Reliable Protein Folding on Non-Funneled Energy Landscapes: The Free Energy Reaction Path

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Protein Folding

As temperature decreases, a linear chain of amino acids collapses into a reproducible three dimensional structure.



Levinthal's Paradox (1968): (as paraphrased by Zwanzig, 1992) If each amino acid can pair with at least 2 others, and if conformations are randomly sampled no faster than 10^{15} per second.



time to fold >
$$2^{500} \times 10^{-15} \,\mathrm{s} \approx 10^{135} \,\mathrm{years}$$

Modern View: Funneled Energy Landscapes

Conformation space is not sampled randomly:

In equilibrium,

Probability = $\exp(-F/T)$ with F = E - TS

Out of equilibrium, dynamics bias the search.

Energy Landscapes are shaped like funnels: Out of equilibrium, dynamics go to N In equilibrium, there is a phase transition



If there are many minima of E then there are many minima of F



at T_1 the time to fold is $\propto \exp(\Delta F/T_1)$

Given that $T(t) = T_0(1 - rt)$ this sets a bound on r. If $r > r^f$ the protein can fall into a metastable state

If there are many minima of E then there are many minima of F



If there are many minima of E then there are many minima of F



If there are many minima of E then there are many minima of F







Simulations

A particular two dimensional C^{α} model



Folding is induced by lowering temperature or increasing attractive strength

$$c \equiv \frac{|E_{\rm att}|}{T} = rt$$











Free Energy Reaction Path



We calculate r^f and r^s for this transition

Reliable Folding



<u>Summary</u>

- Reliable Folding can occur on Non-Funneled Energy Landscapes, depending on the foldinginduction rate r.
- The Free Energy Reaction Path is a useful framework to understand the dynamics.
- Folding can occur either as an equilibrium process or out of equilibrium.
- The native state can be a global or local minimum of free energy.
- These predictions can be tested in simulations and experiments by investigating rate dependence.