



# Evolution and Thermodynamics

## Useful and Misleading Analogies

Peter Schuster

From Thermodynamics to Dynamical Systems

Emmerich Wilhelm's 60th Birthday

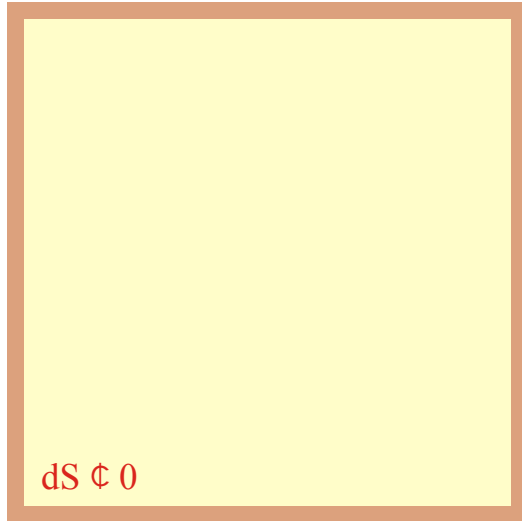
Universität Wien, 17.05.2002

Equilibrium thermodynamics is based on two major statements:

1. The energy of the universe is a constant (first law).
2. The entropy of the universe never decreases (second law).

Carnot, Mayer, Joule, Helmholtz, Clausius, .....

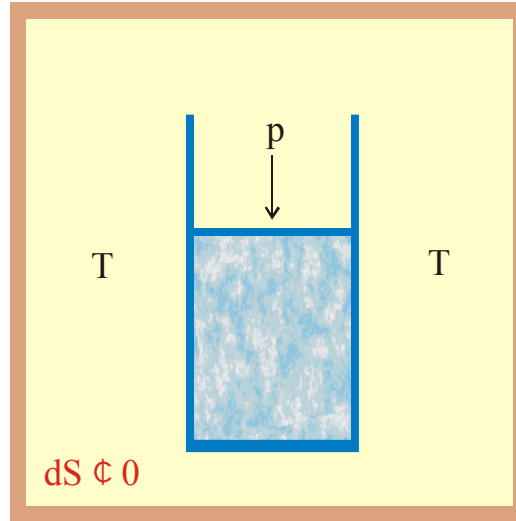
D.Jou, J.Casas-Vázquez, G.Lebon, *Extended Irreversible Thermodynamics*, 1996



### Isolated system

$$U = \text{const.}, V = \text{const.},$$

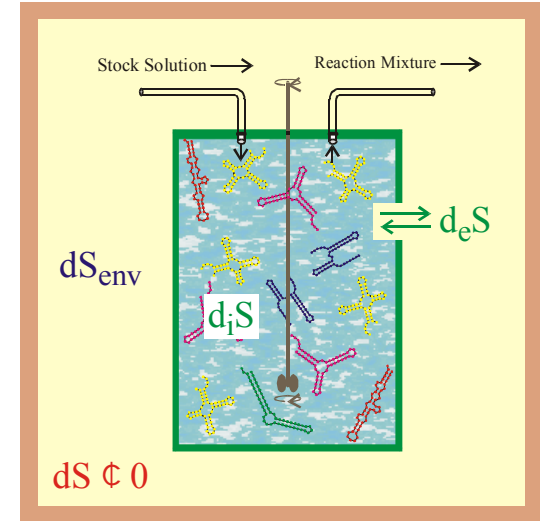
$$dS \leq 0$$



### Closed system

$$T = \text{const.}, p = \text{const.},$$

$$dG = dU - pdV - TdS < 0$$



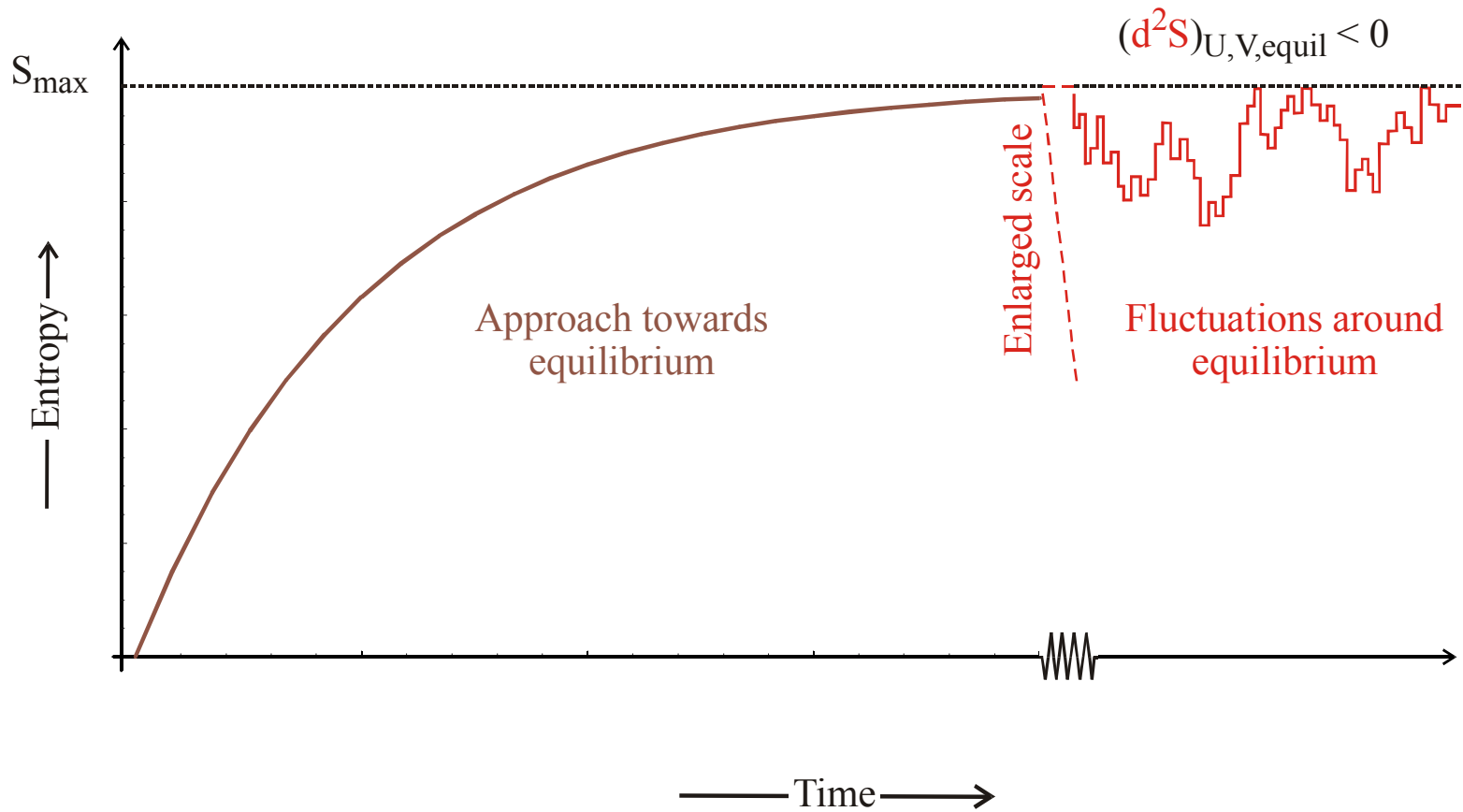
### Open system

$$dS = dS_{\text{env}} + dS \leq 0$$

$$dS = d_i S + d_e S$$

$$d_i S \leq 0$$

Entropy changes in different thermodynamic systems



Entropy and fluctuations at equilibrium

Thermodynamics of closed systems: Entropy is a non-decreasing function

Second law

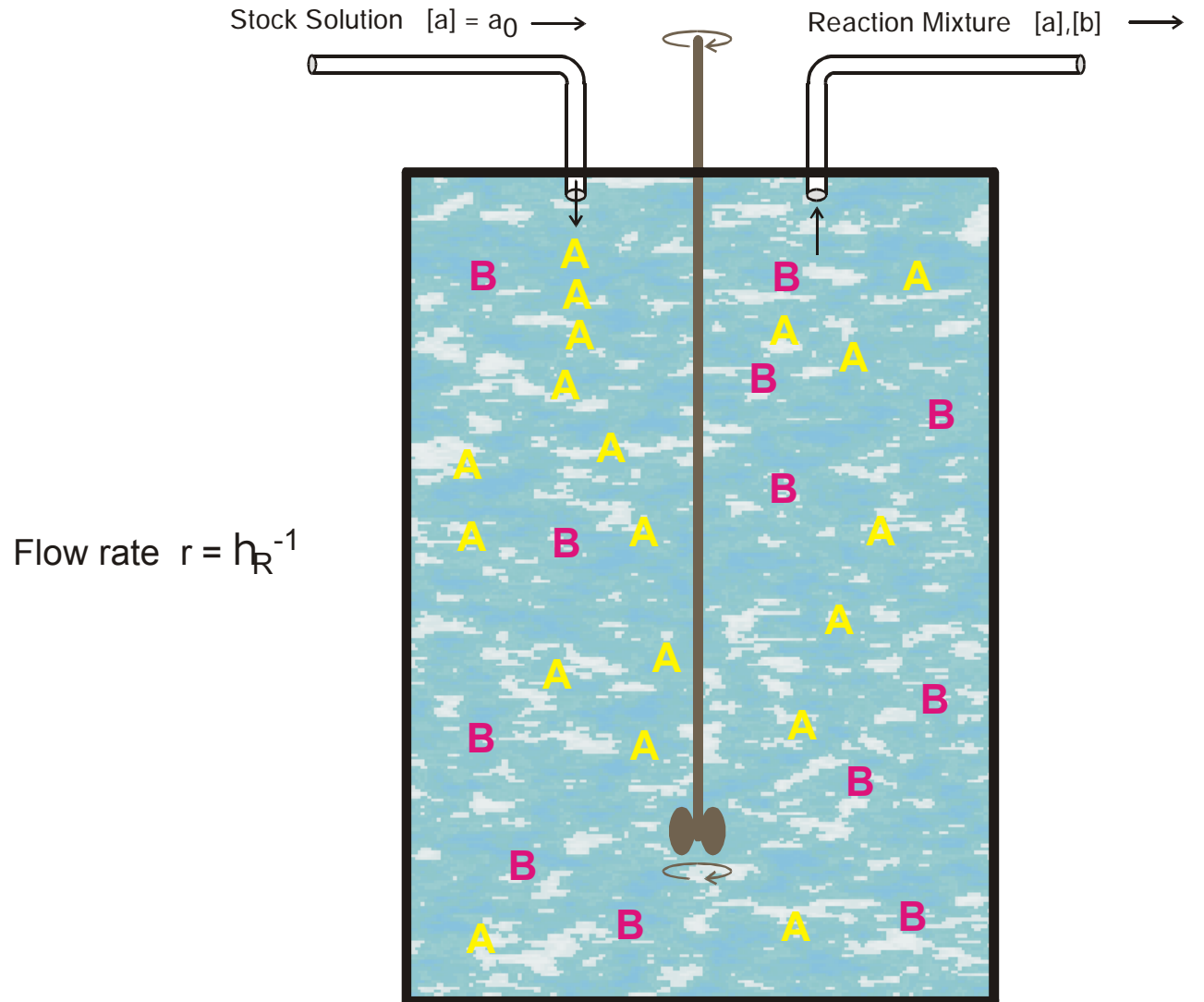
$$S(t) \rightarrow S_{\max}$$

Evolution of Populations:

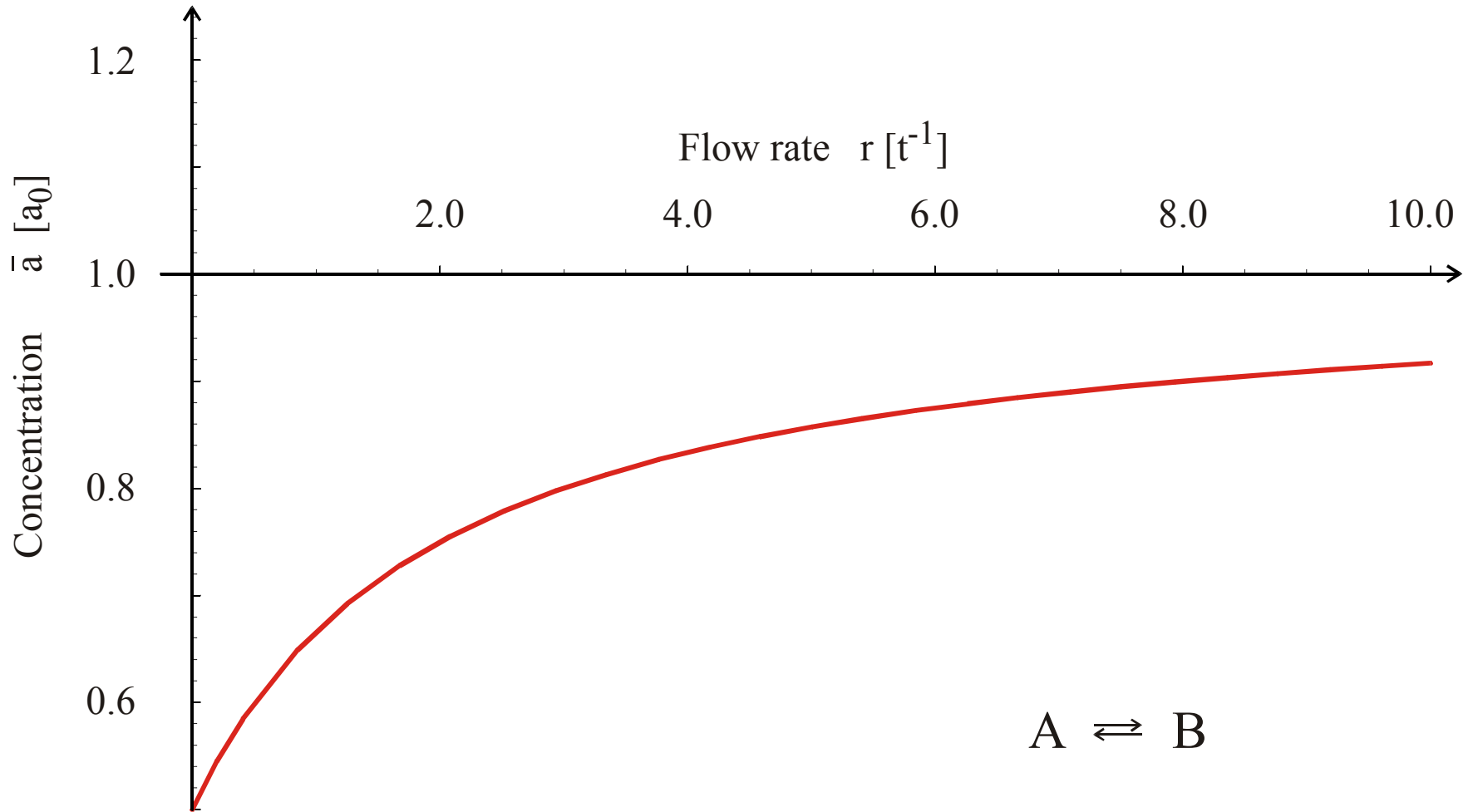
Mean fitness is a non-decreasing function

Ronald Fisher's conjecture

$$f(t) = \frac{\sum_k x_k(t) f_k}{\sum_k x_k(t)} \nearrow f_{\max}$$

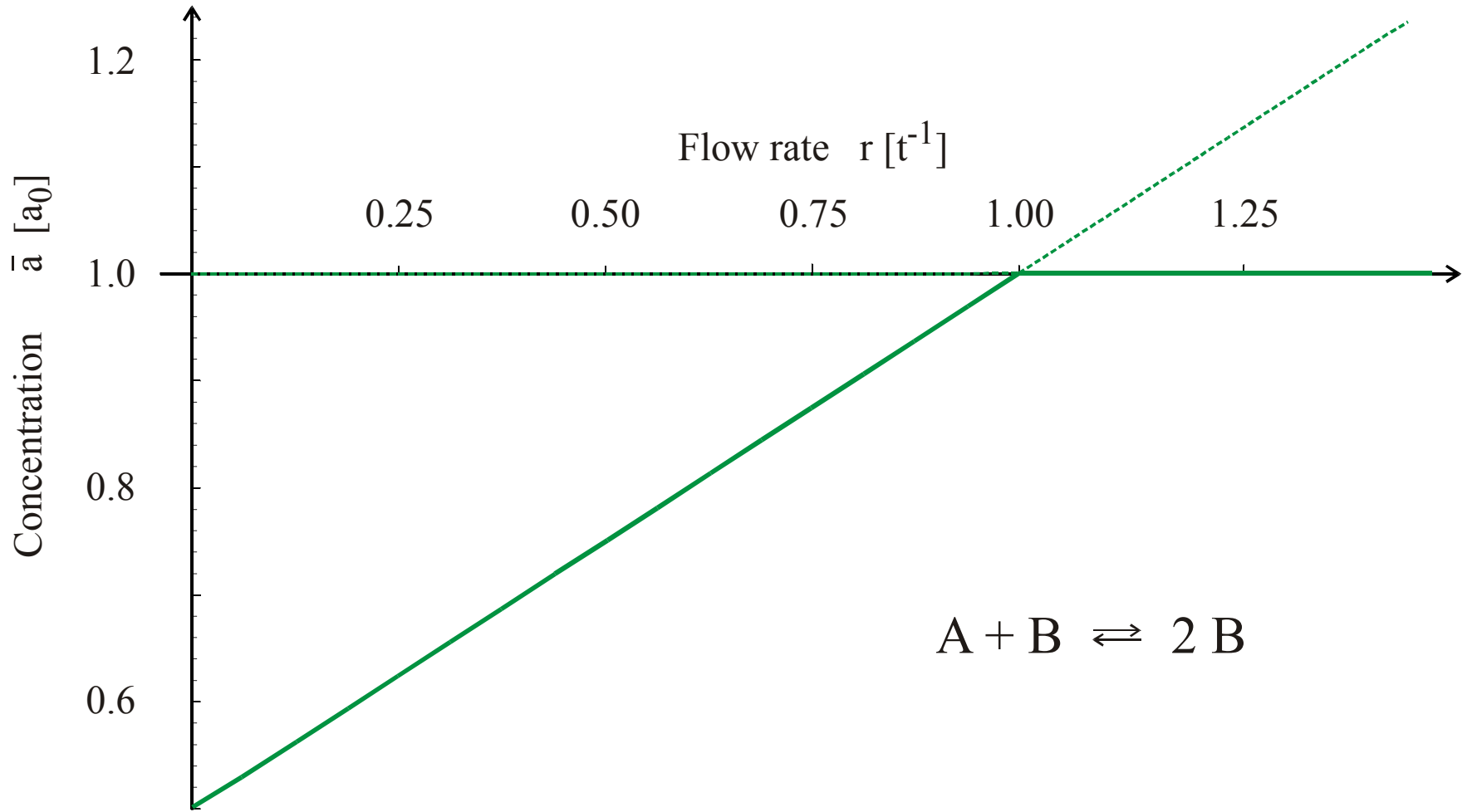


Reactions in the continuously stirred tank reactor (CSTR)

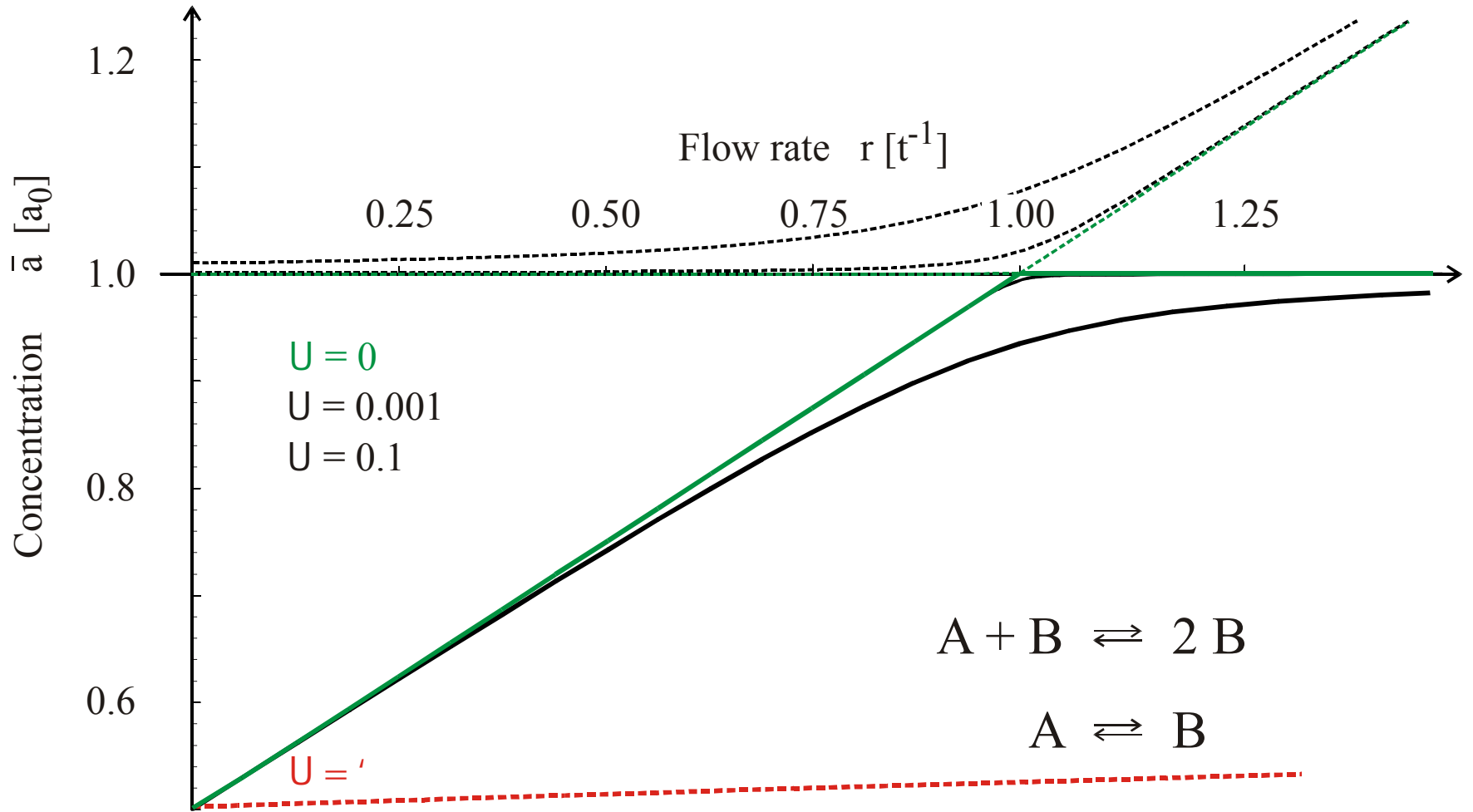


Reversible first order reaction in the flow reactor

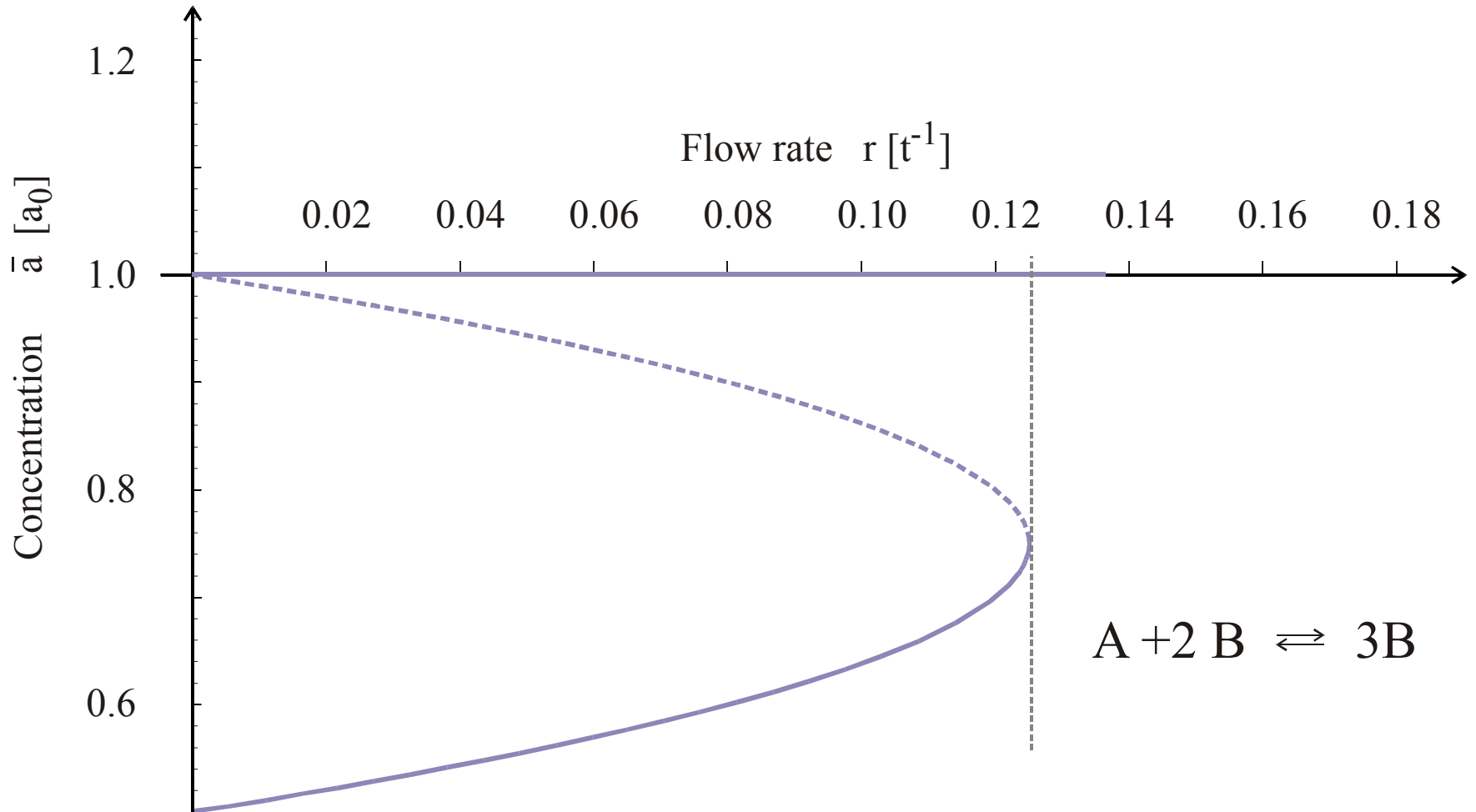




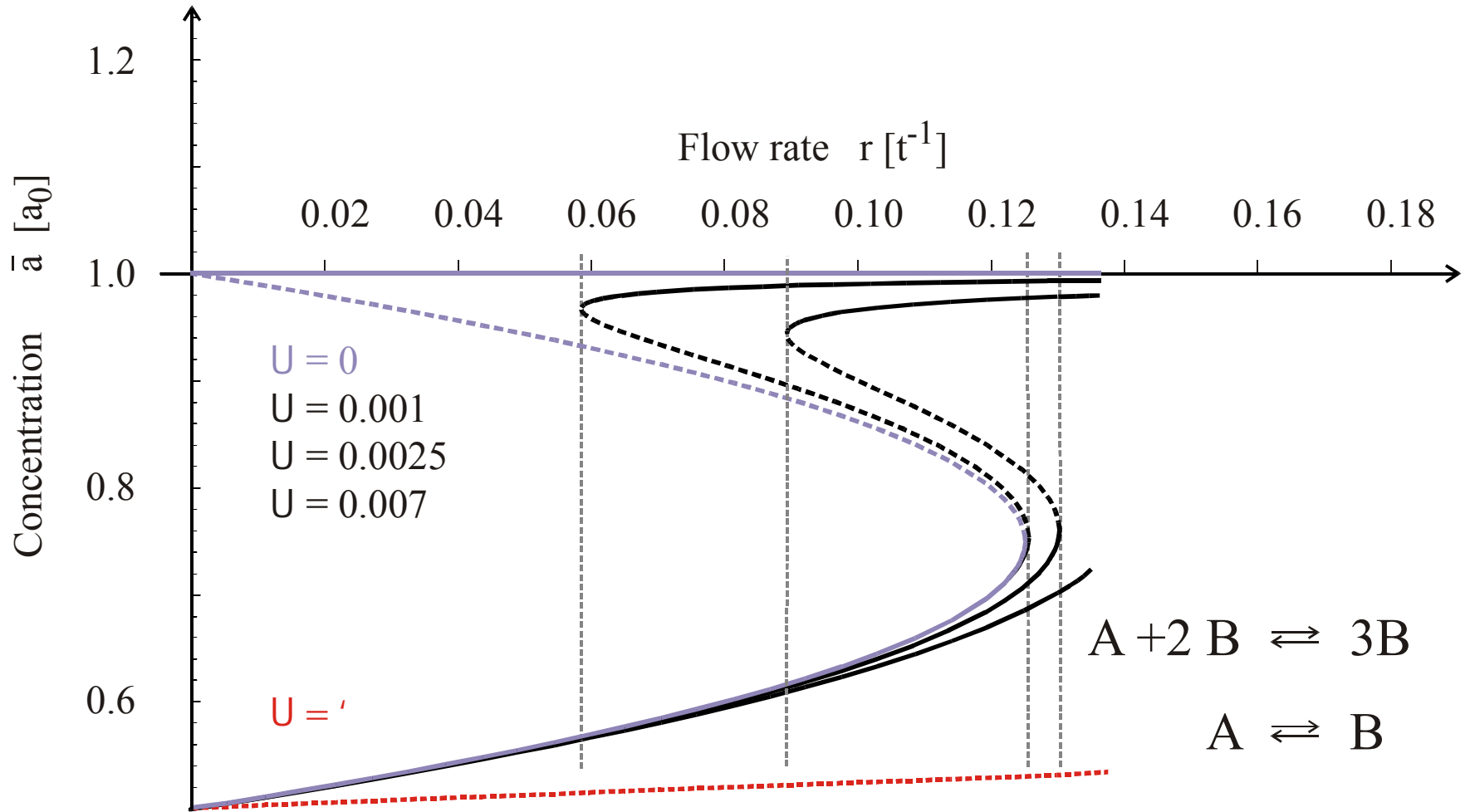
Autocatalytic second order reaction in the flow reactor



Autocatalytic second order and uncatalyzed reaction in the flow reactor



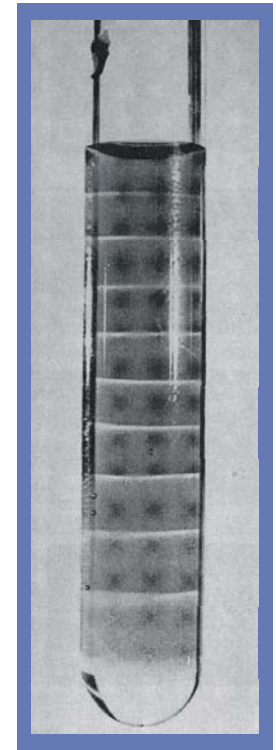
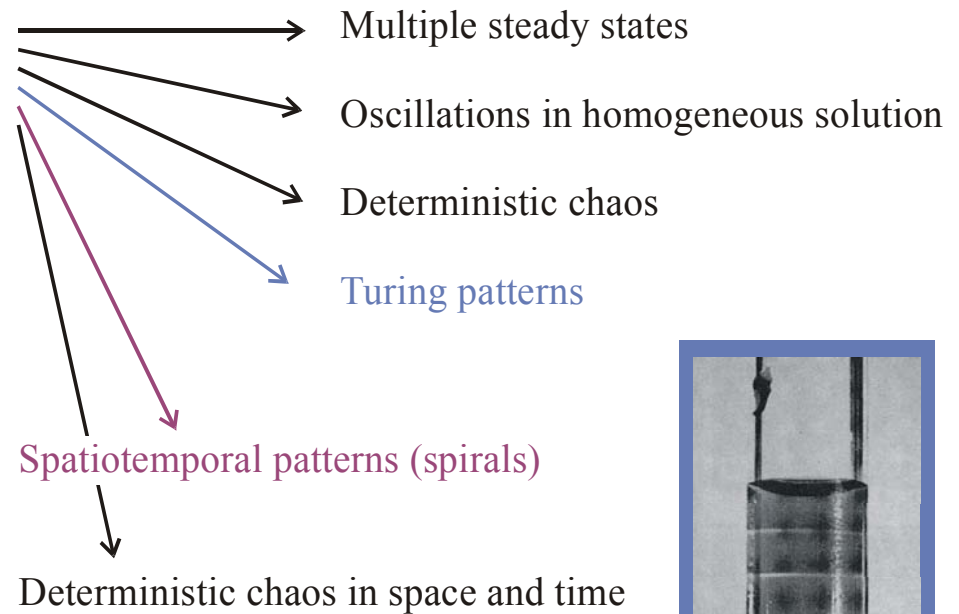
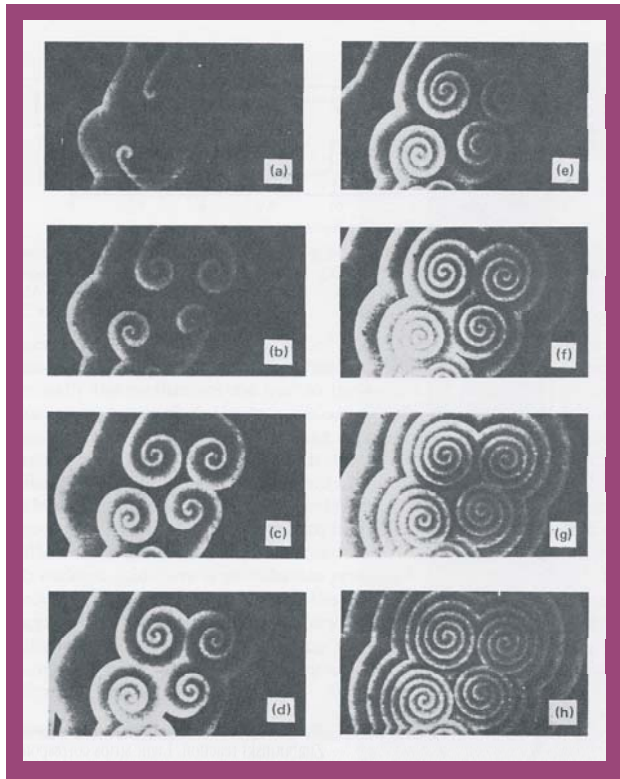
Autocatalytic third order reaction in the flow reactor



Autocatalytic third order and uncatalyzed reaction in the flow reactor

## Autocatalytic third order reactions

Direct,  $A + 2X \rightarrow 3X$ , or hidden in the reaction mechanism (Belousov-Zhabotinskii reaction).

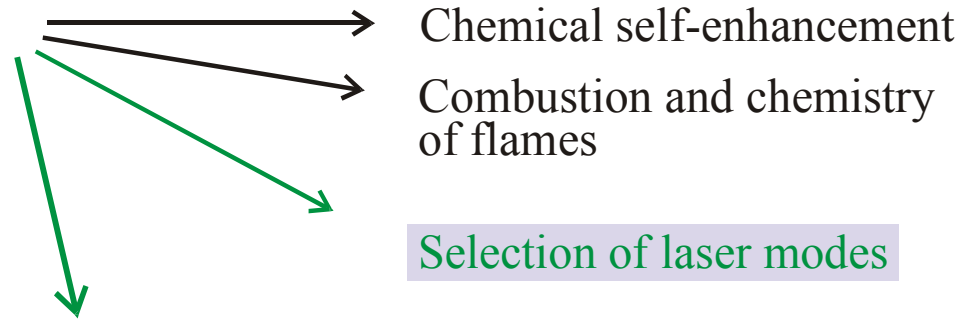


## Pattern formation in autocatalytic third order reactions

G.Nicolis, I.Prigogine. *Self-Organization in Nonequilibrium Systems. From Dissipative Structures to Order through Fluctuations*. John Wiley, New York 1977

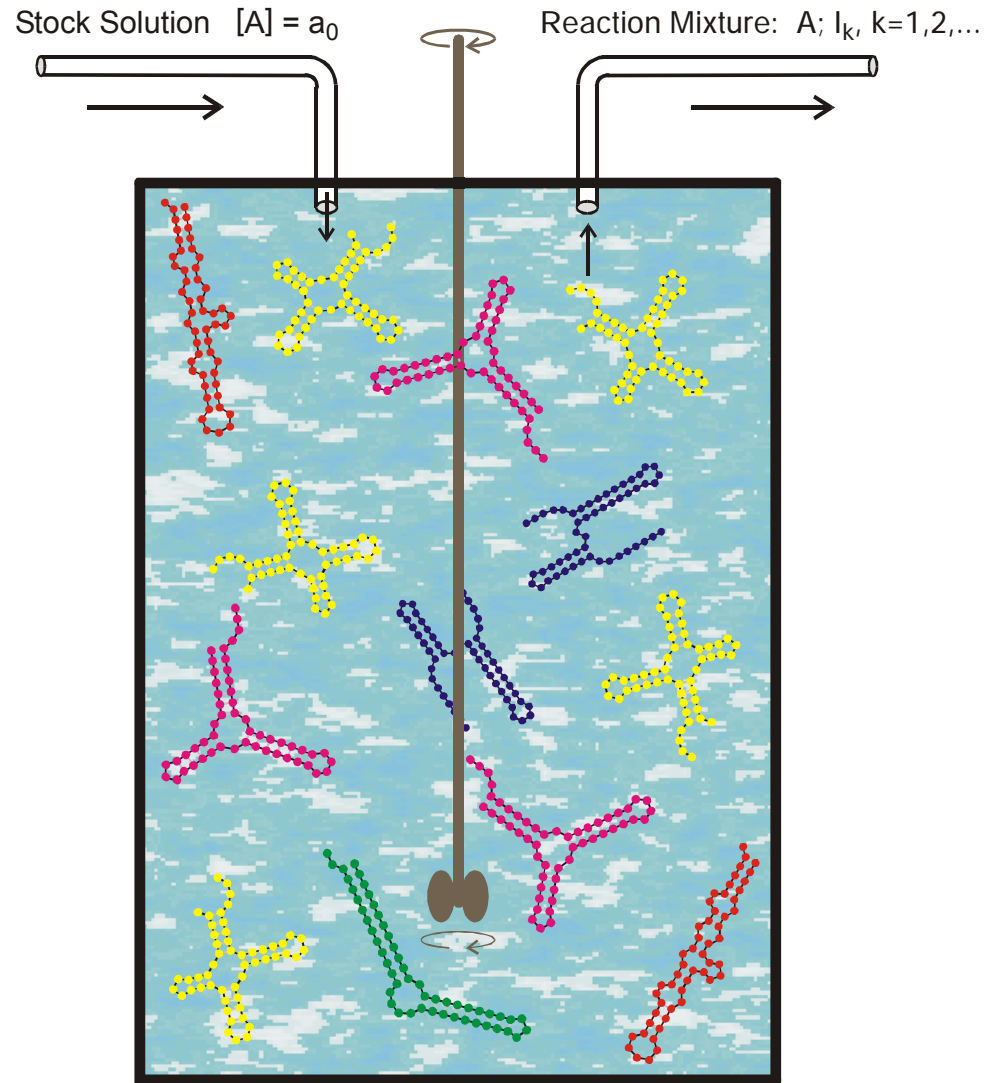
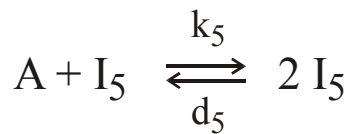
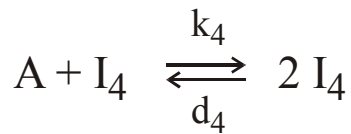
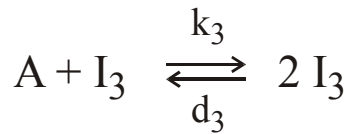
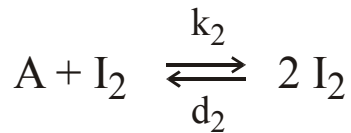
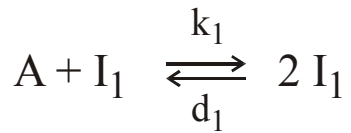
## Autocatalytic second order reactions

Direct,  $A + I \xrightarrow{k} 2I$ , or hidden in the reaction mechanism



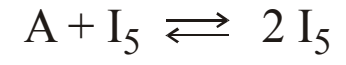
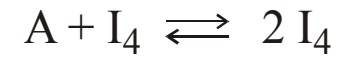
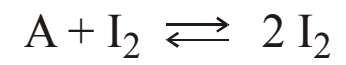
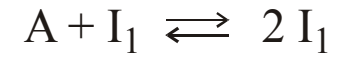
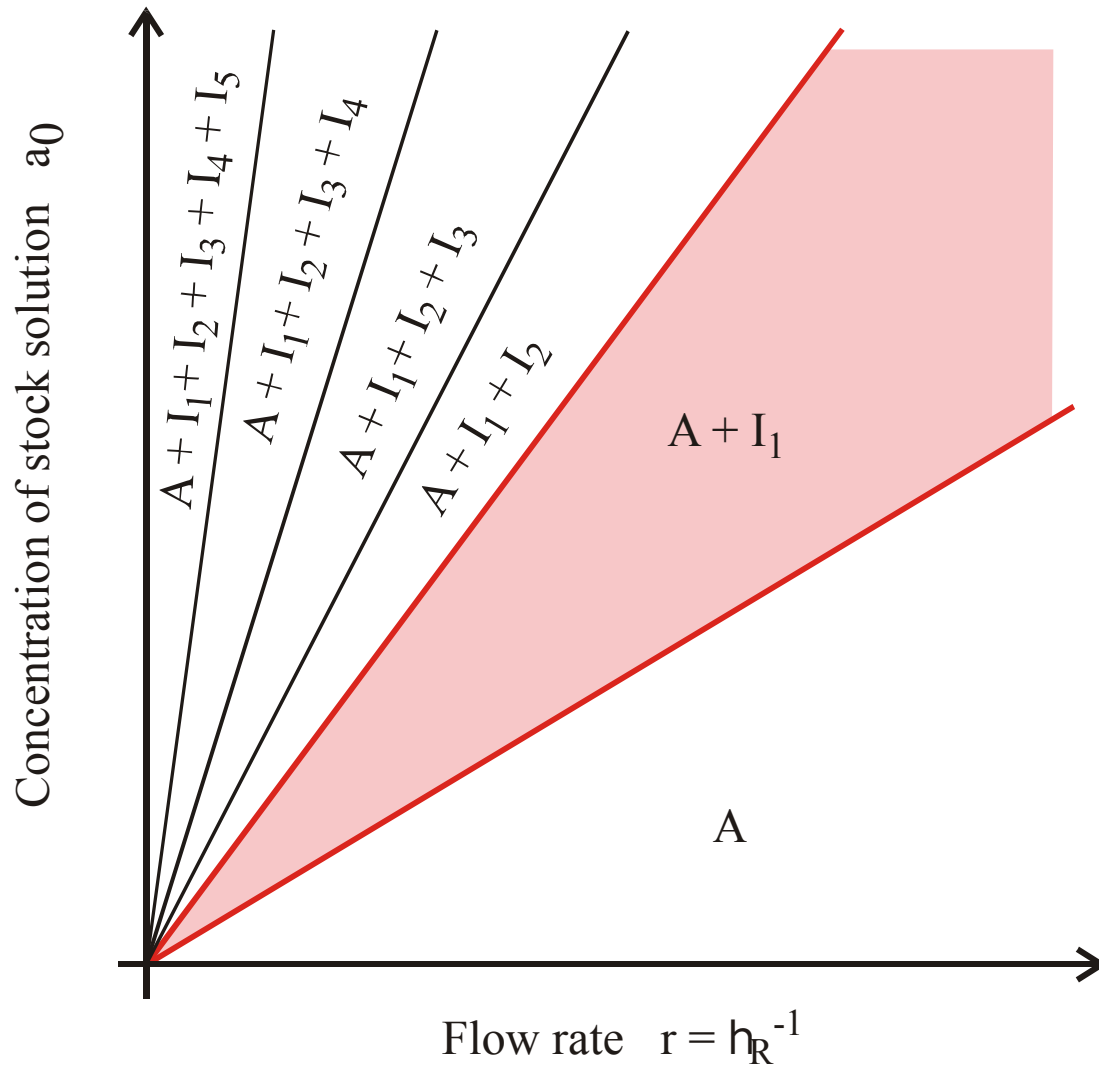
Autocatalytic second order reaction as basis for selection processes.

The autocatalytic step is formally equivalent to replication or reproduction.



## Replication in the flow reactor

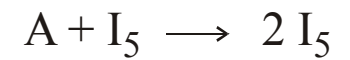
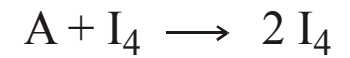
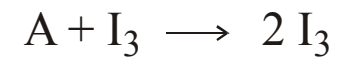
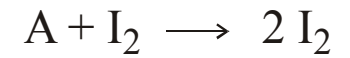
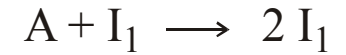
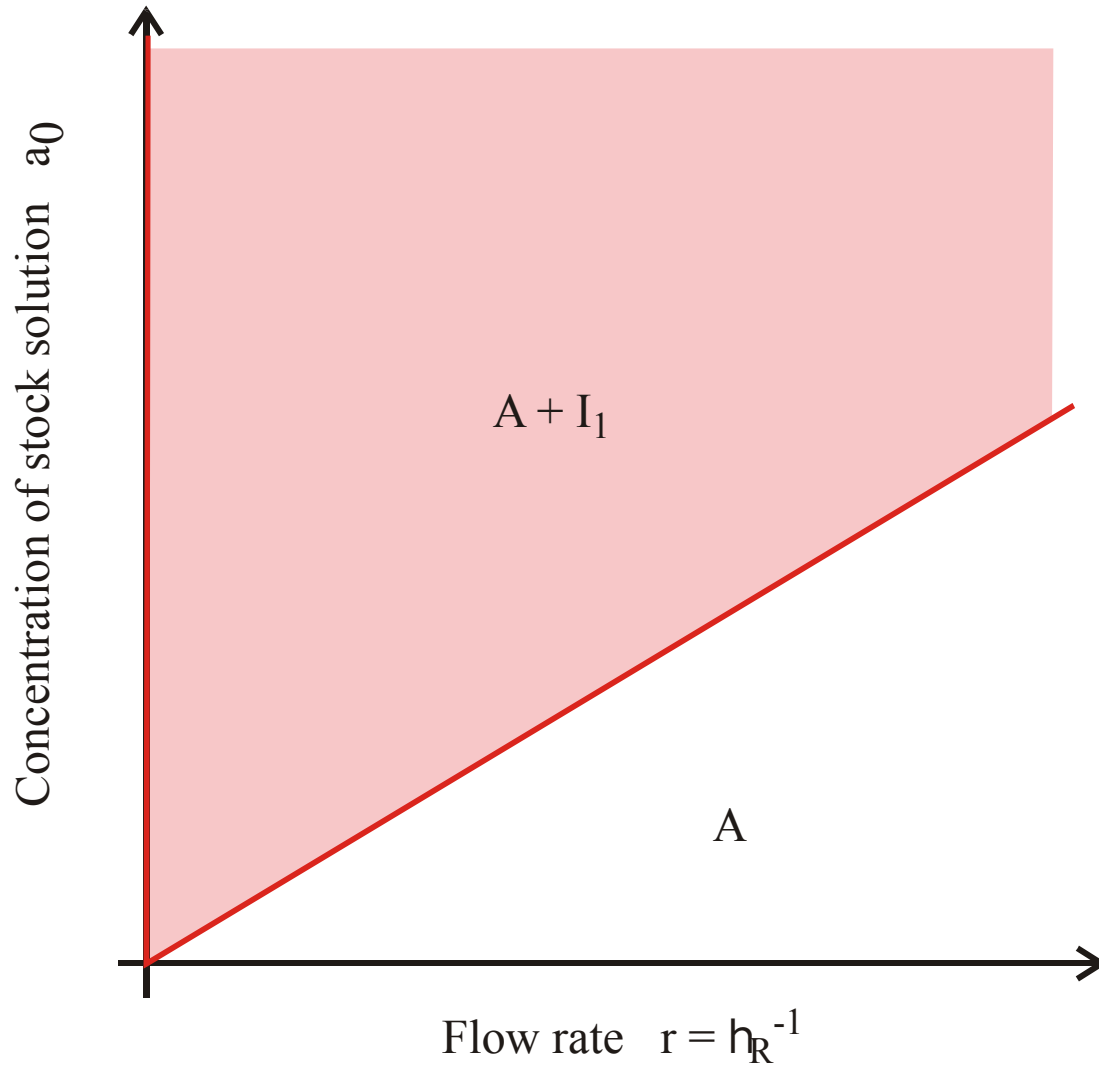
P.Schuster & K.Sigmund, Dynamics of evolutionary optimization, *Ber.Bunsenges.Phys.Chem.* **89**: 668-682 (1985)



$$k_1 > k_2 > k_3 > k_4 > k_5$$

Selection in the flow reactor: Reversible replication reactions





$$k_1 > k_2 > k_3 > k_4 > k_5$$

Selection in the flow reactor: Irreversible replication reactions

$$dx_j / dt = \sum_i k_i x_i - x_j \Phi$$

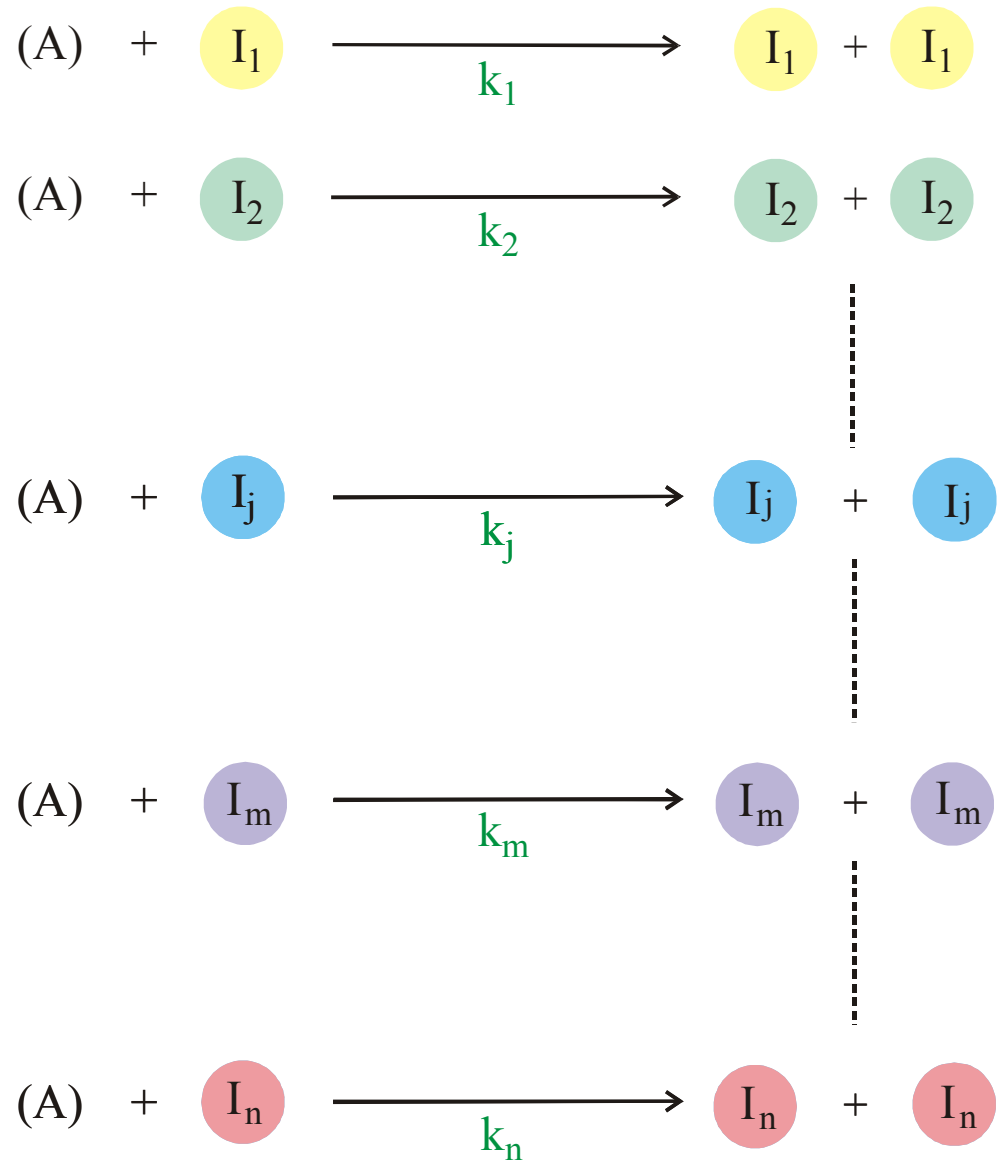
$$\Phi = \sum_i k_i x_i ; \quad \sum_i x_i = 1$$

$$[A] = a = \text{constant}$$

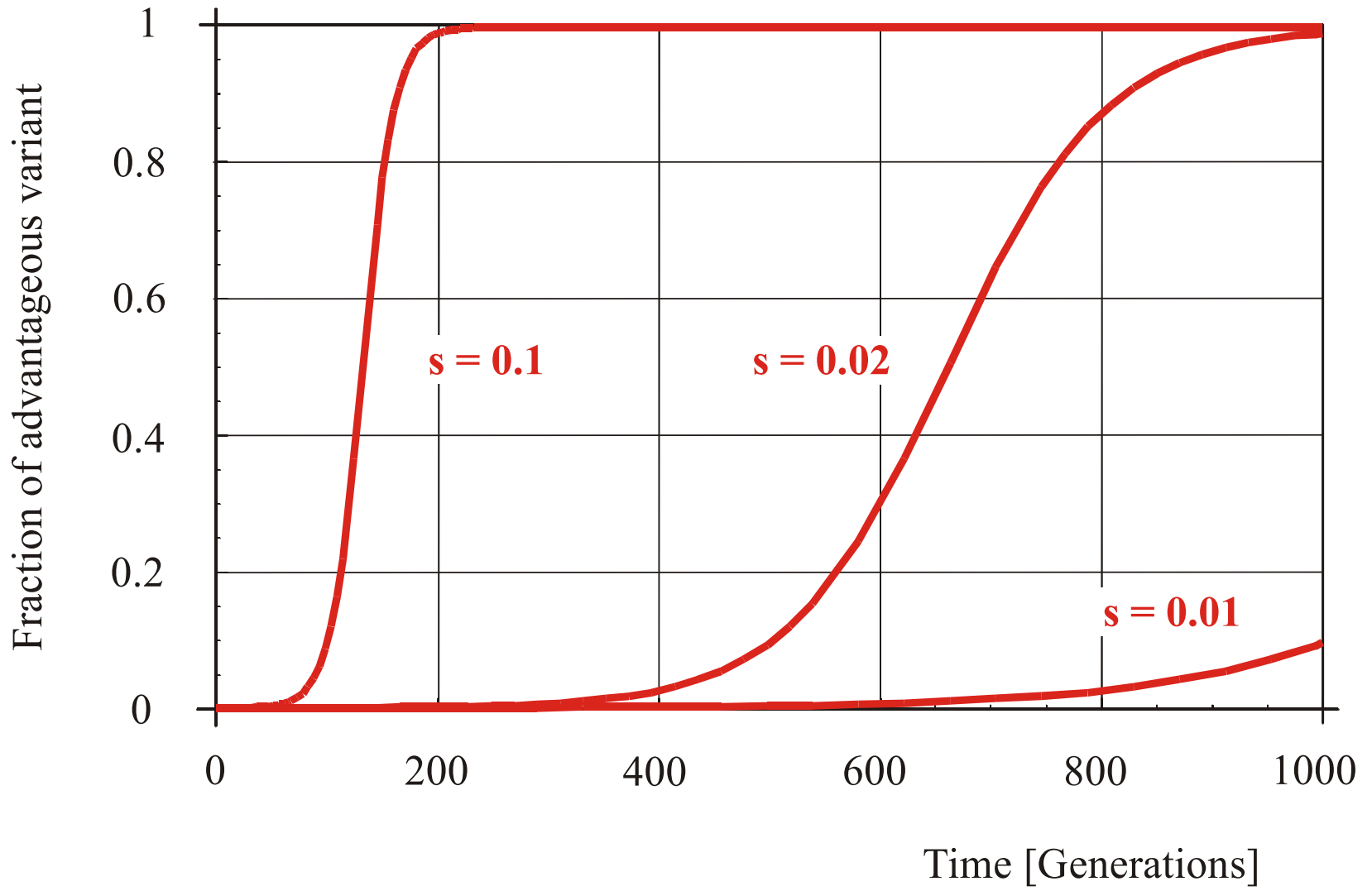
$$k_m = \max \{k_j; j=1,2,\dots,n\}$$

$$x_m(t) \approx 1 \text{ for } t \gg \tau$$

$$s = (k_{m+1} - k_m) / k_m$$



Selection of the „fittest“ or fastest replicating species



Selection of advantageous mutants in populations of  $N = 10\,000$  individuals

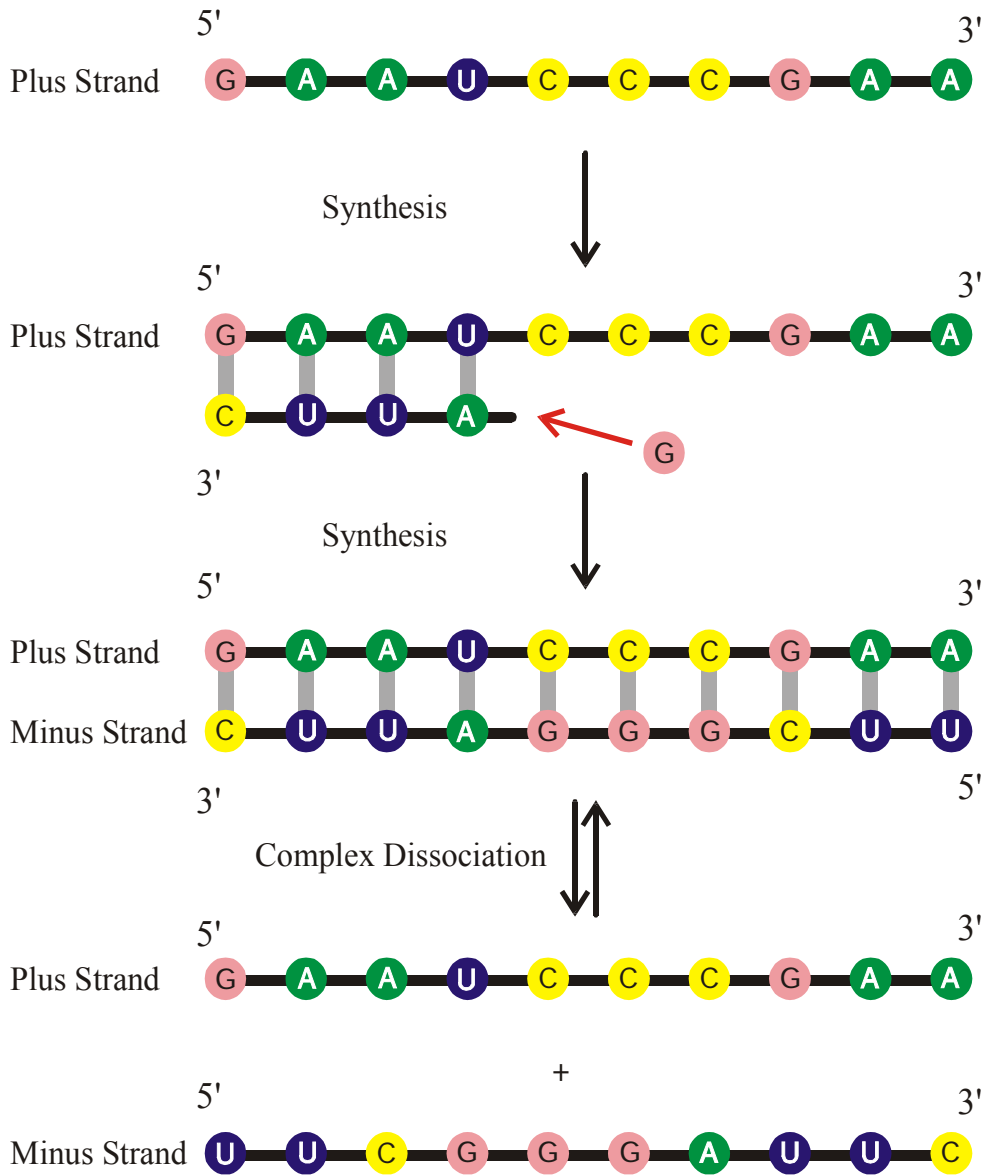


$4^{27} = 1.801 \times 10^{16}$  possible different sequences

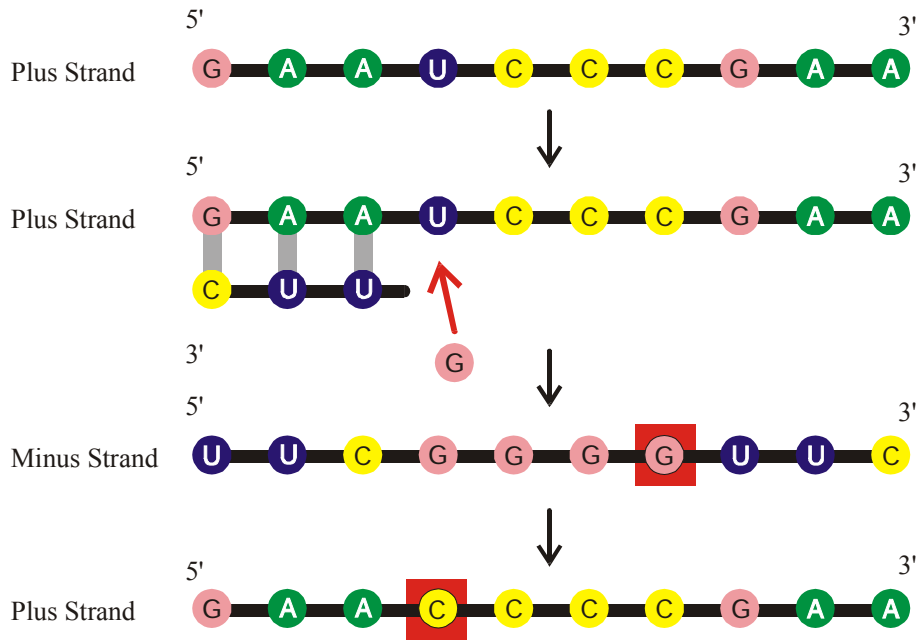
Combinatorial diversity of sequences:  $N = 4^0$

- A** = adenylate
- U** = uridylate
- C** = cytidylate
- G** = guanylate

Combinatorial diversity of heteropolymers illustrated by means of an RNA aptamer that binds to the antibiotic tobramycin



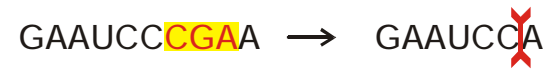
Complementary replication as the simplest copying mechanism of RNA



**Point Mutation**



**Insertion**



**Deletion**

Mutations represent the mechanism of variation in nucleic acids

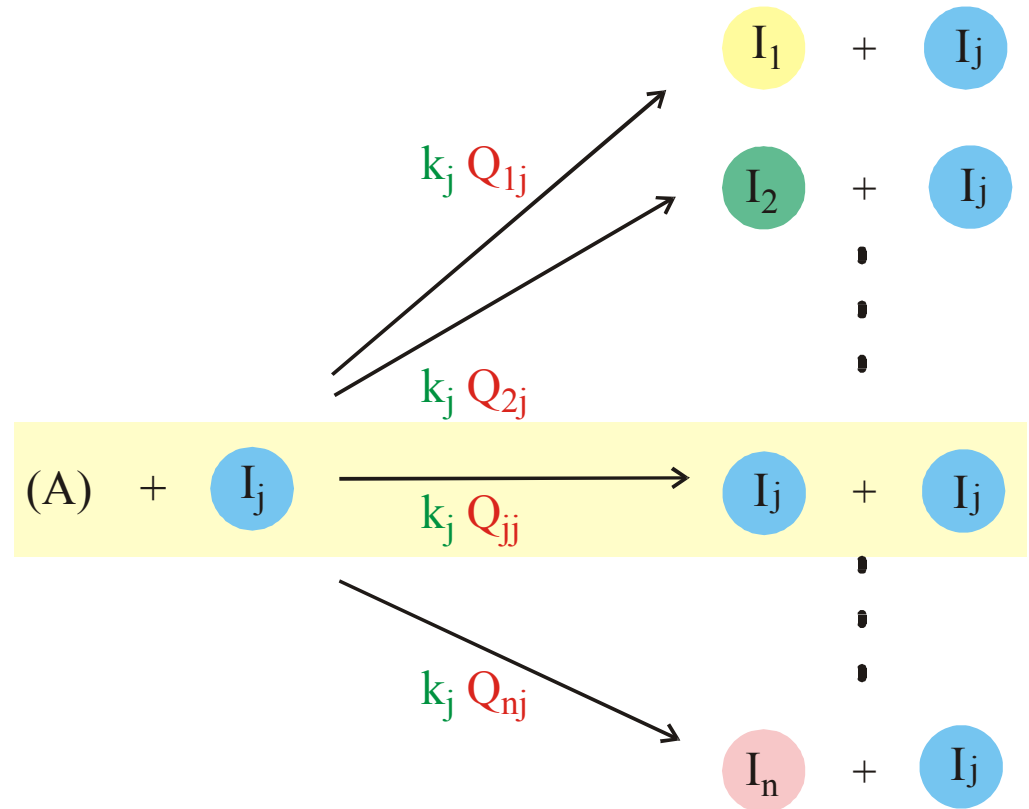
$$dx_j / dt = \sum_i k_i Q_{ji} x_i - x_j \Phi$$

$$\Phi = \sum_i k_i x_i ; \quad \sum_i x_i = 1 ; \quad \sum_i Q_{ij} = 1$$

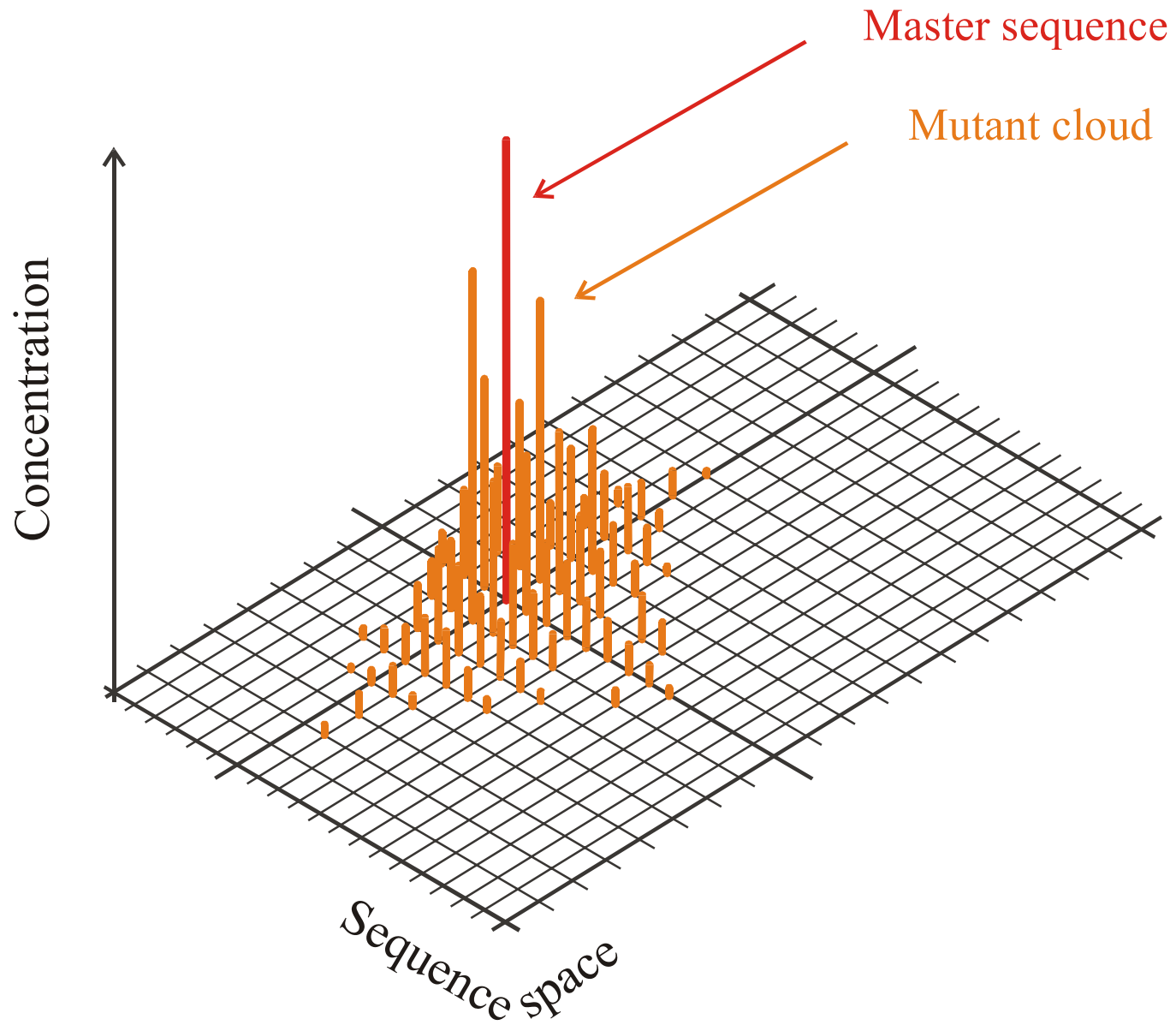
$$Q_{ij} = (1-p)^{n-d(i,j)} p^{d(i,j)}$$

p ..... Error rate per digit

d(i,j) .... Hamming distance  
between  $I_i$  and  $I_j$

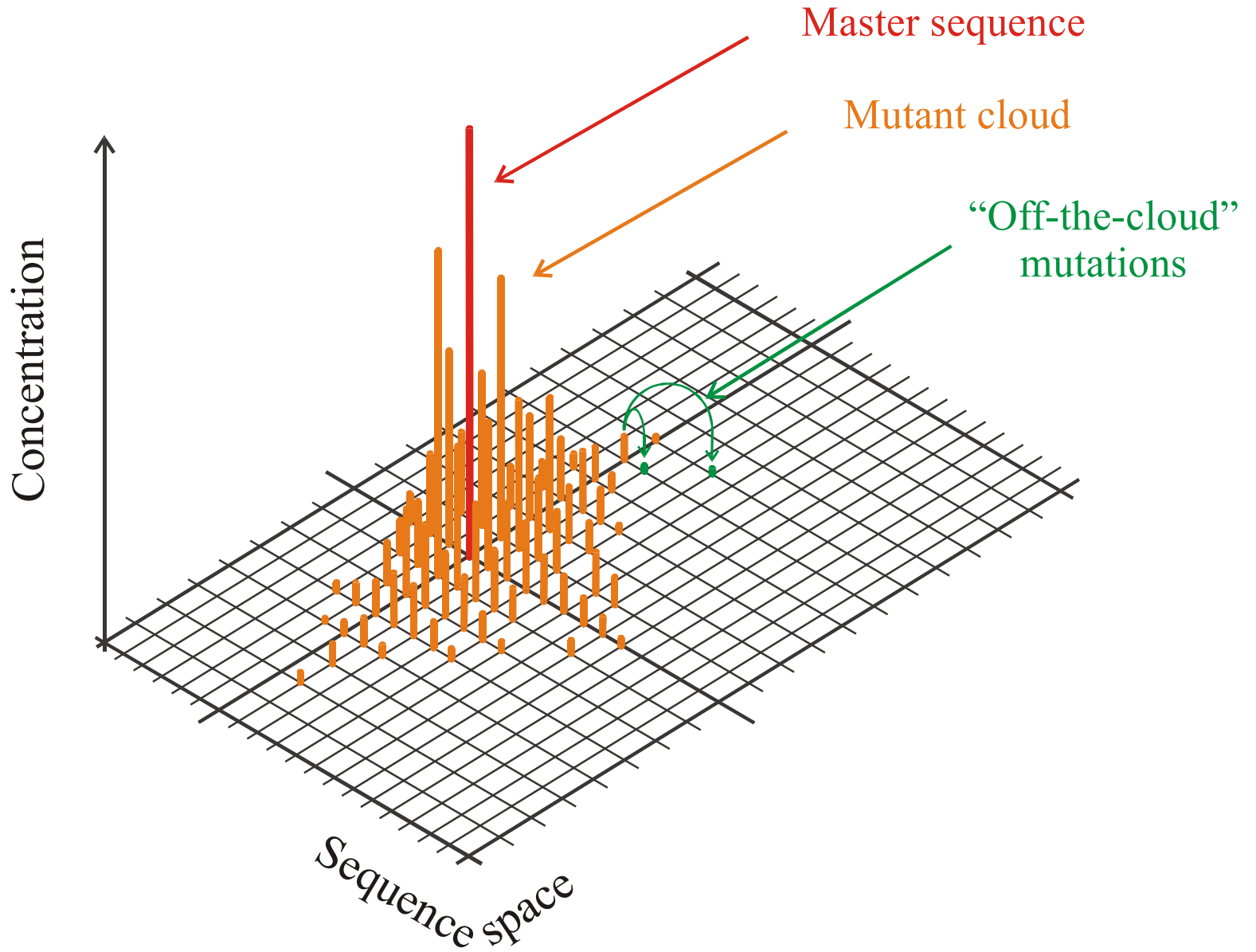


Chemical kinetics of replication and mutation



The molecular quasispecies in sequence space





The molecular quasispecies and mutations producing new variants

Ronald Fisher's conjecture does not hold in general for **replication-mutation systems**: In general evolutionary dynamics the mean fitness of populations may also decrease monotonously or even go through a maximum or minimum. It does also not hold in general for **recombination of many alleles** and general multi-locus systems in population genetics.

**Optimization of fitness** is, nevertheless, fulfilled in most cases, and can be understood as a useful heuristic.

## **Optimization of RNA molecules *in silico***

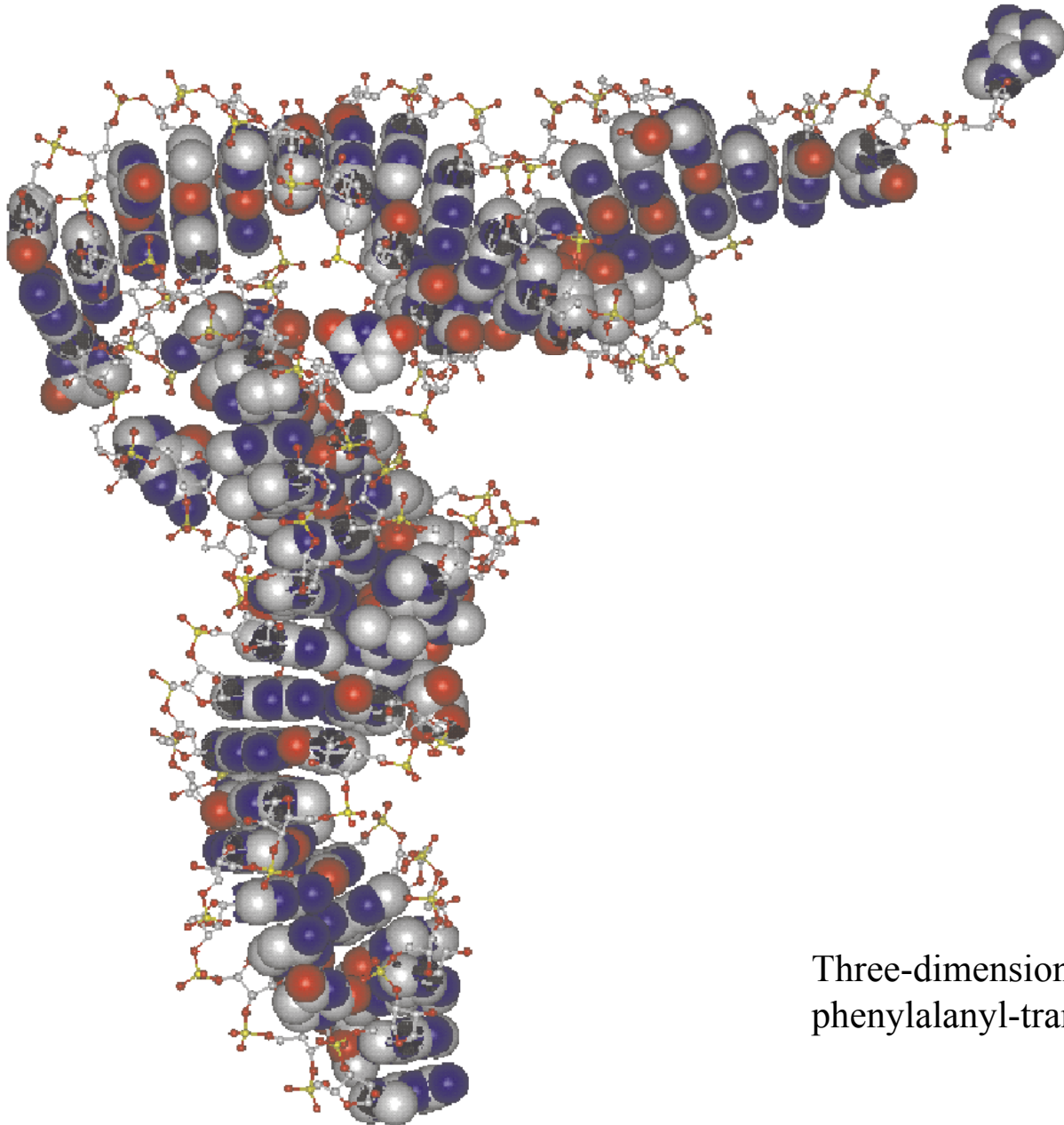
W.Fontana, P.Schuster, *A computer model of evolutionary optimization*. Biophysical Chemistry **26** (1987), 123-147

W.Fontana, W.Schnabl, P.Schuster, *Physical aspects of evolutionary optimization and adaptation*. Phys.Rev.A **40** (1989), 3301-3321

M.A.Huynen, W.Fontana, P.F.Stadler, *Smoothness within ruggedness. The role of neutrality in adaptation*. Proc.Natl.Acad.Sci.USA **93** (1996), 397-401

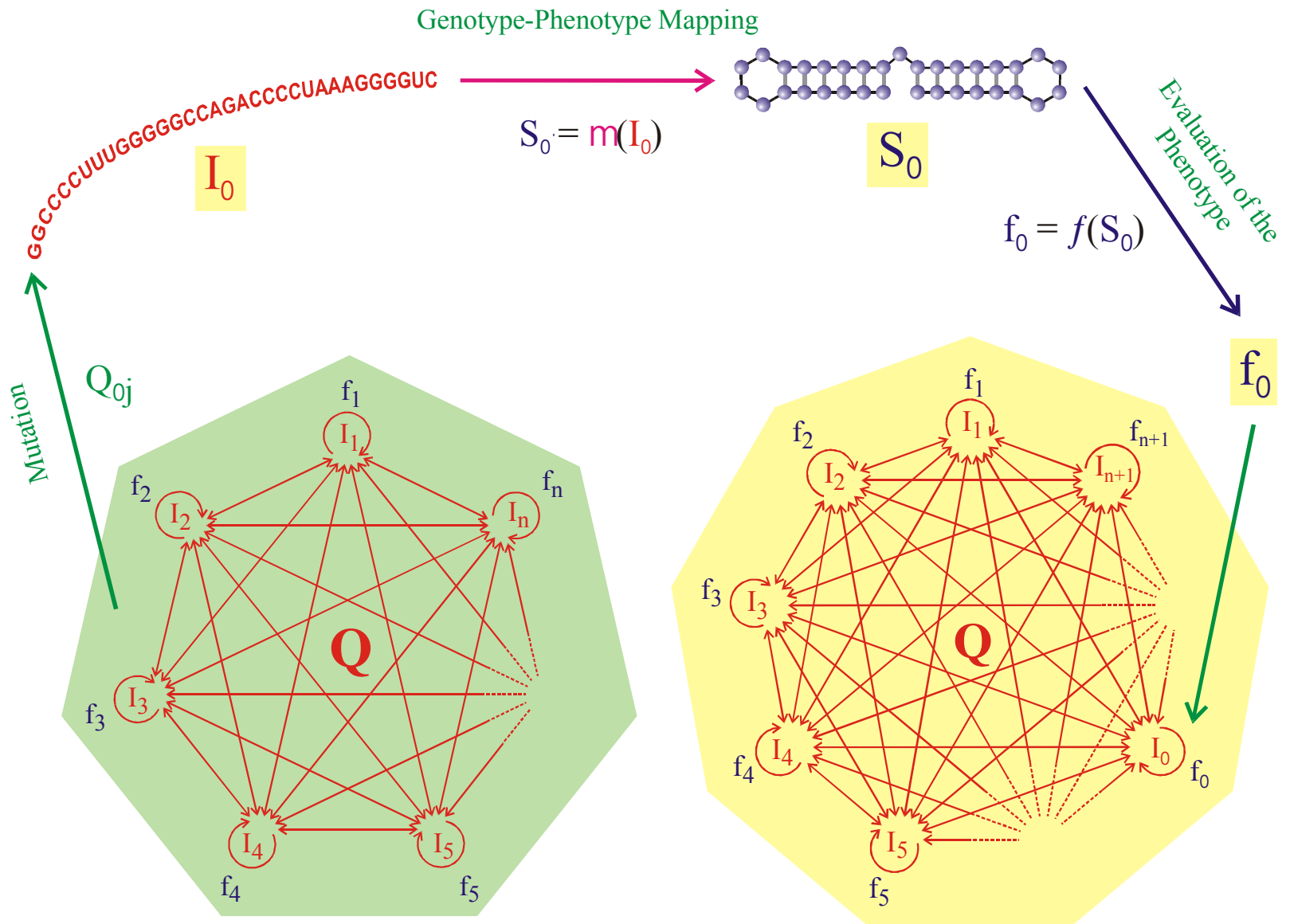
W.Fontana, P.Schuster, *Continuity in evolution. On the nature of transitions*. Science **280** (1998), 1451-1455

W.Fontana, P.Schuster, *Shaping space. The possible and the attainable in RNA genotype-phenotype mapping*. J.Theor.Biol. **194** (1998), 491-515



Three-dimensional structure of phenylalanyl-transfer-RNA

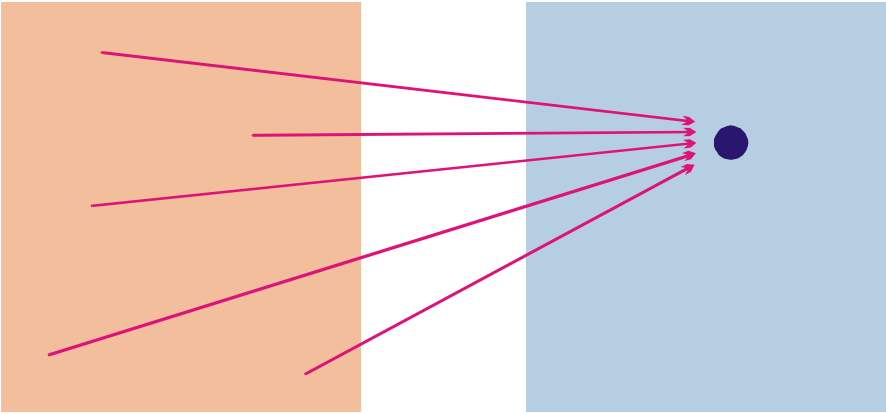
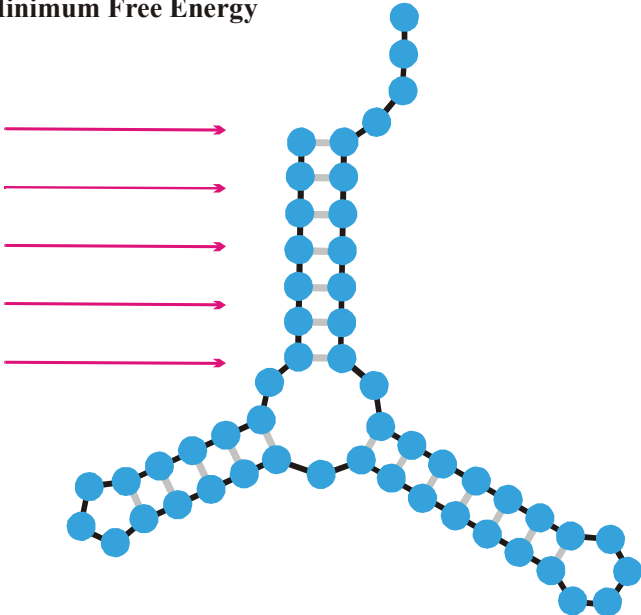




Evolutionary dynamics  
including molecular phenotypes

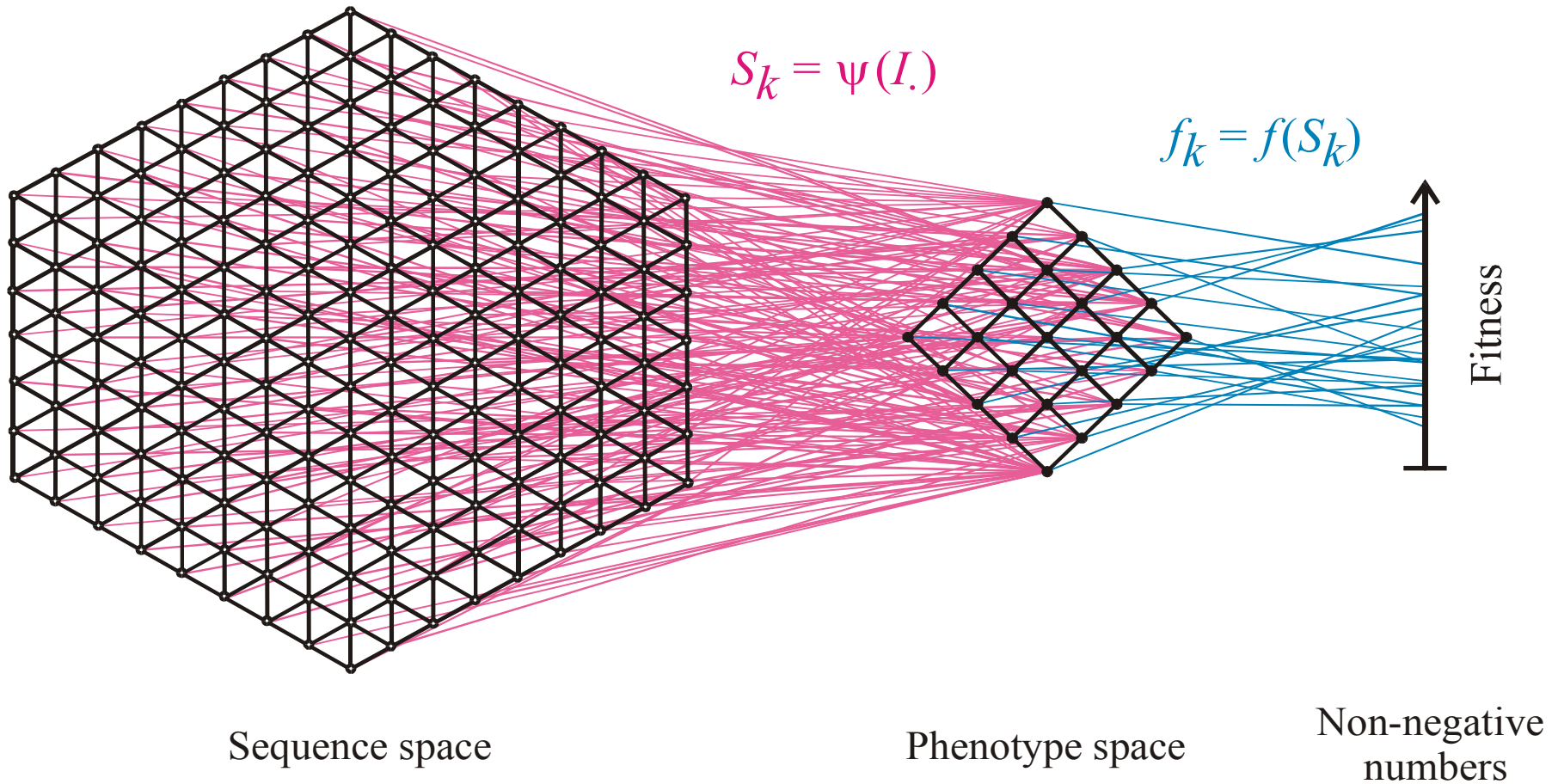
**Criterion of  
Minimum Free Energy**

UUUAGCCAGCGCGAGUCGUGCGGACGGGGUUAUCUCUGUCGGGCUAGGGCGC  
GUGAGCGCGGGGCACAGUUUCUCAAGGAUGUAAGUUUUUGCCGUUUUUCUGG  
UUAGCGAGAGAGAGGAGGCUUCUAGACCCAGCUCUCUGGGUCGUUGCUGAUGCG  
CAUUGGUGCUAAUGAUUUAGGGCUGUAUJCCUGUAUAGCGAUCAGUGUCCG  
GUAGGCCUCUUGACAUAAGAUUUUUCCAUGGUGGGAGAUGGCCAUUGCAG



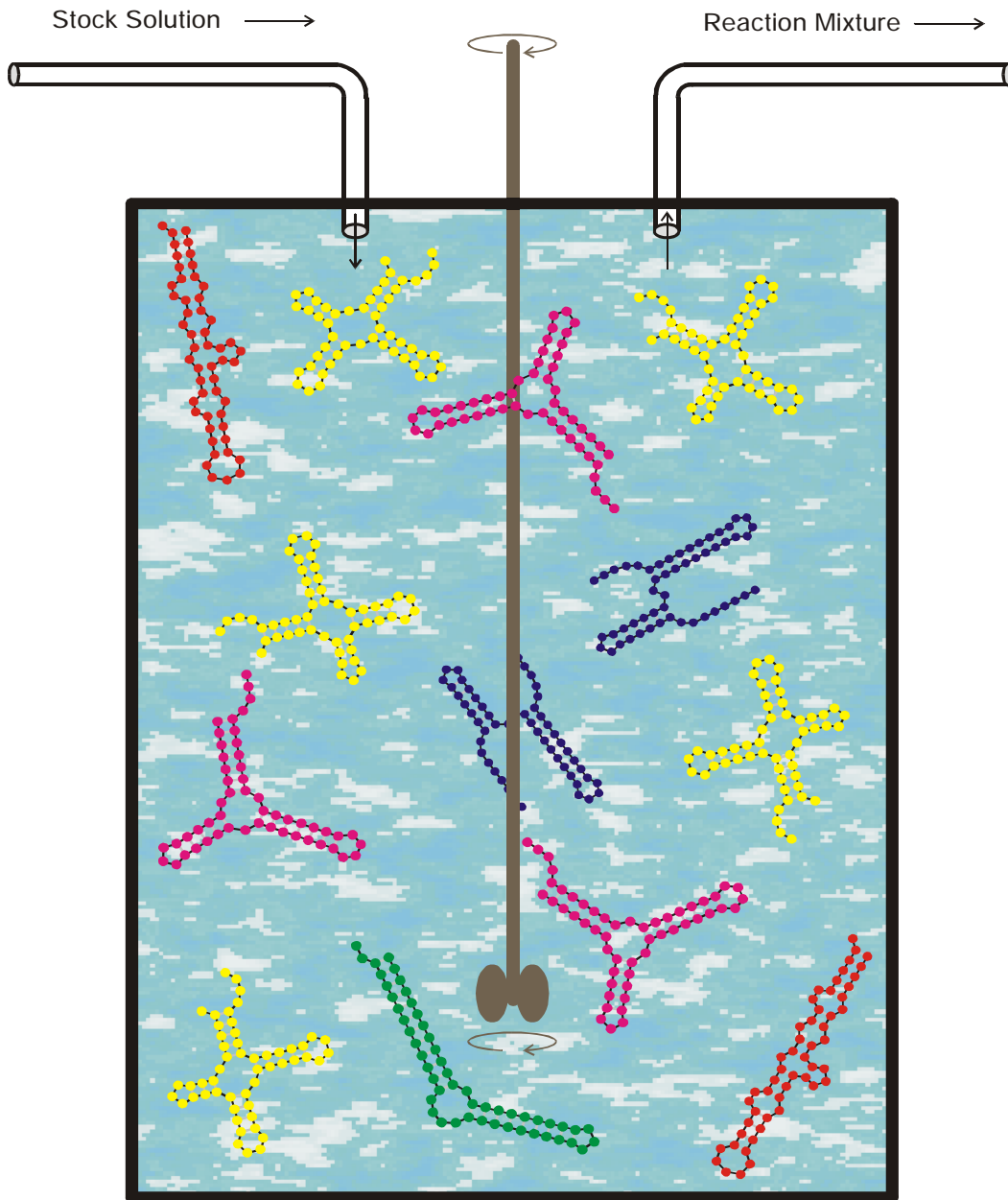
Sequence Space

Shape Space

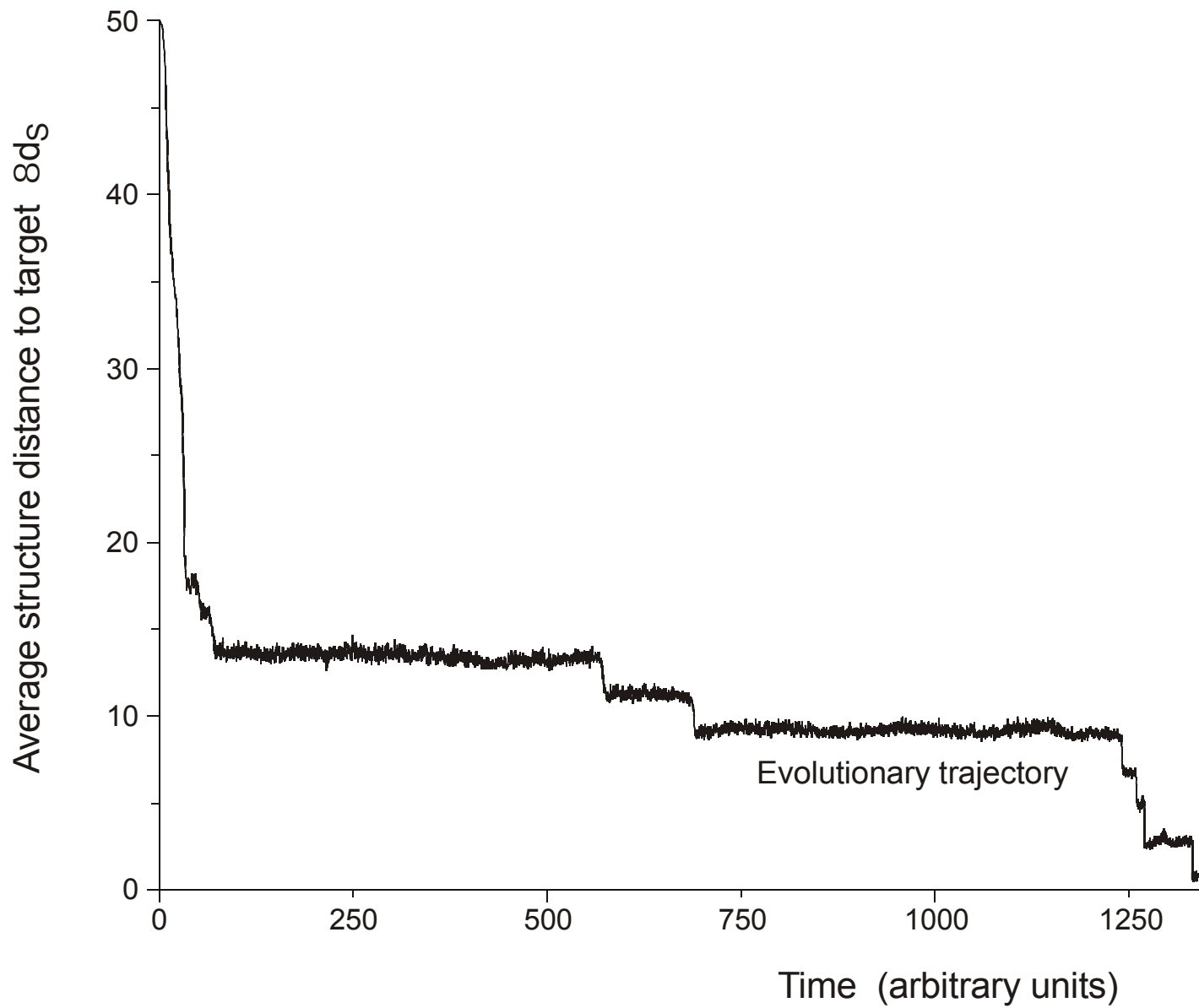


Mapping from sequence space into phenotype space and into fitness values

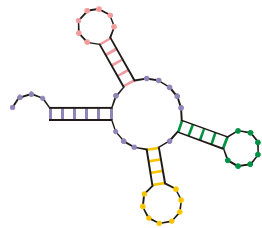
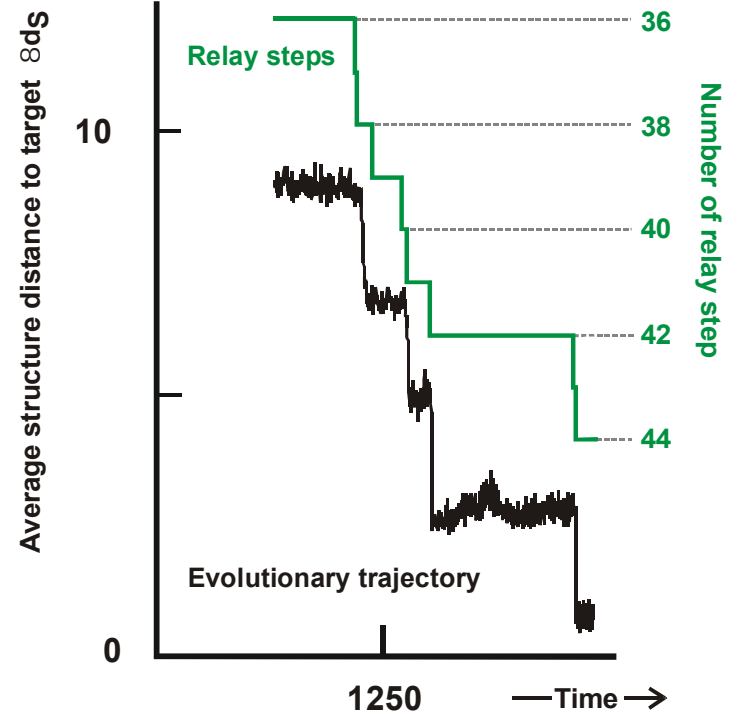




The flowreactor as a device for studies of evolution *in vitro* and *in silico*

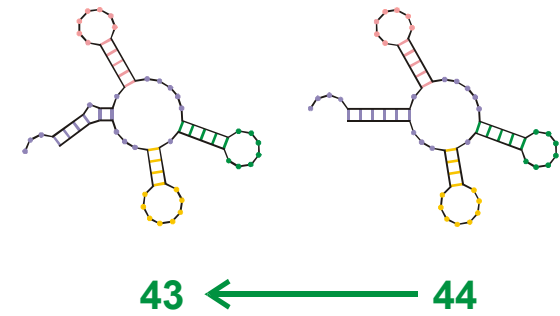
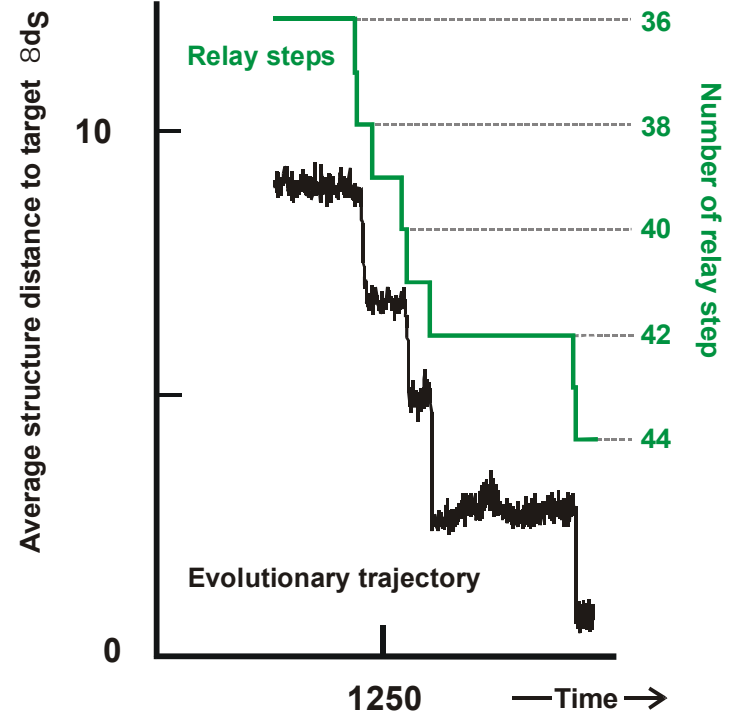


*In silico* optimization in the flow reactor: Trajectory

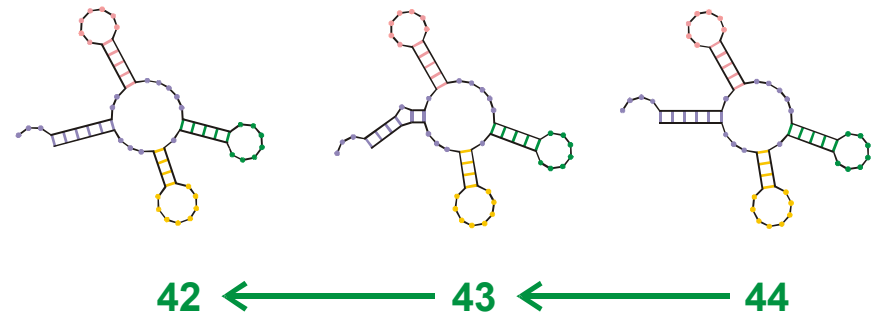
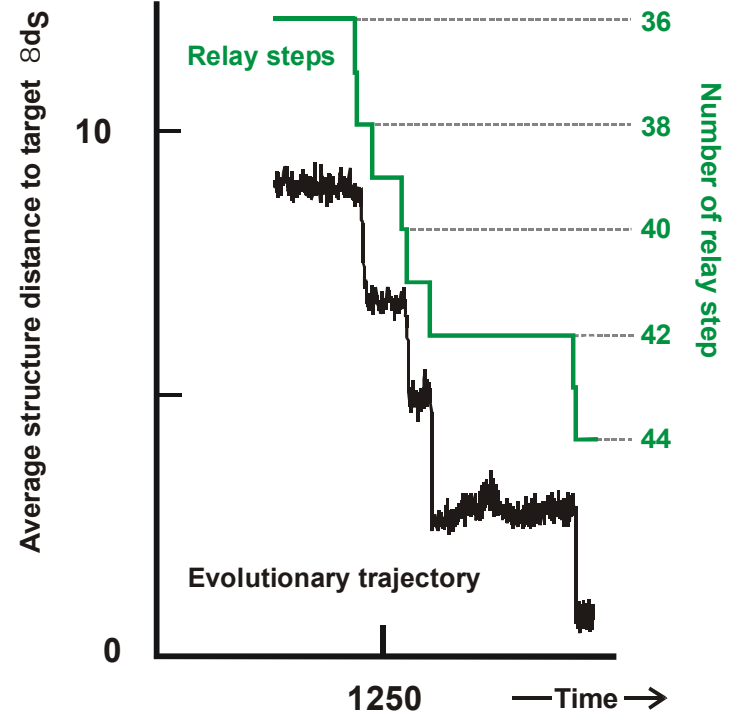


**44**

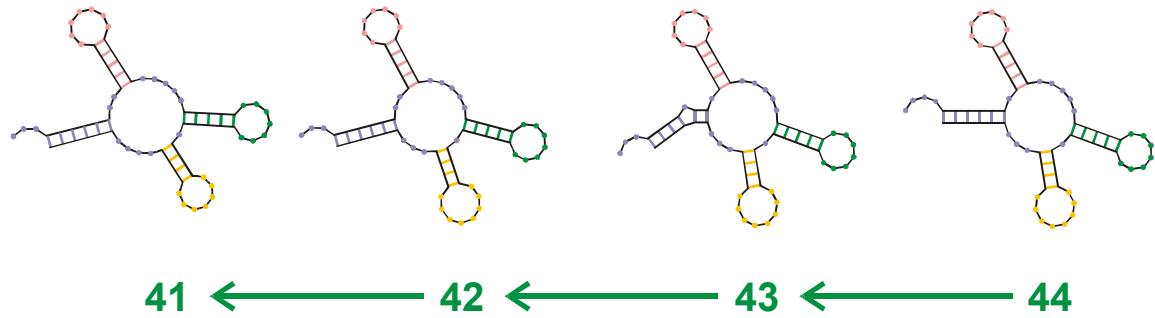
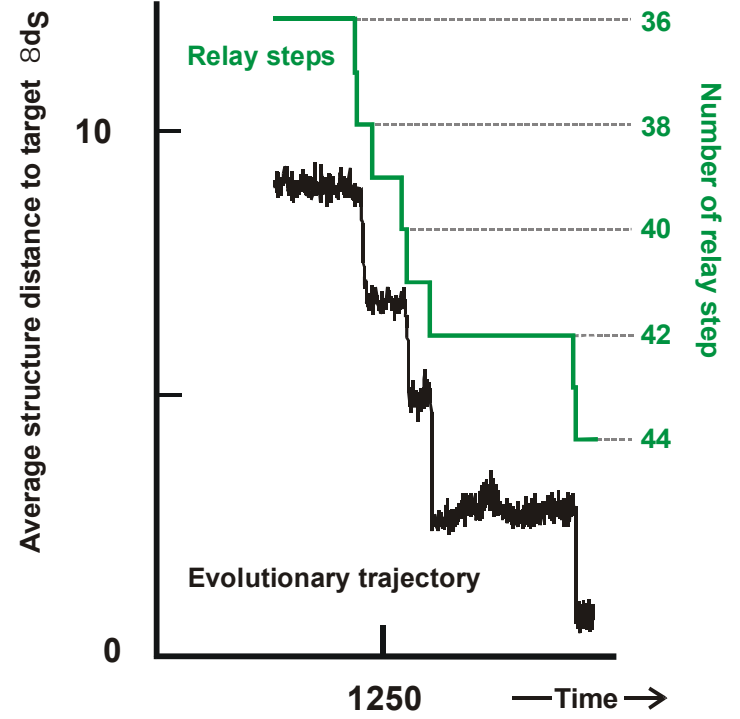
Endconformation of optimization



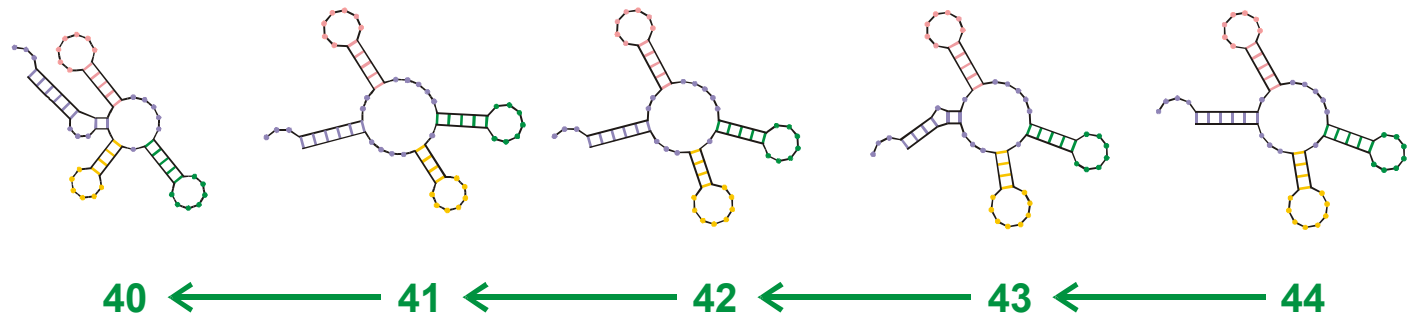
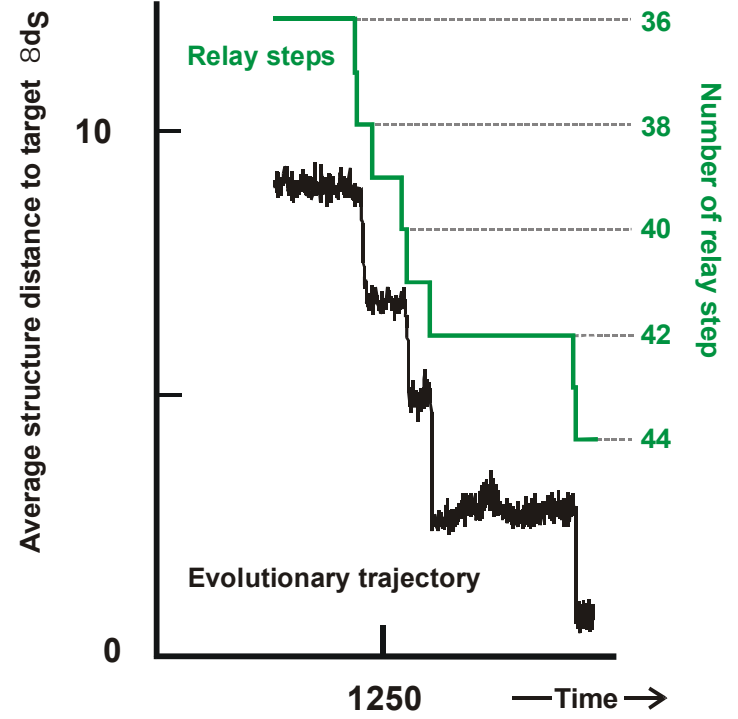
Reconstruction of the last step 43  $\dot{\simeq}$  44



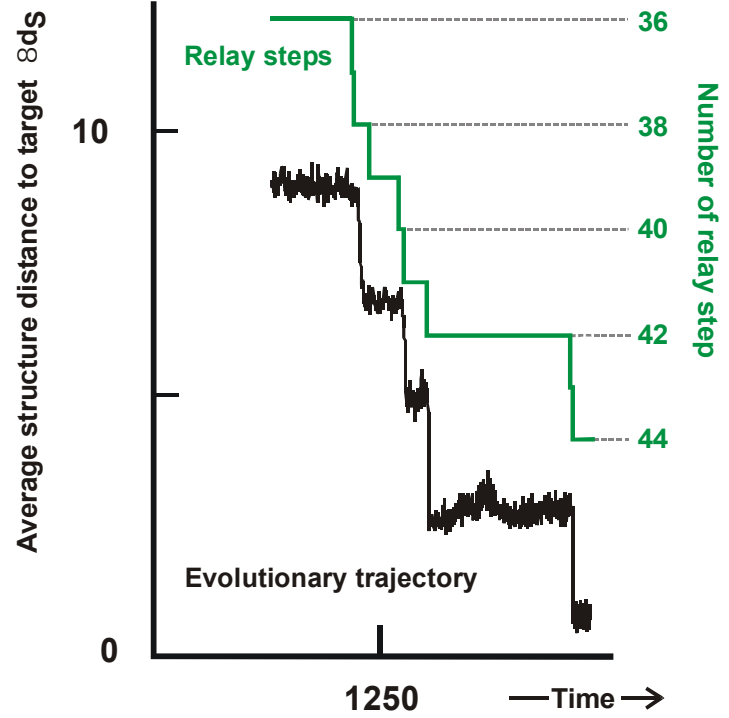
Reconstruction of last-but-one step 42  $\checkmark$  43 ( $\checkmark$  44)



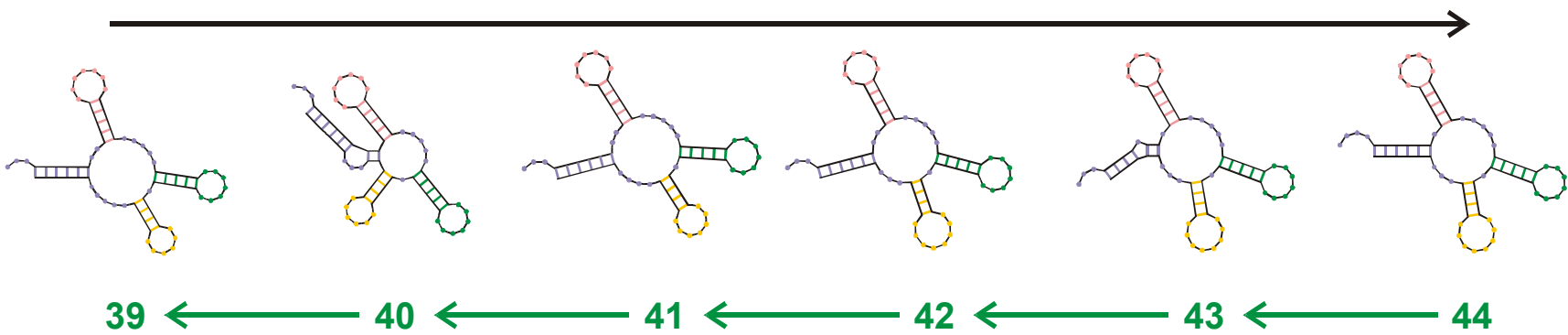
Reconstruction of step 41 š 42 (š 43 š 44)



Reconstruction of step 40 š 41 (š 42 š 43 š 44)



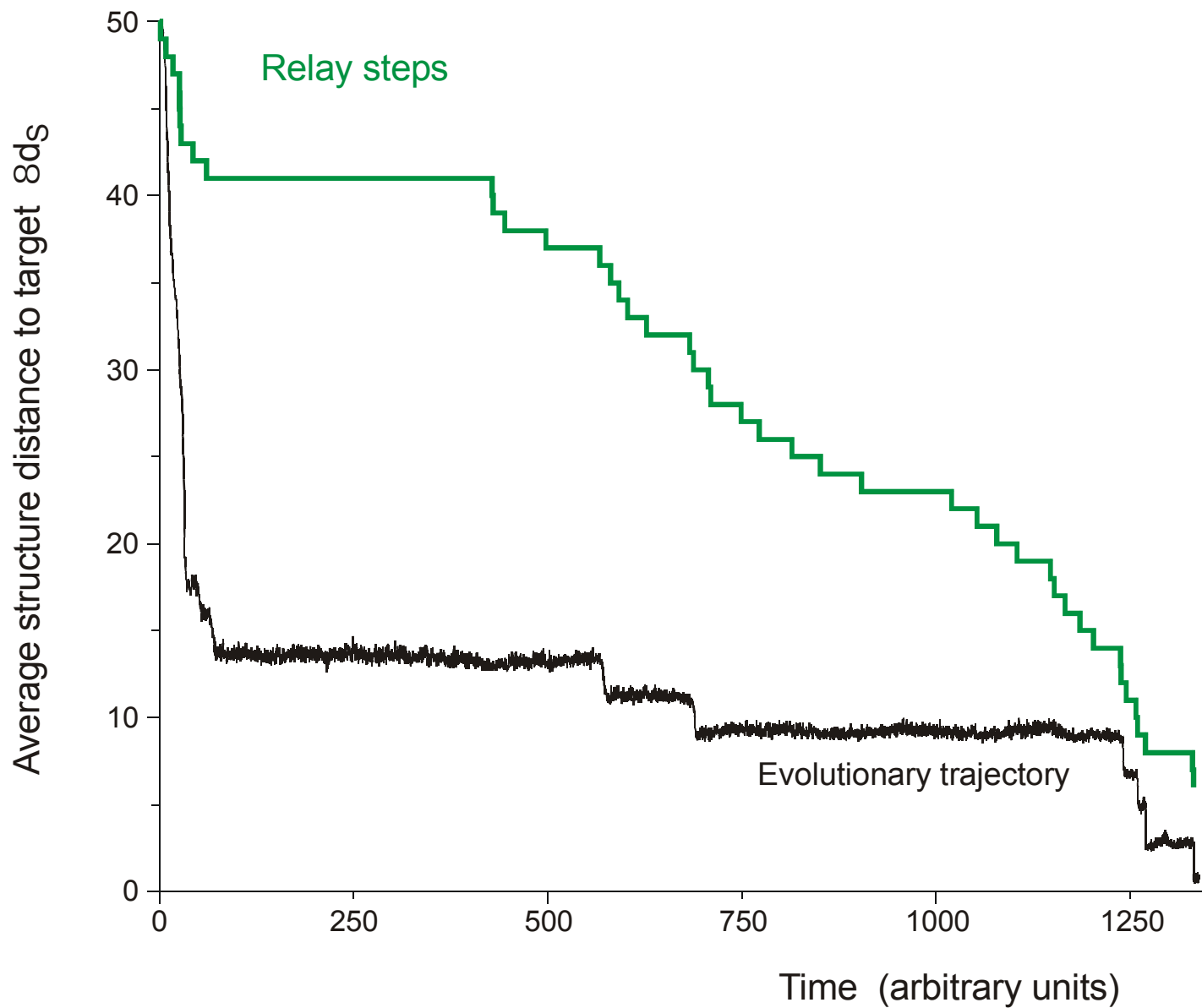
Evolutionary process



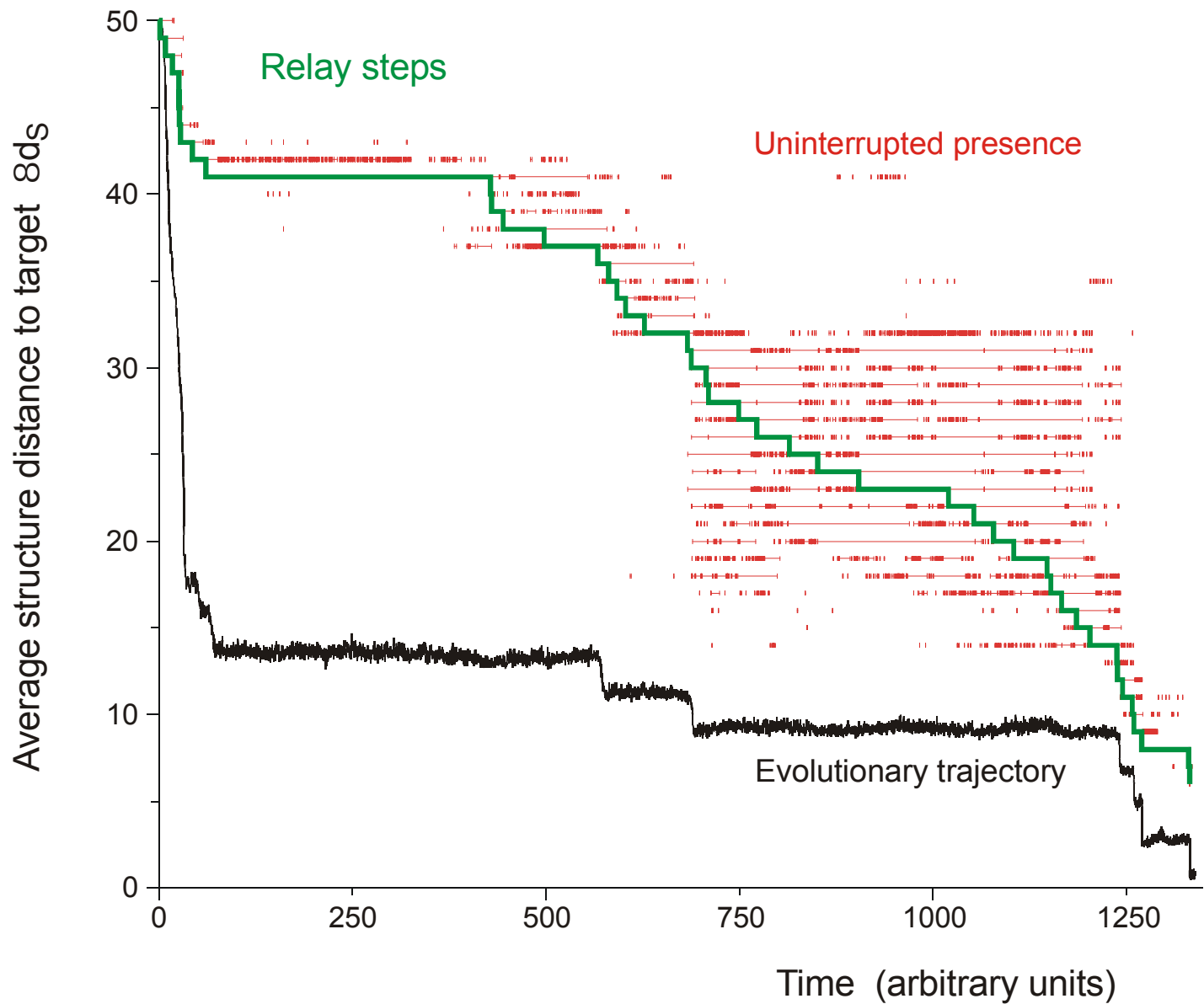
Reconstruction

Reconstruction of the relay series

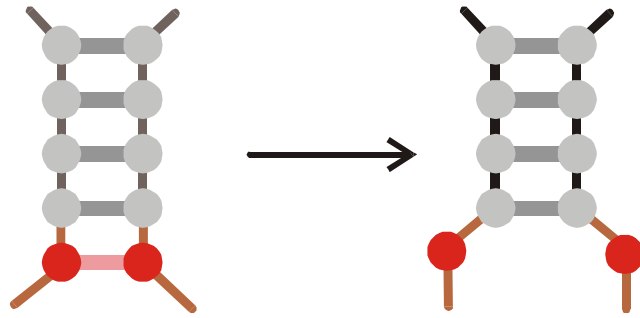




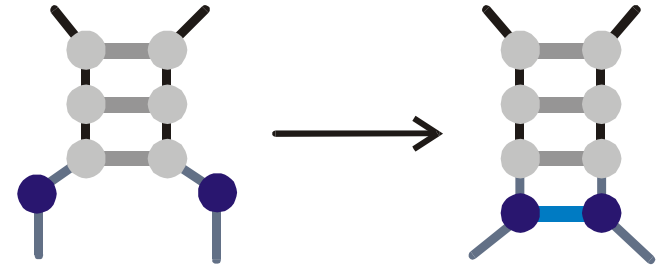
*In silico* optimization in the flow reactor: Trajectory and relay steps



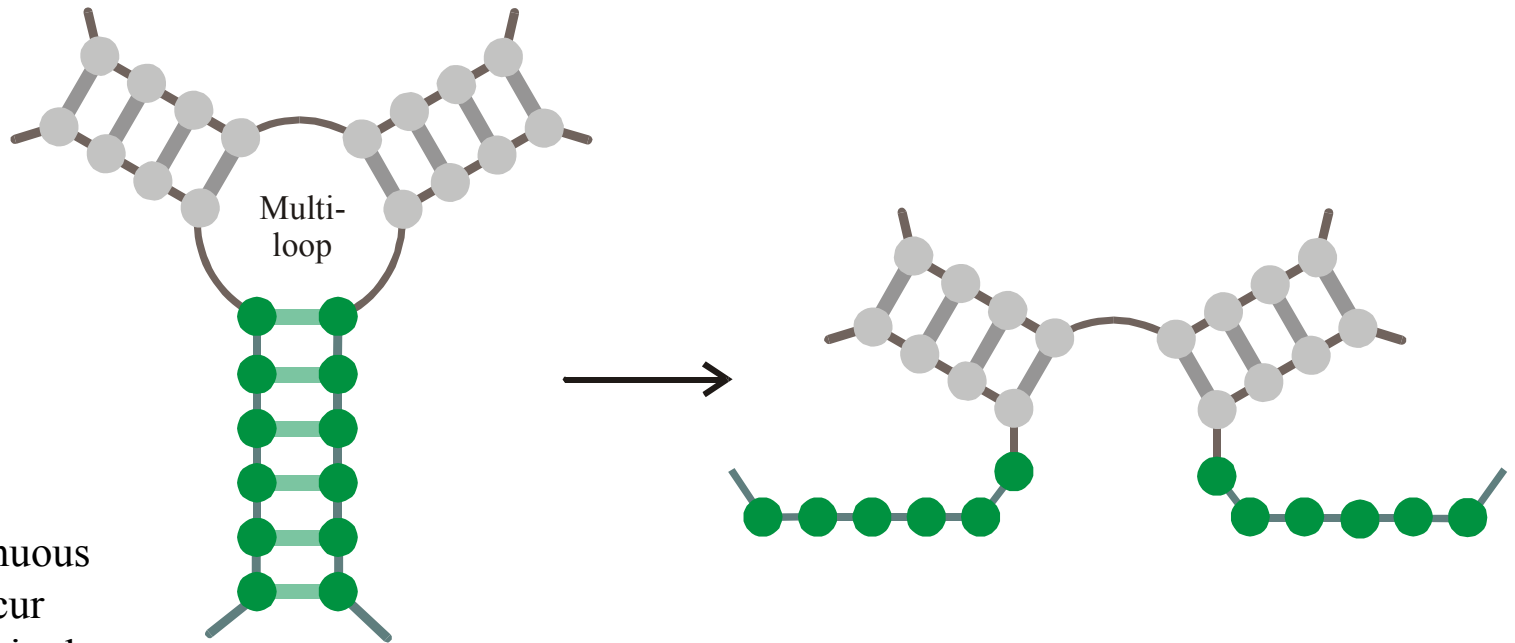
*In silico* optimization in the flow reactor: Uninterrupted presence



Shortening of Stacks

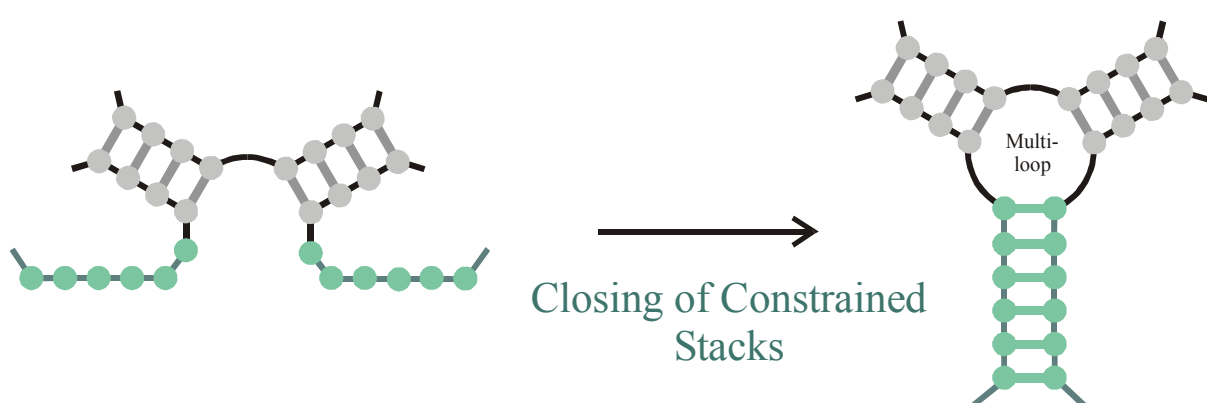
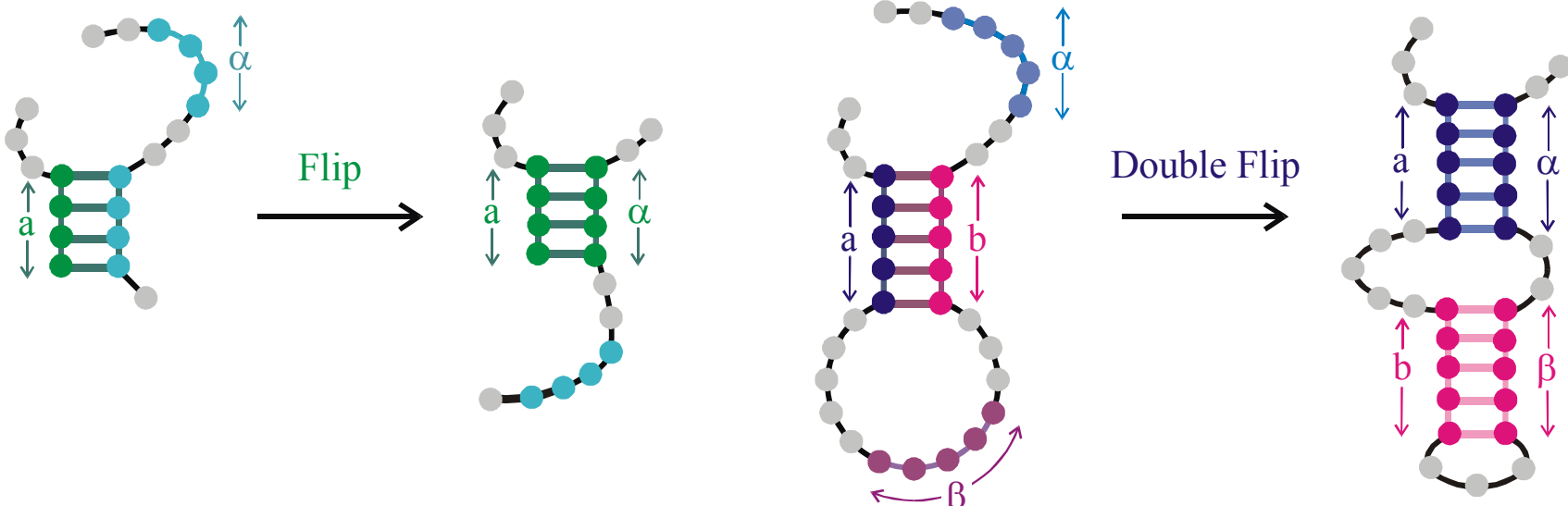
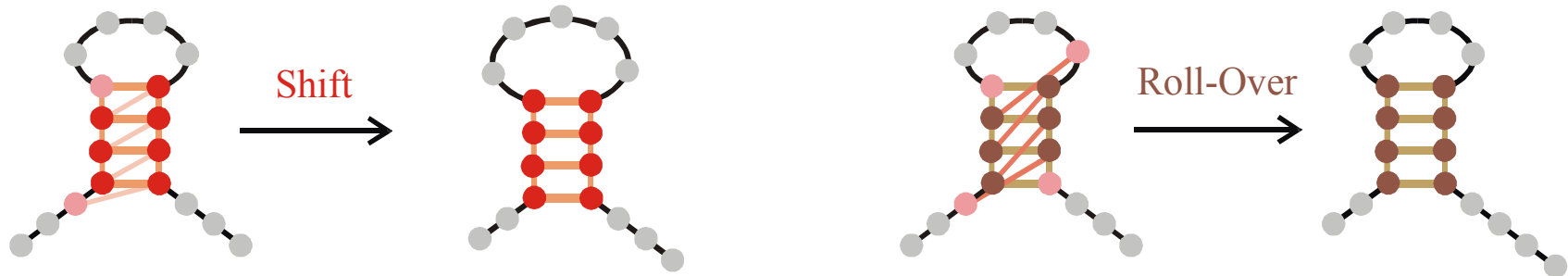


Elongation of Stacks

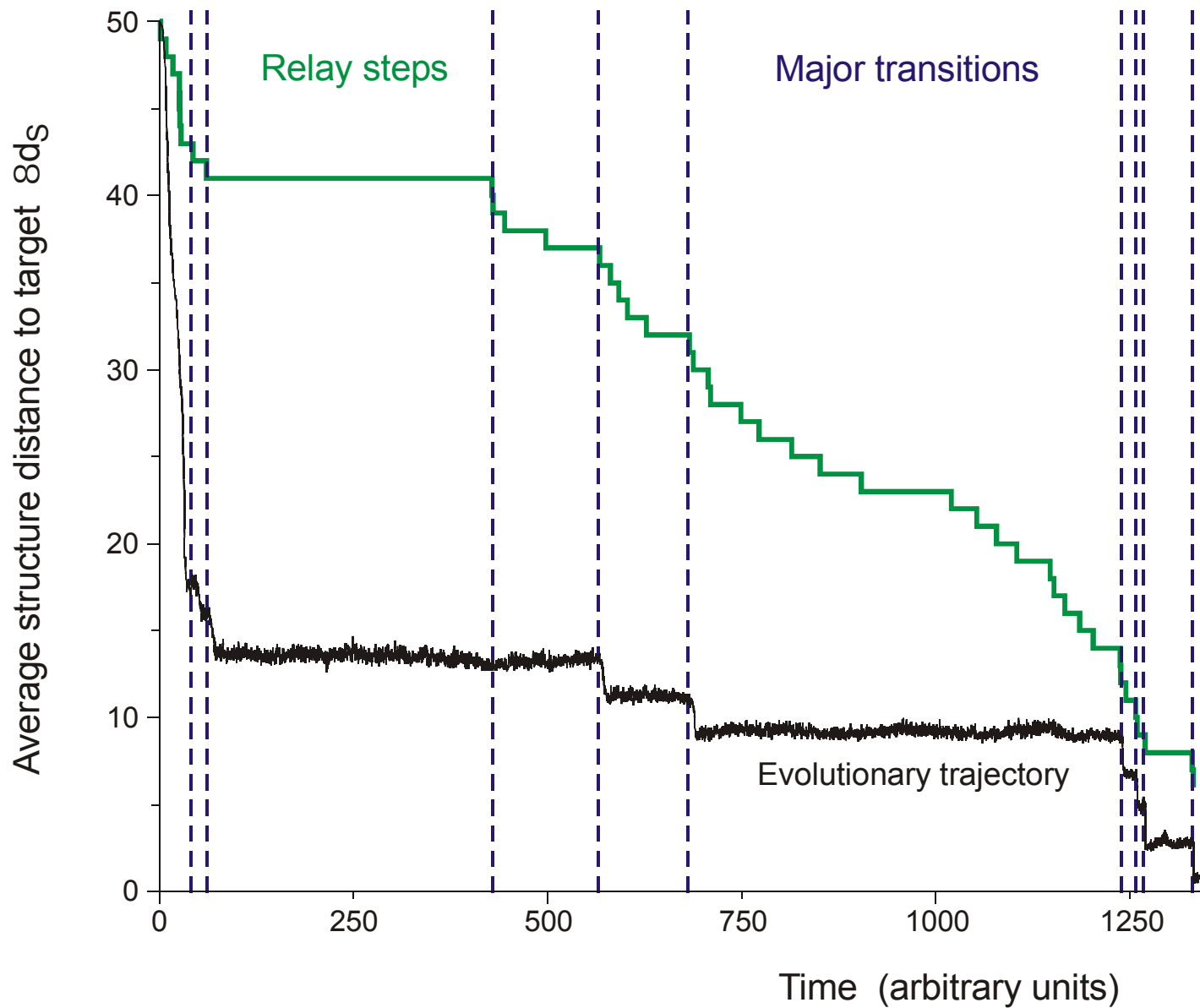


Opening of Constrained Stacks

Minor or continuous transitions: Occur **frequently** on single point mutations

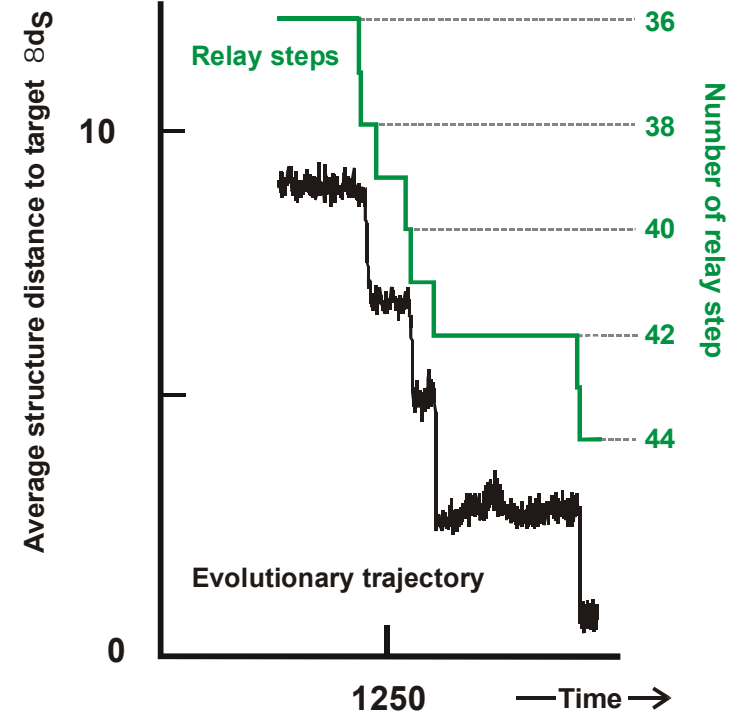
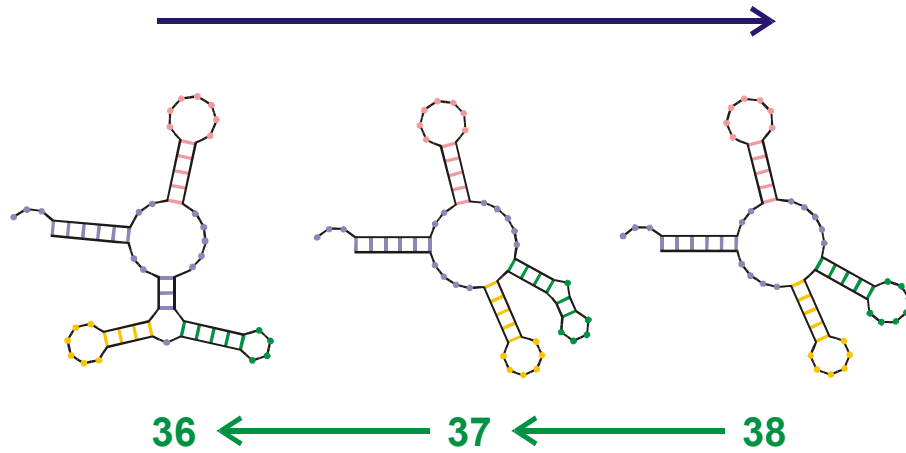


Major or discontinuous transitions: **Structural innovations**, occur rarely on single point mutations



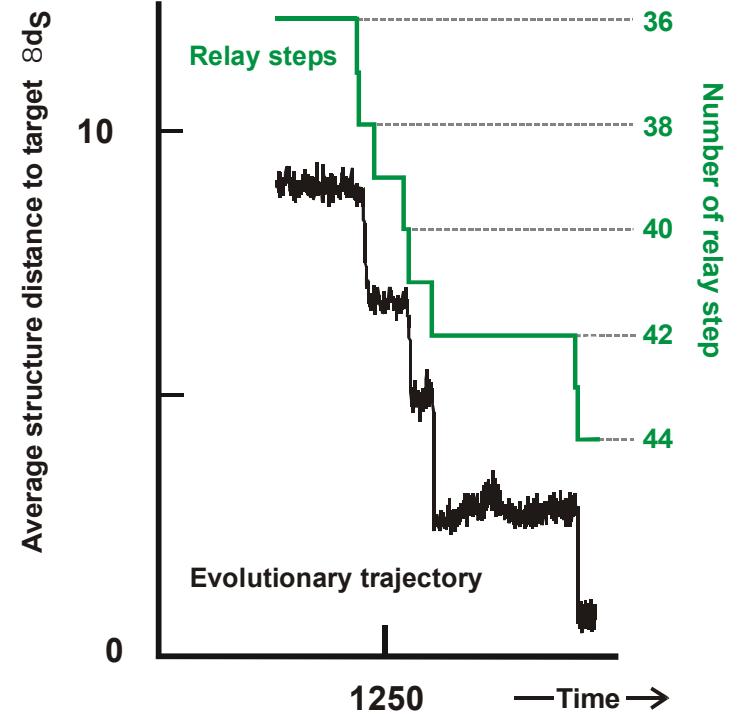
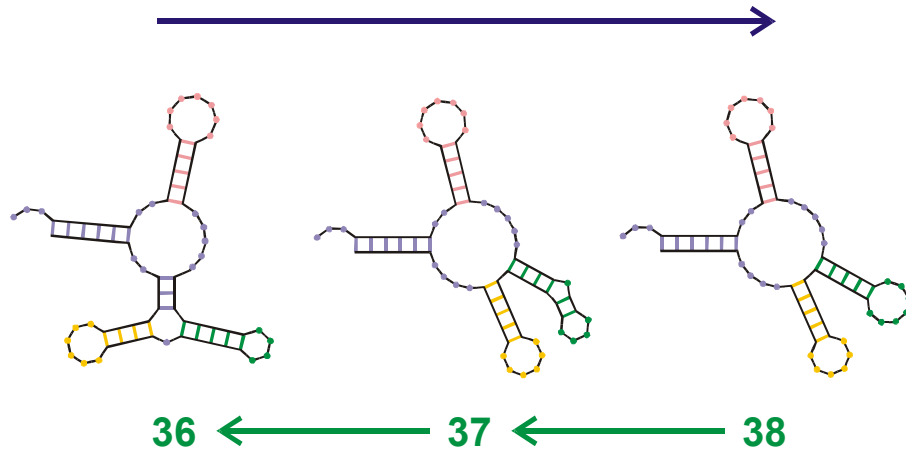
*In silico* optimization in the flow reactor: Major transitions

## Major transition leading to clover leaf

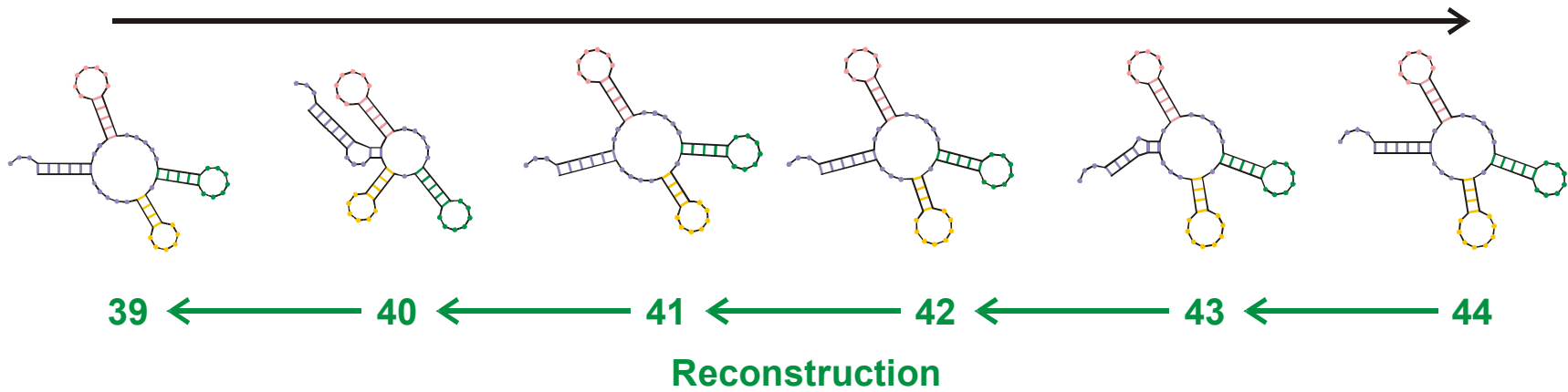


Reconstruction of a major transitions 36  $\rightarrow$  37 ( $\rightarrow$  38)

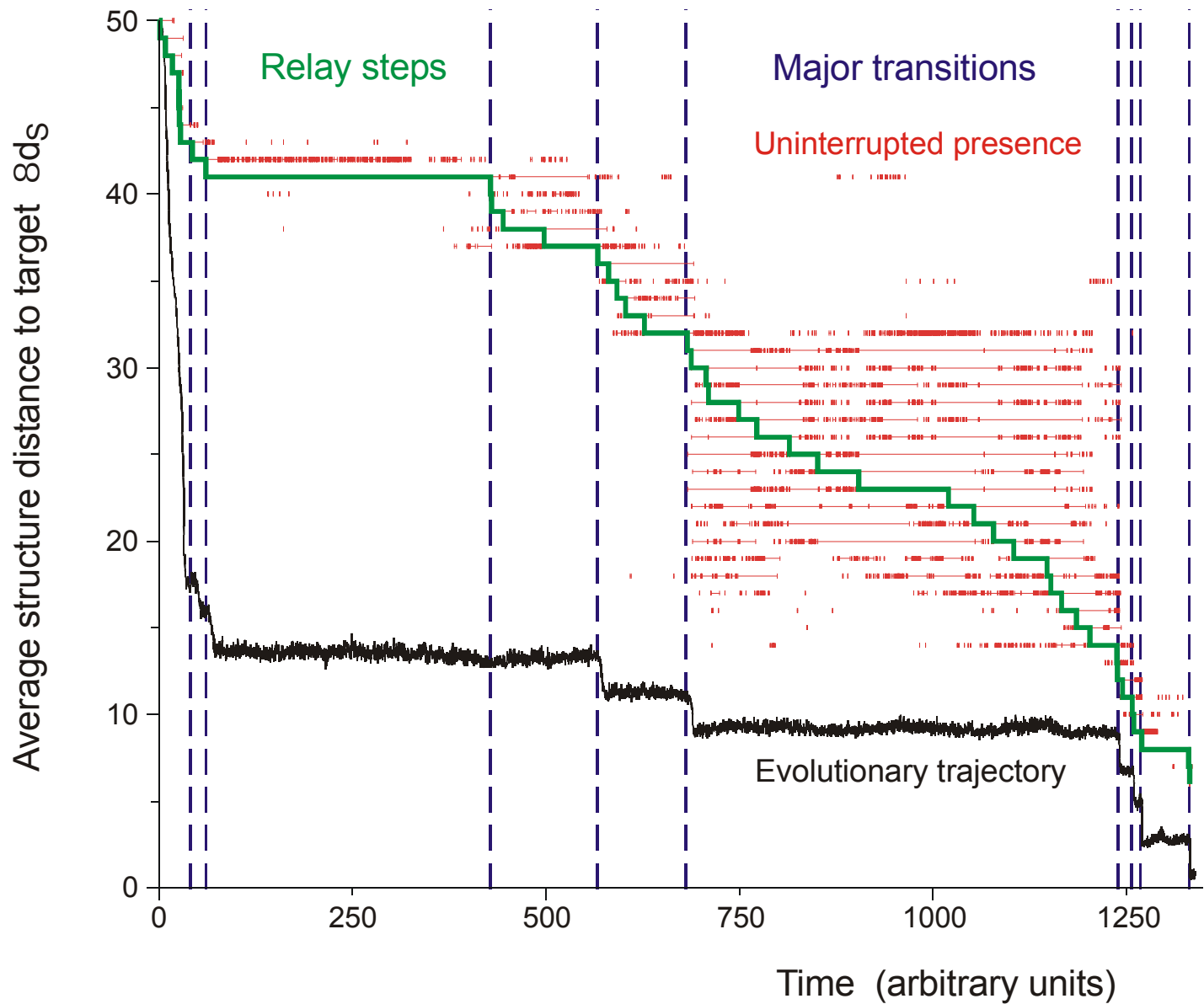
## Major transition leading to clover leaf



## Evolutionary process

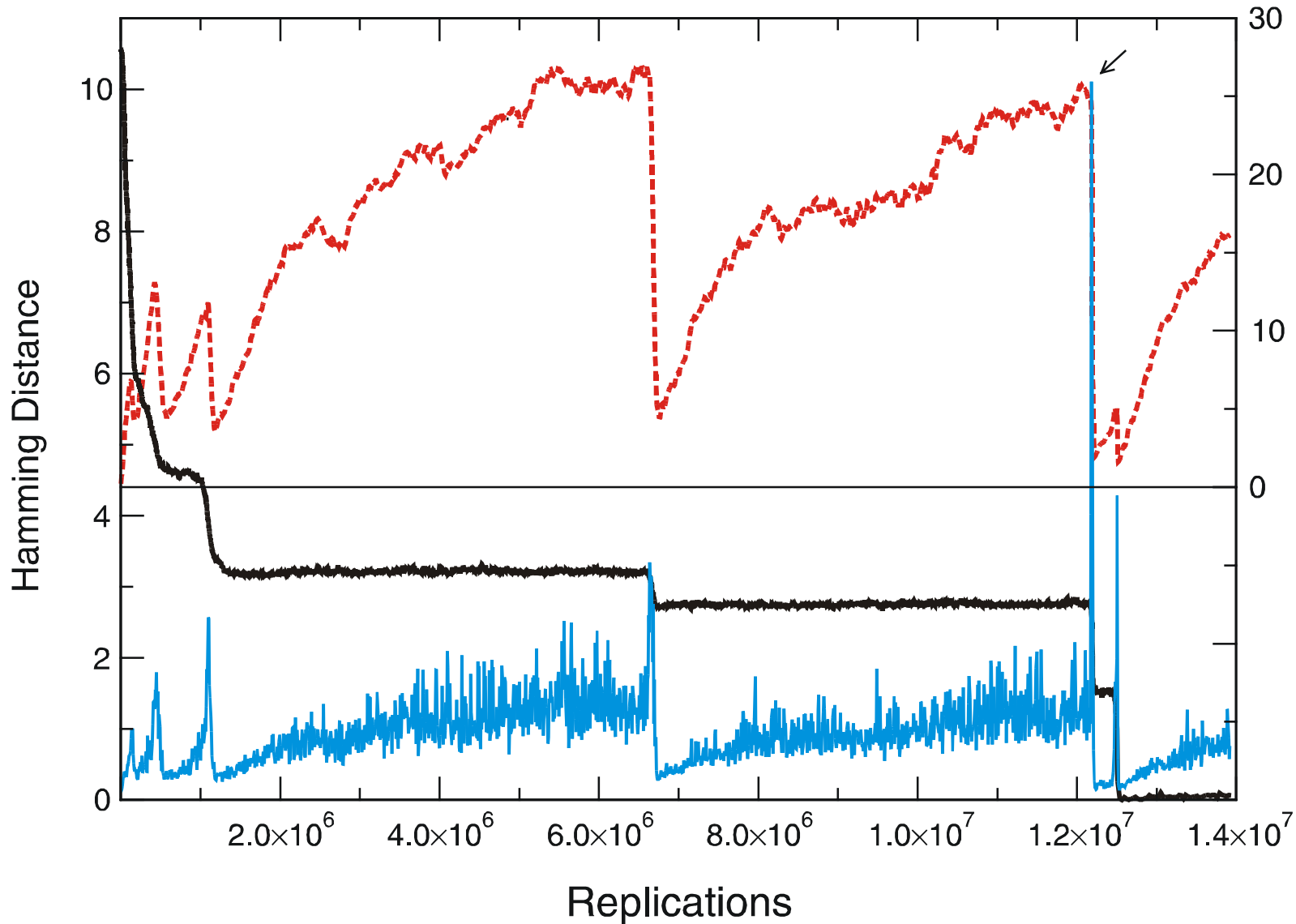


Final reconstruction 36  $\hat{S}$  44



*In silico* optimization in the flow reactor





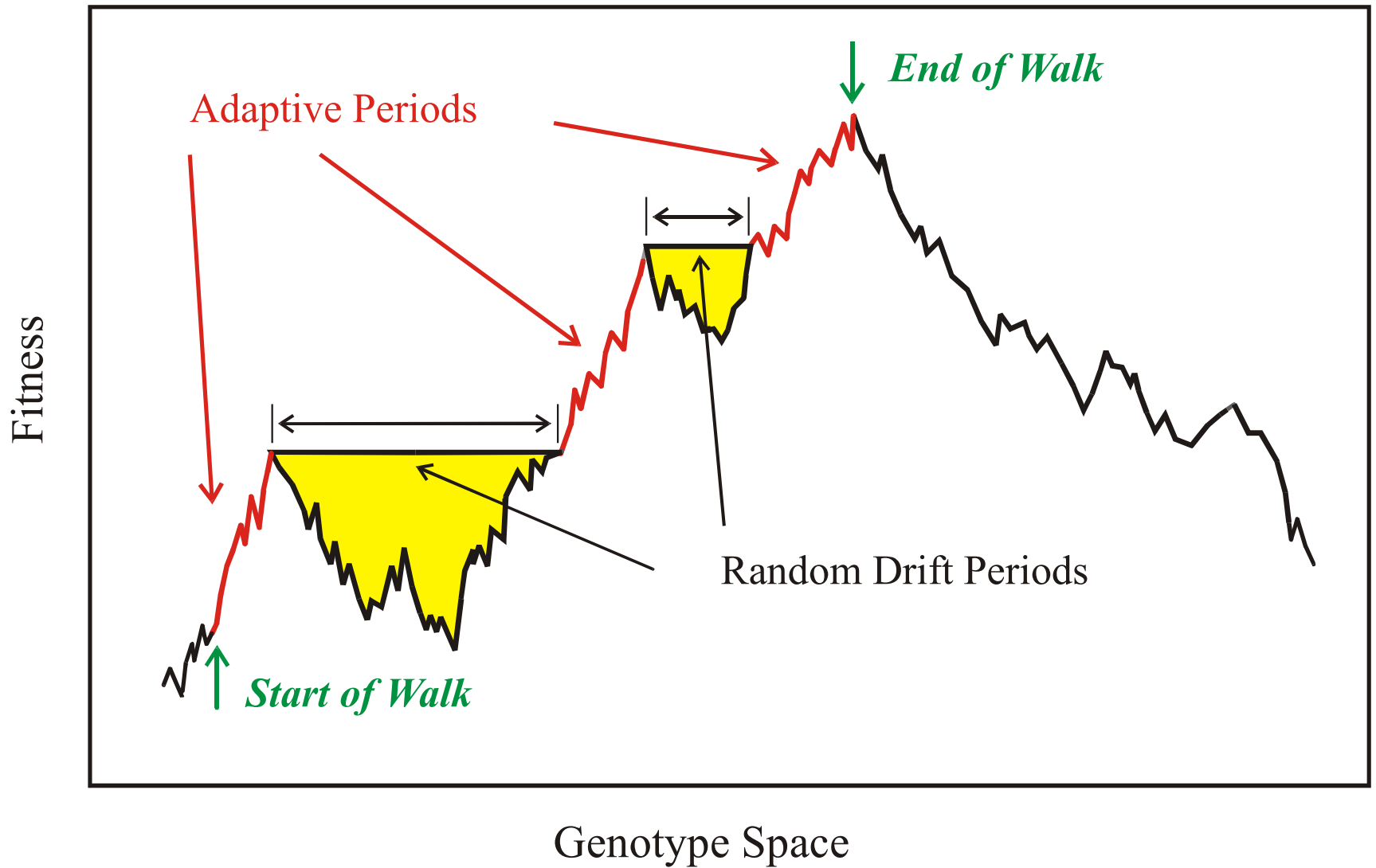
Variation in genotype space during optimization of phenotypes

## Statistics of evolutionary trajectories

Population Size $N$	Number of Replications $\langle n_{\text{rep}} \rangle$	Number of Transitions $\langle n_{\text{tr}} \rangle$	Number of Major Transitions $\langle n_{\text{dtr}} \rangle$	Epochal Phase $\langle d_{\tau}^s(t_{\text{ep}}) \rangle$
1 000	$(5.5 \pm [6.9, 3.1]) \times 10^7$	$92.7 \pm [80.3, 43.0]$	$8.8 \pm [2.4, 1.9]$	$23.7 \pm [5.0, 4.1]$
2 000	$(6.0 \pm [11.1, 3.9]) \times 10^7$	$55.7 \pm [30.7, 19.8]$	$8.9 \pm [2.8, 2.1]$	$22.2 \pm [5.1, 4.2]$
3 000	$(6.6 \pm [21.0, 5.0]) \times 10^7$	$44.2 \pm [25.9, 16.3]$	$8.1 \pm [2.3, 1.8]$	$20.9 \pm [2.4, 2.2]$
10 000	$(1.2 \pm [1.3, 0.6]) \times 10^8$	$35.9 \pm [10.3, 8.0]$	$10.3 \pm [2.6, 2.1]$	$18.4 \pm [2.3, 2.1]$
20 000	$(1.5 \pm [1.4, 0.7]) \times 10^8$	$28.8 \pm [5.8, 4.8]$	$9.0 \pm [2.8, 2.2]$	$17.5 \pm [2.5, 2.2]$
30 000	$(2.2 \pm [3.1, 1.3]) \times 10^8$	$29.8 \pm [7.3, 5.9]$	$8.7 \pm [2.4, 1.9]$	$16.7 \pm [2.0, 1.8]$
100 000	$(3 \pm [2, 1]) \times 10^8$	$24 \pm [6, 5]$	$9 \pm 2$	$17 \pm 1$

„...Variations neither useful not injurious would not be affected by natural selection, and would be left either a fluctuating element, as perhaps we see in certain polymorphic species, or would ultimately become fixed, owing to the nature of the organism and the nature of the conditions.  
...“  
...

Charles Darwin, Origin of species (1859)



Evolution in genotype space sketched as a non-descending walk in a fitness landscape

# **Coworkers**

**Walter Fontana**, Santa Fe Institute, NM

**Christian Reidys, Christian Forst**, Los Alamos National Laboratory, NM

**Peter Stadler**, Universität Wien, AT

**Ivo L.Hofacker**

**Christoph Flamm**

**Bärbel Stadler, Andreas Wernitznig**, Universität Wien, AT

**Michael Kospach, Ulrike Mückstein, Stefanie Widder, Stefan Wuchty**

**Jan Cupal, Kurt Grünberger, Andreas Svrček-Seiler**

**Ulrike Göbel**, Institut für Molekulare Biotechnologie, Jena, GE

**Walter Grüner, Stefan Kopp, Jaqueline Weber**