New LAMMPS Modules for the Simulation of Protein-Surface Interactions with CHARMM

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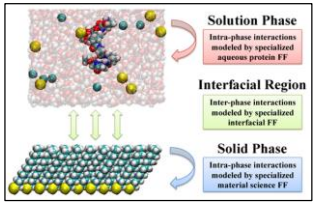
Introduction

- Protein-surface interactions important for broad range of application in bioengineering and biotechnology.
- Simulations of protein-surface interactions require:
  - Force fields for protein, surface, and interface
  - Advanced sampling for ensemble avg. properties
- The Latour group previously developed these capabilities for use with the CHARMM simulation program [1-4].

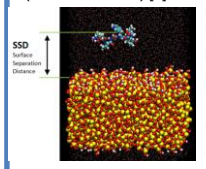
Independent Force Fields for Each Phase of System

Interfacial force field (IFF) to separately represent protein-surface interactions (both Lennard-Jones (ε, σ) and partial charge (q) parameters [1].

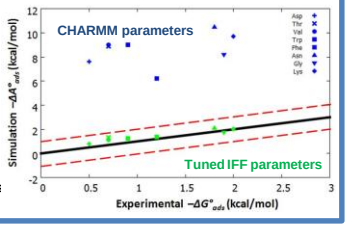


IFF Parameters Tuned To Match Experimental Data

Tuning of IFF parameters based on experimental measurements of peptide adsorption free energy using a host-guest peptide model (TGTG-X-GTGT) [2].

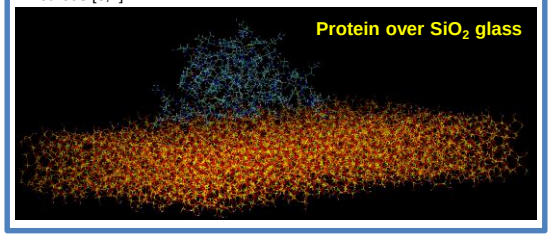


Peptide over SiO_2 glass



Tuned IFF Applied for Protein Adsorption Simulation

Application of IFF parameter set to simulate lysozyme adsorption to silica glass using TIGER2A. TIGER2/TIGER2A: Replica-exchange (REX) sampling algorithm for systems too large for conventional REX methods [3,4].



Objective

- Development of these capabilities in LAMMPS:
  - Modules to incorporate an interfacial force field including both L-J and partial charge parameter sets [1].
  - New fix_cmap module for CHARMM CMAP parameters
  - Modules for TIGER2 and TIGER2A advance sampling [3,4].

LAMMPS Modules:

- Modified LAMMPS data file format to include IFF partial charge in Atoms section.
- Perl scripts to convert CHARMM and LAMMPS regular data files into IFF-formatted LAMMPS data files.

IFF-Formatted LAMMPS Data File with qiff Column

Atoms

			q	X	Y	Z	qiff	
1	1	20	-0.470000	-15.363500000	1.139500000	19.847231000	-0.470000	# NH1
2	1	1	0.310000	-14.785500000	1.881500000	19.516231000	0.310000	# H
3	1	11	0.070000	-14.678500000	-0.118500000	20.263231000	0.070000	# CT1
4	1	4	0.090000	-15.153500000	-0.501500000	21.151231000	0.090000	# HB1
5	1	12	-0.180000	-14.759500000	-1.168500000	19.155231000	-0.180000	# CT2
6	1	7	0.090000	-13.983500000	-0.902500000	18.399231000	0.090000	# HA2
7	1	7	0.090000	-14.027500000	-0.946500000	18.392231000	0.090000	# HA2
8	1	12	-0.140000	-16.161500000	-1.148500000	18.544231000	-0.140000	# CT2
9	1	7	0.090000	-16.436500000	-2.159500000	18.176231000	0.090000	# HA2
10	1	7	0.090000	-16.401500000	-2.150500000	18.222231000	0.090000	# HA2
11	1	28	-0.090000	-16.442500000	-0.039500000	17.142231000	-0.090000	# S
12	1	14	-0.220000	-18.251500000	-0.091500000	17.172231000	-0.220000	# CT3
13	1	8	0.090000	-18.603500000	0.205500000	18.149231000	0.090000	# HA3
14	1	8	0.090000	-18.643500000	0.584500000	16.427231000	0.090000	# HA3
15	1	8	0.090000	-18.586500000	-1.095500000	16.959231000	0.090000	# HA3
16	1	9	0.510000	-13.208500000	0.178500000	20.567231000	0.510000	# C
17	1	24	-0.510000	-12.784500000	1.317500000	20.546231000	-0.510000	# O
18	2	20	-0.470000	-12.463500000	-0.855500000	20.846231000	-0.470000	# NH1
19	2	1	0.310000	-12.766500000	-1.807500000	20.860231000	0.310000	# H

New Section in LAMMPS Data File for CMAP Parameters

4153 atoms
3057 bonds
2644 angles
2695 dihedrals
136 impropers
54 crossterms

32 atom types
50 bond types
113 angle types
261 dihedral types

CMAP

Atom numbers for amino acid phi-psi dihedrals

1	1	16	18	20	30	32
2	1	30	32	34	51	53
3	1	51	53	55	73	75
4	1	73	75	77	92	94
5	1	92	94	96	111	113
6	1	111	113	115	130	132
7	1	130	132	134	144	146
8	5	144	146	148	151	153
9	1	151	153	155	173	175
10	1	173	175	177	187	189
11	1	187	189	191	206	208
12	1	206	208	210	228	230

Separate LAMMPS Data File for IFF L-J Parameters

IFF Pair Coeffs for protGI.data CREATED BY charmm2lammpsIFF

TypeNum	Epsilon	Sigma	TypeName
	IFF		
1	0.0460	0.4000135	# H
2	0.0460	0.4000135	# HC
3	0.0300	2.4200370	# HP
4	0.0220	2.3519730	# HB1
5	0.0280	2.3876090	# HB2

Utility Files to Facilitate IFF Parameter Adjustment

- Text file to facilitate modification of default CHARMM parameters to define new IFF parameters:
  - Section I.A to modify L-J ε and σ for existing Atom Types
  - Section I.B for creation of new Atom Types
  - Section II to modify partial charges for Atoms
  - Section III providing list of all atoms and associations
- Perl script to update LAMMPS data files with IFF parameters

IFF TUNING for protGI. CREATED BY charmm2lammpsIFF v1.8.2.iff.1 ON Mon Feb 16 09:47:37 EST 2015

SECTION I.A: LIST OF ORIGINAL ATOM TYPES IN SYSTEM

TypeNum	Mass	Original FF Type TypeName	Epsilon	Sigma	IFF Epsilon	Sigma	Flag
1	1.00800	H	0.0460	0.4000135	0.0460	0.4000135	
2	1.00800	HC	0.0460	0.4000135	0.0460	0.4000135	
3	1.00800	HP	0.0300	2.4200370	0.0300	2.4200370	
4	1.00800	HB1	0.0220	2.3519730	0.0220	2.3519730	
5	1.00800	HB2	0.0280	2.3876090	0.0280	2.3876090	

SECTION I.B: NEW ATOM TYPES ADDED TO SYSTEM

TypeNum	(eg: ALA) ResID	(eg: CA) ResAtomID	Original FF Type TypeName	Epsilon	Sigma	NewName	IFF Epsilon	Sigma	Flag

SECTION II: LIST OF MODIFICATIONS TO IFF PARTIAL CHARGE PARAMETERS

(ex:ALA) ResID	(eg: CA) ResAtomID	Orig FF PartialChrg	IFF PartialChrg	Flag

SECTION III: ATOMS IN MOLECULAR SYSTEM

AtomNum	ResID	ResAtomID	AtomTypeNum	IFF PartialChrg
1	MET	N	20	-0.4700
2	MET	HN	1	0.3100
3	MET	CA	11	0.0700
4	MET	HA	4	0.0900
5	MET	CB	12	-0.1800

Further Developments Required

- Fix remaining bugs in fix_cmap.cpp module
- Develop capability for 'special_bonds charmm' command to only be applied to CHARMM atoms in a hybrid CHARMM-Class II simulation .

Acknowledgements

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References

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2. Snyder J.A., et al., *Biointerphases*, 2008.
3. Li X., Stuart S.J., Latour R.A., *J. Chem. Phys.*, 2009.
4. Li X., Latour R.A., *J. Comput. Chem.*, 2011.

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