Resource for Macromolecular Modeling and Bioinformatics • National Resource for Automated Molecular Microscopy • National Biomedical Computation Resource present:

### 'Hands-on' Workshop on Computational Biophysics





San Diego, California











The training workshop is organized jointly with the Automated Molecular Imaging Center at The Scripps Research Institute.

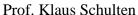
We thanks TSRI for its effort and hospitality. We thank in particular Professors Bridget Carragher and Clint Potter for their support and collegiality.

The Molecular Imaging Center is funded as a National Resource by NIH.

### The Program

### Hands-on Workshop in Computational Biology







Prof. Zan Luthey-Schulten



Prof. Emad Tajkhorshid

Locations at Scripps:

Lectures and labs: Room CB107

Breaks Room CB129



# Mon, 7/12: Introduction to Protein Structure and Dynamics



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09:00-09:10 Opening Remarks

09:10-10:40 Structure and Sequence Analysis with VMD

Break

11:00-12:00 Introduction to Molecular Dynamics with NAMD

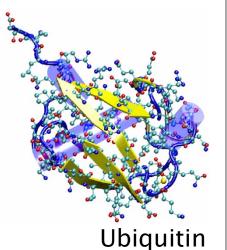
12:00-12:20 Q & A

Lunch

14:00-16:00 VMD Tutorial - Using VMD; NAMD Tutorial

Break

16:15-18:00 VMD Tutorial - Using VMD; NAMD Tutorial



# Tue, 7/13: Statistical Mechanics of Proteins



09:00-10:30 Analysis of Equilibrium and Non-equilibrium Properties of

Proteins with NAMD

Break

10:50-12:00 Exemplary Applications of VMD / NAMD in Modern Research

12:00-12:30 Q & A; Group picture

Lunch

14:00-16:00 Tutorial options: NAMD Tutorial & Stretching Deca-alanine;

Expert NAMD Set Tutorials; Free Energy Set Tutorials

Break

16:15-18:00 Tutorial options: NAMD Tutorial & Stretching Deca-alanine;

Expert NAMD Set Tutorials; Free Energy Set Tutorials



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# Wed, 7/14: Introduction to Bioinformatics



AspRS-tRNA

09:00-10:30	Introduction to Evolutionary Concepts in Bioinformatics:
	7.5.1.6

MultiSeq in VMD

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10:50-12:00 Application of MultiSeq to Evolution of Translation Machinery

12:00-12:20 Daily Q & A

#### Lunch

13:20-14:20 NBCR CADD Pipeline – Rommie Amaro

14:20-16:00 Tutorial options: Basic Sequence Analysis - Aquaporins with VMD;

Expert Sequence Analysis - Evolution of Translation - tRNA,

Ribosome, EF-Tu; Work on own projects

#### Break

16:15-18:00 Tutorial options: Basic Sequence Analysis - Aquaporins with VMD;

Expert Sequence Analysis - Evolution of Translation - tRNA,

Ribosome, EF-Tu; Work on own projects

## Thu, 7/15: Parameters for Classical Force Fields



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09:00-10:30 Int	ntroduction to Topol	ogy, Parameters, ar	d Structure Files
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Break

10:50-12:00 Examples and Applications

12:00-12:20 Q & A

Lunch

14:00-14:30 Overview of NRAMM – Bridget Carragher

14:30-16:30 Parameterizing a Novel Residue

Break

16:45-18:00 Topology File Tutorial

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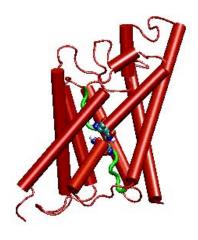
Catalytic domain

## Fri, 7/16: Simulating Membrane Channels

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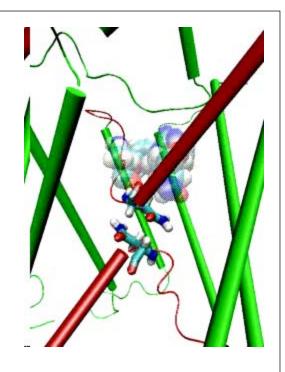


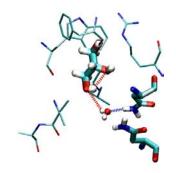
09:00-10:30	Introduction and Examples	
Break		
10:50-12:00	Transport in Aquaporins; Nanotubes	
12:00-12:20	Daily Q&A	
Lunch		Water Permeation through Aquaporin
14:00-16:00	Tutorial options: Membrane Proteins & Nanotubes Tutorials; Expert NAMD Set Tutorials; Free Energy Set Tutorials	
Break		
16:15-18:00 Tutorial options: Membrane Proteins & Nanotubes Tutorials; Expert NAMD Set Tutorials; Free Energy Set Tutorials		•



### General

- The course is a volunteer effort
- The main focus are the hands-on sessions
- The aim is to get you to do computational biology
- The lecturers / teaching assistants provide tutorials for you
- The optimal course is that you help each other
- Model your own system
- Please give us feedback to improve lectures and tutorials
- Please give us feedback to encourage future courses





### Acknowledgements

#### Teaching Assistants



Jen Hsin



J.C. Gumbart



John Eargle

National Institutes of Health, National Center for Research Resources:

National Biomedical Computation Resource Peter Arzberger, Director

National Resource for Automated Molecular Microscopy

Dr. Bridget Carragher, Director