

SCHOOL:

COMPUTER SIMULATIONS OF BIOLOGICAL MEMBRANES

&

FREE ENERGY CALCULATIONS OF BIOMOLECULAR SYSTEMS

DATE: August 13-17, 2018

VENUE: University of Los Andes, Bogotá, Colombia

WEB: https://mptg-cbp.github.io/teaching/mem-fe-2018/

ORGANIZER:

Max Planck Tandem Group in Computational Biophysics



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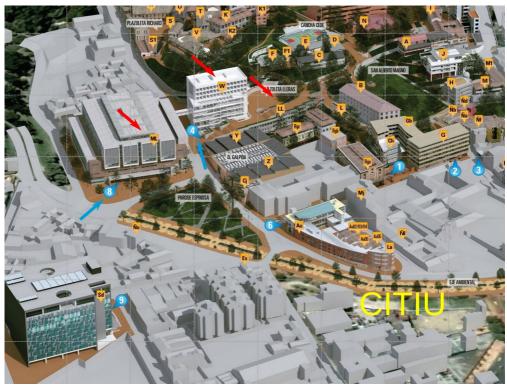
MAPS

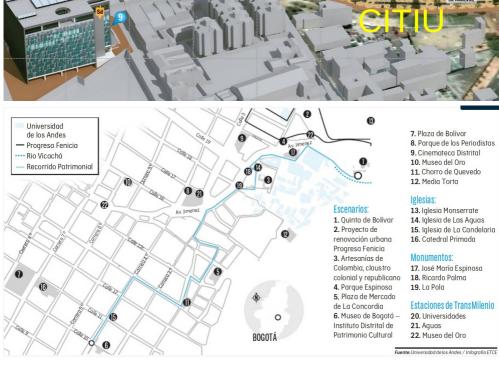
Buildings (red arrows): W, ML, and LL

Entrances (blue arrows):

Entrance 4. "Lleras" Address: Calle 19A Nº 1 - 37 Este

Entrance 8. "Mario Laserna" Address: Cra. 1 Este Nº 19A - 40





PROGR	PROGRAM OVERVIEW (ROOM)						
	PART 1: membranes			PART 2: free energy			
	Monday (13.08)	Tuesday (14.08)	Wed. (15.08)	Thursday (16.08)	Friday (17.08)		
8:00 – 9:00	Registration W101						
9:00 – 9:30	Welcome W101			Gian Pietro Miscione	Bert de Groot		
9:30 -	Bert de Groot	Thomas Walz	Chad Leidy	W101	EG		
10:30	W101	(webinar) MLC	W101	CT4: Hugo J. Bohórquez / W101	Coffee break		
10:30 – 11:00	Coffee break						
11:00 – 12:00	Helgi Ingólfsson W101	Gerhard Hummer MLC	CT2: Karen Palacio CT3: Sergio Mares-Samano W101	Esteban Vohringer- Martínez W101	Hands on LL002 W504		
12:00 – 14:00	Lunch			Lunch			
14:00 - 15:00	Gerhard Hummer W101	Bert de Groot MLC		Andrés González W101			
15:00	Vytas Gapsys / Camilo Aponte /	Helgi	Free program	Coffee break	Vytas Gansys		
16:00	CT1: Florian Franz W101	Ingólfsson MLC	Tree program	CT5: Angélica Sandoval CT6: Stefany	Vytas Gapsys MLC		
16:00 - 16:40	Coffee break			Botero Rodríguez W101	Closing remarks & departure MLC		
16:40 - 19:00	Hands on LL001 LL002	Hands on LL001 LL002		Poster session Hall ML AB			

PROGRAM IN DETAIL

PART 1: COMPUTER SIMULATIONS OF BIOLOGICAL MEMBRANES				
Monday, August 13				
Time	Room			
8:00 – 9:00	W101	Registration		
9:00 – 9:30		Welcome		
9:30 – 10:30	W101	Bert de Groot MPIBPC, Göttingen	The molecular dynamics of solute permeation through biological membranes and membrane proteins	
10:30 - 11:00		Coffee break		
11:00 – 12:00	W101	Helgi Ingólfsson LLNL, Livermore	Coarse-grained simulations: introduction and application to membranes	
12:00 – 14:00		Lunch		
14:00 – 15:00	W101	Gerhard Hummer MPIB, Frankfurt	Large finite-size effects in molecular dynamics simulations of membranes	
15:00 – 15:20	W101	Vytautas Gapsys MPIBPC, Göttingen	Grid-based methods for the analysis of MD simulations of biological membranes I: g_lomempro	
15:20 – 15:40	W101	Camilo Aponte UANDES, Bogotá	Grid-based methods for the analysis of MD simulations of biological membranes II: GROmars	
15:40 – 16:00	W101	Contributed talk 1: Florian Franz IWR, Heidelberg	Stability of Biological Membranes upon Mechanical Indentation	
16:00 – 16:10		Photo		
16:10 – 16:30		Coffee break		
16:30 – 16:40		Heading to computer room		
16:40 – 19:00	LL001/ LL002	Hands on: all-atom MD simulations of biological membranes Introductory (LL001) – Advanced (LL002)		
19:00 –		Invited speakers dinner		
Tuesday,	Tuesday, August 14			
9:30 – 10:30	MLC	Webinar, Thomas Walz Rockefeller, New York	Electron Microscopy Approaches to Studying Lipid-Protein Interactions	
10:30 –		Coffee break		

MLC	Gerhard Hummer MPIB, Frankfurt	Molecular dynamics simulations of proteins that sense the composition and state of lipid membranes	
	Lunch		
MLC	Bert de Groot MPIBPC, Göttingen	Permeation, selectivity and gating of ion channels studied by computational electrophysiology	
MLC	Helgi Ingolfson LLNL, Livermore	Capturing biological membranes in silico at different compositional complexity	
	Coffee break		
	Heading to computer room		
LL001/ LL002	Hands on: coarse-grained MD simulations of biological membranes Introductory (LL001) – Advanced (LL002)		
y, August	15		
W101	Chad Leidy UANDES, Bogotá	Integrating Computational and Experimental Approaches to InvestigateAntimicrobial Peptide Activity in Membranes	
	Coffee break		
W101	Contributed talk 2: Karen Palacio Rodríguez UDEA, Medellín	Exponential consensus ranking improves outcome in docking and receptor ensemble docking	
W101	Contributed talk 3: Sergio Mares-Samano UNAM, México City	Molecular dynamics studies of the solvation effects of water and trifluoroethanol on the peptides pandinin-2 (pin2) and pin2-GVG	
	free program		
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August 16	5		
W101	Gian Pietro Miscione UANDES, Bogotá	Mechanism of L-Tryptophan Prenylation, Catalyzed by FgaPT2: a Computational Study	
W101	Contributed talk 4: Hugo J. Bohórquez FIDIC, Bogotá	The frozen molecule approach in peptide- protein binding energies	
	Coffee break		
W101	Esteban Vohringer- Martínez	Force field improvement with ab-initio methods	
	MLC MLC LL001/ LL002 y, August W101 W101 REE ENE August 16 W101 W101	MPIB, Frankfurt Lunch MLC Bert de Groot MPIBPC, Göttingen MLC Helgi Ingolfson LLNL, Livermore Coffee break Heading to computer root Introductory (LL001) – Mands on: coarse-grain Introductory (LL001) –	

		UCONCEPCIÓN, Concepción		
12:00 – 14:00		Lunch		
14:00 – 15:00	W101	Andrés González UANDES, Bogotá	Applications of product design departing from free energy calculations	
15:00 – 15:30		Coffee break		
15:30 – 16:00	W101	Contributed talk 5: Angélica Sandoval UANDES, Bogotá	Specific at one side unspecific at the other: the interaction of blood proteins with extracellular DNA	
16:00 – 16:30	W101	Contributed talk 6: Stefany Botero Rodríguez UNAL, Bogotá	Computational Tracing of Protein and ncRNA epitopes inside Dengue Virus	
16:30 – 16:40		Heading to poster room		
16:40 – 19:00	Hall ML AB	Poster session (with wine and finger food)		
Friday, Aug	just 17			
9:00 – 10:00	MLC	Bert de Groot MPIBPC, Göttingen	Introduction to alchemical free energy calculations	
10:00 – 10:45		Coffee break		
10:45 – 12:45	LL002 W504	Hands on: Free energy calculations Introductory (LL002) – Advanced (W504)		
12:45 – 15:00		Lunch		
15:00 – 16:00	MLC	Vytas Gapsys MPIBPC, Göttingen	Application of the alchemical free energy calculations to proteins, nucleic acids and ligands	
16:00 – 16:30	MLC	Closing remarks and departure		

POSTERS

FU.	STERS	
1	Diego Gomez Hernandez UDISTRITAL, Bogotá	In silico evaluation of the potential afinity of anandamide analogues for CB1 receptor.
2	Carlos Pinilla UNORTE, Barranquilla	FeS all0ys at conditions of the Earth Interior
3	Juan David Orjuela UANDES, Bogotá	Effect of the lipid-protein interaction on the assembly of the platelet Glycoprotein-IB
4	Markus Kurth Heidelberg U. Heidelberg	Probing the lipid environment of the Metabotropic glutamate receptor 2
5	Laura Pinto Herrera UANDES, Bogotá	Effect of particulate matter on the lung surfactant at a high altitude city: Review
6	Johann Bedoya Cardona UNAL, Medellín	Applicability of some force field parameters of biomolecules to model the surface tension of hexadecane
7	Yaritza Fortaleché Rodríguez UNAL, Bogotá	Agonist, antagonist or super-activator effect of different ligands in the receptor-ligand interaction of the TraR protein
8	Paula Giraldo Hincapie UNAL, Medellín	Understanding insecticide peptides: Modeling peptide-membrane interactions with Molecular Dynamics
9	Jessica Martinez UAN, Bogotá	Does Using Virtual Sites in Proteins Affect the Protein Fold?
10	Juan Zarate Moreno SENA, Bogotá	Kinetic models for chitosan membranes on biological systems, a computational approach.
11	Cesar Quintana Cataño UANDES, Bogotá	Force spectroscopy of T4 bacteriophage adhesion during infection.
12	Santiago Agudelo Gómez UDEA, Medellín	Preferred sites of glycosaminoglycans in the envelope protein of the Zika virus
13	Alberto Mario Castillo UBJTL, Bogotá	Spring Network Model of Trypanosoma Cruzi bloodstream trypomastigote
14	Gesivaldo Santos State U. Bahia	Autism Spectro Disorder & Alzheimer Disease: different conditions linked by mTOR pathway
15	Helman Amaya Espinosa UANDES, Bogotá	Cooperative dynamics of self-interacting Biopolymers in blood elucidated by Coarse-Grained Brownian Dynamics Simulations

16	Valeria Mejía Restrepo UANDES, Bogotá	The effect of G1324A and G1324S mutations on the complex formed by the von Willebrand factor A1 domain and the glycoprot lba-platelet receptor, studied through molecular dynamics simulations and free energy calculations.	
17	Andrés Cifuentes López UDISTRITAL, Bogotá	In silico evaluation of the potential afinity of anandamide analogues for CB1 receptor	
18	Jhoan Ortiz Giron UDEA, Medellín	A novel methodology for cryo-EM map validation	