

EXPLORING CRITICAL CONFORMATIONS:
STATE SEARCHING AND SAMPLING IN BOTH
GERMANIUM CHAINS AND ICE INTERFACES
{EARLY DRAFT}

By

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Abstract: Molecular conformation plays a critical role in the properties of systems in either the condensed or vapor states. The ensemble of conformations dictates structural properties, energies, heat capacities, and other thermodynamic and dynamic quantities. Here, we explore the role of conformation in proton ordering and orientational defect formation in ice as well as strategies for exhaustive conformer searching for molecules using Group IV element backbones. In the ice systems, we show algorithmic strategies for seeking optimized proton disordered crystals that satisfy the Bernal-Fowler ice rules. In the Group IV molecule investigations, we develop an automated strategy for seeking the optimal low energy conformer and uncover previously unreported deficiencies in common computational software used in investigating Germanium complex energies.

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NOMENCLATURE

Variables

ϵ	Lennard-Jones Potential well depth
r	Lennard-Jones Potential distance between center of two particles
σ	Lennard-Jones Potential intermolecular contact distance
V	Lennard-Jones Potential intermolecular potential

Subscripts/Superscripts

0	Initial condition
---------	-------------------

CHAPTER 1

Introduction

I want a first paragraph that inspires the reader to continue reading. Maybe something with a quote or a question. Maybe not.

The idea for an introduction is to interest the reader and provide general background information. For my work, the interesting part is how impactful computational science (specifically chemistry) has been in research and on society. The background information will start extremely generic and then go into some overarching themes. Generically, I'll include the development of computational science in the 20th century and the vast applications of computational chemistry specifically. Overarching themes are related, but don't have to be explicitly relevant. For example, Levinthal's paradox is a fun example showing the problem of conformation landscape searches. Also,

1.1 Reason for Study

The studies conducted that comprise this work were determined as a combination of collaborative efforts and larger research group goals with novel discoveries worth reporting. Collectively, they explore conformations of internal bond dihedrals, molecule orientations of microstates, and properties of interfacing substrates. These efforts are categorized and separated into three categories: ice crystal states, conformation landscapes, and ice interfaces. A brief introduction of each and a literature review of relevant information is given below.

1.1.1 Generation of Ice I_h Crystal Structure

Ice crystals can take many forms based on properties like temperature and pressure. The proton-disorganized orthorhombic form of ice known as I_h is the form of ice most commonly found on earth (general understanding, CITATION NEEDED). Due to the inherent randomness of the disorganization of the molecules within the crystal, computational efforts are limited in scope or instead utilize the proton-ordered orthorhombic form of ice XI (general understanding, CITATION NEEDED). This project explores a method to produce a high quality pseudorandom ice I_h crystal structure.

1.1.2 Conformation Landscapes of Group IV Chains

Any molecule with a chain length of at least four contains at least one dihedral. In small molecules, the steric hindrance between the head and tail atoms are usually minimized in the fully gauche conformation to produce the lowest-energy conformer. In larger and more bulky molecules, additional interactions may cause the dihedral to take other conformations in search of the lowest-energy conformation. This project details the search for the lowest-energy conformer of a bulky hexagermane molecule in collaboration with Oklahoma State University’s Charles Weinert and the complications and curiosities found within.

1.1.3 Ice Interfaces in Two Dimensions

Ice is capable of interfacing with hydrophobic and amphipathic molecules. These interfaces often have a specific range of polarity and **physicochemical** properties like atom type, charge, and the spacing of interfaces. While usually considered in the biochemical sense, molecular interfaces with water have additional applications. If, for example, an interface had the properties to encourage ice growth, then it may be possible to observe significant ice growth above the expected freezing temperature.

Modeling water systems can be computationally intensive and require significant resources or a limited scope of system. One proven method of simplifying water modeling is to reduce the system by one dimension, creating a two-dimensional water. The 'Mercedes Benz' BN2D model and the more recent rose potential model are two examples of two-dimensional water models. Exploring and studying a two-dimensional water system allows for computationally-efficient investigating and can provide relevant information for a similar simulation with three-dimensional water. This project covers the usage of the two-dimensional rose potential model to observe ice growth on a substrate with varying properties.

1.2 Ice Annealing

EACH SUBSECTION: DEFINITION OF TERMS

1.2.1 Bernal - Fowler Ice Rules

Citation! Bernal and Fowler (1933)

There have been many works published on this topic, so I will have no problem obtaining a cohesive review. I plan to include the various forms of ice and focus on I_h and XI. This includes differences between the two in prevalence, environment, and synthesis (is synthesis the correct term here?).

I expect to focus on many thermodynamic properties and to focus on entropy as a driving force of difference in the modeled system. I will include publications of the effort to model a truly proton-disordered system and focus on the computational aspect.

1.2.2 Structures of Ice

Ice contains many structures. These structures are typically orthorhombic, which means rectangular at non-90 angles. They can also be hexagonal, cubic, else. These

different structures form based on temperature and pressure. Ice I_h is the most prevalent form of ice found normally on earth, forming at pressures around 1 atm and temperatures around 0C. (source needed?).

More detail on ice I_h .

More detail on ice XI.

1.2.3 Residual Entropy of Ice I_h and Ice XI

Residual entropy is a thermodynamic property that greatly differs between ice I_h and XI. In general, entropy can be calculated for a system of N molecules as $S = Nk \ln(w)$, where k is the Boltzmann constant and w is the number of real microstates corresponding to any macrostate. Residual entropy differs in calculation from entropy in that it generally refers to the entropy of a crystal near zero kelvin. Linus Pauling (1935) described the w of very low temperature crystals to approach the number of orientations possible for each molecule with consideration to immediate neighbors. Since ice I_h is a

For a proton-disordered ice I_h crystal, w becomes $\frac{x}{24}$ where x is the number of acceptable orientations within the crystal.

1.2.4 Hydrogen Bond Defects in Ice Crystals

Speak here about defects and how they quantitatively harm stability and why the defects need to be reduced in general ice I_h structures.

1.2.5 Literature Review on Relevant Works

1.3 Conformation Landscapes

EACH SUBSECTION: DEFINITION OF TERMS

For ROUGHLY forty years, computational programs have allowed investigators to model chemical systems with high accuracy to determine their physical properties.

1.3.1 A Brief History of Conformation Landscapes

1.3.1.1 Levinthal's Paradox

Discuss history of Levinthal and his paradox. Provide the non-paradoxical solution.

Next: Levinthal golf courses by Ken Dill.

1.3.2 Computational Modeling

Introduce importance and impact. Bigly important.

1.3.2.1 History of Chemical Modeling

Here I will introduce molecular modeling. This will begin with a brief history of the development of the field. It will continue through to mention the styles and goals of molecular modeling. Upon reaching modern techniques, I will discuss the benefits and costs associated with the major types of calculations (QM, MD, MC, etc).

1.3.2.2 Hardware: Oklahoma State University's Cowboy Cluster

It would also be appropriate to mention the computational capabilities of OSU's Cowboy cluster.

1.3.2.3 Software

Software to mention:

Visualizing Avogadro, UCSF Chimera(?),

Computing GAMESS(?), Gaussian, NWChem(?), OOPSE

This also includes brief pros and cons about the programs and the general purpose of use in case.

1.3.2.4 Programming Languages

Another hugely important portion of this will include a choice in the programming languages used (mostly python (Cython-compiled!), some Perl and Bash).

1.3.3 Literature Review on Relevant Works

1.4 Modeling Germanium Compounds

EACH SUBSECTION: DEFINITION OF TERMS

This will be an interesting section as there is extremely little in terms of Ge computational work. Perhaps a broader search will yield interesting results. For sake of thoroughness, I will also include work on computational energy optimization in general and work through complications brought by the size of Ge. I might also include a portion on the statistical spread of conformations at a given temperature (internal energy?) I may include a sentence or paragraph on Gaussian-based publications.

1.4.1 Tools for Modeling Germanium

Computational Requirements and reasons for those requirements.

Germanium is not the most-studied atom in computational works. The majority of Germanium studies are done with Gaussian (citation needed?).

1.4.2 Computational Complexity of Germanium Compounds

Draw-backs of modeling Germanium. Uncommon but still necessary for wetwork.

1.4.3 Literature Review on Relevant Works

Make note of various Germanium modeling research. Make note of tools and methods used.

1.5 Two-Dimensional Water

EACH SUBSECTION: DEFINITION OF TERMS

Rose water is fairly new on the computational scene and so I may also include a review on the Mercedez-Benz water system as well as any other attempts to model water in two dimensions. For the rose potential system, I will review the Lennard-Jones potential as well as any other equations/systems related to the rose potential.

1.5.1 Lennard-Jones Potential

The Lennard-Jones Potential well is a soft-sphere model of interaction between two spheres described with

$$V_{LJ} = 4\epsilon[(\frac{\sigma}{r})^{12} - (\frac{\sigma}{r})^6] \quad (1.1)$$

where V is the potential, r is the distance between the center of two particles, σ is the specific distance between the two particles where the potential is zero, and $-\epsilon$ is the minimum potential of the plot. **REFINE WORDING:** The plot is defined in $[0, \infty)$. As two particles approach from infinity, their interaction become negative - which is an attractive force - and will approach the global minimum of $-\epsilon$. The r of this interaction is slightly larger than the combined radii of the two particles - which means they aren't quite touching - and is the equilibrium distance between the two particles. As r decreases beyond the minimum and toward σ , the interaction strength increases and reaches zero as $r = \sigma$. At $r < \sigma$,

Potential digression: In a "hard-sphere" model, a particle's radius is firm, which is to say that the interaction potential is infinite at r less than σ . Basically a vertical line between two discrete values (usually ϵ and ∞) as the potential shifts from $r \geq \sigma$ to $r < \sigma$ (maybe include image?). The Lennard-Jones potential is a "soft-sphere" model, which blurs the line and replaces the vertical line with a functional representation.

This breaks with reality as the particles become "squishy" and the potential ramps up toward infinity as r decreases. The benefit to the soft-sphere model is that modeling programs can more-easily account for overlaps in particles during time steps than with hard-sphere models. For example, a hard-sphere model of two particles interacting will likely not have a position where $r = \sigma$ and will potentially overlap. At this overlap, the potential is infinity and will introduce a nearly infinite force at that instant of time. Computer systems do not like having infinitely large repulsions suddenly introduced into a simulation.

1.5.2 Modeling Water in Two Dimensions

Modeling in two dimensions sacrifice the "realism" of models in three dimensions, but reduce the computational load significantly. This allows researchers (scientists, chemists, digital magicians?) to test more simple designs in two dimensions as well as a higher volume of simulations at the same time/computational cost.

1.5.2.1 Mercedes-Benz Model

The "Mercedes-Benz" BN2D model of water first proposed by Ben-Naim (1971) as "waterlike particles" are a popular two-dimensional representation of water. ROUGH: details of shape of MB water

The mathematical model used in the BN2D model is generated from the Percus-Yevick equation by substituting the approximation

$$c(X_1, X_2) = y(X_1, X_2)f(X_1, X_2) \quad (1.2)$$

into the Percus-Yevick equation obtained from the Ornstein-Zernike relation

$$h(X_1, X_2) = c(X_1, X_2) + \frac{\rho}{2\pi} \int c(X_1, X_3)h(X_3, X_2)dX_3 \quad (1.3)$$

to produce the overall relation

$$y(X_1, X_2) = 1 + \frac{\rho}{2\pi} \int y(X_1, X_3) f(X_1, X_3) \times \left[y(X_3, X_2) f(X_3, X_2) + y(X_3, X_2) - 1 \right] dX_3 \quad (1.4)$$

1.5.2.2 Rose Potential Model

The rose potential is another model first introduced by Williamson et al. (2017). This model, while similar to the three-pronged BN2D, is notably different in that the rose potential model simplifies the model by use of a radial sinusoidal plot to make the three "prongs" of the particle.

1.5.2.3 Two-Dimensional Modeling

Something other than OOPSE? (not seeing obvious answer other than "custom code modified/forked from existing 3D tools")

The Object Oriented Parallel Simulation Engine (OOPSE) was introduced by A. et al. (n.d.) as a relatively light-weight molecular dynamics simulation package focused on "efficiently integrating equations of motion for atom types with orientational degrees of freedom" (from abstract). While OOPSE was further developed and renamed OpenMD, a fork of OOPSE was developed specifically to model water in two dimensions.

1.5.3 Literature Review on Relevant Works

TODO: Work with MB water,

CHAPTER 2

On Algorithms for Building and Sampling Disordered Crystal States

2.1 States and Properties of Ice

Ice is cool. Ice has many forms, each with unique environments and structures that give rise to similar and unique properties.

2.1.1 Bernal-Fowler Ice Rules

Bernal-Fowler Ice Rules are the basic rules for how water molecules interact in an ice structure. DETAILS ON BF PAPER

Basically, water’s tetrahedral structure allows for four interactions on each molecule. The two protons allow for a hydrogen bond with a lone pair from a neighboring oxygen atom. Similarly, the oxygen atom’s two lone pairs allow for a hydrogen bond with a neighboring proton. These rules are fairly rigid in the sense that every water molecule can interact with two oxygen atoms and two protons from four surrounding water molecules. These are also free-form in the sense that each of the four attached water molecules can occupy one of three rotational microstates, allowing for 81 possible configurations (including rotational duplicates).

2.1.2 Forms of Ice

While ubiquitous in the ‘ I_h ’ form, ice water has many known forms. As of the writing of this work, there are 17 established forms of ice. These forms usually occur in cubic, hexagonal, and orthorhombic crystal structures. The relationship between external pressure and temperature are the primary defining characteristics of which form will

form in a given system. Do other characteristics come into play???????

2.1.3 Ice I_h

As the most commonly found form on earth, ice I_h is a highly desired form for computational studies involving ice systems.

2.1.4 Efforts to Generate Ice I_h

Has anyone else published efforts to generate Ice I_h ? I'm sure someone has.

2.1.5 Comparison between Ice XI and Ice I_h

While ice I_h is known as the most common form of ice found on the planet, it is much more difficult to computationally generate than an ice XI crystal. The ease of generation of an ice XI structure stems from the repetition of a unit cell with consistent layering and orientation throughout the crystal lattice.

With ice I_h crystals, the proton-disordered form introduces entropy by way of rotational disorder. As the protons and lone pairs are no longer consistently ordered, hydrogen bonds may no longer form properly at all interaction sites. The interaction of proton with proton or lone pair with lone pair are not hydrogen bonds and are considered defects in the lattice. An ice structure of randomly oriented molecules without consideration of hydrogen bonds will likely produce defects at many interaction sites across the lattice and weaken the integrity of the system, leading to stability problems while running simulations. In generating the crystal, the cause of these defects must be considered and countered effectively.

2.2 Method Design

2.2.1 Overview

The big idea is to convert an easy-to-make ice XI crystal into an ice Ih crystal. Because the key difference in structure is the proton-orderedness, it might be possible to rearrange the water molecule orientations in a pseudorandom way to create an ice Ih crystal. This section walks through the method developed to convert ice XI into ice Ih, the results of initial testing, and imperfections discovered in the design.

2.2.2 Selection of Software Tools

Python was chosen as the language of the tool due to the versatility of the language and the ease of development due to the "pseudocode" written style of the language and the availability of scientific packages including SciPy and NumPy. Python version 2.7 was specifically chosen due to familiarity with the language. Crystal files were defined and saved as Protein Data Bank (.pdb) files as this format allows for defining multiple molecules within a larger structure with a simple X, Y, Z grid position format.

2.2.3 Generation of Source Ice XI

This is Dr. Fennell's method to create an ice XI pdb file. Basically, the ice XI unit cell of eight water molecules is repeated as desired to create a sufficiently large crystal. The primarily used crystal consists of a 3 x 3 x 6 unit cell repetition totaling 432 water molecules.

2.2.4 Source Ingestion

It is important that the crystal be read and stored in an efficient method to keep relevant information about each molecule easily accessible. As the file is read in, each

molecule is stored as an entry in a multidimensional array where the first index is the molecule number. Further, the second index defines the molecule number where 0 is oxygen and 1 and 2 are the protons. The third, fourth, and fifth indices define the X, Y, and Z position coordinates.

2.2.5 Identifying Neighboring Molecules

Identifying the neighboring molecules proved computationally difficult. The most effective method is to find the closest four molecules by computing a distance calculation between every two oxygen atoms. This ensures every molecule is considered, but also presents significant hurdles. First, a distance calculation utilizes an extremely computationally-inefficient square root calculation, which can be ignored by instead calculating the squared-distance between molecules and finding the lowest values.

Second, molecules on the walls and edges of the molecule will not have four neighbors in the non-periodic crystal. This is accounted for by shifting all six sides to make a pseudo-periodicity for these edge cases. Those periodically-neighboring molecules are flagged with a shifting value in the neighboring atom array by specifying a translation in the x, y, or z axis values. Unfortunately, the necessary code to implement the periodically-neighboring molecule detections requires a major rewrite of the entire tool and has not yet been implemented.

Once these closest neighboring oxygen atoms have been discovered, the appropriate interacting tetrahedral position is identified by finding the closest of the four tetrahedral positions using the same squared-distance calculation with the four defined tetrahedral positions detailed in the next subsection.

2.2.6 Defining Tetrahedral Positions

An important aspect of pseudorandom selection is the existence of a bank of options. Using the ingestion portion to calculate and store all tetrahedral possibilities proves

useful. For each water molecule, the first two tetrahedral positions are known by the positions of the two hydrogen atoms. The other two positions are found by rotating one hydrogen atom 120° twice about the vector from the oxygen atom through the other hydrogen atom and storing the resulting positions as tetrahedral positions three and four.

This does not produce an exactly correct tetrahedral position of potential hydrogen atoms due to the slight acuteness of the H-O-H bond created by the variance in repulsive forces between the two lone pairs of electrons and two hydrogen atoms. Fortunately, this difference is sufficiently small for visualization programs like Avogadro to still recognize hydrogen bonds between a rotated hydrogen atom and corresponding neighboring lone pair. Currently, the method relies on a very soft annealing process by a simulation package to minimize the effect of this hydrogen bond imperfection. Future versions of this method may account for the variations.

2.2.7 Pseudorandom Rearrangement of Water Molecules

Once the tetrahedral positions have been defined, each water molecule is ready to rotate. What may seem the most crucial step in this methods ends up being the most simple. As designed, the rotation of water molecules is as simple as using a stepwise iterator to pseudorandomly select two tetrahedral positions for the hydrogen bonds and store the new positions in a new crystal array. An extremely important note is that this rearrangement does not consider the orientations of neighboring molecules and likely introduces defects of hydrogen - hydrogen and lone pair - lone pair interactions. The likelihood of a defect-free interaction lattice forming is nearly zero and is assumed to have a great deal of defects within the lattice.

2.2.8 Detecting Hydrogen Bond Defects

After all water molecules have been rearranged, defects between incorrectly-interacting hydrogen bonds must be found and corrected. Discovering the defects relies on the detection of neighboring molecules and the appropriate interacting hydrogen atom or electron lone pair. As previously discussed, the initial data ingest records and detects the nearest water molecules and determines the tetrahedral position containing the interacting space, be it electron lone pair or hydrogen atom. From that data, the detection of a valid hydrogen bond is as simple as checking both all interacting tetrahedral positions and confirming that they both do not contain or lack a hydrogen atom.

2.2.9 Correcting Hydrogen Bond Defects

Once the hydrogen bond defects have been discovered and marked, each needs to be corrected. The most direct approach to this is to sequentially walk through each defect and repeat the pseudorandom rotation until the number of defective regions is zero or a user-specified value.

The current design of the method allows for the user to specify a threshold of defects as an average per molecule. For example, a threshold of 2.5 will allow a maximum of 3 defects on any given molecule and will continue to correct defects until the average number of defects per molecule is equal to or below 2.5. As of the current implementation, the method cannot reliably produce a crystal with a threshold below 2 as it will continue to search until the system runs out of available memory and crash without recording any new structure.

2.3 Results of Method

When supplied with an input ice XI crystal, an output structure with rotated water molecule orientations strictly consistent with ice Ih describes a success at the most

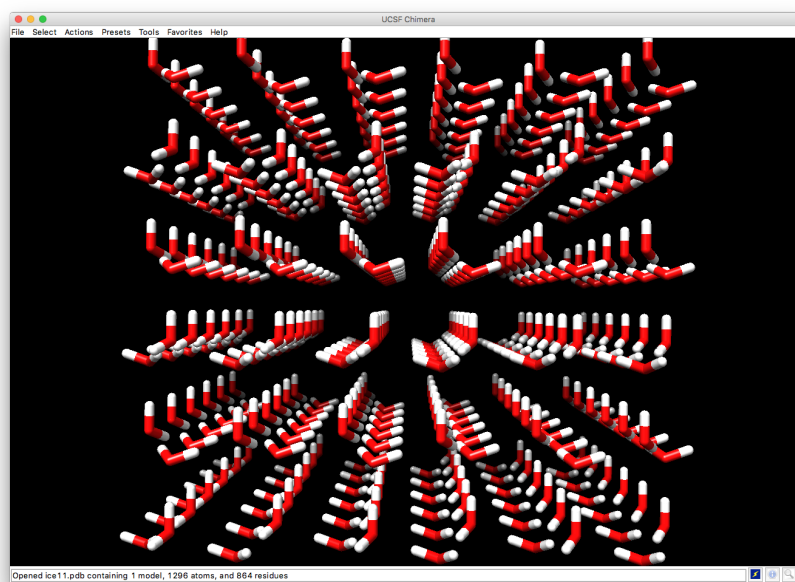


Figure 2.1: "Before" image of Ice XI

basic level. An example before and after of the method is given in figures 2.1 and 2.2. The generated ice Ih has been rotated. When following the subsequent layers in the crystal, patterns emerge. Inconsistently, some rows of waters remain consistent. Some of these are a uniform rotation of both hydrogen atoms, while others are just one consistently placed hydrogen atom. Multiple trials yield internally unique results, yet all contain these consistent layers.

2.4 Comments on Limitations and Proposed Improvements

During the hydrogen bond defect correction step, a weakness in the design is that any clustering or regions of high defect density will not be noticed. This allows the existence of a highly-defective region within the larger structure that could potentially cause problems when the crystal is used in simulations. The prevalence and occurrence of these defects have not been studied, but seem a natural inevitability of statistics.

A potential solution with partial development will score regions based on the number of defects as a weighted function expanding out from a central molecule for

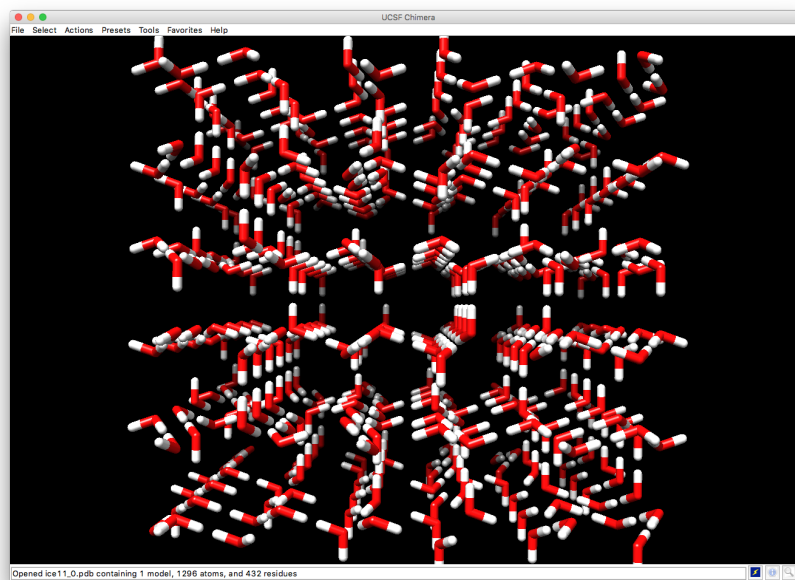


Figure 2.2: "After" image of generated ice Ih

N connections. For example,

CHAPTER 3

Sampling Conformation Landscapes by Rotatable Bond Degrees of Freedom

3.1 Conformation Landscapes

EACH SUBSECTION: DEFINITION OF TERMS

For ROUGHLY forty years, computational programs have allowed investigators to model chemical systems with high accuracy to determine their physical properties.

3.1.1 A Brief History of Conformation Landscapes

3.1.1.1 Levinthal's Paradox

Discuss history of Levinthal and his paradox. Provide the non-paradoxical solution.

Next: Levinthal golf courses by Ken Dill.

3.1.2 Computational Modeling

Introduce importance and impact. Bigly important.

3.1.2.1 History of Chemical Modeling

Here I will introduce molecular modeling. This will begin with a brief history of the development of the field. It will continue through to mention the styles and goals of molecular modeling. Upon reaching modern techniques, I will discuss the benefits and costs associated with the major types of calculations (QM, MD, MC, etc).

3.1.2.2 Hardware: Oklahoma State University's Cowboy Cluster

It would also be appropriate to mention the computational capabilities of OSU's Cowboy cluster.

3.1.2.3 Software

Software to mention:

VisualizingAvogadro, UCSF Chimera(?),

ComputingGAMESS(?), Gaussian, NWChem(?), OOPSE

This also includes brief pros and cons about the programs and the general purpose of use in case.

3.1.2.4 Programming Languages

Another hugely important portion of this will include a choice in the programming languages used (mostly python (Cython-compiled!), some Perl and Bash).

3.1.3 Literature Review on Relevant Works

intro: Reference introduction: inherent complexity of "objective" or "exhaustive" search, levinthal's paradox as it applies to non-biological systems, ELSE?

3.2 Approach to Solution: Variable-Resolution Search

Run through a set of dihedral positions at a constant interval. Selection of lowest-energy optimization organized on dihedral values. Quick determination of importance of dihedral based on how heavily it impacts internal energy. Splitting "best" dihedral into smaller interval to repeat the process.

This method produces an interesting visual plot with varying resolution at different X values (if plotting energy vs. dihedral). Example given on 3.1.

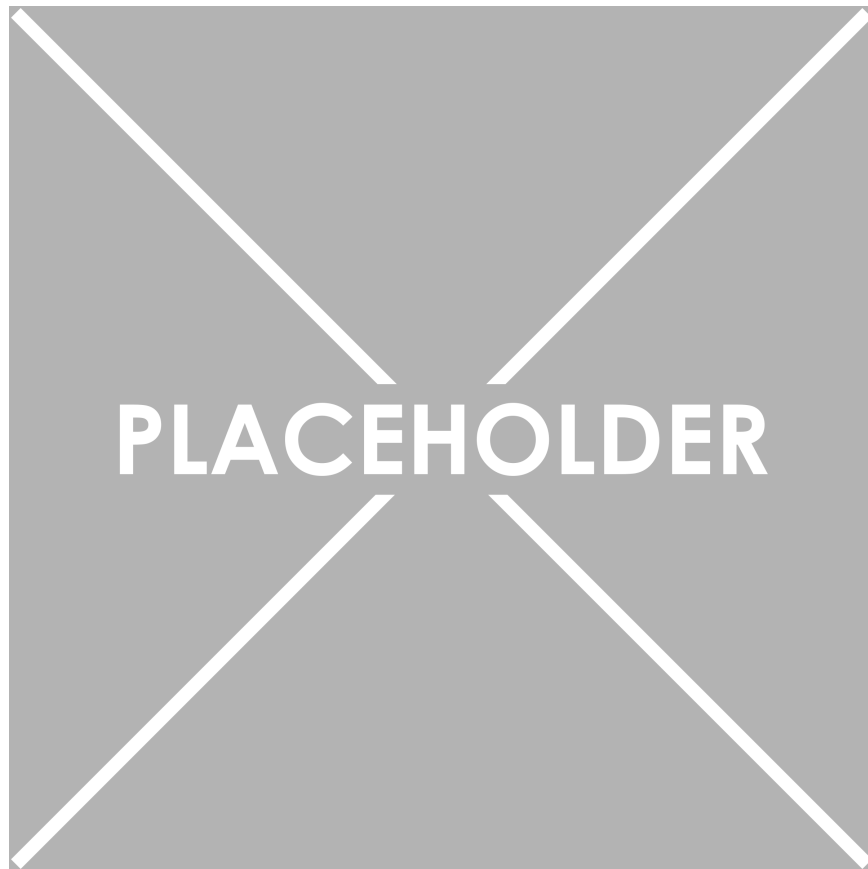


Figure 3.1: example VR chart (exploding like molecule/cell/fiber/muscle)

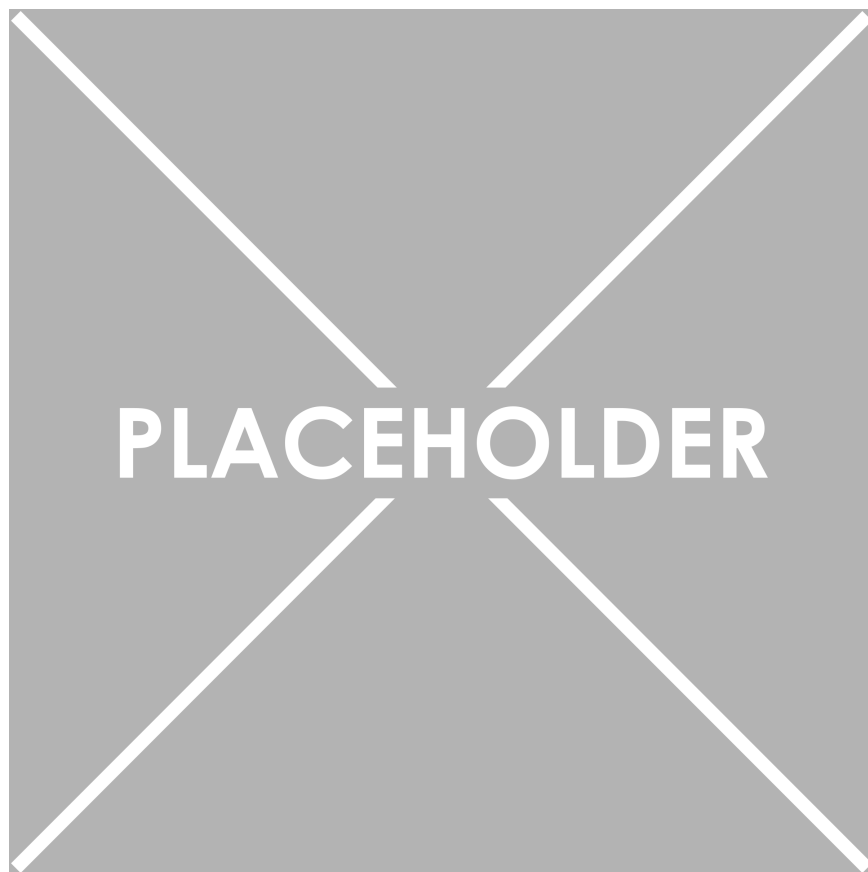


Figure 3.2: Flow of method design for variable resolution conformation landscape search.

3.2.1 Design of System

System designed in Python for ease of development and compiled via Cython for computational efficiency. Utilizes Gaussian and UCSF Chimera, but can be redesigned for any computational programs that accomplish the desired tasks. Overview of system flow given in 3.2.

This design, with implementation being a current work in progress, but shouldTM work as a cascade toward the lowest energy conformation in each case.

3.2.1.1 Variation of Theory and Basis Set Usage by System Size and largest atom type

System will have inherent restrictions. Give an example of large system with simple atoms, small system with complex atoms. System estimates quantity and cost of calculations based on computational limits defined by user for various theory-basis set pairings. System optimizes calculations for the scale of run (is it the first broad-scope search, or a final near-exact search).

Good to have: data on how theory and basis set alter computational requirement. Available in literature? Create data from runs?

3.2.1.2 Computational Optimization by Varying Resolution

Extant work not optimized for a general search (negative claim: make sure literature has nothing). Design should work with additional development (primary focus this semester) as a general search tool.

3.2.2 Inherent Complications

Complications of size and atom type, impossible conformations, duplications, limited computational resources, GERMANIUM.

3.3 Results

Current success: finding accepted lowest energy conformer of a two-dihedral system by manually cranking each step. Self-running is still a work in progress.

3.3.1 Problems

Difficulty in defining an abstract system based on arbitrary hardware limitations. Propose a test-run to determine efficiency and resource availability.

3.3.2 Anticipated Approaches for Future Work

Putting system into a single cohesive program. Further optimizing Theory/Basis Set determination by computational efficiency as well as system size (determine an upper-limit of computation?)

CHAPTER 4

Germanium Compounds and QM Concerns

4.1 Modeling Germanium Compounds

EACH SUBSECTION: DEFINITION OF TERMS

This will be an interesting section as there is extremely little in terms of Ge computational work. Perhaps a broader search will yield interesting results. For sake of thoroughness, I will also include work on computational energy optimization in general and work through complications brought by the size of Ge. I might also include a portion on the statistical spread of conformations at a given temperature (internal energy?) I may include a sentence or paragraph on Gaussian-based publications.

4.1.1 Tools for Modeling Germanium

Computational Requirements and reasons for those requirements.

Germanium is not the most-studied atom in computational works. The majority of Germanium studies are done with Gaussian (citation needed?).

4.1.2 Computational Complexity of Germanium Compounds

Draw-backs of modeling Germanium. Uncommon but still necessary for wetwork.

4.1.3 Literature Review on Relevant Works

Make note of various Germanium modeling research. Make note of tools and methods used.

Table 4.1: Collaborator’s Hexagermane Energies by Conformation
(Density Function Theory, Unknown Basis Set)

Conformation	Energy (E_h)	Δ Energy (E_h)	Δ Energy ($\frac{Kj}{mol}$)
Trans-coplanar	-15014.8403143	0.0066255	17.39525025
Cis-Trans-Cis	-15014.7983311	0.0486087	127.6221418
Trans-Cis-Trans	-15014.8469398	0.0000000	0
Cis-Trans-Trans	-15014.8246918	0.0222480	58.412124

In the fall of 2016, the Fennell Group was contacted by Dr. Scott Weinert to study a germanium-based compound comprised of a backbone hexagermane chain, two phenyl rings off the internal atoms, and isopropyl groups on the terminal germanium atoms (hereafter referred to as "hexagermane"). Dr. Weinert’s lab had received curious results from a prior collaborator and sought confirmation by a second computational group.

4.2 Current Methods

Reiterate the scarcity of extant Germanium studies. Probably definitely reference Dr. Weinert’s work.

4.2.1 Precursory Work

Dr. Weinert’s lab had received curious results from a prior collaborator and sought confirmation by a second group.

From the information provided in 4.1, the energy from Density Functional Theory calculations suggest that the most energetically-favorable conformation of hexagermane be the trans-cis-trans form.

4.3 Modeling Germanium molecules in Gaussian

This is the meat of the chapter - the Gaussian problem.

4.3.1 Recognition of Problem

Include Dr. Fennell's image. Relate to strangeness of collaborator's data. FRAME
PROBLEM WITH THEORY AND BASIS SET

4.3.2 Confirmation of Germanium consistency from other systems

A minor note of confirmation of Gaussian problem from consistent results from other programs with same theory and basis set.

4.3.3 Correcting the Issue

Use basis set from Basis Set Exchange, detail selection and usage in input settings.

CHAPTER 5

Crystal and Liquid 2D Water at Interfaces

5.1 Two-Dimensional Water

EACH SUBSECTION: DEFINITION OF TERMS

Rose water is fairly new on the computational scene and so I may also include a review on the Mercedez-Benz water system as well as any other attempts to model water in two dimensions. For the rose potential system, I will review the Lennard-Jones potential as well as any other equations/systems related to the rose potential.

5.1.1 Lennard-Jones Potential

The Lennard-Jones Potential well is a soft-sphere model of interaction between two spheres described with

$$V_{LJ} = 4\epsilon[(\frac{\sigma}{r})^{12} - (\frac{\sigma}{r})^6] \quad (5.1)$$

where V is the potential, r is the distance between the center of two particles, σ is the specific distance between the two particles where the potential is zero, and $-\epsilon$ is the minimum potential of the plot. **REFINE WORDING:** The plot is defined in $[0, \infty)$. As two particles approach from infinity, their interaction become negative - which is an attractive force - and will approach the global minimum of $-\epsilon$. The r of this interaction is slightly larger than the combined radii of the two particles - which means they aren't quite touching - and is the equilibrium distance between the two particles. As r decreases beyond the minimum and toward σ , the interaction strength

increases and reaches zero as $r = \sigma$. At $r < \sigma$,

Potential digression: In a "hard-sphere" model, a particle's radius is firm, which is to say that the interaction potential is infinite at r less than σ . Basically a vertical line between two discrete values (usually ϵ and ∞) as the potential shifts from $r \geq \sigma$ to $r < \sigma$ (maybe include image?). The Lennard-Jones potential is a "soft-sphere" model, which blurs the line and replaces the vertical line with a functional representation. This breaks with reality as the particles become "squishy" and the potential ramps up toward infinity as r decreases. The benefit to the soft-sphere model is that modeling programs can more-easily account for overlaps in particles during time steps than with hard-sphere models. For example, a hard-sphere model of two particles interacting will likely not have a position where $r = \sigma$ and will potentially overlap. At this overlap, the potential is infinity and will introduce a nearly infinite force at that instant of time. Computer systems do not like having infinitely large repulsions suddenly introduced into a simulation.

5.1.2 Modeling Water in Two Dimensions

Modeling in two dimensions sacrifice the "realism" of models in three dimensions, but reduce the computational load significantly. This allows researchers (scientists, chemists, digital magicians?) to test more simple designs in two dimensions as well as a higher volume of simulations at the same time/computational cost.

5.1.2.1 Mercedes-Benz Model

The "Mercedes-Benz" BN2D model of water first proposed by Ben-Naim (1971) as "waterlike particles" are a popular two-dimensional representation of water. ROUGH: details of shape of MB water

The mathematical model used in the BN2D model is generated from the Percus-Yevick equation by substituting the approximation

$$c(X_1, X_2) = y(X_1, X_2)f(X_1, X_2) \quad (5.2)$$

into the Percus-Yevick equation obtained from the Ornstein-Zernike relation

$$h(X_1, X_2) = c(X_1, X_2) + \frac{\rho}{2\pi} \int c(X_1, X_3)h(X_3, X_2)dX_3 \quad (5.3)$$

to produce the overall relation

$$y(X_1, X_2) = 1 + \frac{\rho}{2\pi} \int y(X_1, X_3)f(X_1, X_3) \times \left[y(X_3, X_2)f(X_3, X_2) + y(X_3, X_2) - 1 \right] dX_3 \quad (5.4)$$

5.1.2.2 Rose Potential Model

The rose potential is another model first introduced by Williamson et al. (2017). This model, while similar to the three-pronged BN2D, is notably different in that the rose potential model simplifies the model by use of a radial sinusoidal plot to make the three "prongs" of the particle.

5.1.2.3 Two-Dimensional Modeling

Something other than OOPSE? (not seeing obvious answer other than "custom code modified/forked from existing 3D tools")

The Object Oriented Parallel Simulation Engine (OOPSE) was introduced by A. et al. (n.d.) as a relatively light-weight molecular dynamics simulation package focused on "efficiently integrating equations of motion for atom types with orientational degrees of freedom" (from abstract). While OOPSE was further developed and renamed OpenMD, a fork of OOPSE was developed specifically to model water in two dimensions.

5.1.3 Literature Review on Relevant Works

intro: Paragraph refreshing current work. Emphasize computational efficiency of Rose-Potential over Mercedez-Benz model.

5.2 Goal of Project

The objective of this work was to model two-dimensional water with a surface designed to discourage crystal growth at freezing temperatures. The design of the surface was the primary focus. Successfully designing a surface capable of discouraging water ice formation at freezing temperatures would provide valuable information in designing a three-dimensional model of the same type at a reduced computational cost.

Idea: adjust freezing point depression to be freezing point modification.

5.3 Tools and Terms

Either a refresh from intro or a detailed explanation of OOPSE and the reduced terms.

5.3.1 OOPSE in 2D

Detail differences in computation system that Dr. Fennell developed to allow 2D MD(?) on a 3D program.

5.3.2 Reduced Terms: 2D analogues

Detail differences in dimensionality and define the reduced dimensions. Still working on the understanding/equations.

5.4 Designing System

Include: ensemble, thermodynamic variables, box attributes (size, pressure, temp, etc), number of waters, surface (size, spacing between beads of surface, charges, LJ values, etc)

5.4.1 Defining the Surface

Explain how to develop the surface in the program and how to build a custom surface

5.4.1.1 Manipulation of LJ Potential

Manipulate σ and ϵ values to effectively adjust the radius and interaction strength of surface beads.

5.4.1.2 Manipulation of bead spacing

Detail design of optimizing bead spacing for freezing encouragement or disruption.

5.5 Results

Success of freezing point elevation, pending results for freezing point depression

5.5.1 Future Work

Continued efforts to disrupt crystal growth on the surface.

CHAPTER 6

Conclusion

6.1 Ice I_h Generation

Review:

6.1.1 Purpose

6.1.2 Results

6.1.3 Flaws/Improvements

6.1.4 Practical Implications

Easier to generate crystals for modeling research

6.2 Conformation Landscapes

Review:

6.2.1 Purpose

6.2.2 Results

6.2.3 Flaws/Improvements

6.2.4 Practical Implications

Collected Program for general use

6.3 Modeling Germanium Compounds

Review:

6.3.1 Purpose

6.3.2 Results

6.3.3 Flaws/Improvements

6.3.4 Practical Implications

Discovered mistake to be fixed

6.4 Two-Dimensional Water

Review:

6.4.1 Purpose

6.4.2 Results

6.4.3 Flaws/Improvements

6.4.4 Practical Implications

super-duper anti-freeze? also freezing point elevation.

6.5 Super Duper Final Conclusion

References

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APPENDIX A

Ice Ih to Ice XI Conversion

Listed below is the source code utilized in the conversion of a PDB Ice Ih structure into an Ice XI structure.

A.1 Code: PDBDisorganize.py

```
1
2 #!/usr/bin/python
3
4 # Author = Gentry Smith
5 # Copyright 2016, all rights reserved
6
7 # this reads in a .PDB file , takes an argument for deformities per
8 # molecules , and randomly organizes the crystal
9 # structure into a disordered proton formation
10
11 # import sample: python PDBDisorganize.py arg1 arg2 arg3
12 # where:
13 # arg1 = source pdb file to be read (ex: acetone.pdb or acetone)
14 # arg2 = number of defects per molecule (in H2O, num of non-hydrogen-
15 # bonds. from 0 to 4)
16 # arg3 = desired output pdb file name
17
18 import sys
19 print sys.path
20 import string
21 import numpy as np
22 import math
23 import random
24
25 sys.setrecursionlimit(10000000) # maximum recursive depth. Set to
26 (10,000,000) as under maximum
27
28 pdbIN = file(sys.argv[1]) # source PDB file
29 maxErr = int(sys.argv[2]) # max errors allowed
30 pdbOUT = str(sys.argv[3]) # output file name
31 finalData = [ [ [ 0 for i in range(3) ] for j in range(3) ] for k in
32 range(300) ]
33
34 # looks at args validity
35 def checkArgs(arg1, arg2, arg3):
36     returnBool = False
37     if type(arg1) != file: # check arg1
```

```

35         print "Bad arg", arg1, " must be a file "
36         returnBool = True
37     if type(arg3) != str: # check arg3
38         print "Bad arg", arg3, ", must be a file name"
39         checkPDBSuffix(arg3)
40         print arg3
41         returnBool = True
42     if type(arg2) != int: # check arg2 type
43         print "Bad arg2: ", arg2, " is not an int."
44         returnBool = True
45     elif type(arg2) == int:
46         if arg2 < 0 or arg2 > 4: # check arg2 range
47             print "arg2 is not in a valid range 0 <= arg2 <= 4"
48             returnBool = True
49     return returnBool
50
51 def checkPDBSuffix(pdbFile):
52     if string.find(pdbFile, '.pdb', 0, len(pdbFile)) == -1:
53         print("did not find 'pdb' in ", pdbFile, ". Appending...")
54         pdbFile += '.pdb'
55
56
57
58 # reads in file ,
59 def readfile(fileName):
60     print "Reading file..."
61     # gets number of atoms
62     atoms = 0
63     for line in fileName:
64         data = line.split()
65         if len(data) > 0:
66             if data[0] != "CONNECT" and data[0] != "END":
67                 atoms += 1
68     # print "atoms: ", atoms
69     numMol = atoms / 3 # assumes 3-atom water molecule
70     dataTable = [ [ [ 0 for i in range(3) ] for j in range(3) ] for k in
71                   range(numMol) ]
72     fileName.seek(0)
73     iter0 = 0
74     iter1 = 0
75     pdbType = -1
76     for line in fileName:
77         data = line.split()
78         if pdbType == -1:
79             if data[0] == "ATOM":
80                 pdbType = 0
81             elif data[0] == "HETATM":
82                 pdbType = 1
83         # print "LineTuple=", data
84         if len(data) > 1 and ( data[0] == "ATOM" or data[0] == "HETATM"
85                               ):
86             if data[0] == "ATOM":
87                 newData = getDataATOM(data)
88                 for i in range(3):

```



```

87         #data[molecule][atom][X/Y/Z]
88         dataTable[iter0][iter1 % 3][i] = newData[i]
89     elif data[0] == "HETATM":
90         dataTable[iter0][iter1 % 3] = getDataHETATM(data)
91     if iter1 == 2:
92         iter0 += 1
93         iter1 = 0
94     elif iter1 != 2:
95         iter1 += 1
96 # print "DataTable: ", dataTable
97 print "File read"
98 return dataTable, pdbType
99
100
101 # Split by index
102 # if having a problem with reading data, check .pdb to see if data
103 # has a space between each value
104 # reads XYZ coordinate data from ATOM-type pdb
105 def getDataATOM(strLine):
106     # print "Getting ATOM Data..."
107     dataLine = strLine[5:8]
108     # print "dataline: ", dataLine
109     i = 0
110     while i < 3:
111         # print "dataline[", i, "]: ", dataLine[i]
112         dataLine[i] = float(dataLine[i])
113         # print "dataline[", i, "]" type: ", type(dataLine[i])
114         i += 1
115     return dataLine
116
117
118 # reads XYZ coordinate data from HETATM-type pdb
119 def getDataHETATM(strLine):
120     # print "Getting HETATM Data..."
121     dataLine = strLine[5:8]
122     # print "dataline: ", dataLine
123     i = 0
124     while i < 3:
125         # print "dataline[", i, "]: ", dataLine[i]
126         dataLine[i] = float(dataLine[i])
127         # print "dataline[", i, "]" type: ", type(dataLine[i])
128         i += 1
129     return dataLine
130
131
132 # gets all four position vectors of hydrogen/lone pair as offset of
133 # oxygen molecule
134 def getOrientations( molecule ):
135     # 120 degrees = ( 2 * pi ) / 3 radians
136     theta = ( ( 2 * math.pi ) / 3 )
137     newMol = zeroOrientation(molecule)
138     returnInt1 = rotateMolecule(newMol[1], newMol[2], theta)
139     returnInt2 = rotateMolecule(newMol[1], newMol[2], (-1 * theta) )

```

```

139     return [returnInt1, returnInt2]
140
141
142 # randomly selects new orientation, returns two unique ints, from 0 to 3
    inclusively
143 def newRandOrientation( positions ):
144     # print "Changing orientation"
145     randVal1 = random.randint(0,3)
146     randVal2 = random.randint(0,3)
147     while randVal1 == randVal2:
148         randVal2 = random.randint(0,3)
149     newMol = [ [ 0, 0, 0 ],
150                positions[ randVal1 ],
151                positions[ randVal2 ] ]
152     return newMol
153
154 # selects new orientation from list. Reduces computational overhead in
    re-orientation option traversal
155 def newSetOrientation( positions, pos1, pos2 ):
156     newMol = [ [ 0, 0, 0 ],
157                positions[ pos1 ],
158                positions[ pos2 ] ]
159     return newMol
160
161
162 # sets molecule coordinates so that oxygen is the origin
163 def zeroOrientation(source):
164     # print "Zeroing Molecule..."
165
166     oxy = source[0]
167     hyd1 = source[1]
168     hyd2 = source[2]
169
170     # print "Oxygen pos: ", oxy
171     # print "Hydrogen 1: ", hyd1
172     # print "Hydrogen 2: ", hyd2
173
174     zeroedOrigin = [0, 0, 0]
175     zeroedHyd1 = [0, 0, 0]
176     zeroedHyd2 = [0, 0, 0]
177     for i in range(3):
178         zeroedHyd1[i] = hyd1[i] - oxy[i]
179         zeroedHyd2[i] = hyd2[i] - oxy[i]
180
181     # print "Zeroed Hydrogen 1: ", zeroedHyd1
182     # print "Zeroed Hydrogen 2: ", zeroedHyd2
183
184     # return new molecule position
185     newMol = [zeroedOrigin, zeroedHyd1, zeroedHyd2]
186     return newMol
187
188 # resets the zeroed molecule to the original oxygen position
189 def resetOrientation(oxygenPos, molecule):
190     # print "Resetting molecule..."

```

```

191 rO = oxygenPos
192 rH1 = [0,0,0]
193 rH2 = [0,0,0]
194 newMol = []
195 for i in range(3):
196     rH1[i] = molecule[1][i] + rO[i]
197     rH2[i] = molecule[2][i] + rO[i]
198     newMol = [rO, rH1, rH2]
199 # print "Rebuilt Molecule: ", newMol
200 return newMol
201
202 # rotates vector about axis for theta degrees
203 # Handler for rotationMatrix function below
204 def rotateMolecule(vector, axis, theta):
205     rotMatx = rotationMatrix(axis, theta)
206     return np.dot(rotMatx, vector)
207
208
209 # Creates Rotation matrix for a given axis and theta
210 # from stackoverflow user unutbu
211 # page: http://stackoverflow.com/questions/6802577/python-rotation-of-3d-vector
212 def rotationMatrix(axis, theta):
213     """
214
215     :type axis: list
216     :type theta: union
217     """
218     axis = np.asarray(axis)
219     theta = np.asarray(theta)
220     axis /= math.sqrt(np.dot(axis, axis))
221     a = math.cos(theta/2.0)
222     b, c, d = -axis*math.sin(theta/2.0)
223     aa, bb, cc, dd = (a * a), (b * b), (c * c), (d * d)
224     bc, ad, ac, ab, bd, cd = (b * c), (a * d), (a * c), (a * b), (b * d), (c * d)
225     return np.array([ [ (aa + bb - cc - dd), ( 2 * ( bc + ad ) ), ( 2 *
226         ( bd - ac ) ) ],
227         [ ( 2 * ( bc - ad ) ), (aa + cc - bb - dd), ( 2 *
228         ( cd + ab ) ) ],
229         [ ( 2 * ( bd + ac ) ), ( 2 * ( cd - ab ) ), (aa +
230         dd - bb - cc) ] ] )
231
232 # gets results from rotateAboutAxis plus two Hydrogens to get the
233 # tetrahedron positions
234 def getTetrahedronPositions(molecule):
235     positions = [ [ 0 for i in range(3) ] for j in range(4) ]
236     newMol = zeroOrientation(molecule) # zero molecule
237     positions[0] = newMol[1]
238     positions[1] = newMol[2]
239     newPos = getOrientations(molecule) # get final two positions
240     positions[2] = list(newPos[0])
241     positions[3] = list(newPos[1])

```

```

239     return positions                                # return all four positions
240
241
242 # checks distance of new positions from zero
243 def checkDist(posArray):
244     distance = [0 for i in range(len(posArray))]
245     for i in range(len(posArray)):
246         distance[i] = ( (posArray[i][0] * posArray[i][0]) +
247                         (posArray[i][1] * posArray[i][1]) +
248                         (posArray[i][2] * posArray[i][2]) )
249         # print "Distance", i, ": ", distance[i]
250     avg = 0
251     for i in range(len(posArray)):
252         avg += distance[i]
253     averageDistance = ( avg / len(posArray) )
254     # print "Average Distance: ", averageDistance
255     return averageDistance
256
257
258 # prints data given a 3D table of water molecules
259 def printData(data):
260     print "Data: "
261     strData = [" O", "H1", "H2"]
262     dimData = ["X", "Y", "Z"]
263     bigAvg = 0
264     numAtoms = 0
265     for mol in range(len(data)):
266         for atom in range(len(data[mol])):
267             printStr = str(mol) + ": " + strData[atom] + ": "
268             for dimension in range(3):
269                 printStr += dimData[atom] + ":" + "{:7.3f}".format(data[
270 mol][atom][dimension]) + "\t"
271             print printStr
272             bigAvg += checkDist(zeroOrientation(data[mol])[1:])
273             numAtoms += 1
274             print ""
275     print "total average distance: ", bigAvg / numAtoms
276
277 # checks validity of molecule
278 def isDefectiveCheck(err, neighborData, posData, index):
279     # find nearby molecules (avg oxygen distance???)
280     print "checking for defects at index", index, "..."
281     print "neighbor indices: ", neighborData[index]
282     returnBool = False
283     neighbors = 4
284     for i in range(4): # count real neighbors
285         if neighborData[index][1][i] == -1:
286             neighbors -= 1
287     if neighbors <= err: # de facto good if num(neighbors) <
288 maxErrAllowed
289     # print "Fewer neighbors than allowed errors. de facto Good
290 Orientation"
291     returnBool = True

```

```

290     elif neighbors > err: # enough neighbors to require check
291         # print "More neighbors than error threshold"
292         defectCount = 0
293         for neighbor in range(4): # check each neighbor
294             if neighborData[index][1][neighbor] != -1: # skip over non-
existent neighbors
295                 molA = posData[index]
296                 molB = posData[ neighborData[index][1][neighbor] ]
297                 oxyDist = getDistBetweenAtoms(molA[0], molB[0])
298
299                 if minHydrogenDistance(molA, molB) > oxyDist: # check
for facing lone pairs
300                     print "Double Lone Pair defect"
301                     defectCount += 1
302                     break
303                 else: # check for facing protons
304                     smallerHydrogenDistanceCount = 0
305                     isDefective = False
306                     for first in range(2):
307                         if not isDefective:
308                             for second in range(2):
309                                 newDist = getDistBetweenAtoms(molA[ first
+ 1], molB[second + 1])
310                                     if newDist < oxyDist:
311                                         smallerHydrogenDistanceCount += 1
312                                     if smallerHydrogenDistanceCount > 1:
313                                         print "Double Hydrogen defect"
314                                         defectCount += 1
315                                         isDefective = True
316             # print "Defects found:", defectCount
317             if defectCount > 4:
318                 print "IMPOSSIBLE AMOUNT OF DEFECTS DETECTED!!!!"
AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA
319             if defectCount > err:
320                 # print "Found a bad molecule!"
321                 returnBool = False
322             else:
323                 # print "Molecule is within parameters."
324                 returnBool = True
325
326         return returnBool
327
328
329 # randomly re-reorients molecule and neighbors, rechecks all
330 def rerunMolAndNeighbors(err, neighborData, posData, index):
331     # print "Re-reordering molecule at", index
332     # err - max errors allowed
333     # neighborData - int[4] of neighbor indices
334     # posData - array of all molecule position vectors
335     # index - location of focus molecule in posData
336     isGood = False
337     timeCount = 0
338     while not isGood:

```

```

339         # re-rotate molecule through all positions (iterated through all
orientations)
340         positions = getTetrahedronPositions(posData[index])
341         zeroedMol = newRandOrientation(positions)
342         # print "isGood CHECK", isGood
343         isGood, posData = iterThroughRotations(err, neighborData,
posData, index)
344         posData[index] = resetOrientation(posData[index][0], zeroedMol)
345         if timeCount >= 13: # { (1 - 1/6)^n < 0.05 } says n = 17
346             # BROKEN - need to rebuild
347             # 0. evaluated molecule has too many defects
348             # 1. reorient molecule statistically probable amount of
times to cover all orientations
349             # 2. Repeat 1. with neighbor 1
350             # 2a repeat 1. with original molecule
351             # 3. Repeat 2. with neighbor 2, 3, 4, as/if necessary
352             for neighborIndex in range(4):
353                 if neighborData[index][1][neighborIndex] != -1:
354                     positions = getTetrahedronPositions(posData[
neighborIndex])
355                     zeroedMol = newRandOrientation(positions)
356                     posData[neighborIndex] = resetOrientation(posData[
neighborIndex][0], zeroedMol)
357                     # isGood = isDefectiveCheck(err, neighborData,
posData, neighborIndex)
358                     isGood = isDefectiveCheck(err, neighborData, posData, index)
359                     if not isGood:
360                         isGood, posData = rerunMolAndNeighbors(err, neighborData
, posData, neighborData[index][1][neighborIndex])
361                     finalData = posData
362                     return True, finalData
363
364 # iterates molecule through all possible rotations
365 def iterThroughRotations(err, neighborData, posData, index):
366     isGood = False
367     pos1 = 0 # tetrahedral position for H1
368     pos2 = 0 # tetrahedral position for H2
369     while not isGood or (pos1 != 3 and pos2 != 3): # iterates through
all orientations, stops if good orientation
370         if pos1 != pos2:
371             posData[index] = newSetOrientation(posData[index][0], pos1,
pos2)
372             isGood = isDefectiveCheck(err, neighborData, posData, index)
373             if pos2 < 3:
374                 pos2 += 1
375             elif pos2 == 3:
376                 if pos1 < 3:
377                     pos1 += 1
378                 pos2 = 0
379             return isGood, posData
380 # determines minimum hydrogen distance between two atoms
381 def minHydrogenDistance(mol1, mol2):
382     minDist = 100
383     for first in range(2):

```

```

384         for second in range(2):
385             newDist = getDistBetweenAtoms(mol1[first+1], mol2[second+1])
386             if newDist < minDist:
387                 minDist = newDist
388         return minDist
389
390
391
392
393
394 # finds neighboring molecules of each molecule
395 def getNeighbors(data):
396     returnData = [ [ [ 0 for i in range(4) ] for j in range(2) ] for k
397                     in range(len(data)) ] # data[molecule][distance,index][four values]
398     for mol1 in range(len(data)):
399         minDist = [100, 100, 100, 100]
400         minIndex = [0, 0, 0, 0]
401         for mol2 in range(len(data)):
402             if mol1 != mol2:
403                 newMin = getDistBetweenAtoms(data[mol1][0], data[mol2
404                                                 ][0])
405                 bigIndex = indexOfBiggest(minDist)
406                 if newMin < minDist[bigIndex]:
407                     minDist[bigIndex] = newMin
408                     minIndex[bigIndex] = mol2
409                 for i in range(4):
410                     if minDist[i] >= 9:
411                         minDist[i] = -1
412                         minIndex[i] = -1
413                 # print "Four smallest Distances of", mol1, ": ", minDist
414                 # print "Four smallest Indices of", mol1, ": ", minIndex
415                 returnData[mol1] = [minDist, minIndex]
416         return returnData
417
418 # finds distance between oxygen atoms
419 def getDistBetweenAtoms( mol1, mol2 ):
420     distance = ( ( ( mol1[0] - mol2[0] ) * ( mol1[0] - mol2[0] ) ) +
421                 ( ( mol1[1] - mol2[1] ) * ( mol1[1] - mol2[1] ) ) +
422                 ( ( mol1[2] - mol2[2] ) * ( mol1[2] - mol2[2] ) ) )
423     return distance
424
425 # gets index of largest item from a list
426 def indexOfBiggest(check):
427     bigIndex = 0
428     for i in range(len(check)):
429         if check[i] > check[bigIndex]:
430             bigIndex = i
431     return bigIndex
432
433
434 # writes data to PDB file
435 def writeDataPDB(data, pdbType):

```

```

436     print "Writing Data to", str(pdbOUT)
437     fileName = str(pdbOUT)
438     output = open(fileName, 'w')
439     if pdbType == 0:
440         writeDataPDBATOM(data, output)
441     elif pdbType == 1:
442         writeDataPDBHETATM(data, output)
443     output.close()
444
445
446 # Writes data to PDB file style = ATOM
447 def writeDataPDBATOM(data, inFile):
448     iterator = 0
449     for molecule in range(len(data)):
450         for atom in range(3):
451             iterator += 1
452             outStr = "ATOM "
453             outStr += str(iterator)
454             while len(outStr) < 11:
455                 outStr = outStr[:6] + " " + outStr[6:]
456             outStr += " "
457             if atom == 0:
458                 outStr += " O " + " WAT"
459             elif atom == 1:
460                 outStr += " H1 " + " WAT"
461             elif atom == 2:
462                 outStr += " H2 " + " WAT"
463             outStr += str(molecule)
464             while len(outStr) < 26:
465                 outStr = outStr[:20] + " " + outStr[20:]
466             outStr += " "
467             outStr += "{:8.3f}".format(data[molecule][atom][0])
468             outStr += "{:8.3f}".format(data[molecule][atom][1])
469             outStr += "{:8.3f}".format(data[molecule][atom][2])
470             outStr += " 1.00" + " 0.00"
471             outStr += " "
472             if atom == 0:
473                 outStr += " O "
474             elif atom == 1:
475                 outStr += " H "
476             elif atom == 2:
477                 outStr += " H "
478             outStr += "\n"
479             inFile.write(outStr)
480
481
482 # Writes data to PDB file style = HETATOM
483 def writeDataPDBHETATM(data, inFile):
484     iterator = 0
485     for molecule in range(len(data)):
486         for atom in range(3):
487             iterator += 1
488             outStr = "HETATM"
489             outStr += str(iterator)

```



```

490         while len(outStr) < 11:
491             outStr = outStr[:6] + " " + outStr[6:]
492         outStr += " "
493         if atom == 0:
494             outStr += " O " + " WAT"
495         elif atom == 1:
496             outStr += " H1 " + " WAT"
497         elif atom == 2:
498             outStr += " H2 " + " WAT"
499         outStr += str(molecule)
500         while len(outStr) < 26:
501             outStr = outStr[:20] + " " + outStr[20:]
502         outStr += " "
503         outStr += "{:8.3f}".format(data[molecule][atom][0])
504         outStr += "{:8.3f}".format(data[molecule][atom][1])
505         outStr += "{:8.3f}".format(data[molecule][atom][2])
506         outStr += " 1.00" + " 0.00"
507         outStr += " "
508         if atom == 0:
509             outStr += " O "
510         elif atom == 1:
511             outStr += " H "
512         elif atom == 2:
513             outStr += " H "
514         outStr += "\n"
515         inFile.write(outStr)
516
517
518 # runs program
519 def testRun(inFile, err, outFile):
520     print "Running Test Version of Program..."
521
522
523 # this is the parent runner for the program
524 def runPgm(inFile, err):
525     print "Running Program..."
526     data, pdbType = readFile(inFile)
527     newData = [ [ [ 0 for i in range(3) ] for j in range(3) ] for k in
528 range(len(data)) ]
529     print "Reordering Molecules..."
530     for i in range(len(data)):
531         positions = getTetrahedronPositions(data[i])
532         zeroedMol = newRandOrientation(positions)
533         newMol = resetOrientation( data[i][0], zeroedMol )
534         newData[i] = newMol
535     print "Molecules Reordered"
536     connectedMolecules = getNeighbors(newData) # -1 index = not
537     neighboring
538     finalData = newData
539     for i in range(len(connectedMolecules)):
540         # print "check defects"
541         isFine = isDefectiveCheck(err, connectedMolecules, finalData, i)
542         # print "isFINE CHECK", isFine
543         if not isFine:

```

```

542         # print "fixing defects"
543         while not isFine:
544             # print "RerunMol"
545             isFine, finalData = rerunMolAndNeighbors(err,
connectedMolecules, finalData, i)
546             # print "rerunDone"
547             writeDataPDB(finalData, pdbType)
548             # printData(newData)
549
550
551 badArgs = checkArgs(pdbIN, maxErr, pdbOUT) # stop in case of bad
argument
552
553 # check input args
554 if not badArgs: # stop in case of bad argument
555     print "Good Arguments, Initializing Reorientation with", maxErr, "
maximum defects"
556     # testRun(pdbIN, maxErr, pdbOUT)
557     runPgm(pdbIN, maxErr)
558 elif badArgs:
559     print "Bad Arguments, Quitting..."

```

APPENDIX B

Conformation Landscapes

APPENDIX C

Germanium Landscape

Listed below are two example Germanium PDB files. The first is for the end-goal hexagermane in the trans-trans-trans conformation with isopropyl groups on the terminal Ge atoms. The second is for the simplified butagermane with fully protonated Germanium atoms.

C.1 Code: hexagermane-transall.pdb

```
1 HEADER
2 REMARK Title: hexagermane-transall system
3 HETATM 1 Ge 1 -4.399 0.008 0.355 0.00 0.00
   Ge
4 HETATM 2 Ge 1 -1.965 0.138 -0.022 0.00 0.00
   Ge
5 HETATM 3 C 1 -4.822 1.886 0.961 0.00 0.00
   C
6 HETATM 4 C 1 -5.008 -1.297 1.715 0.00 0.00
   C
7 HETATM 5 C 1 -5.256 -0.261 -1.445 0.00 0.00
   C
8 HETATM 6 C 1 -1.213 1.435 1.157 0.00 0.00
   C
9 HETATM 7 Ge 1 -0.756 -1.988 0.223 0.00 0.00
   Ge
10 HETATM 8 C 1 -1.297 -2.917 1.805 0.00 0.00
   C
11 HETATM 9 Ge 1 1.647 -1.496 0.371 0.00 0.00
   Ge
12 HETATM 10 C 1 -1.182 -3.010 -1.339 0.00 0.00
   C
13 HETATM 11 C 1 2.131 -0.425 1.877 0.00 0.00
   C
14 HETATM 12 C 1 2.111 -0.634 -1.269 0.00 0.00
   C
15 HETATM 13 Ge 1 2.889 -3.585 0.738 0.00 0.00
   Ge
16 HETATM 14 C 1 2.287 -4.358 2.378 0.00 0.00
   C
17 HETATM 15 Ge 1 5.327 -3.386 1.080 0.00 0.00
   Ge
18 HETATM 16 C 1 2.766 -4.685 -0.813 0.00 0.00
   C
19 HETATM 17 C 1 5.688 -2.615 2.887 0.00 0.00
   C
```

20	HETATM	18	C	1	6.239	-2.415	-0.417	0.00	0.00
		C							
21	HETATM	19	C	1	5.893	-5.324	0.888	0.00	0.00
		C							
22	HETATM	20	C	1	-3.527	2.543	1.328	0.00	0.00
		C							
23	HETATM	21	C	1	-5.754	1.844	2.133	0.00	0.00
		C							
24	HETATM	22	H	1	-5.303	2.355	0.072	0.00	0.00
		H							
25	HETATM	23	H	1	-5.269	1.358	2.999	0.00	0.00
		H							
26	HETATM	24	H	1	-6.679	1.287	1.913	0.00	0.00
		H							
27	HETATM	25	H	1	-6.047	2.856	2.449	0.00	0.00
		H							
28	HETATM	26	H	1	-3.043	2.019	2.171	0.00	0.00
		H							
29	HETATM	27	H	1	-3.683	3.585	1.642	0.00	0.00
		H							
30	HETATM	28	H	1	-2.818	2.559	0.490	0.00	0.00
		H							
31	HETATM	29	H	1	-4.336	-1.167	2.589	0.00	0.00
		H							
32	HETATM	30	C	1	-4.907	-2.680	1.154	0.00	0.00
		C							
33	HETATM	31	C	1	-6.417	-0.909	2.051	0.00	0.00
		C							
34	HETATM	32	H	1	-3.858	-2.985	0.982	0.00	0.00
		H							
35	HETATM	33	H	1	-5.433	-2.773	0.187	0.00	0.00
		H							
36	HETATM	34	H	1	-5.349	-3.420	1.836	0.00	0.00
		H							
37	HETATM	35	H	1	-6.488	0.167	2.302	0.00	0.00
		H							
38	HETATM	36	H	1	-6.802	-1.477	2.909	0.00	0.00
		H							
39	HETATM	37	H	1	-7.103	-1.094	1.205	0.00	0.00
		H							
40	HETATM	38	C	1	5.200	-6.127	1.944	0.00	0.00
		C							
41	HETATM	39	C	1	7.384	-5.453	0.966	0.00	0.00
		C							
42	HETATM	40	H	1	5.523	-5.590	-0.126	0.00	0.00
		H							
43	HETATM	41	H	1	7.790	-4.974	1.874	0.00	0.00
		H							
44	HETATM	42	H	1	7.885	-4.994	0.099	0.00	0.00
		H							
45	HETATM	43	H	1	7.691	-6.509	0.992	0.00	0.00
		H							
46	HETATM	44	H	1	5.502	-5.821	2.960	0.00	0.00
		H							

47	HETATM	45	H	1	5.436	-7.197	1.849	0.00	0.00
		H							
48	HETATM	46	H	1	4.106	-6.027	1.879	0.00	0.00
		H							
49	HETATM	47	C	1	6.243	-1.232	2.746	0.00	0.00
		C							
50	HETATM	48	C	1	6.612	-3.524	3.636	0.00	0.00
		C							
51	HETATM	49	H	1	4.684	-2.582	3.376	0.00	0.00
		H							
52	HETATM	50	H	1	7.535	-3.731	3.068	0.00	0.00
		H							
53	HETATM	51	H	1	6.139	-4.497	3.853	0.00	0.00
		H							
54	HETATM	52	H	1	6.913	-3.088	4.599	0.00	0.00
		H							
55	HETATM	53	H	1	7.243	-1.234	2.279	0.00	0.00
		H							
56	HETATM	54	H	1	6.347	-0.742	3.725	0.00	0.00
		H							
57	HETATM	55	H	1	5.589	-0.589	2.128	0.00	0.00
		H							
58	HETATM	56	C	1	5.630	-1.055	-0.555	0.00	0.00
		C							
59	HETATM	57	H	1	6.024	-3.039	-1.315	0.00	0.00
		H							
60	HETATM	58	C	1	7.712	-2.342	-0.145	0.00	0.00
		C							
61	HETATM	59	H	1	7.923	-1.890	0.839	0.00	0.00
		H							
62	HETATM	60	H	1	8.227	-1.728	-0.898	0.00	0.00
		H							
63	HETATM	61	H	1	8.188	-3.335	-0.163	0.00	0.00
		H							
64	HETATM	62	H	1	4.573	-1.106	-0.861	0.00	0.00
		H							
65	HETATM	63	H	1	6.155	-0.455	-1.314	0.00	0.00
		H							
66	HETATM	64	H	1	5.675	-0.486	0.391	0.00	0.00
		H							
67	HETATM	65	H	1	-5.890	-1.163	-1.302	0.00	0.00
		H							
68	HETATM	66	C	1	-4.220	-0.487	-2.505	0.00	0.00
		C							
69	HETATM	67	C	1	-6.093	0.945	-1.729	0.00	0.00
		C							
70	HETATM	68	H	1	-6.841	1.122	-0.939	0.00	0.00
		H							
71	HETATM	69	H	1	-6.644	0.838	-2.676	0.00	0.00
		H							
72	HETATM	70	H	1	-5.478	1.858	-1.818	0.00	0.00
		H							
73	HETATM	71	H	1	-3.754	-1.481	-2.414	0.00	0.00
		H							

74	HETATM	72	H	1	-3.411	0.262	-2.459	0.00	0.00
		H							
75	HETATM	73	H	1	-4.659	-0.429	-3.512	0.00	0.00
		H							
76	HETATM	74	C	1	-1.706	1.681	2.429	0.00	0.00
		C							
77	HETATM	75	C	1	-0.128	2.155	0.679	0.00	0.00
		C							
78	HETATM	76	H	1	0.268	1.941	-0.323	0.00	0.00
		H							
79	HETATM	77	C	1	0.451	3.147	1.465	0.00	0.00
		C							
80	HETATM	78	C	1	-1.134	2.678	3.216	0.00	0.00
		C							
81	HETATM	79	C	1	-0.058	3.415	2.731	0.00	0.00
		C							
82	HETATM	80	H	1	-1.525	2.873	4.219	0.00	0.00
		H							
83	HETATM	81	H	1	1.306	3.716	1.086	0.00	0.00
		H							
84	HETATM	82	H	1	0.391	4.199	3.349	0.00	0.00
		H							
85	HETATM	83	C	1	-1.557	-4.274	1.694	0.00	0.00
		C							
86	HETATM	84	C	1	-0.365	-3.088	-2.455	0.00	0.00
		C							
87	HETATM	85	C	1	-2.027	-4.985	2.796	0.00	0.00
		C							
88	HETATM	86	H	1	-1.378	-4.792	0.742	0.00	0.00
		H							
89	HETATM	87	C	1	-1.446	-2.277	3.025	0.00	0.00
		C							
90	HETATM	88	C	1	-0.752	-3.866	-3.544	0.00	0.00
		C							
91	HETATM	89	H	1	0.592	-2.548	-2.482	0.00	0.00
		H							
92	HETATM	90	C	1	-2.386	-3.699	-1.304	0.00	0.00
		C							
93	HETATM	91	C	1	-2.219	-4.336	4.011	0.00	0.00
		C							
94	HETATM	92	H	1	-2.237	-6.056	2.707	0.00	0.00
		H							
95	HETATM	93	C	1	-1.915	-2.983	4.130	0.00	0.00
		C							
96	HETATM	94	H	1	-1.159	-1.217	3.132	0.00	0.00
		H							
97	HETATM	95	C	1	-2.771	-4.484	-2.388	0.00	0.00
		C							
98	HETATM	96	H	1	-3.043	-3.610	-0.422	0.00	0.00
		H							
99	HETATM	97	C	1	-1.952	-4.568	-3.509	0.00	0.00
		C							
100	HETATM	98	H	1	-0.105	-3.928	-4.425	0.00	0.00
		H							

101	HETATM	99	H	1	-3.721	-5.027	-2.358	0.00	0.00
		H							
102	HETATM	100	H	1	-2.253	-5.182	-4.364	0.00	0.00
		H							
103	HETATM	101	H	1	-2.596	-4.891	4.876	0.00	0.00
		H							
104	HETATM	102	H	1	-2.041	-2.474	5.091	0.00	0.00
		H							
105	HETATM	103	C	1	2.487	-3.679	3.571	0.00	0.00
		C							
106	HETATM	104	C	1	1.701	-5.563	-0.935	0.00	0.00
		C							
107	HETATM	105	C	1	3.733	-4.618	-1.807	0.00	0.00
		C							
108	HETATM	106	H	1	0.940	-5.615	-0.140	0.00	0.00
		H							
109	HETATM	107	C	1	1.598	-6.382	-2.057	0.00	0.00
		C							
110	HETATM	108	C	1	1.690	-5.609	2.382	0.00	0.00
		C							
111	HETATM	109	C	1	2.102	-4.259	4.776	0.00	0.00
		C							
112	HETATM	110	H	1	2.956	-2.680	3.567	0.00	0.00
		H							
113	HETATM	111	C	1	1.520	-5.523	4.784	0.00	0.00
		C							
114	HETATM	112	H	1	2.260	-3.721	5.716	0.00	0.00
		H							
115	HETATM	113	C	1	1.311	-6.197	3.585	0.00	0.00
		C							
116	HETATM	114	H	1	1.504	-6.131	1.431	0.00	0.00
		H							
117	HETATM	115	C	1	2.562	-6.313	-3.057	0.00	0.00
		C							
118	HETATM	116	H	1	0.754	-7.074	-2.153	0.00	0.00
		H							
119	HETATM	117	C	1	3.630	-5.430	-2.933	0.00	0.00
		C							
120	HETATM	118	H	1	4.590	-3.931	-1.700	0.00	0.00
		H							
121	HETATM	119	H	1	4.391	-5.376	-3.718	0.00	0.00
		H							
122	HETATM	120	H	1	2.481	-6.954	-3.941	0.00	0.00
		H							
123	HETATM	121	H	1	1.223	-5.984	5.731	0.00	0.00
		H							
124	HETATM	122	H	1	0.844	-7.187	3.587	0.00	0.00
		H							
125	HETATM	123	C	1	1.878	0.732	-1.306	0.00	0.00
		C							
126	HETATM	124	C	1	1.530	-0.534	3.120	0.00	0.00
		C							
127	HETATM	125	C	1	2.642	-1.289	-2.370	0.00	0.00
		C							

128	HETATM	126	C	1	2.179	1.455	-2.458	0.00	0.00
		C							
129	HETATM	127	H	1	1.444	1.239	-0.432	0.00	0.00
		H							
130	HETATM	128	C	1	3.179	0.461	1.679	0.00	0.00
		C							
131	HETATM	129	C	1	2.005	0.227	4.186	0.00	0.00
		C							
132	HETATM	130	H	1	0.661	-1.197	3.265	0.00	0.00
		H							
133	HETATM	131	C	1	2.940	-0.568	-3.524	0.00	0.00
		C							
134	HETATM	132	H	1	2.840	-2.370	-2.334	0.00	0.00
		H							
135	HETATM	133	C	1	2.710	0.804	-3.567	0.00	0.00
		C							
136	HETATM	134	H	1	1.989	2.533	-2.491	0.00	0.00
		H							
137	HETATM	135	H	1	3.358	-1.081	-4.396	0.00	0.00
		H							
138	HETATM	136	H	1	2.944	1.370	-4.475	0.00	0.00
		H							
139	HETATM	137	C	1	3.067	1.105	3.998	0.00	0.00
		C							
140	HETATM	138	H	1	1.534	0.140	5.170	0.00	0.00
		H							
141	HETATM	139	C	1	3.650	1.229	2.740	0.00	0.00
		C							
142	HETATM	140	H	1	3.633	0.553	0.682	0.00	0.00
		H							
143	HETATM	141	H	1	4.480	1.926	2.585	0.00	0.00
		H							
144	HETATM	142	H	1	3.439	1.703	4.836	0.00	0.00
		H							
145	HETATM	143	C	1	-2.039	0.838	-1.804	0.00	0.00
		C							
146	HETATM	144	C	1	-1.525	0.195	-2.916	0.00	0.00
		C							
147	HETATM	145	C	1	-2.655	2.077	-1.927	0.00	0.00
		C							
148	HETATM	146	C	1	-1.618	0.802	-4.168	0.00	0.00
		C							
149	HETATM	147	H	1	-1.048	-0.789	-2.818	0.00	0.00
		H							
150	HETATM	148	C	1	-2.746	2.686	-3.175	0.00	0.00
		C							
151	HETATM	149	H	1	-3.084	2.566	-1.036	0.00	0.00
		H							
152	HETATM	150	C	1	-2.223	2.047	-4.296	0.00	0.00
		C							
153	HETATM	151	H	1	-1.210	0.296	-5.049	0.00	0.00
		H							
154	HETATM	152	H	1	-3.229	3.663	-3.275	0.00	0.00
		H							

155	HETATM	153	H		1		-2.292	2.524	-5.279	0.00	0.00
		H									
156	HETATM	154	H		1		-2.539	1.081	2.827	0.00	0.00
		H									
157	CONECT	3	1	20	21	22					
158	CONECT	4	1	29	30	31					
159	CONECT	5	1	65	66	67					
160	CONECT	6	74	75	2						
161	CONECT	8	83	87	7						
162	CONECT	10	84	90	7						
163	CONECT	11	124	128	9						
164	CONECT	12	123	125	9						
165	CONECT	14	103	108	13						
166	CONECT	16	104	105	13						
167	CONECT	17	15	47	48	49					
168	CONECT	18	56	57	58	15					
169	CONECT	19	15	38	39	40					
170	CONECT	20	3	26	27	28					
171	CONECT	21	3	23	24	25					
172	CONECT	30	4	34	32	33					
173	CONECT	31	4	35	36	37					
174	CONECT	38	19	44	45	46					
175	CONECT	39	19	41	42	43					
176	CONECT	47	54	55	17	53					
177	CONECT	48	17	50	51	52					
178	CONECT	56	62	63	64	18					
179	CONECT	58	59	60	61	18					
180	CONECT	66	71	72	73	5					
181	CONECT	67	68	69	70	5					
182	CONECT	74	78	154	6						
183	CONECT	75	76	77	6						
184	CONECT	77	75	79	81						
185	CONECT	78	74	79	80						
186	CONECT	79	77	78	82						
187	CONECT	83	85	86	8						
188	CONECT	84	88	89	10						
189	CONECT	85	83	91	92						
190	CONECT	87	93	94	8						
191	CONECT	88	84	97	98						
192	CONECT	90	95	96	10						
193	CONECT	91	85	93	101						
194	CONECT	93	87	91	102						
195	CONECT	95	90	97	99						
196	CONECT	97	88	95	100						
197	CONECT	103	109	110	14						
198	CONECT	104	106	107	16						
199	CONECT	105	117	118	16						
200	CONECT	107	104	115	116						
201	CONECT	108	113	114	14						
202	CONECT	109	103	111	112						
203	CONECT	111	109	113	121						
204	CONECT	113	108	111	122						
205	CONECT	115	107	117	120						
206	CONECT	117	105	115	119						

207	CONECT	123	126	127	12
208	CONECT	124	129	130	11
209	CONECT	125	131	132	12
210	CONECT	126	123	133	134
211	CONECT	128	139	140	11
212	CONECT	129	124	137	138
213	CONECT	131	125	133	135
214	CONECT	133	126	131	136
215	CONECT	137	129	139	142
216	CONECT	139	128	137	141
217	CONECT	143	144	145	2
218	CONECT	144	143	146	147
219	CONECT	145	143	148	149
220	CONECT	146	144	150	151
221	CONECT	148	145	150	152
222	CONECT	150	146	148	153
223	CONECT	1	2	3	4
224	CONECT	2	1	143	6
225	CONECT	7	2	8	9
226	CONECT	9	7	11	12
227	CONECT	13	9	14	15
228	CONECT	15	13	17	18
229	CONECT	22	3		
230	CONECT	23	21		
231	CONECT	24	21		
232	CONECT	25	21		
233	CONECT	26	20		
234	CONECT	27	20		
235	CONECT	28	20		
236	CONECT	29	4		
237	CONECT	32	30		
238	CONECT	33	30		
239	CONECT	34	30		
240	CONECT	35	31		
241	CONECT	36	31		
242	CONECT	37	31		
243	CONECT	40	19		
244	CONECT	41	39		
245	CONECT	42	39		
246	CONECT	43	39		
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250	CONECT	49	17		
251	CONECT	50	48		
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253	CONECT	52	48		
254	CONECT	53	47		
255	CONECT	54	47		
256	CONECT	55	47		
257	CONECT	57	18		
258	CONECT	59	58		
259	CONECT	60	58		
260	CONECT	61	58		

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261 CONECT    62    56
262 CONECT    63    56
263 CONECT    64    56
264 CONECT    65     5
265 CONECT    68    67
266 CONECT    69    67
267 CONECT    70    67
268 CONECT    71    66
269 CONECT    72    66
270 CONECT    73    66
271 CONECT    76    75
272 CONECT    80    78
273 CONECT    81    77
274 CONECT    82    79
275 CONECT    86    83
276 CONECT    89    84
277 CONECT    92    85
278 CONECT    94    87
279 CONECT    96    90
280 CONECT    98    88
281 CONECT    99    95
282 CONECT   100    97
283 CONECT   101    91
284 CONECT   102    93
285 CONECT   106   104
286 CONECT   110   103
287 CONECT   112   109
288 CONECT   114   108
289 CONECT   116   107
290 CONECT   118   105
291 CONECT   119   117
292 CONECT   120   115
293 CONECT   121   111
294 CONECT   122   113
295 CONECT   127   123
296 CONECT   130   124
297 CONECT   132   125
298 CONECT   134   126
299 CONECT   135   131
300 CONECT   136   133
301 CONECT   138   129
302 CONECT   140   128
303 CONECT   141   139
304 CONECT   142   137
305 CONECT   147   144
306 CONECT   149   145
307 CONECT   151   146
308 CONECT   152   148
309 CONECT   153   150
310 CONECT   154    74
311 END

```

The above molecule contains 154 atoms and 153 bonds, making it extremely computationally expensive for regular(WHICH) QM calculations. This made utilizing

the large molecule as a trial system unreasonable due to the prohibitively long computation time for each conformation, assuming the conformation calculation would complete at all.

The below PDB file is the simplified butagermane with fully protonated Germanium atoms. As a significantly smaller system with only 14 atoms and 13 bonds, the relatively short computation time allowed the trial system to move with relative ease.

C.2 Code: ge4h.pdb

```

1 COMPND      UNNAMED
2 AUTHOR      GENERATED BY OPEN BABEL 2.3.90
3 HETATM      1 GE      UNL      1      -3.520      1.842      -0.078      1.00      0.00
               Ge3—
4 HETATM      2 GE      UNL      1      -1.368      2.888      -0.034      1.00      0.00
               Ge2—
5 HETATM      3 GE      UNL      1      0.324      1.200      0.059      1.00      0.00
               Ge3—
6 HETATM      4 GE      UNL      1      2.475      2.248      0.099      1.00      0.00
               Ge
7 HETATM      5 H      UNL      1      -4.622      2.930      -0.135      1.00      0.00
               H
8 HETATM      6 H      UNL      1      -3.699      0.985      1.202      1.00      0.00
               H
9 HETATM      7 H      UNL      1      -3.621      0.932      -1.328      1.00      0.00
               H
10 HETATM     8 H      UNL      1      -1.258      3.797      1.217      1.00      0.00
               H
11 HETATM     9 H      UNL      1      -1.178      3.740      -1.314      1.00      0.00
               H
12 HETATM    10 H      UNL      1      0.213      0.288      -1.189      1.00      0.00
               H
13 HETATM    11 H      UNL      1      0.135      0.352      1.342      1.00      0.00
               H
14 HETATM    12 H      UNL      1      2.655      3.095      -1.186      1.00      0.00
               H
15 HETATM    13 H      UNL      1      3.578      1.161      0.165      1.00      0.00
               H
16 HETATM    14 H      UNL      1      2.574      3.167      1.343      1.00      0.00
               H
17 CONECT      1      2      5      6      7
18 CONECT      2      1      3      8      9
19 CONECT      3      2      4     10     11
20 CONECT      4      3     12     13     14
21 CONECT      5      1
22 CONECT      6      1
23 CONECT      7      1
24 CONECT      8      2
25 CONECT      9      2
26 CONECT     10      3
27 CONECT     11      3
28 CONECT     12      4
29 CONECT     13      4
30 CONECT     14      4

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31	MASTER	0	0	0	0	0	0	0	0	14	0	14	0
32	END												

APPENDIX D

Two-Dimensional Rose-Potential Water

words

VITA

Gentry H. Smith

Candidate for the Degree of
Master of Science

Thesis: EXPLORING CRITICAL CONFORMATIONS

Major Field: Chemistry

Biographical:

Personal Data: Born in Olathe, KS in November 1993.

Education:

Received a Bachelors of Science in Chemistry at Southern Nazarene University in May 2016.

Completed the requirements for the degree of Master of Science with a major in Chemistry at Oklahoma State University in May 2018.

Experience:

Professional Affiliations:

American Chemical Society

Awards

Colonel Andre Whitely Scholarship in Chemistry