Exit Time Problems for Protein Folding

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Exit Time Problems in Protein Folding

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Inference in single-molecule biophysics

Goal: Inference of mechanical strength/functional characteristics/energies of chemical bonds from atomic force spectroscopy or optical tweezers experiments.

Modes of operation:

- Force ramp mode: v > 0
- Force clamp mode: v = 0

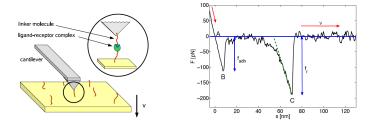


Figure: Left: Atomic force microscopy applied to ligand-receptor complex. Right: Possible force-extension curve generated by AFM when v > 0.

Over the past two decades, these experiments have given us new insights into physics and biology at single-molecule lengthscales.

The data from these experiments can take many forms:

- Rupture force distributions (Dudko, Hummer, Szabo, 2008)
- Rupture time distributions (Evans et al., 2001)
- Dwell time distributions (Woodside and Block, 2014)

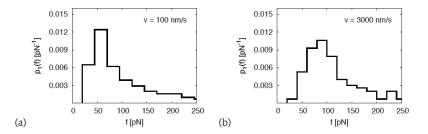
Big-picture question: How do we interpret these data sets to inform our understanding of chemical bond breaking, protein folding, DNA zipping/unzipping etc.?

Physical model: Microscopic, stochastic evolution of a reaction coordinate on 1D energy landscape (Freund, 2009; Evans and Ritchie, 1997)

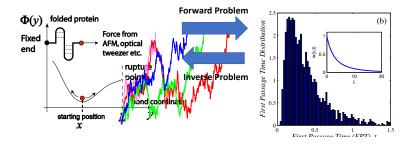
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Force ramp mode and a stochastic model

- For fixed v, rupture does not always occur at the same force \Rightarrow rupture force *distribution*
- When v is larger, the rupture distribution shifts to higher values
- Bond rupture could be modeled by *thermally-activated escape* (stochastic model).



Exit Time or First Passage Time Problem



- Given $\Phi(y)$, find distribution of FPT w(t) (forward problem)
- Given w(t), find $\Phi(y)$ (inverse problem)
- Smoluchowski dynamics. Underlying stochastic model is diffusive in position: $dX = -\frac{D\Phi'(X)}{k_BT}dt + \sqrt{2D}dW$ (Fok & Chou, Proc. Royal Soc. 2010)

Let $w(x_0, t)$ be the exit time distribution given that $X(t = 0) = x_0$. Then $w(x_0, t)$ satisfies the *backward* Smoluchowski equation

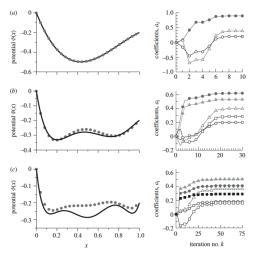
$$\frac{\partial w}{\partial t} + \underbrace{\frac{D}{k_B T} \frac{d\Phi}{dx_0}}_{-U(x_0)} \frac{\partial w}{\partial x_0} = D \frac{\partial^2 w}{\partial x_0^2}$$

subject to initial and boundary conditions

$$\begin{array}{lll} w(x_0,0) &=& 0, \\ \left. \frac{\partial w}{\partial x_0} \right|_{x_0=0} &=& 0, \\ w(L,t) &=& \delta(t). \end{array}$$

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Potential Reconstruction



Outline of algorithm

• Represent $U = \sum_{k=1}^{N} a_k \varphi_k(x)$

• Forward problem:

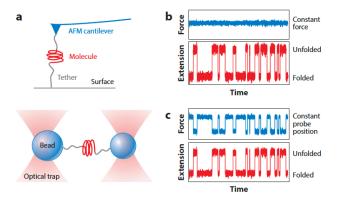
$$w = w(x_0, t; a_1, \dots, a_N)$$

$$||w_{\text{data}}(t) - w(x_0, t; \mathbf{a})||^2$$

is minimized

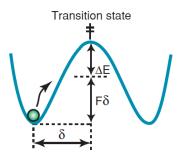
Force clamp AFM

- No bond breaking/rupture; dwell times only
- Two-state stochastic model



(From Woodside and Block, Annual Reviews of Biophysics 2014).

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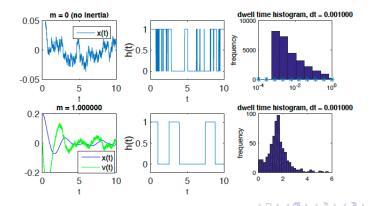
- Left of maximum \Leftrightarrow State 0
- $\bullet \ {\sf Right \ of \ maximum} \Leftrightarrow {\sf State \ 1}$
- Stochastic transitions between two states
- Kramers escape problem
- Multiple crossings and importance of inertia (next slide)

Preliminary Results from Simulation

Coupled stochastic differential equation:

$$dx = vdt$$

$$mdv = -\left[\frac{d\Phi}{dx} + \gamma v\right] dt + \sqrt{2\gamma k_B T} dW$$



Exit Time Problems in Protein Folding

Fokker-Planck (Kramers) equation for P(x, v, t):

$$\frac{\partial P}{\partial t} + v \frac{\partial P}{\partial x} = \frac{1}{m} \frac{\partial}{\partial v} \left(\left[\frac{d\Phi}{dx} + \gamma v \right] P \right) + \frac{\gamma k_B T}{m^2} \frac{\partial^2 P}{\partial v^2}$$

- In principal, given appropriate boundary conditions, the dwell times can be computed from this PDE
- Goal: infer the potential Φ from the dwell time distribution

Tools:

- Backward Equation
- Survival Probability
- Conservation laws

- No notion of initial position/velocity; random walk is sampling from a stationary distribution
- How to incorporate multiple crossings into the backward equation?
- Need to derive the backward Kramers equation
- Need value of drag coefficient γ