Simulating the Aggregation of Globular Protein in Solution at Various Salt Concentrations

By: Alexander Olinger Millsaps College REU KSU Summer 2010

Proteins

Amino Acid Structure



- Linear polymers of amino acids which compose a peptide chain
- Globular-have a folded chain

My Proteins

- Spherical
- 3-4 nm in diameter
- Uniform surface charge distribution

My Project

- To study the kinetic and aggregation of these proteins in solution and what happens as you vary the salt concentration
- Use the condition of constant temperature and number of proteins since those conditions are similar to those of the human body



Applications worth exploring

- Insulin delivery
- Eliminate diseases
- Destroy bacteria

Equations

Modified Lennard-Jones Potential

$$V(r) = \frac{4\epsilon}{\alpha^2} \left(\frac{1}{(r^2 - 1)^6} - \frac{\alpha}{(r^2 - 1)^3} \right)$$

Yukawa Potential

$$V(r) = A \frac{e^{-kr}}{r}, \quad 0 < r < r_{cutoff}$$

ε-relative potential
well depth
α-relative potential
well width
A-relative surface
charge distribution
Γ-damping coefficient

Brownian Equation of Motion

$$\vec{\overrightarrow{r_i}} = -\overrightarrow{\bigtriangledown}U_i - \Gamma \vec{\overrightarrow{r_i}} + \vec{W_i}(t)$$

Potential Plot

V-total for T=1





Other Similar Potentials

- DLVO Potential
- Asakura-Oosawa Potential

Lysozyme





Aggregation

- Diffusion Limited Cluster Aggregation (DLCA)
 - Stingry, fractal aggregates
 - Fractal dimension of 1.8

Reaction Limited Cluster Aggregation(RLCA) Fatter cluster Fractal dimension of 2.1

Snapshots

• K=5











Overall Assessment

- Took a while to get programs to work properly
- Obtained reasonable date that is physically proper
- Got a good feel for how this system works under various concentrations!

Future

- Nucleating cluster with at concentrations that have a potential barrier
- Include patchy interactions since the charge distribution of proteins is actually non-uniform

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Sources

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