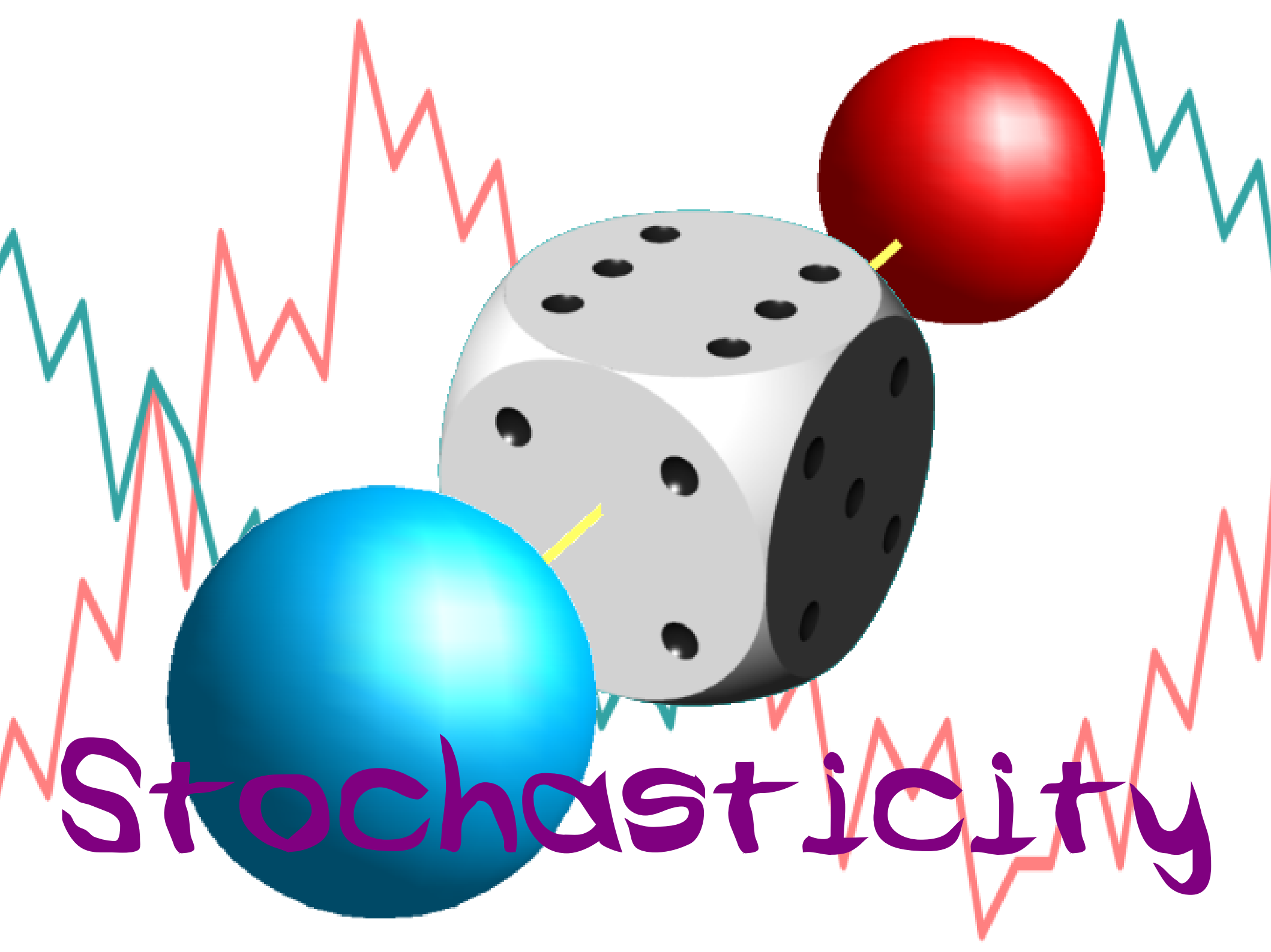
Mesoscopic simulations of receptive lattices

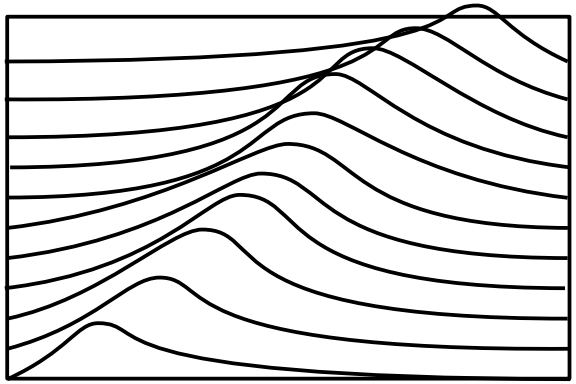
Limitation of deterministic approaches

Continuous, deterministic models can’t cope with:

1. Sensitivity to a very small number of molecules
2. Protein complexes with many states
3. Spatial heterogeneity

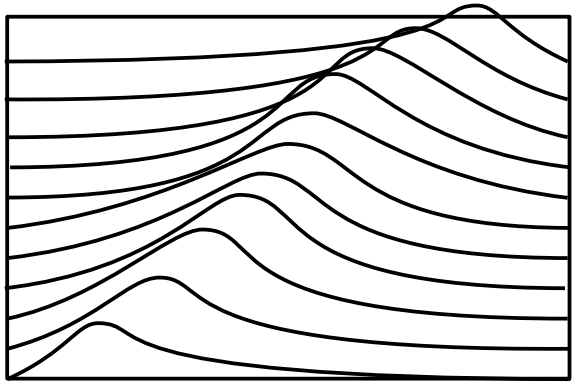

Stochasticity

Different modelling approaches



Grand Probability function: P(X,t)

Different modelling approaches



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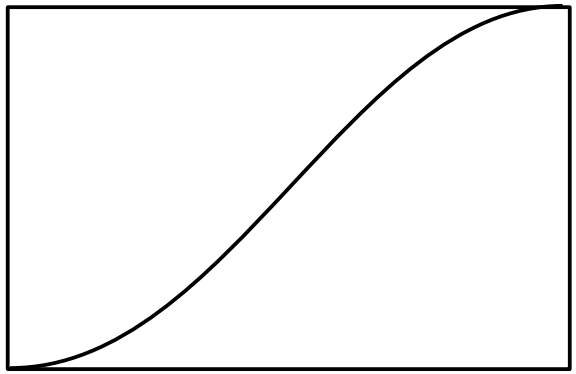
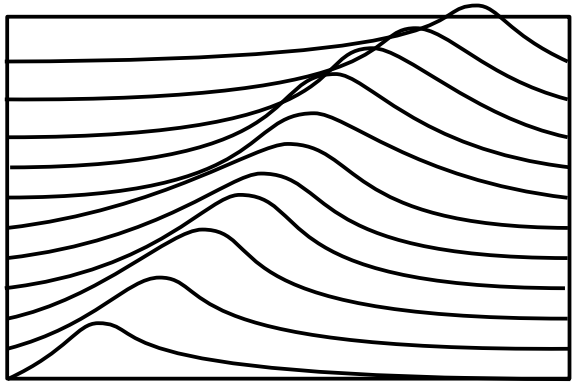


typologic view of the world: (X)=f(t)

Different modelling approaches



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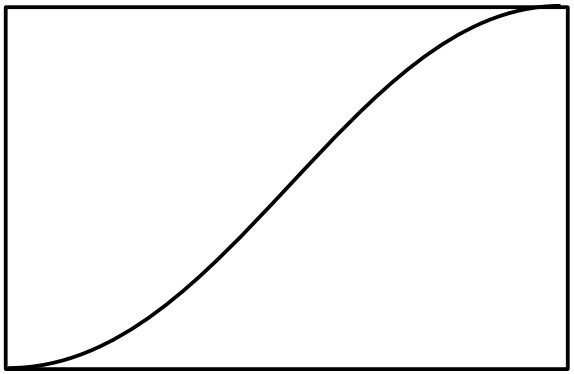

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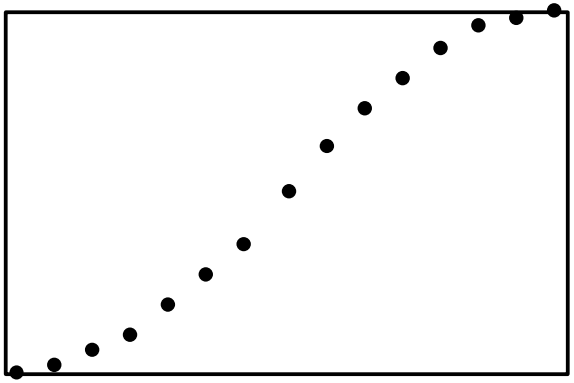
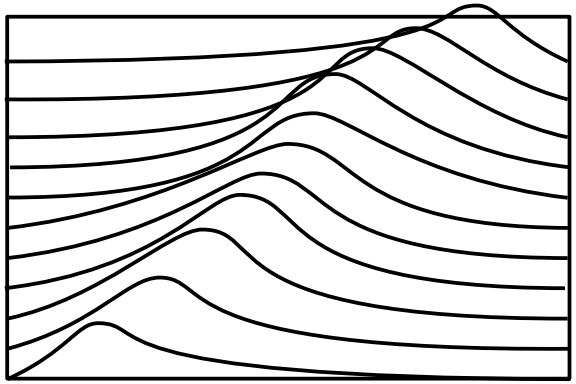


deterministic approach: (X,t)=f(X',t-1)

Different modelling approaches



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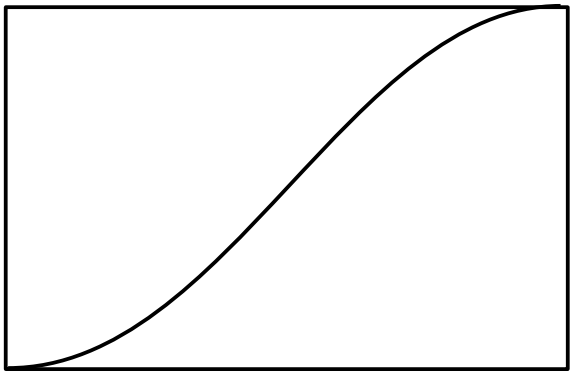
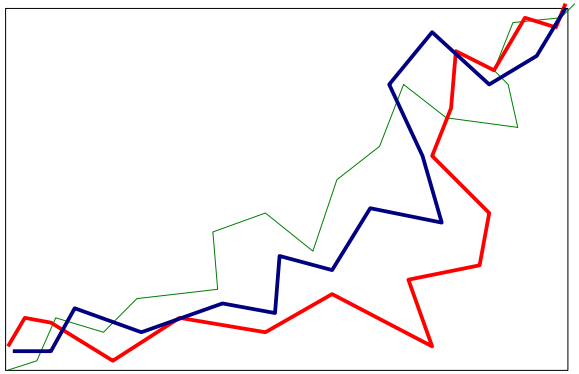
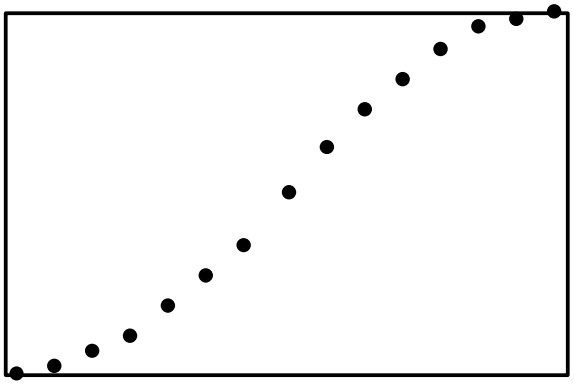


typologic view of the world: (X)=f(t)

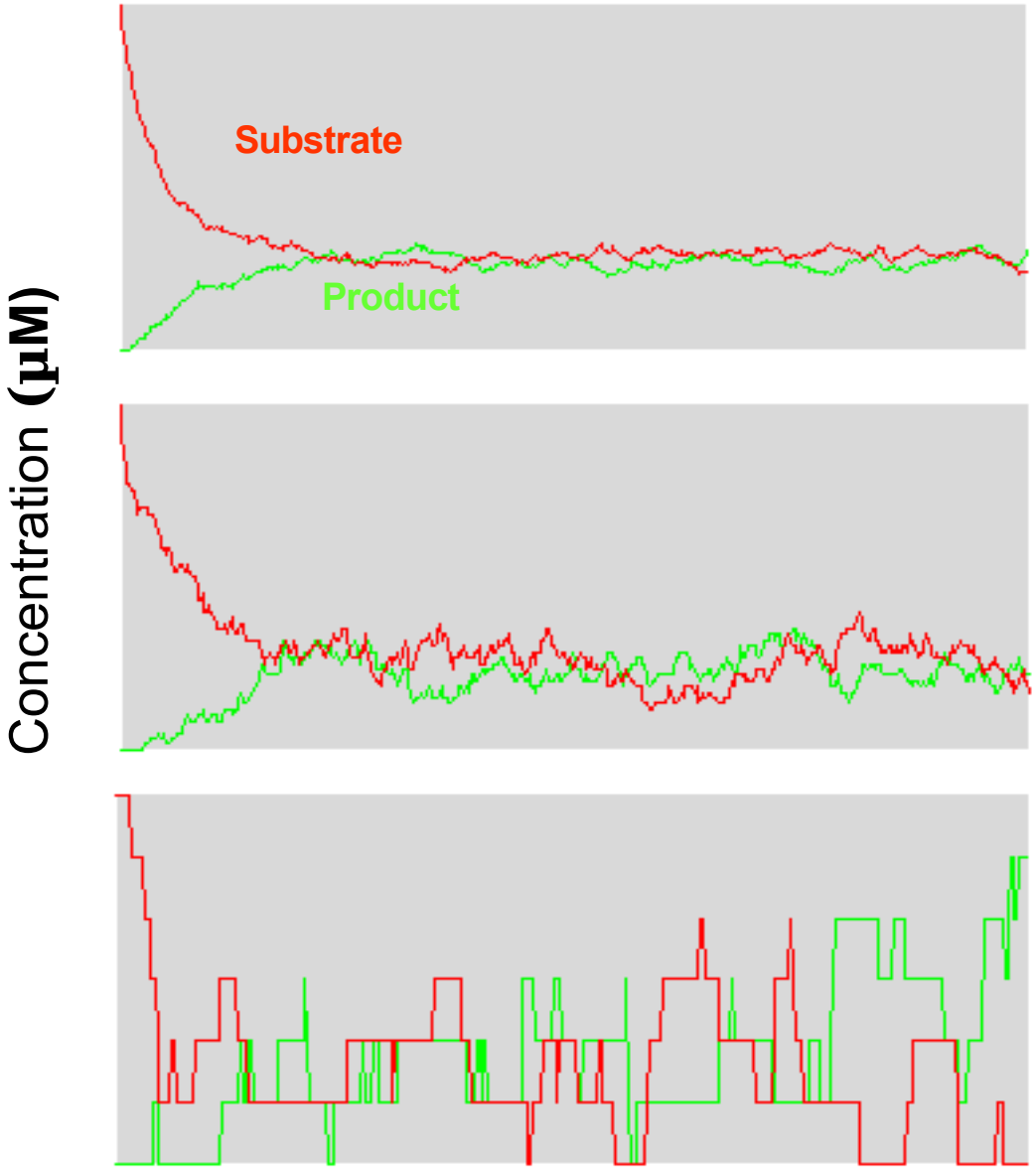


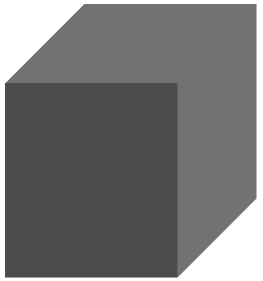
stochastic approach: P(X,t)/(X',t-1)



deterministic approach: (X,t)=f(X',t-1)

On small numbers





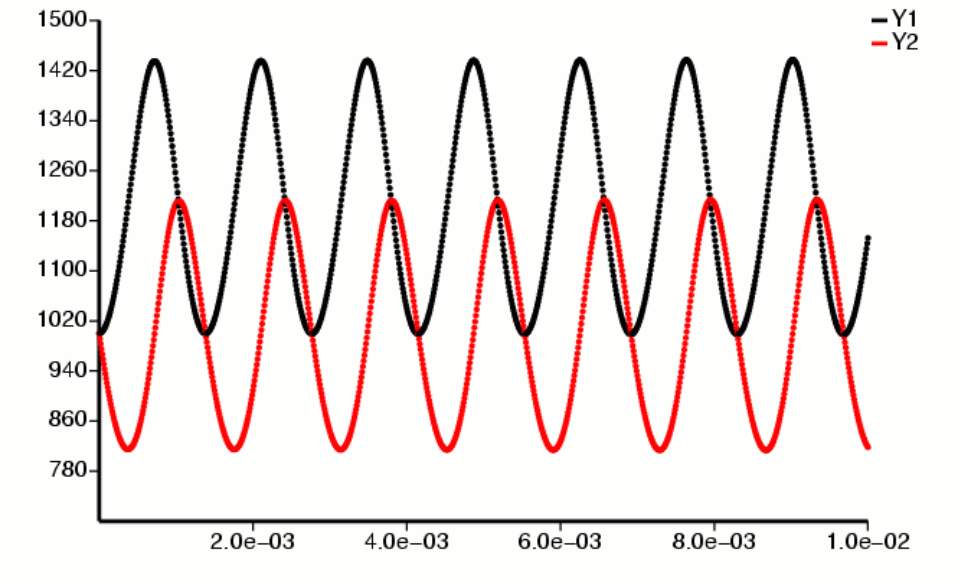
10^{-15} litres

10^{-16} litres

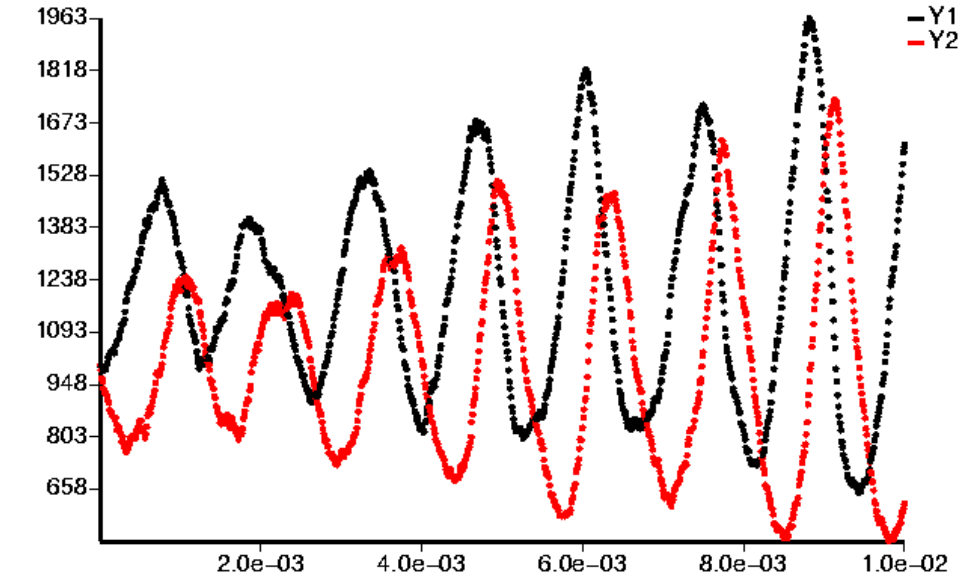
10^{-17} litres

Resting number of calcium ions in a dendritic spine = 3-5 ...

On determinism and reproducibility

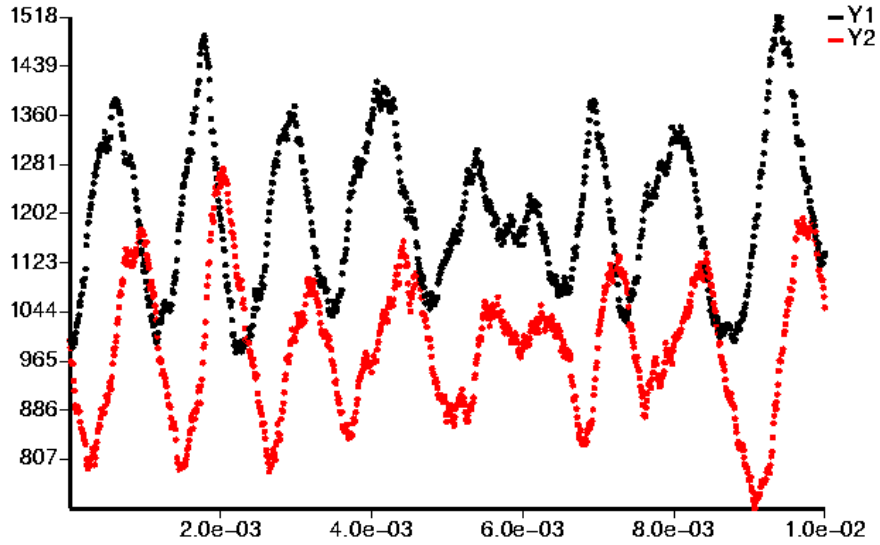


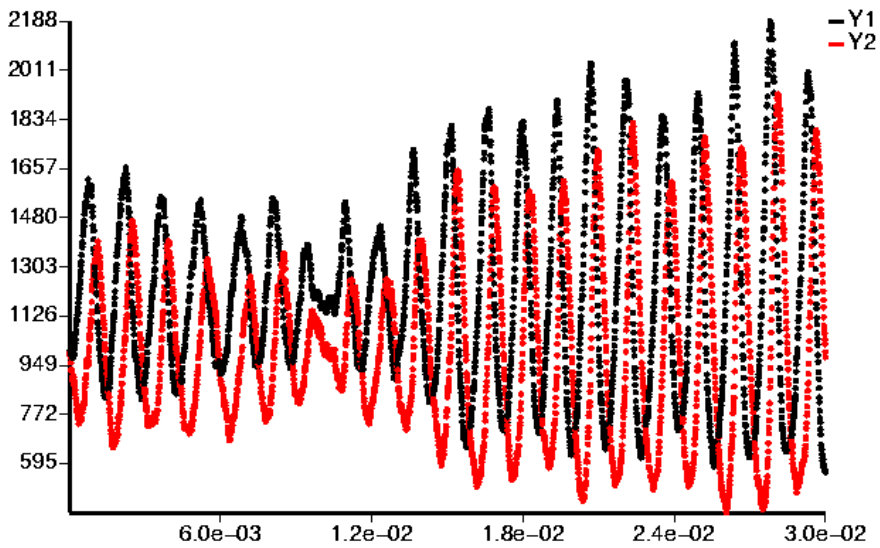
deterministic result

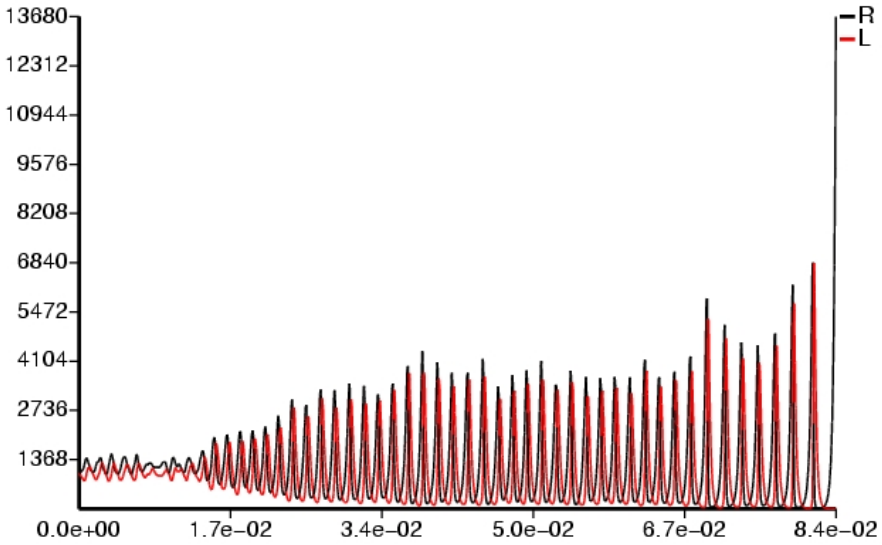


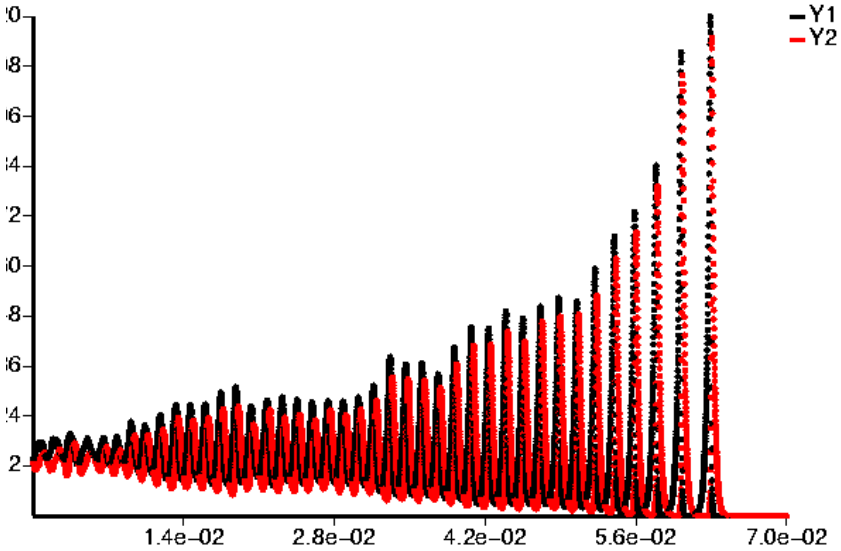
stochastic result

"Pathologic" behaviour







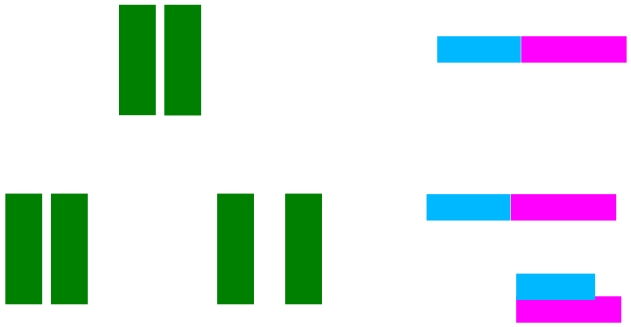



Combinatorial
Explosion

Combinatorial explosion

NMDA + CaMKII <=> NMDA-CaMKII

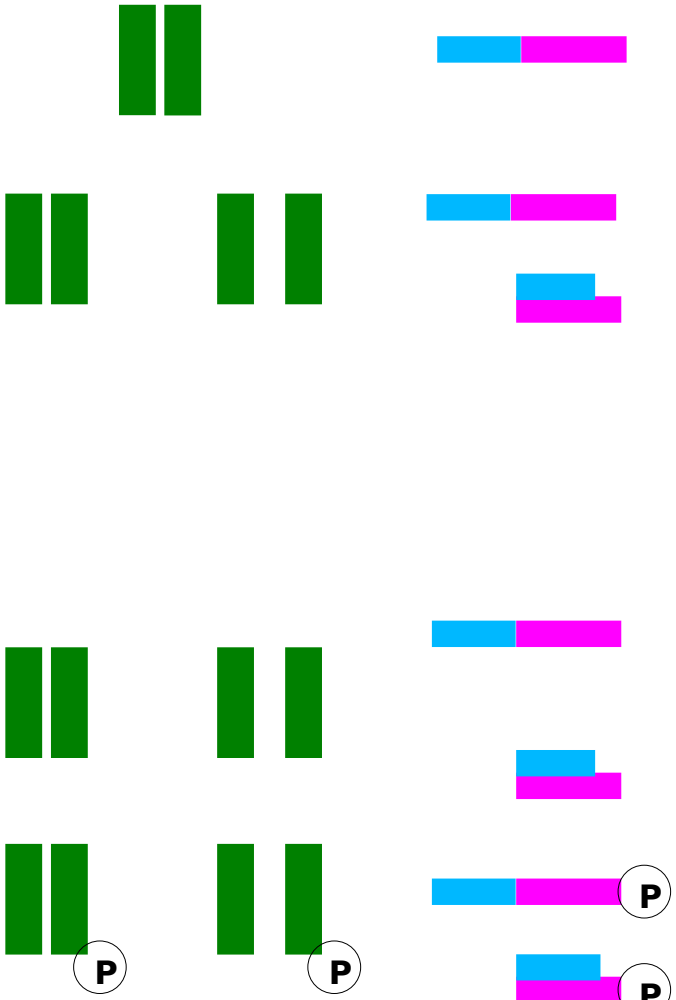
Combinatorial explosion



NMDA + CaMKII <=> NMDA-CaMKII

NMDAc + CaMKIIc <=> NMDAc-CaMKIIc
NMDAo + CaMKIIc <=> NMDAc-CaMKIIc
NMDAc + CaMKIIo <=> NMDAc-CaMKIIo
NMDAo + CaMKIIo <=> NMDAc-CaMKIIo

Combinatorial explosion



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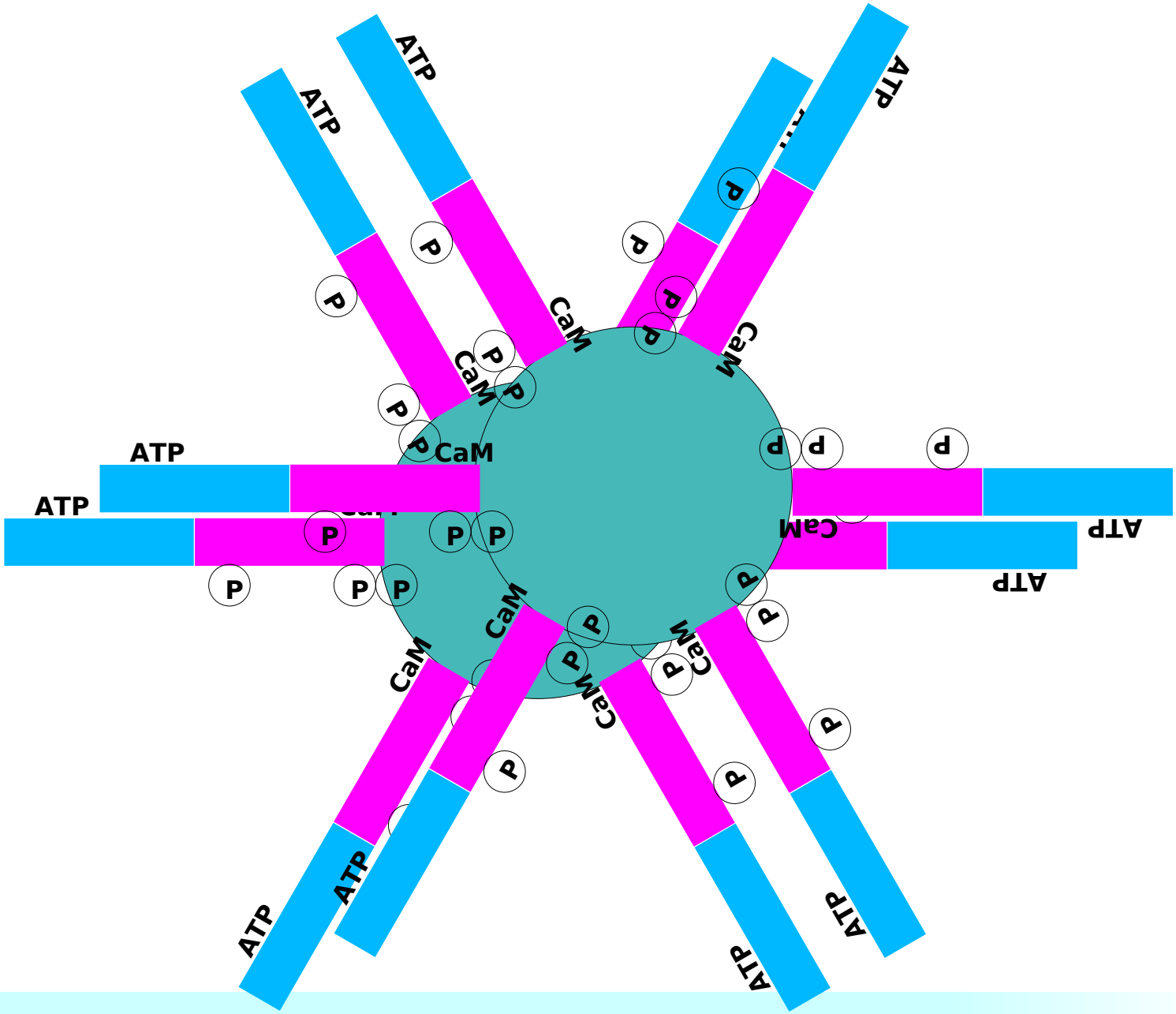
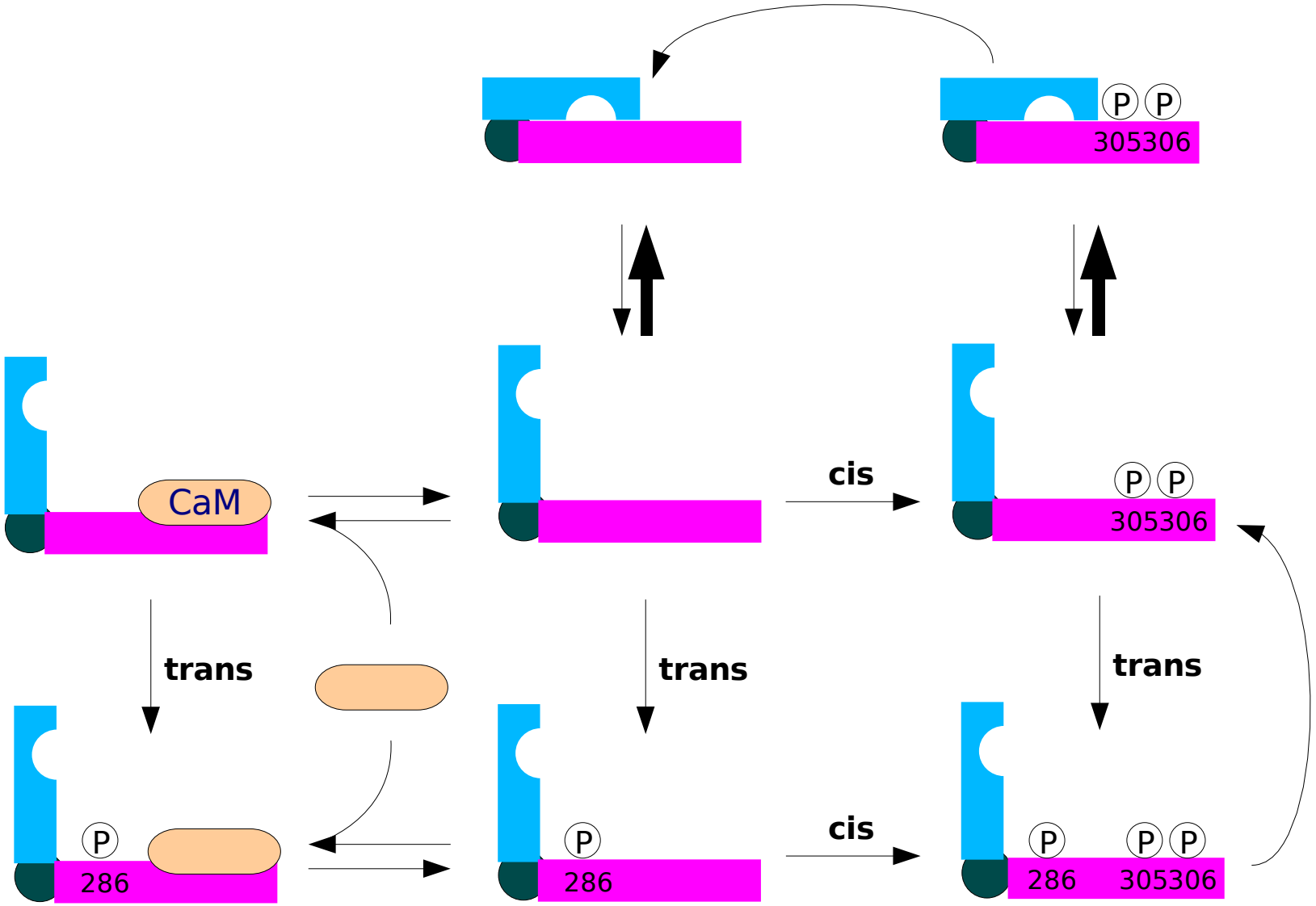
NMDAc + CaMKIIo <=> NMDAc-CaMKIIo
NMDAo + CaMKIIo <=> NMDAc-CaMKIIo
pNMDAc + CaMKIIc <=> pNMDAc-CaMKIIc
pNMDAo + CaMKIIc <=> pNMDAc-CaMKIIc
pNMDAc + CaMKIIo <=> pNMDAc-CaMKIIo
pNMDAo + CaMKIIo <=> pNMDAc-CaMKIIo
NMDAc + pCaMKIIc <=> NMDAc-pCaMKIIc
NMDAo + pCaMKIIc <=> NMDAc-pCaMKIIc
NMDAc + pCaMKIIo <=> NMDAc-pCaMKIIo
NMDAo + pCaMKIIo <=> NMDAc-pCaMKIIo
pNMDAc + pCaMKIIc <=> pNMDAc-pCaMKIIc
pNMDAo + pCaMKIIc <=> pNMDAc-pCaMKIIc
pNMDAc + pCaMKIIo <=> pNMDAc-pCaMKIIo
pNMDAo + pCaMKIIo <=> pNMDAc-pCaMKIIo

Combinatorial explosion



Additional reactions



Combinatorial explosion

- number of states = 2^n
- A molecule with 10 features = 2^{10} = 1024 states, that is 1024 pools. But most signalling molecules are present a few hundred times ...
- number of state conversions= n x 2^{n-1}
- A molecule with 10 features reacting with a molecule with 10 features =

Combinatorial explosion

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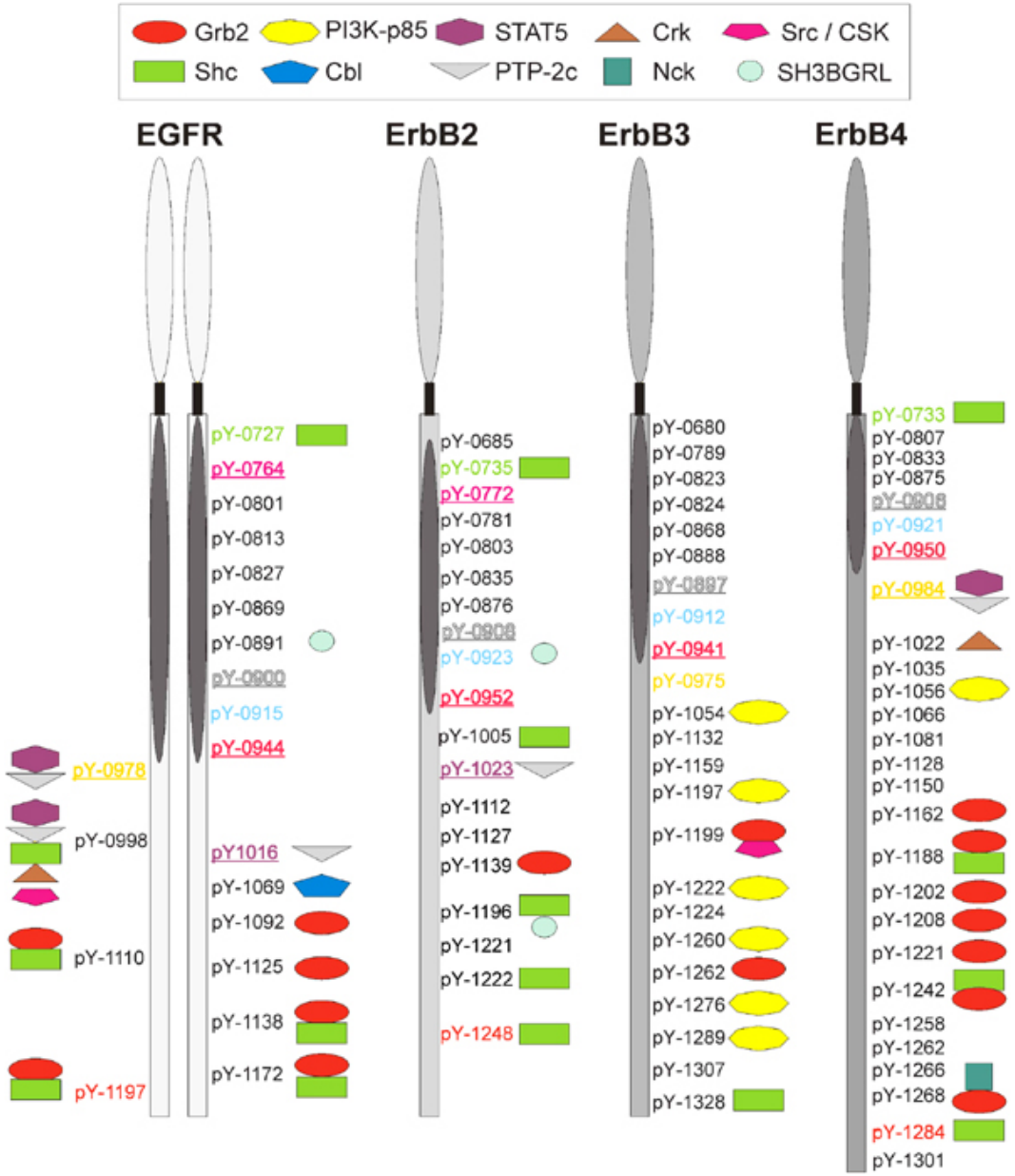
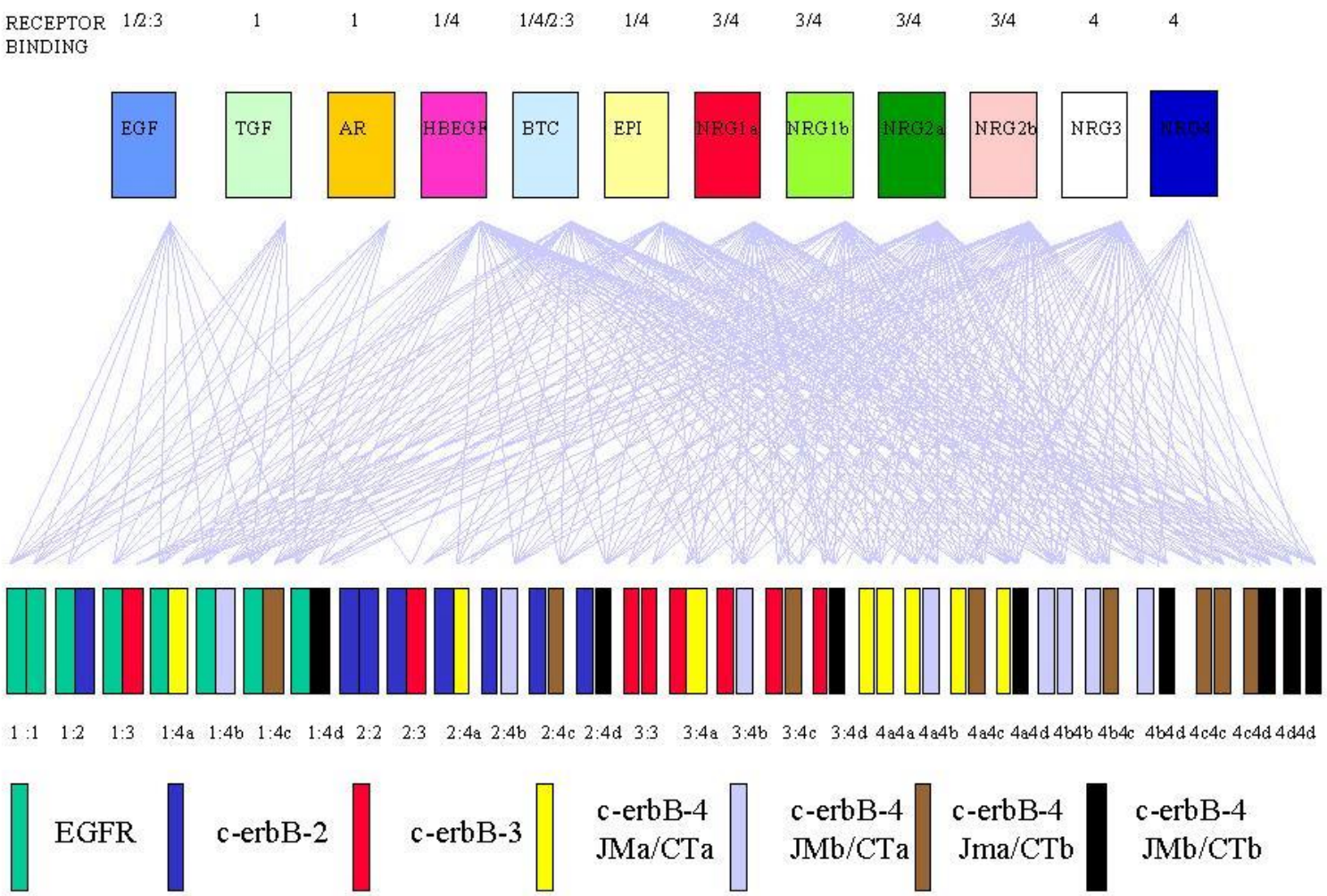
- number of state conversions= n x 2^{n-1}
- A molecule with 10 features reacting with a molecule with 10 features = 1058816 possible reactions!

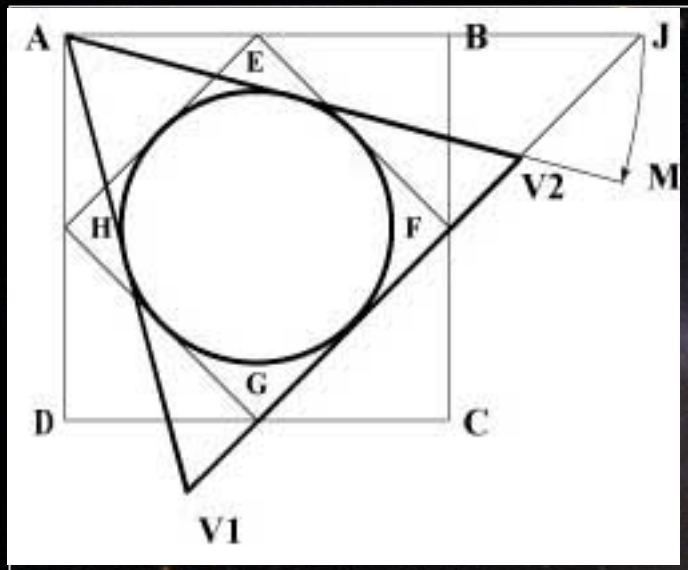
Ugly beast

Schulze *et al*. (2005)
Mol Sys Bio,
doi: 10.1038/msb4100012



Ugly beast

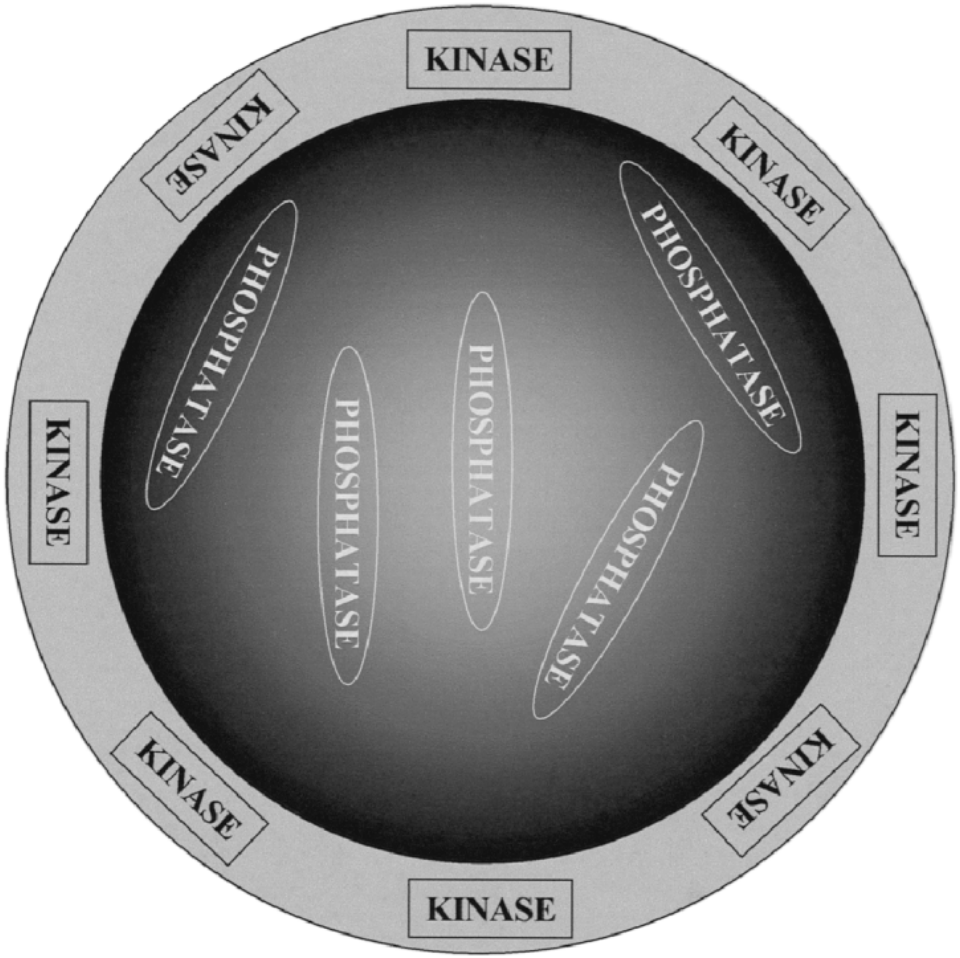

RECEPTOR BINDING
1/2:3
1
1
1/4
1/4/2:3
1/4
3/4
3/4
3/4
3/4
4
4
EGF
TGF
AR
HBEGF
BTC
EPI
NRG1a
NRG1b
NRG2a
NRG2b
NRG3
NRG4
1:1 1:2 1:3 1:4a 1:4b 1:4c 1:4d 2:2 2:3 2:4a 2:4b 2:4c 2:4d 3:3 3:4a 3:4b 3:4c 3:4d 4a4a 4a4b 4a4c 4a4d 4b4b 4b4c 4b4d 4c4c 4c4d 4d4d
EGFR
c-erbB-2
c-erbB-3
c-erbB-4 JMa/CTa
c-erbB-4 JMb/CTa
c-erbB-4 Jma/CTb
c-erbB-4 JMb/CTb

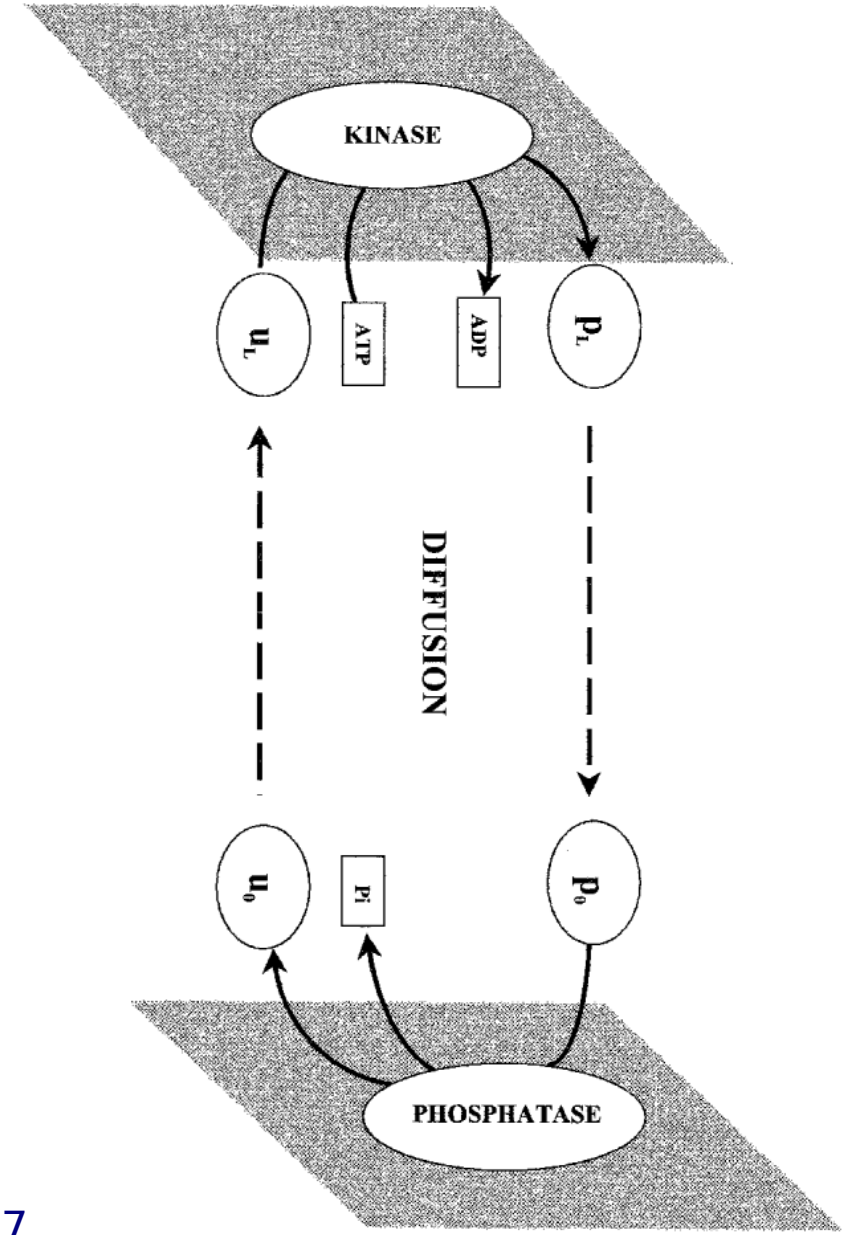


Space and geometry

ESO, geoman.net

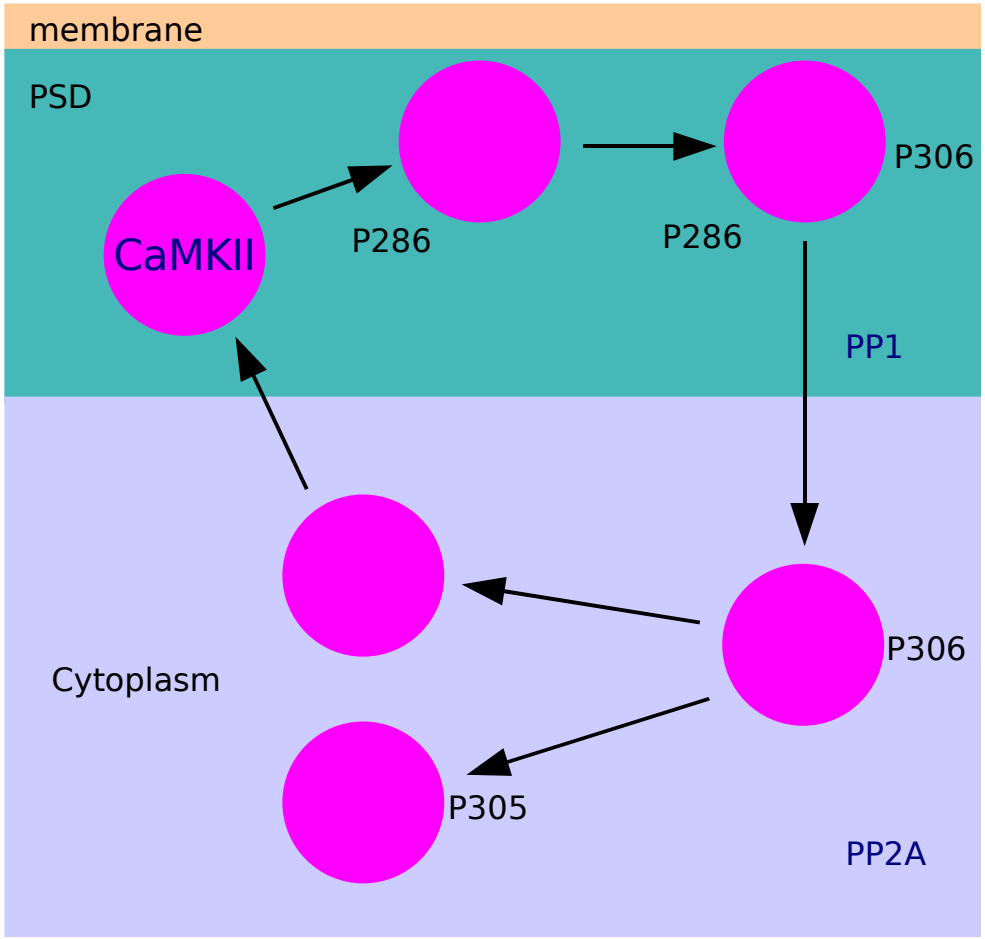
Spatial hysteresis





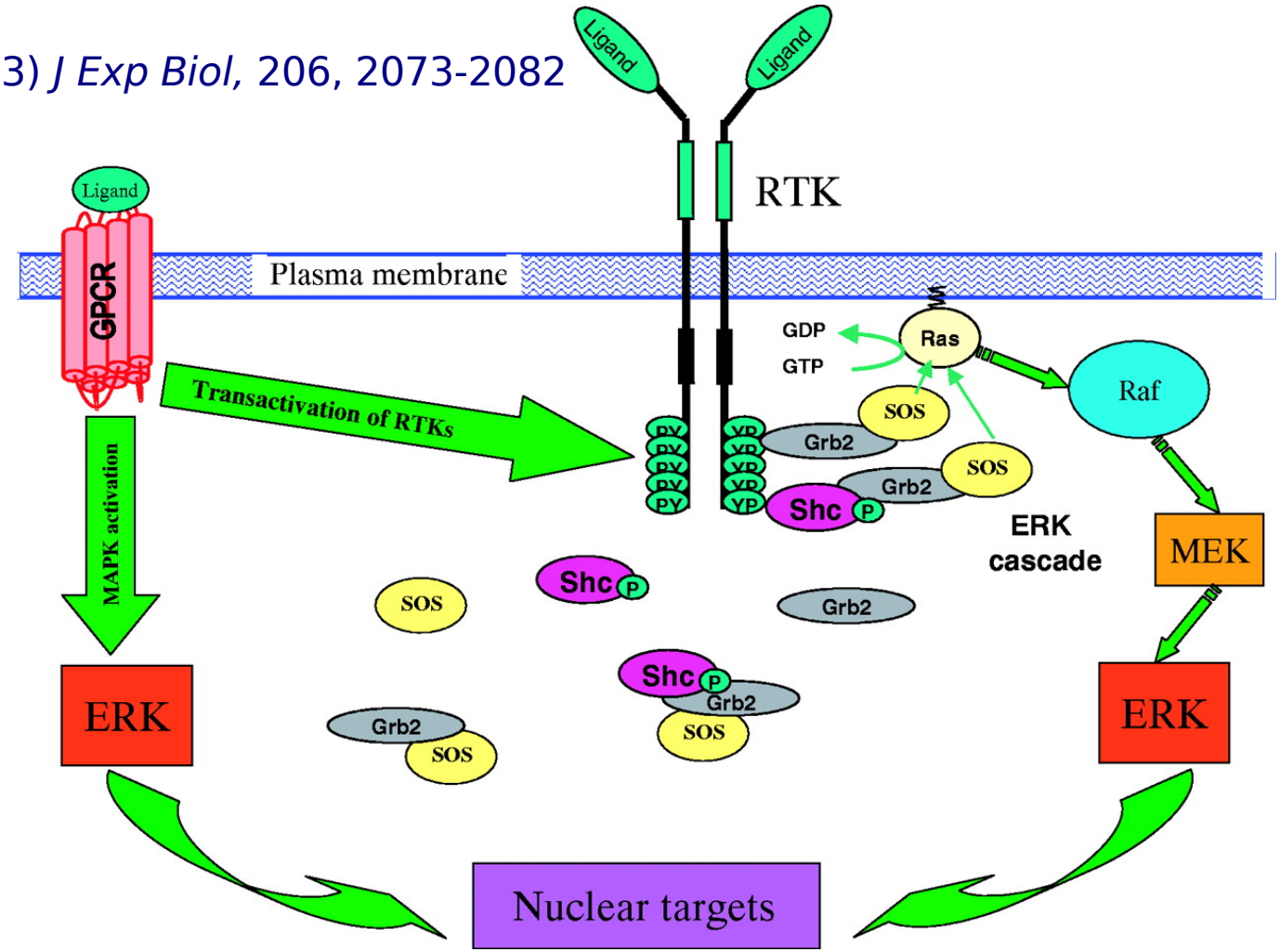
Kholodenko et al. *Biochem. J.* (2000) 350: 901–907

Spatial hysteresis



Spatial cascades

Kholodenko (2003) *J Exp Biol,* 206, 2073-2082



Need another paradigm of simulation

Population-based simulation

- Continuous representation of populations
- Generally deterministic algorithms to simulate the evolution of populations (but not always: Gillespie)
- Generally no representation of space (but not always: finite elements)
- No movements (but not always: PDE or reaction-diffussion)
- Molecules under different states are represented by different pools

Particle-based simulation

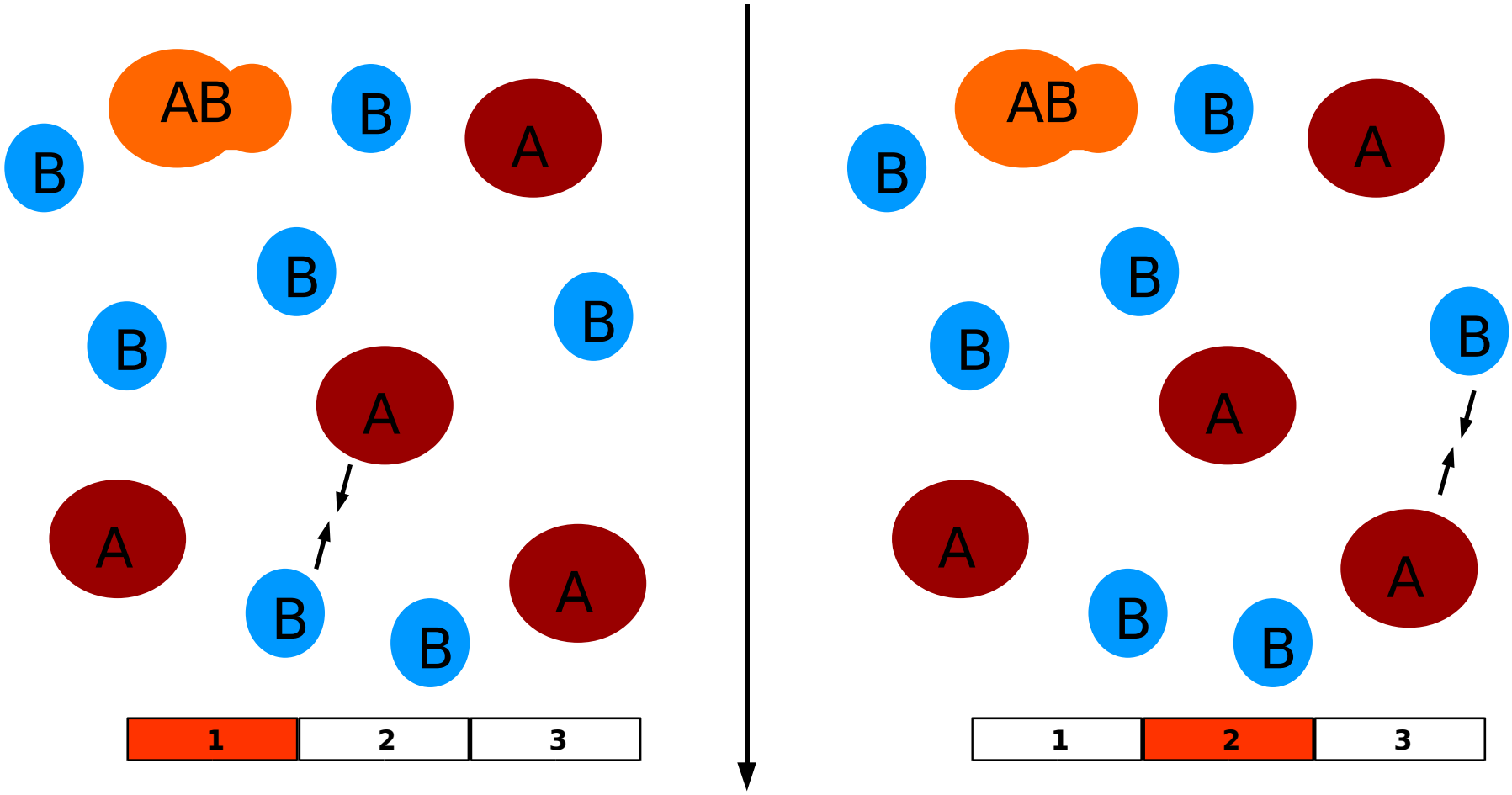
- Discrete representation of molecules
- Generally stochastic algorithms (but not always: deterministic automata)
- Generally location of molecules (but not always: StochSim v1)
- Representation of the movements of (some) molecules
- Possibility of multistates molecules

StochSim: Stochastic cellular automata

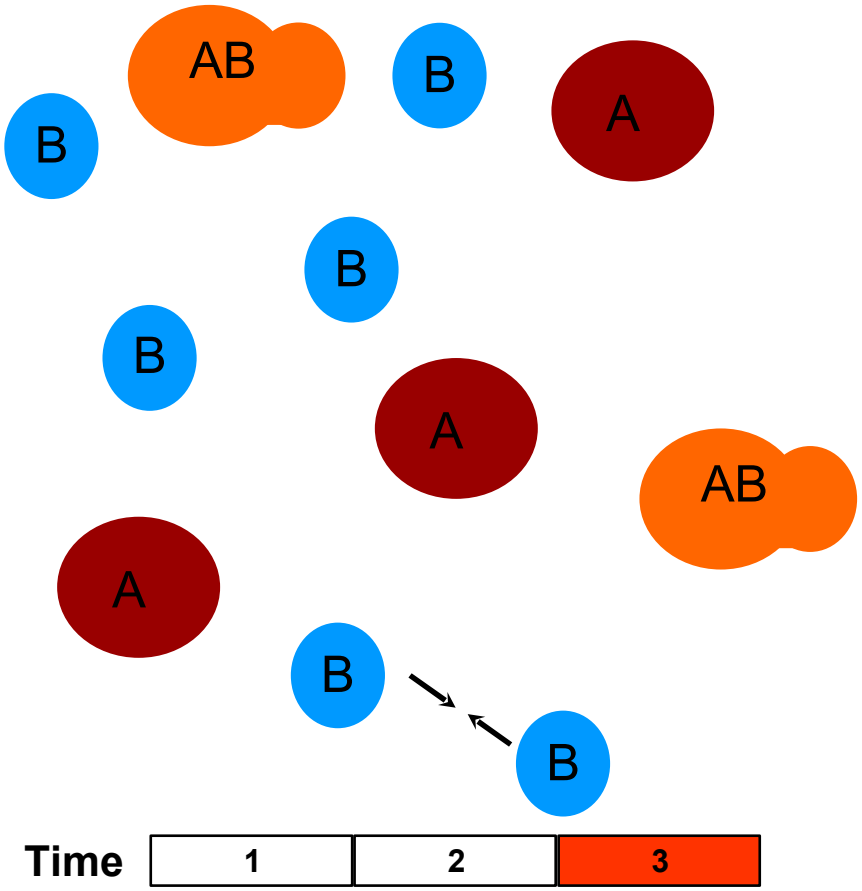
- Morton-Firth CJ, Bray D (1998) *J. Theor. Biol.* 192: 117–128.
- Le Novère N, Shimizu TS (2001) *Bioinformatics* 17: 575-576

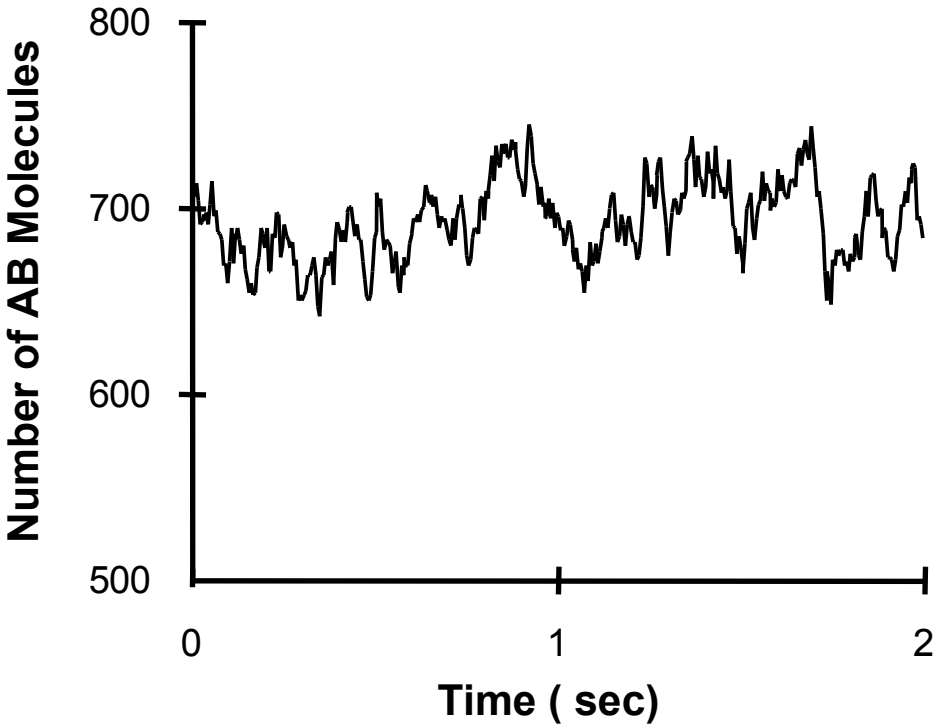
- Particle-based stochastic simulations
- Possibility of multistate complexes
- Rapid equilibria to reduce stiffness problems
- 2D lattices of various geometry

StochSim algorithm



StochSim algorithm





Kinetic constant to probability

$$\Delta n_A = P(\text{pick A}) * P(\text{pick pseudo-mol}) * P1 * \Delta t$$
$$+ P(\text{pick pseudo-molecule}) * P(\text{pick A}) * P1 * \Delta t$$

$$\Delta n_A = kon * [A] * \Delta t$$

$$kon * n_A/(Va*Na) = 2 * n_A/n * n_0/(n+n_0) * P1 * \Delta t$$

n: # molecules in the system
n_0: # pseudomolecules in the system
V: volume of the system
N_A: Avogadro constant

Kinetic constant to probability

$$d[A]/dt = -k[A] \qquad P1 = \frac{k\, n(n+n_0)\Delta t}{n_0}$$

$$d[A]/dt = -k[A][B] \qquad P2 = \frac{k\, n(n+n_0)\Delta t}{2VN_A}$$

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Kinetic constant to probability

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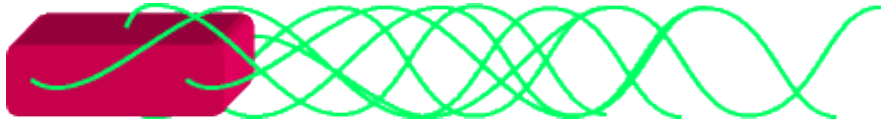
$$d[A]/dt = -k[A][B] \qquad P2 = \frac{k\, n(n+n_0)\Delta t}{2VN_A}$$

n_0 optimized to limit the stiffness between unimolecular and bimolecular reactions

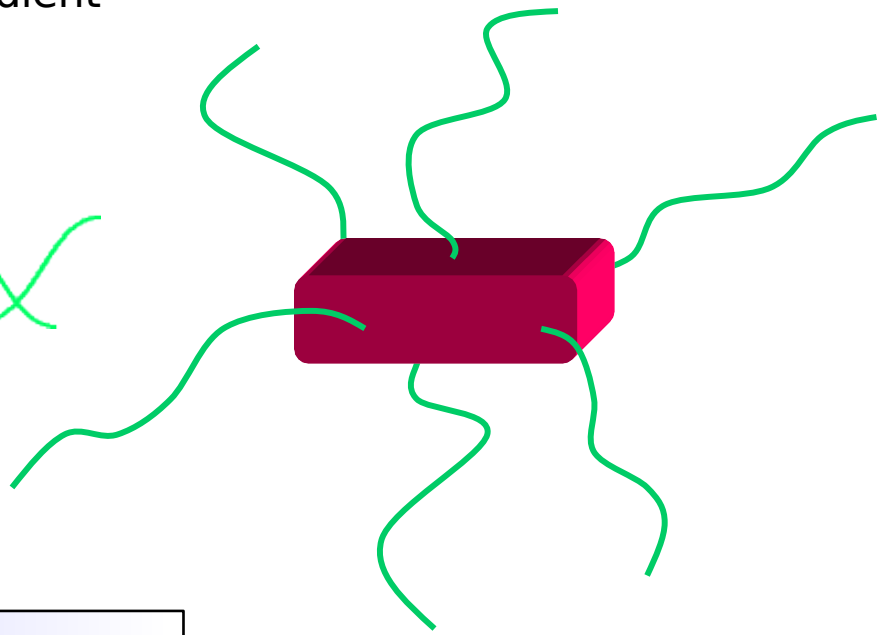
n: # molecules in the system
n_0: # pseudomolecules in the system
V: volume of the system
N_A: Avogadro constant

Mechanism of bacterial chemotaxis

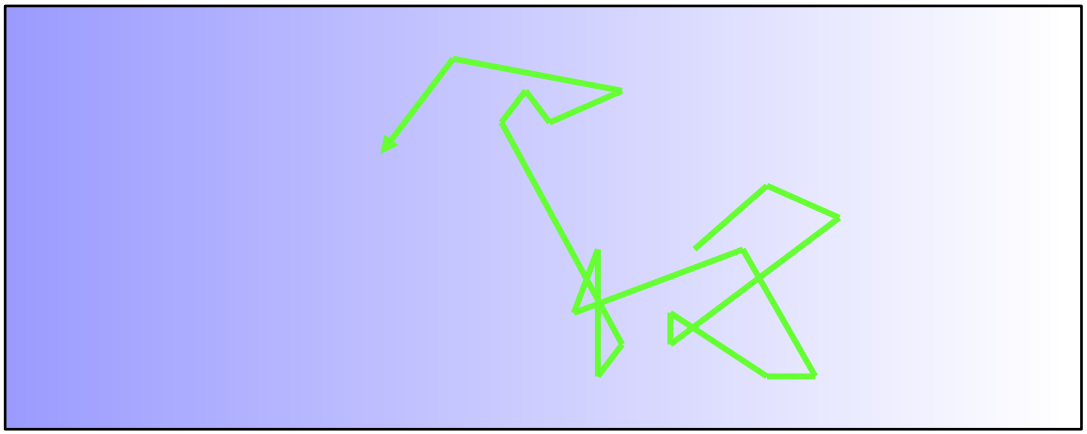
- small size ⇒ unable to read gradient
- small weight ⇒ no inertia



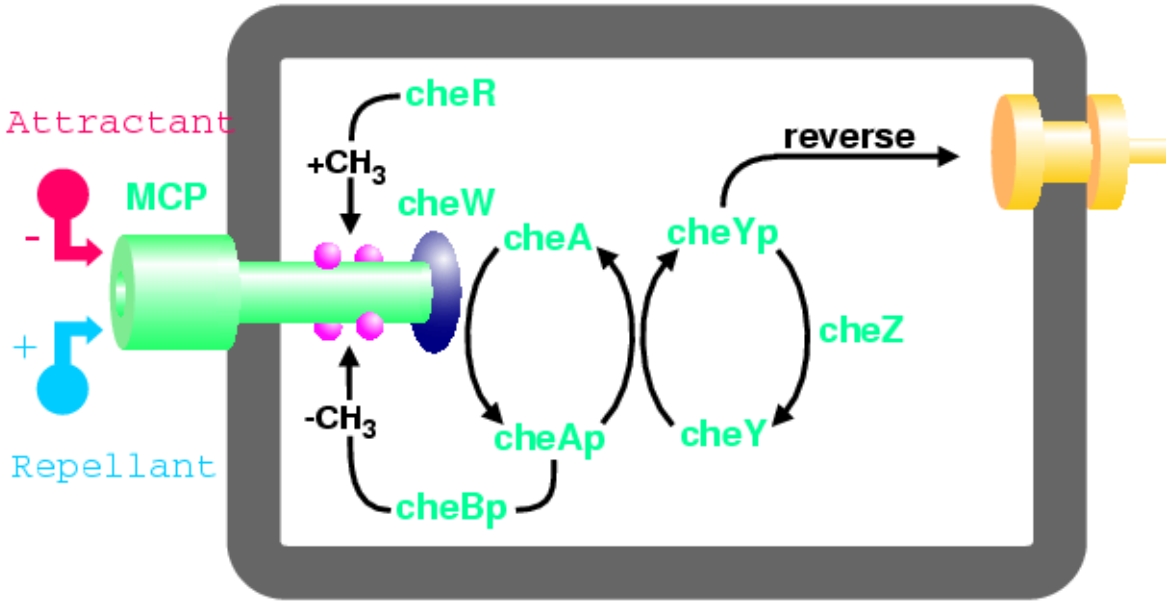
CCW = smooth



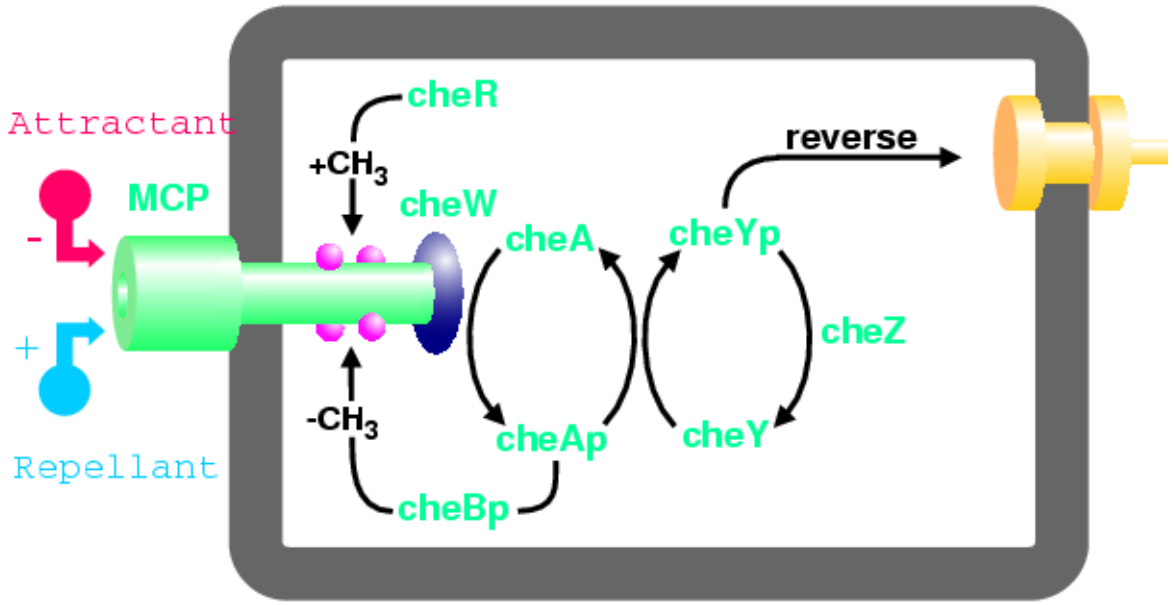
CW = tumble

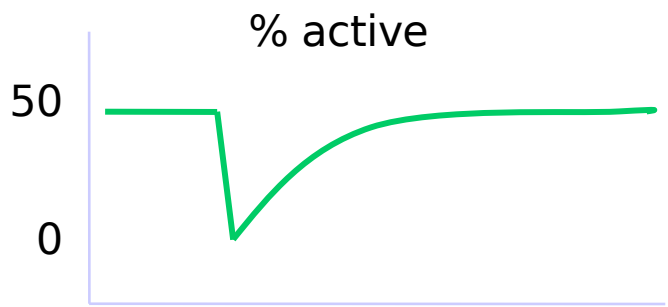


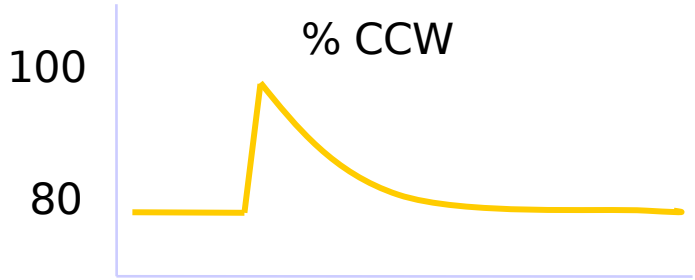
Mechanism of bacterial chemotaxis



Mechanism of bacterial chemotaxis

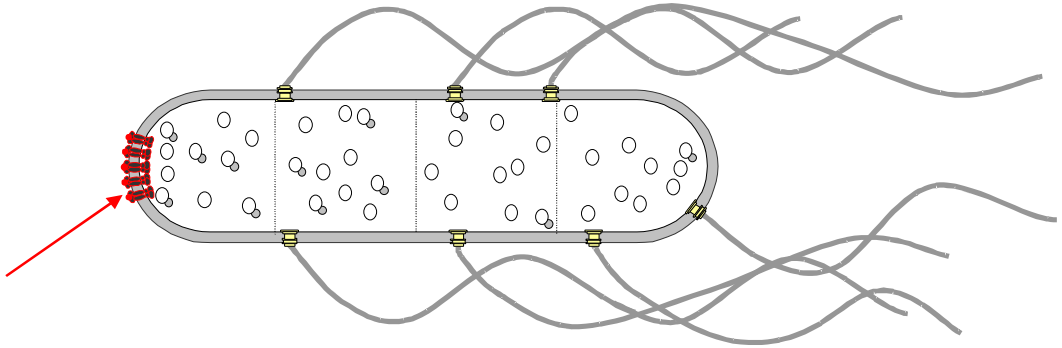


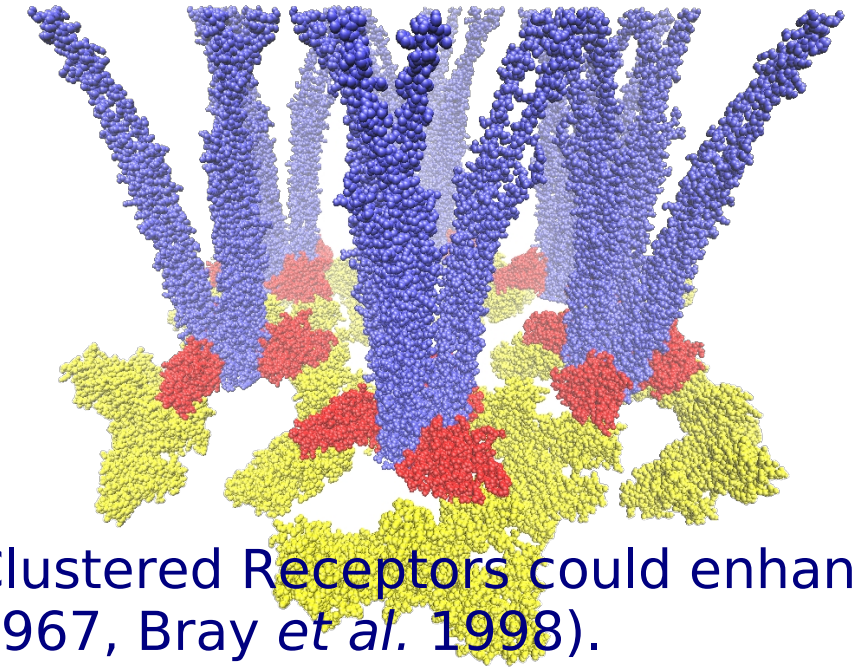


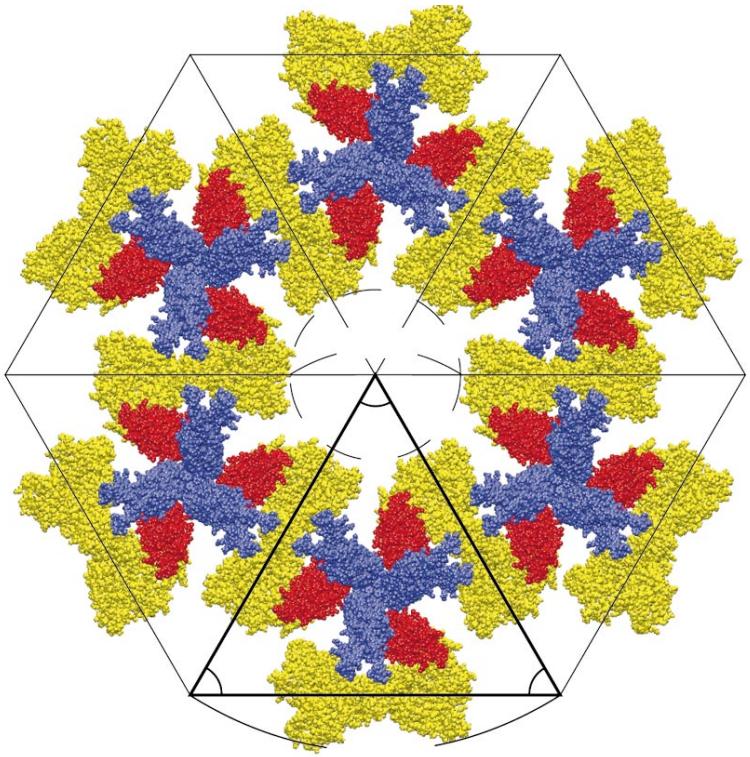


Receptor clustering and sensitivity

Chemotactic receptors form clusters at cell poles in E. coli (Shimizu *et al.* (2000) *Nat Cell Biol* 2: 792-796).







Clustered Receptors could enhance sensitivity (Changeux *et al.* 1967, Bray *et al.* 1998).

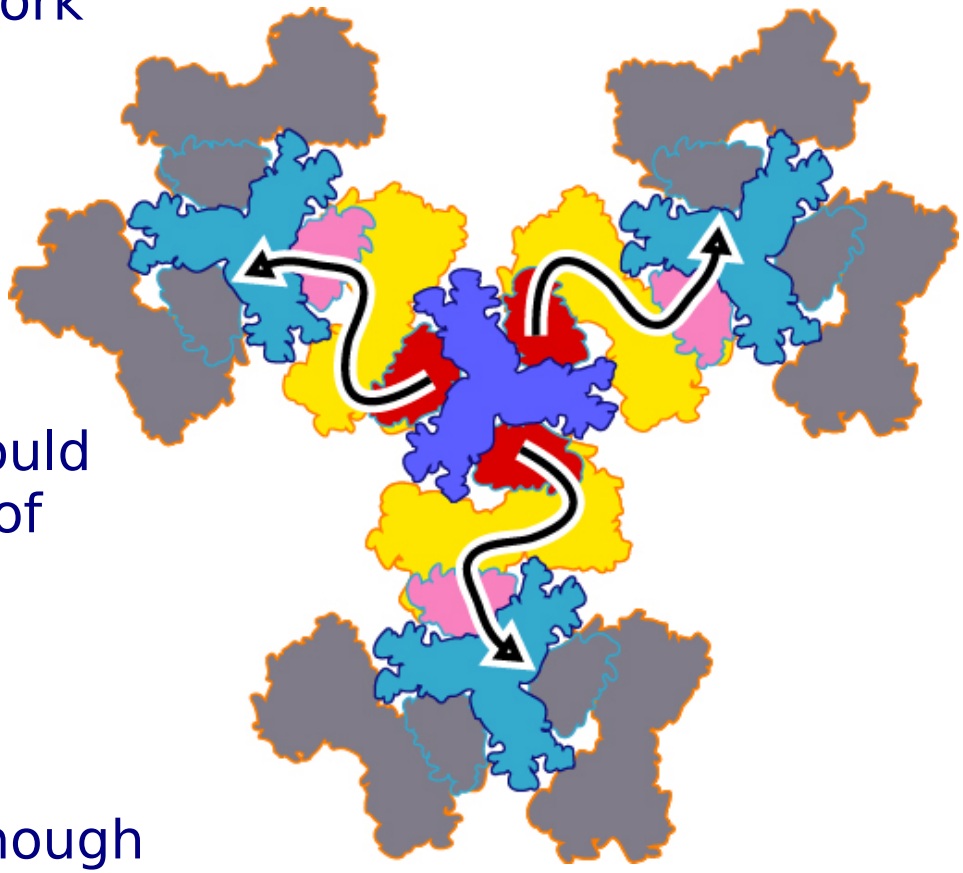
Integration of various signals (Hazelbauer et al. 1989).

Consequences for signalling

- Conformational changes could be propagated through the network via CheA/CheW
  Enhanced gain;

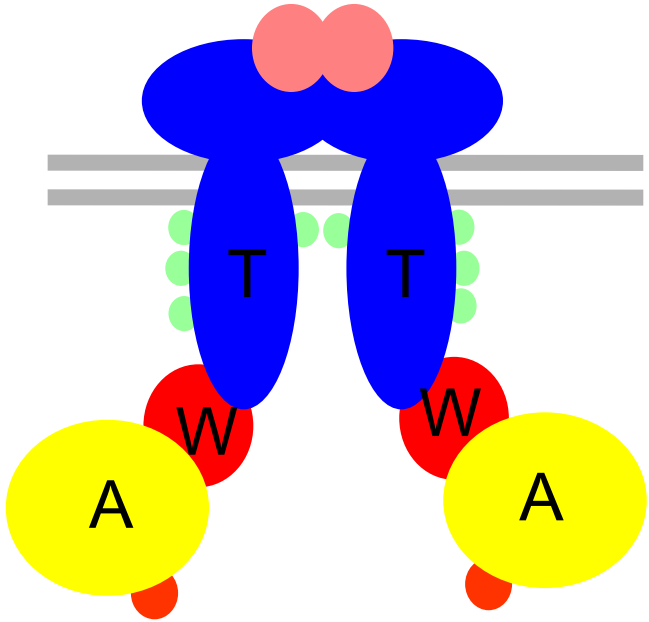
- Hybrid networks containing multiple types of receptors could integrate signals at the level of CheA activity;

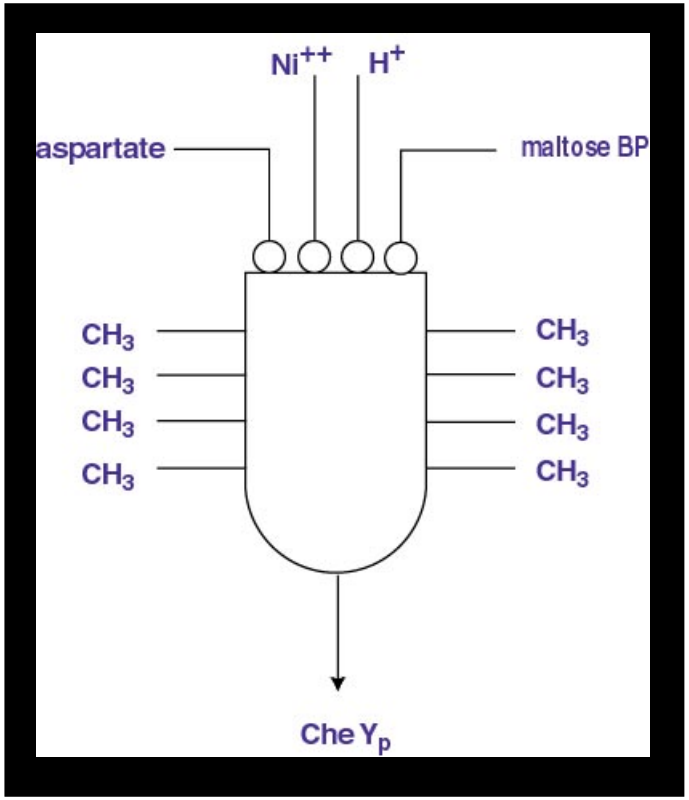
- Receptor dimers are close enough (6-10 nm) for adaptational cross-talk.



Multistate molecules

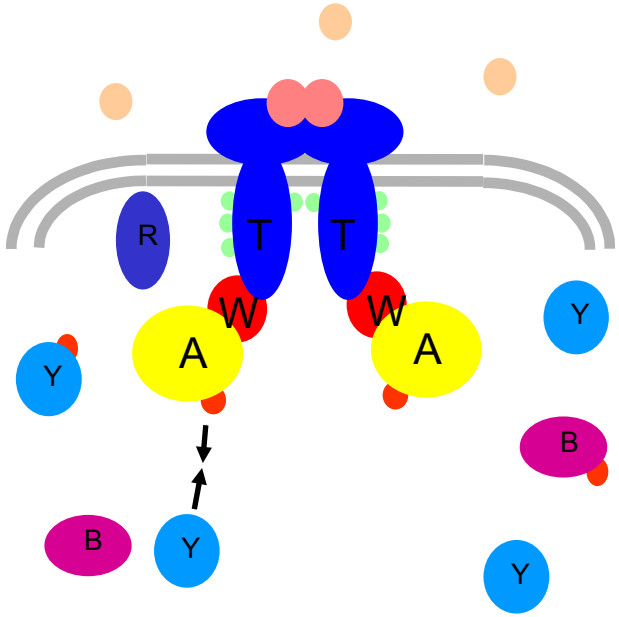
Internal features represented by binary flags. States are vectors of flags.





Multistate reactions

Reaction probabilities can be modified by the state of a participating multistate complex



$$p_{MS} = p_{base} \times p_{rel}$$

Where p_{base} is the base probability, and is p_{rel} the state-dependent relative probability.

Multistate reactions

$$(???0???) \xrightarrow{p_{base}} (???1???)$$

$$(0??0???) \xrightarrow{p_{base} \times p_{rel(0,0)}} (0??1???)$$

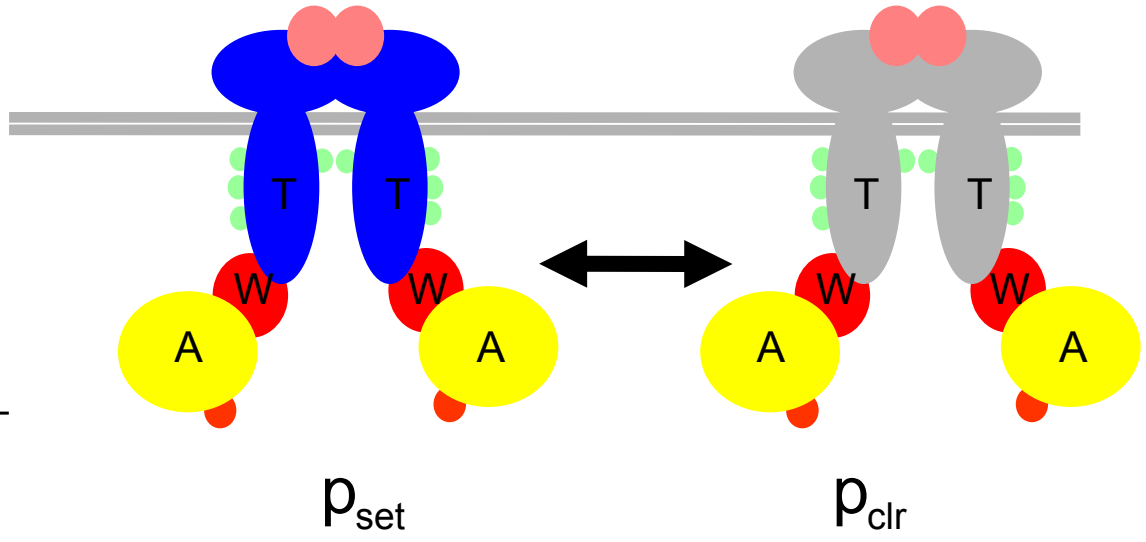
$$(1??0???) \xrightarrow{p_{base} \times p_{rel(0,1)}} (1??1???)$$

- '?' Flags do not affect the reaction
- only 4 species are needed instead of 128

Multistate rapid equilibria

- *Instantaneously* determines state of flag according to predefined probabilities.
- Probability can depend on the state of other flags.
- Primarily used to represent conformational 'flipping'.

$$\Delta G_0 = -RT \ln \frac{p_{set}}{p_{clear}}$$



Free-energy based activation probabilities

no attractant bound			attractant bound		
Species	p	ΔG (kcal/mol)	Species	p	ΔG (kcal/mol)
	0.017	2.37		0.003	3.55
	0.125	1.18		0.017	2.37
	0.500	0.00		0.125	1.18
	0.874	1.18		0.500	0.00
	0.997	3.55		0.980	2.37

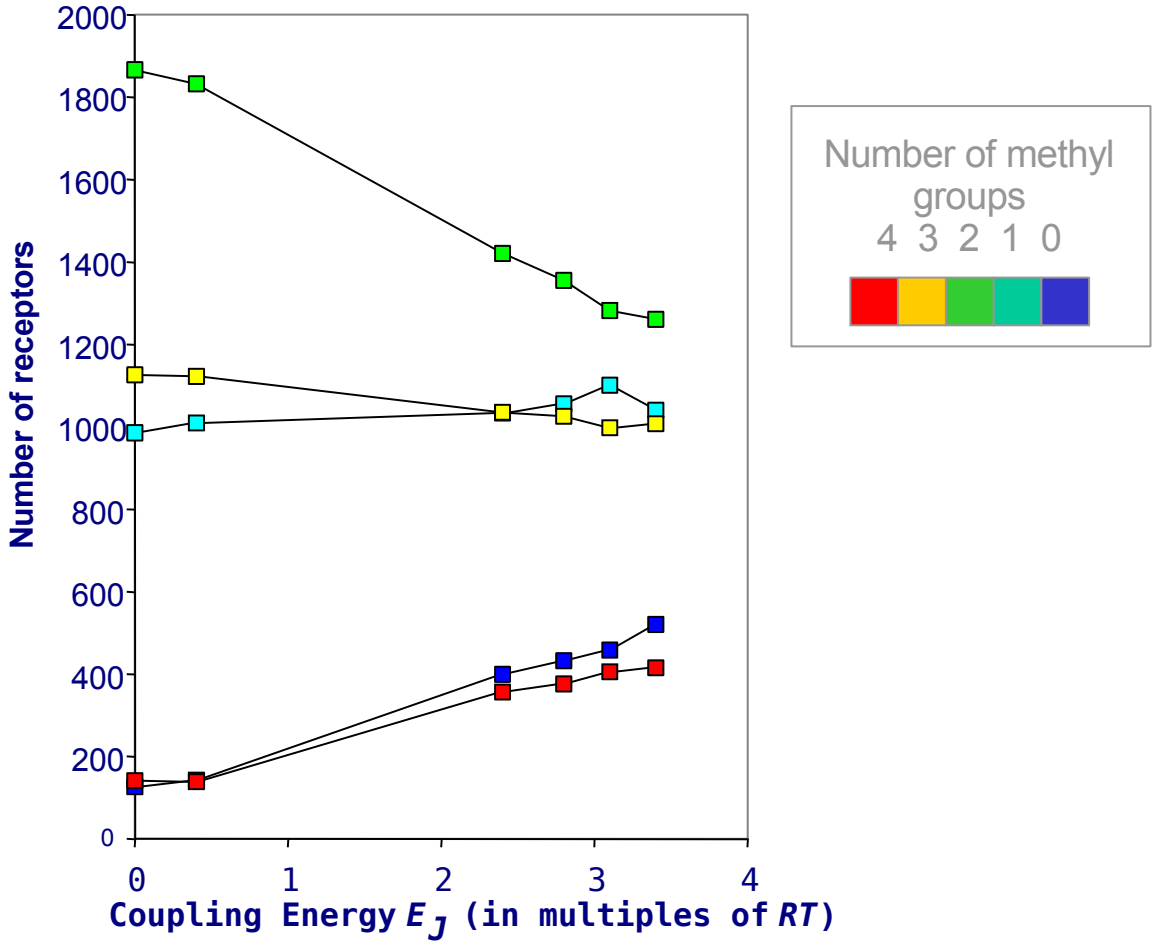
Free-energy values for coupled receptors

	no attractant bound						attractant bound					
	active neighbours	0	1	2	3	4	active neighbours	0	1	2	3	4
p		0.00	0.00	0.02	0.08	0.30		0.00	0.00	0.00	0.01	0.07
ΔG		4.47	3.49	2.50	1.51	0.53		5.55	4.56	3.58	2.59	1.61
p		0.01	0.03	0.13	0.41	0.78		0.00	0.00	0.02	0.08	0.30
ΔG		3.17	2.18	1.20	0.21	-0.77		4.47	3.49	2.50	1.51	0.53
p		0.04	0.17	0.50	0.83	0.96		0.01	0.03	0.13	0.41	0.78
ΔG		1.97	0.99	0.00	-0.99	-1.97		3.17	2.18	1.20	0.21	-0.77
p		0.22	0.58	0.87	0.97	0.99		0.04	0.17	0.50	0.83	0.96
ΔG		0.78	-0.21	-1.19	-2.18	-3.16		1.97	0.99	0.00	-0.99	-1.97
p		0.93	0.99	1.00	1.00	1.00		0.67	0.91	0.98	1.00	1.00
ΔG		-1.61	-2.59	-3.58	-4.56	-5.55		0.43	-1.41	-2.40	-3.38	-4.37

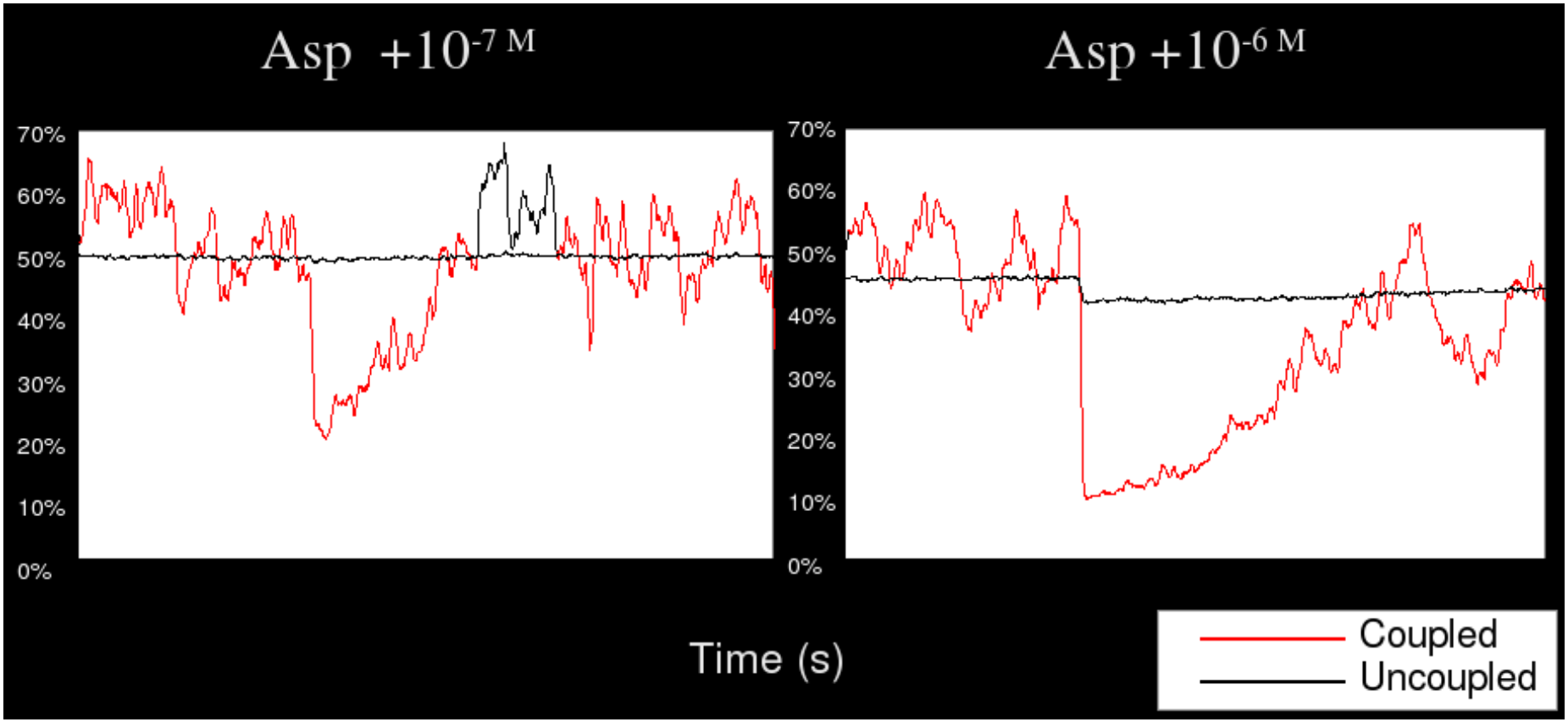
Shimizu *et al.* (2003) J Mol Biol 329: 291-309.

Quantitative patterns of methylation

- Steady-state population profile of receptor methylation states changes with degree of coupling

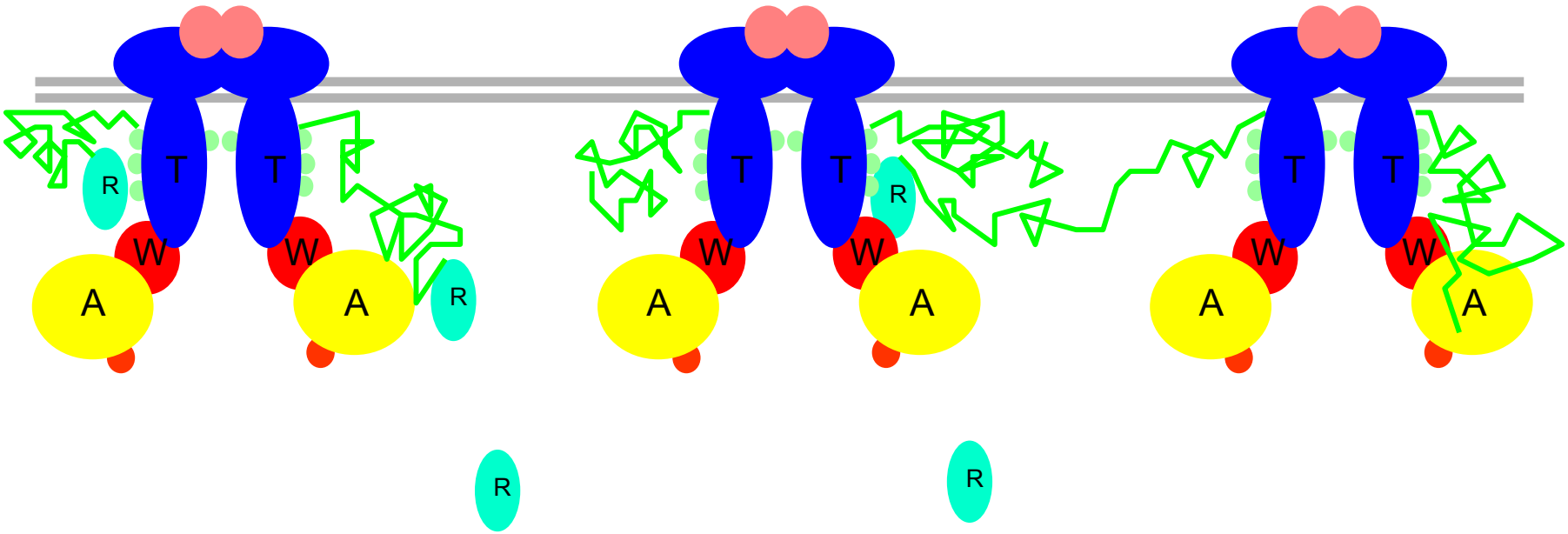


Gain

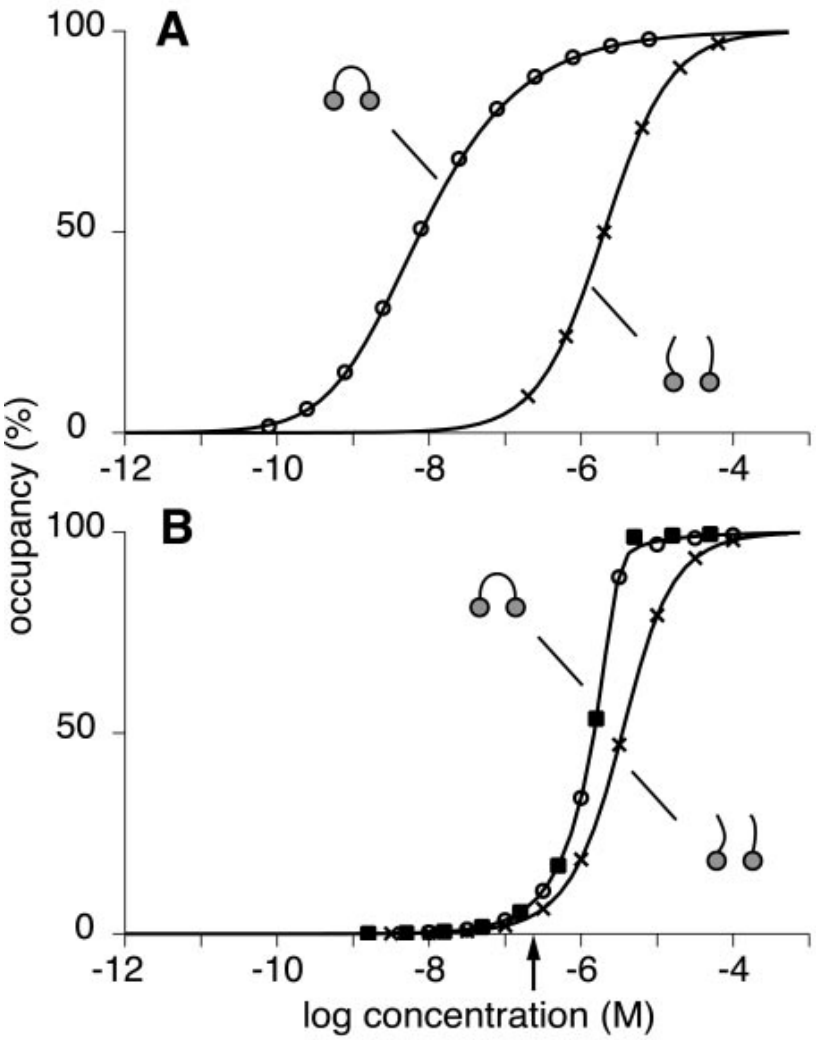

Asp +10-7 M
Asp +10-6 M
70%
60%
50%
40%
30%
20%
10%
0%
Time (s)
Coupled
Uncoupled

"Molecular brachiation"

Interaction between receptors and CheR (methyltransferase)



Effective Kd

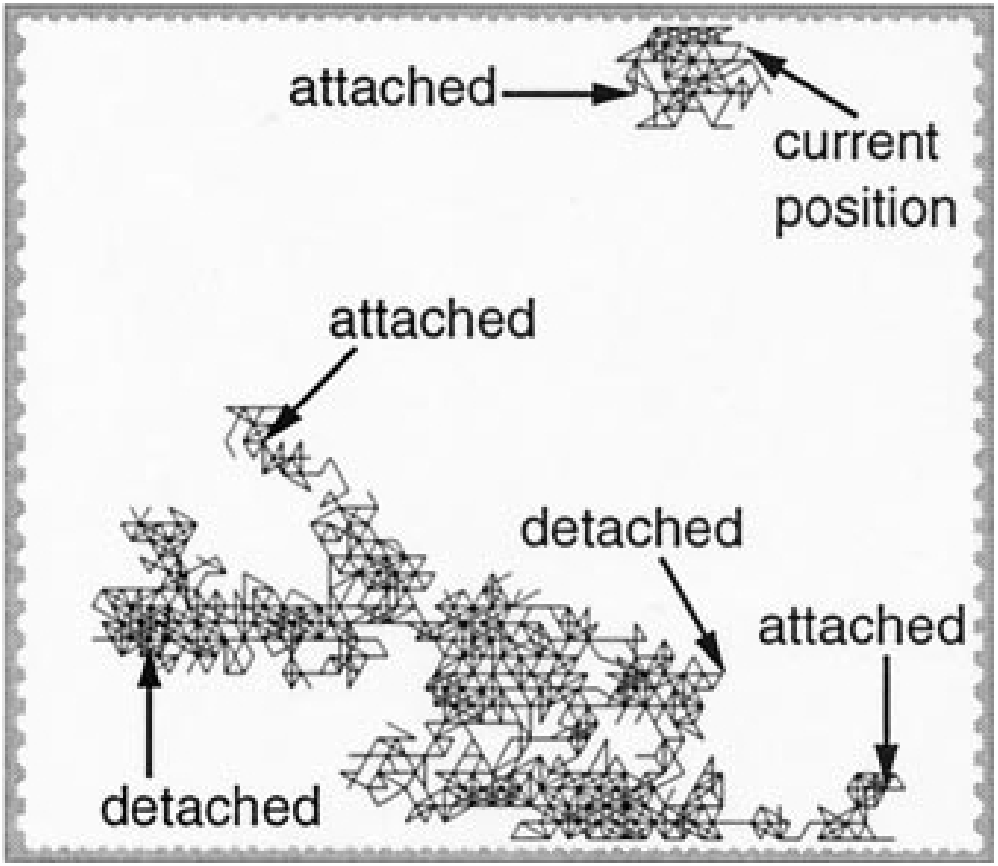


Excess brachiating molecule

Limiting brachiating molecule

Levin et al. (2002) *Biophys J* 82:1809-1817.

Segregation by affinity



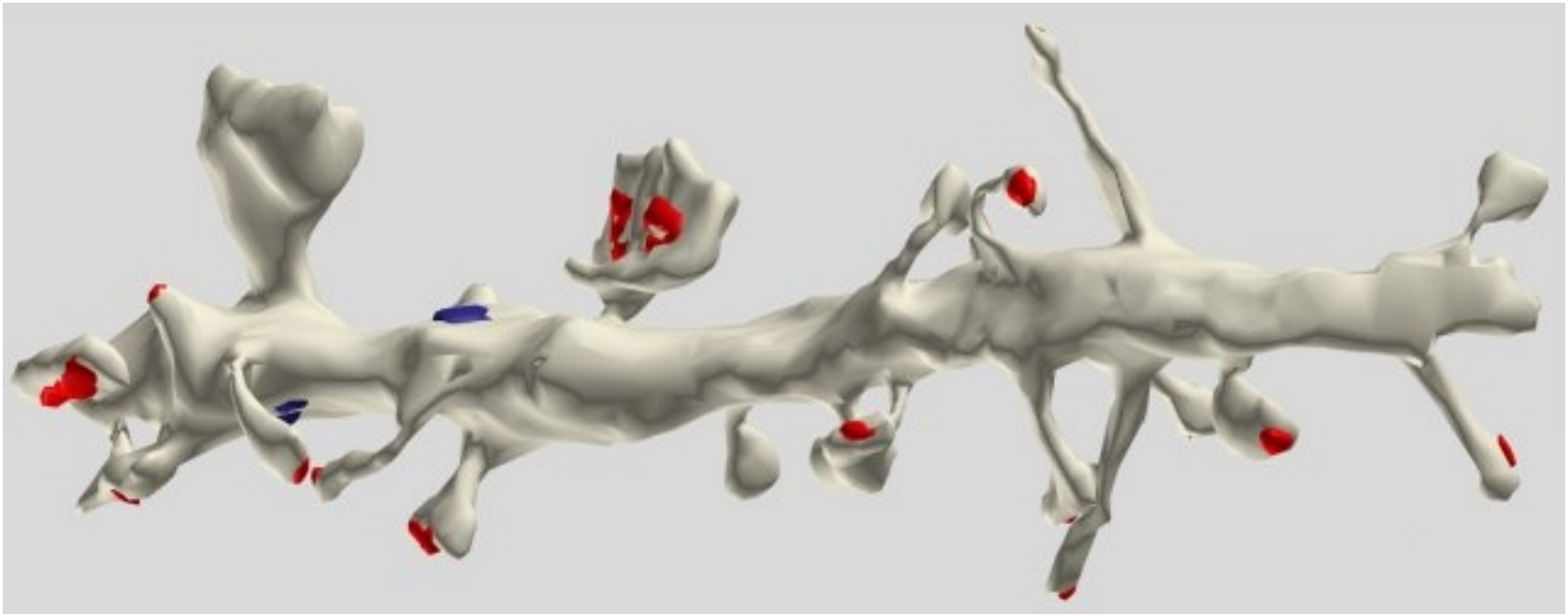
Each CheR molecule visits more receptors, some of them repetitively;

CheR molecules are trapped into the receptor lattice.

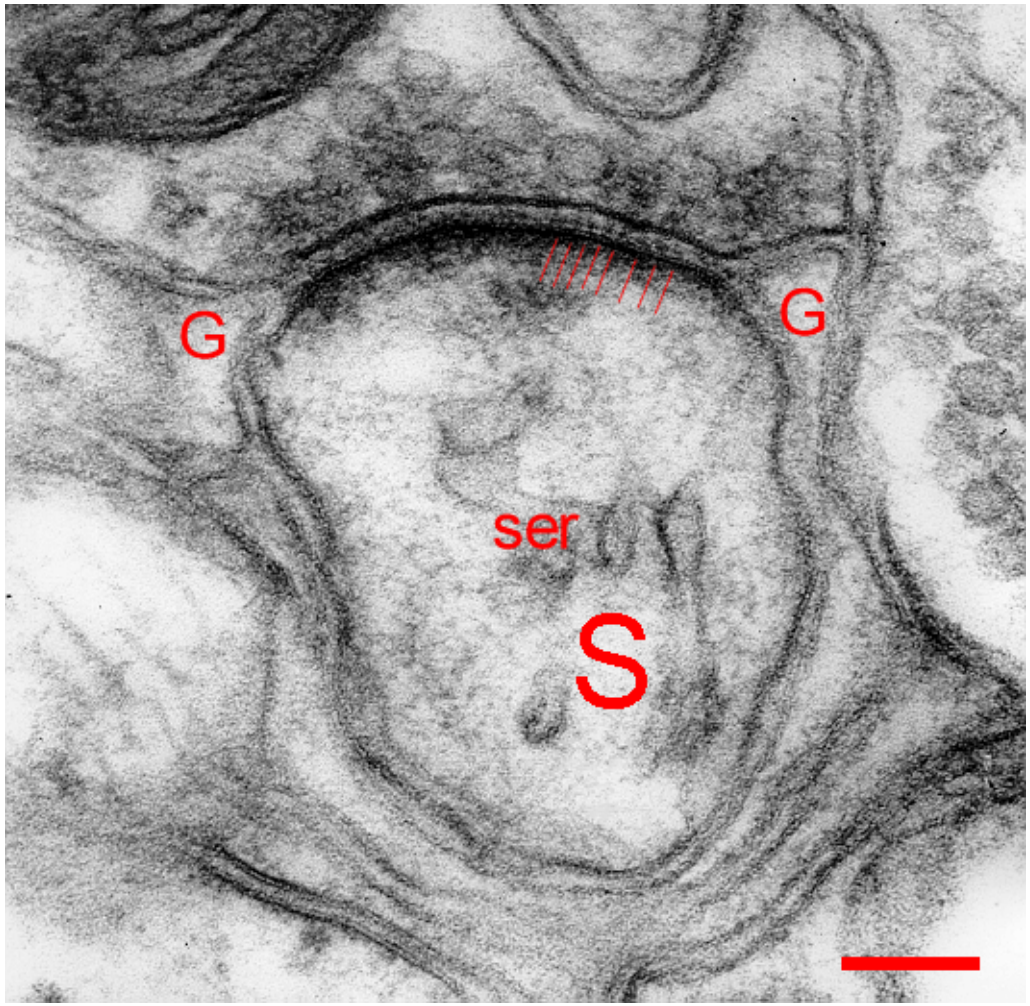
Future of StochSim?

- 3D lattice
- Reactions between different multistate molecules
- New native format based on XML (extension of SBML)
- New GUI

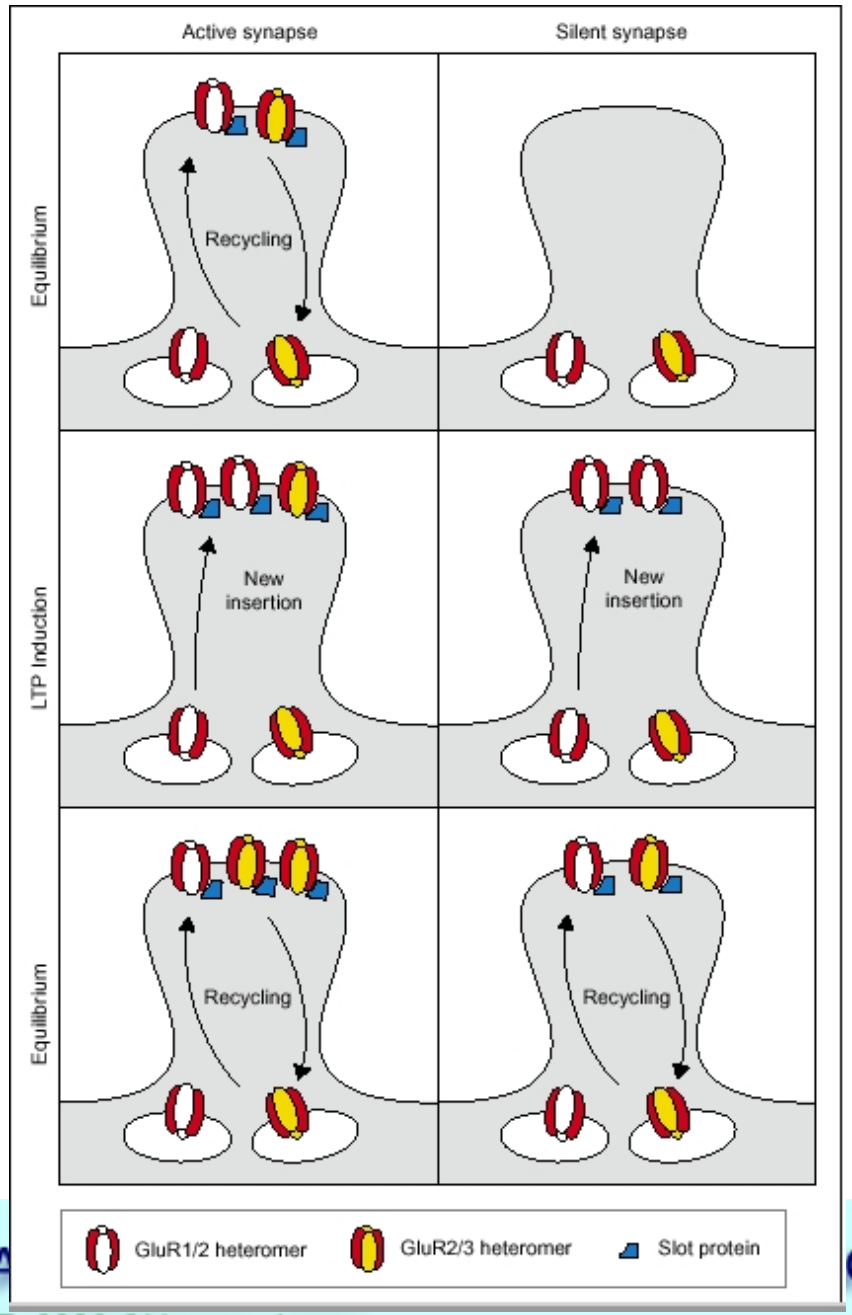
A spiny dendrite



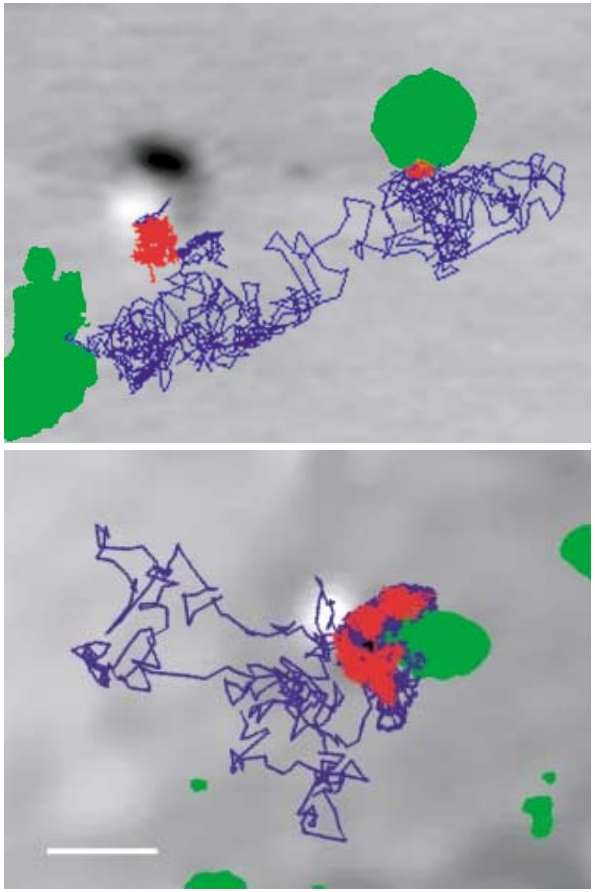
Dendritic spine



Receptors for neurotransmitters are moving



Barry and Ziff. (2002)
Curr Opin Neurobiol, 12: 279-286



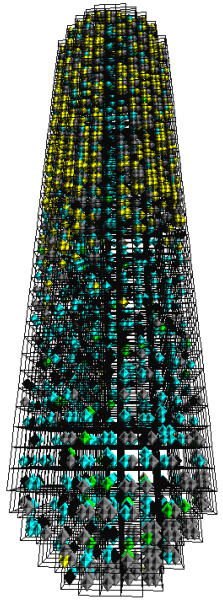
Choquet & Triller (2003)
Nat Rev Neurosci, 4: 251-265

The mesoscopic scale

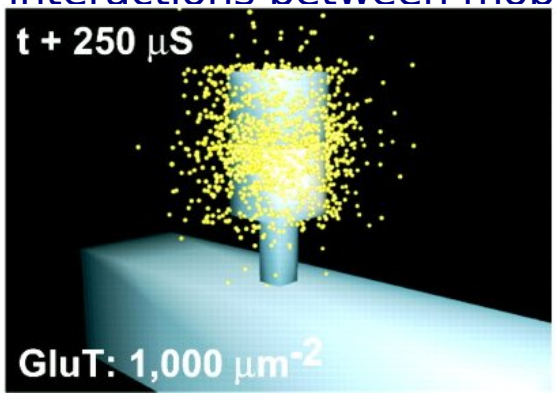
- molecule abstracted ⇒ macroscopic scale
- atomic details ⇒ microscopic scale
- Abstracted but realistic geometry ⇒ mesoscopic scale
- Relative size of object respected
- Differential location of binding sites
- realistic movements (speed and topology)

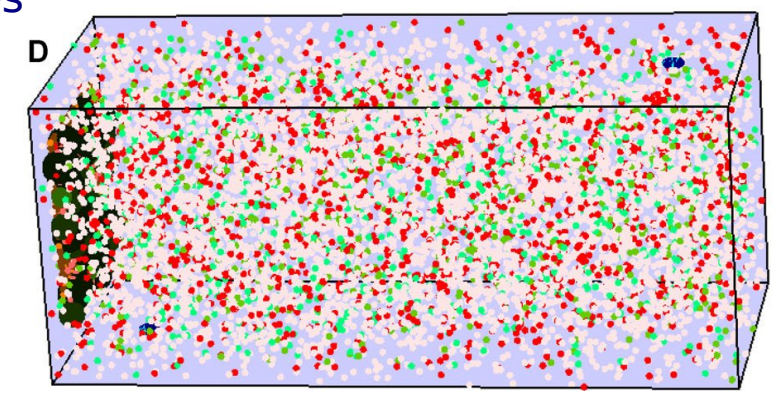
Existing software

- Population based ("spatial Gillespie")
  - SmartCell, Mesord
  - finite elements (voxels), no individual molecules



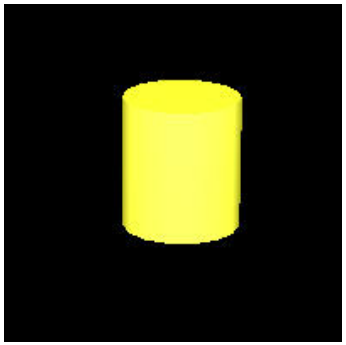
- Single-particle based
  - MCell: individual small molecules, ray-tracing. Immobile reactive surfaces. no interactions between mobile molecules

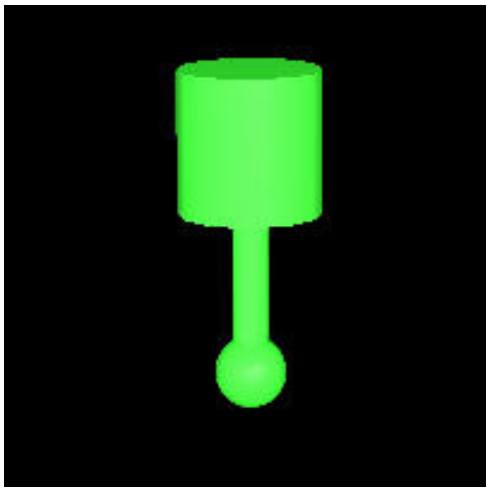


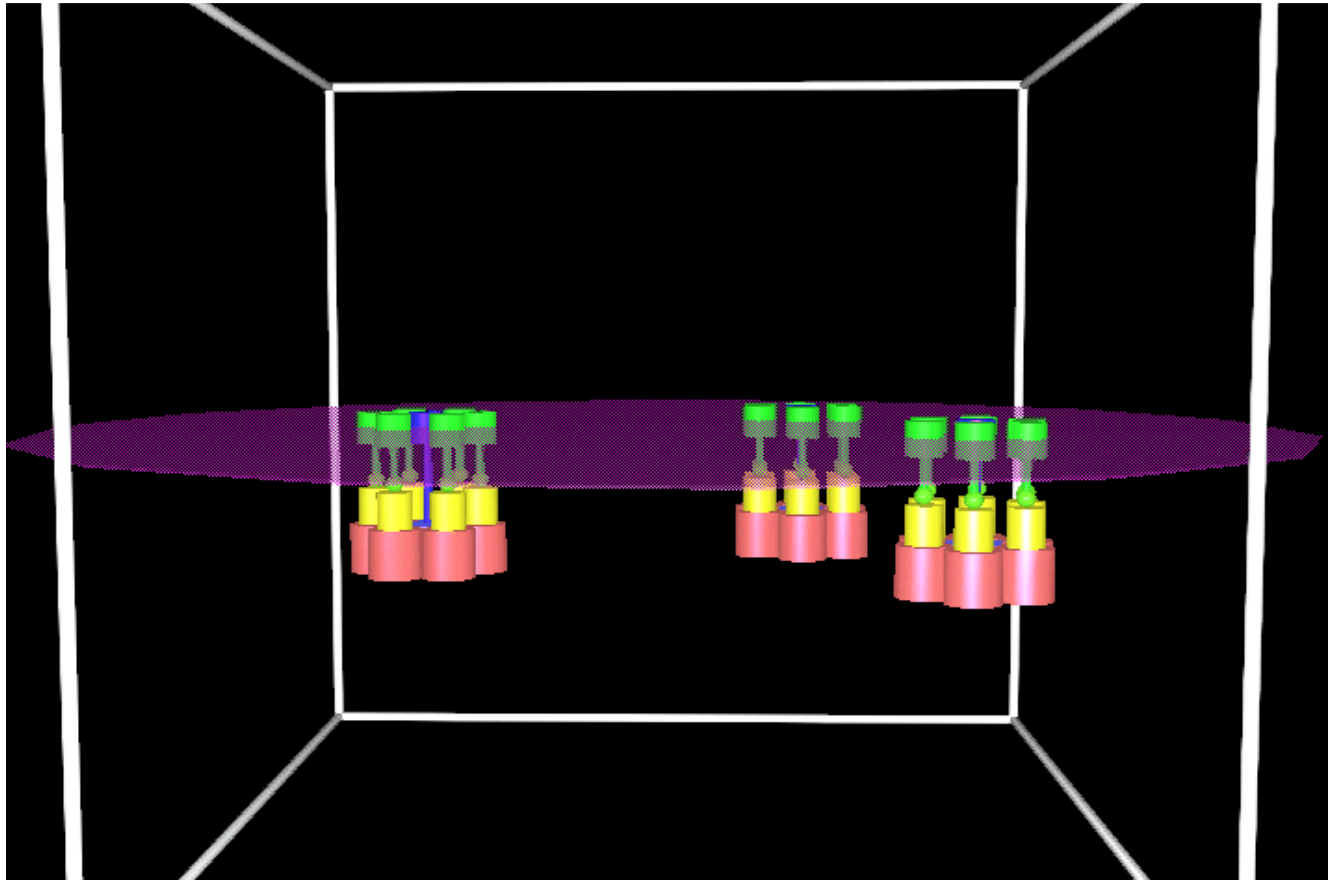


  - Smoldyn: individual small molecules, reactions between them
  - Meredys: Everything plus topology of molecules

Meredys: Particles, Objects and Clusters







Particles carry binding sites

Cluster class allows recording of Center Of Mass, radius, RMS displacement;
possibility of cluster state

Clusters are dynamically created and destroyed – transient.

Molecule diffusion

- Different diffusion spaces:
  - Static; Free diffusion; Membrane diffusion; Above membrane; Below membrane
- Two types of motion:
  - Translational $\bar{r^2} = 2\mathrm{D}_T t = 2\mathrm{kb}_T t$
  - Rotational $\bar{\theta^2} = 2 D_R t = 2\mathrm{kb}_R t$
- random walk algorithm

$$p(x,t) = \frac{1}{\sqrt{4\pi Dt}} \exp - \frac{x^2}{4\mathrm{Dt}}$$ gaussian with $\sigma^2 = 2Dt$

  - Translational $\Delta(x,y,z) = \sqrt{2\mathrm{D}_T t} \times gaussRand$
  - Rotational $\Delta\theta = \frac{\sqrt{2\mathrm{D}_R t}}{r} \times gaussRand$
- Two types of diffusion equations:
  - unrestricted brownian motion – Low Trans/Rot
  - intra-membrane diffusion (Saffman and Delbrück 1975) – High Trans/Rot

Molecule diffusion

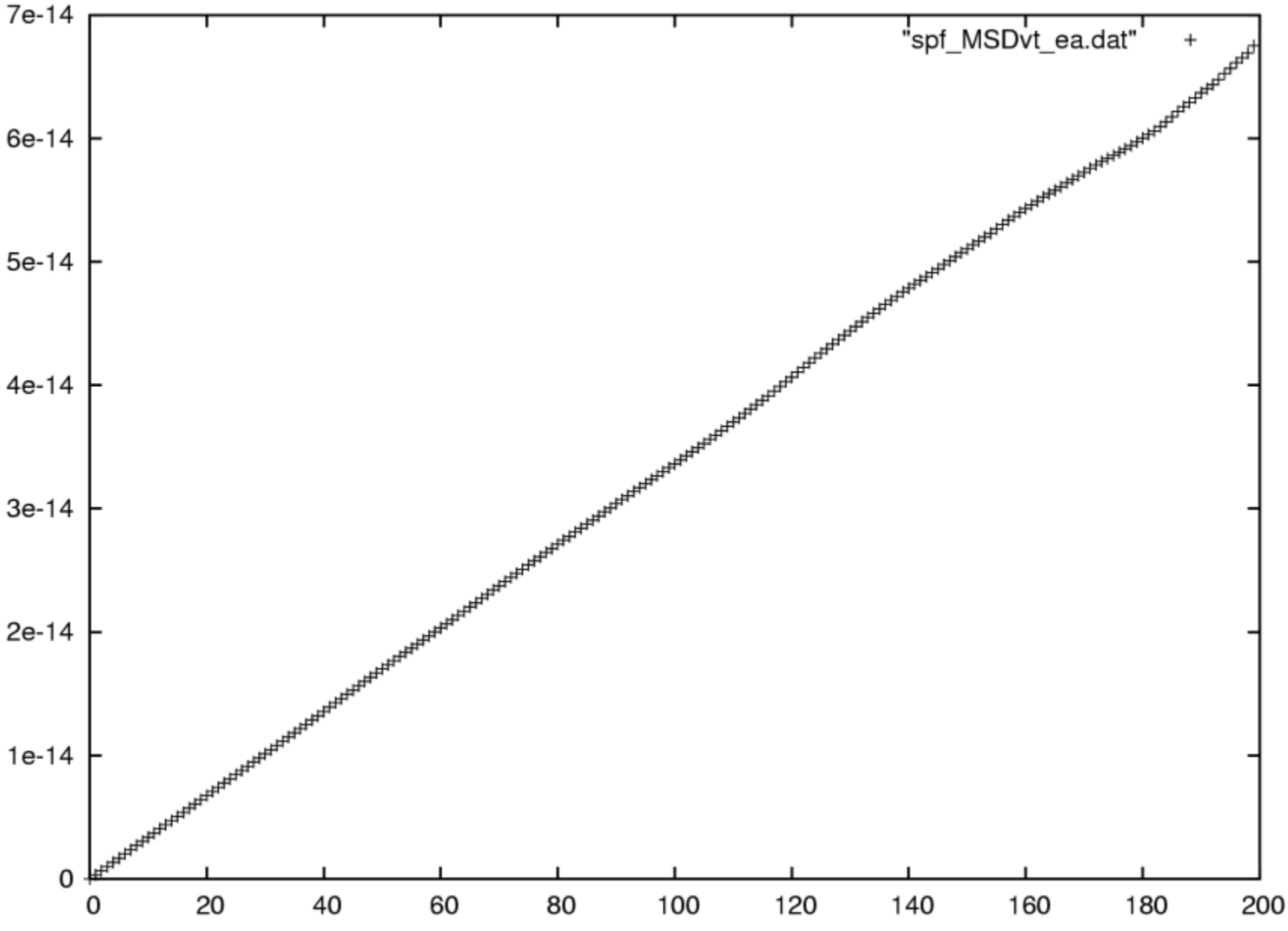
- Unrestricted brownian motion – Low Translation/Rotational

$$b_T = \frac{1}{6\pi\mu r} \qquad b_R = \frac{1}{8\pi\mu r^3} \qquad \frac{b_T}{b_R} = \frac{4}{3}r^2$$

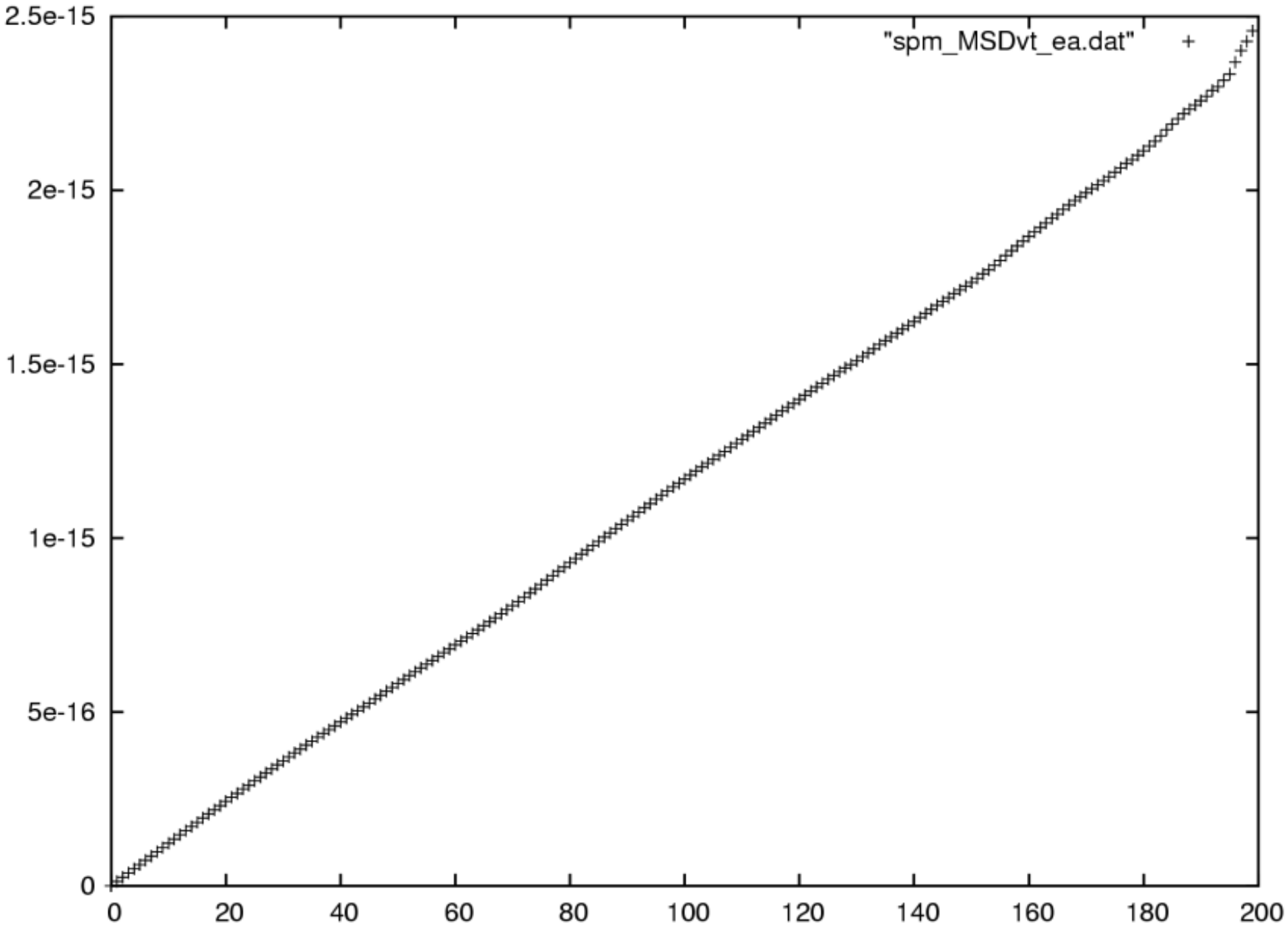
- Intra-membrane diffusion (Saffman and Delbrück 1975) High Translational/Rotational

$$b_T = \frac{1}{4\pi\mu h}\left(\log\left(\frac{\mu' h}{\mu r}\right) - \gamma\right) \qquad b_R = \frac{1}{4\pi\mu r^2 h} \qquad \frac{b_T}{b_R} = \left(\log\left(\frac{\mu' h}{\mu r}\right) - \gamma\right) \times r^2$$

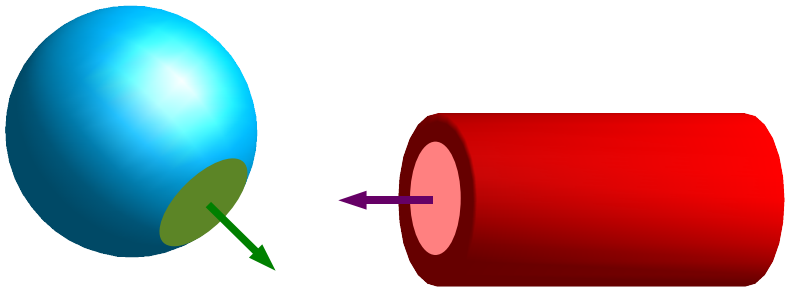
RMS displacement for free diffusion



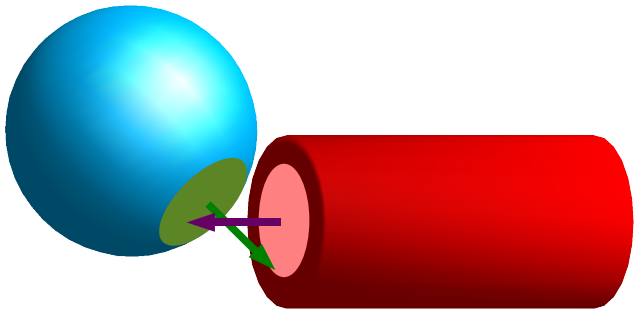
RMS displacement for membrane diffusion



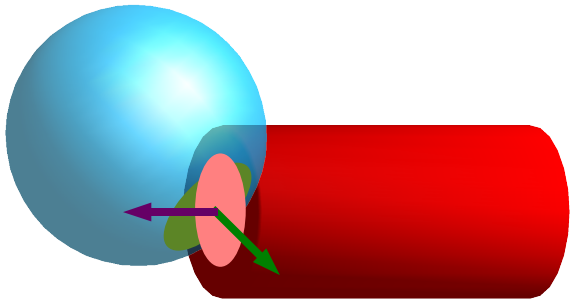
Reactions and complex formation



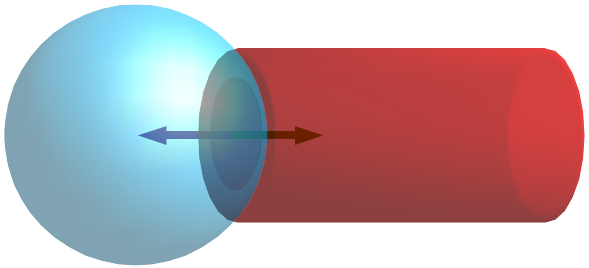
Reactions and complex formation

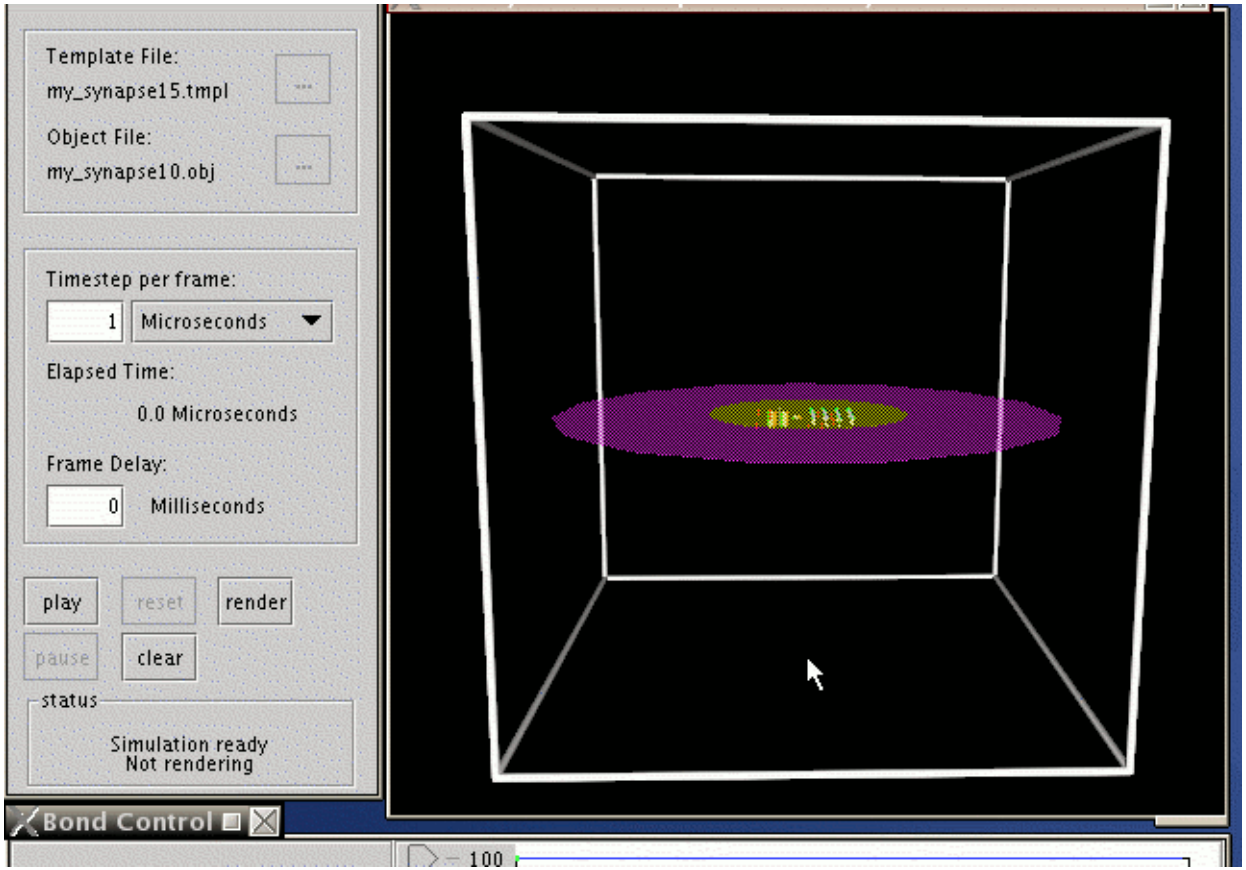


Reactions and complex formation



Reactions and complex formation

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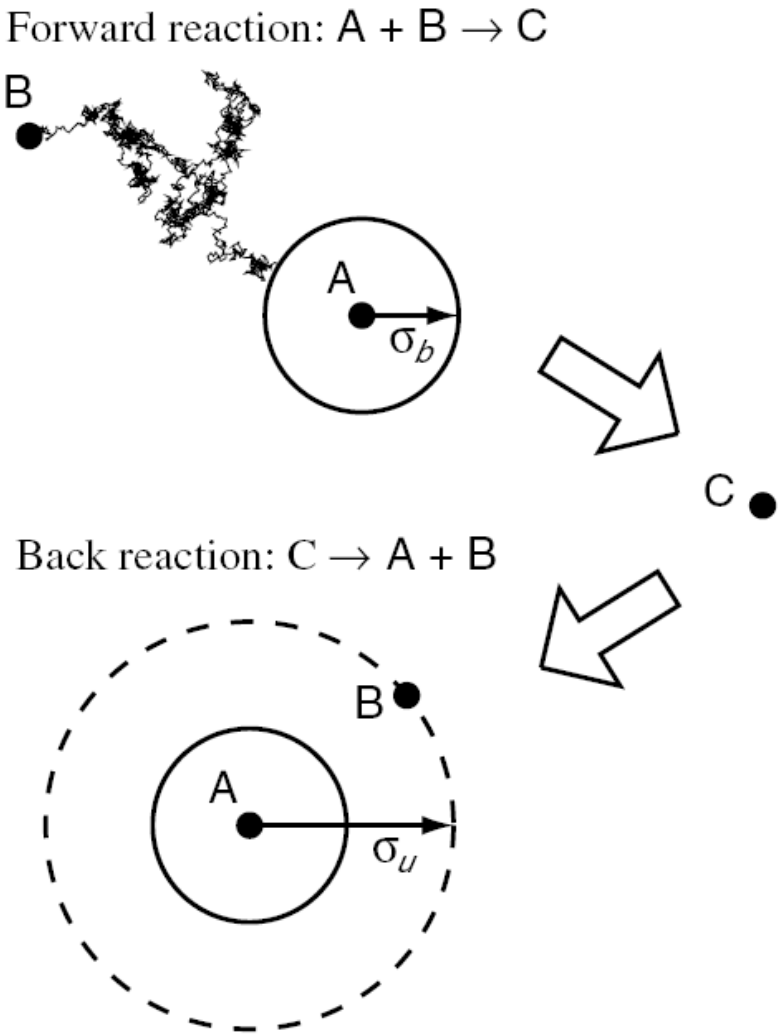
my_synapse15.tmpl
Object File:
my_synapse10.obj
Timestep per frame:
1
Microseconds
Elapsed Time:
0.0 Microseconds
Frame Delay:
0
Milliseconds
play
reset
render
pause
clear
status
Simulation ready
Not rendering
Bond Control
100

Remaining problems

- Probabilities of reactions are hard-coded
- Molecules can have several states, but a state does not affect the reactions
- Shape of molecules does not affect diffusion
- ...

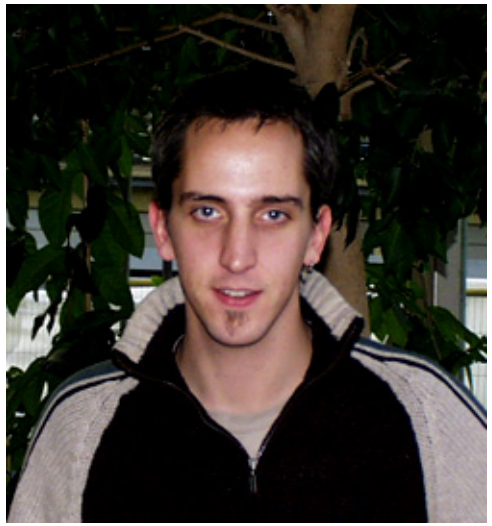
Smoluchovski model

- Smoldyn
  (Andrews and Bray (2004) *Phys Biol* 1: 137-151)
  - + single-particle
  - + binding radius (probability of reaction) related to kinetics
  - - no volume, shape, mass,
  - - No complexes
  - - No multistate molecules



Acknowledgements

- Dennis Bray
- Matthew Levin
- Carl Morton-Firth
- Thomas Simon Shimizu



Dominic Tolle

- Fred Howell
- Dan Mossop