

SI2-SSE #1440581

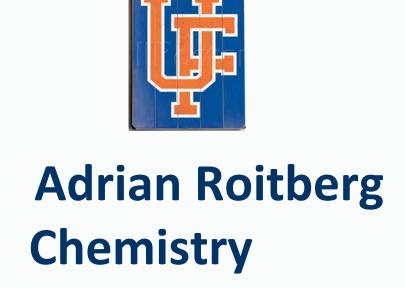
**NSF ACI** 

A Plug-and-Play Software Platform of Robotics-Inspired Algorithms for Modeling Biomolecular Structures and Motions

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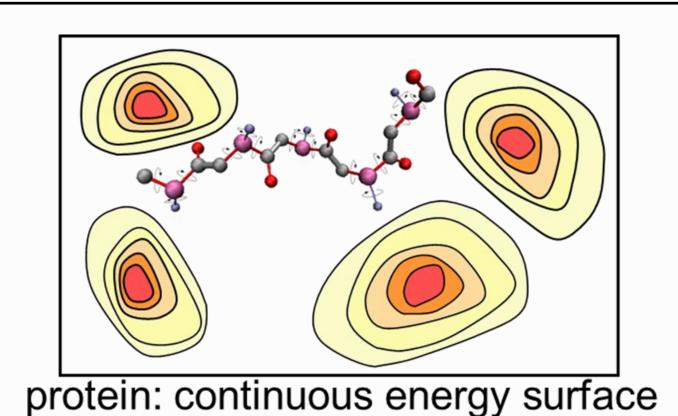
Project Page: http://cs.gmu.edu/~ashehu/?q=SI2-SSE15Project

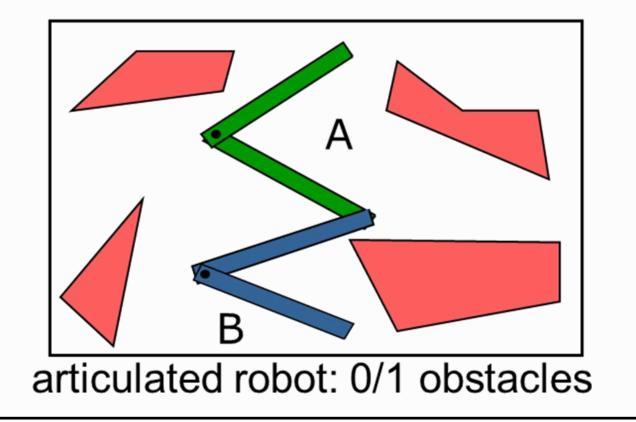
- □ <u>Objective</u>: Address algorithmic impasse on characterizing *protein and peptide structural dynamics* through a *plug-and-play platform of open-source software elements*.
- ☐ <u>Premise:</u> Address by integrating algorithmic efforts of AI researchers on *search and optimization* and modeling efforts of biophysics researchers on molecular mechanics and energetics.

## Application Setting:

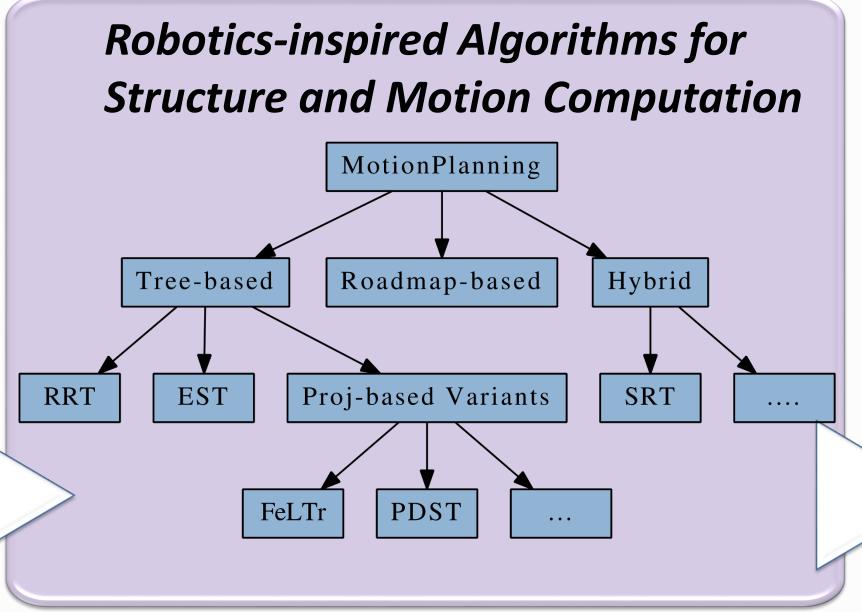
Protein and peptide structure and dynamics.

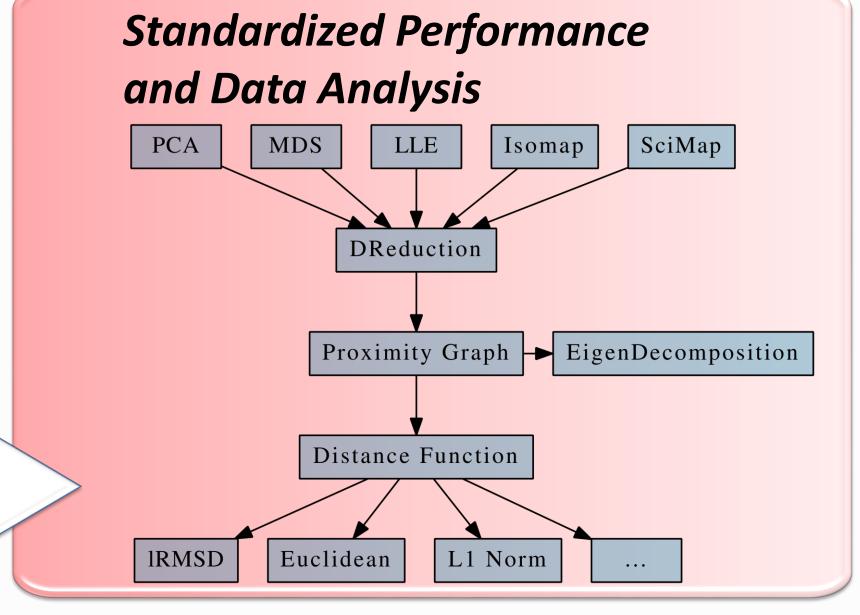
<u>Software elements</u> integrate search and optimization algorithms inspired from robot motion planning with sophisticated molecular models grounded in the latest understanding of protein biophysics.





State-of-the-art Molecular Representations and Energetic Models Structure Molecular Tree Conformation Building Blocks Kinematic Representation Structure Medium Cartesian Coarse Energy Structure Conformation Head-Gordon Rosetta FLibs Protocols Mover AMBER **Building Block** Rosetta Fragment





## **Dissemination:**

- ☐ Open-source software (ROMEO) on gitlab.
- Workshops at ACM BCB 2018-2016, IEEE BIBM 2015, ACM GECCO 2017-2015.
- ☐ Tutorials on ROMEO at ACM BCB 2018, 2017.
- ☐ Testing labs of research collaborators (Ruth Nussinov/NCI, John Choy/Catholic Univ. of America, Carla Mattos/Northeastern Univ., Christopher McDermott-Roe/University of Pennsylvania).
- ☐ Educational partners (Nurit Haspel/Univ Mass Boston, Jing He/Old Dominion Univ., Brian Chen/Lehigh Univ, Lydia Tapia/Univ New Mexico, and others).
- Research articles (BMC Genomics 2018, JCB 2017, IEEE BIBM 2017, IEEE ICCABS 2017, JAIR 2016, ACM BCB 2016, IEEE/ACM TCBB 2016, Robotica 2016, IEEE NanoBioScience 2016, IEEE BIBM 2016, BICoB 2015).

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