Implementing Spherical Harmonics in the Poisson Boltzmann Equation for the Electrostatic-Potential

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Background - Potential

Electrostatic Potential why important? -electrostatic forces are derived from this -changes with each configuration change

- clearly the potential is a vital yet complex calculation which needs to be performed optimally
- -solved with the Poisson Boltzmann equation



Background – Poisson Boltzmann Equation



The Poisson Boltzmann Equation (PBE) is a <u>complex</u> <u>second order non-linear partial differential equation used</u> <u>the electrostatic potential</u>. It takes the following form.

$$\begin{aligned} -\nabla \cdot \left(\epsilon(\mathbf{r}) \nabla \Phi(\mathbf{r})\right) + \bar{\kappa}^2 \left(\frac{k_B T}{e_c}\right) \sinh\left(\frac{e_c \Phi(\mathbf{r})}{k_B T}\right) \\ &= 4\pi \sum_{i=1}^{N_m} q_i \delta(\mathbf{r} - \mathbf{r}_i) \end{aligned}$$

The hyperbolic sine term can be linearized resulting in the Linearized PBE (LPBE)

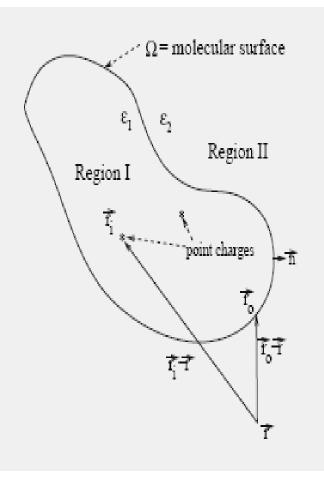
$$-\nabla \cdot (\epsilon(\mathbf{r})\nabla \Phi(\mathbf{r})) + \bar{\kappa}^2 \Phi(\mathbf{r}) = 4\pi \sum_{i=1}^{N_m} q_i \delta(\mathbf{r} - \mathbf{r}_i).$$

Background- Molecular Case of the LPBE

- Discontinuous piecewise constant dielectric term
- Discrete individual point charges on molecule
- The LPBE splits into the following system

$$\nabla^2 \phi_1(\vec{r}) = -\sum_{i=1}^{n_e} \frac{q_i}{\epsilon_1} \delta(\vec{r} - \vec{r}_i) \quad (\text{Region I})$$

$$\nabla^2 \phi_2(\vec{\textbf{r}}) - \kappa^2 \phi_2(\vec{\textbf{r}}) = 0 \quad \ (\text{Region II})$$





Background- Boundary Element Method



 Using Green's function we can convert the previous system of 2nd order PDEs to a system of <u>surface integrals</u> of the following form

$$\begin{split} \varphi_1(\vec{r}) &= \int_{\Omega} \left[G_1(\vec{r};\vec{r}') \frac{\partial \varphi_1}{\partial n}(\vec{r}') - \varphi_1(\vec{r}') \frac{\partial G_1}{\partial n}(\vec{r};\vec{r}') \right] d\vec{r}' \\ &+ \sum_{i=1}^{n_e} \frac{q_i}{\epsilon_1} G_1(\vec{r};\vec{r}_i), \end{split}$$

$$\varphi_2(\vec{r}) = \int_{\Omega} \left[-G_2(\vec{r};\vec{r}') \frac{\partial \varphi_2}{\partial n}(\vec{r}') + \varphi_2(\vec{r}') \frac{\partial G_2}{\partial n}(\vec{r};\vec{r}') \right] d\vec{r}',$$

This system is approximated using finite element methods creating a non sparse matrix

Project Idea

 Computational Speed and Efficiency -Matrix Compression :

ACA algorithm

Accuracy

 Flexible approximation techniques: we can specify the order of approximating polynomial
Accurate functional representation: Spherical Harmonics



Project Idea part 1: Implementing ACA Algorithm

- Matrix manipulations are often the most computationally expensive
- Finite Element and Finite Difference Methods
 - Sparse large matrices
- Boundary Element Method
 - Smaller matrix but *not sparse*
- ACA compresses nearly singular portions of a surface integral matrix
- ACA programming and setting up the surface integral matrix consists of the bulk of the project



Project Idea part 2: Implementing Spherical Harmonics

- Clearly the solution of the PBE hinges on surface integrals
- To integrate over the surface we need a functional representation of the surface
- previously naive attempts were made fitting an ellipse over target molecule
- Spherical Harmonics can produce better shapes



Spherical Harmonics-What are they?



- an ortho-normal series of functions defined on the unit sphere (defined for all (phi,theta))
- a generalization of the Fourier series to the sphere
- an infinite dimension basis for all continuous functions defined on the unit sphere

$$Y_{\ell}^{m}(\theta,\varphi) = \sqrt{\frac{(2\ell+1)}{4\pi} \frac{(\ell-m)!}{(\ell+m)!}} P_{\ell}^{m}(\cos\theta) e^{im\varphi}$$

Spherical Harmonics-Why use them?



- we can express the radius of a star surface with a central point as a function of (phi,theta)
- this function can be then be written as an infinite sum of spherical harmonics
- we can specify the degree of accuracy by the adding harmonics
- for star shaped objects the spherical harmonics should converge to the shape

Spherical Harmonics-Coefficients

For each function there exists a unique spherical harmonic $\underline{coefficient}$ for each harmonic $f_{\ell}^{m} = \int_{\Omega} f(\theta, \varphi) Y_{\ell}^{m*}(\theta, \varphi) d\Omega$

The coefficients obey the following property
$$f(heta, arphi) = \sum_{\ell=0}^{\infty} \sum_{m=-\ell}^{\ell} f_{lm} Y_{lm}(heta, arphi).$$

The coefficients also minimize the following quantity

$$\int_{H} (r(\theta,\varphi) - \sum C_{nk} Y_{nk}(\theta,\varphi))^2 d\omega$$



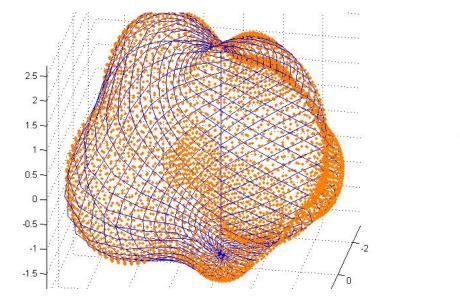
Spherical Harmonics- Process

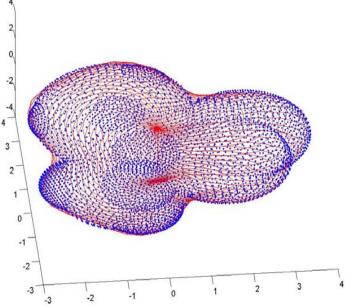
- Start with a PDB file containing atomic coordinates of the nuclei of the molecule/protein
- Use Dr. Connolly's msroll program to generate a larger series of coordinates representing the dot surface of the molecule/protein
- Run spherical harmonics approximation of the desired degree



Results : Simple Amino Acids

• Alanine: only 13 atoms, a common residue

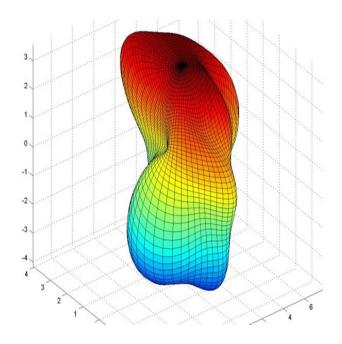


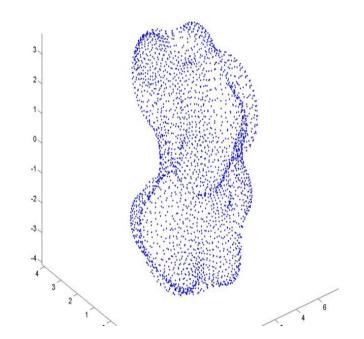




Results : Complex Amino Acids

• Tryptophan: 27 atoms

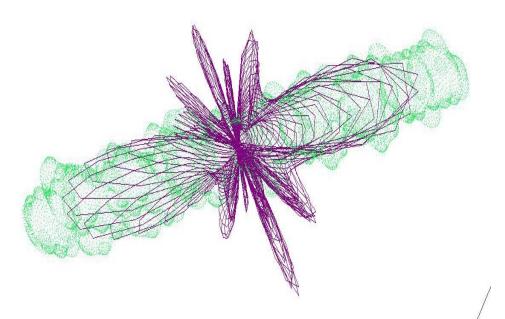


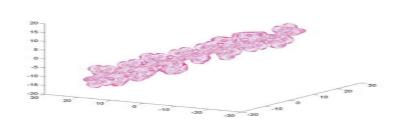


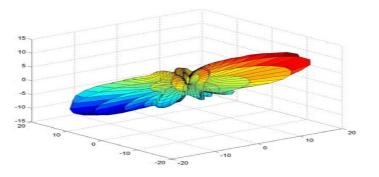


Results: Secondary Structure

Beta Pleated Sheets ~ 15 residues



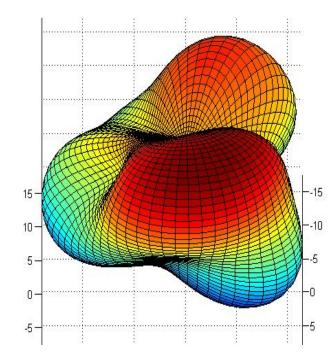


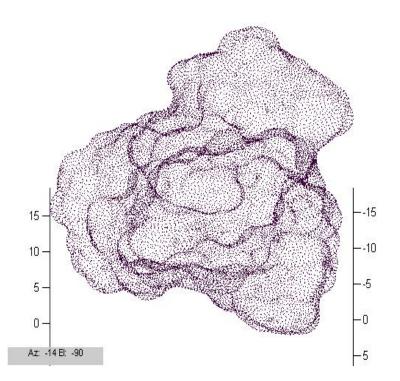




Results- Simple Proteins

Due to slightly more regular shape these fit fairly well Crambin: only 46 residues

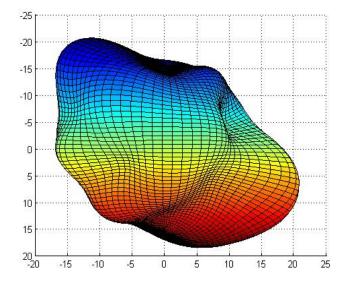


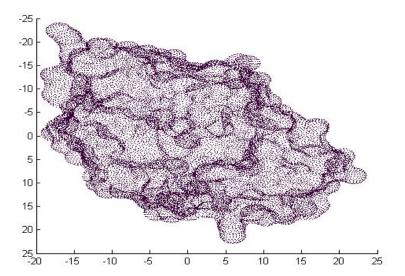




Results –Not so simple protein

• Lysozyme: 129 Residues







Results - Summary

- Single Amino Acids: excellent fit
- Secondary Structure: way off because of poor shape
- Proteins: doesn't capture everything, but gives a pretty good general idea
- Overall fairly successful attempt



Thank You Slide

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References



- Altman, Bardhan, Kuo, Tidor and White "Fast Methods for Simulation of Biomolecule Electrostatics," *IEEE* 2002.
- Baker, Holst and Wang "Adaptive Multilevel Finite Element Solution of the Poisson-Boltzmann Equation 1 Algorithms and Examples," *Journal of Computational Chemistry*, 2000.
- Boschitsch, Fenley and Zhou "Fast Boundary Element Method for the Linear Poisson-Boltzmann Equation," *Journal of Physical Chemistry*, 2002.
- Connolly, "Solvent-Accessible Surface of Proteins and Nucleic Acids," Science, Aug. 1983.
- Getzoff and Max "Spherical Harmonic Molecular Surfaces," *IEEE Computer Graphics & Applications,* July, 1988.
- Grandison, Penfold and Vanden-Broeck "A rapid boundary integral equation technique for protein electrostatics," Journal of Computational Physics, 2006.
- Lee, Vouvakis and Zhao "The Adaptive Cross Approximation Algorithm for Accelerated Method of Moments Computations of EMC Problems," IEEE 2005.