

# Rare switching events in non-stationary and non- Markovian systems

N. Becker, R. Allen, P. R. ten Wolde

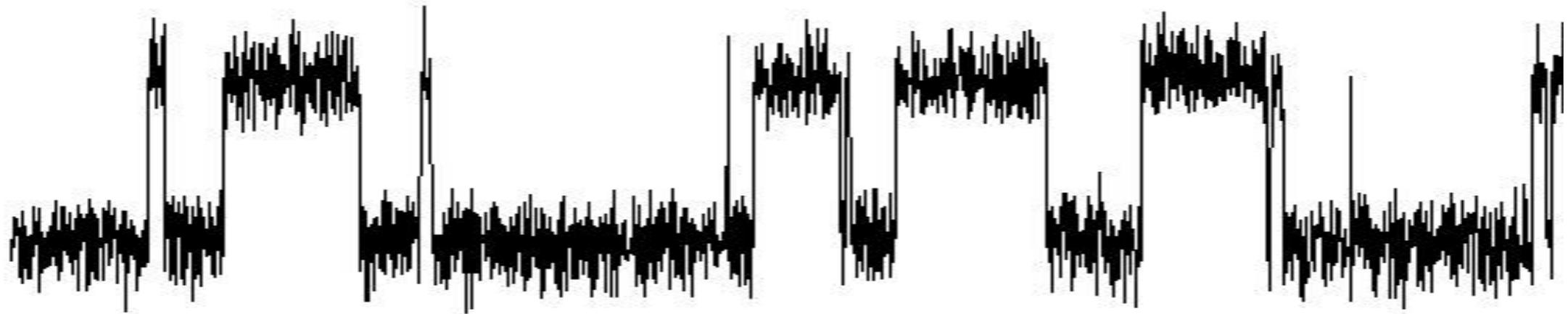
*Computation of transition trajectories and rare events in  
in non-equilibrium systems*

Lyon, June 11-15, 2012

# Rare events in non-equilibrium systems

- protein and DNA pulling
- polymer collapse under flow
- crystal nucleation under shear
- traffic jams
- (bio)polymer translocation
- DNA condensation
- switches in biochemical networks

# Rare events in stationary, Markovian systems



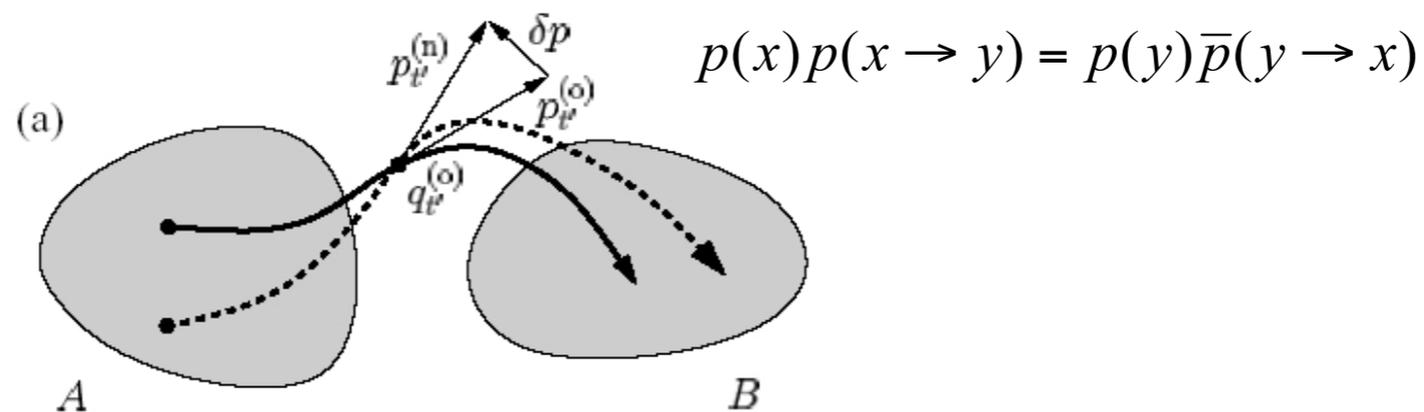
- Mean waiting time much longer than duration of switching event itself
- Time-homogeneous Markov systems:  
transitions are independent and intervals are uncorrelated and exponentially distributed

# Non-equilibrium systems

- Dynamics do not satisfy detailed balance
- Stationary distribution is not known

# Simulating rare events in non-equilibrium systems

- Biasing potentials cannot be used
- Problems with transition path sampling and transition interface sampling



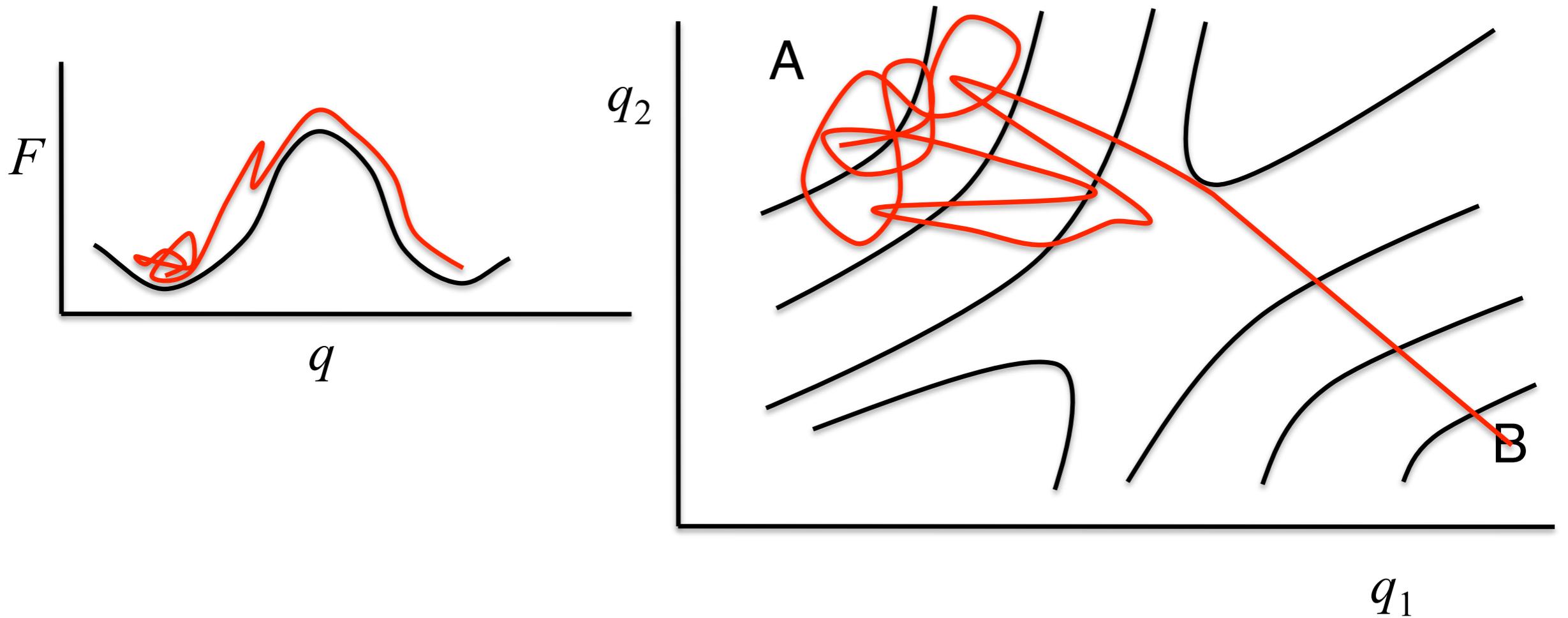
C. Dellago, P. G. Bolhuis, F. S. Csajka & D. Chandler, *J. Chem. Phys.* **108**, 1964 (1998)

C. Dellago, P. G. Bolhuis & P. L. Geissler, *Adv. Chem. Phys.* **123**, 1 (2002)

# Path sampling in non-equilibrium systems

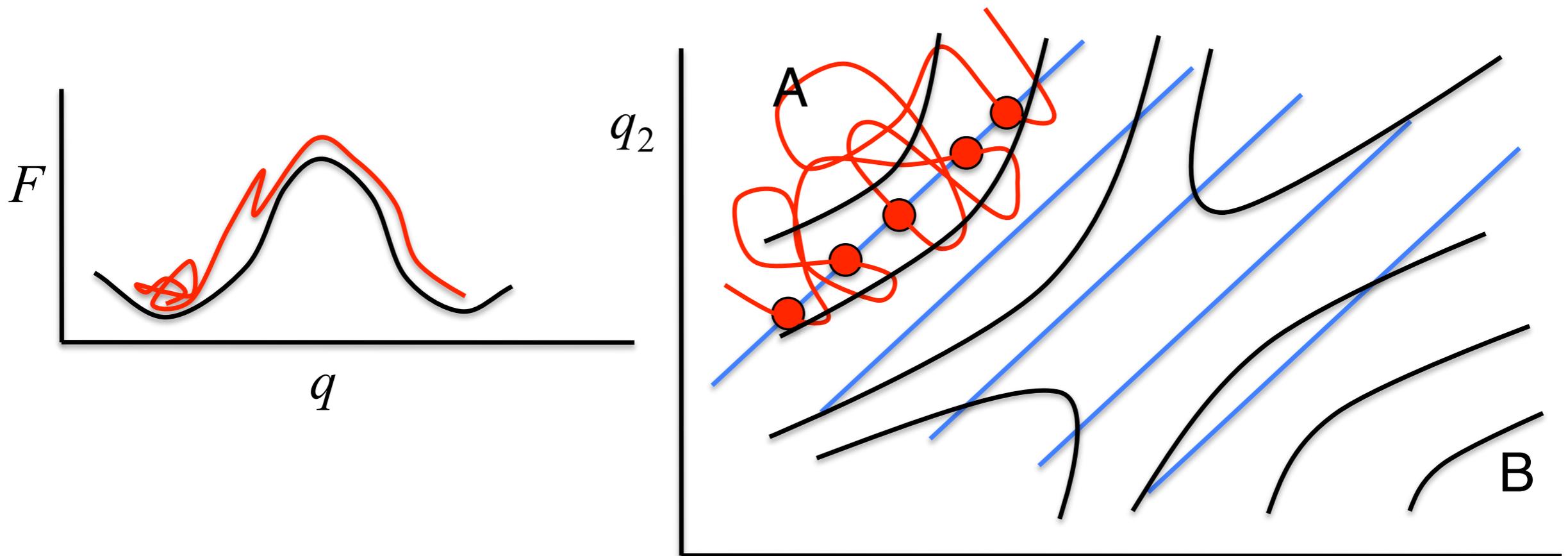
- Often only transition rates between states are known
- Detailed balance is not satisfied
- Phase-space density is not known
- Cannot propagate backwards in time
- Cannot calculate weight of paths

# Rare-event problem



Can we drive the system over the barrier by only propagating forward in time?

# Forward-Flux Sampling



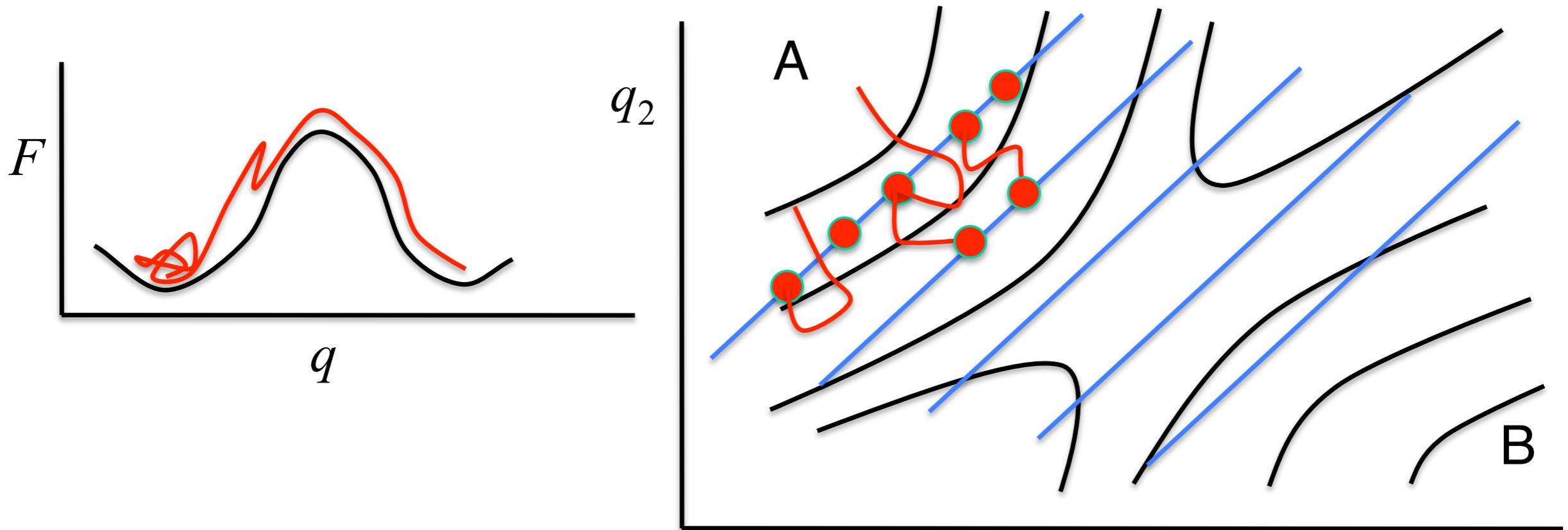
$$k_{AB} = \frac{\bar{\Phi}_{A,B}}{\bar{h}_A} = \frac{\bar{\Phi}_{A,1}}{\bar{h}_A} P(\lambda_B | \lambda_1)$$

$$P(\lambda_B | \lambda_1) = \prod_{i=1}^{n-1} P(\lambda_{i+1} | \lambda_i) \times P(\lambda_B | \lambda_n)$$

Allen et al, PRL (2005); JCP (2006)

T. S. van Erp, D. Moroni & P. G. Bolhuis, *J. Chem. Phys.* **118**, 7762 (2003)

# Forward-Flux Sampling



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Allen et al, PRL (2005); JCP (2006)

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# Forward-Flux Sampling

- Different versions:
  - **Static MC:**
    - Direct FFS (just shown)
    - Branched-Growth (BG) FFS (PERM, Grassberger)
  - **Dynamic MC:**
    - Rosenbluth (RB) FFS
- FFS can be used to compute stationary distributions
- Committors can be extracted on the fly and used to identify reaction coordinates (Borrero & Escobedo)

Review: Allen et al, JPCM (2009)

# Forward-Flux Sampling

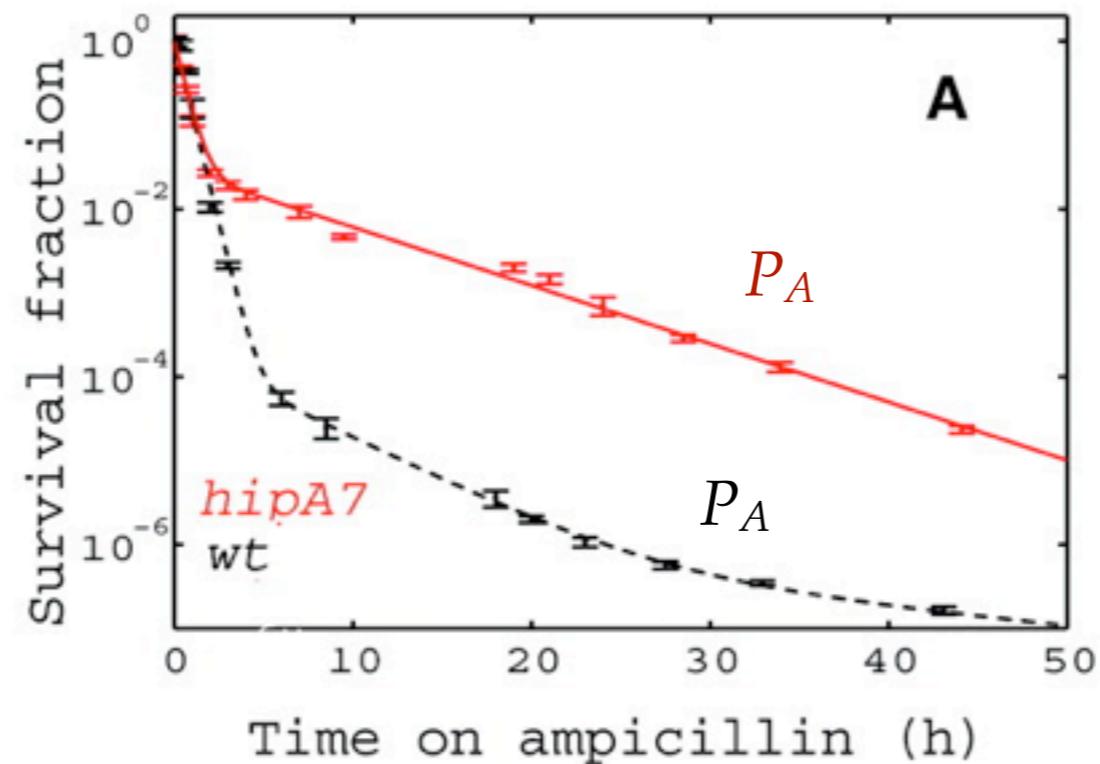
- **Widely used:**
  - crystal nucleation and gas-liquid nucleation
  - DNA condensation
  - membrane pore formation
  - translocation of DNA and proteins through pores
  - protein folding
  - droplet coalescence
  - polymer collapse under flow
  - diffusion-limited aggregation
  - nucleosome dynamics
  - switches in biochemical networks

Review: Allen et al, JPCM (2009)

# Rare events in non-stationary and non-Markovian systems

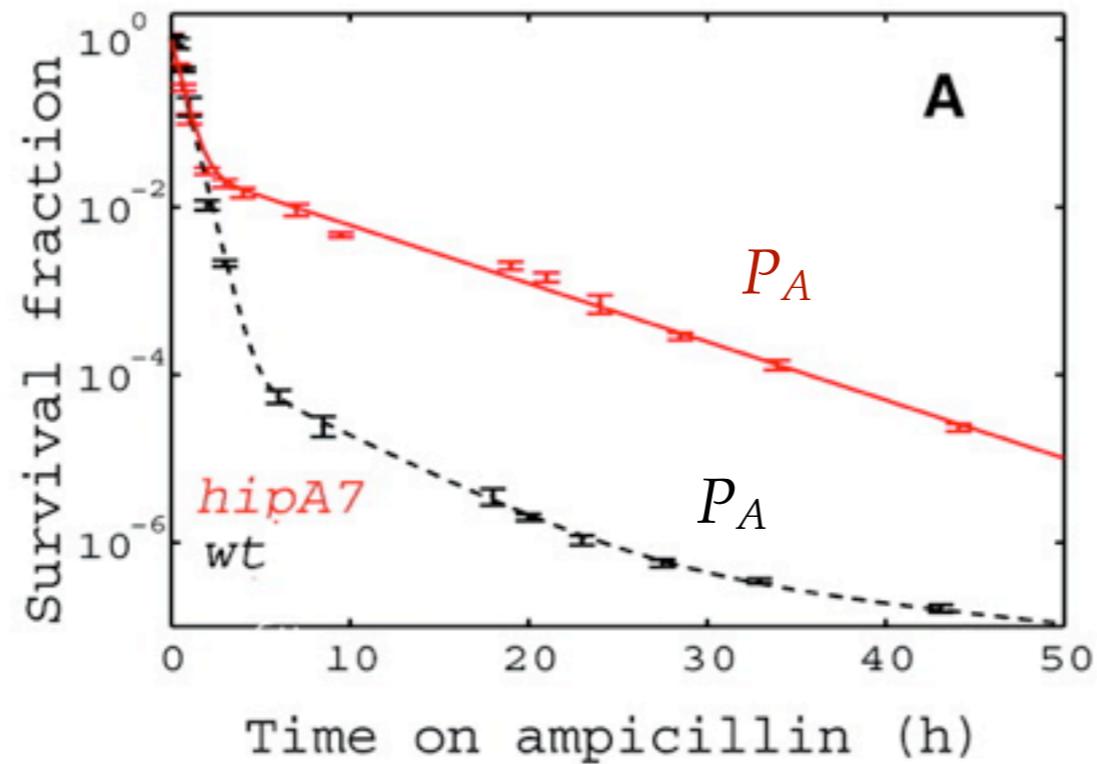
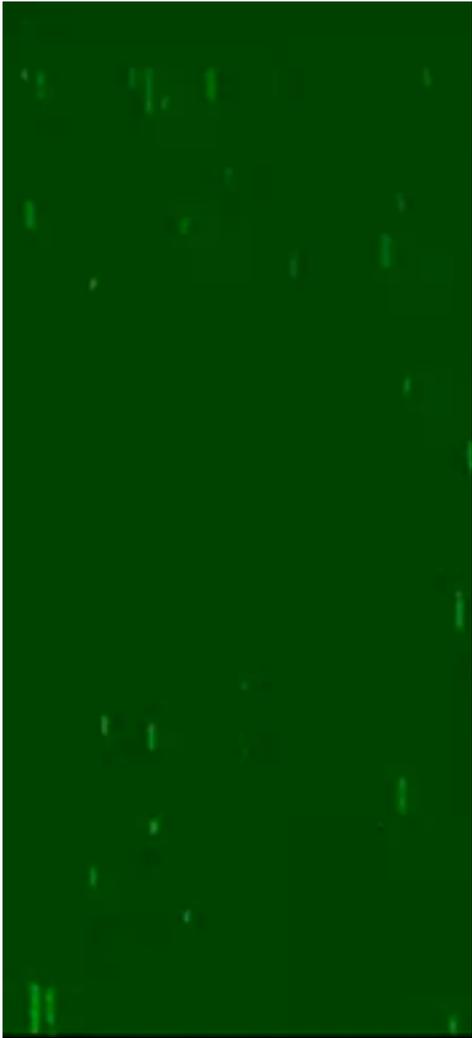
- Externally driven systems
  - protein folding under force
  - nucleation during temperature quench
- Robustness against transient perturbations
  - power grid
  - traffic jams
  - biological systems
- (In) sensitivity to transient driving or pulses
  - signaling networks, e.g. cell differentiation and cell cycle
  - **antibiotics**
- **Non-Markovian transitions**

# Resistance against antibiotics: A non-stationary rare event



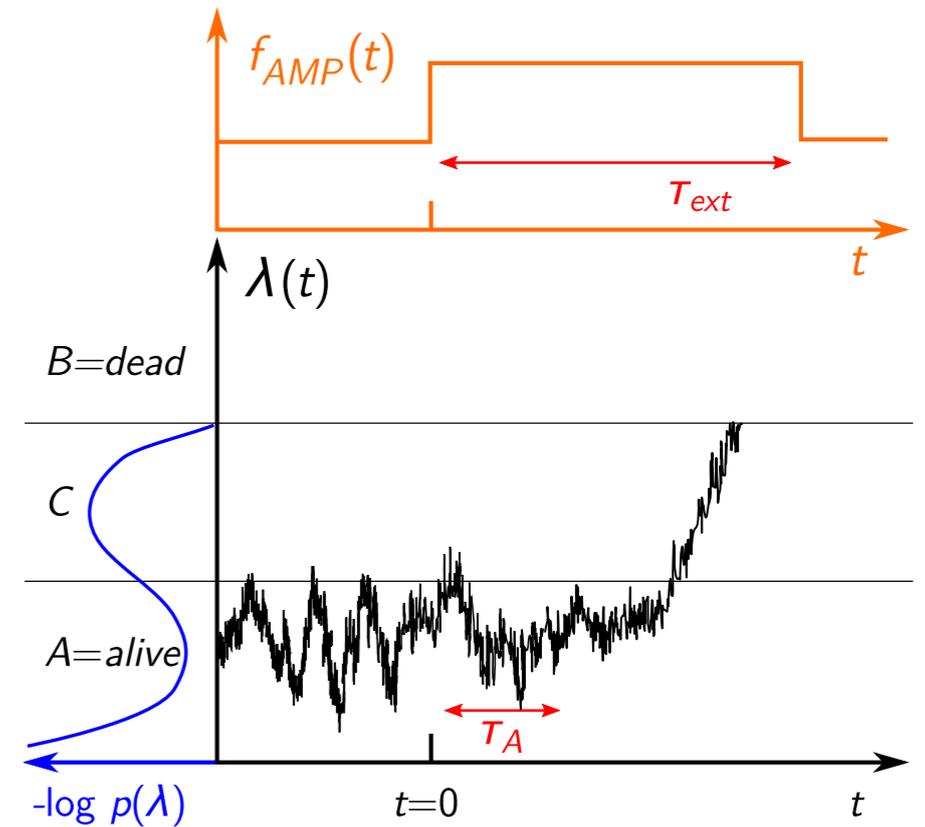
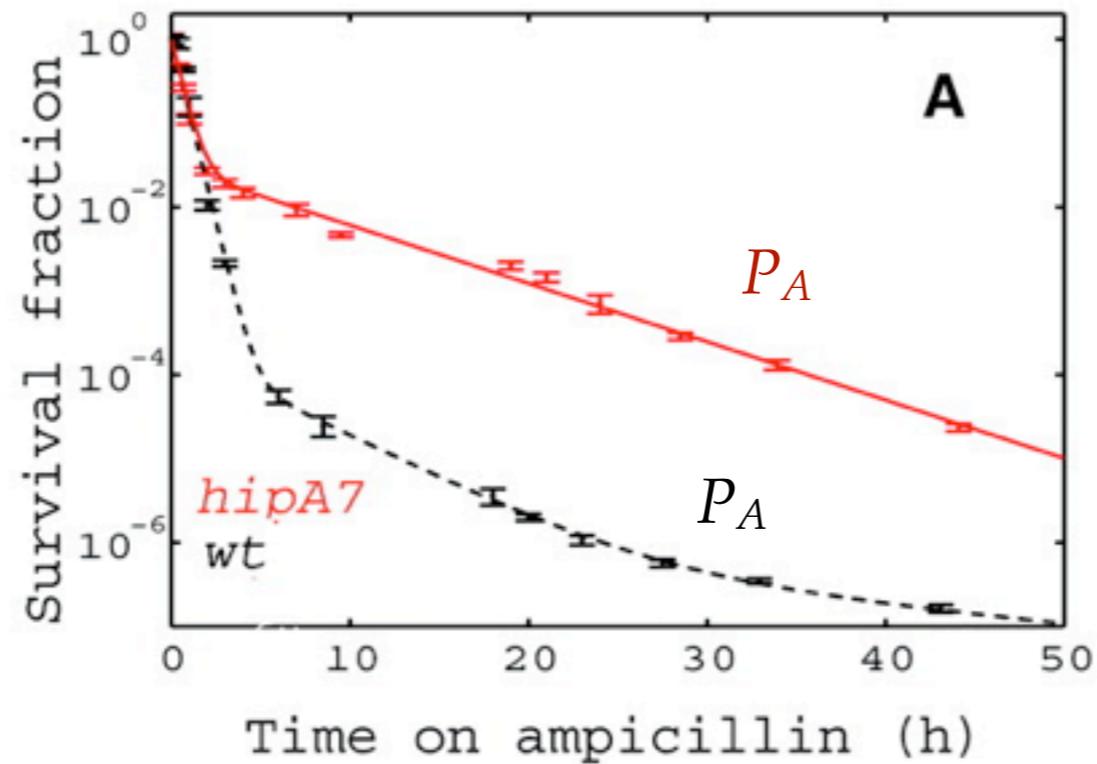
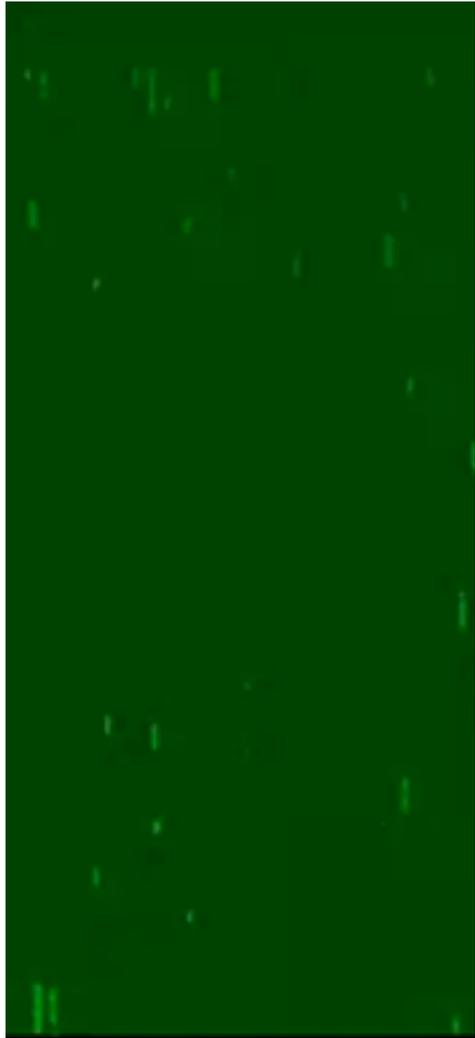
Balaban et al., Science, 2004

# Resistance against antibiotics: A non-stationary rare event



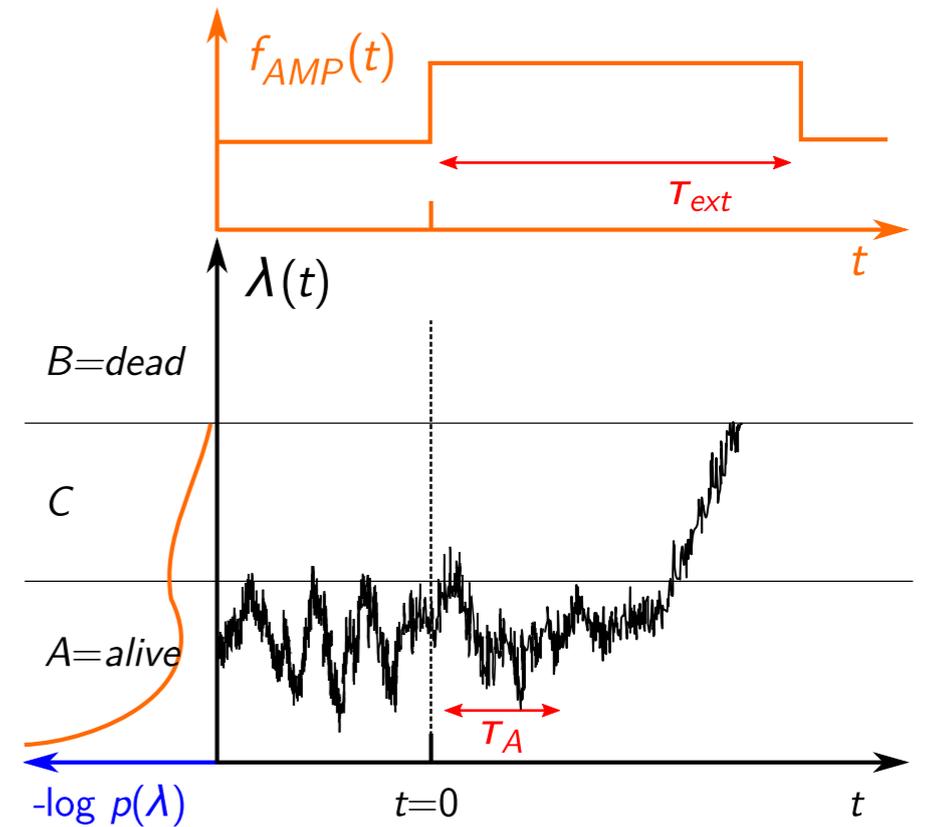
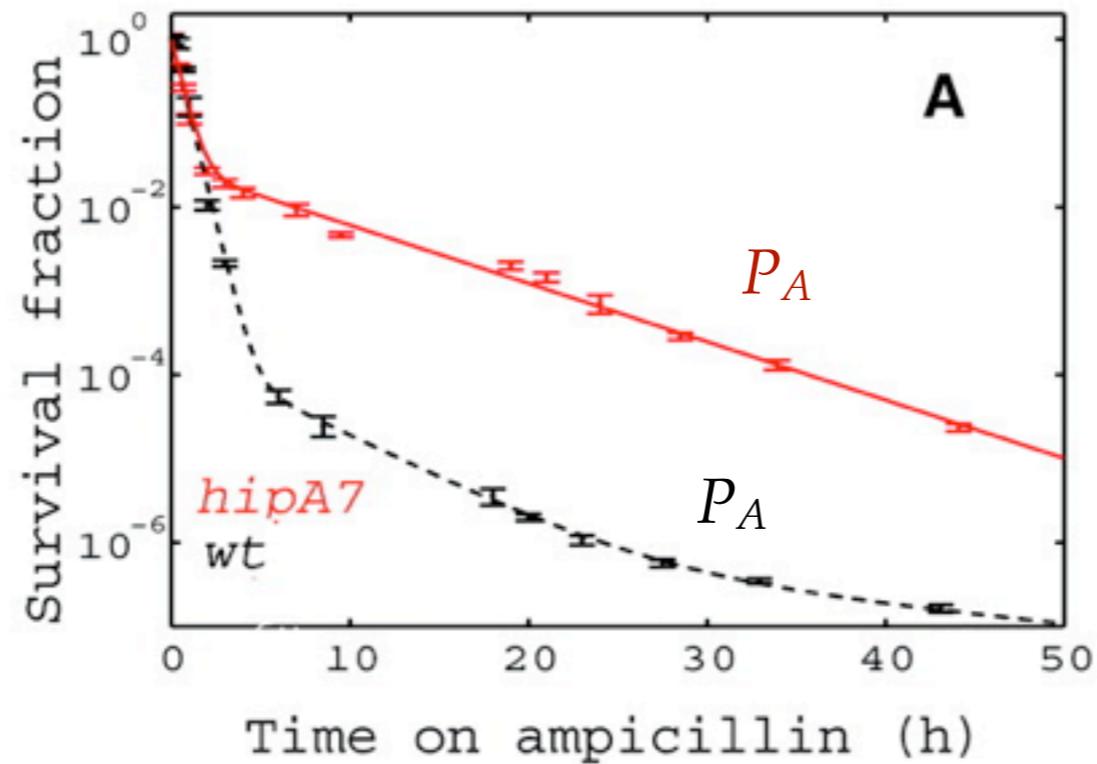
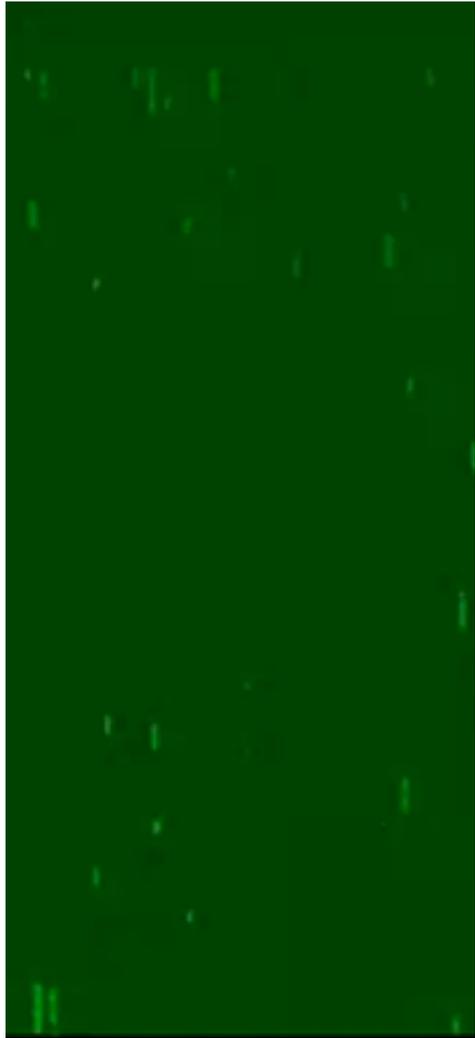
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# Resistance against antibiotics: A non-stationary rare event



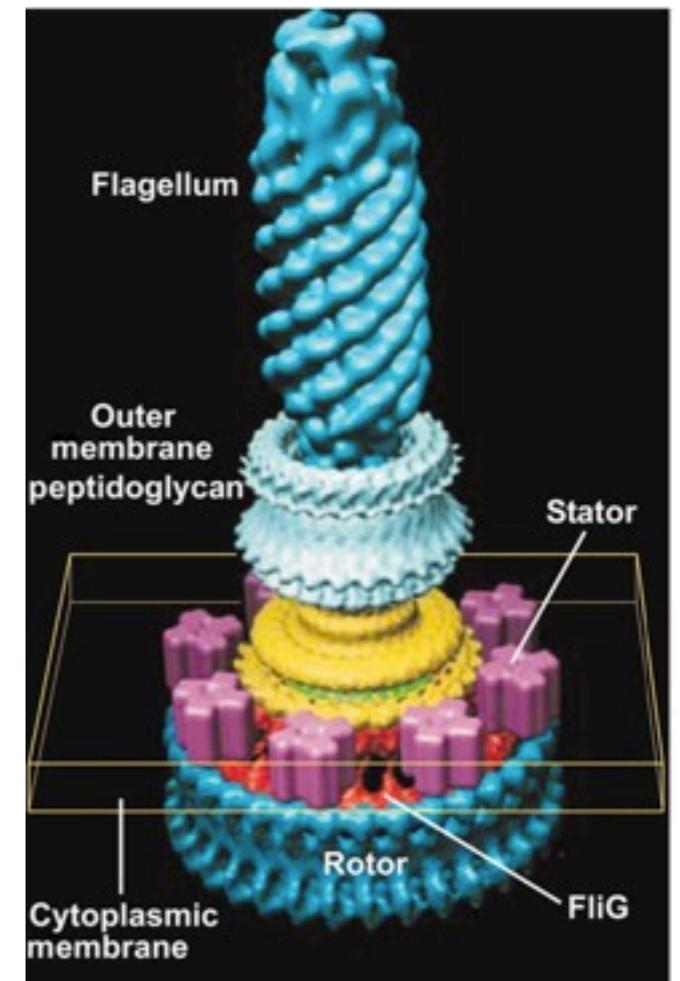
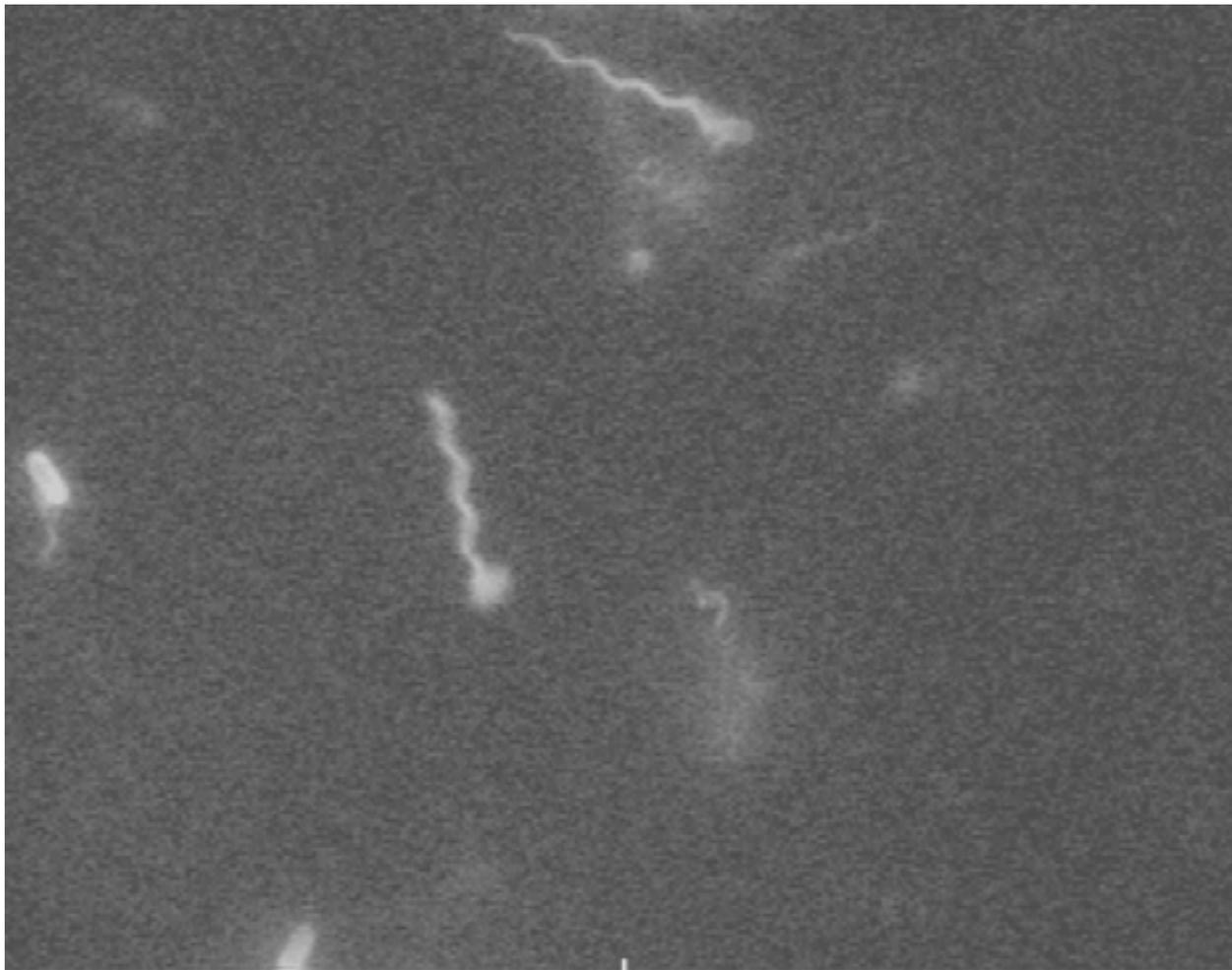
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# Resistance against antibiotics: A non-stationary rare event



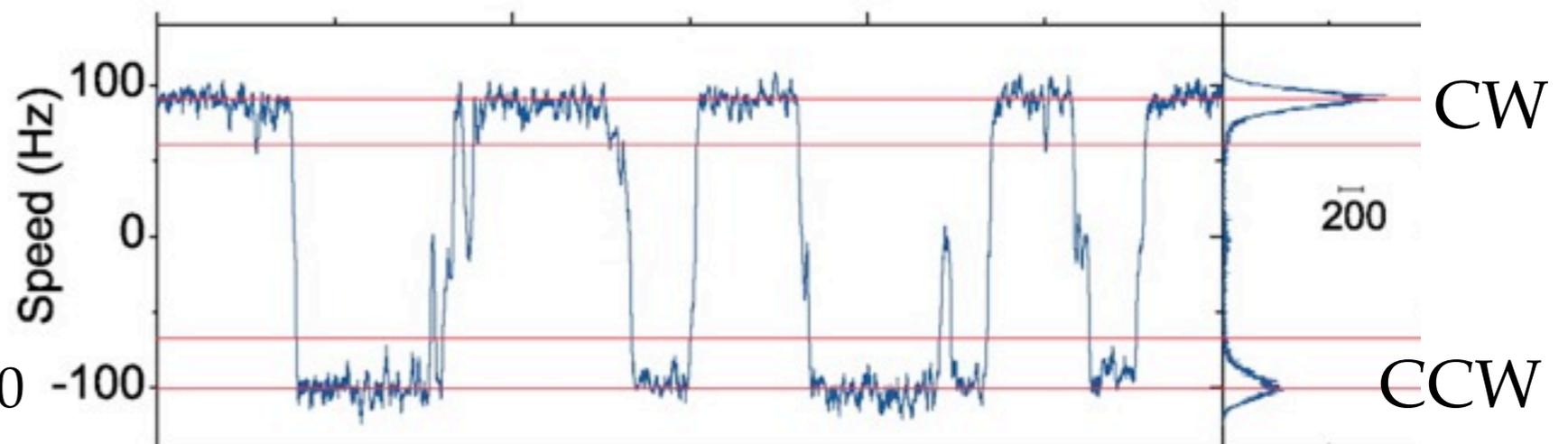
Balaban et al., Science, 2004

# Switching of the bacterial flagellar motor: Non-Markovian dynamics

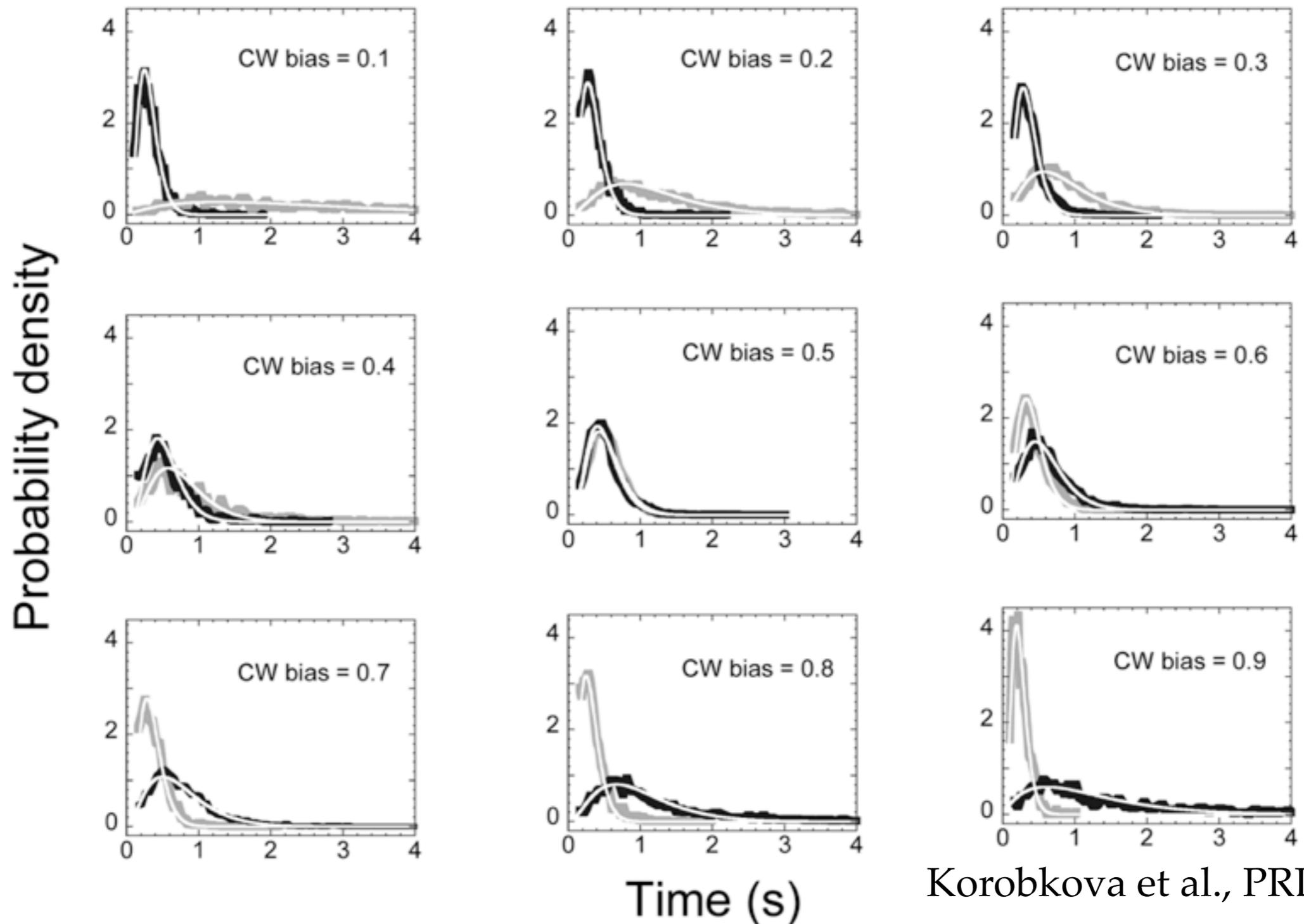


Howard Berg lab

Berry et al., Science 2010



# Switching of the bacterial flagellar motor: Non-Markovian dynamics



Korobkova et al., PRL, 2006

# Questions

- How do we describe these systems?
- Can we derive microscopic expressions in terms of correlation functions for the macroscopic rate constants and rate kernels?
- Can we simulate these non-stationary and non-Markovian systems efficiently?

# Macroscopic description of two-state system



- Waiting time longer than transition time: two-state description

$$\begin{aligned} \frac{\partial}{\partial t} P_B(t; t', t'', \dots) &= \delta(t - t') k_{AB}(t' | t'', \dots) P_A(t'; t'', \dots) \\ &\quad - k_{BA}(t | t', t'', \dots) P_B(t; t', t'', \dots) \end{aligned}$$

$$\frac{d}{dt} P_B(t) = \int_{t \leq t' \leq t'' \leq \dots} \frac{\partial}{\partial t} P_B(t; t', t'', \dots) dt' dt'' \dots$$

- Eqs. cannot be solved in general Chandler, JCP (1978)
- Experiment has to inform us about most meaningful model

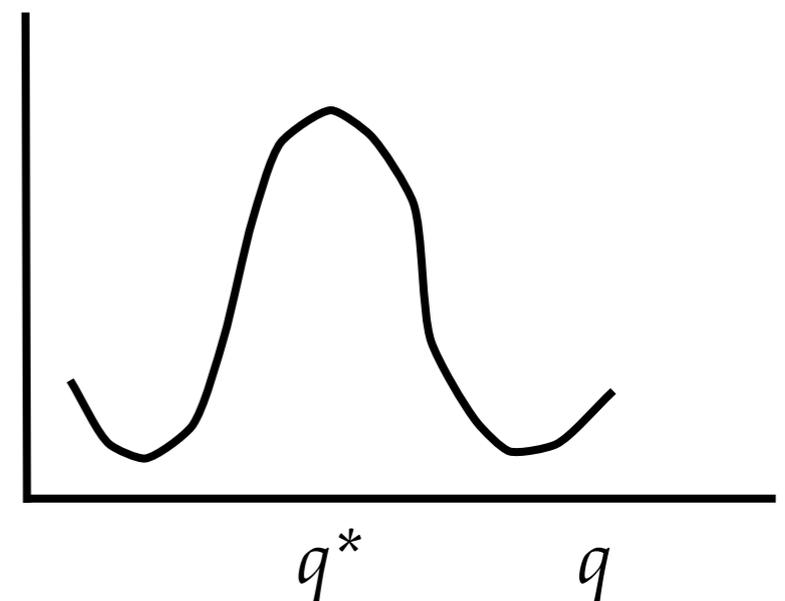
# Microscopic description

- Define macroscopic states in terms of microscopic indicator functions:

$$h_A(x_t) = \theta[q^* - q(x_t)],$$

$$h_B(x_t) = \theta[q(x_t) - q^*].$$

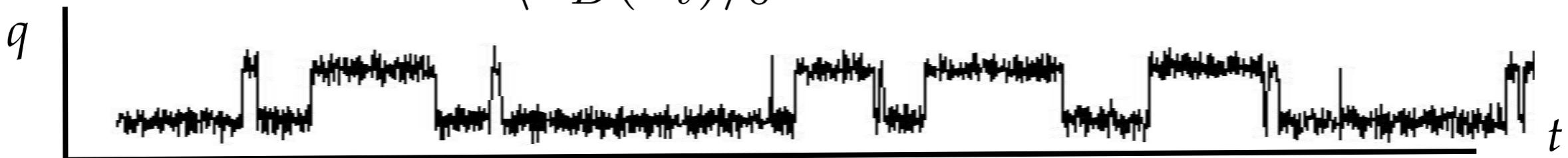
$-\ln[P(q)]$



- Macroscopic rate constants are related to time derivative of:

$$C(t) = \int dx_0 dx_t \rho(x_0) p(x_t | x_0) h_B(x_t)$$

$$= \langle h_B(x_t) \rangle_0$$



# Markov systems

- Experiment reveals that there exists a macroscopic time resolution  $\Delta t$  on which the propensity to switch is independent of the history:

$$k_{AB}(t|t', t'', \dots) = k_{AB}(t)$$

- Rate equation:

$$\frac{d}{dt}P_B(t) = k_{AB}(t)P_A(t) - k_{BA}(t)P_B(t)$$

# Markov systems

- Consider:

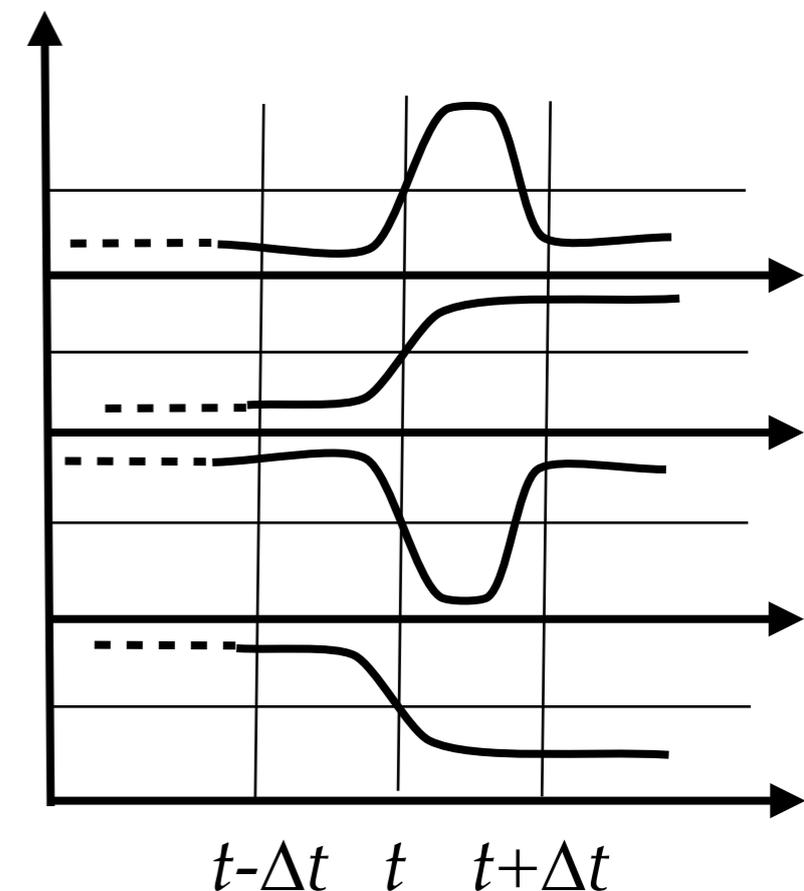
$$\dot{C}(t) = \langle \dot{h}_B(t) \rangle_{A_0}$$

- Insert:

$$h_A(t - \Delta t) + h_B(t - \Delta t) = 1$$

$$h_A(t + \Delta t) + h_B(t + \Delta t) = 1$$

$$\begin{aligned} \dot{C}(t) &= \langle h_A(t - \Delta t) \rangle_{A_0} \langle \dot{h}_B(t) h_A(t + \Delta t) \rangle_{A_{t-\Delta t}} \\ &+ \langle h_A(t - \Delta t) \rangle_{A_0} \langle \dot{h}_B(t) h_B(t + \Delta t) \rangle_{A_{t-\Delta t}} \\ &+ \langle h_B(t - \Delta t) \rangle_{A_0} \langle \dot{h}_B(t) h_B(t + \Delta t) \rangle_{B_{t-\Delta t}} \\ &+ \langle h_B(t - \Delta t) \rangle_{A_0} \langle \dot{h}_B(t) h_A(t + \Delta t) \rangle_{B_{t-\Delta t}} \\ &\equiv j_{AA}(t) + j_{AB}(t) + j_{BB}(t) + j_{BA}(t) \end{aligned}$$



# Markov systems

- If system is time reversible or time-homogeneous or memoryless on time scale  $\Delta t$ , then  $j_{AA}(t)$  and  $j_{BB}(t)$  are zero:

$$\begin{aligned}\dot{C}(t) &= \langle h_A(t - \Delta t) \rangle_{A_0} \langle \dot{h}_B(t) h_A(t + \Delta t) \rangle_{A_{t-\Delta t}} \\ &+ \langle h_B(t - \Delta t) \rangle_{A_0} \langle \dot{h}_B(t) h_A(t + \Delta t) \rangle_{B_{t-\Delta t}} \\ &\simeq P_A(t) \langle \dot{h}_B(t) h_B(t + \Delta t) \rangle_{A_{t-\Delta t}} + P_B(t) \langle \dot{h}_B(t) h_A(t + \Delta t) \rangle_{B_{t-\Delta t}} \\ &= dP_B(t)/dt\end{aligned}$$

- Hence, time-dependent rate constants are given by:

$$k_{AB}(t) = \langle \dot{h}_B(t) h_B(t + \Delta t) \rangle_{A_{t-\Delta t}},$$

$$k_{BA}(t) = -\langle \dot{h}_B(t) h_A(t + \Delta t) \rangle_{B_{t-\Delta t}}.$$

Bennett, Chandler

# Markov system with external driving

- Two-state system with driving force that varies on time scale  $\tau_\phi$
- Markov description requires that  $\tau_{\text{trans}} < \Delta t \ll \tau_{\text{rxn}}$
- Two simple scenarios:

- quasi-static case:

$$\tau_{\text{trans}} < \Delta t < \tau_\phi \ll \tau_{\text{rxn}} : k(t) = k(\phi(t))$$

- rapidly varying force:

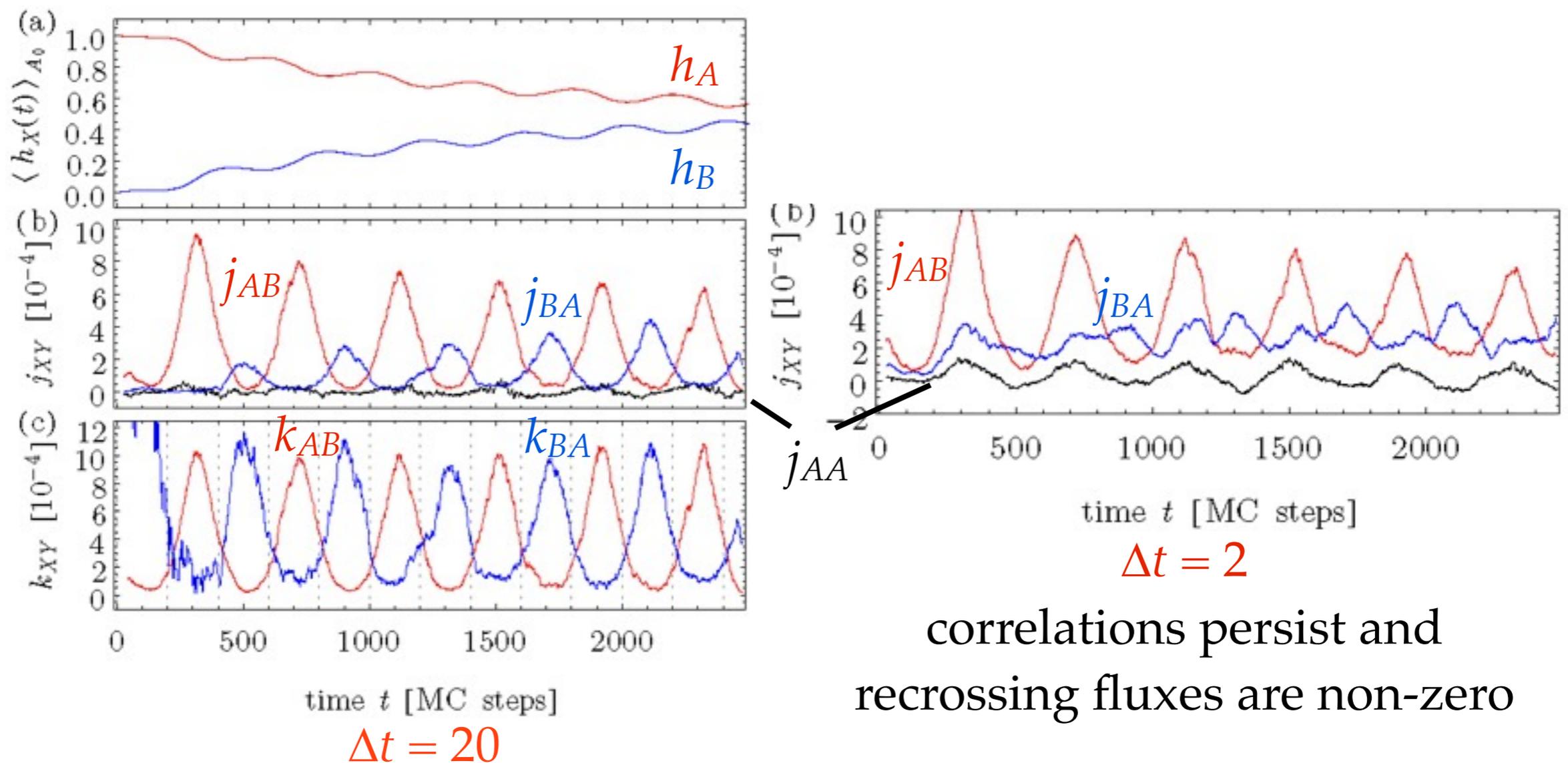
$$\tau_{\text{trans}}, \tau_\phi < \Delta t \ll \tau_{\text{rxn}}$$

# Markov system with external driving

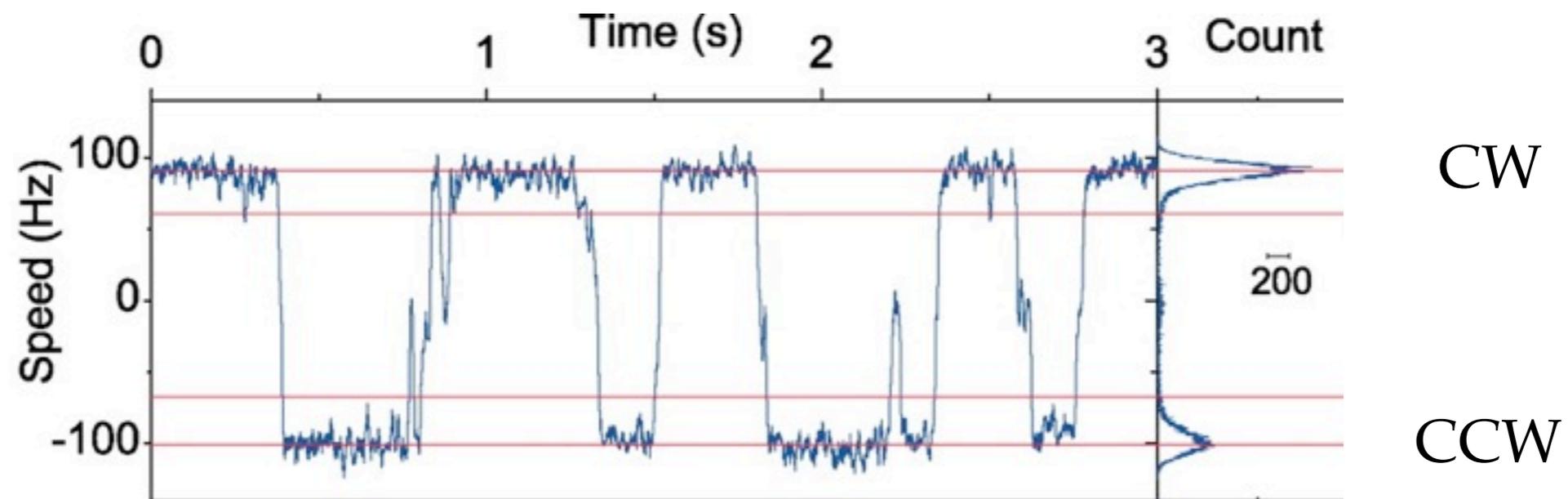
- One-dimensional barrier with oscillatory force

- Quasi-static case:

$$\tau_{\text{trans}} < \Delta t < \tau_{\phi} \ll \tau_{\text{rxn}} : k(t) = k(\phi(t))$$

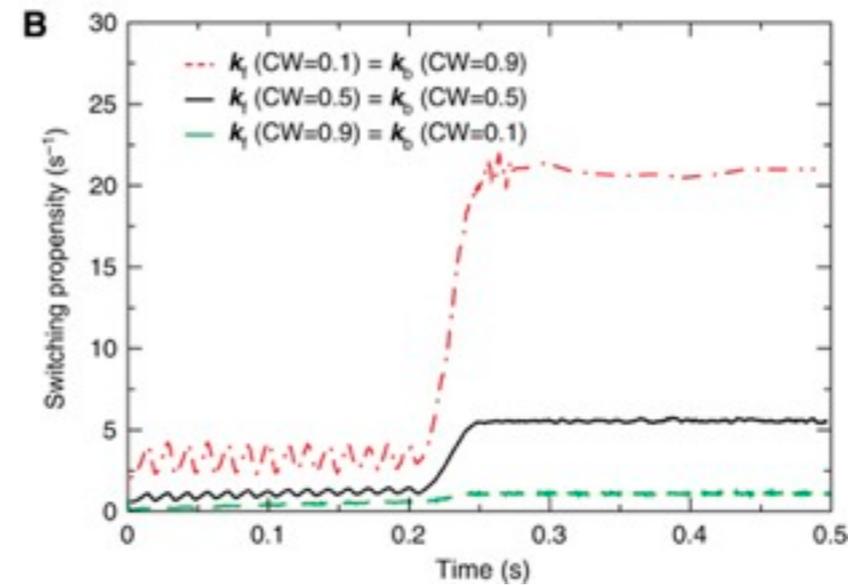
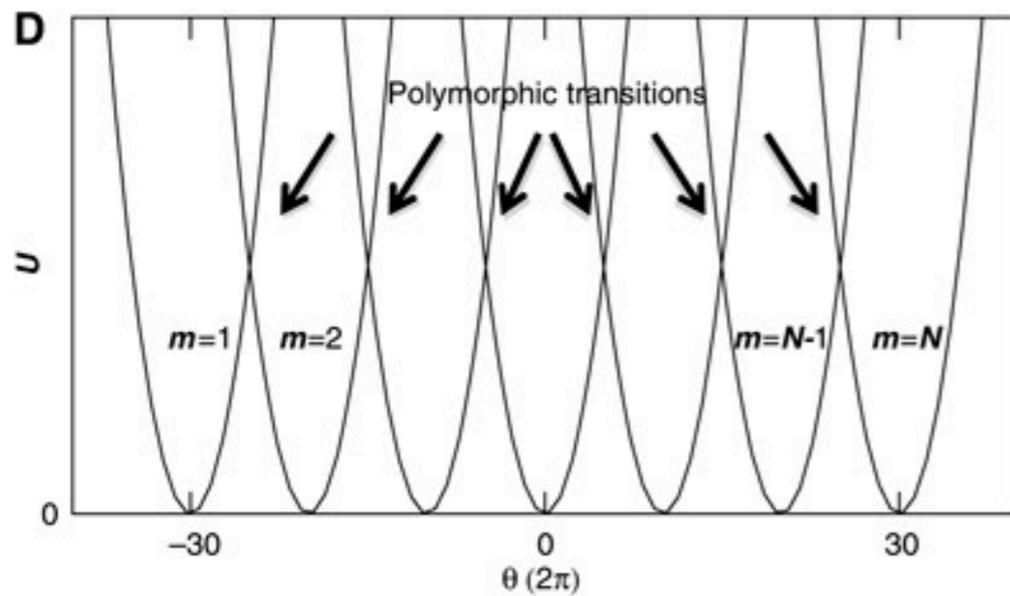
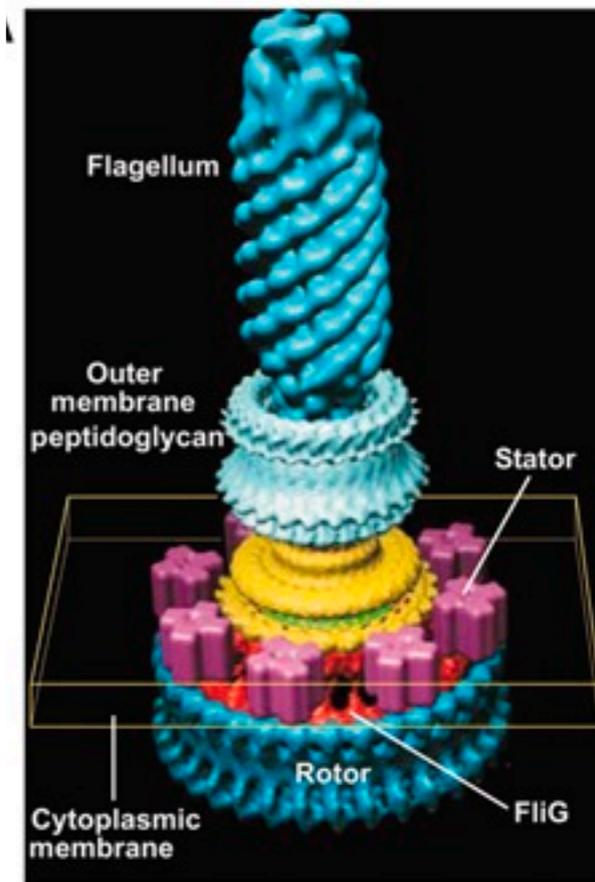
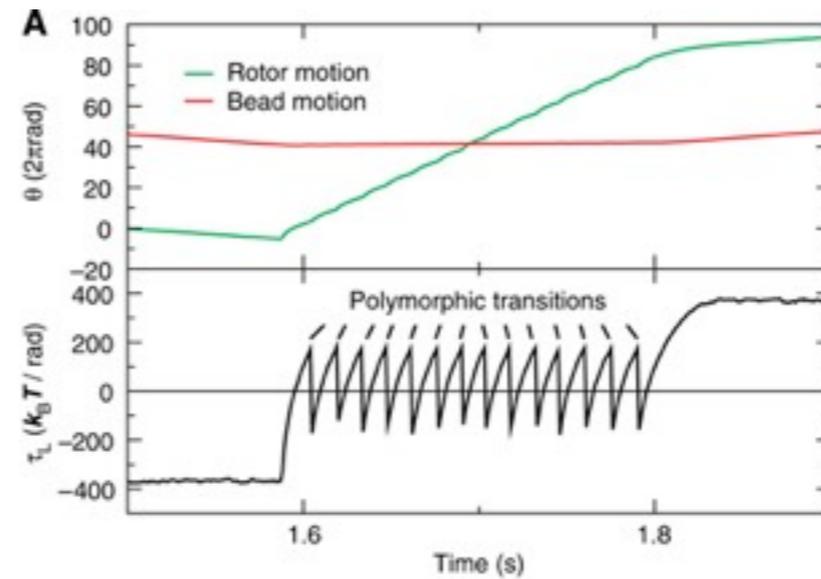
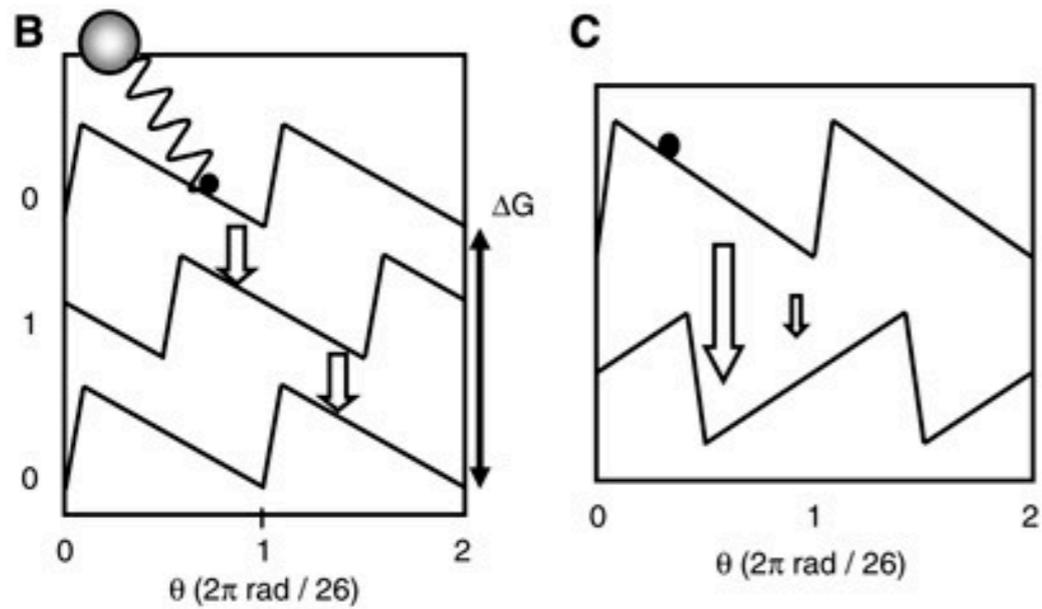


# Non-Markov system: flagellar motor



- Randomly shuffling clockwise and counterclockwise intervals does not change power spectrum; moreover, power spectrum can be reproduced from waiting-time distributions only
- System is a time-homogeneous non-Markovian system: transitions are independent and the different intervals are temporally uncorrelated, but they are *not* exponentially distributed.
- Switching propensity depends only upon the time that has passed since the last switching event.

# The flagellar motor



Albada, Tanase-Nicola, PRtW, Nat MSB (2009)

# Non-Markov systems

## Macroscopic description

- Clock resetting:

$$\frac{d}{dt}P_B(t) = \int_{t \leq t'} [k_{AB}(t|t')P_A(t; t') - k_{BA}(t|t')P_B(t; t')]dt'$$

- $P_A(t; t')$ : Probability that the system is in  $A$  at time  $t$  and has switched into that state for the last time within an earlier time interval  $(t', t'+dt)$
- $k_{AB}(t|t')$  : The propensity that the system switches from  $A$  to  $B$  at time  $t$  given that it has switched into  $A$  at time  $t' < t$  and is still in  $A$  at time  $t$

# Non-Markov systems

## microscopic description

- Need indicator function that measures time since last switching event:

$$H_X(t, t') \equiv \prod_{t \geq t'' > t'} h_X(t''); \quad H_X(t, t) = 1$$

- Relate macroscopic rate equation to:

$$\begin{aligned} \dot{h}_B(t) &= \dot{h}_B(t) \sum_{X=A,B} H_X(t, t) \\ &= \partial_t H_B(t, t_0) - \partial_t H_A(t, t_0) \\ &\quad + \int_{t_0}^t [\partial_t \partial_{t'} H_B(t, t') - \partial_t \partial_{t'} H_A(t, t')] dt' \end{aligned}$$

# Non-Markov system microscopic description

- Microscopic expressions for  $P_B(t,t')$  and  $k_{AB}(t,t')$ :

$$\begin{aligned}\partial_{t'} \langle H_B(t, t') \rangle dt' &= \langle H_B(t, t') \dot{h}_B(t') \rangle dt' \\ &= P_B(t; t') dt',\end{aligned}$$

$$\begin{aligned}\frac{\partial_t \partial_{t'} \langle H_B(t, t') \rangle}{\partial_{t'} \langle H_B(t, t') \rangle} &= \frac{\langle \dot{h}_B(t) H_B(t, t') \dot{h}_B(t') \rangle}{\langle H_B(t, t') \dot{h}_B(t') \rangle} \\ &= -k_{AB}(t|t')\end{aligned}$$

# Non-Markov system microscopic description

- Integrate over transient crossings over the dividing surface:

$$h_B(t; \Delta t) = \theta \left[ \int_{t-\Delta t}^t h_B(t') dt' - \Delta t/2 \right]$$

glasses, Chandler et al.

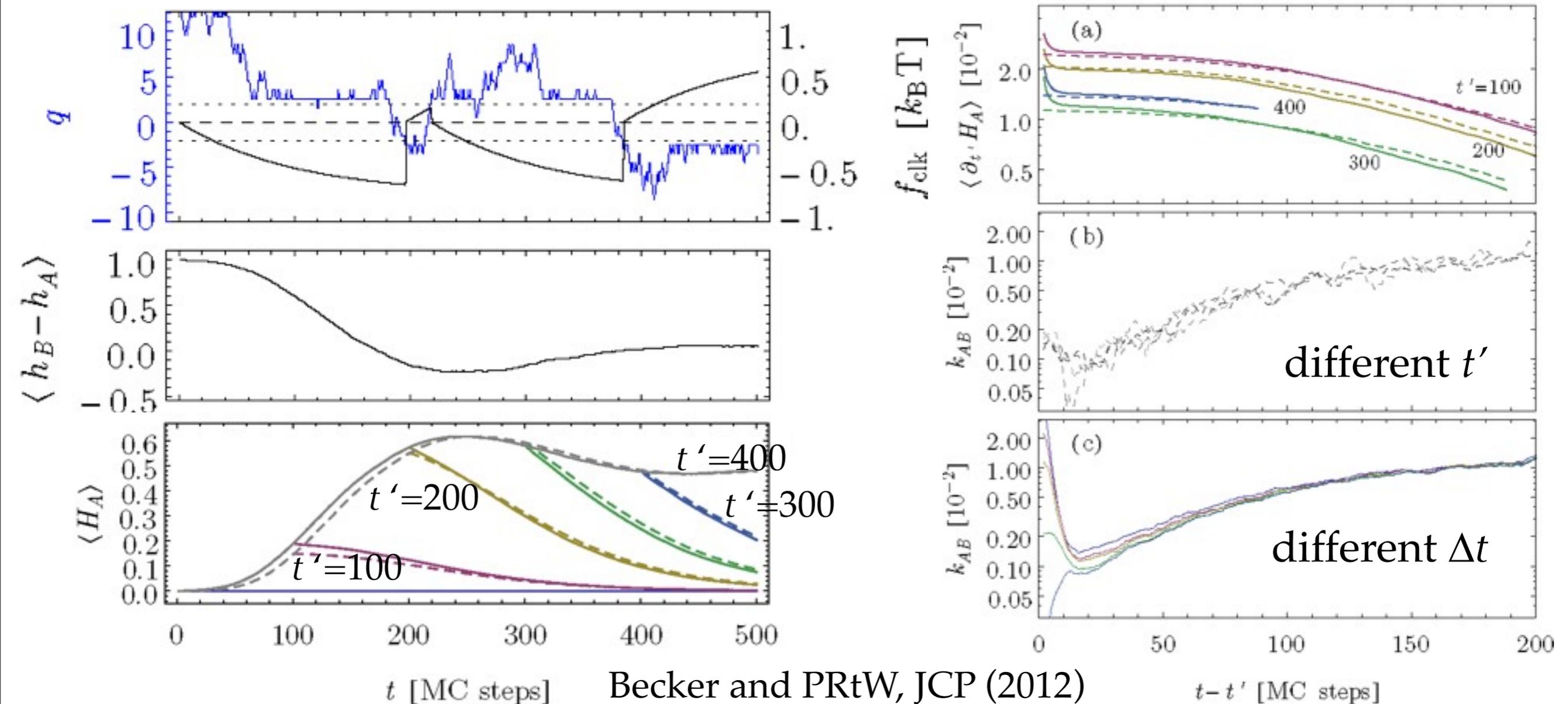
- Microscopic expressions for  $P_B(t, t')$  and  $k_{AB}(t, t')$  depend on  $\Delta t$ :

$$P_B(t; t'; \Delta t) dt' = \partial_{t'} \langle H_B(t, t'; \Delta t) \rangle dt',$$

$$k_{AB}(t|t'; \Delta t) = - \frac{\partial_t \partial_{t'} \langle H_B(t, t'; \Delta t) \rangle}{\partial_{t'} \langle H_B(t, t'; \Delta t) \rangle}$$

# Non-Markov system microscopic description

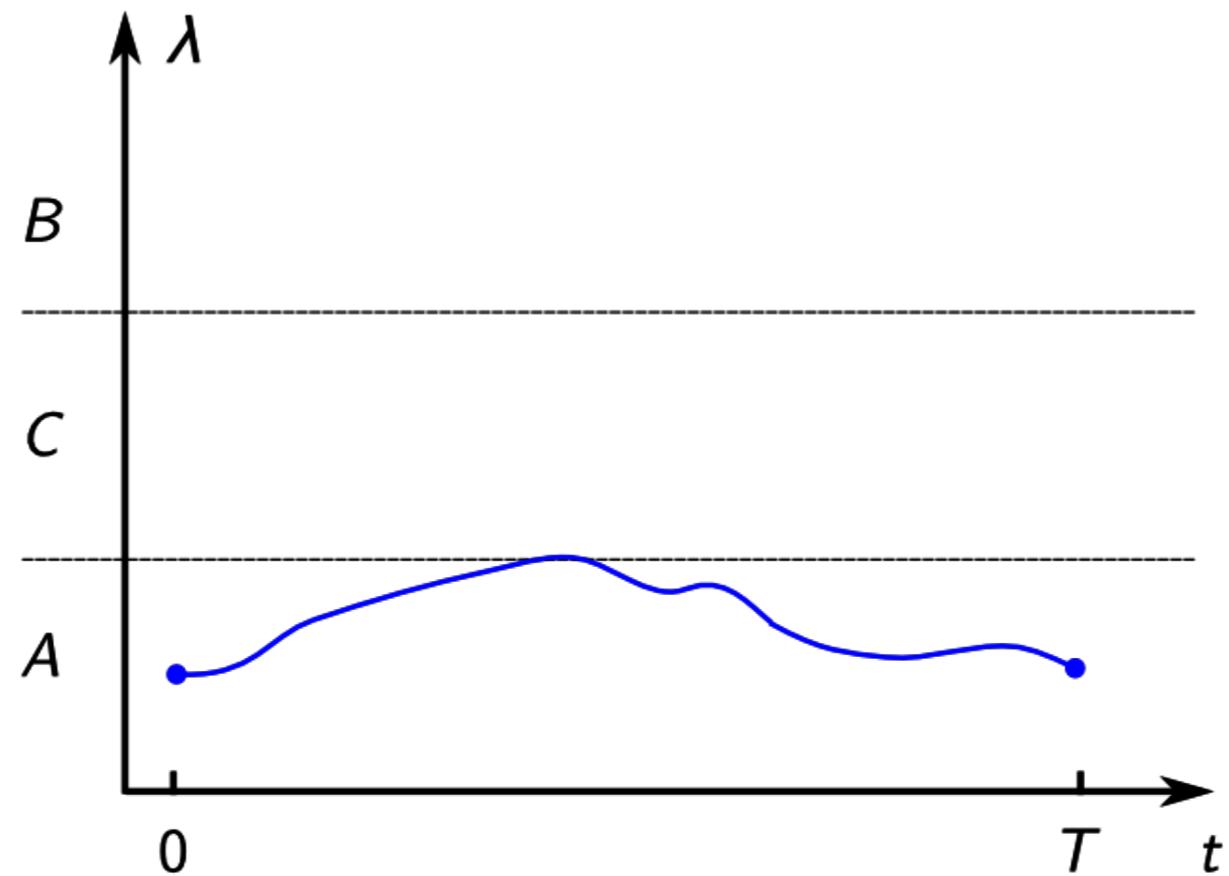
- One-dimensional barrier problem where after a barrier-crossing event the other state becomes progressively more stable



# How to simulate non-stationary and non-Markovian rare events?

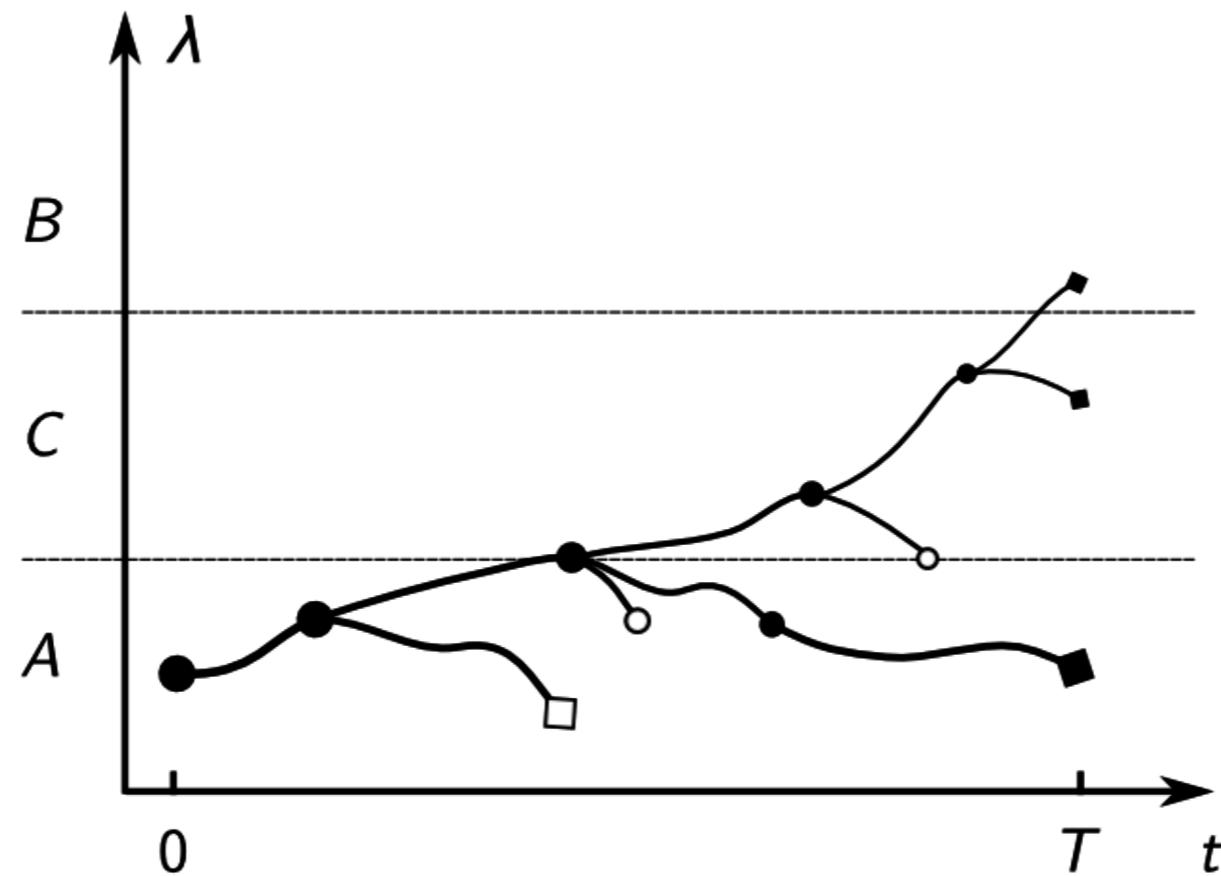
Non-Stationary Forward Flux Sampling

# Non-Stationary FFS



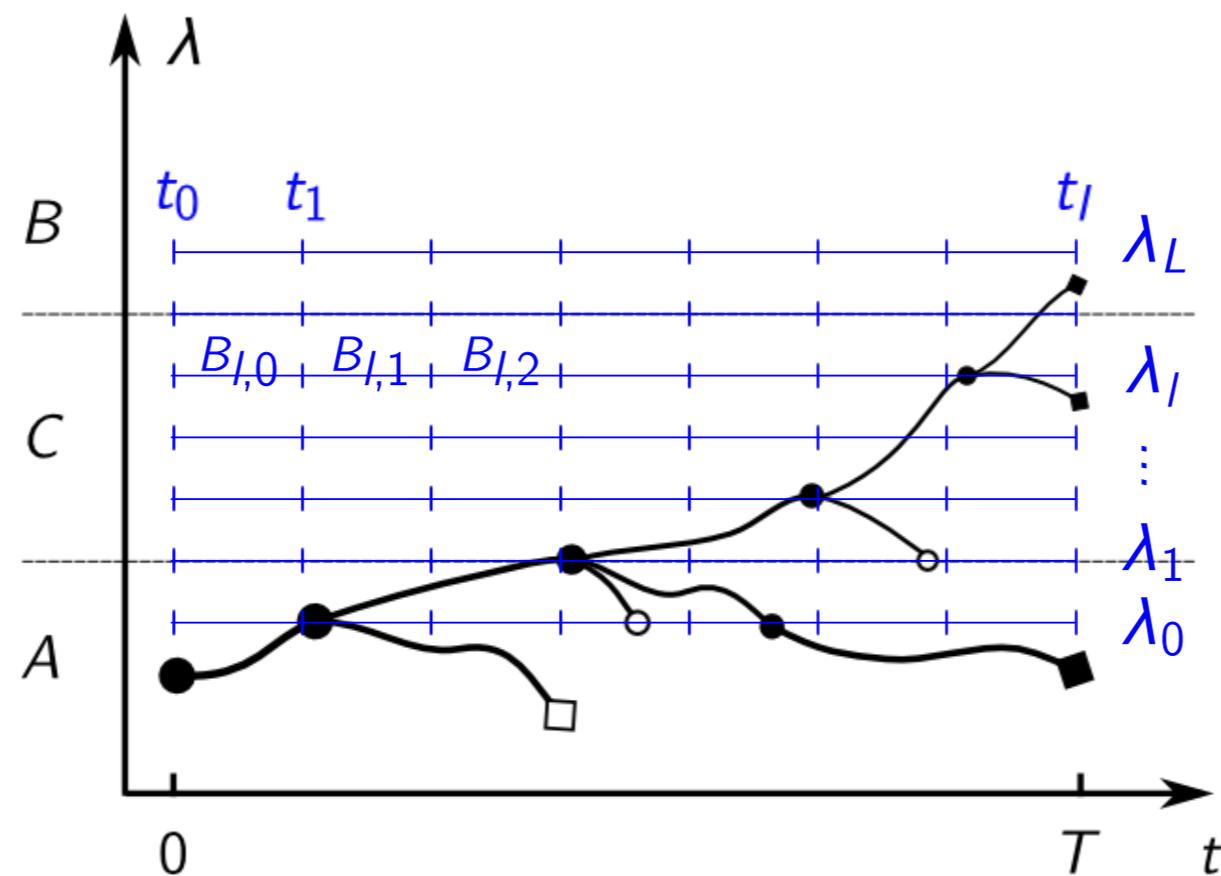
- Approach the saddle by ratcheting (FFS)
- Trigger branching / pruning on crossing

# Non-Stationary FFS



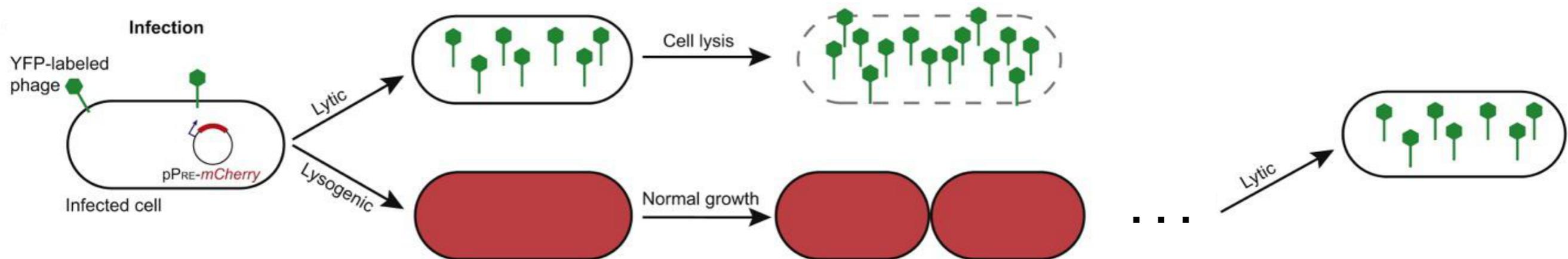
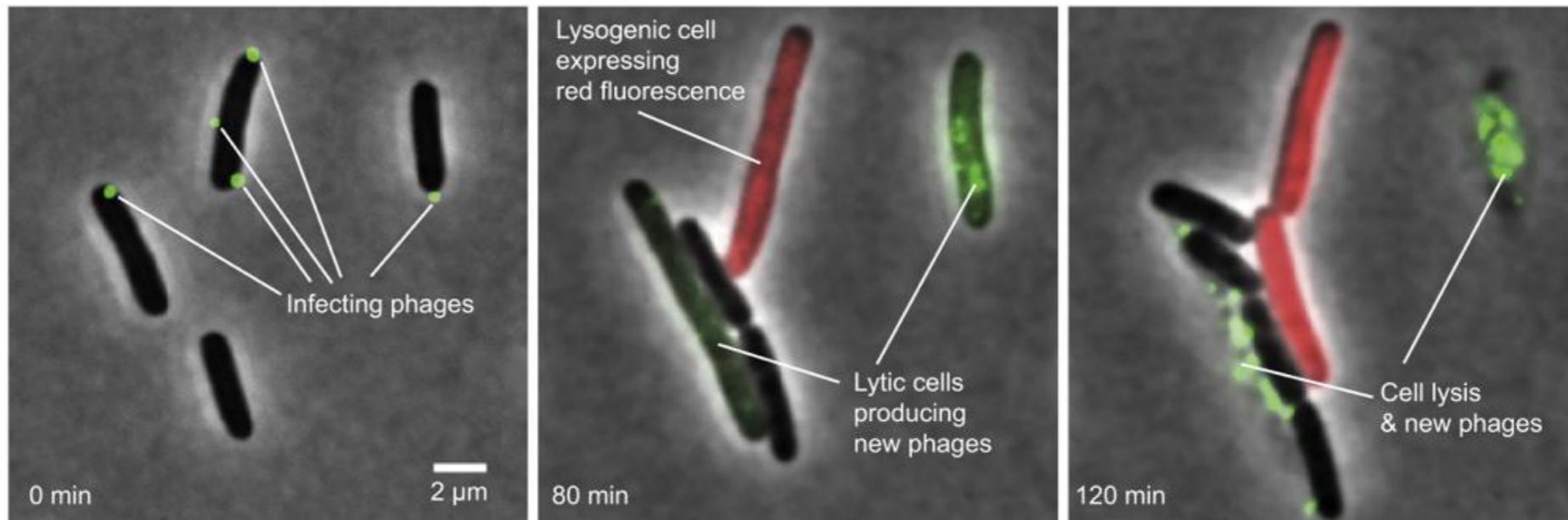
- Approach the saddle by ratcheting (FFS)
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# NS-FFS: flatPERM branching rule

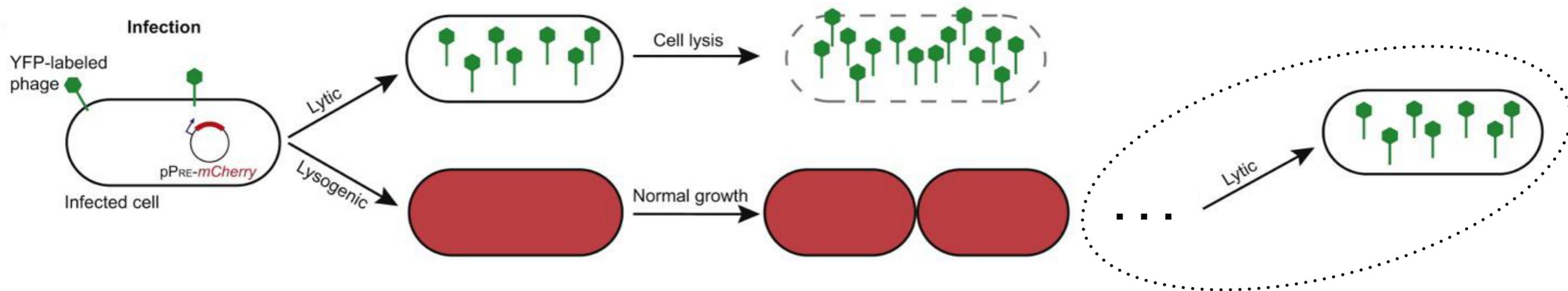
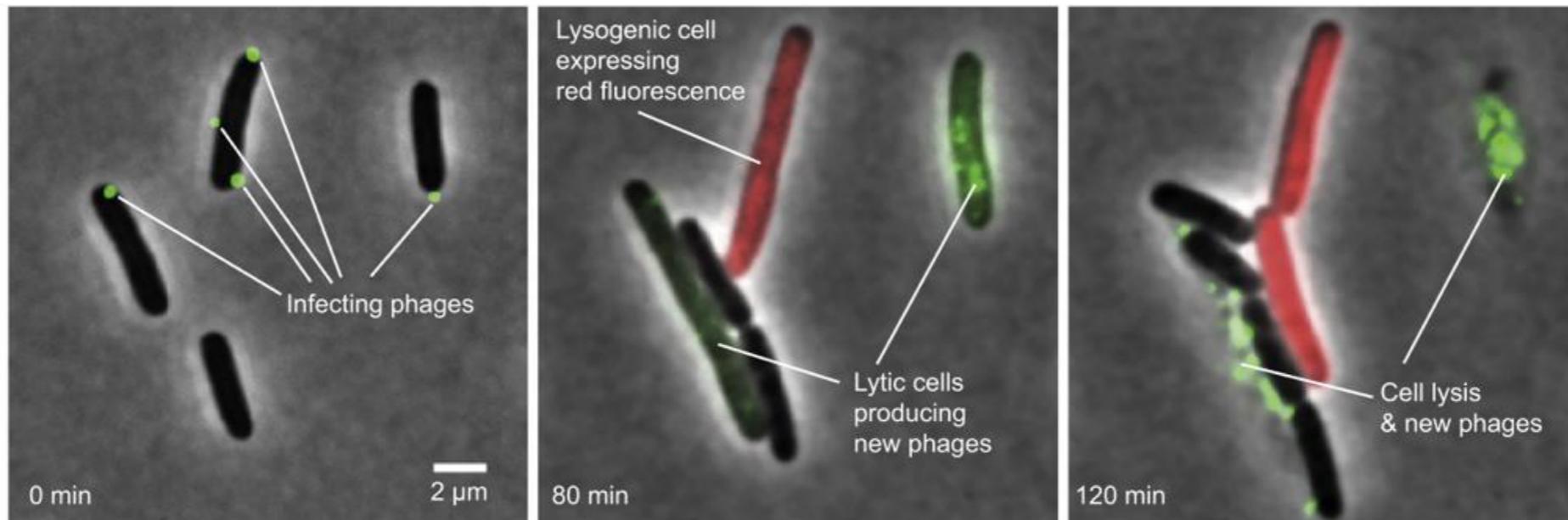


- ‘Branch uphill, prune downhill’
- Sampling uniformly by branching / pruning (flatPERM)  
Prellberg, T. & Krawczyk, J. PRL (2004); Grassberger, P. PRE (1997)
- Flat sampling of trajectory space Becker, Allen, PRtW, JCP (2012)

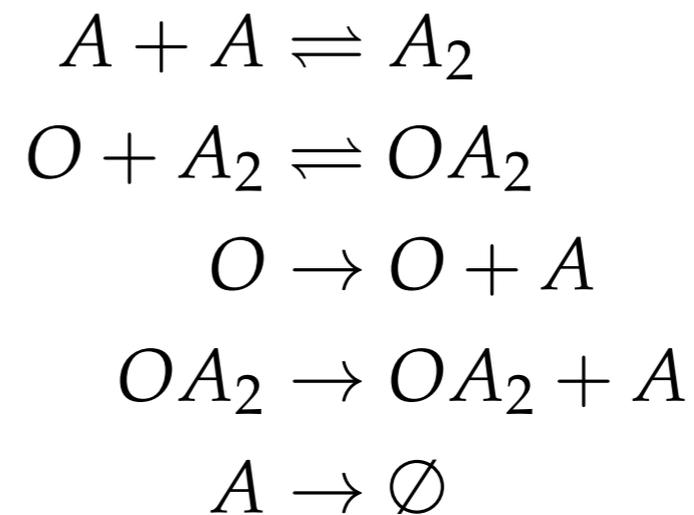
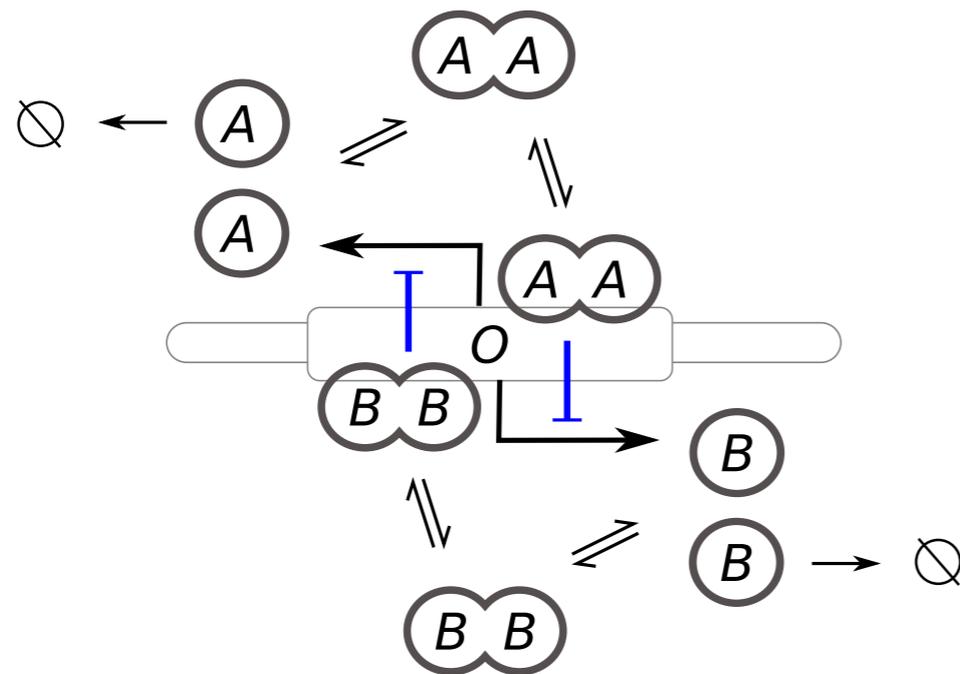
# Bacteriophage- $\lambda$ infection



# Bacteriophage- $\lambda$ infection



# The toggle switch



- Toy model of the phage- $\lambda$  genetic switch.
- Progress coordinate: total  $B$  monomers - total  $A$  monomers

$$\lambda = [B] + 2[B_2] + 2[OB_2] - ([A] + 2[A_2] + 2[OA_2])$$

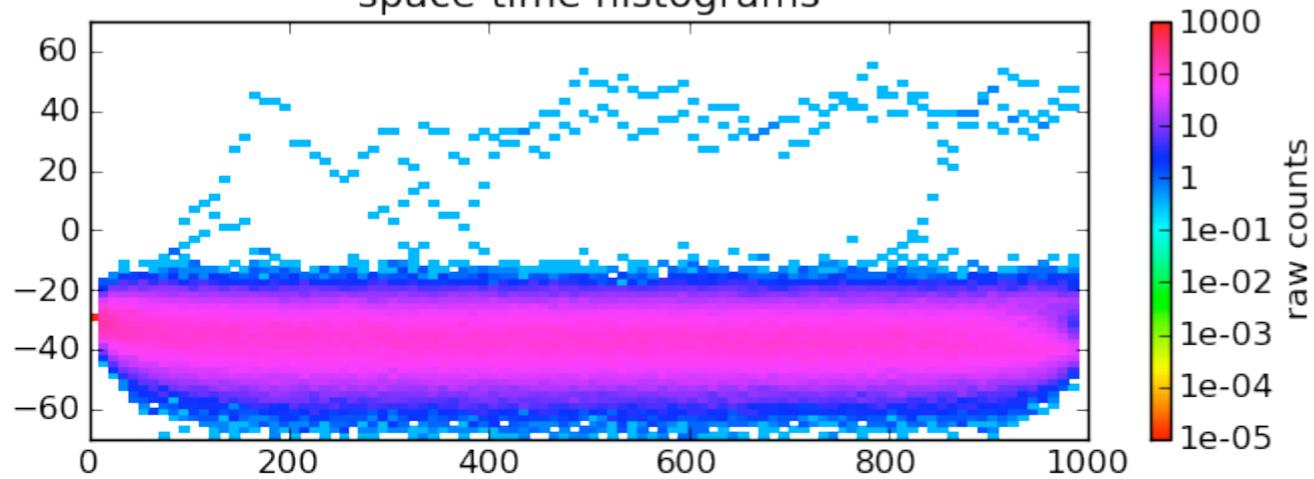
*e.g. Allen et al, JCP 2006*

# Spontaneous transitions

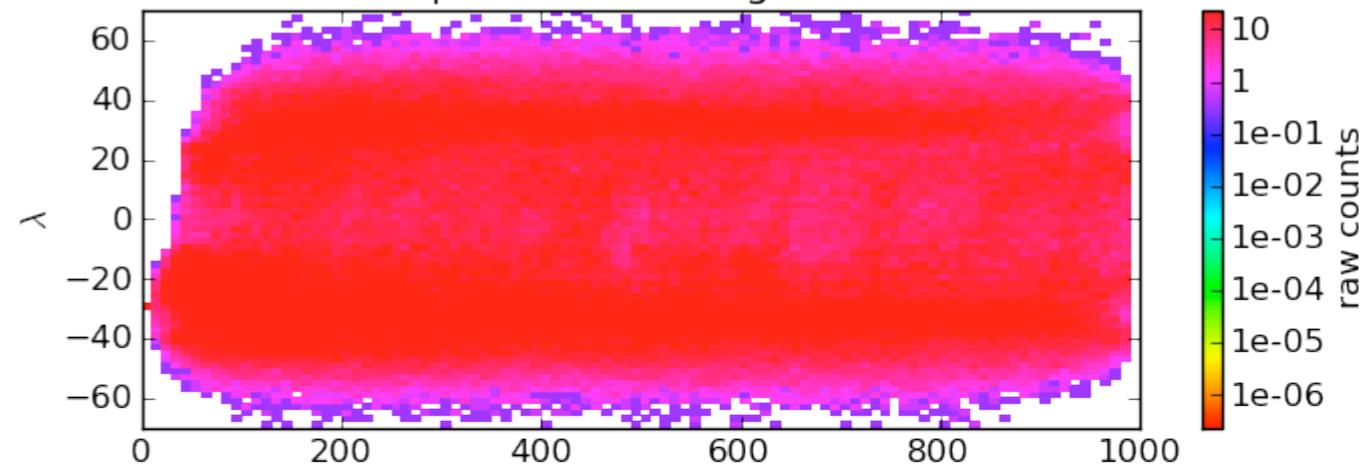
brute force

NS-FFS

space-time histograms



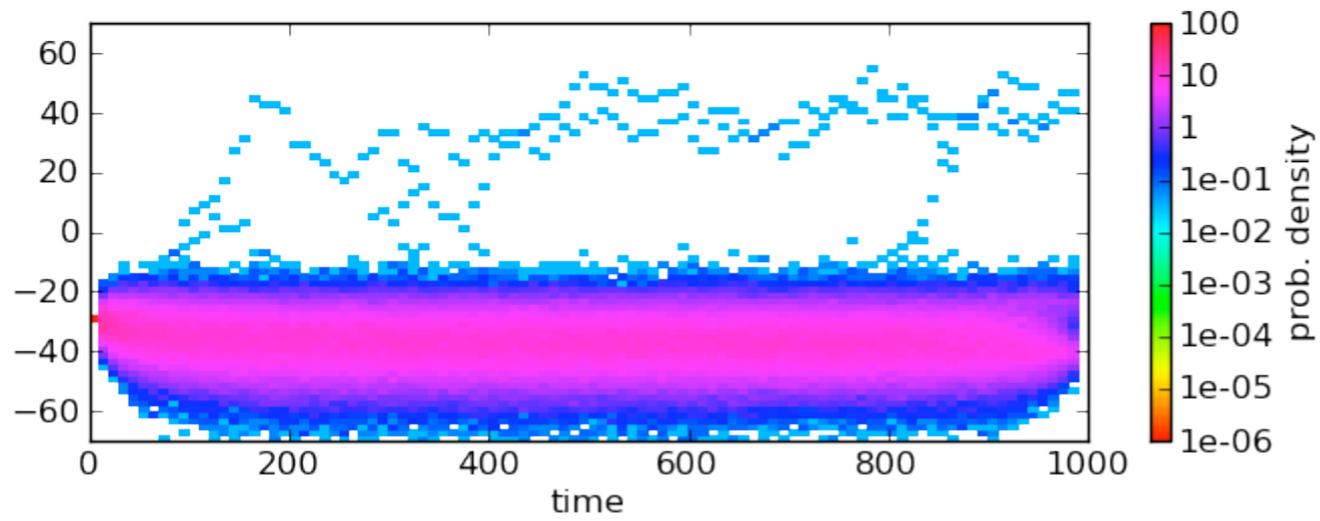
space-time histograms



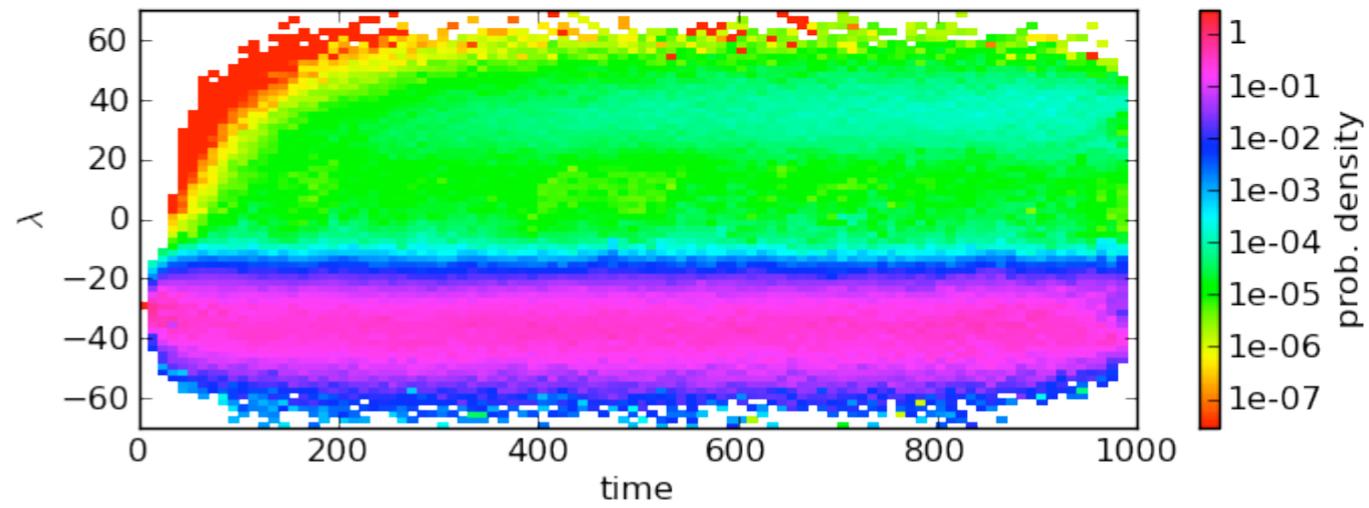
$\text{Prob}(\text{flipped until } t = 800) = .07\%$

# Spontaneous transitions

brute force

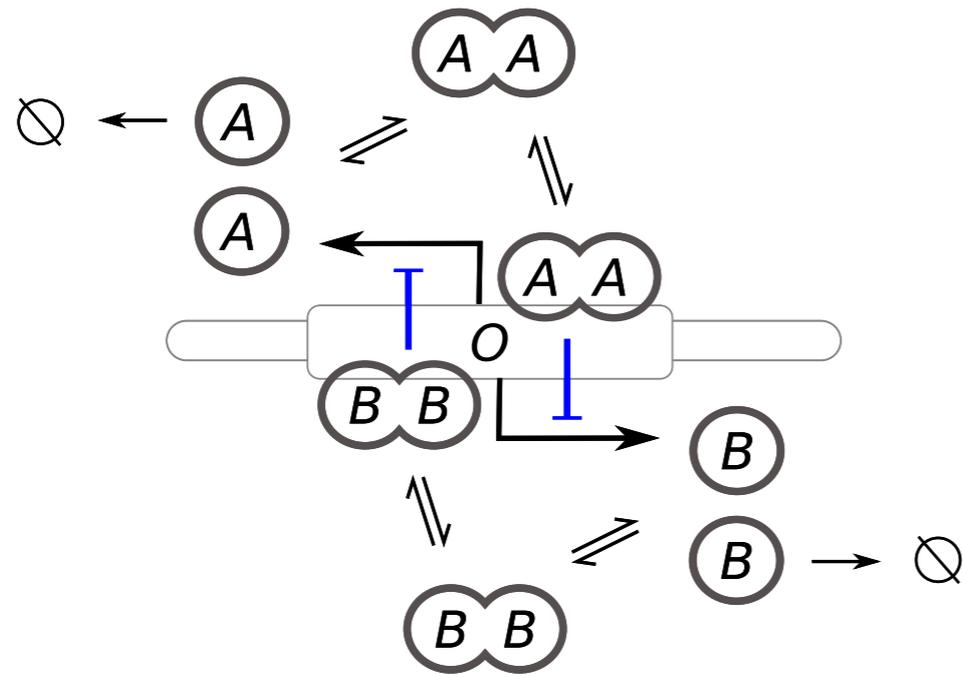


NS-FFS



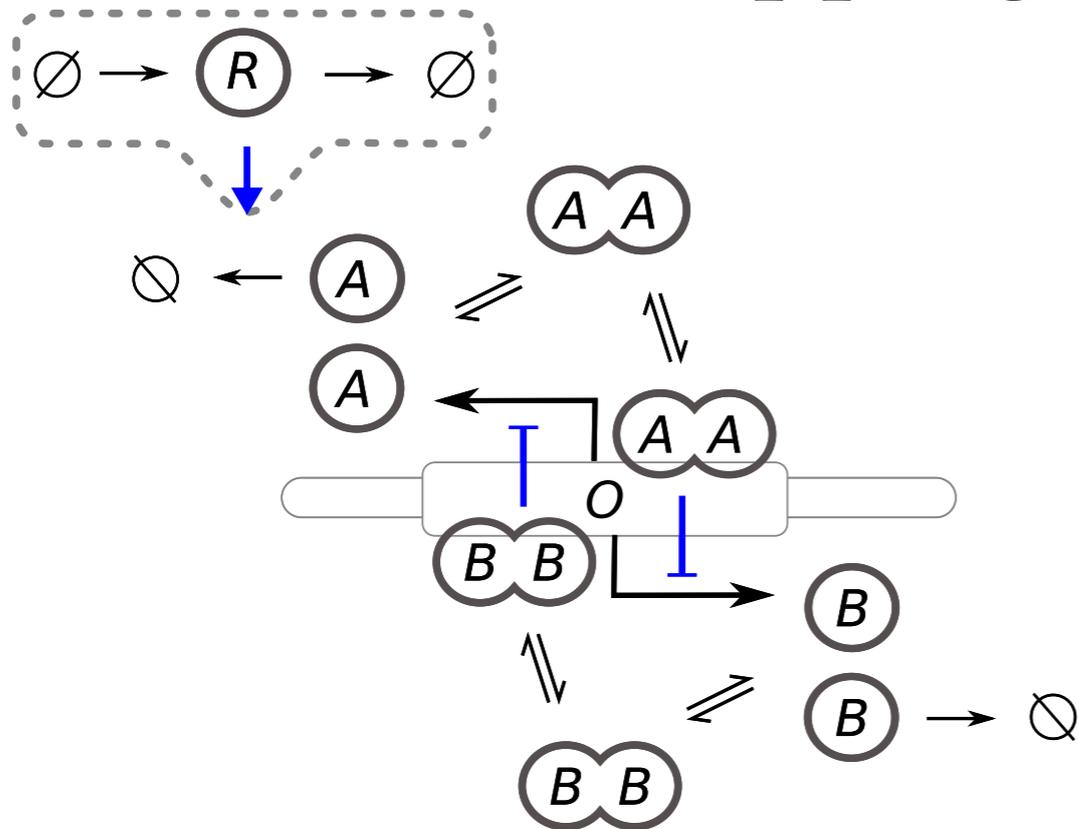
Prob(flipped until  $t = 800$ ) = .07%

# Flipping the switch



mean-field forcing:  $\gamma n_R^\infty = \text{fixed}$

# Flipping the switch



mean-field forcing:  $\gamma n_R^\infty = \text{fixed}$

- New chemical species:  $R$  ( $\sim$  RecA in phage  $\lambda$ )
- $R$  degrades  $A$  monomers  $\rightarrow$  flips the switch from  $A$  to  $B$

# Flipping the switch with a **ramp**

- accumulation of  $R$  :

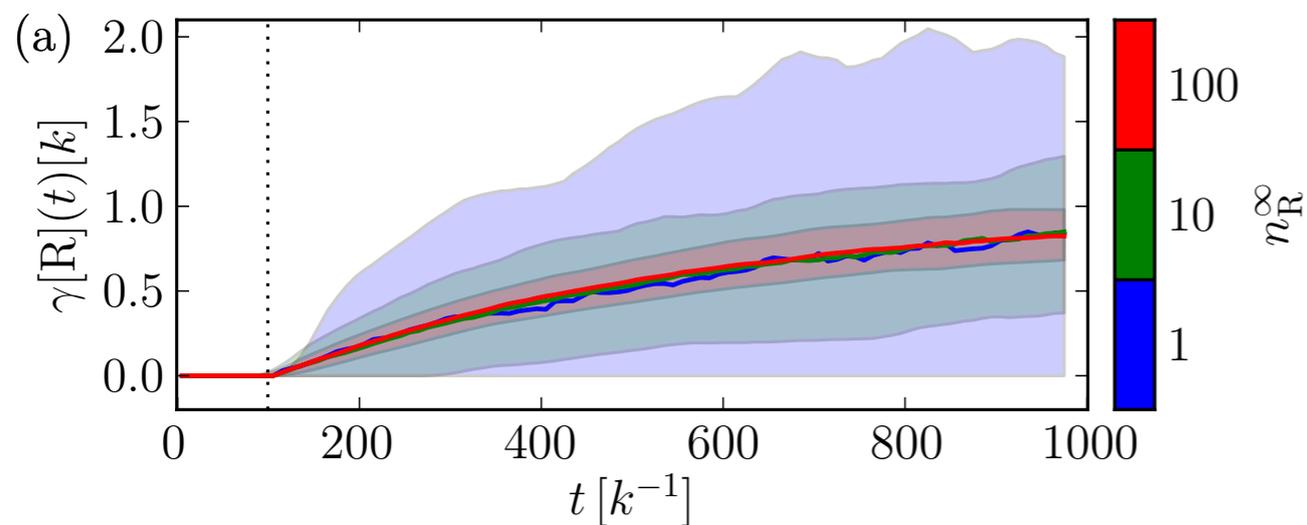
$$\langle R(t) \rangle = n_R^\infty (1 - e^{-\mu_R t})$$

- steady-state:  $n_R^\infty = k_R / \mu_R$

- mean-field forcing:  $\gamma n_R^\infty = \text{fixed}$

- increasing fluctuations:

$$n_R^\infty = 100, 10, 1$$

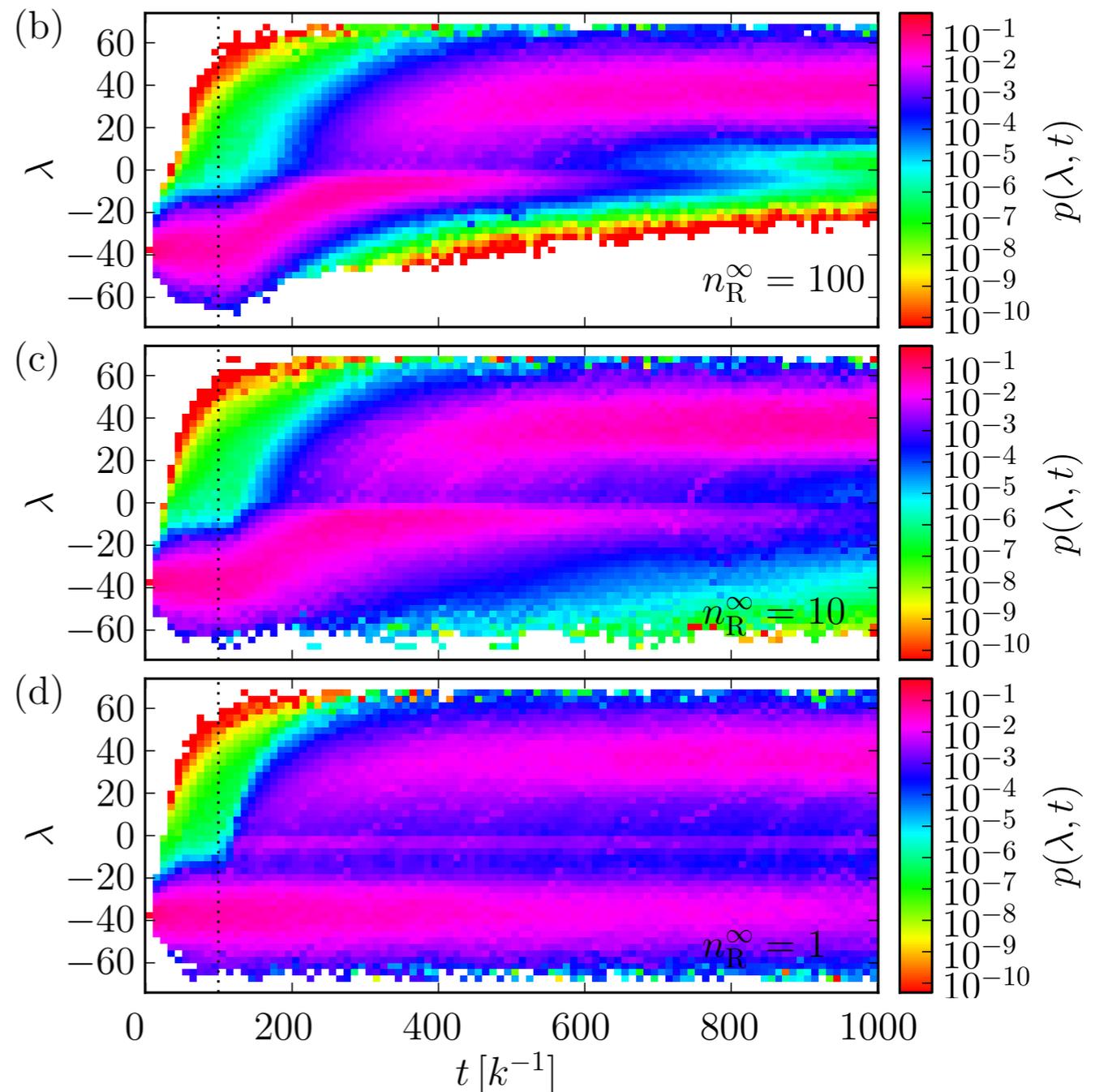
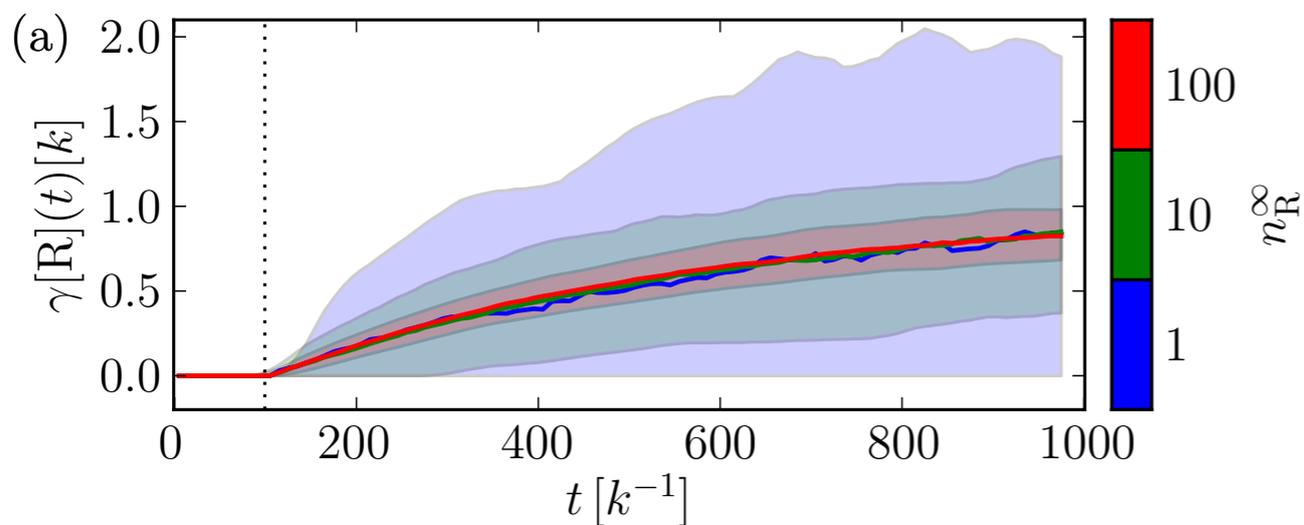


# Flipping the switch with a ramp

- accumulation of  $R$  :  

$$\langle R(t) \rangle = n_R^\infty (1 - e^{-\mu_R t})$$
- steady-state:  $n_R^\infty = k_R / \mu_R$
- mean-field forcing:  $\gamma n_R^\infty = \text{fixed}$
- increasing fluctuations:

$$n_R^\infty = 100, 10, 1$$



# Flipping the switch with a pulse

- decaying  $R$  pulse:

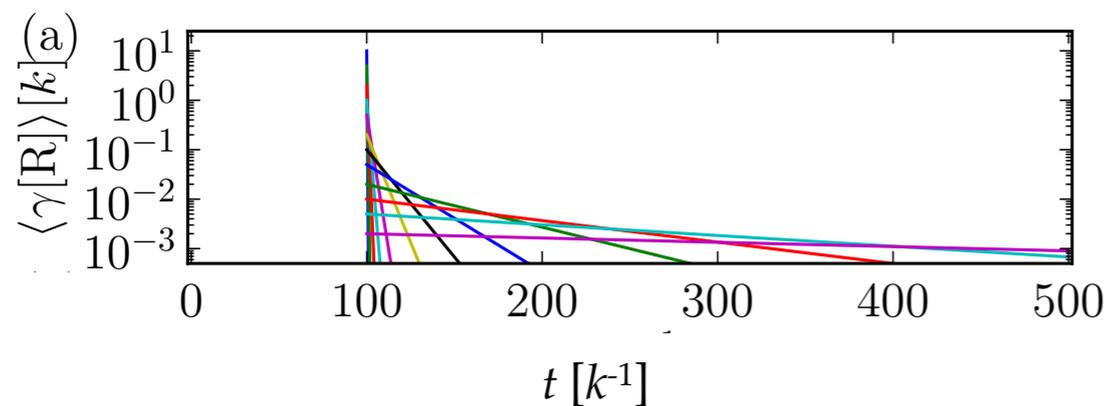
$$\langle R(t) \rangle = R_0 e^{-\mu_R(t-t_0)} \Theta(t-t_0)$$

- time-integrated bias:

$$\gamma \int_0^{\infty} \langle R(t) \rangle dt = \text{fixed}$$

- decreasing pulse duration:

$$\mu_R^{-1} = 100, 1, 0.1$$



# Flipping the switch with a pulse

- decaying  $R$  pulse:

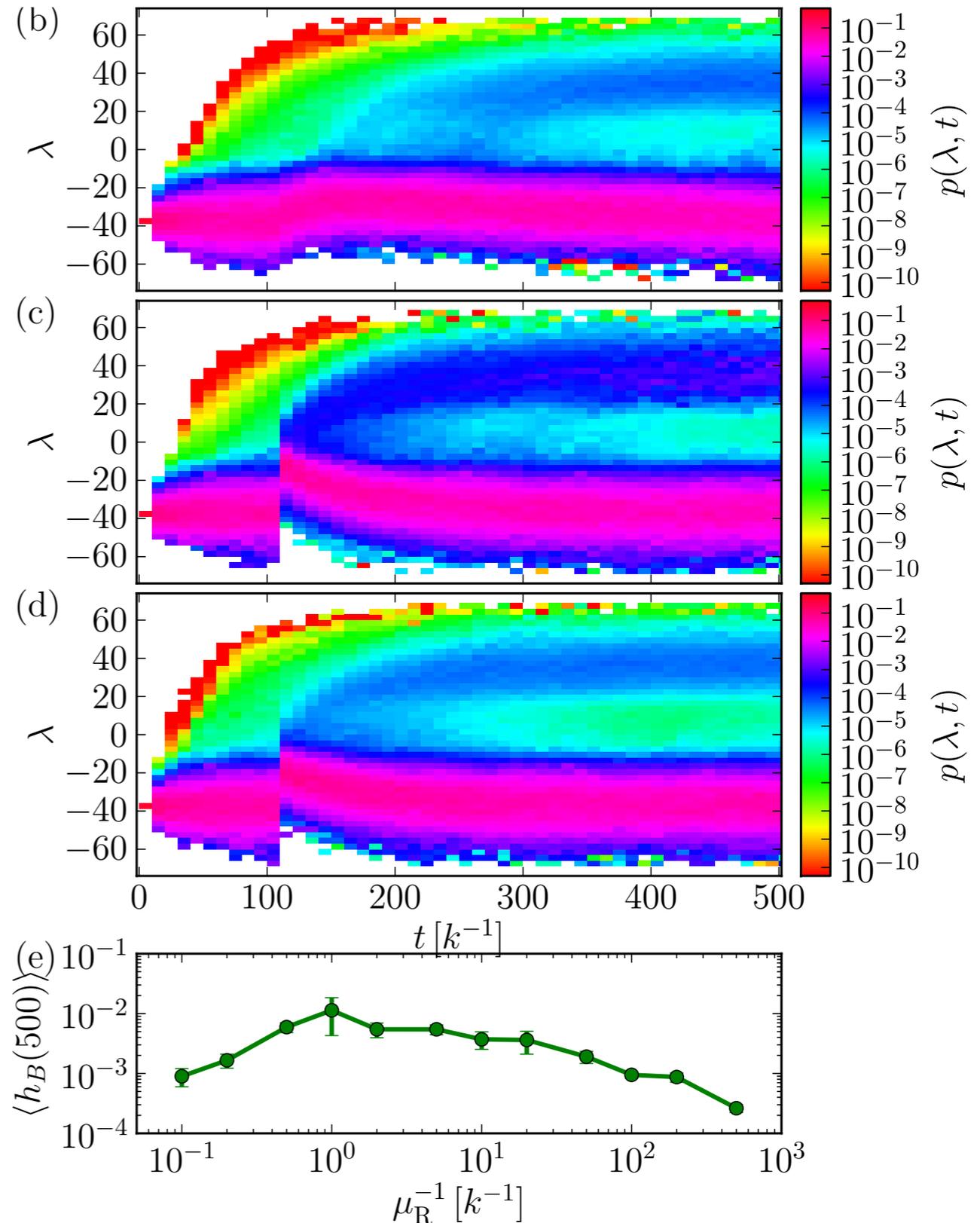
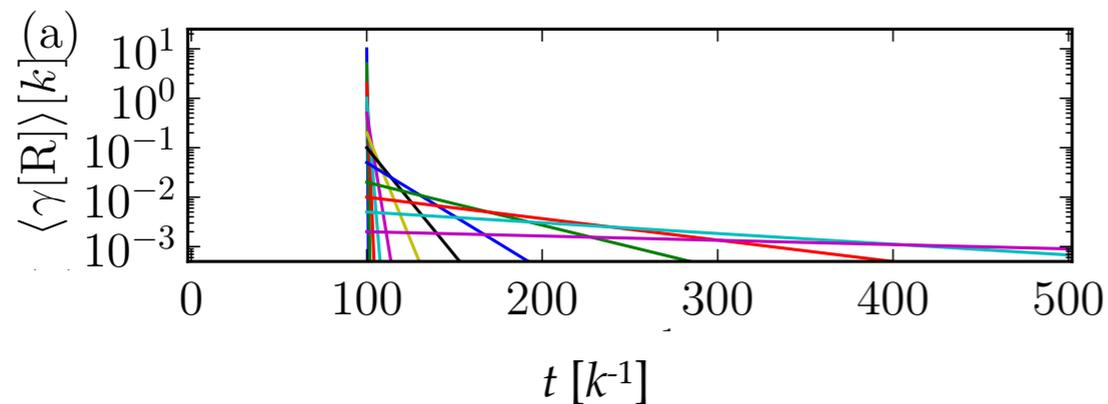
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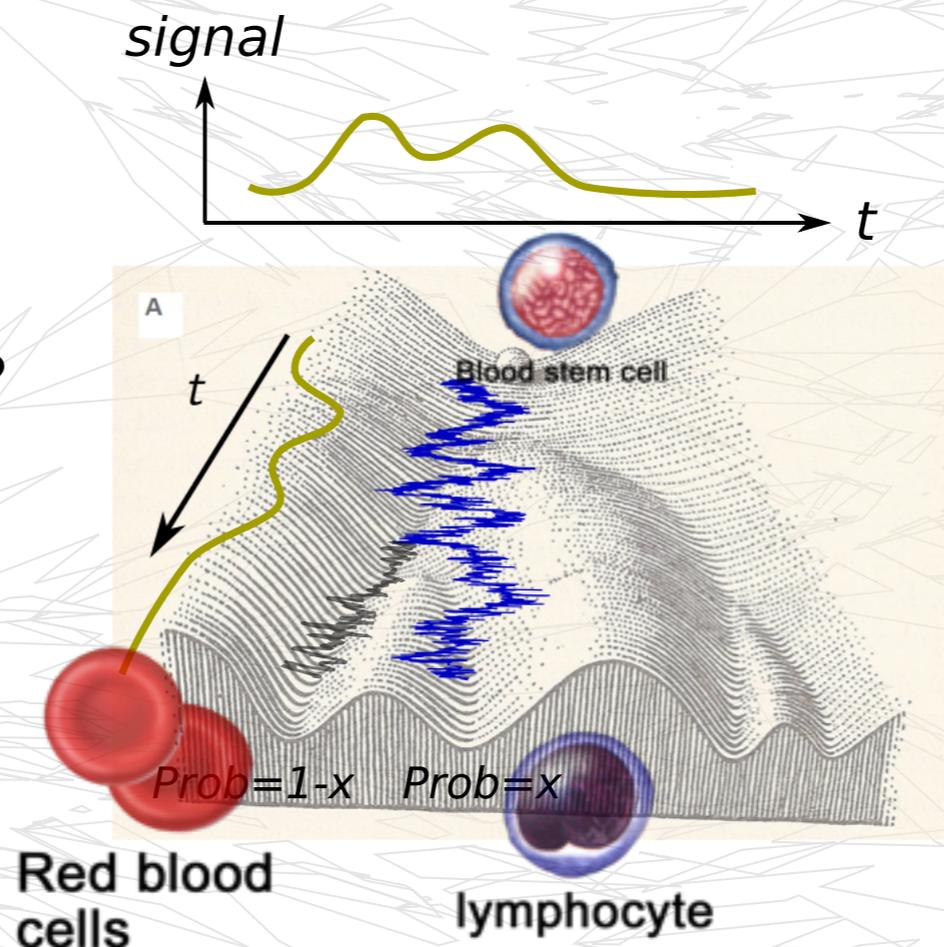


# Summary

- Non-stationary rare events are omnipresent, interesting and relevant
- A non-Markovian state model can be a useful coarse-grained description
- NS-FFS is a novel method for enhanced sampling of non-stationary rare events.
- *Outlook:* Cell differentiation occurs via induced switching and is stable afterwards. *How?*

Becker, Allen, PRtW, JCP (2012)

Becker, PRtW, JCP (2012)



# Extra slides

# Microscopic expressions for rate functions

time-inhomogeneous Markov case:

$$k_{AB}(t) = \langle \dot{h}_B(t) h_B(t + \Delta t) | h_A(t - \Delta t) \rangle$$

non-Markovian case:

$$h_A(t; \Delta t) = \theta[\int_{t-\Delta t}^t h_A(t') dt' - \Delta t/2]$$

$$H_A(t; t'; \Delta t) = \prod_{t \geq t'' > t'} h_A(t''; \Delta t)$$

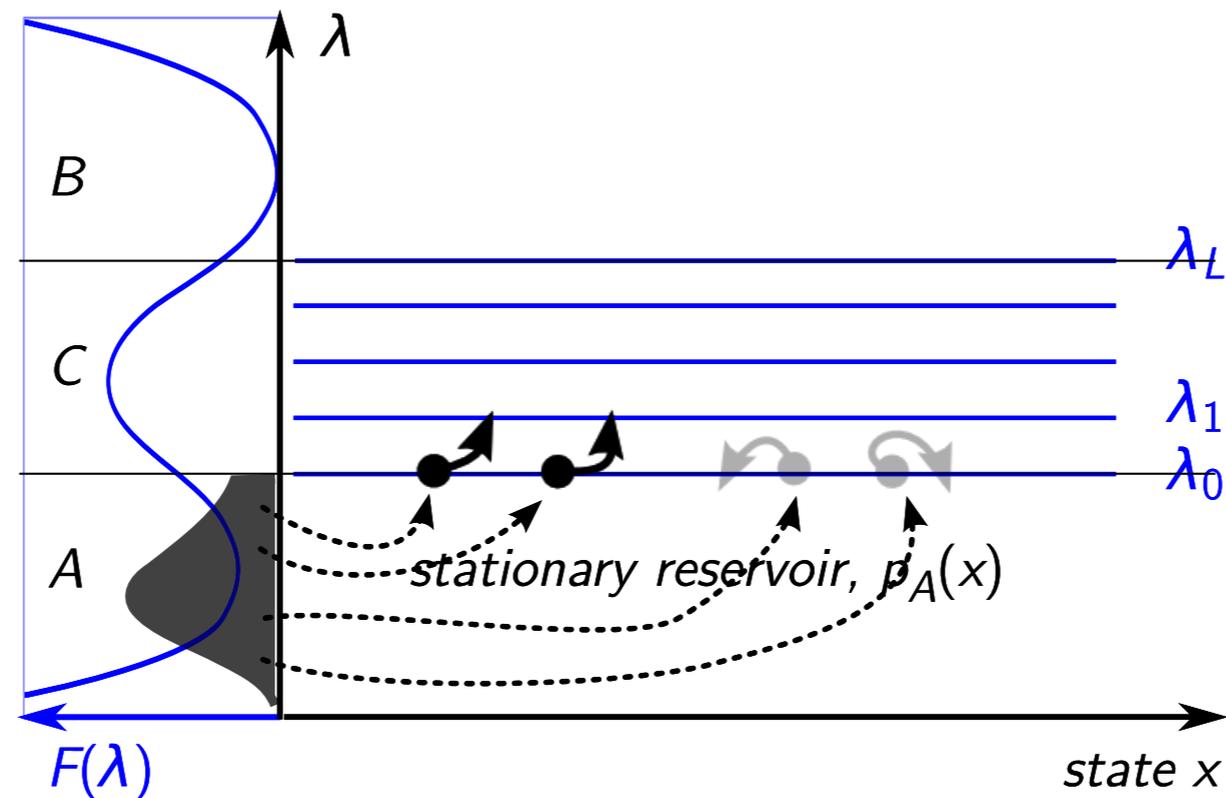
$$k_{AB}(t|t') = - \frac{\langle \partial_t \partial_{t'} H_A(t; t'; \Delta t) \rangle}{\langle \partial_{t'} H_A(t; t'; \Delta t) \rangle}$$

# NS-FFS algorithm

- ▶ *Init.* Weight histogram  $H_{li} = 0$ , tree count  $S = 0$ , growing branch list  $G = \{\}$
- ▶ *Run.* Iterate until convergence:
  - ▶ If  $G$  is empty, start a new trajectory with weight  $w = 1$  at  $t = 0$  and add it to  $G$
  - ▶ Pick and remove a trajectory from  $G$
  - ▶ Propagate to  $t = T$ , unless an interface is crossed; then:
    - ▶ increase  $H_{li}$  by the current weight  $w$
    - ▶ draw a child number  $n(S, H_{li}) = 0, 1, \dots$
    - ▶ add  $n$  children with weight  $wr(n)$  to  $G$ .

back

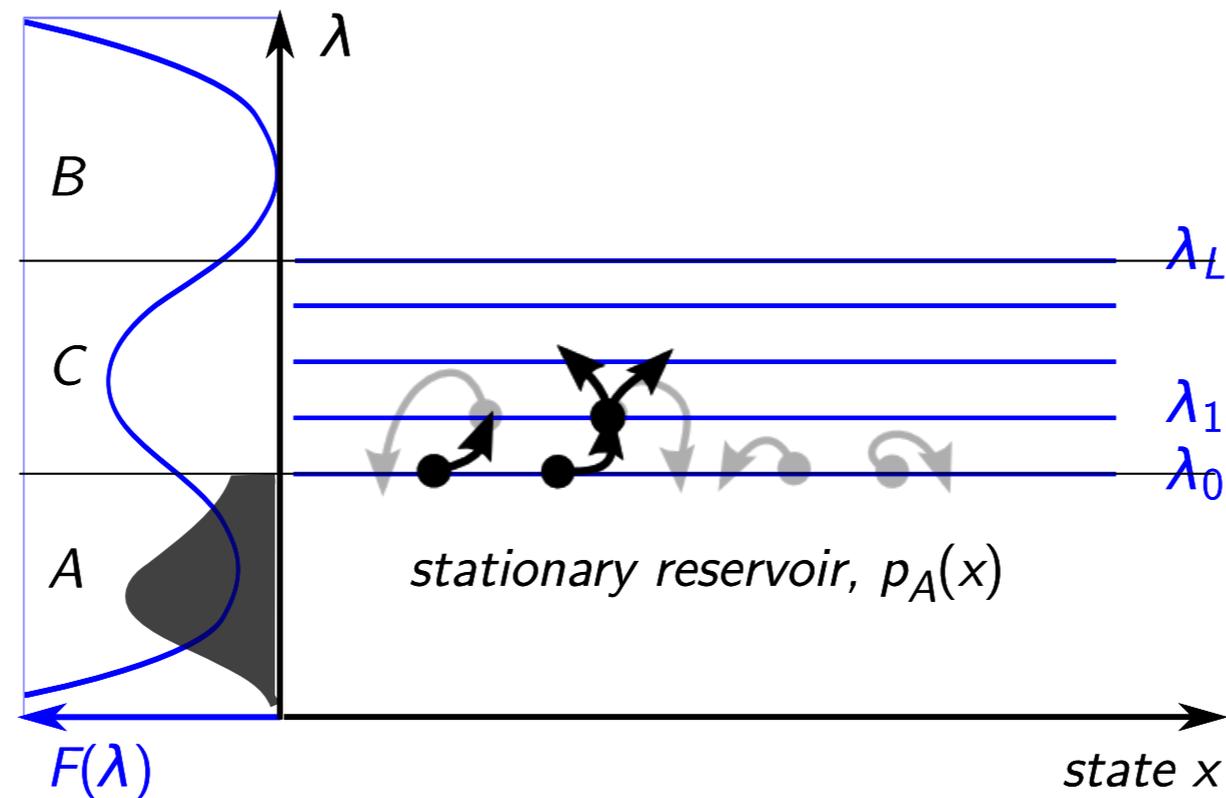
# Enhanced sampling in stationary state (FFS)



1. Simulate stationary distribution in  $A$  once and for all
2. Shoot short trajectories from each interface to the next

*Allen et al, JCP 2006*

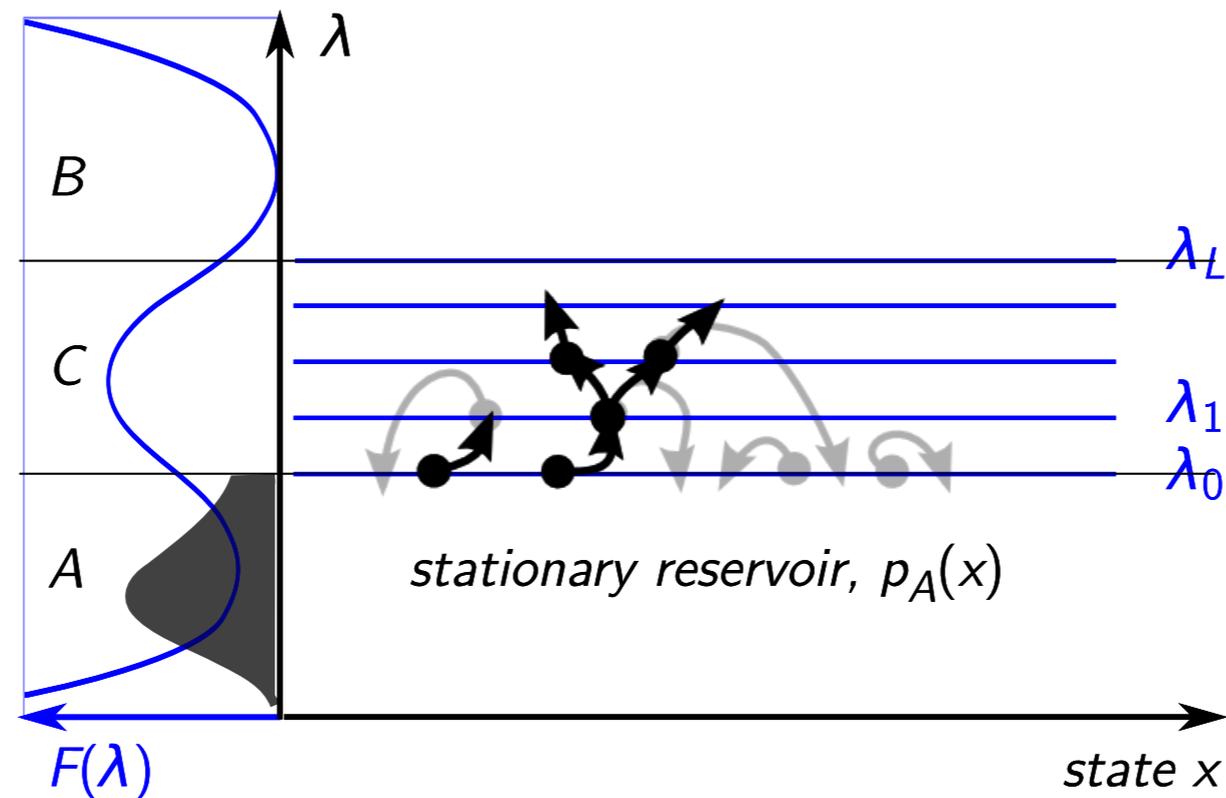
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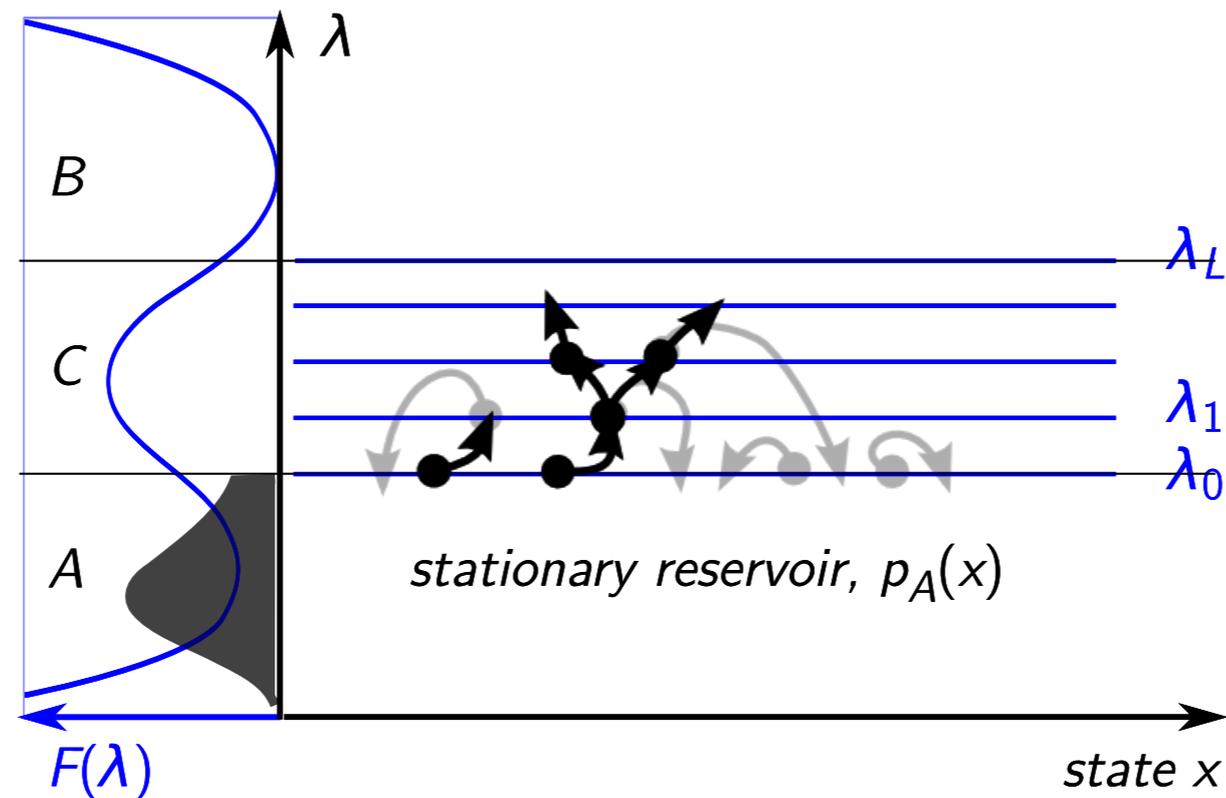
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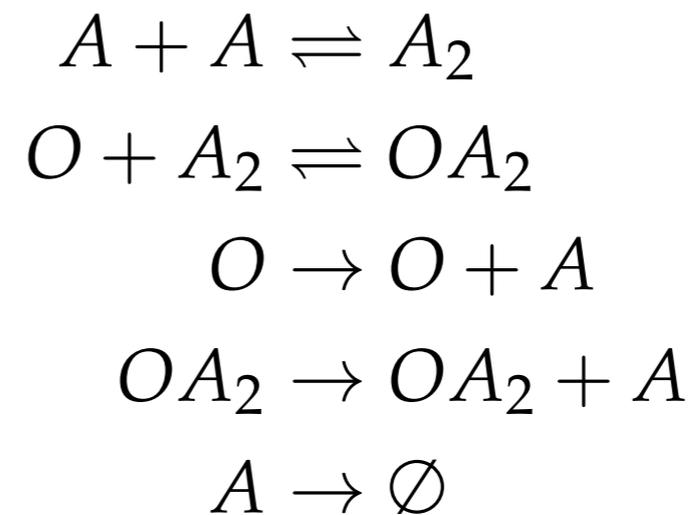
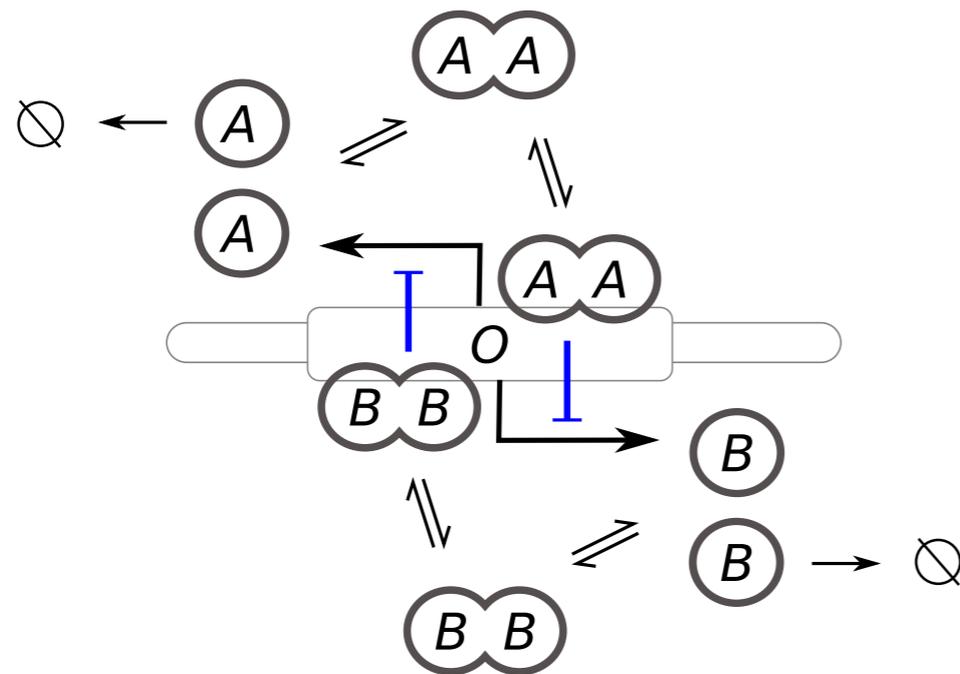


1. Simulate stationary distribution in  $A$  once and for all
2. Shoot short trajectories from each interface to the next



*Allen et al, JCP 2006*

# The toggle switch



- Toy model of the phage- $\lambda$  genetic switch.
- Progress coordinate: total  $B$  monomers - total  $A$  monomers

$$\lambda = [B] + 2[B_2] + 2[OB_2] - ([A] + 2[A_2] + 2[OA_2])$$

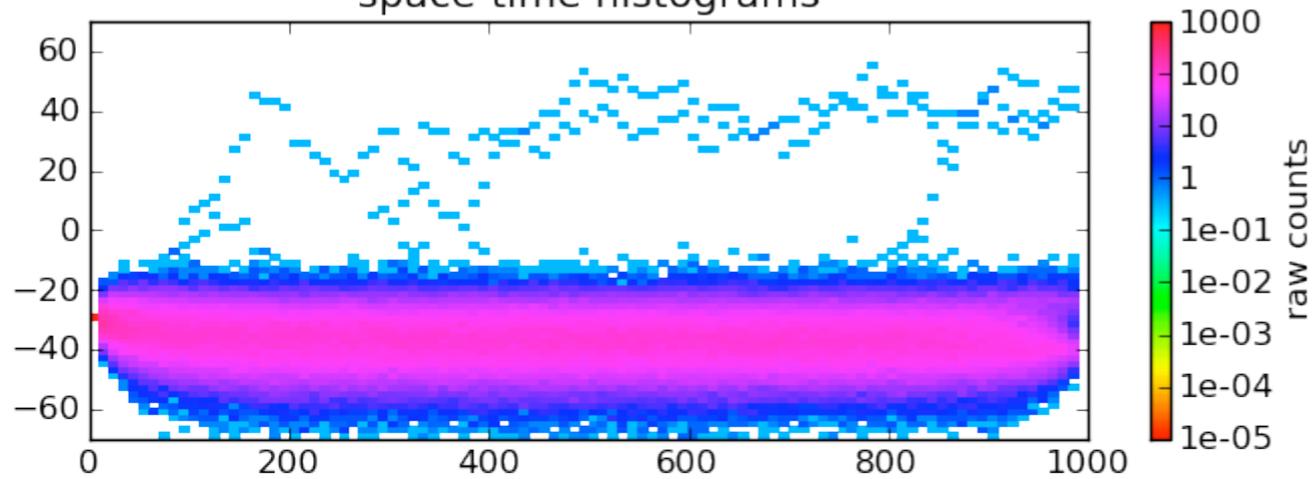
*e.g. Allen et al, JCP 2006*

# Spontaneous transitions

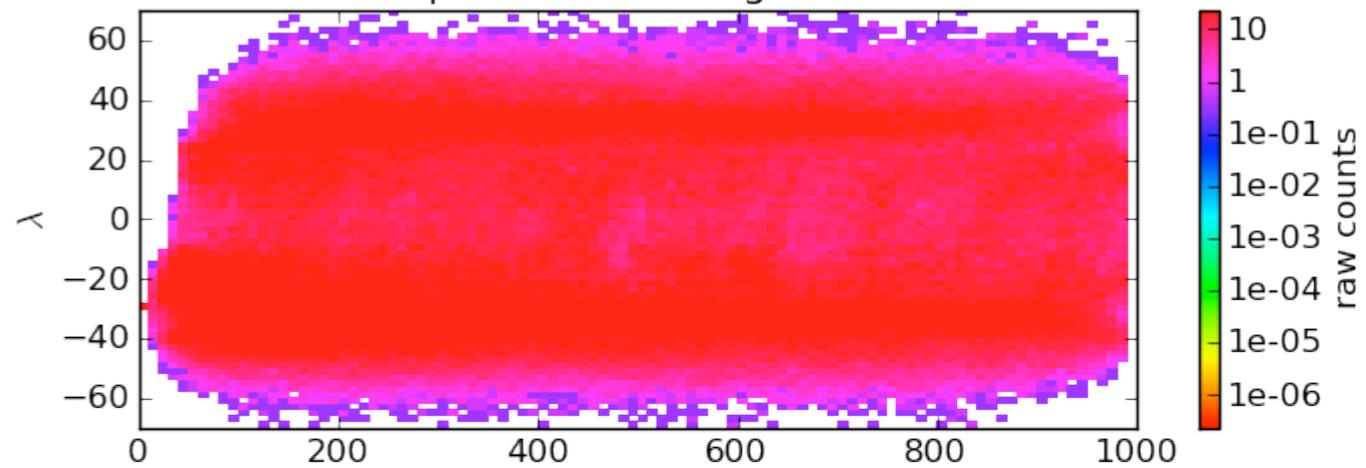
brute force

NS-FFS

space-time histograms



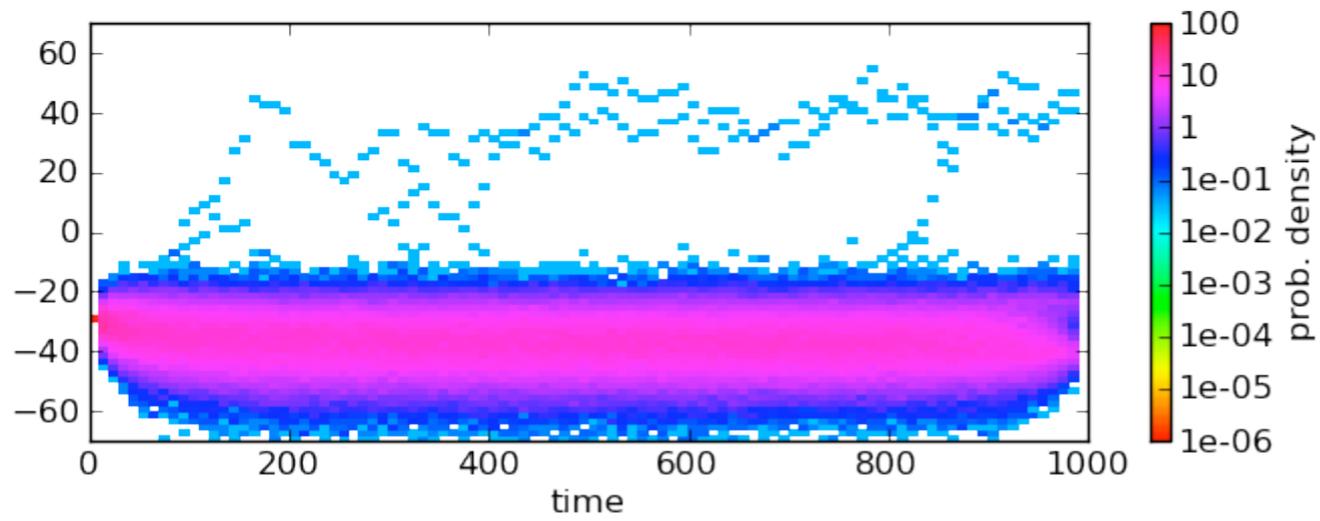
space-time histograms



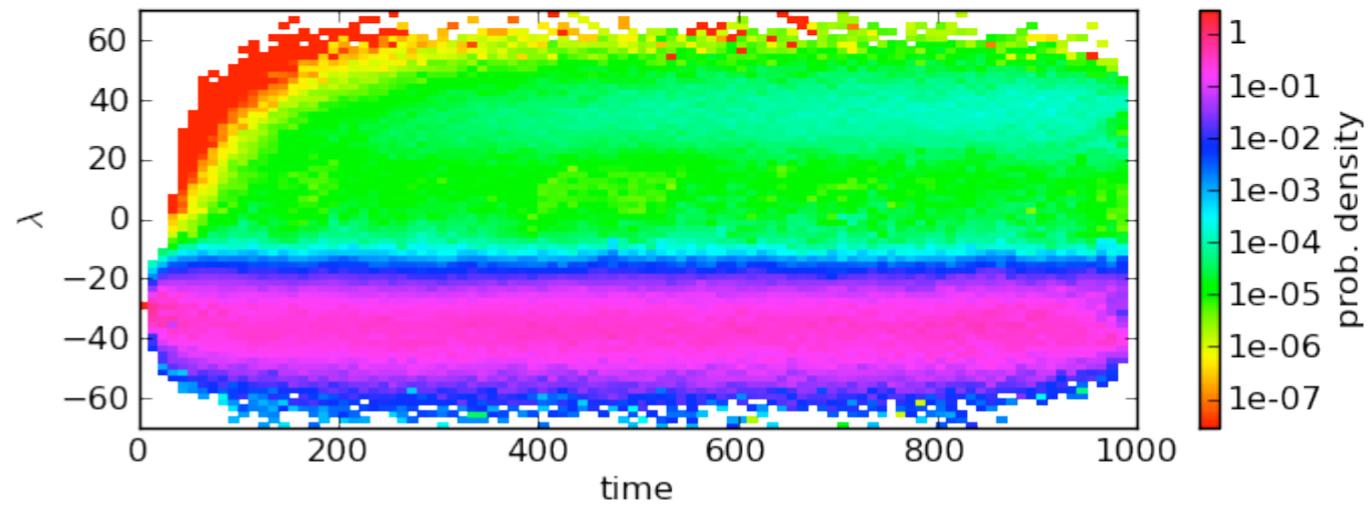
$\text{Prob}(\text{flipped until } t = 800) = .07\%$

# Spontaneous transitions

brute force

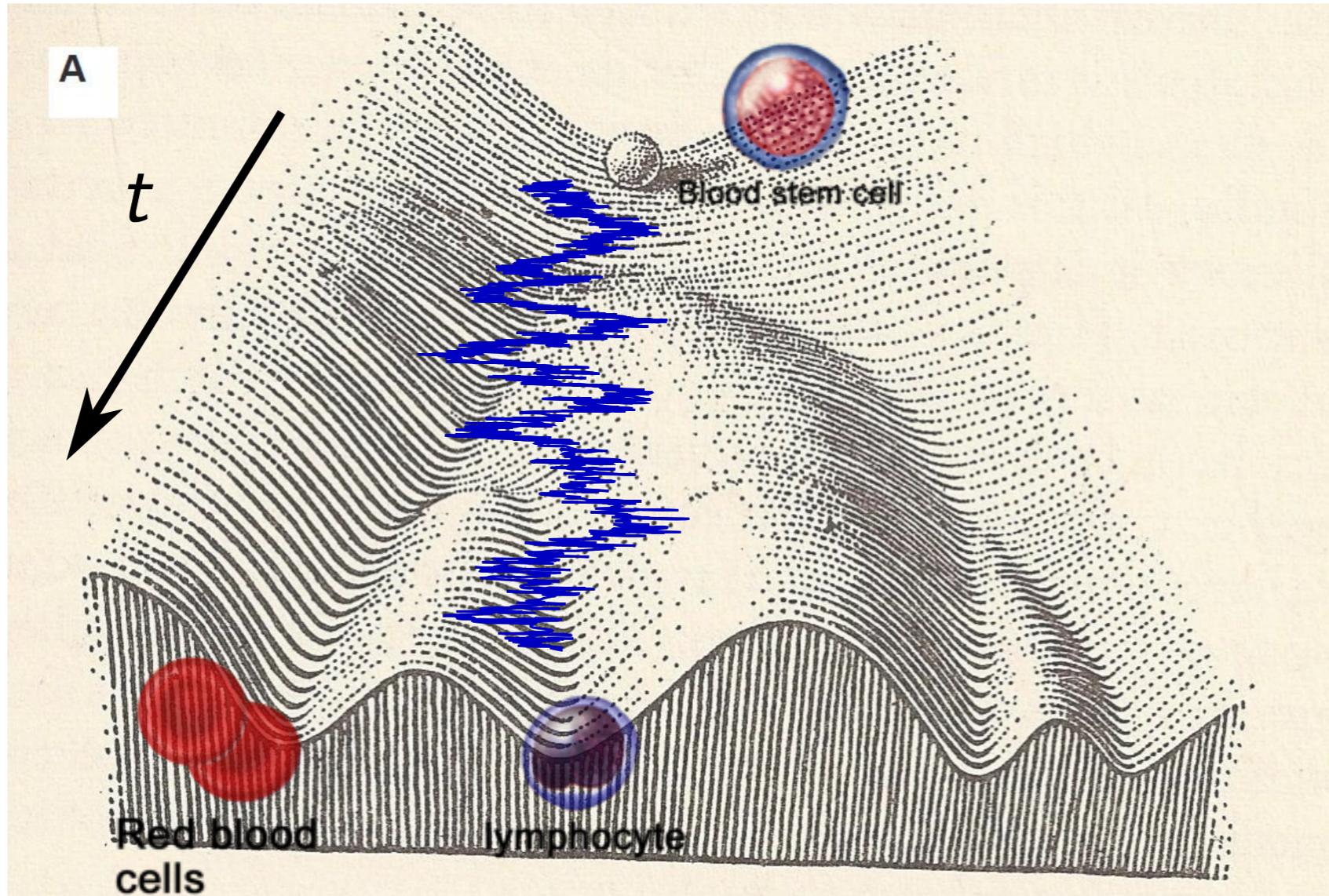


NS-FFS



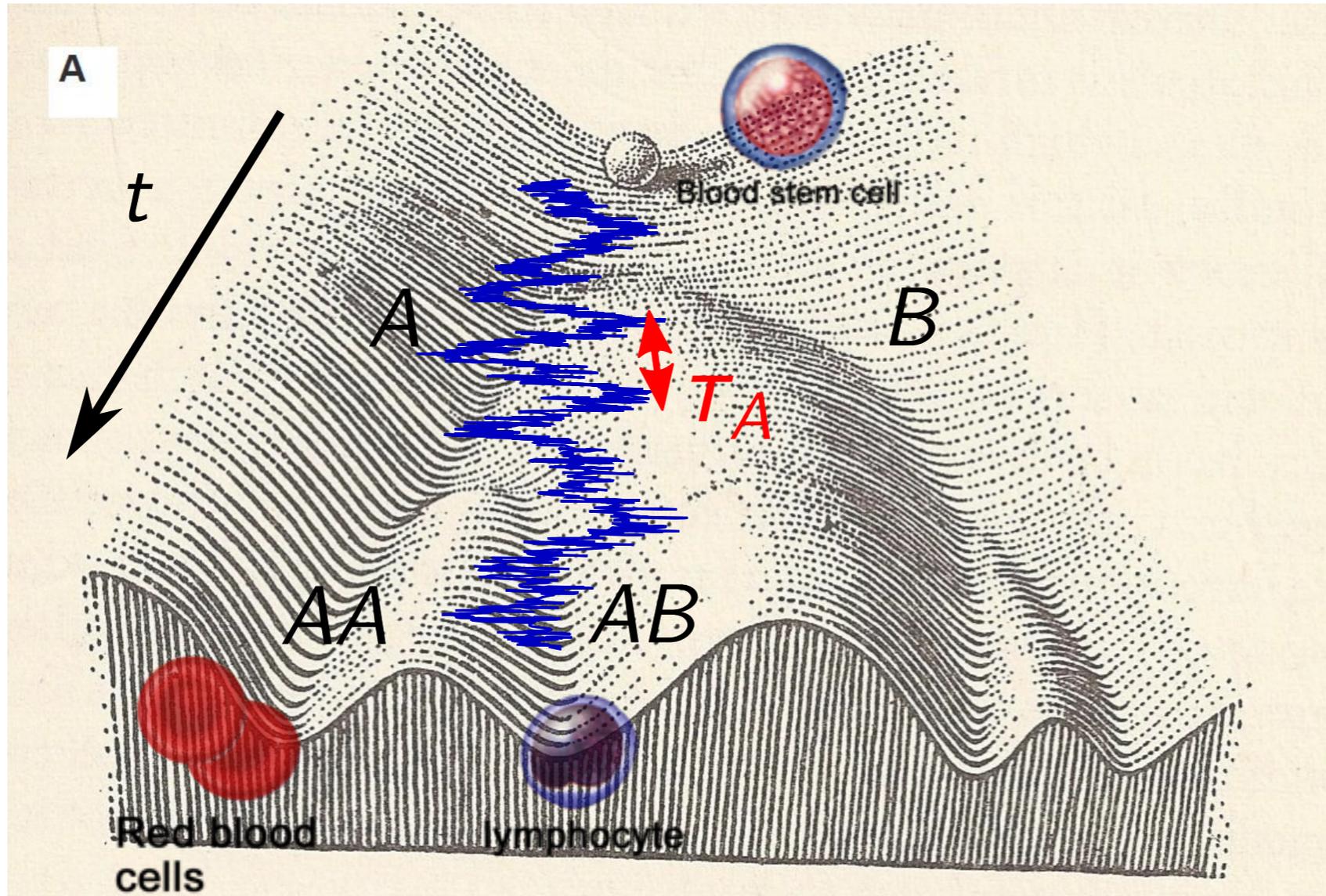
Prob(flipped until  $t = 800$ ) = .07%

# Outlook



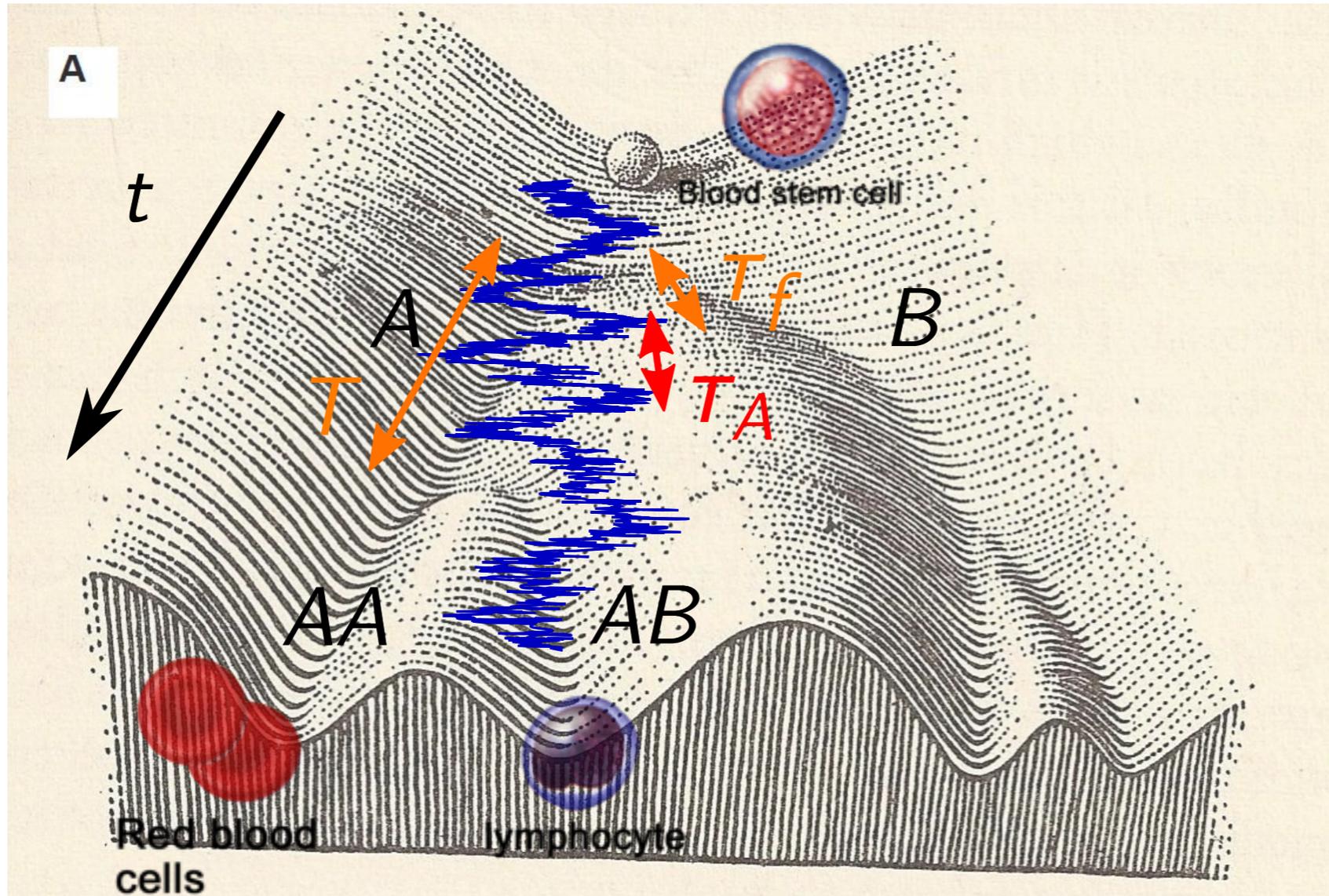
*Waddington (1940s), e.g. S. Huang, Cell & Molecular Biology (2011)*

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