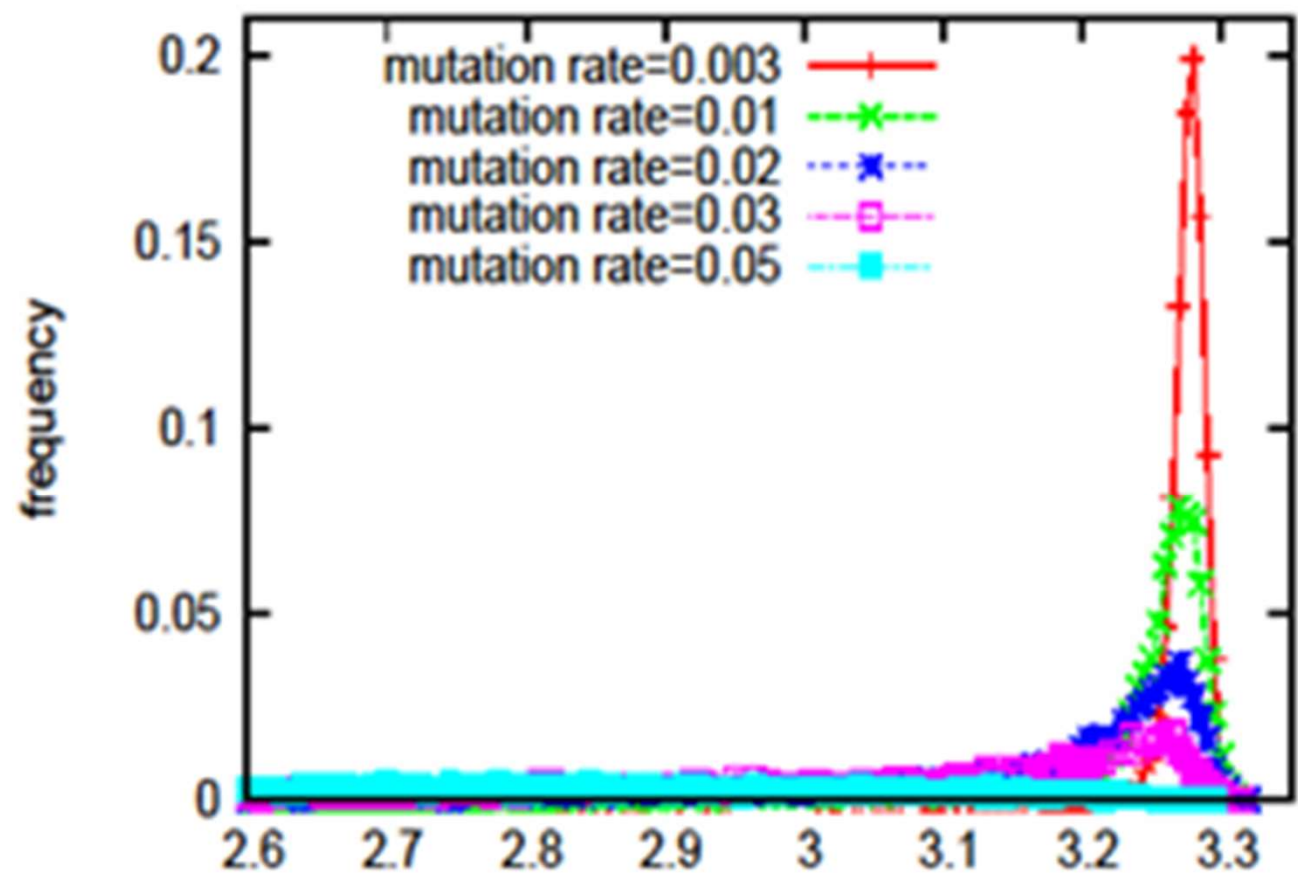
(2) evolution no longer progresses beyond  $\mu_{max}$

evolution speed is maximal at  $\mu \sim \mu_{max}$

(3)  $V_g$  approaches  $V_p$

$V_p$

distribution of genotype



As  $\mu$  is increased,  
The distribution  
'collapses'

Error catastrophe

Consider 2-variable distrib

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

Keep a single-peak (stability condition).

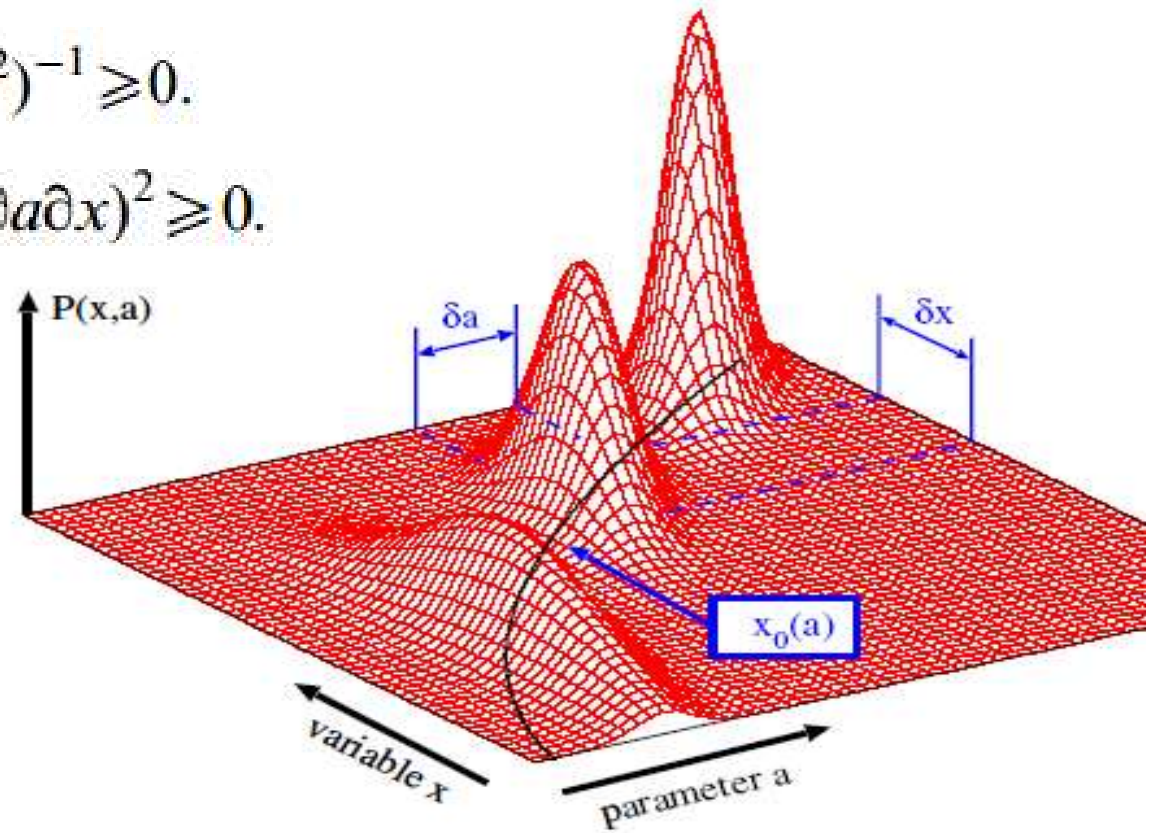
KK, Furusawa, 2006 JTB

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

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

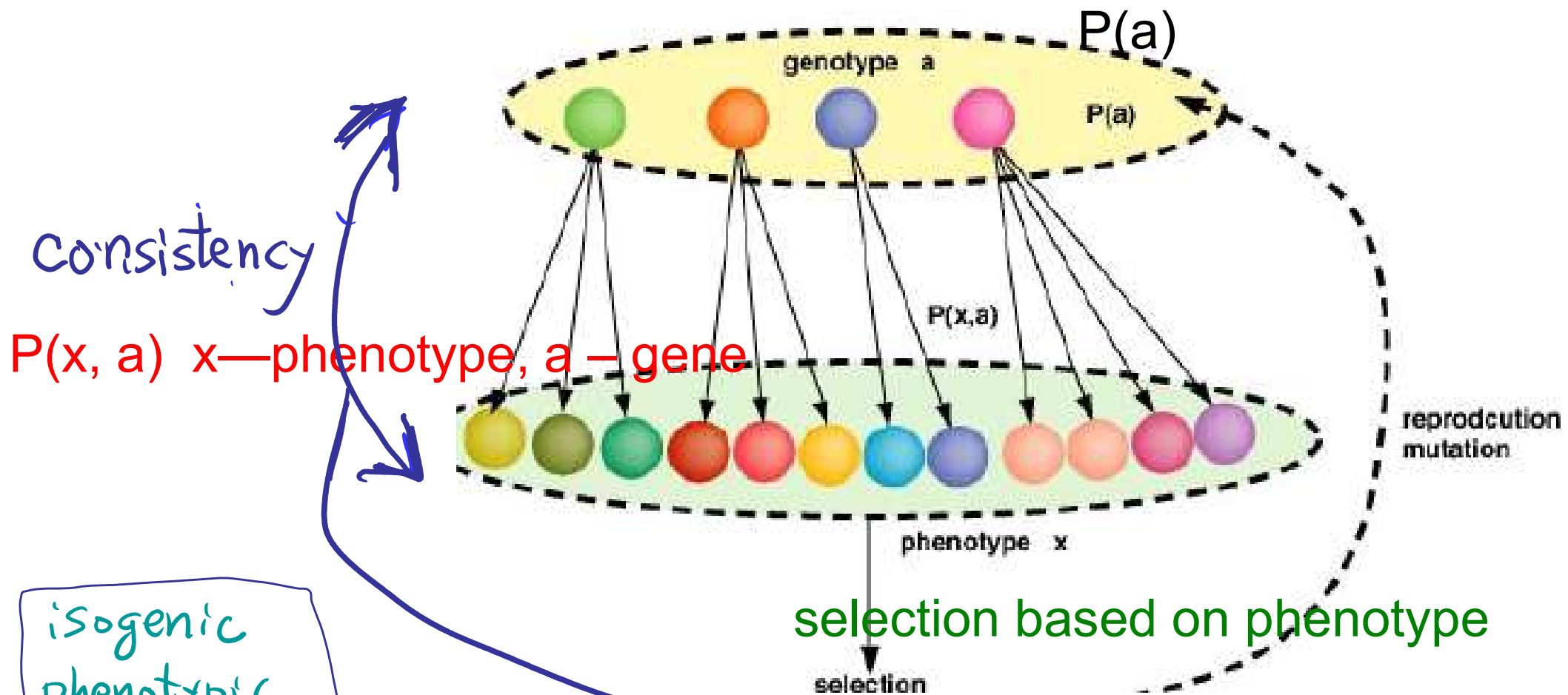
Hessian condition

Leads to relationship  
between  $V_{ip}$  and  $V_g$

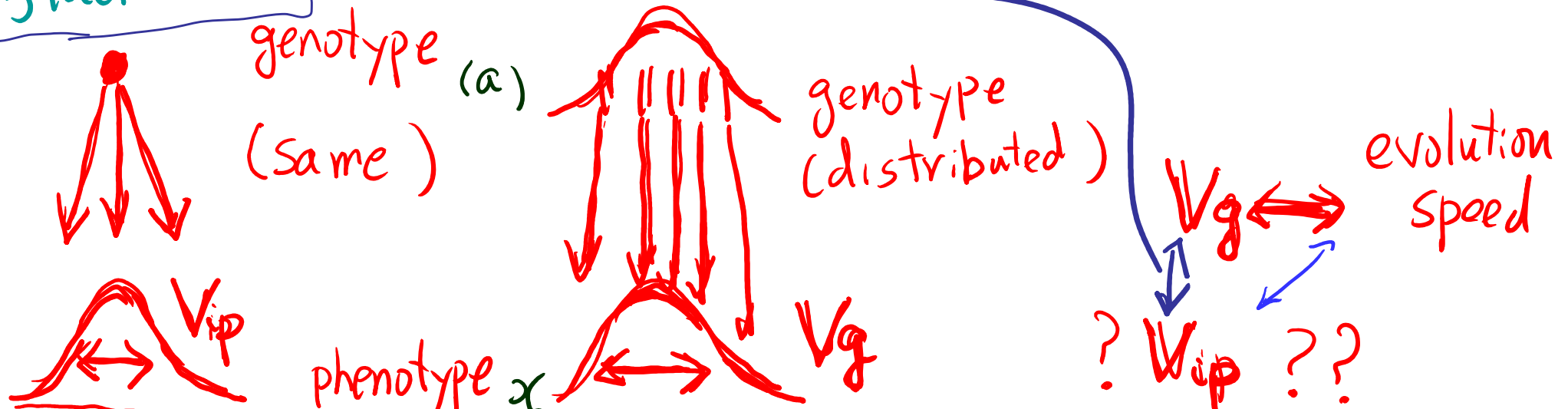


KK, Furusawa, 2006 JTB





isogenic phenotypic fluctuation



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



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

$$\mu \leq \frac{1}{\alpha C^2} \equiv \mu_{max}.$$

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

$$V_g = \langle \overline{(x(a) - X_0)^2} \rangle = \frac{\mu C^2 \alpha^2}{1 - \mu C^2 \alpha} = \alpha \frac{\frac{\mu}{\mu_{max}}}{1 - \frac{\mu}{\mu_{max}}}.$$

Vip=α

If mutation rate  $\mu$  is small,  $V_g < V_{ip}$ ,

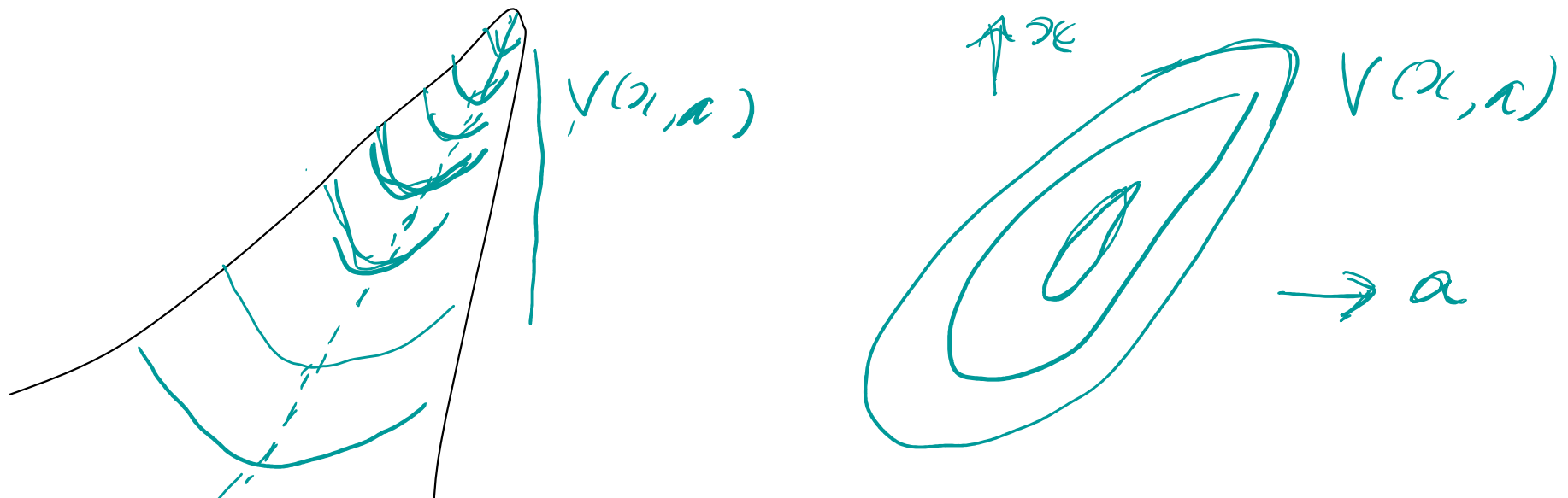
$$V_g \sim (\mu/\mu_{max}) V_{ip} \propto V_{ip}$$

- P(x,a) theory; **assumption** --- 2- variable distribution (potential in geno- and phenotype)
- **Q: x and a are represented in a single potential?**

Consequence of Genetic Variation to phenotype already exists in phenotype fluctuation

e.g., Variation of chemical abundances  $X_i$

← correspond to → change in reaction network of  $J_{ij}$  by mutation in reaction  $X_i X_j \xrightarrow{J_{ij}}$



• (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 higher noise leads to robust evolution?

---

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

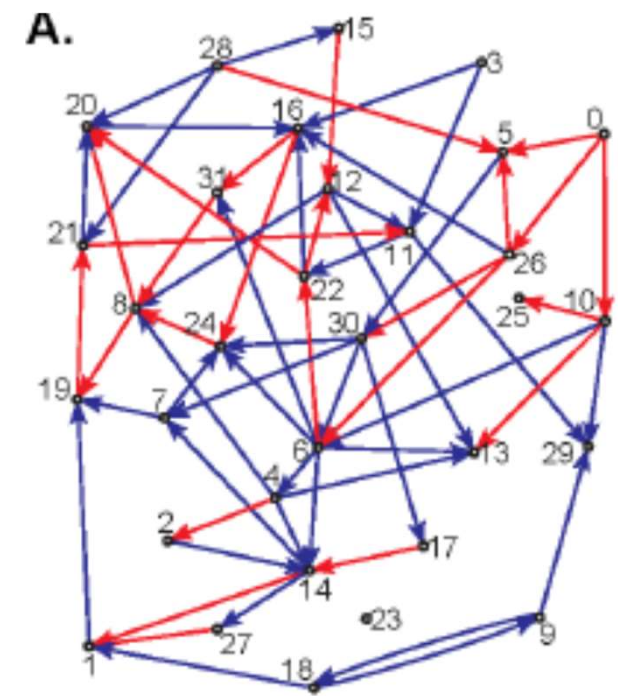
# Gene expression dynamics model:: Relevance of Noise to evolution?

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

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

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

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



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

**Gaussian white**

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

**Noise strength  $\sigma$**

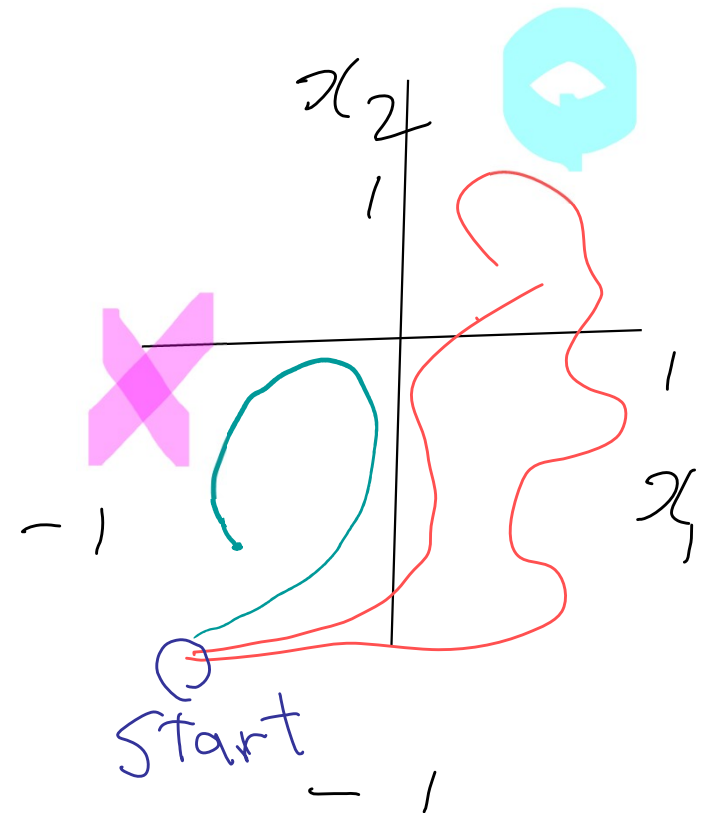
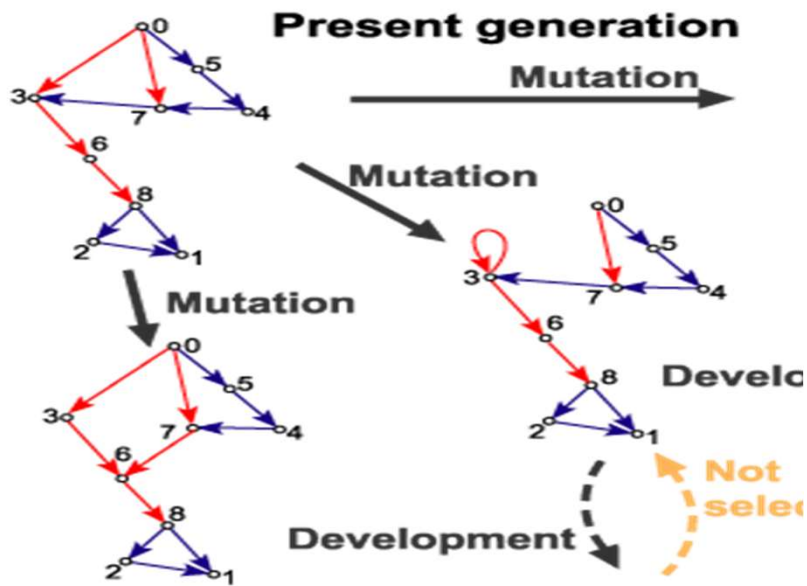
- Fitness: Starting from off of all genes, after development genes  $x_i$   $i=1, 2, \dots, k$  should be on (Target Gene Pattern)

Fitness  $F = - (\text{Number of off } x_i)$

## Genetic Algorithm

Mutate networks and Select those with higher  $\langle F \rangle$

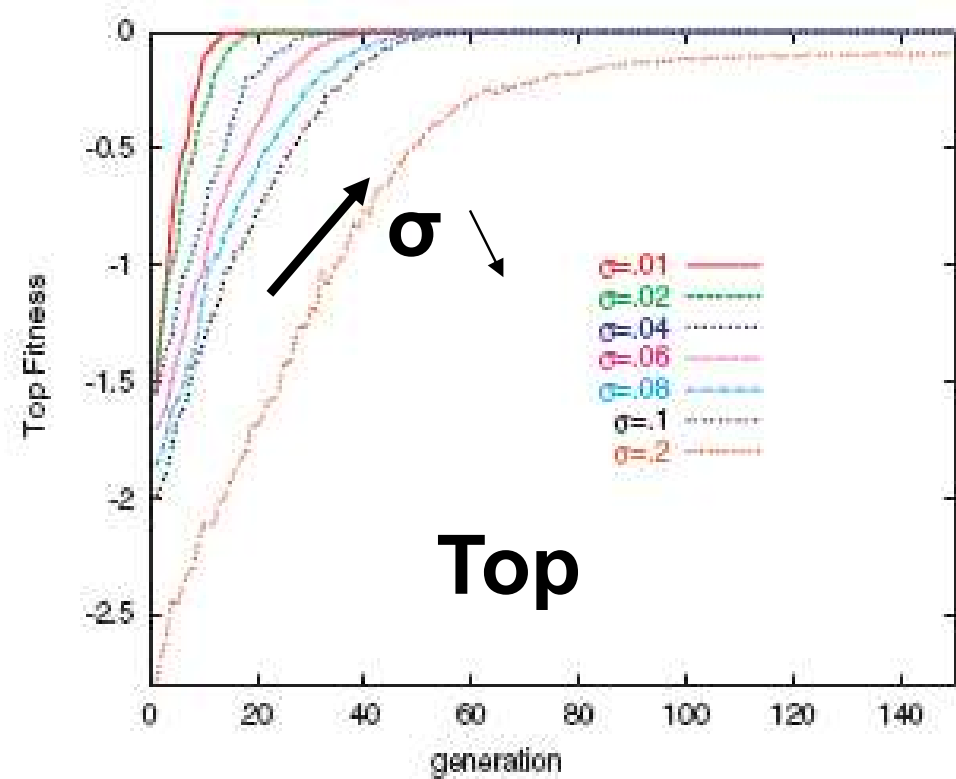
Choose top  $n$  networks among total  $N$ , and mutate with rate  $\mu$  to keep  $N$  networks



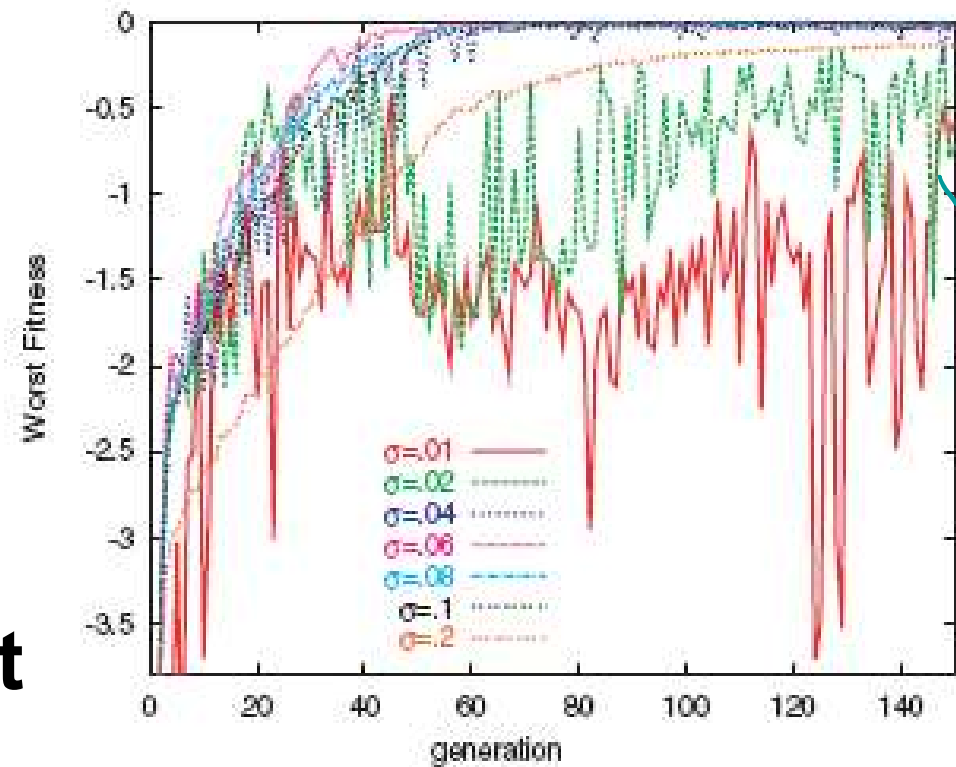
# Result of evolution

Top: reaches the fittest  
faster for lower noise( $\sigma$ )

Lowest; cannot evolve  
for low noise( $\sigma$ )

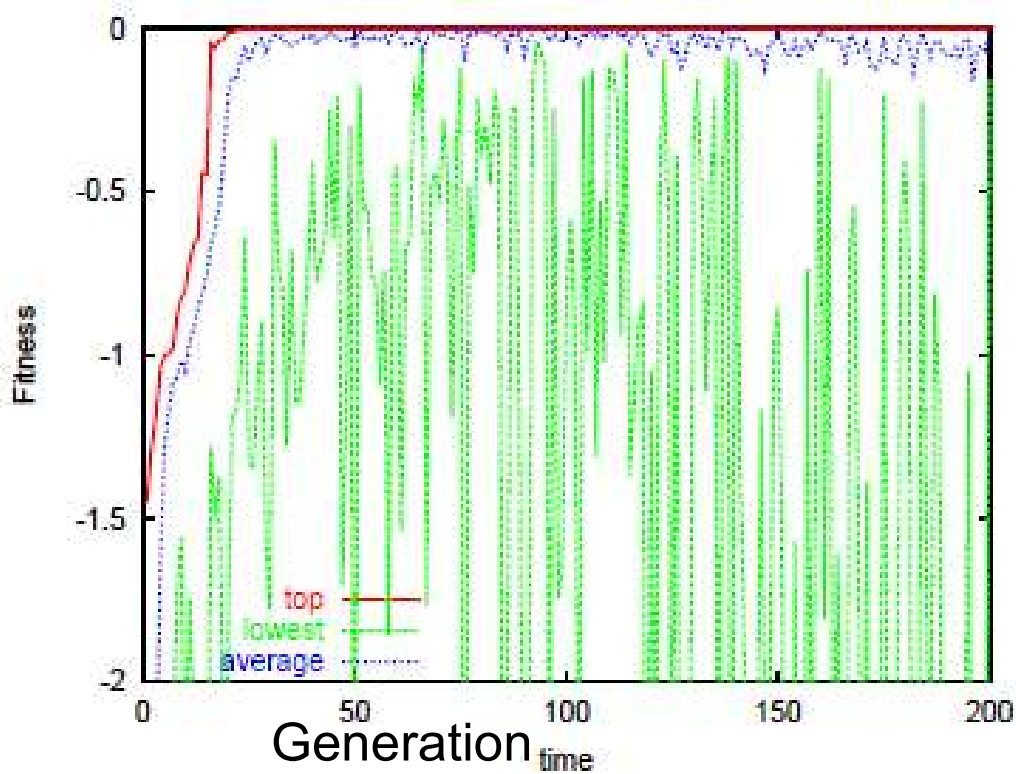


(a)

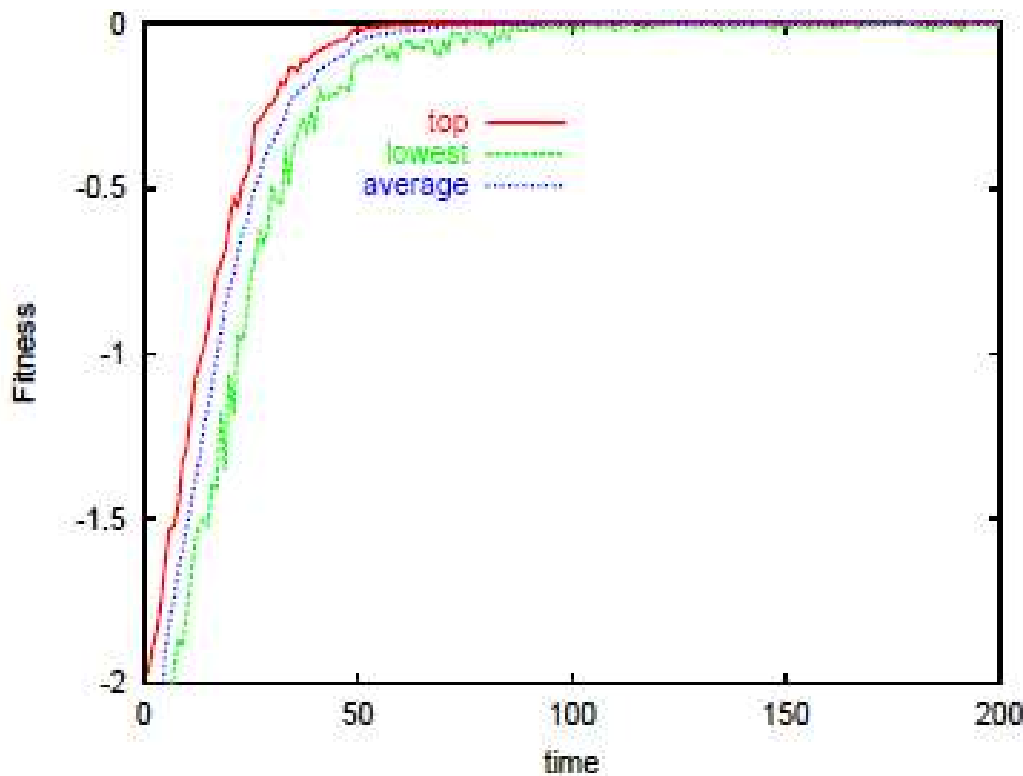


(b)

**Lowest**

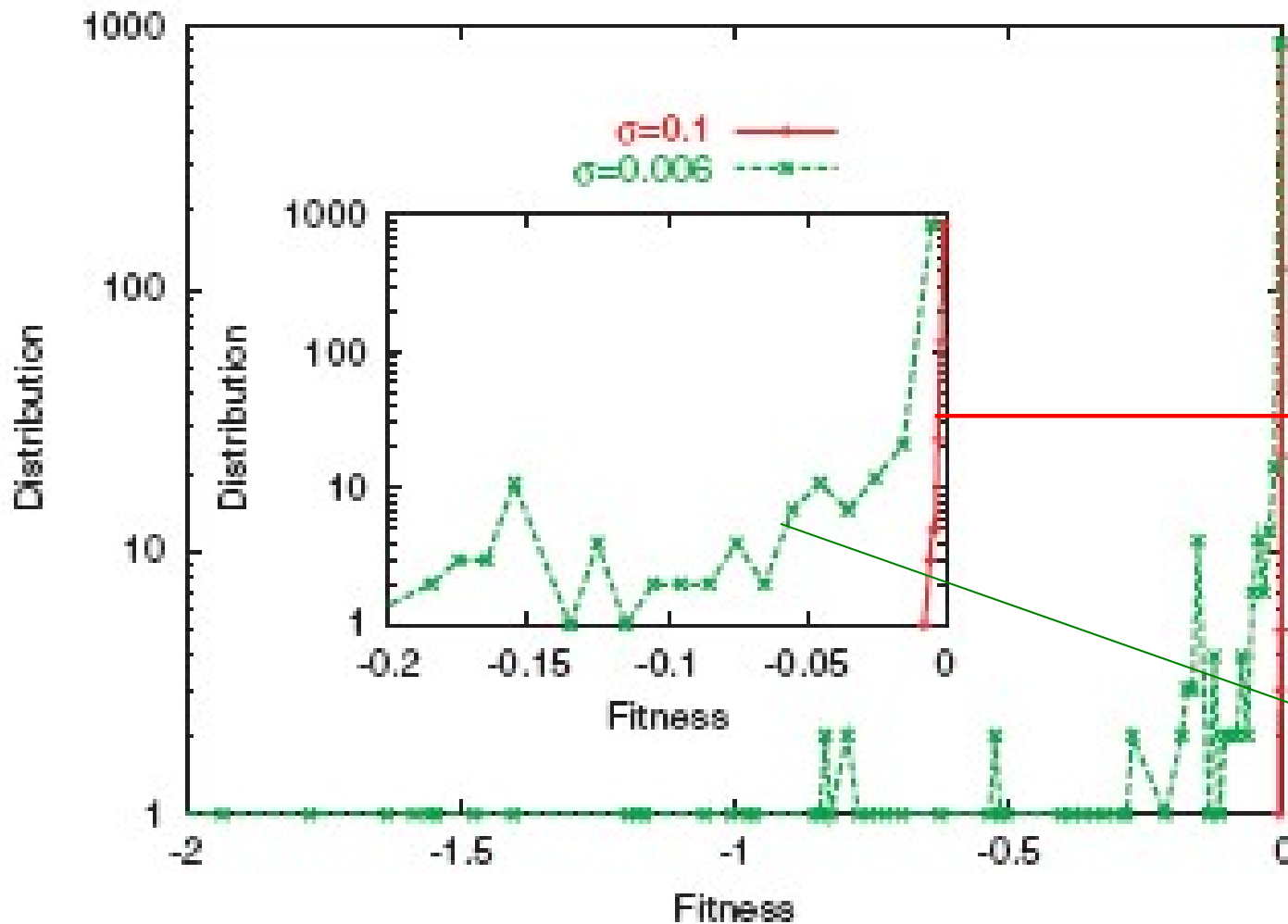


Low noise case:  
 top reaches the fittest  
 but low-fitness  
 mutants remain



High Noise case:  
 top-lowest  
 All reach the fittest





## Result of evolution

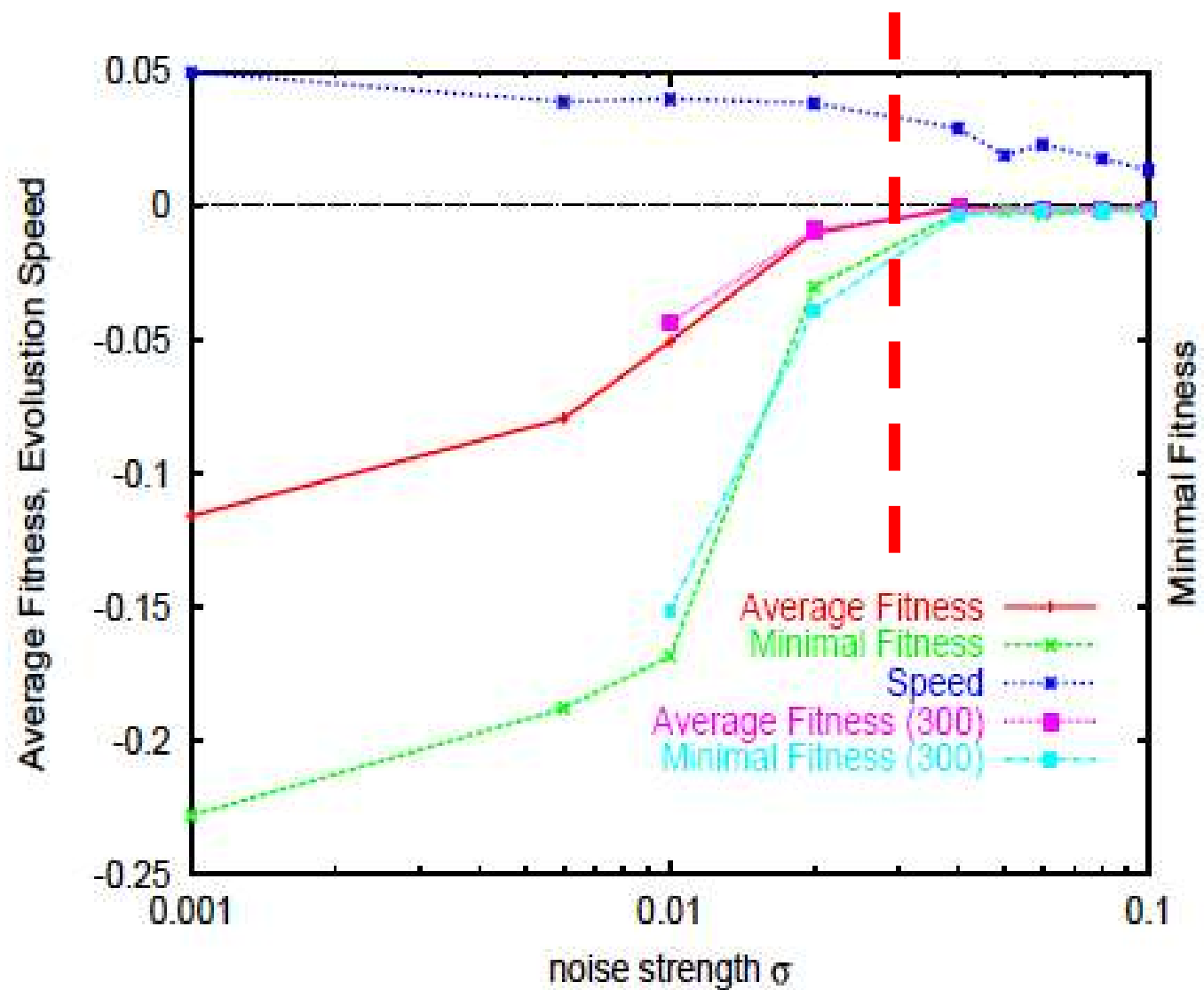
Top:reaches the fittest  
 Lowest;cannot evolve  
 for low noise( $\sigma$ )

$\sigma > \sigma_c$

$\sigma < \sigma_c$

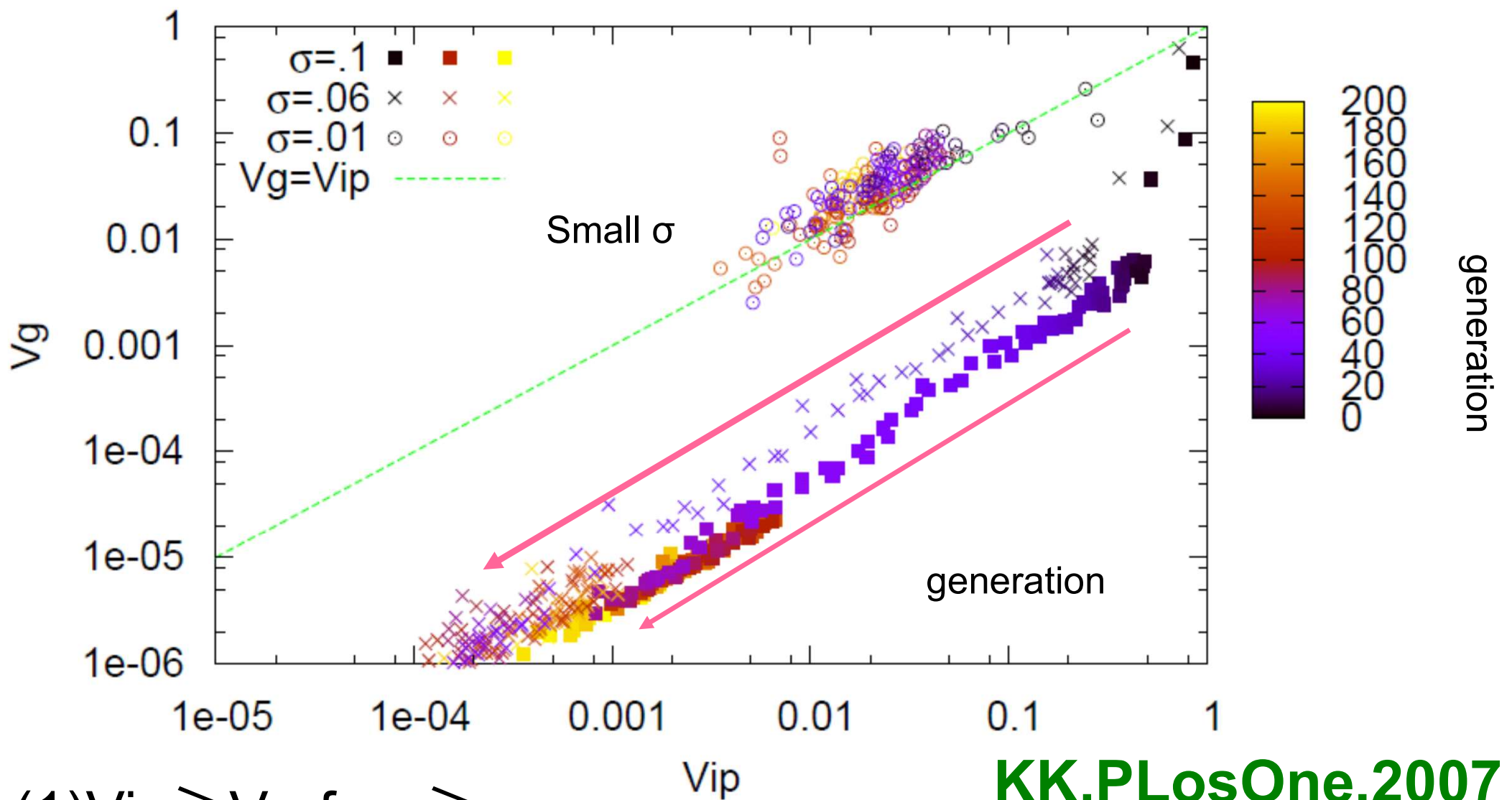
## Fitness Distribution

$\sigma < \sigma_c$  --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)**

- **Comment on error catastrophe**
- Error Catastrophe (Eigen, Schuster)
  - combinatorial explosion of unfit states (static)
  - catastrophe w.r.t. mutation rate
- \*the robustness transition here
  - combinatorial explosion of orbits reaching unfit states
  - catastrophe w.r.t. noise and mutation rate
- ? In EC by Eigen, discontinuous transition
  - (even top fitness is not sustained)
- Here, continuous transition?
  - condition for it?



(1)  $Vip \geq Vg$  for  $\sigma \geq \sigma_c$

(2)  $Vg \rightarrow Vip$  as  $\sigma \rightarrow \sigma_c$

(3) evolution progresses only for  $Vip \geq Vg$

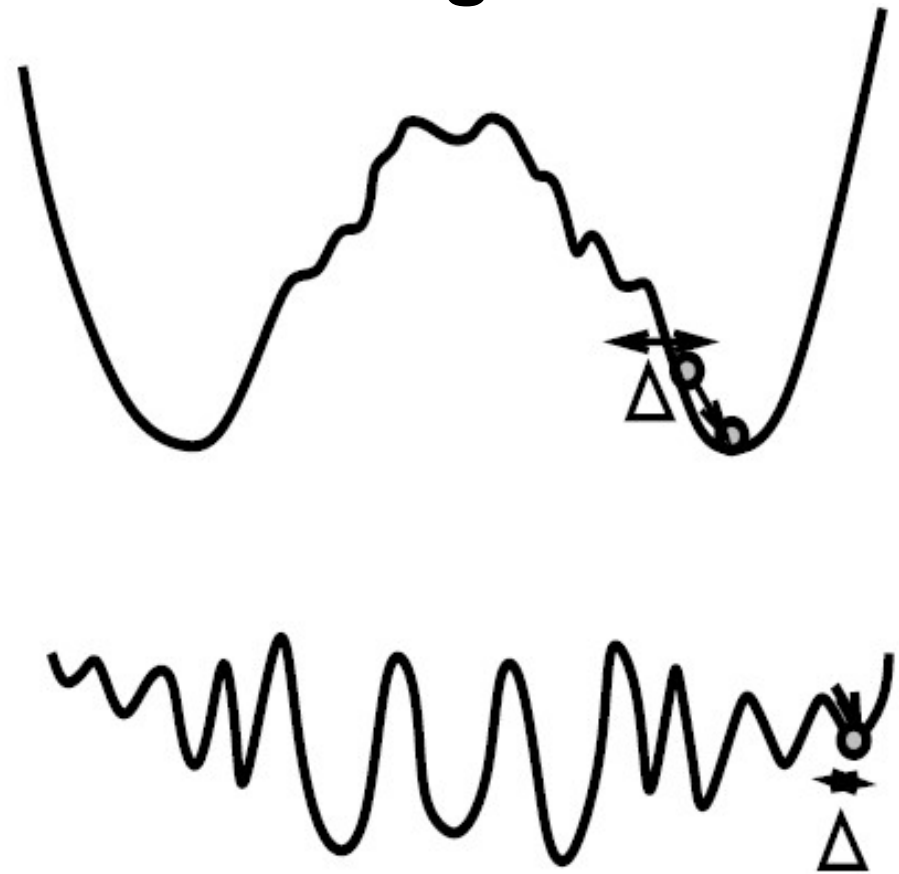
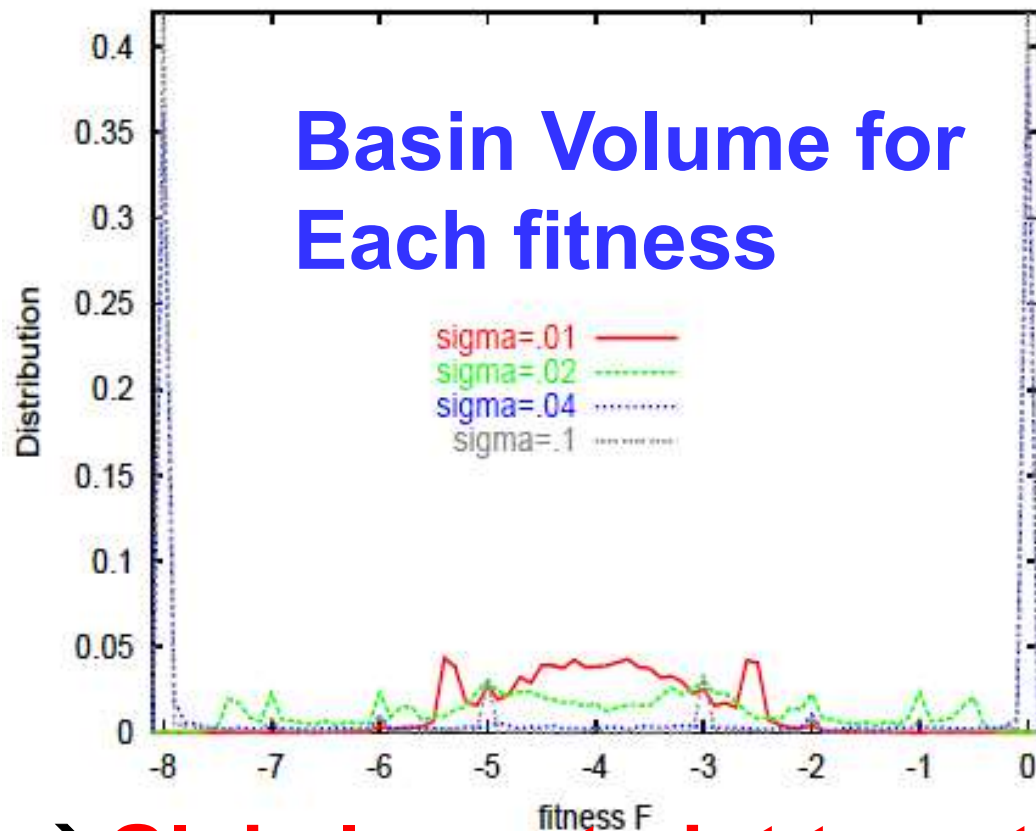
(4)  $Vip \propto Vg$  through evolution course

**Distribution Theory confirmed**

Why?; difference in basin structure

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

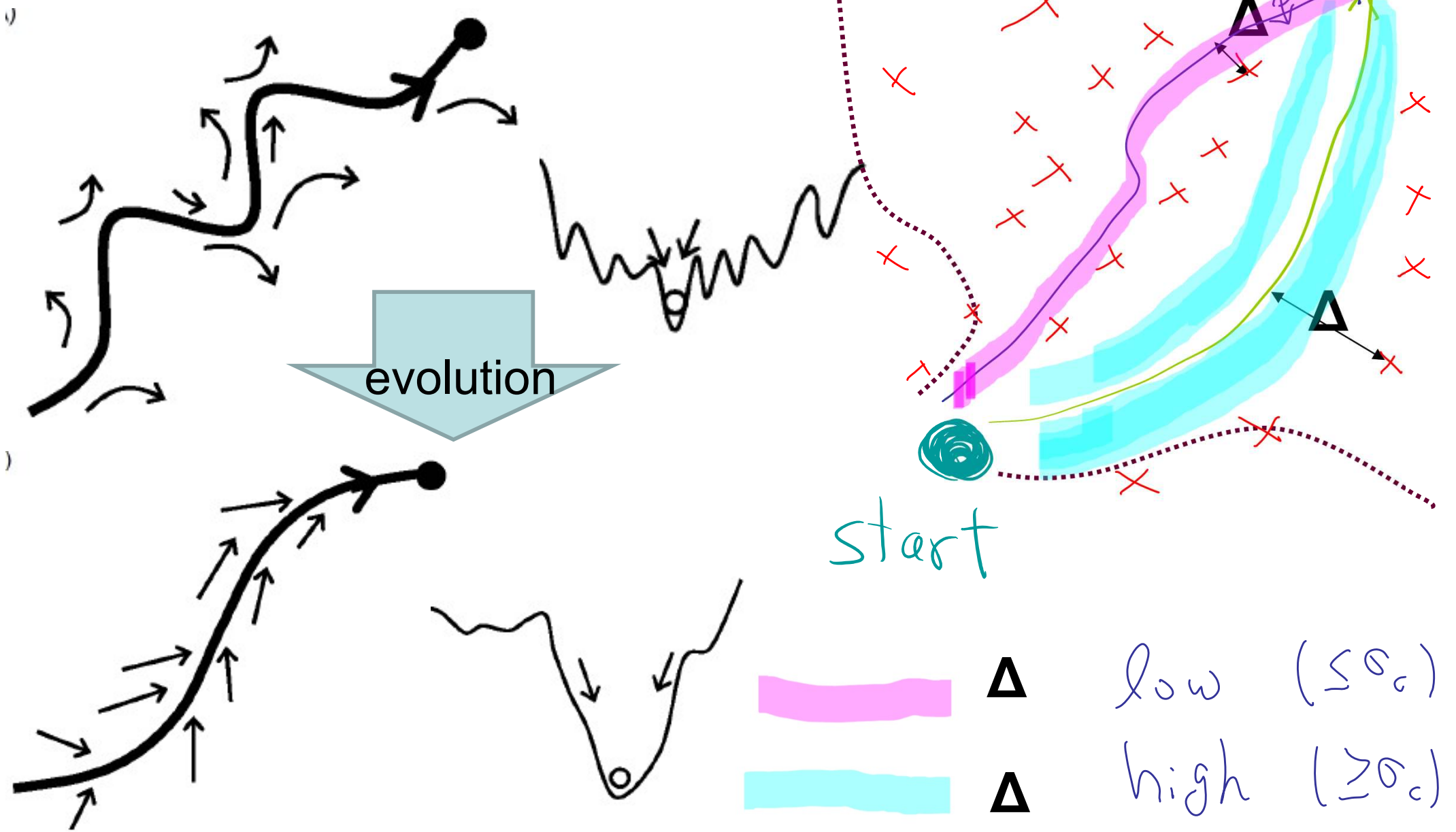
$\sigma < \sigma_c \rightarrow$  only tiny basin around target orbit  
 $\Delta$  remains small



$\rightarrow$  **Global constraint to potential landscape (funnel?)**  
cf. protein; gene-expression (Li, Long, Lu, Ouyang, Tang)

# Evolution of dynamical systems

- dynamical systems whose attractor is robust to noise
- robust to parameter changes (mutation)



**Deviation of basin  
boundary (turning points)**

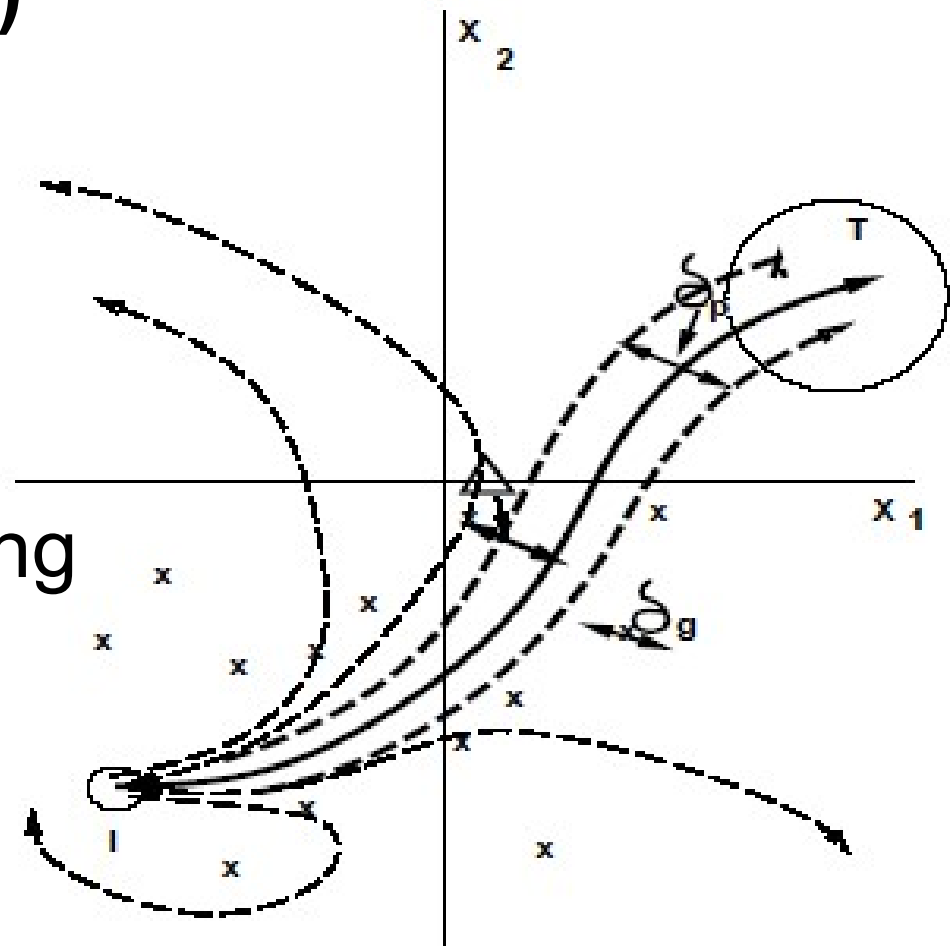
**$\Delta$  increases**

**$\rightarrow$  robustness increases**

why threshold?

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

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



**$\Delta \sim$  distance to turning points  
(basin boundary)**

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

- Robustness to mutation is increased for network evolved under higher noise

$$F = -c(\sigma) m ;$$

$$C(\sigma) > 0 \text{ if } \sigma < \sigma_c$$

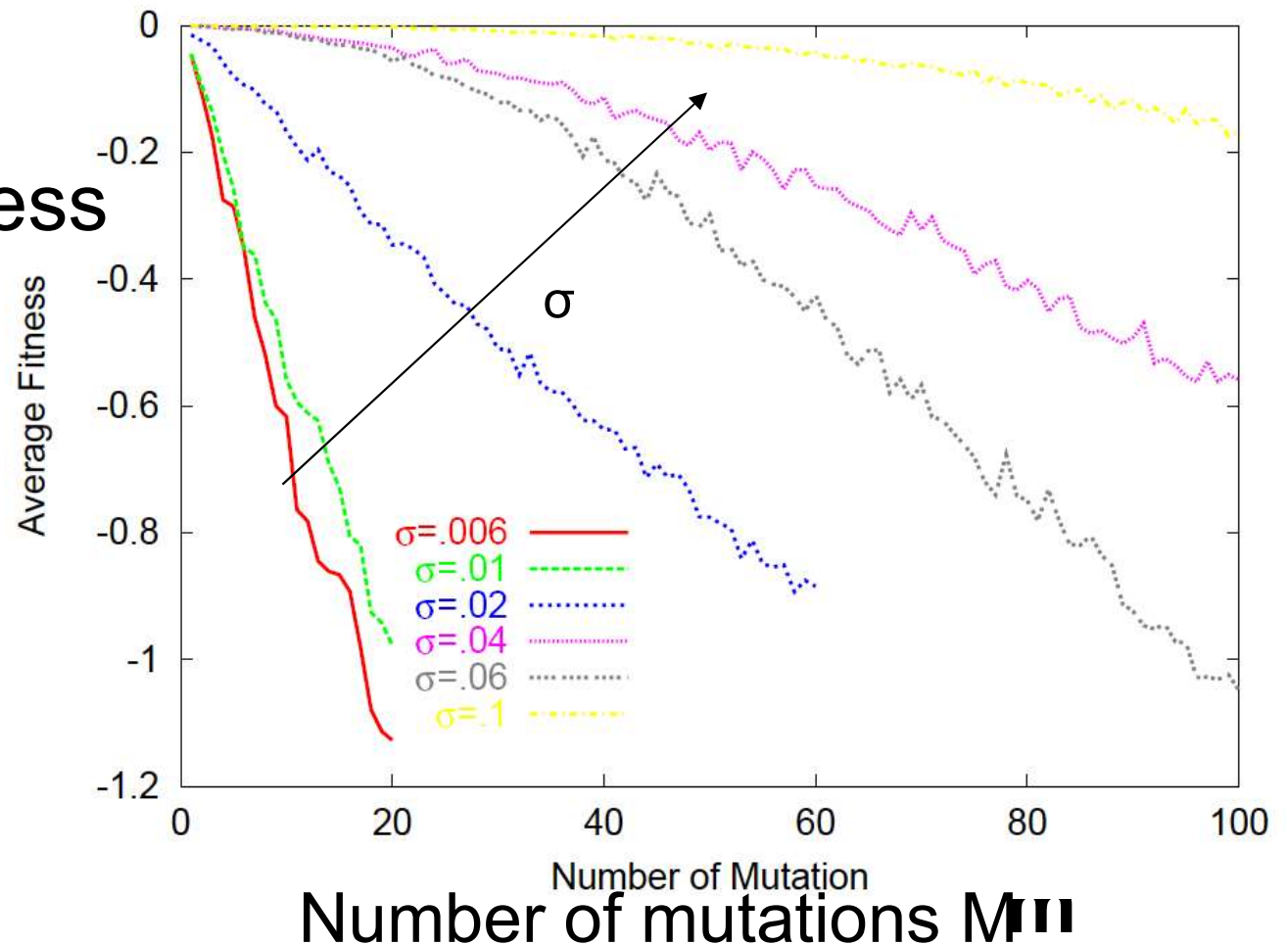
$$C(\sigma_c) = 0$$

Almost Neutral of fitness over mutations

accordingly robust case ( high  $\sigma$  ) allow for higher genetic diversity

Cf Tomoko Ohta

Average fitness over mutants with M mutations



Number of mutations M



# 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 increases

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

(cf. Ancel-Fontana J Exp Zool B 2000

A Wagner et al, PLoS Comp Biol 2007)

# Waddington's and Einstein's Legacy

Robustness is Essential

- Canalization
- Genetic Assimilation

→ These are linked through potential picture  
Environmental change → potential change  
how it is buffered in genetic change

We represented by  $P(x,a)$  and in terms of  
fluctuations based on consistency between  
geno and pheno fluctuation

Einstein's Brownian motion theory (consistency  
between micro fluct vs macro motion)

Ours: that between geno and pheno fluctuation

- Q again: Why phenotypic fluctuation is favored for evolutionary stability?

(1) 'fatal' states around highly optimized state

(2) Small noise case

Trapped at 'metastable' state in 'model' space

(3) simple structure both in 'gene' direction and 'phenotype' direction is favored

(Funnel-like structure is preferred (even though complex dynamics may be hidden somewhere))

Protein (Go), Gene expression dynamics (Tang-Ouyang), Developmental process

- **Nature vs Nurture?**
- Standard population genetics:  
non-genetic variations are regarded to be **due to environmental variation** instead of fluctuation
- The ratio of genetic variation to total variation is called "**heritability**". This value, for most cases is less than .5 (cf: data in *Drosophilla* 0.2-0.5)
- Our argument shows heritability  $< 1/2$ , as **heritability =  $V_g / (V_{ip} + V_g)$**  (if  $V_{ip}$ ,  $V_g$  are added independently) by regarding  $V_{ip}$  as origin of non-genetic variation
  - (?Nature < Nurture? But the precise formula is  $V_{ip} > V_g$ : but if selection is strong -?  $< .5$ )

- **Generality?** For a system satisfying:
    - (1) fitness is determined after developmental dynamics
    - (2) **developmental dynamics is complex**  
(eg., with distributed catastrophic pts.  
( $\Rightarrow$  deleterious mutants, error catastrophe )
    - (3) effective equivalence between mutations and noise with regards to the consequence to fitness
- 

\* $V_{ip}$  variance of phenotype over isogenic individuals

\* $V_g$  variance of average phenotype over heterogenic population

**Plasticity**  $\propto$   **$V_{ip}$**   $\propto$   **$V_g$**   $\propto$  evolution speed

through evolution course

and **over genes at given snapshot**

Spin Model for evolution [Sakata.Hukushima. KK, PRL 2009](#)

eg. Protein folding dynamics

spin configuration --- configuration in protein

H folding dynamics

$$H(\mathbf{S}|\mathbf{J}) = -\frac{1}{\sqrt{N}} \sum_{i < j} J_{ij} S_i S_j$$

Fitness; to align target spins  
evolve  $J_{ij}$

Again transition;

As noise is increased

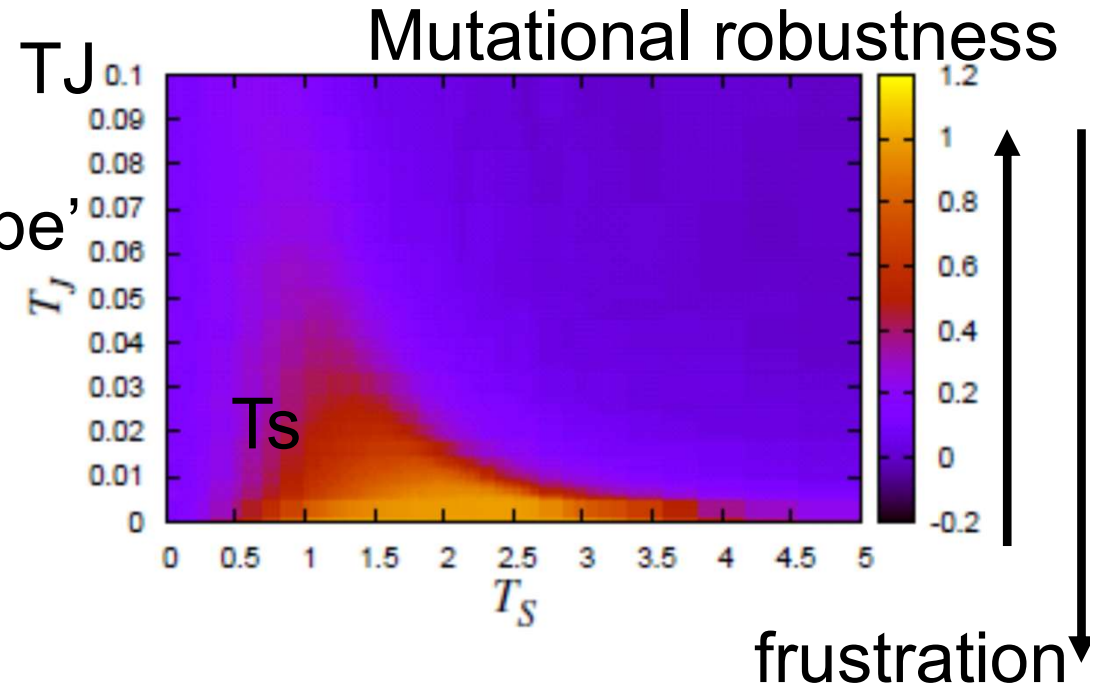
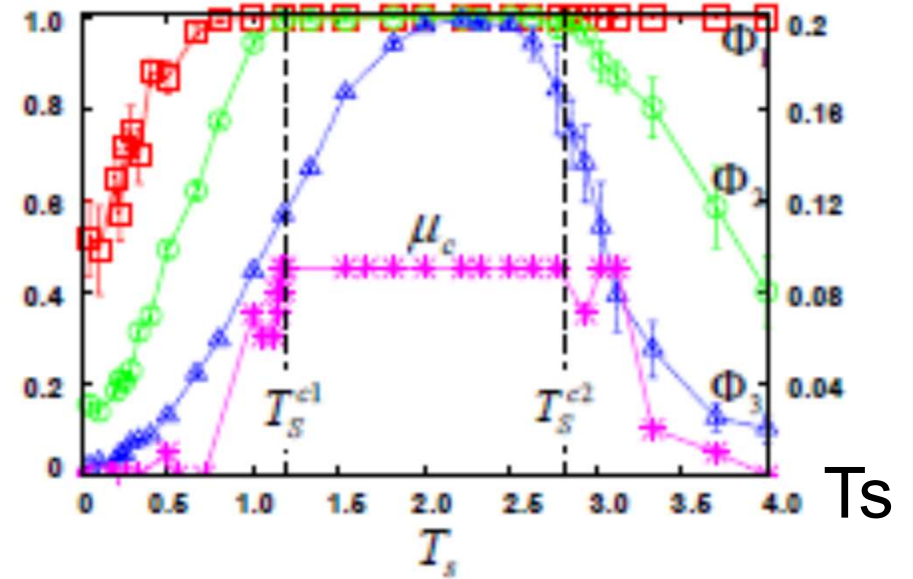
high fitness with robustness

to mutation is achieved

Form  $J_{ij}$  to have 'funnel landscape'

$T_S$  noise during  
'developmental' dynamics

$T_J$  selection pressure  
( high as  $T_J \rightarrow 0$ )



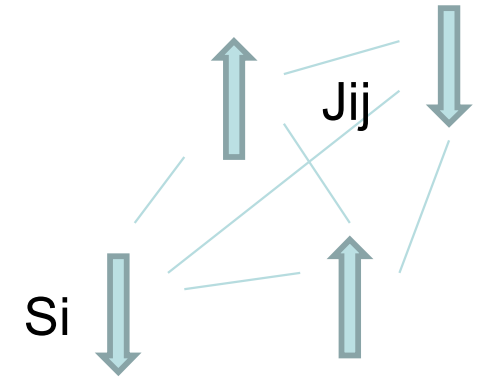
Spin Model for evolution (Sakata.Hukushima, KK, PRL 2009)

eg. Protein folding dynamics

spin configuration --- configuration in protein

H folding dynamics

$$H(\mathbf{S}|\mathbf{J}) = -\frac{1}{\sqrt{N}} \sum_{i<j} J_{ij} S_i S_j$$



librium distribution for a given  $\mathbf{J}$ ,  $P(\mathbf{S}|\mathbf{J}, T_S) = e^{-\beta_S H(\mathbf{S}|\mathbf{J})} / Z_S(T_S)$ , where  $\beta_S = 1/T_S$  and  $Z_S(T_S) = \text{Tr}_{\mathbf{S}} \exp[-\beta_S H(\mathbf{S}|\mathbf{J})]$ . In the steady state of the dynamics, the phenotype  $\mathbf{S}$

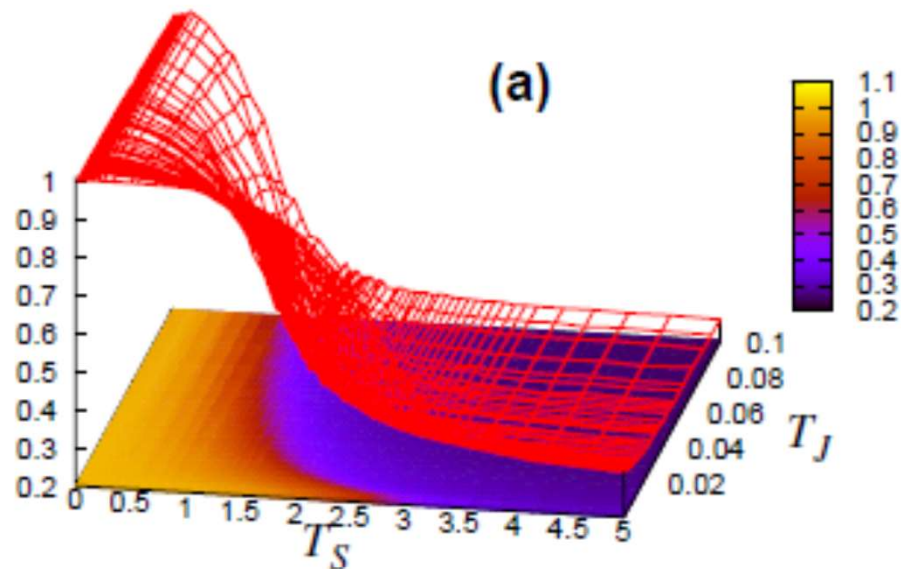
$$Fit(\mathbf{J}|T_S) = \left\langle \prod_{i<j \in \mathbf{t}} \delta(S_i - S_j) \right\rangle \quad \mathbf{t} : \text{target spin; fitted if aligned}$$

tionary distribution,  $P(\mathbf{J}, T_S, T_J) = e^{\beta_J Fit(\mathbf{J}, T_S)} / Z_J(T_S, T_J)$ , where  $\beta_J = 1/T_J$  and  $Z_J(T_S, T_J) = \text{Tr}_{\mathbf{J}} \exp[\beta_J Fit(\mathbf{J}, T_S)]$ .

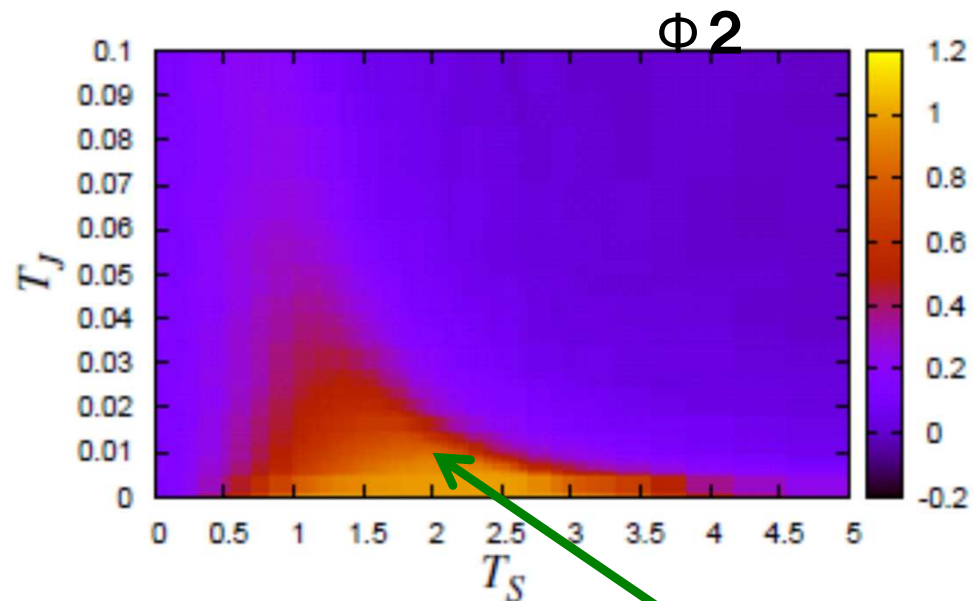
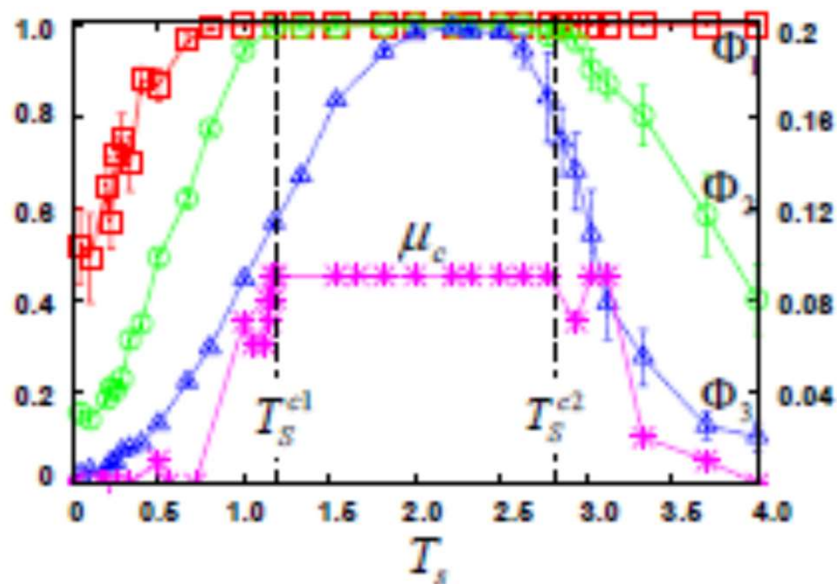
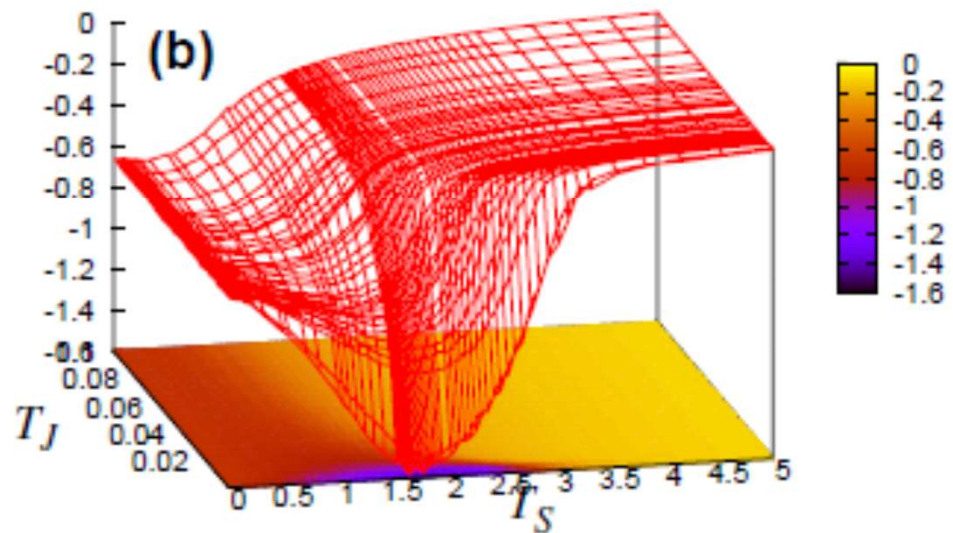
$T_S$  noise during 'developmental' dynamics

$T_J$  mutation-selection process (selection pressure)

Fitness



Energy



1- $\Phi_2$ : Frustration in spins around the target

Funnel Phase

$\mu_c$ : mutation in network necessary to destroy the target config



- Phase transition

$T_s < T_{c1}$  – high fitness state is achieved, but not robust to mutation: Spin-glass phase

$T_{c1} < T_s < T_{c2}$  -- high fitness state. Robust to mutation. No frustration around the target spins, but frustration remains elsewhere: ‘local Mattis’ state; ~

funnel developmental landscape

the target equilibrium reached globally and fast

$T_s > T_{c2}$ , -- high fitness is not achieved. ‘paramagnetic’ phase

\*Ubiquity of funnel developmental landscape--result of evolution under noise, which also leads to robustness to mutation

\*\*\*Evolutionary Meaning of RSB! \*\*\*

# Double-replica theory for evolution of genotype-phenotype interrelationship

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<sup>2</sup> *Center for Complex Systems Biology, Universal Biology Institute, University of Tokyo, Komaba, Tokyo 153-8902, Japan*

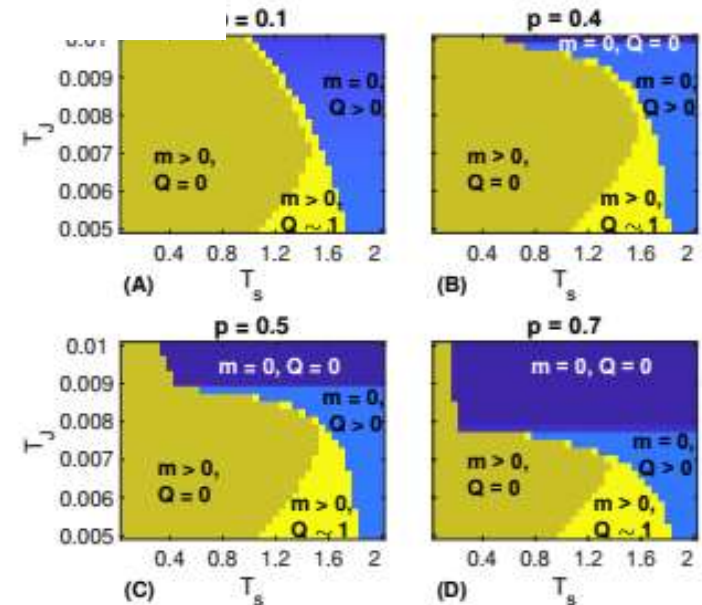
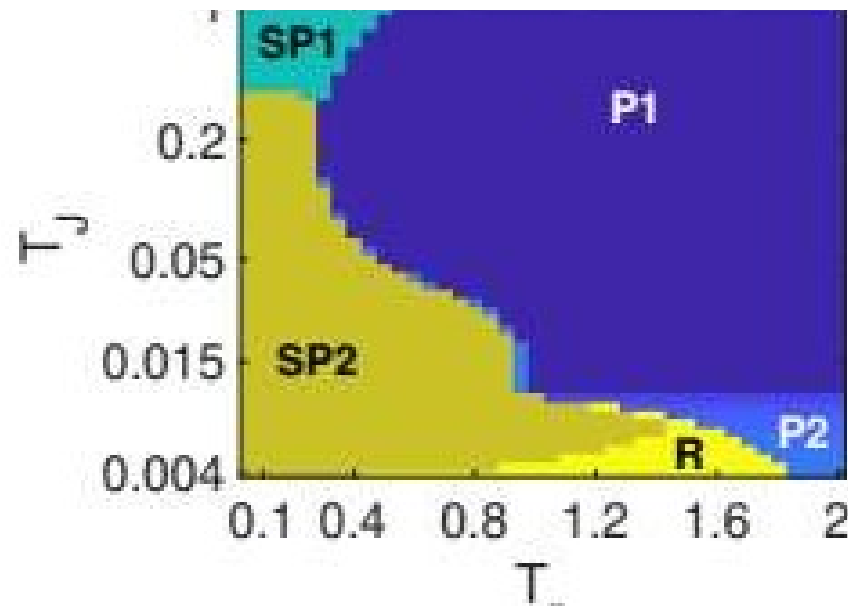
(Dated: November 29, 2022)

The relationship between genotype and phenotype plays a crucial role in determining the function and robustness of biological systems. Here the evolution progresses through the change in genotype, whereas the selection is based on the phenotype, and genotype-phenotype relation also evolves. Theory for such phenotypic evolution remains poorly-developed, in contrast to evolution under the fitness landscape determined by genotypes. Here we provide statistical-physics formulation of this problem by introducing replicas for genotype and phenotype. We apply it to an evolution model, in which phenotypes are given by spin configurations; genotypes are interaction matrix for spins to give the Hamiltonian, and the fitness depends only on the configuration of a subset of spins called target. We describe the interplay between the genetic variations and phenotypic variances by noise in this model by our new approach that extends the replica theory for spin-glasses to include spin-replica for phenotypes and coupling-replica for genotypes. Within this framework we obtain a phase diagram of the evolved phenotypes against the noise and selection pressure, where each phase is distinguished by the fitness and overlaps for genotypes and phenotypes. Among the phases, robust fitted phase, relevant to biological evolution, is achieved under the intermediate level of noise (temperature), where robustness to noise and to genetic mutation are correlated, as a result of replica symmetry. We also find a trade-off between maintaining a high fitness level of phenotype and acquiring a robust pattern of genes as well as the dependence of this trade-off on the ratio between the size of the functional (target) part to that of the remaining non-functional (non-target) one. The selection pressure needed to achieve high fitness increases with the fraction of target spins.

arXiv

Dual Replicas for  
Spin(phenotype)  
Jij-interaction (genotype)

Replica Symmetric Phase  
-robust to noise and mutation



Through directed evolution; fluctuations decrease

(\*\*Model, experiments, theory, i.e., increase of robustness through evolution.)

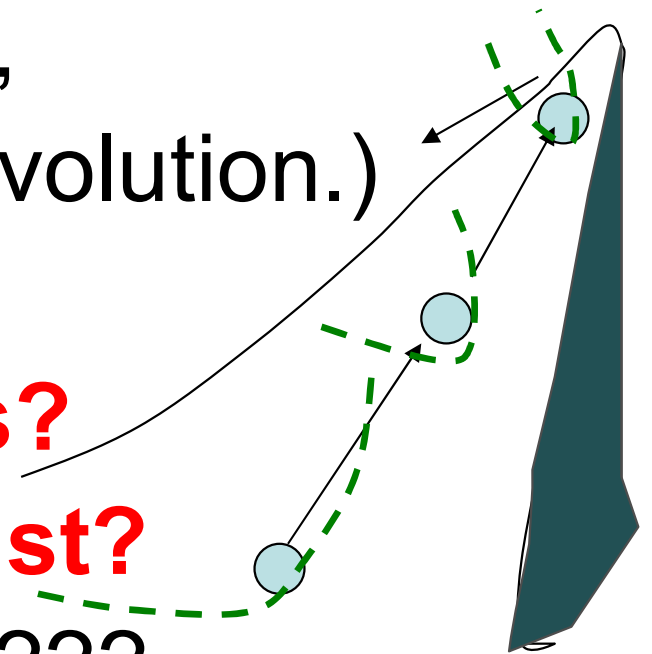
Then, evolution slows down..

↔ **How Evolution continues?**

**Why Large Fluctuations exist?**

?? **Is there regain of fluctuations????**

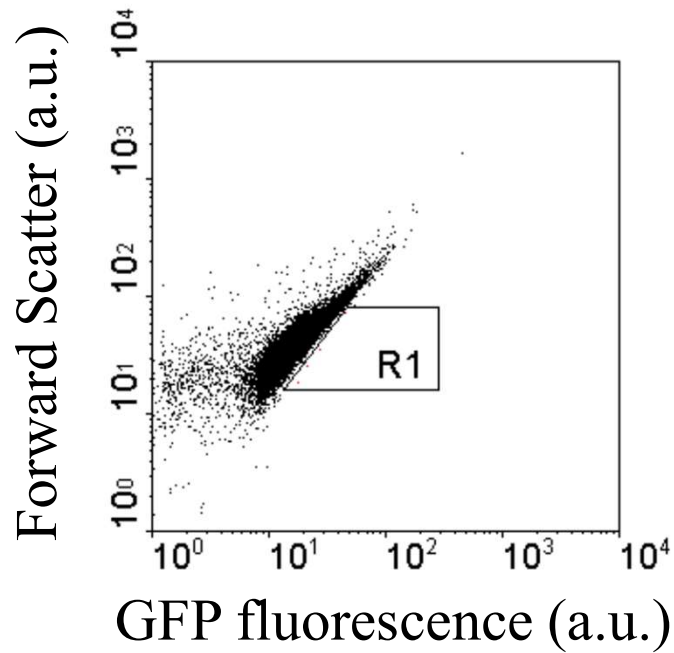
- Experimentally Observed: Appearance of mutants with large fluctuations at further evolution. (← interference with other processes) (Ito, etal, MSB 2009)
- → **Restoration of Plasticity**



# Strategy for survival with the increase of fluctuation

Fig.1

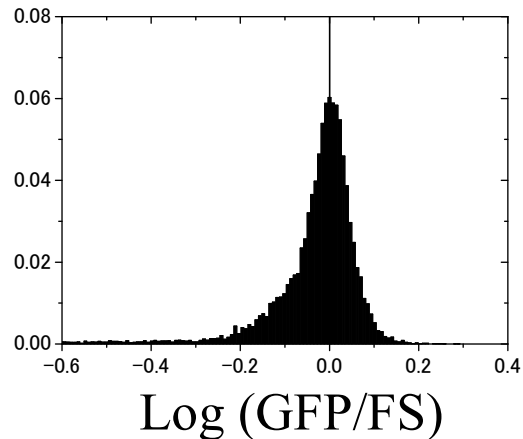
A



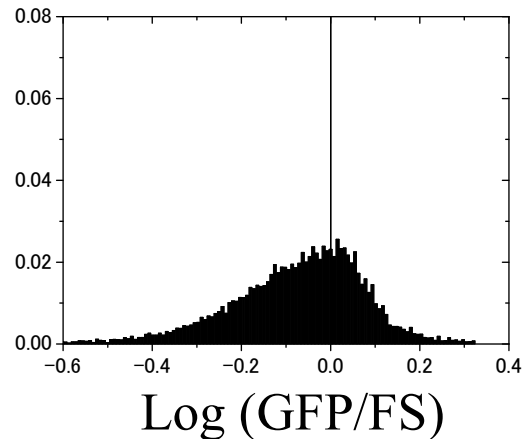
Selection experiment  
at individual level  
(strong selective pressure)  
(Ito et al, *Molecular Systems  
Biology* 2009)

Appearance of 'broad  
mutants'

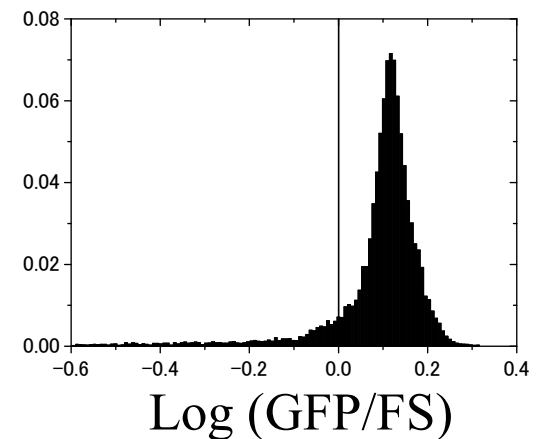
B

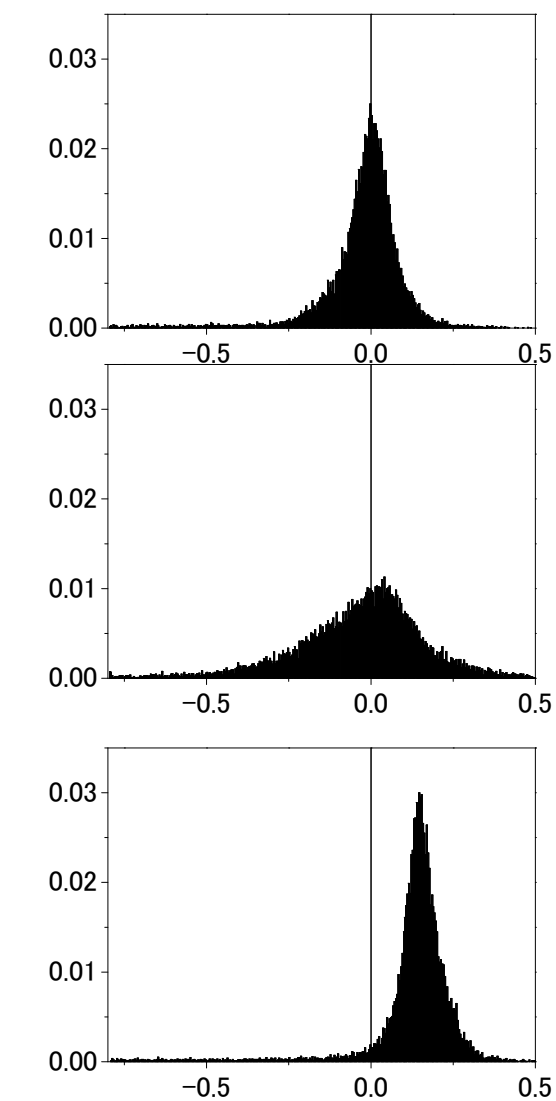
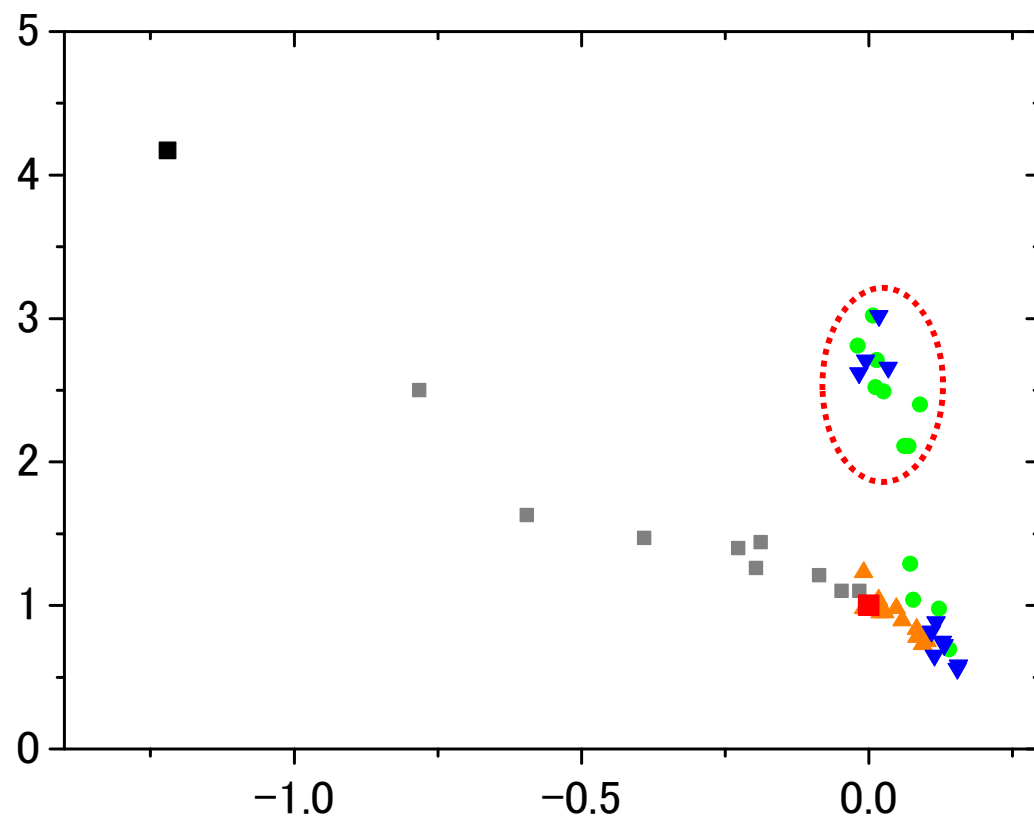


C

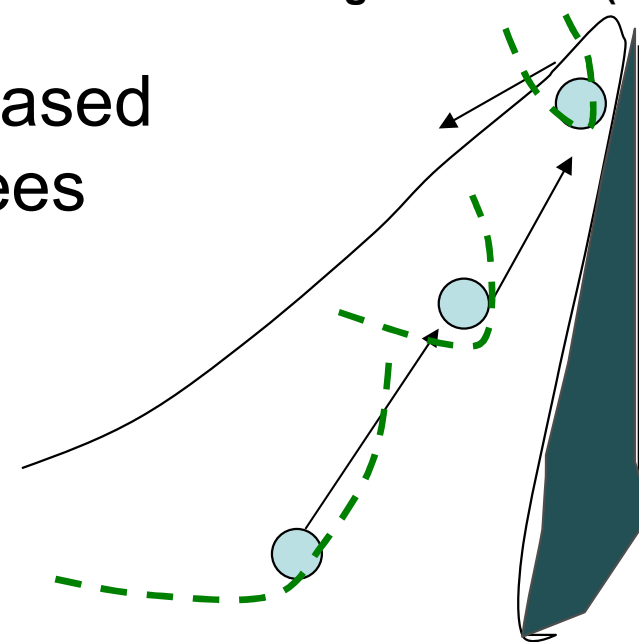


D



**A****B****C****Log (GFP FL/FS) (a.u.)****Full width at half-maximum****Log Peak value (a.u.)**

Here Fluctuation in  
mRNA conc. Is increased  
→ Use of 'new' degrees  
of freedom



# Figure S1 C

Selected clone (4<sup>th</sup> round)

The initial clone

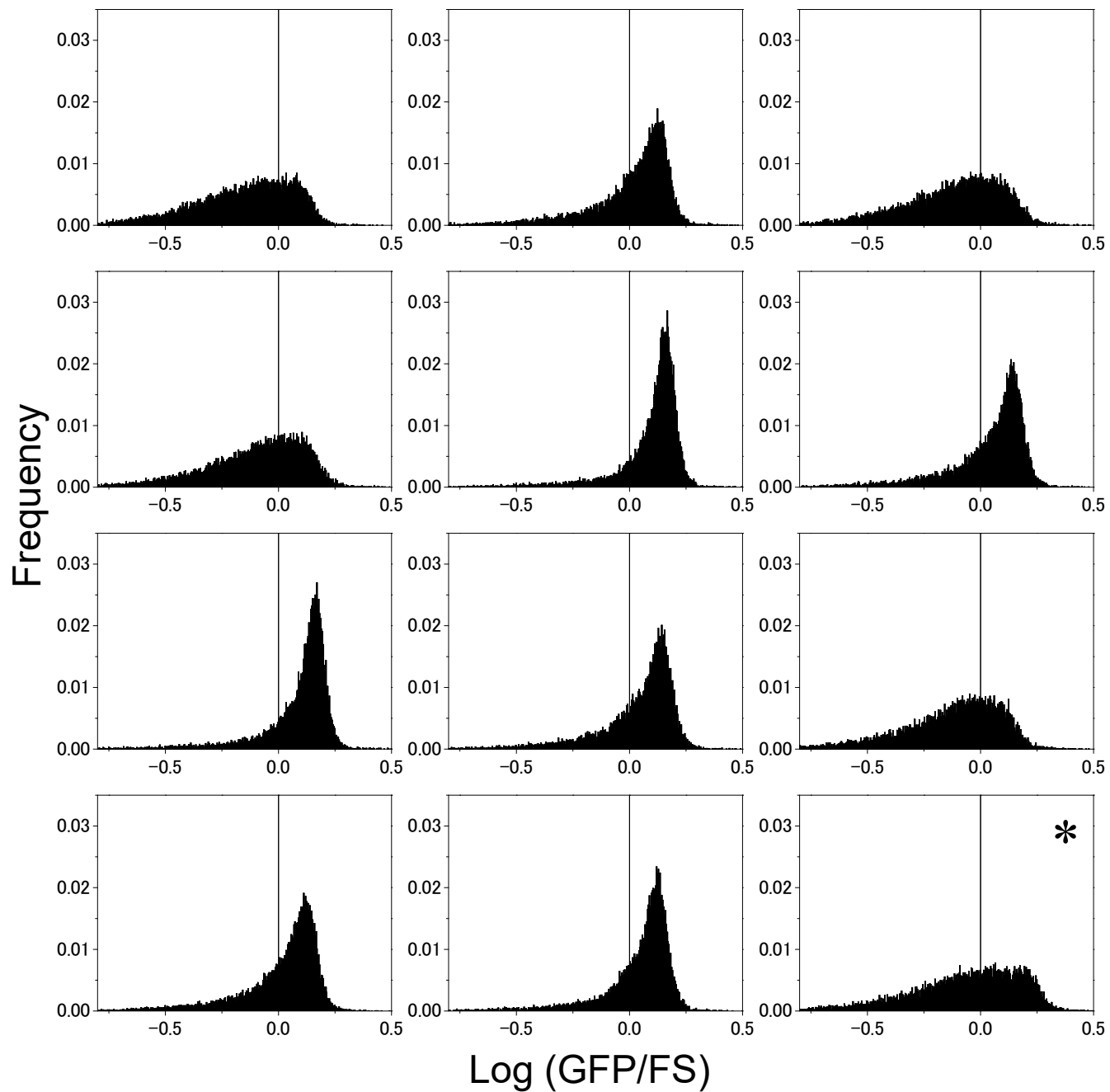
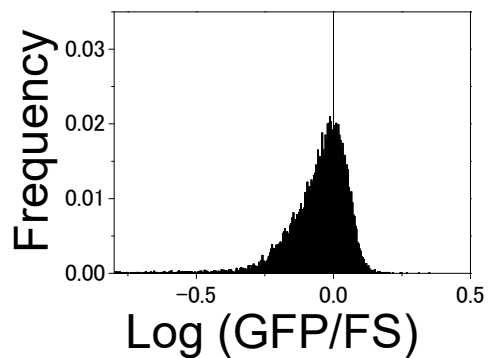
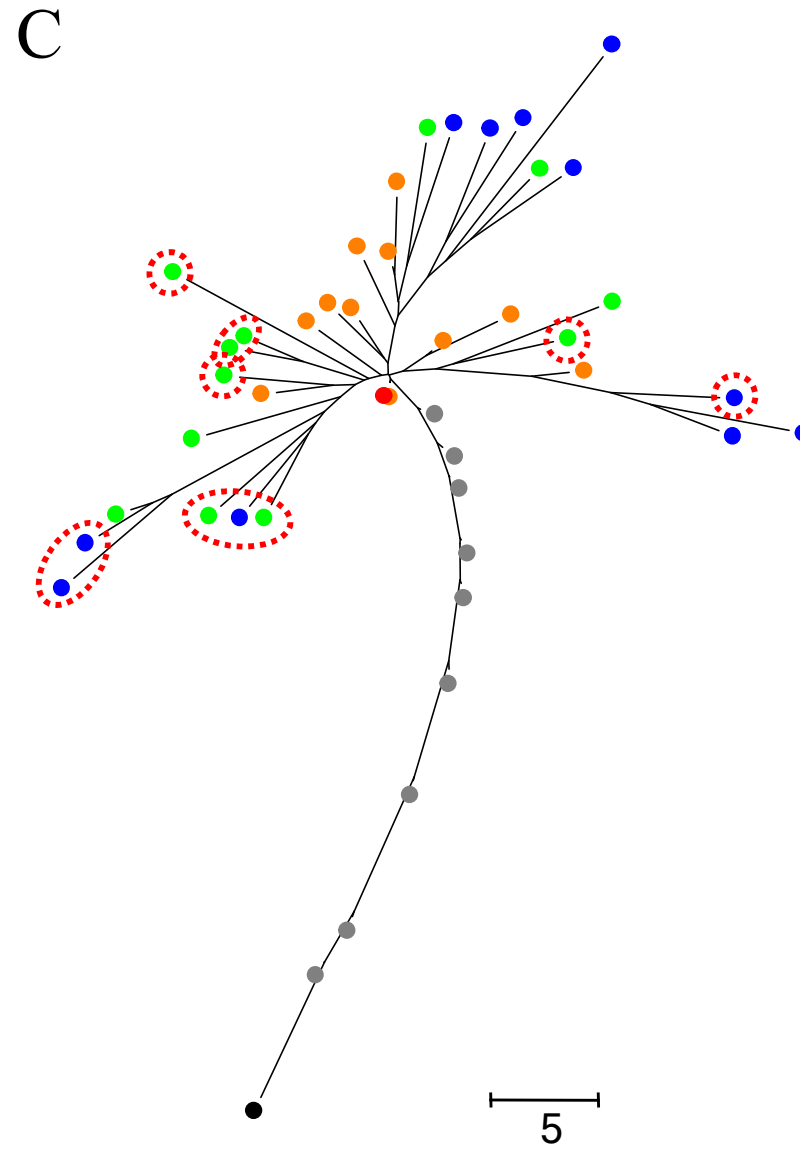
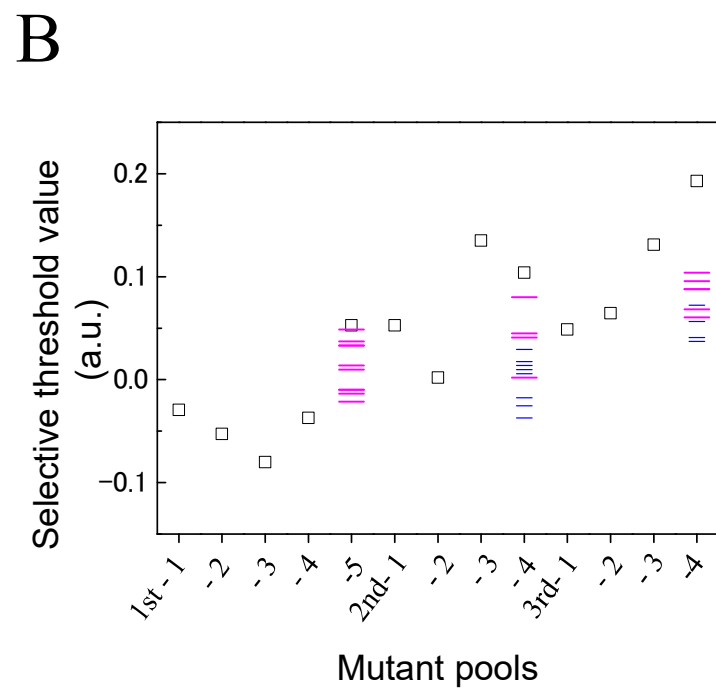
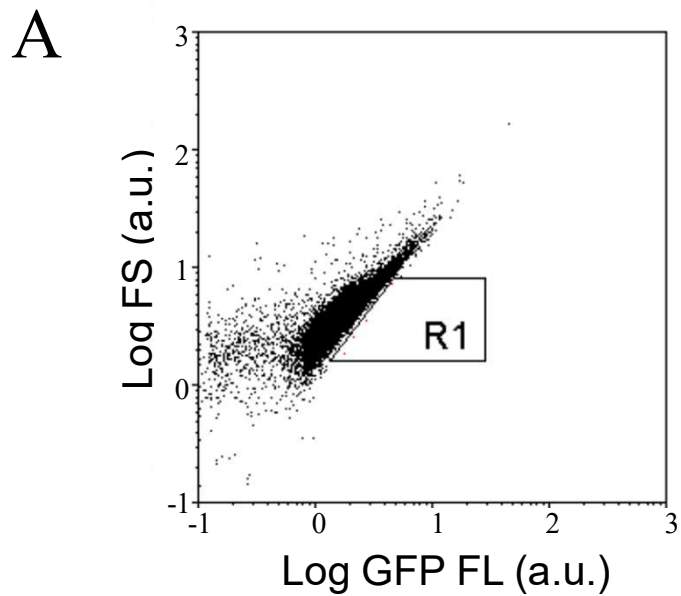
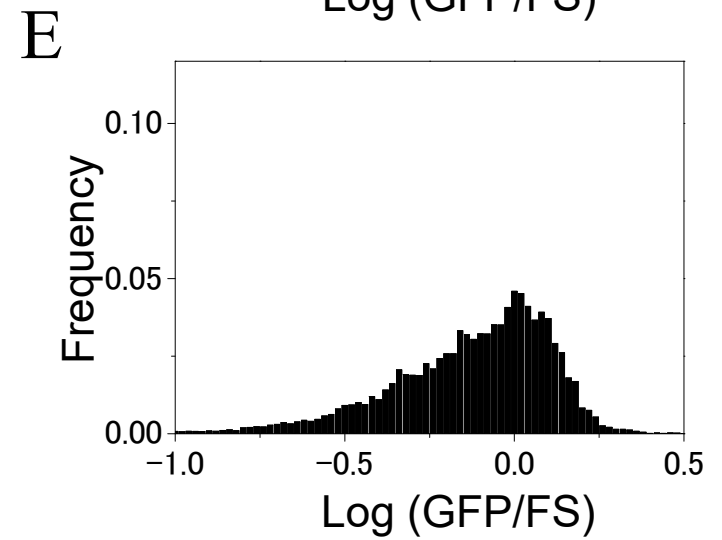
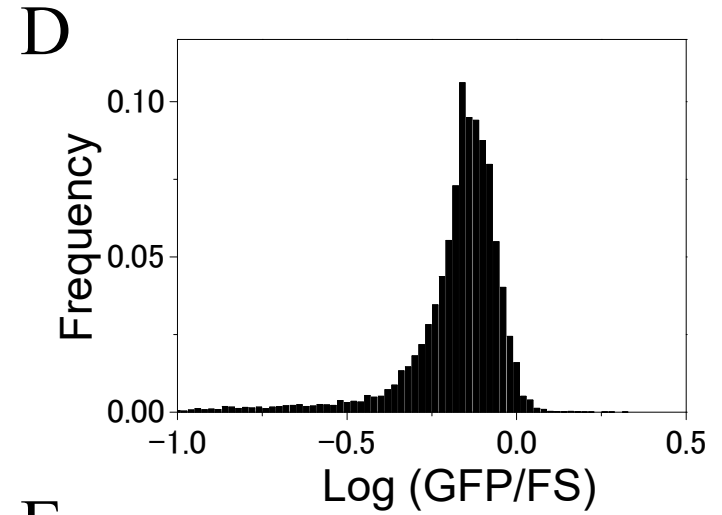
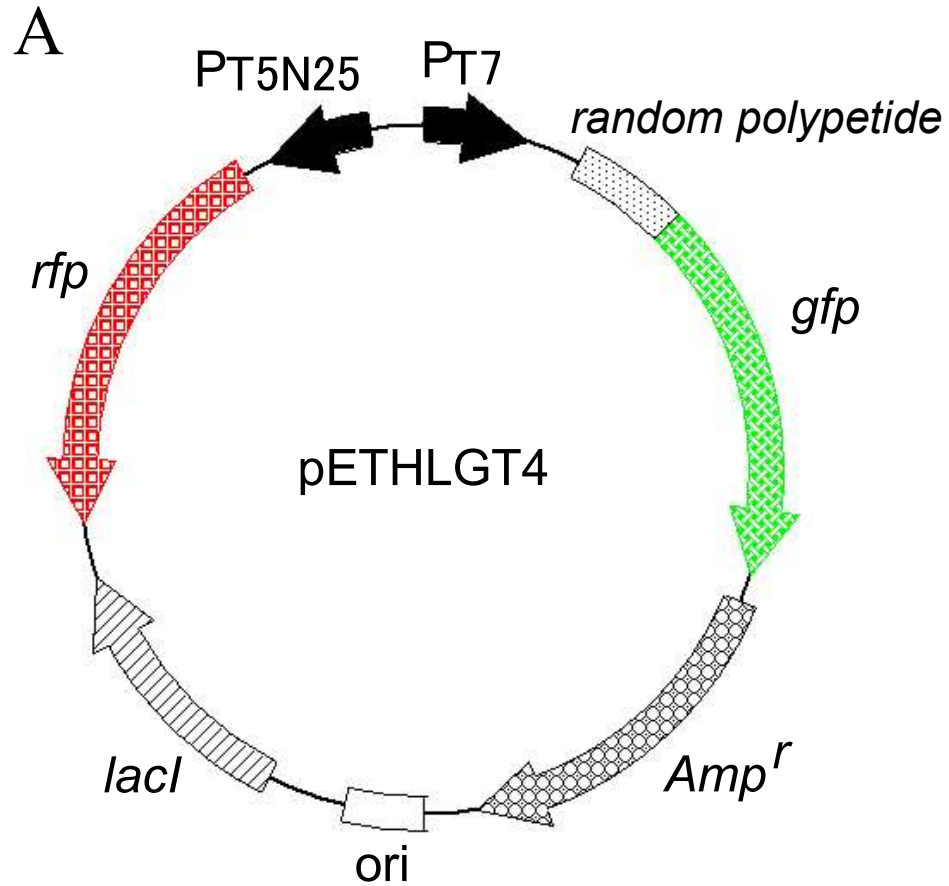


Figure 1



# Figure S3





A possible scenario:

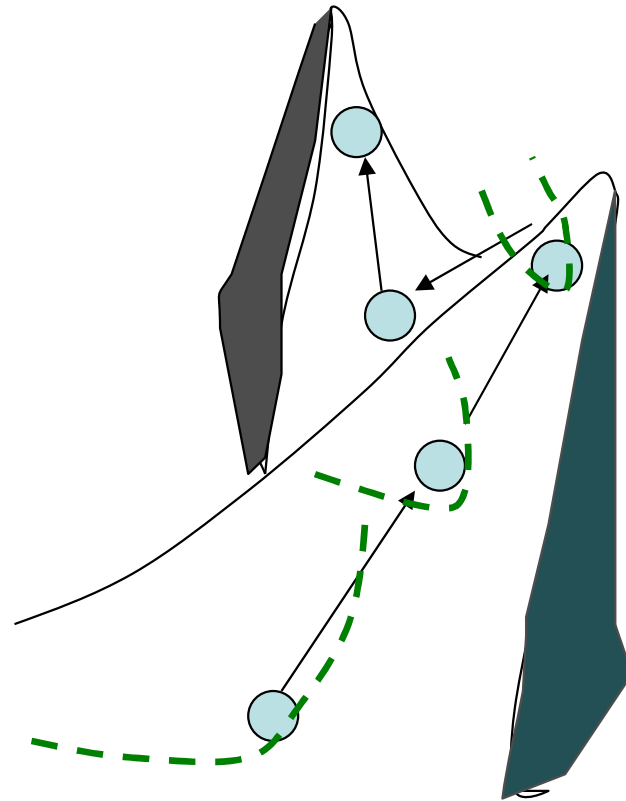
directed evolution → decrease in fluctuation and plasticity,

loss of evolvability

Cliff Landscape (fall down to some other directions than the original 1-dimensional direction)

Re-increase of fluctuation → Recovery of evolvability

Evolve to  
some other  
direction →  
(Gain of novel  
function)



Modularity?

- Fluorescence Intensity

combination of several factors

(1) Solubility ← indeed major source for the initial stage

(2) Fluorescence in single molecule

(3) Expression level

(3.1) plasmid copy number

(3.2) mRNA level

← also related with cell growth

Change in broad mutants

neither (1) nor (2) (average, variance)

(3) –

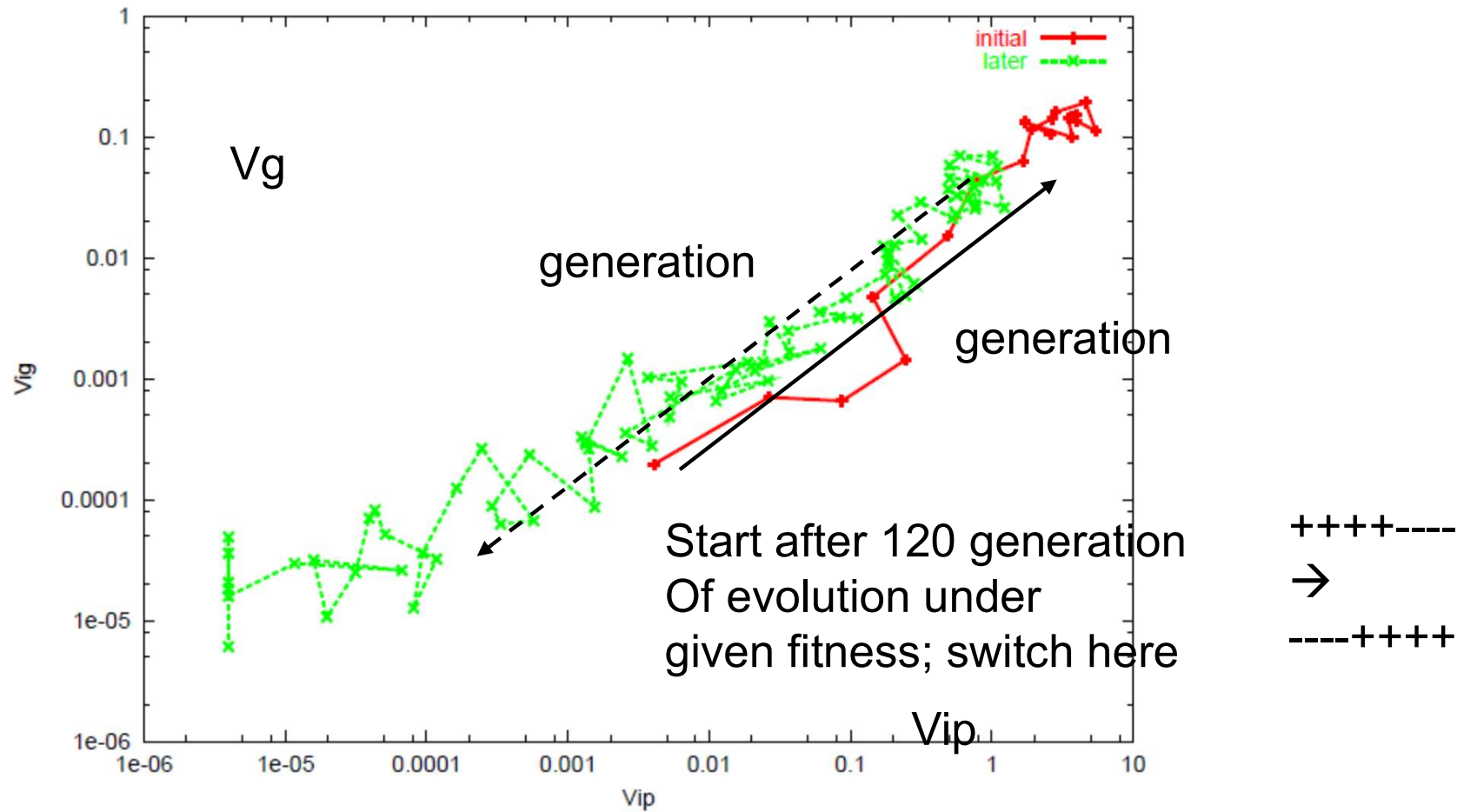
average decreased, variance is increased

not (3.1), but (3.2)

- Toxicity in GFP?
- influences cell growth
- Broad; GFP synthesis/growth are suppressed for many cells, but some continue
  - difference in timing in suppression
  - source of increase in fluctuation?

(‘heterochrony’ in Gould?)

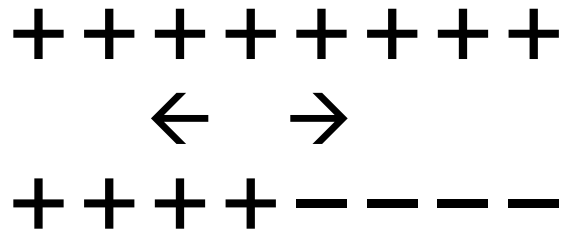
When environmental condition is **switched** in the model  
 → fluctuation once **increases to regain evolvability**  
 and then decreases



?? Increase in fluctuation also proportionally??

# Continuous environmental change

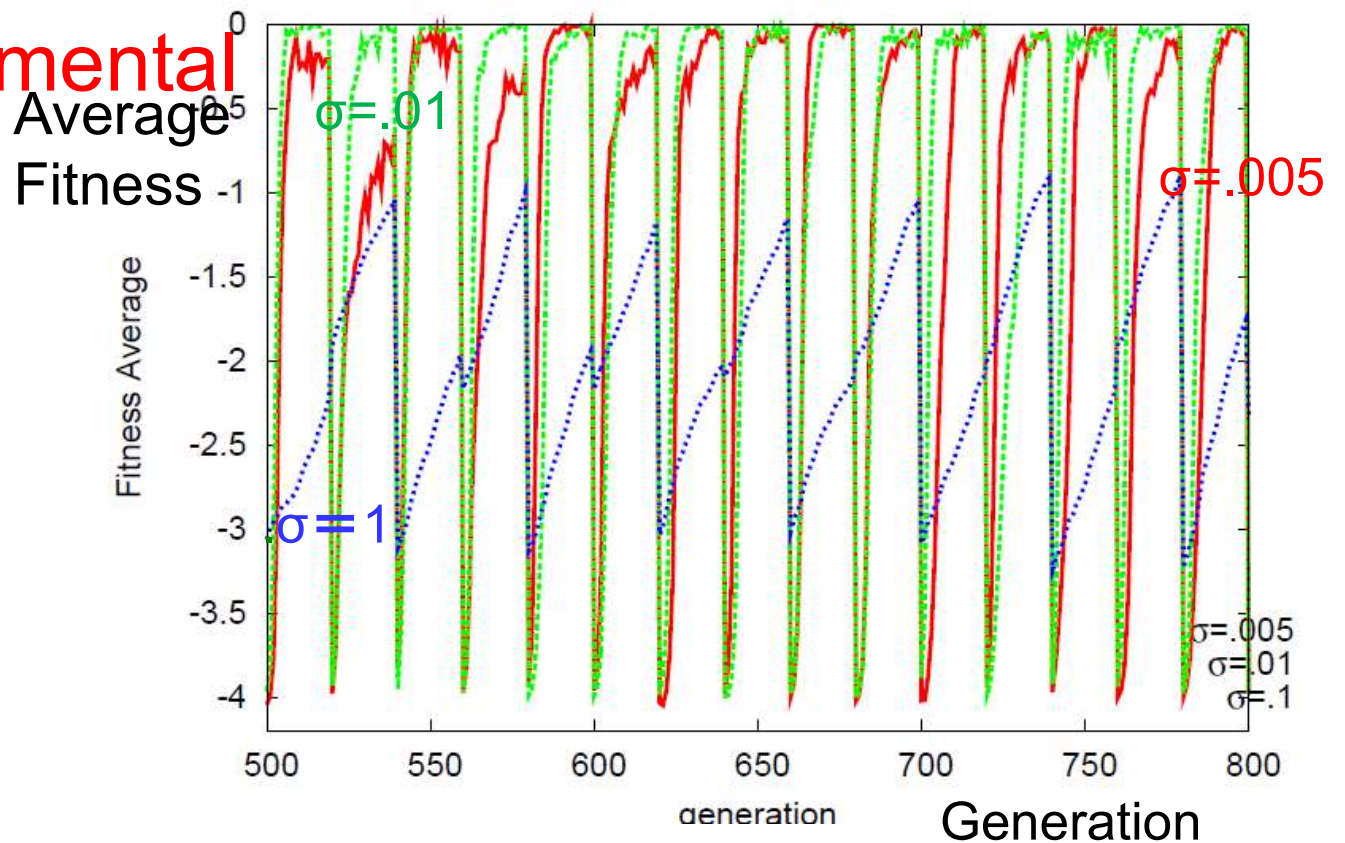
Switch the Fitness Condition per 20 generations



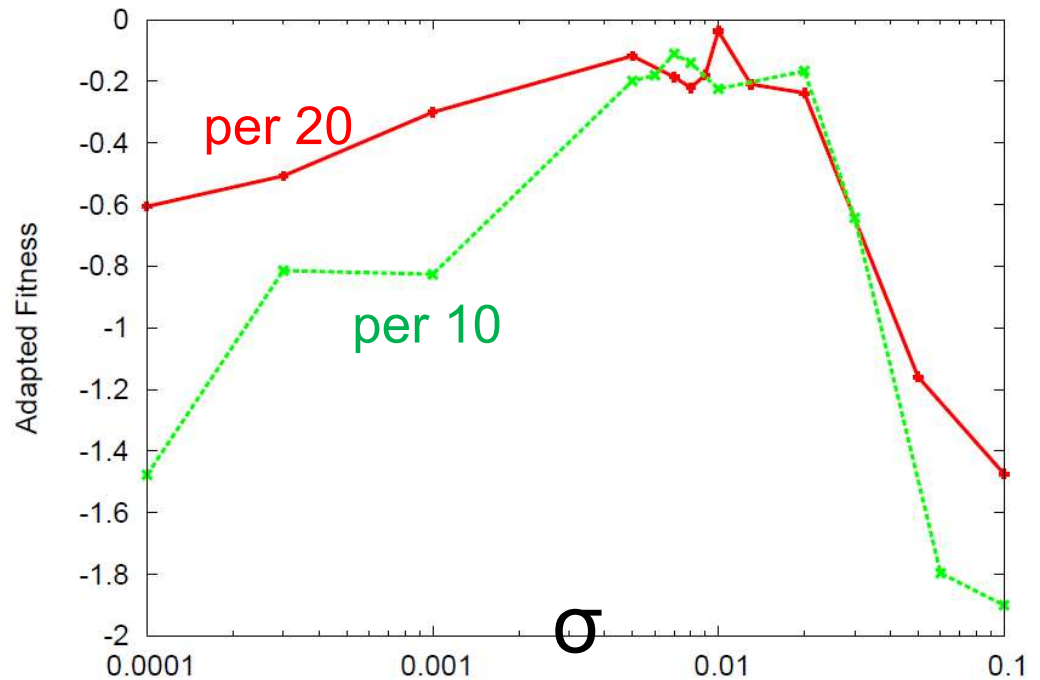
Large  $\sigma$  (low  $V_g/V_{ip}$ ) cannot follow the environmental change

Small  $\sigma$  (high  $V_g/V_{ip}$ ) non-fit mutants remain

Near  $\sigma \sim \sigma_c$  cope with environmental change satisfy both adaptation to new environment and robustness



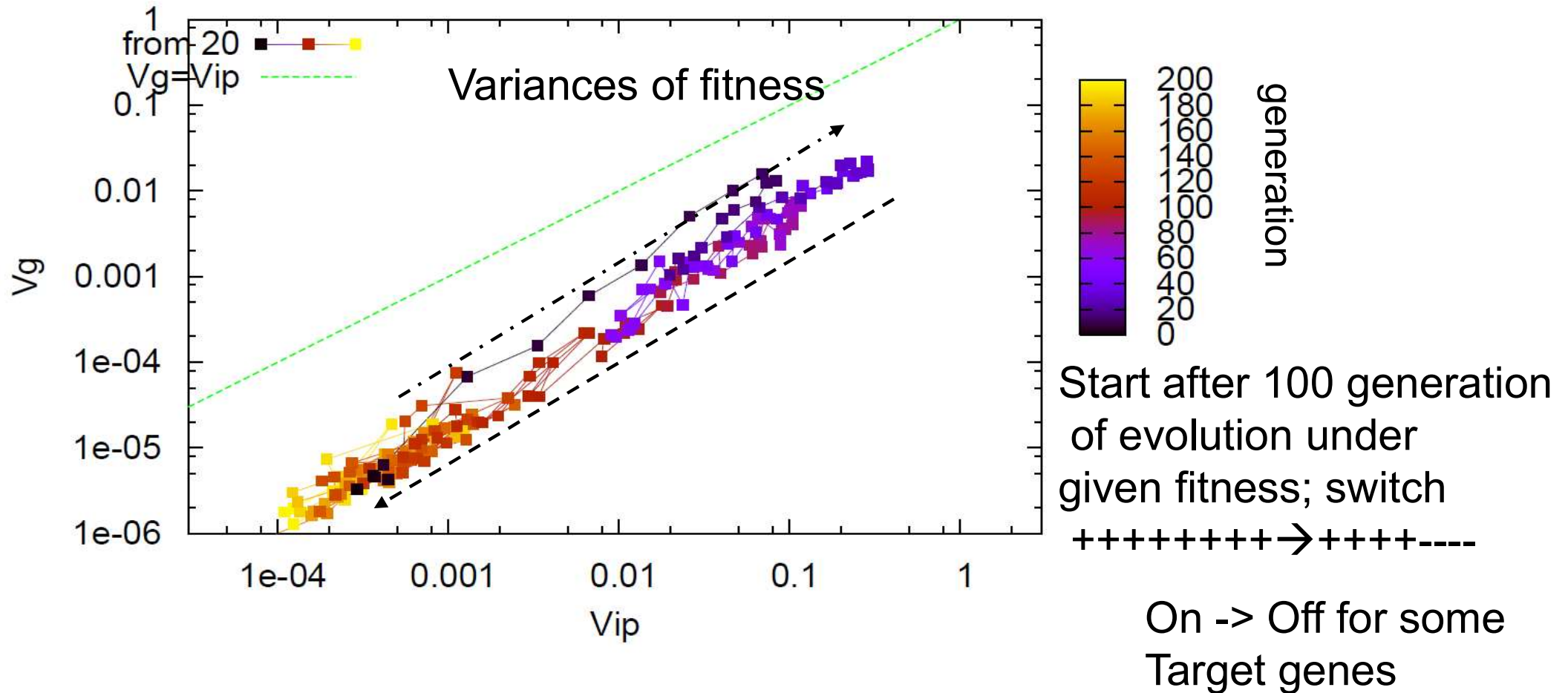
Average fitness after adaptation



In fixed environment/fitness, plasticity decreases.

When environmental condition is **switched** in the model

→ fluctuation once **increases to regain plasticity**  
( **evolvability** ) and then decreases

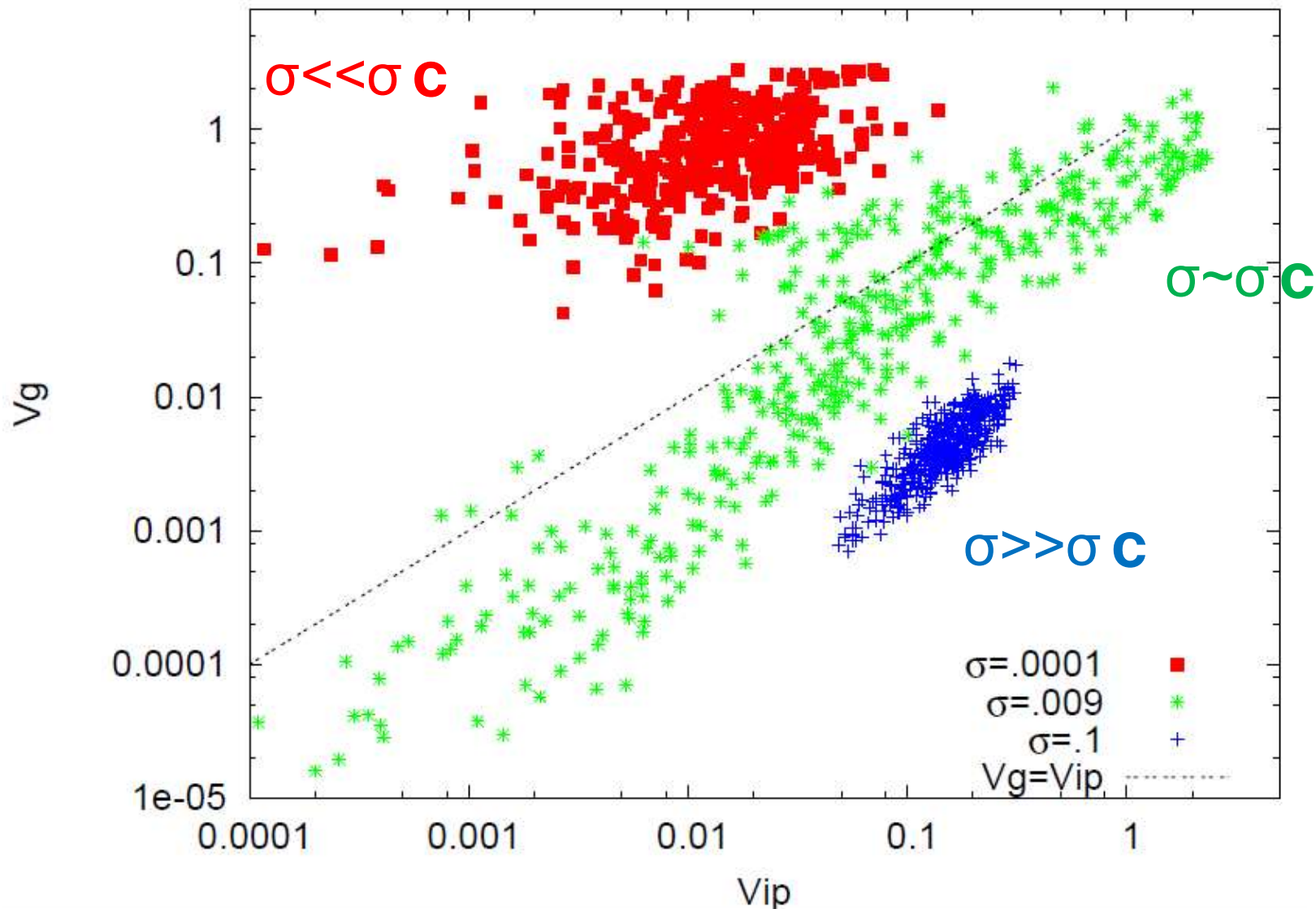


In a fluctuating environment, fluctuation (plasticity) is sustained

(Increase of fluctuation in bacterial evolution; Ito-Toyota-KK-Yomo)

# Critical State can adapt most efficiently to environmental change

Vip-Vg of fitness temporally varies to a large degree



## (B) Environmental variation?

Noise level  $\sigma > \sigma_c \rightarrow$  robustness increases and

$V_g, V_{ip}$  decreases (loss of evolvability)

In wildtype fluctuation and plasticity are maintained

How? ( $\leftarrow$  environmental fluctuation, interactions)

(a) individual environmental variation within each generation

(b) environmental change over generations (n)

$$\frac{dx_i}{dt} = F\left[\sum_j^M J_{ij}x_j - \theta_i\right] - x_i + I_i(n) + (\sigma\eta_i(t))$$

$$F(X) = 1/(\exp(-\beta X) + 1)$$

The Model

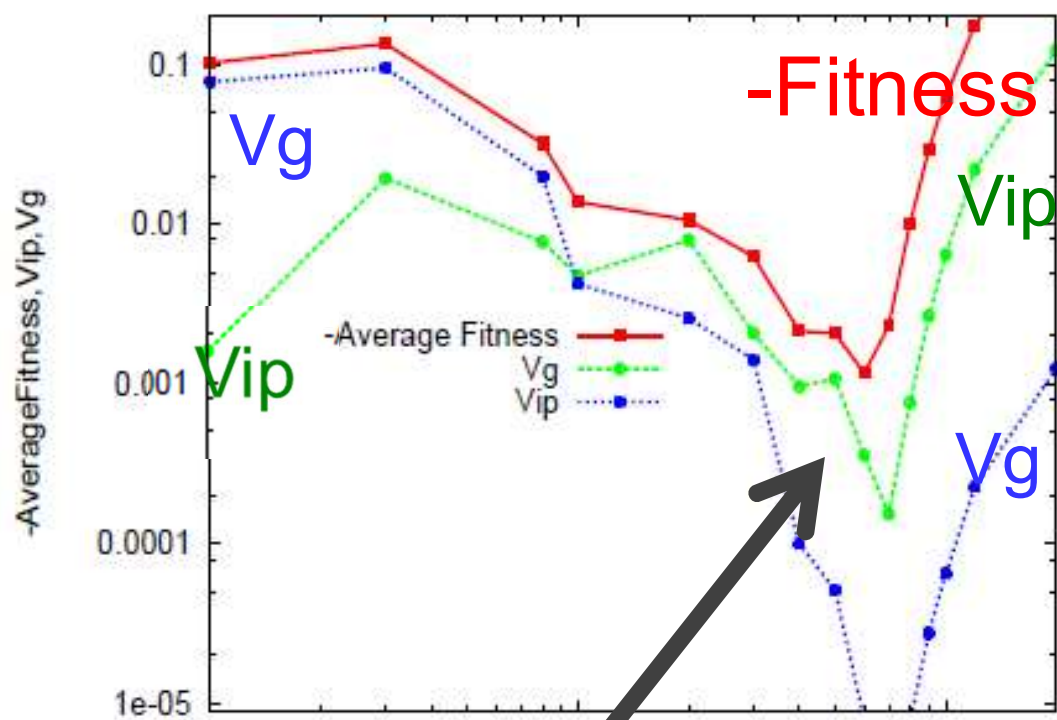
$I_i=0$  except for few input genes

(a)  $I_i = \xi_i(n)$  (b)  $I_i = \xi(n)$  (not dep on t but varies by generation n)



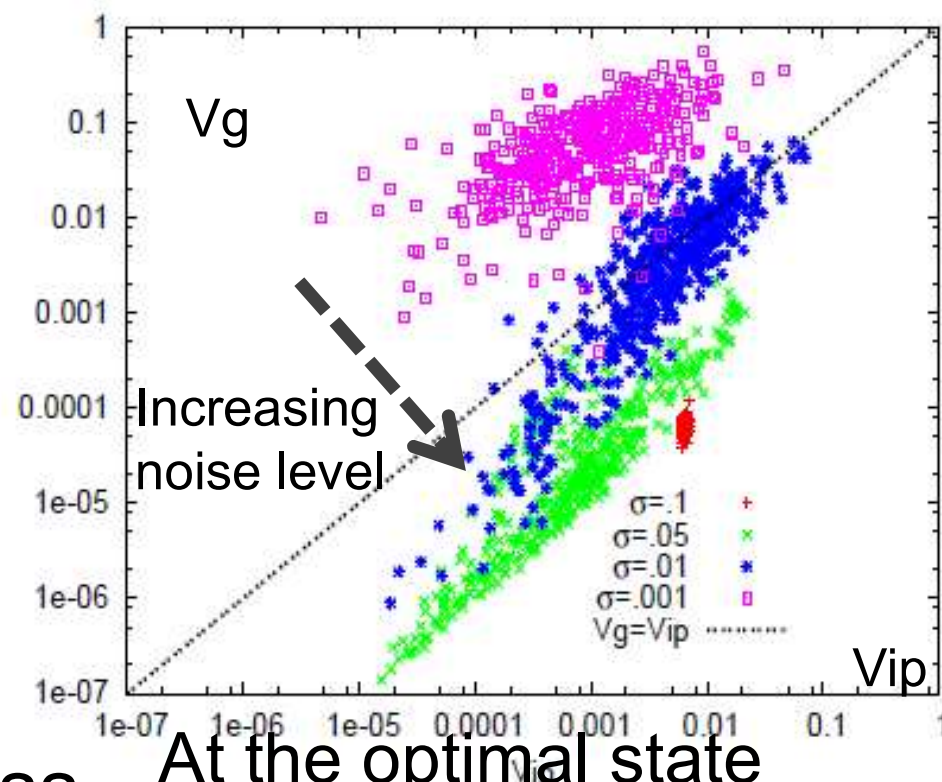
# Similar behaviors are observed by the input-change model

Average Fitness, Vip, Vg over generations



Near  $\sigma \sim \sigma_c$ , highest fitness where average Vip and average Vg crossovers

- Generation-to generation
- change of Vip and Vg



At the optimal state Vip and Vg goes up and down over generations, following proportionality

# Symbiotic Sympatric Speciation

KK etal 2000  
ProcRoySoc

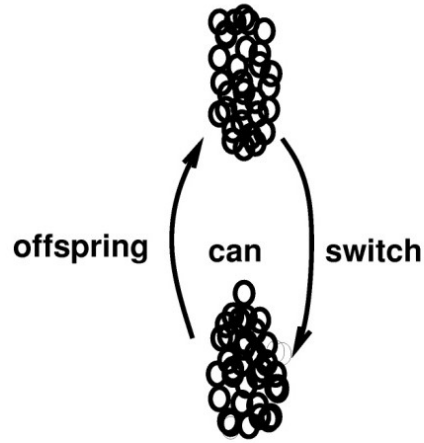
- So far, no interaction, evolution under fixed environment --  
– single-peaked distribution
- Speciation → change to double peaked distribution
- \*\* Sympatric Speciation -- fundamental but difficult?
- Our scenario for sympatric speciation (confirmed by several models):
  - (1) Isologous diversification ( 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

P (phenotype)



G (Genotype) a)

P Differentiation to two types



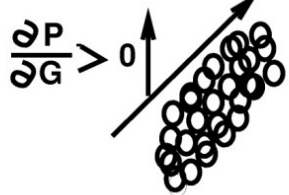
G b)

Cf: pithcfork possible

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

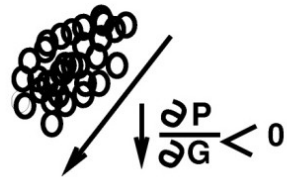
a increases with # of units

P



Growth Rate

Growth Rate



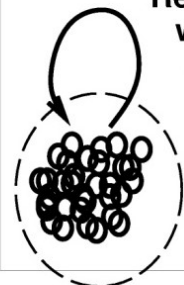
G c)

P



Recursive without the other group

Recursive without the other group



G d)

