**What We Do**

We are interested in the structure and dynamics of condensed phase systems, and in particular, in the theory of time-dependent phenomena in liquids. Experimentally, one important approach for determining the structure and dynamics of condensed matter involves linear and non-linear vibrational spectroscopy. Typically, such spectroscopy contains information about local molecular environments, whose extraction, however, usually requires theoretical models and their solutions. In order to accomplish this, we use ab initio calculations, molecular dynamics simulations, statistical mechanics, and basically any theoretical approach that will enable us to further our understanding. The systems we are working on include water, peptides and proteins, interfaces, membranes etc.

**New Water Model**

The most common potentials used in classical simulations of liquid water assume a pairwise additive form. But none is able to describe accurately water throughout its complicated phase diagram. The primary reason for this is the neglect of many-body interactions. To this end, we introduce a new water model E3B2 that explicitly includes three-body interactions. The model was parameterized by fitting to a wide range of experimental properties (diffusion constant, rotational correlation time, etc.). The robustness was verified by calculating many other quantities such as the temperature-dependant third virial coefficient.

**Spectroscopy of Ice**

- In ice, the directions of the protons vary from totally disordered in ice I and I to perfectly ordered in ice XI.
- We want to reveal the effects of proton disorder in spectroscopic observables from an atomistic level.
- We use the ES/MD method to interpret IR, Raman and ultrarapid spectroscopy, which probe the structure and dynamics in ice.

**Water in Heterogeneous Systems**

**SFG at Water Liquid/Vapor Interface**

- Inclusion of many-body interactions in the E3B2 model is critical in the description of the air/water interface.
- Shape of the SFG spectrum is determined by a delicate cancellation of positive and negative contributions.
- Simulations show that the air/water interface is not ionic.

**Reverse Micelles**

In a reverse micelle, water is confined in a nanopool by surfactant molecules and its dynamics are greatly altered from the bulk as the size of the micelle decreases.

**Water at lipid bilayer surfaces**

Lipid bilayer hydration strongly influences both water and membrane properties in biological systems. Using vibrational spectroscopy, we have studied the structure and dynamics of water in lipid bilayer systems as a function of the hydration level.

**IR Spectroscopy of Peptides and Proteins**

Linear and two-dimensional IR are being tailored to determine the structures and dynamics of peptides and proteins. A rapid and accurate structure interpretation method has implications into drug design and also for understanding the reaction pathways.

- Expand current spectroscopic methods for NMA and acetamide to polypeptides.
- Simulate 1D and 2D spectra of the amide-I band.
- Understand how and what structural information can be obtained through spectra.

**Transferable Peptide Maps**

- IR experiments usually focus on the amide I vibrational mode, which is primarily the peptide bond C=O stretch.
- Different protein secondary structures, such as α-helix and β-sheet, have distinct spectral features in the amide I region.
- Theoretical modeling of the peptide IR spectra requires an accurate and efficient description of the amide I frequencies.
- We have developed frequency maps for both the protein backbone and side-chain amide groups from simple model compounds. The maps relate the amide I frequencies with local electric fields and are designed to be transferable to different electrostatic environment.
- The maps have been validated by the FTIR spectra for peptides with well-defined secondary structures.

**M2 Proton Channel**

The M2 protein from influenza A virus is a proton-selective ion channel protein. It serves as a target for amineadamantane antflu agents that block its H+ channel activity. We proposed a new H+ gating mechanism based on theoretical and experimental linear and two-dimensional IR spectra. In the new mechanism, pH change induces helix rotation which closes opens channel.

**Ovispirin**

- An 18-residue antimicrobial peptide
- Theory = Experiment to identify most likely position of Ovispirin on/in the membrane
- Investigate mechanism of antimicrobial action

**Amylin**

- A 37 residue peptide hormone secreted by pancreatic β-cells
- Also called Islet Amyloid Polypeptide, or IAPP
- Islet amyloid is a characteristic pathological finding in patients with type II diabetes
- Rat amylin (rAAPP) differs from human amylin (hAAPP) at 6 residues, but it has no amyloid fibril formation.
- Investigate aggregation mechanism and how the aggregation harms cells

**The Skinner Group:** (L to R)

Liang Shi, Yicun Ni, Dr. Piotr Pieniazek, Fu Li, Prof. Jim Skinner, Lu Wang, Dr. Scott Gruenbaum, Josh Carr, Craig Tainter