A method for redesigning molecular mechanics force field parameterization by use of a Bayesian statistical framework

Bryce C. Manubay^{1,*}

¹University of Colorado - Department of Chemical and Biological Engineering (Dated: October 5, 2016)

This document describes a collected set of best practices for computing various physical properties from molecular simulations of liquid mixtures.

Keywords: best practices; molecular dynamics simulation; physical property computation

 $^{^{}st}$ bryce.manubay@colorado.edu

6 Todo list

10

11

12

13

14

15

16

17

18

19

21

22

23

24

I. Outline

A. Objectives

- Molecular dynamics simulation is becoming more integral to many scientific studies
 - Observing physical phenomena at a molecular scale (phase changes, ligand docking, etc.
 - Drug discovery and deisgn of new molecules
- The necessity for transferable and accurate force fields is therefore imperative
 - Transferability encourages use and provides convenience for scientists with wide arrays of research interests
 - Inaccurate force fields have been shown to grossly misrepresent even somewhat simple molecular systems (gaff2 lol, check for some other cites)
- A possible solution to the given problem can be by recasting the force field parameterization issue as a bayesian inference problem
- The objective of this paper is introduce a framework for using disparate experimental data in order to parameterize molecular mechanics force fields
- In this paper I will describe the process of collecting and organizing large amounts of high quality thermochemical data and preliminary use of the Multistate Bennett Acceptance Ratio (MBAR) as a means to improve sampling speed during the parameterization process.