

Protein Folding & Self-Organized Criticality

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INTRODUCTION

Proteins are known to fold into tertiary structures that determine their functionality in living organisms. However, the complex dynamics of protein folding and the way they consistently fold into the same structures is unknown. Self-organized criticality (SOC) has provided a framework for understanding complex systems in various scientific disciplines through scale invariance and the associated "fractal" power law behavior. In this research, we use a simple hydrophobic-polar lattice-bound computational model to investigate self-organized criticality as a possible mechanism for generating complexity in protein folding.

SELF-ORGANIZED CRITICALITY (SOC)

SOC system is a dynamical system at a critical state that is characterized by power law behavior. It follows that these systems are both time and scale invariant.

The Sand Pile Model is the first and most well known example of a selforganizing system.

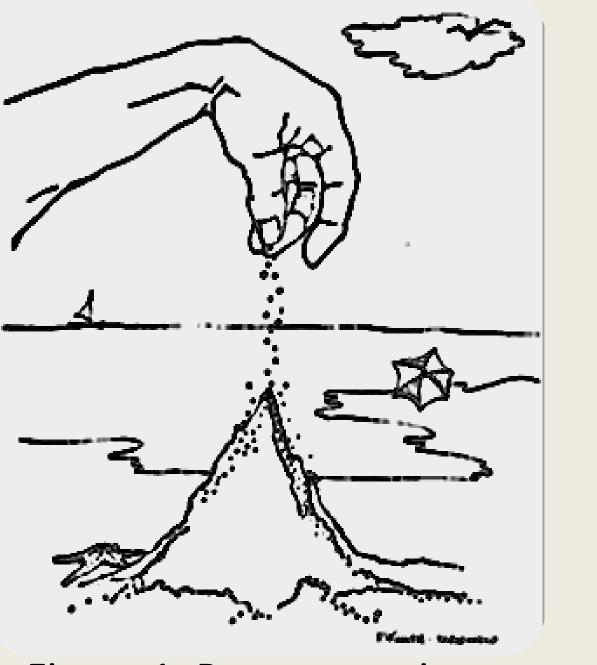
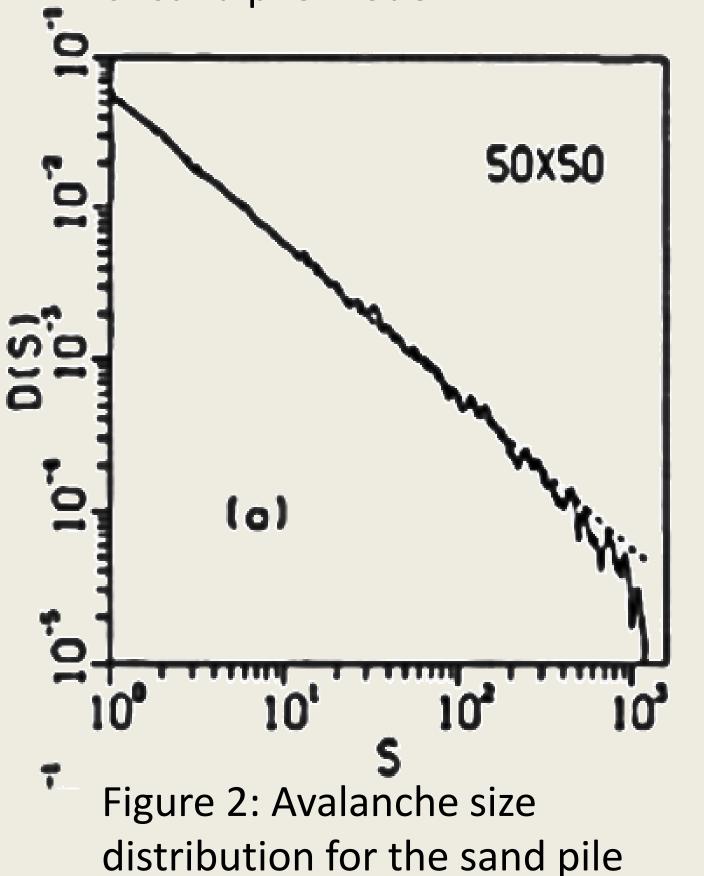


Figure 1: Representation of sand pile model



SAND PILE MODEL

Grains of sand are individually dropped onto a flat plane.

<u>Critical Trait</u>: steepness of slope<u>Critical State</u>: slope is reached<u>Avalanches</u>: grains of sand falling from steep slopes

Avalanche Size: number of grains falling

The distribution of avalanches follow a power law behavior

PROTEIN FOLDING MODEL

<u>Critical Trait</u>: minimizing energy<u>Critical State</u>: non-native structure<u>Avalanches</u>: rapid changes in structure(due to overcoming energy barriers)<u>Avalanche Size</u>: consecutive folds

ALGORITHM

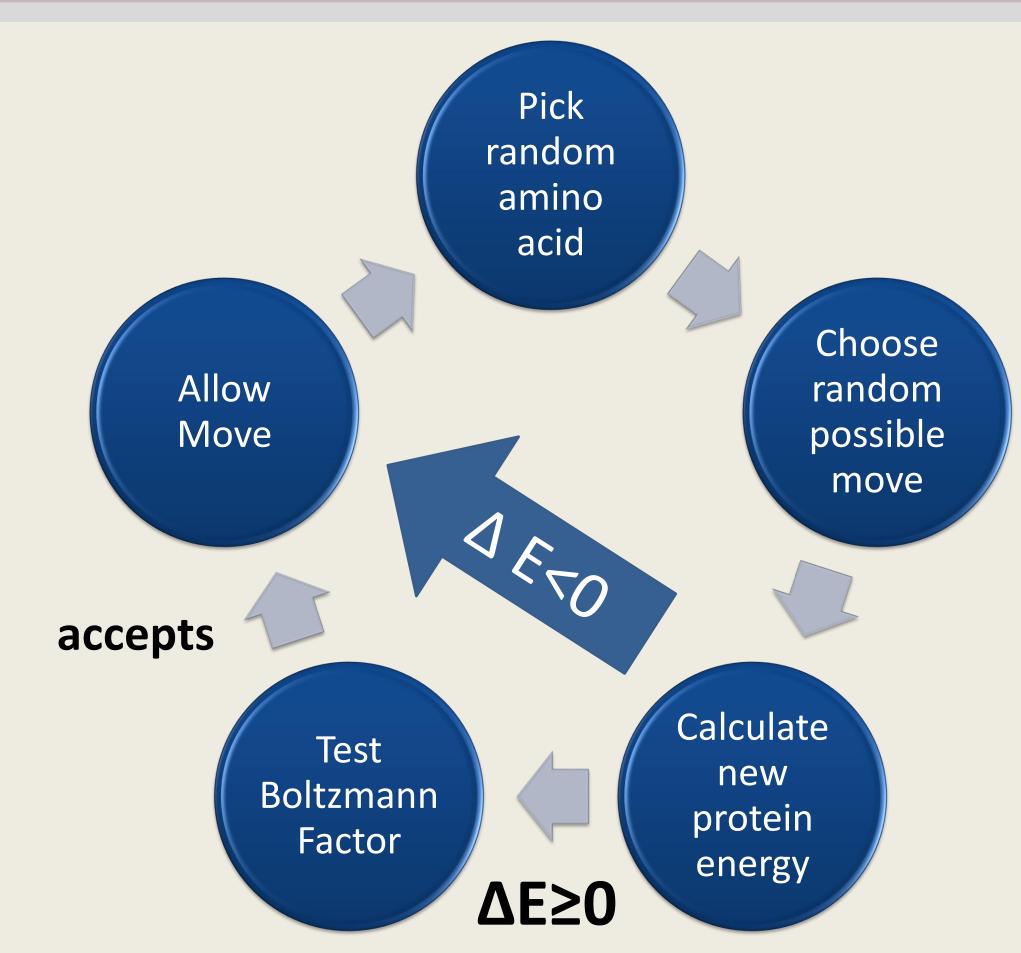


Figure 4: Flow diagram representing the computation sequence of the folding process

AVALANCHE DISTRIBUTION

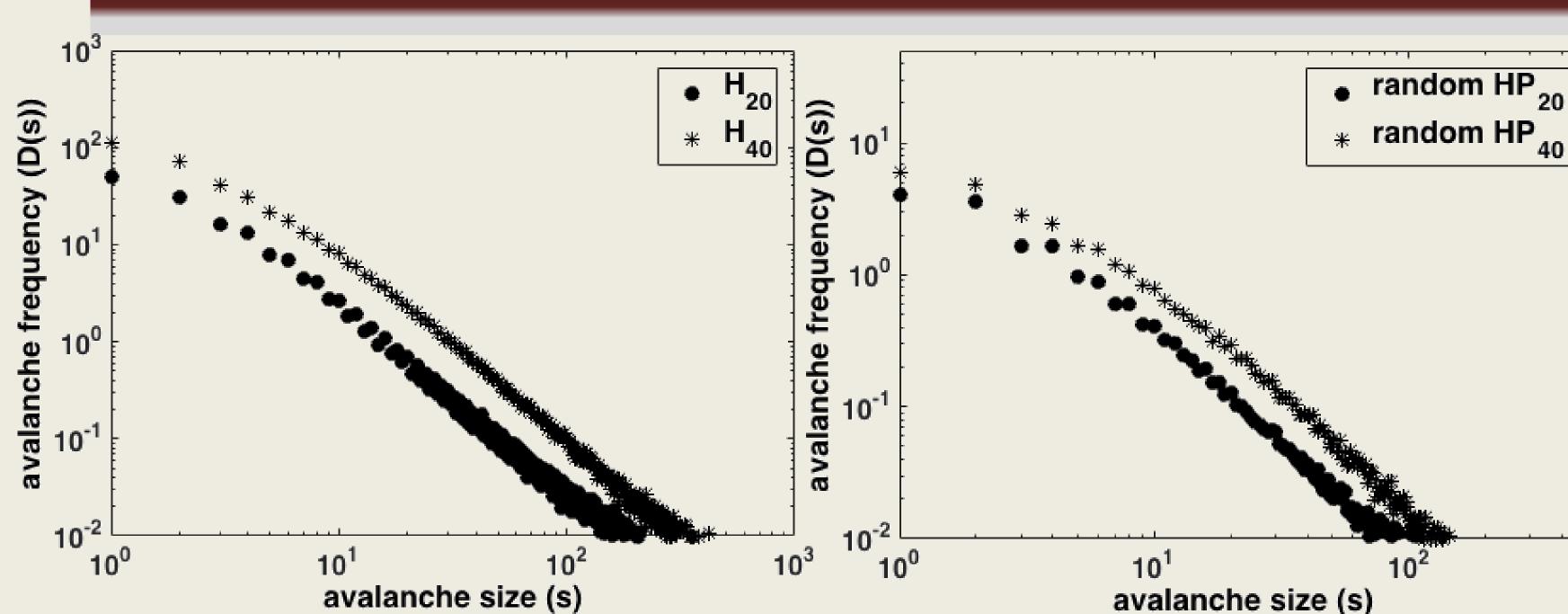


Figure 5: Avalanche distributions for 20 and 40 amino acid chain. Since SOC systems follow a power law, an avalanche distribution on a log plot should show a straight line

- Individual folds are randomly prevented throughout the folding process
- What impact does random stopping have on the avalanche distribution?

Figure 6: Stopping avalanches to inspect SOC resilience

HYDROPHOBIC-POLAR (HP) MODEL

Simplified model for understanding how a protein folds in space.

- •3D lattice: 1 bond length, no stretching
- •HP model: 2 types of amino acidshydrophobic (H) and polar (P)
- One amino acid moves at a time

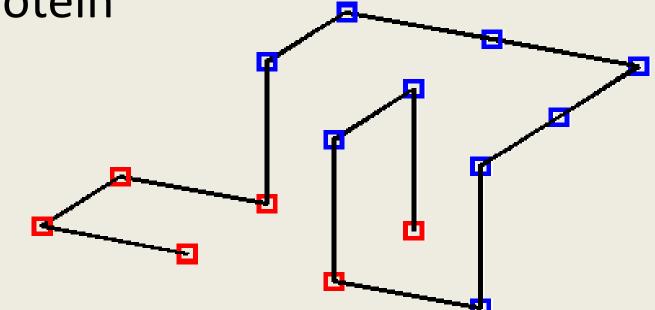


Figure 3: 3D lattice protein model in its native (folded) state

DISCUSSION

- Avalanche distributions in figure 5
 exhibits power law, although this
 feature alone doesn't support the
 presence of SOC
- Avalanche stopping alters SOC characteristics

FUTURE RESEARCH

- Does the model exhibit other SOC features? For longer protein chains?
- Do more sophisticated models exhibit SOC?
- Is tertiary structure connected to SOC?

H. Frauenfelder, Proc. Natl. Acad. Sci. U. S. A. **99 Suppl 1**, 2479 (2635 (1995002)