

Stochastic Thermodynamics and Thermodynamics of Information

Lecture V: Stochastic thermodynamics in biological
systems

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May 18, 2018

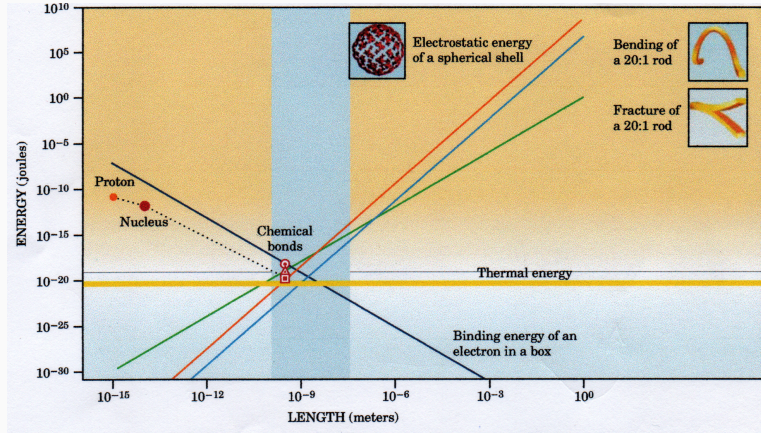
Statistical Physics, SISSA and SMRI (Italy)



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3. Molecular motors
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5. Summary

Energy scale vs. length scale

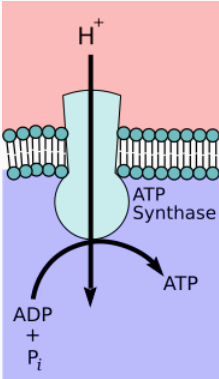
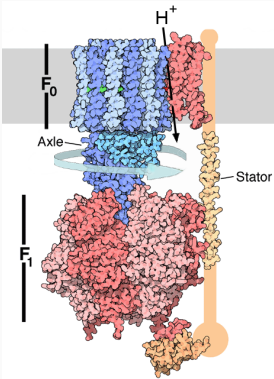


□: hydrogen bond; △: phosphate bond; ○: covalent bond

PHILLIPS AND QUAKE, 2006

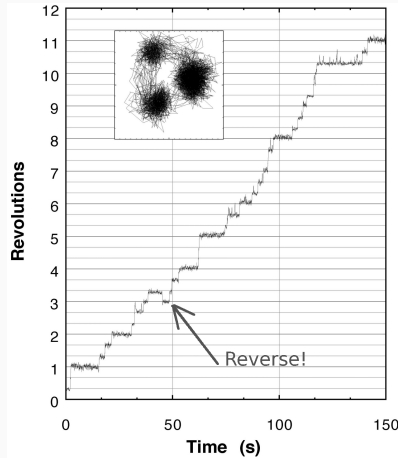
A rotary motor: ATP synthase

YASUDA ET AL., 2002



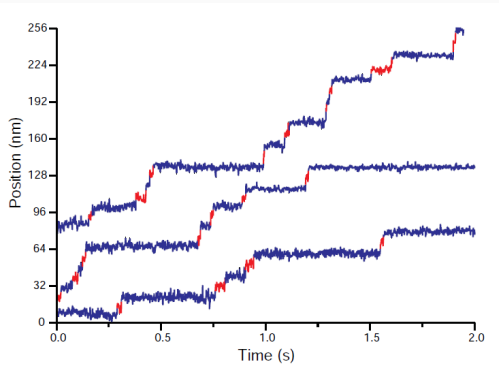
A rotary motor: ATP synthase

YASUDA ET AL., 2002



ATP Synthase motion is *reversible*: ATP degradation \rightarrow proton gradient

A processing motor: kinesin



FEHR, ASBURY AND BLOCK, 2008

A signalling network

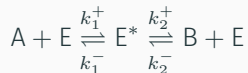


MA, BUER AND ZENG, 2004

Passive catalysis

Formalism developed in a simple case

- Enzyme E catalyzing the isomerization:



- Define $\epsilon^* = \epsilon_{E^*} - \epsilon_E$
- Ratios of reaction rates:

$$\frac{k_1^+}{k_1^-} = e^{-(\epsilon^* - \epsilon_A)/k_B T} \quad \frac{k_2^+}{k_2^-} = e^{(\epsilon^* - \epsilon_B)/k_B T}$$

- Therefore

$$\frac{k_1^+ k_2^+}{k_1^- k_2^-} = e^{-(\epsilon_B - \epsilon_A)/k_B T}$$

Passive catalysis

- Set

$$\begin{aligned}k_1^+ &= \omega_1 e^{-(\epsilon^* - \epsilon_A)/k_B T} & k_1^- &= \omega_1 \\k_2^+ &= \omega_2 & k_2^- &= \omega_2 e^{-(\epsilon^* - \epsilon_B)/k_B T}\end{aligned}$$

- Rate equations (average):

$$\begin{aligned}\frac{d\langle n \rangle}{dt} &= k_2^+ [E^*] - k_2^- [E][B] \\ \frac{d[E^*]}{dt} &= k_1^+ [E][A] + k_2^- [E][B] - (k_1^- + k_2^+) [E]\end{aligned}$$

- Production of B-molecules vanishes at equilibrium:

$$\frac{[B]}{[A]} = \frac{k_1^+ k_2^+}{k_1^- k_2^-} = e^{-(\epsilon_B - \epsilon_A)/k_B T}$$

i.e.

$$[A] e^{-\epsilon_A/k_B T} = [B] e^{-\epsilon_B/k_B T}$$

Master equation

Beyond the rate equations:

- Number of B-molecules synthesized: n
- Enzyme free (0) or bound (1)
- Chemostats fix $[A]$ and $[B]$
- Master equation for p_{in} , $i \in \{0, 1\}$, $n \in \mathbb{Z}$

$$\begin{aligned}\frac{dp_{0n}}{dt} &= k_1^- p_{1n} + k_2^+ p_{1,n-1} - (k_1^+ [A] + k_2^- [B]) p_{0n} \\ \frac{dp_{1n}}{dt} &= k_1^+ [A] p_{0n} + k_2^- [B] p_{0,n+1} - (k_1^- + k_2^+) p_{1n}\end{aligned}$$

Non-equilibrium steady state

Chemostat [A] and [B] away from the equilibrium values:

$$[A] e^{-\epsilon_A/k_B T} \neq [B] e^{-\epsilon_B/k_B T}$$

Free-energy imbalance:

$$\Delta G = \epsilon_B - k_B T \log[B] - (\epsilon_A - k_B T \log[A]) = k_B T \log \frac{k_1^+ k_2^+ [A]}{k_1^- k_2^- [B]}$$

Steady-state probability of charged enzyme:

$$p_1 = \frac{k_1^+ [A] + k_2^- [B]}{k_1^- - k_1^+ [A] + k_2^+ - k_2^- [B]}$$

Net production rate (cf. rate equation):

$$\frac{d \langle n \rangle}{dt} = \frac{k_1^+ k_2^+ [A] - k_1^- k_2^- [B]}{k_1^- - k_1^+ [A] + k_2^+ - k_2^- [B]}$$

Large deviations

Generating function:

$$\Psi_\alpha(\mu, t) = \sum_{n=-\infty}^{+\infty} e^{\mu(n+\alpha/2)} p_{\alpha,n}(t) \quad \alpha \in \{0, 1\}$$

Evolution equation:

$$\frac{d}{dt} \begin{pmatrix} \Psi_0 \\ \Psi_1 \end{pmatrix} = \mathcal{L}(z) \begin{pmatrix} \Psi_0 \\ \Psi_1 \end{pmatrix} \quad z = e^{\mu/2}$$

$$\mathcal{L}(z) = \begin{pmatrix} -(k_1^+[A] + k_2^-[B]), & z^{-1}k_1^- + zk_2^+ \\ zk_1^+[A] + z^{-1}k_2^-[B], & -(k_1^- + k_2^+) \end{pmatrix}$$

$$\Psi \sim e^{t\theta(\mu)} \quad \theta(\mu) : \text{largest e.v. of } \mathcal{L}$$

Large deviations

Distribution function of n : $P(n, t) = e^{-t\omega(J)}$, $J = n/t$

$$\theta(\mu) = \max_J (\mu J - \omega(J))$$

E.v.'s of $\mathcal{L}(z)$ depend only on $z^{-2}k_1^+k_2^+[\text{A}] + z^2k_1^-k_2^-[\text{B}]$

Gallavotti-Cohen symmetry: $z \rightarrow \bar{z}$:

$$\bar{z}^{-2}k_1^-k_2^-[\text{B}] = z^2k_1^+k_2^+[\text{A}] \quad \Leftrightarrow \quad \mu \rightarrow \bar{\mu} = \Delta G/k_{\text{B}}T - \mu$$

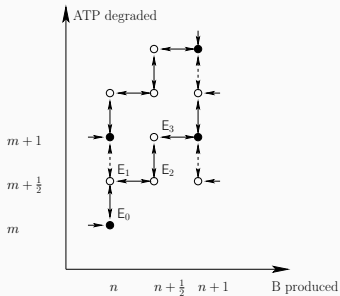
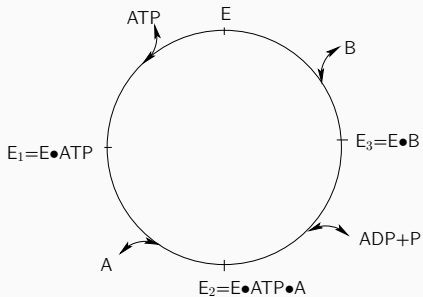
$$\theta(\mu) = \theta(\Delta G/k_{\text{B}}T - \mu)$$

$$J(\mu) = -J(\Delta G/k_{\text{B}}T - \mu)$$

$$\omega(J) - \omega(-J) = J \Delta G/k_{\text{B}}T = \dot{S}$$

Active catalysis

Reaction scheme: $\text{ATP} + \text{A} \rightleftharpoons \text{ADP} + \text{P} + \text{B}$



Rate equations

$$\begin{aligned}\frac{d[E]}{dt} &= k_4^+ [E_3] + k_1^- [E_1] - k_1^+ [E][ATP] - k_4^- [E][B] \\ \frac{d[E_1]}{dt} &= k_1^+ [E][ATP] + k_2^- [E_2] - k_1^- [E_1] - k_2^+ [E_1][A] \\ \frac{d[E_2]}{dt} &= k_2^+ [E_1][A] + k_3^- [E_3][ADP][P] - (k_2^- + k_3^+) [E_2] \\ \frac{d[E_3]}{dt} &= k_3^+ [E_2] + k_4^- [E][B] - (k_4^+ + k_3^- [ADP][P]) [E_3]\end{aligned}$$

Detailed balance:

$$\begin{aligned}\frac{k_i^+}{k_i^-} &= e^{-\Delta\epsilon_i/k_B T} \\ \frac{k_1^+ k_2^+ k_3^+ k_4^+}{k_1^- k_2^- k_3^- k_4^-} &= e^{-(\Delta\epsilon_A + \Delta\epsilon_{ATP})/k_B T}\end{aligned}$$

$$\Delta\epsilon_A = \epsilon_B - \epsilon_A$$

$$\Delta\epsilon_{ATP} = \epsilon_{ADP} + \epsilon_P - \epsilon_{ATP}$$

Generating function

$$\frac{\partial \Psi_0}{\partial t} = k_4^+ e^{\mu_1/2} \Psi_3 + k_1^+ e^{-\mu_2/2} \Psi_1 - (k_1^+ [\text{ATP}] + k_4^-) \Psi_0$$

$$\frac{\partial \Psi_1}{\partial t} = k_1^+ [\text{ATP}] e^{\mu_2/2} \Psi_0 + k_2^- e^{-\mu_1/2} \Psi_2 - (k_1^- + k_2^+ [\text{A}]) \Psi_1$$

$$\frac{\partial \Psi_2}{\partial t} = k_2^+ [\text{A}] e^{\mu_1/2} \Psi_1 + k_3^- [\text{ADP}][\text{P}] e^{-\mu_2/2} \Psi_3 - (k_2^- + k_3^+) \Psi_2$$

$$\frac{\partial \Psi_3}{\partial t} = k_3^+ e^{\mu_2/2} \Psi_2 + k_4^- [\text{B}] e^{-\mu_1/2} \Psi_0 - (k_4^- + k_3^+ [\text{ADP}][\text{P}]) \Psi_3$$

$$\frac{\partial \Psi}{\partial t} = \mathcal{L}_\mu \Psi,$$

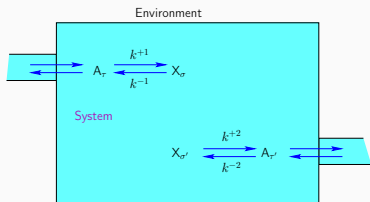
The Gallavotti-Cohen symmetry involves the simultaneous change of μ_1, μ_2 :

$$\mathcal{L}_{\bar{\mu}} = \mathbf{Q}^{-1} \mathcal{L}_\mu^\dagger \mathbf{Q}$$

$$e^{\bar{\mu}_1} = \frac{k_2^- k_4^- [\text{B}]}{k_2^+ k_4^+ [\text{A}]} e^{-\mu_1}$$

$$e^{\bar{\mu}_2} = \frac{k_1^- k_3^- [\text{ADP}][\text{P}]}{k_1^+ k_3^+ [\text{ATP}]} e^{-\mu_2}$$

Chemical Reaction Network:



$$\sum_{\sigma} \nabla_{+\rho}^{\sigma} X_{\sigma} + \sum_{\tau} \nabla_{+\rho}^{\tau} A_{\tau} \xrightleftharpoons[k^{+\rho}]{k^{-\rho}} \sum_{\sigma} \nabla_{-\rho}^{\sigma} X_{\sigma} + \sum_{\tau} \nabla_{-\rho}^{\tau} A_{\tau}$$

Stoichiometric matrix:

$$\begin{aligned} \nabla_{\pm\rho} &= (\nabla_{\pm\rho}^{\sigma,\tau}) & \nabla_{\pm\rho}^{\sigma,\tau} &\in \mathbb{N} \\ \nabla_{\rho} &= \nabla_{-\rho} - \nabla_{+\rho} & \nabla_{\rho}^{\sigma,\tau} &\in \mathbb{Z} \end{aligned}$$

Chemical species: $X = (X_{\sigma})$, $A = (A_{\tau})$

X_{σ} : intermediate A_{τ} : chemostatted

Transitions

Elementary transitions:

$$X \xrightarrow{\pm\rho} X' : \quad X' - X = \pm\nabla_\rho$$

Mass-action law:

$$R_{X'X}^{\pm\rho} = \delta_{X', X \mp \nabla_\rho} \Omega k_{\pm\rho} \prod_{\tau} [A_\tau]^{\nu_{\pm\rho}^\tau} \\ \times \prod_{\sigma} \left(\frac{X^\sigma}{\Omega} \frac{X^\sigma - 1}{\Omega} \dots \frac{X^\sigma - \nabla_{\pm\rho}^\sigma + 1}{\Omega} \right)$$

Master equation:

$$\frac{dp_X}{dt} = \sum_{\epsilon=\pm 1} \sum_{\rho} [R_{XX'}^{\epsilon\rho} p_{X'} - R_{X'X}^{-\epsilon\rho} p_X] = (\mathcal{L}p)_X$$

Steady state $p^{\text{ss}}(X)$ (not trivial to evaluate)

Average entropy production

Entropy of a state p_X :

$$S(P) = \underbrace{\sum_X S^{(0)}(X)p_X}_{\text{"internal"}} - \underbrace{k_B \sum_X p_X \log p_X}_{\text{Shannon}}$$

Total average entropy production:

$$\dot{S}^{\text{tot}} = \frac{dS}{dt} - \frac{dS^{(r)}}{dt}$$

$$J_\rho(X; t) = R_{X', X}^\rho p_X - R_{X X'}^{-\rho} p_{X'}$$

$$A_\rho(X; t) = k_B \log \frac{R_{X X'}^\rho p_{X'}}{R_{X', X}^{-\rho} p_X}$$

$$-\frac{dS^{(r)}}{dt} = \underbrace{\sum_{X, \rho} S^{(0)}(X) J_\rho(X; t)}_{\text{advection}} - \underbrace{\frac{1}{2} \sum_{X, \rho} J_\rho(X; t) \log \frac{R_{X X'}^\rho}{R_{X', X}^{-\rho}}}_{\text{Heat flow } Q/T}$$

$$\dot{S}^{\text{tot}} = \frac{1}{2} \sum_{X, \rho} J_\rho(X; t) A_\rho(X; t) \geq 0$$

Fluctuation relation

- Trajectory:

$$\mathbf{X} = (X(t)) = (X_0, t_0) \xrightarrow{\rho_1} (X_1, t_1) \xrightarrow{\rho_2} \dots \xrightarrow{\rho_n} (X_n, t_n) \rightarrow t_f$$

- Time-reversed trajectory $\hat{\mathbf{X}}$
- Probability density of a path $\mathcal{P}(\mathbf{X})$
- Detailed fluctuation relation:

$$\frac{\mathcal{P}(\mathbf{X}|X_0)}{\mathcal{P}(\hat{\mathbf{X}}|X_f)} = \prod_{k=1}^n \frac{R_{X_k X_{k-1}}}{R_{X_{k-1} X_k}} = e^{Q(\mathbf{X})/k_B T}$$

- $Q/T \neq -\Delta S^{(r)}$ because of the advection term
- Integral fluctuation relation:

$$\frac{\mathcal{P}(\mathbf{X})}{\mathcal{P}(\hat{\mathbf{X}})} = e^{(Q(\mathbf{X}) - \Delta S(\mathbf{X}))/k_B T}$$

- ΔS cancels the advection term...

Thus

$$\left\langle e^{-(Q - \Delta S)/k_B T} \right\rangle = 1$$

Generating function

Define

$$\Psi_X(\mu; t) = \int d\mathbf{X} \mathcal{P}^{\text{ss}}(\mathbf{X}) \delta_{X(t)X} e^{-\mu Q(\mathbf{X})/k_B T}$$

it satisfies

$$\Psi_X(\mu; t_0) = p_X^{\text{ss}}$$

$$\frac{\partial \Psi_X}{\partial t} = (\mathcal{L} \Psi)_X - \sum_{\rho} \sum_{X' (\neq X)} ' \left(\frac{R_{XX'}^{\rho}}{R_{X'X}^{-\rho}} \right)^{\mu} \Psi_{X'} = (\mathcal{L}_{\mu} \Psi)_X$$

Therefore

$$\Psi \underset{t \rightarrow \infty}{\sim} e^{-t \theta(\mu)}$$

where

$$\theta(\mu) = -\log \Lambda_{\max}(\mathcal{L}_{\mu})$$

Gallavotti-Cohen symmetry

We have of course

$$\mathcal{P}^{\text{ss}}(\mathbf{X}) \left(\frac{\mathcal{P}^{\text{ss}}(\hat{\mathbf{X}})}{\mathcal{P}^{\text{ss}}(\mathbf{X})} \right)^\mu = \mathcal{P}^{\text{ss}}(\hat{\mathbf{X}}) \left(\frac{\mathcal{P}^{\text{ss}}(\mathbf{X})}{\mathcal{P}^{\text{ss}}(\hat{\mathbf{X}})} \right)^{1-\mu} = \mathcal{P}^{\text{ss}}(\mathbf{X}) \left(\frac{\mathcal{P}^{\text{ss}}(\mathbf{X})}{\mathcal{P}^{\text{ss}}(\hat{\mathbf{X}})} \right)^{1-\mu}$$

which implies the Gallavotti-Cohen symmetry:

$$\theta(\mu) = \theta(1 - \mu)$$

The large-deviation (Cramér) function $\omega(s)$ is defined by

$$\text{Prob}(Q, t) \underset{t \rightarrow \infty}{\sim} e^{-t\omega(s)}, \quad \frac{Q}{k_B T} = s t$$

since

$$\int dQ \text{Prob}(Q, t) e^{-\mu Q/k_B T} = \sum_X \Psi_X(\mu; t) \sim e^{-t\theta(\mu)}$$

we have (if the saddle-point integration can be inverted!)

$$\omega(s) = \max_{\mu} (\theta(\mu) - \mu s)$$

and $\omega(s) - \omega(-s) = -s$

Simulation of chemical reactions

Chemical reaction rates with a given number of particles:

$$\sum_{\sigma} \nabla_{+\rho}^{\sigma} X_{\sigma} + \sum_{\tau} \nabla_{+\rho}^{\tau} A_{\tau} \xrightleftharpoons[k_{+\rho}]{k_{-\rho}} \sum_{\sigma} \nabla_{-\rho}^{\sigma} X_{\sigma} + \sum_{\tau} \nabla_{-\rho}^{\tau} A_{\tau}$$

Rates for reaction $\rho (= \pm\rho)$:

$$R_{X'X}^{\rho} = \delta_{X', X + \nabla_{\rho}} \Omega k_{\rho} \prod_{\tau} [A_{\tau}]^{\nu_{\rho}^{\tau}} \\ \times \prod_{\sigma} \left(\frac{X^{\sigma}}{\Omega} \frac{X^{\sigma} - 1}{\Omega} \dots \frac{X^{\sigma} - \nabla_{\rho}^{\sigma} + 1}{\Omega} \right)$$

Simulation of chemical reactions

Simulation algorithm:

GILLESPIE, 1976, 1977

1. Given the time t number $\{n_\sigma\}$ of all species involved, evaluate the rates R_ρ of all possible reactions
2. Define $R = \sum_\rho R_\rho$ and extract the time τ to the next reaction, exponentially distributed with average R^{-1} : update t to $t + \tau$
3. Choose the next reaction ρ^{next} with probability R_ρ/R
4. Change the number of the affected species according to the stoichiometry of the reaction ρ^{next} and return to step 1

Difficulties:

- The number of possible reactions can become large
- Thus τ can become too small—simulation sluggish!
- Several tricks have been invented to speed up the simulation, at some cost in precision

Simulation of chemical reactions

```
# Schlögl model (1972)

FIX: A B

# Reactions
R1:
  A + {2} X > {3} X
  1/2*c1*A*X*(X-1)

R2:
  {3} X > A + {2} X
  1/6*c2*X*(X-1)*(X-2)

R3:
  B > X
  c3 * B

R4:
  X > B
  c4*X

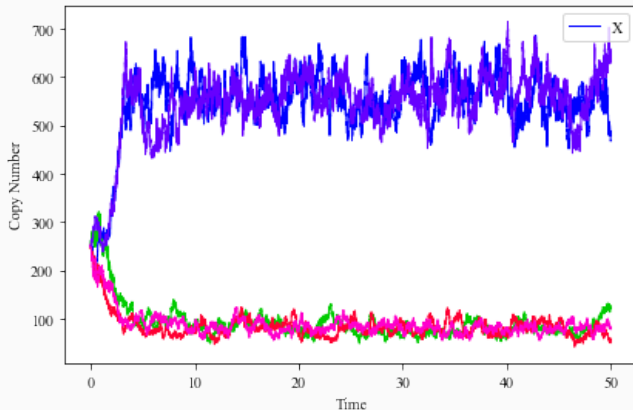
# Fixed species
A = 100000
B = 200000

# Variable species
X = 250

c1 = 3*10**-7
c2 = 10**-4
c3 = 10**-3
c4 = 3.5
```

Simulation of chemical reactions

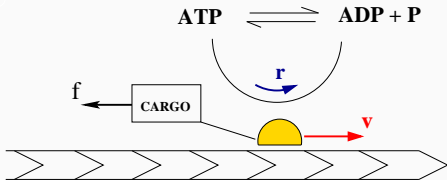
Python module: `stochpy`



Fluctuation Theorem for molecular motors

GASPARD, 2006; LACOSTE, LAU AND MALLICK, 2008

A model of a molecular motor:



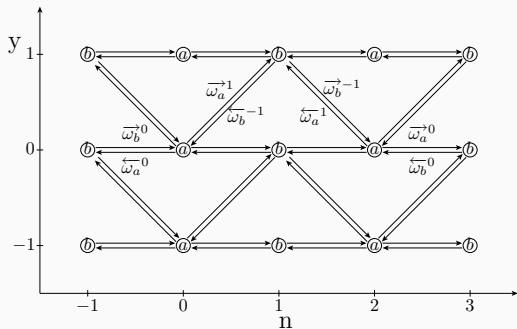
The motor is kept in a nonequilibrium state by the chemical imbalance of the $\text{ATP} \rightleftharpoons \text{ADP} + \text{P}$ reaction:

$$\frac{[\text{ATP}]}{[\text{ADP}][\text{P}]} \neq e^{(\epsilon_{\text{ATP}} - \epsilon_{\text{ADP}} - \epsilon_{\text{P}})/k_{\text{B}}T}$$

The “product” is displacement

The model

NISHINARI ET AL., 2005 *et al.*



States:

1: Bound to ATP

2: Bound to ADP or empty

Moves:

Brownian motion: $(i, 2) \xrightarrow{\omega_B} (i \pm 1, 2)$

ATP binding: $(i, 2) \xrightarrow{\omega_s} (i, 1)$

Ratchet: $(i, 1) \xrightarrow{\omega_+} (i + 1, 2)$

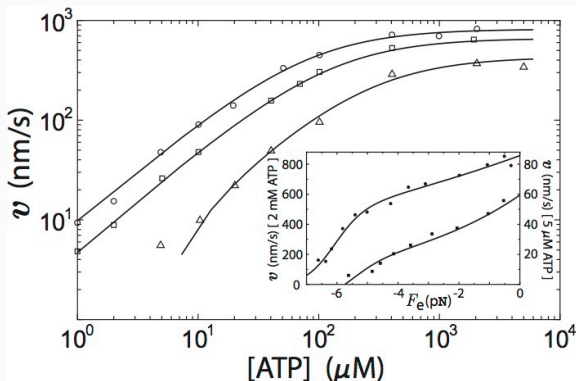
Reverse ratchet: $(i, 2) \xrightarrow{\omega_-} (i - 1, 1)$

Hydrolysis: $(i, 1) \xrightarrow{\omega_h} (i, 2)$

Rates $\omega = \{\omega(f, \Delta\mu)\}$ with a few measurable and 4 adjustable kinetic parameters, constrained by a thermodynamic relation

Application to kinesin

LACOSTE, LAU AND MALLICK, 2008



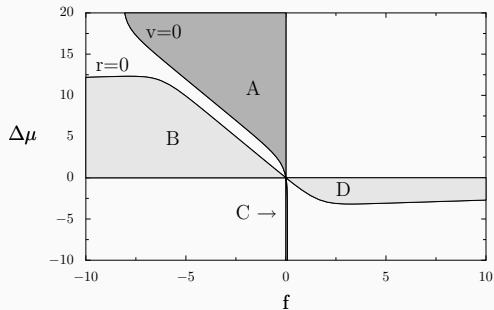
Data from SCHNITZER AND BLOCK, 1995

Lines for $f = -1.05, -3.59, -5.63$ pN

Inset: v vs. f for fixed $[ATP]$ 2 μM 5 μM

The phase diagram

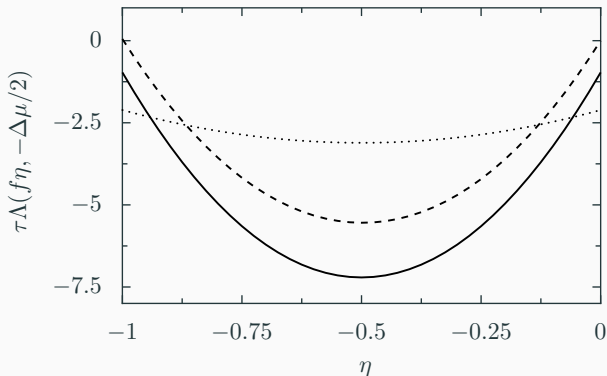
LACOSTE, LAU AND MALLICK, 2008



v : average velocity r : average ATP consumption rate

Modes: A: ATP consumed, work performed; B: work consumed to produce ATP

C: ADP consumed to produce work; D: Work consumed to produce ADP



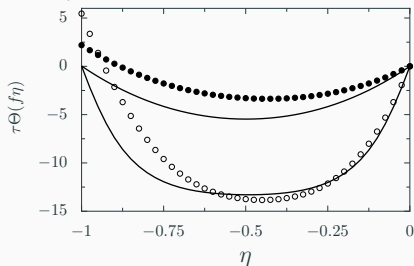
Normalized eigenvalue of $\mathcal{L}_{(fd/k_B T)\eta, -\Delta\mu/2k_B T}$ vs. η (parameter of the generating function) for various values of $(fd/k_B T, \Delta\mu/k_B T)$: (5, 0) (dashed), (5, 10) (solid), (2, 10) (dotted)

Comments

- The Gallavotti-Cohen symmetry appears in the pdf of the fluxes v, r :

$$\ln \frac{P(v, r, \mathcal{T})}{P(-v, -r, \mathcal{T})} \sim \underbrace{[(f/k_B T)v + (\Delta\mu/k_B T)r] \mathcal{T}}_{\text{entropy production}}$$

- The *reduced* distribution $P_i(n, t) = \sum_y P_i(n, y, t)$ does not exhibit the symmetry:



Lack of symmetry hints at the existence of hidden dynamical variables

Information processing

Information processing in the cell:

Copy: Transcription (DNA→RNA), Replication (DNA→DNA)

Translation: DNA→Proteins

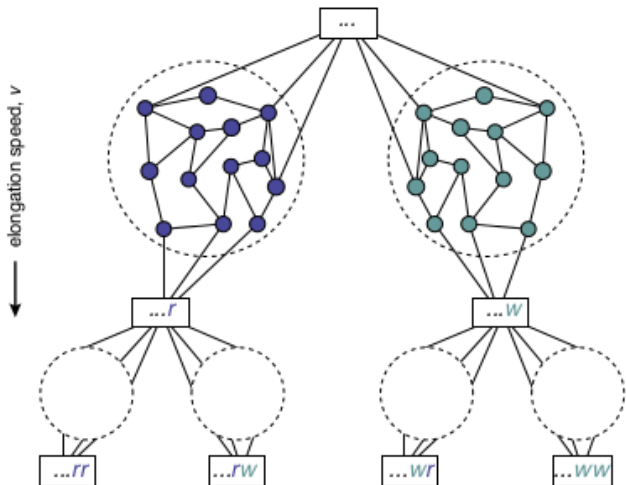
tRNA aminoacylation: The “interpreters” of the genetic code are tRNA, carrying the *anticodon* on one side and the corresponding amino acid on the other. Amino acids are charged by *activation enzymes*

Sensing: All processes which monitor the environment

“High fidelity” is a requirement

Template-assisted polymerization

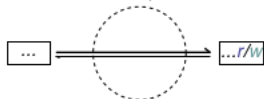
General transition network



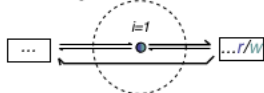
Template-assisted polymerization

Examples

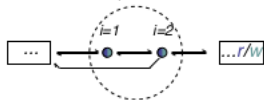
No intermediate states, $n=0$



Proofreading, $n=1$



mRNA translation, $n=2$



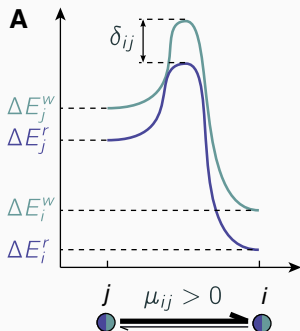
elongation speed, $v \longrightarrow$

- Elongation speed v
- Error rate η
- Rate of “right” incorporations:
 $v^r = (1 - \eta) v$
- Rate of “wrong” incorporations: $v^w = \eta v$
- Equation for the error η :

$$\frac{\eta}{1 - \eta} = \frac{v^w(\eta)}{v^r(\eta)}$$

Reaction rates

Rates: μ_{ij} chemical driving, δ_{ij} kinetic barrier



B

$$k_{ij}^r = \omega_{ij} \exp[(\Delta E_j^r + \mu_{ij} + \delta_{ij})/T]$$

$$k_{ij}^w = \omega_{ij} \exp[(\Delta E_j^w + \mu_{ij})/T]$$

$$k_{ji}^r = \omega_{ij} \exp[(\Delta E_i^r + \delta_{ij})/T]$$

$$k_{ji}^w = \omega_{ij} \exp[\Delta E_i^w/T]$$

Dictionary: $k \rightarrow R$, $T \rightarrow k_B T$

Definitions

Definitions:

- Entropy produced per incorporated monomer: ΔS^{tot}
- Entropy produced per *wrong* incorporated monomer: $\Delta S^{\text{tot,w}}$

$$\Delta W = \sum_{(ij), \alpha \in \{r, w\}} J_{ij}^{\alpha} \mu_{ij} / v$$

$$\Delta F^{\text{eq}} = -k_B T \log \sum_{\alpha} e^{-\Delta E^{\alpha} / k_B T}$$

$$\eta^{\text{eq}} = \exp [(-\Delta E^w + \Delta F^{\text{eq}}) / k_B T]$$

$$D_{\text{KL}}(\eta \| \eta^{\text{eq}}) = \eta \log \frac{\eta}{\eta^{\text{eq}}} + (1 - \eta) \log \frac{1 - \eta}{1 - \eta^{\text{eq}}}$$

$$\Delta W^w = \sum_{(ij)} J_{ij}^w \mu_{ij} / v^w$$

Main results

In the steady state:

$$T\Delta S^{\text{tot}} = \Delta W - \Delta F^{\text{eq}} - k_B T D_{\text{KL}}(\eta \| \eta^{\text{eq}}) \geq 0$$
$$T\Delta S^{\text{tot,w}} = \Delta W^{\text{w}} - \Delta F^{\text{eq}} - k_B T \log \frac{\eta}{\eta^{\text{eq}}} \geq 0$$

Therefore

$$\eta = \eta^{\text{eq}} \exp \left[\frac{-\Delta S^{\text{tot,w}} + (\Delta W^{\text{w}} - \Delta F^{\text{eq}})}{k_B T} \right]$$

Possible copying regimes:

Error amplification: $\Delta W^{\text{w}} - \Delta F^{\text{eq}} > 0$ and $\eta > \eta^{\text{eq}}$

Demon: $\Delta W^{\text{w}} - \Delta F^{\text{eq}} < 0$ and $\eta < \eta^{\text{eq}}$ (but $\Delta W - \Delta F^{\text{eq}} > 0$
due to right matches)

Error correction: $\Delta W^{\text{w}} - \Delta F^{\text{eq}} > 0$ and $\eta < \eta^{\text{eq}}$, thus

$$\eta \geq \eta^{\text{eq}} e^{-\Delta S^{\text{tot,w}}/k_B}$$

Single-step polymerization machines

Two regimes:

Energetic discrimination: $\Delta E = \Delta E^w - \Delta E^r \geq \delta$

Kinetic discrimination: $\Delta E < \delta$

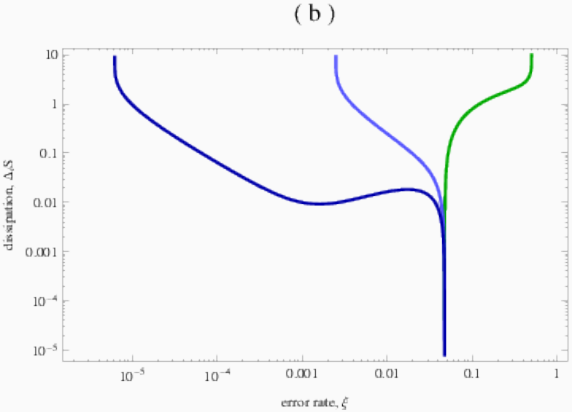
In energetic discrimination:

- $\eta \geq \eta^{\text{eq}}$ (error amplification)
- η monotonically *decreases* as v decreases, minimum error at zero dissipation

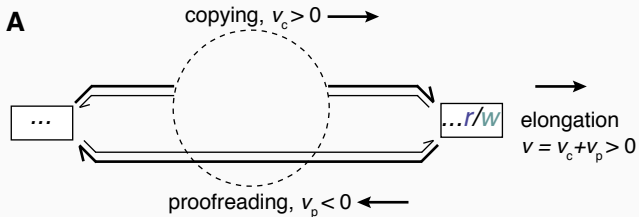
In kinetic discrimination:

- $\eta^{\text{eq}} \geq \eta \geq \eta^{\text{min}} = e^{-\delta/k_B T}$
- η decreases as v and dissipation increases

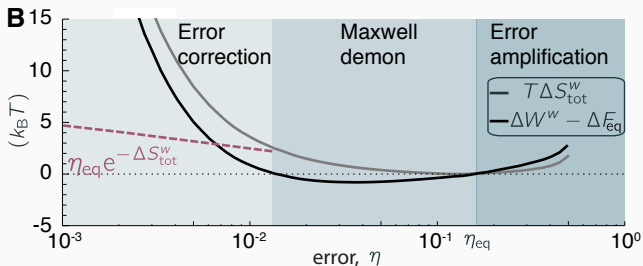
Single-step polymerization machines



NINIO, HOPFIELD, 1974, 1975



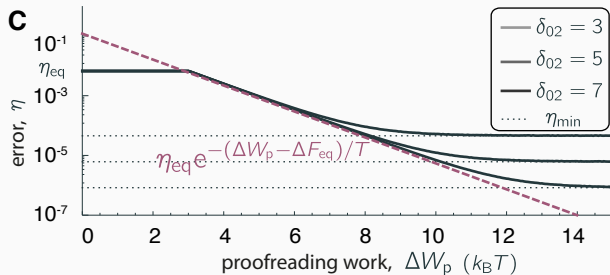
Extra pathway with negative velocity $v_p \leq 0$ preferentially removes wrong monomers



Since $\dot{S}_p^{\text{tot},w} \geq 0$ and $v_p \leq 0$ one can show

$$\eta \geq \eta^{\text{eq}} \exp\left(\frac{-\Delta W_p + \Delta F^{\text{eq}}}{k_B T}\right)$$

Proofreading



$$\eta^{\min} \simeq e^{(-\delta + \delta_p - \Delta E^w + \Delta E^r)/k_B T}$$

Stochastic polymerization dynamics

- State of the growing polymer: $rrwr \dots$
- State of the machine: $i \in \{1, \dots, n\}$
- Intermediate states (with a *tentatively* matched monomer):
 $rrwrr_i$ Or $rrwrw_i$
- Copying protocol: network of transitions $j \rightarrow i$ with rates $R_{ij}^{r,w}$
- Discrimination is due to differences in rates
- Probabilities: $P(\dots r)$, $P(\dots w)$, $P(\dots r_i)$, $P(\dots w_i)$ satisfying master equations:

$$\frac{d}{dt}P(\dots r_i) = \sum_{j=0}^{n+1} \mathcal{J}_{ij}^r(\dots) \quad \frac{d}{dt}P(\dots w_i) = \sum_{j=0}^{n+1} \mathcal{J}_{ij}^w(\dots)$$

- Currents: $\mathcal{J}_{ij}^r(\dots) = R_{ij}^r P(\dots r_j) - R_{ji}^r P(\dots r_i)$
- $j = 0 \rightarrow j = n + 1$ corresponds to the incorporation of a monomer
- All transitions are reversible

Stochastic polymerization dynamics

- Rates of incorporation:

$$\frac{d}{dt}P(\dots w) = \sum_{j=0}^{n+1} \left[\underbrace{\mathcal{J}_{n+1,j}^w(\dots)}_{\text{incorporation}} - \underbrace{\mathcal{J}_{j0}^r(\dots w) + \mathcal{J}_{j0}^w(\dots w)}_{\text{attempted incorp.}} \right]$$

and analog for r

- Assume errors are uncorrelated:

$$P(\dots) \propto \eta^{N_w} (1 - \eta)^{N - N_w}$$

- Then

$$P(\dots r) = P(\dots)(1 - \eta) \quad P(\dots w) = P(\dots)\eta$$

- Assume states i -occupancy $p_i^{r,w}$ to be independent of (\dots) . Then

$$P(\dots r_i) = P(\dots)p_i^r \quad P(\dots w_i) = P(\dots)p_i^w$$

- Occupation fluxes:

$$J_{ij}^r = \mathcal{N} (R_{ij}^r p_j - R_{ji}^r p_i) \quad J_{ij}^r(\dots) = P(\dots)J_{ij}^r/\mathcal{N}$$

Entropy production rate

$$\frac{dS^{\text{tot}}}{dt} = k_B \underbrace{\sum_{\dots} \frac{P(\dots)}{\mathcal{N}}}_{=1} \sum_{(ij), \alpha \in \{r, w\}} \left[J_{ij}^{\alpha} \log \left(\frac{R_{ij}^{\alpha} p_j^{\alpha}}{R_{ji}^{\alpha} p_i^{\alpha}} \right) \right]$$

$$\frac{dS^{\text{tot}}}{dt} = k_B \sum_{(ij), \alpha} \frac{J_{ij}^{\alpha} \mu_{ij}}{k_B T} - \eta v \left(\log \eta + \frac{\Delta E^w}{k_B T} \right) + (1-\eta) v \left(\log \left(1 - \eta + \frac{\Delta E^r}{k_B T} \right) \right)$$

Thus ΔS^{tot} per incorporated monomer is given by

$$\Delta S^{\text{tot}} = \frac{1}{v} \frac{dS^{\text{tot}}}{dt} = \frac{1}{T} (\Delta W - \Delta F^{\text{eq}} - k_B T D_{\text{KL}}(\eta \| \eta^{\text{eq}})) \geq 0$$

Entropy production per *wrong* incorporated polymer:

$$\Delta S^{\text{tot}, w} = \frac{1}{T} \left(\Delta W^w - \Delta F^{\text{eq}} - k_B T \log \frac{\eta}{\eta^{\text{eq}}} \right) \geq 0$$

Summary

- ST helps in setting up a unified frame for discussing dissipation in several biochemical processes
- Several regimes can be exhibited: we discussed no general “tradeoff” principle

The interplay between speed, dissipation and accuracy has been addressed in the so-called “uncertainty relations” in ST

Thank you!

References i



D. Andrieux and P. Gaspard.

Fluctuation theorems and the nonequilibrium thermodynamics of molecular motors.

Physical Review E, 74:011906, Jul 2006.



D. Andrieux and P. Gaspard.

Nonequilibrium generation of information in copolymerization processes.

Proceedings of the National Academy of Sciences USA, 105(28):9516–9521, 2008.



D. Andrieux and P. Gaspard.

Molecular information processing in nonequilibrium copolymerizations.

Journal of Chemical Physics, 130:014901, 2009.

References ii



C. L. Asbury, A. N. Fehr, and S. M. Block.
Kinesin moves by an asymmetric hand-over-hand mechanism.
Science, 302(5653):2130–2134, 2003.



C. H. Bennett.
Dissipation-error tradeoff in proofreading.
Biosystems, 11:85–91, 1979.



A. N. Fehr, C. L. Asbury, and S. M. Block.
Kinesin steps do not alternate in size.
Biophysical journal, 94(3):L20–L22, 2008.



P. Gaspard.
Fluctuation theorem for nonequilibrium reactions.
Journal of Chemical Physics, 120:8898–8905, 2004.

References iii



D. T. Gillespie.

A general method for numerically simulating the stochastic time evolution of coupled chemical reactions.

Journal of Computational Physics, 22(4):403–434, 1976.



D. T. Gillespie.

Exact stochastic simulation of coupled chemical reactions.

The Journal of Physical Chemistry, 81(25):2340–2361, 1977.



J. J. Hopfield.

Kinetic proofreading: A new mechanism for reducing errors in biosynthetic processes requiring high specificity.

Proceedings of the National Academy of Sciences of the United States of America, 71:4135–4139, 1974.

References iv



D. Lacoste, A. W. Lau, and K. Mallick.

Fluctuation theorem and large deviation function for a solvable model of a molecular motor.

Physical Review E, 78:011915, Jul 2008.



H.-W. Ma, J. Buer, and A.-P. Zeng.

Hierarchical structure and modules in the Escherichia coli transcriptional regulatory network revealed by a new top-down approach.

BMC bioinformatics, 5(1):199, 2004.



T. R. Maarleveld, B. G. Olivier, and F. J. Bruggeman.

Stochpy: a comprehensive, user-friendly tool for simulating stochastic biological processes.

PloS one, 8(11):e79345, 2013.

References v



J. Ninio.

La précision dans la traduction génétique.

In C. Sadron, editor, *École de Roscoff 1974. L'évolution des macromolécules biologiques*, pages 51–68. CNRS, 1975.



K. Nishinari, Y. Okada, A. Schadschneider, and D. Chowdhury.
Intracellular transport of single-headed molecular motors KIF1A.

Physical Review Letters, 95:118101, Sep 2005.



R. Phillips and S. R. Quake.

The biological frontier of physics.

Physics Today, 59:38–43, May 2006.



W. H. Press, S. A. Teukolsky, W. T. Vetterling, and B. P. Flannery.

***Numerical Recipes: The Art of Scientific Computing*, chapter 17.7.**

Cambridge University Press, New York, 3rd edition, 2007.

References vi



R. Rao and L. Peliti.

**Thermodynamics of accuracy in kinetic proofreading:
dissipation and efficiency trade-offs.**

Journal of Statistical Mechanics: Theory and Experiment,
2015(6):P06001, 2015.



P. Sartori and S. Pigolotti.

Kinetic versus energetic discrimination in biological copying.

Physical Review Letters, 110:188101, 2013.



P. Sartori and S. Pigolotti.

Thermodynamics of error correction.

Physical Review X, 5(4):041039, 2015.

References vii



J. Schnakenberg.

Network theory of microscopic and macroscopic behavior of master equation systems.

Rev. Mod. Phys., 48:571–585, Oct 1976.



M. J. Schnitzer and S. M. Block.

Statistical kinetics of processive enzymes.

Cold Spring Harb. Symp. Quant. Biol., 60:793–802, 1995.



R. Yasuda, N. Hiroiyuki, K. Kinosita, Jr., and M. Yoshida.

F_1 -ATPase is a highly efficient molecular motor that rotates with discrete 120° steps.

Cell, 93:1117–1124, 1998.