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

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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

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Todo list

I. Outline

A. Objectives $(0.5pages)$

- Molecular dynamics simulation is becoming more integral to many scientific studies
  - Observing physical phenomena at a molecular scale (phase changes, ligand docking, etc.)[1]
  - Drug discovery and deisgn of new molecules[2]
- 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[3, 4]
- 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.

B. Significance $(0.5pages)$

C. Background and related literature $(1.5pages \pm 0.5pages)$

D. Methods $(1.5pages \pm 0.5pages)$

E. Progress $(1.5pages \pm 0.5pages)$

F. Research plan $(0.5pages)$

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[1] G. Jayachandran, V. Vishal, and V. S. Pande, The Journal of Chemical Physics **124**, 164902 (2006).
[2] M. De Vivo, M. Masetti, G. Bottegoni, and A. Cavalli, J. Med. Chem. **59**, 4035 (2016).
[3] O. F. Lange, D. van der Spoel, and B. L. de Groot, Biophys J **99**, 647 (2010).

[4] F. MartÃŋn-GarcÃŋa, E. Papaleo, P. Gomez-Puertas, W. Boomsma, and K. Lindorff-Larsen, PLoS One **10**, (2015).