

# Science at the Edge Seminar Series

Quantitative Biology Graduate Program/  
Gene Expression in Development and Disease

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**When anomalous becomes the norm:  
Lateral (sub)diffusion in cell membranes.**

The plasma membrane of our cells is a complex mixture of hundreds of different lipids, proteins, and cholesterol. Lateral heterogeneity in composition is therefore expected, but the observable signatures and functional consequences of such heterogeneity remain controversial. I will present chemically detailed, "all-atom" simulations of lipid mixtures, which suggest a new model for lateral heterogeneity on the nanoscale. Long (10 microsecond) contiguous trajectories provide evidence for subdiffusive transport, recently corroborated by iSCAT single particle tracking data. These observations motivate a stochastic simulation approach which predicts interesting consequences for subdiffusion on the encounter of signaling partners, suggesting a functional role for membrane heterogeneity.

- E. Lyman, H. Cui, and G. A. Voth, "Water under the BAR," Biophysical Journal 99, 1783 (2010).
- E. Lyman, C. Higgs, B. Kim, D. Lupyan, J. C. Shelley, R. Farid, and G. A. Voth, "A role for a specific cholesterol interaction in stabilizing the Apo configuration of the human A2A adenosine receptor," Structure 17, 1660 (2009).
- E. Lyman, J. Pfandtner, and G. A. Voth, "Systematic multiscale parameterization of heterogeneous elastic network models of proteins," Biophysical Journal 95, 4183 (2008).
- E. Lyman and D. M. Zuckerman "On the structural convergence of biomolecular simulations by determination of the effective sample size," J. Phys. Chem. B 111, 12876 (2007).
- E. Lyman, F. M. Ytreberg, and D. M. Zuckerman, "Resolution exchange simulation," Phys. Rev. Lett. 96, 028105 (2006).
- D. M. Zuckerman and E. Lyman, "A second look at canonical sampling of biomolecules using replica exchange simulation," J. Chem. Theory Comput. 2, 1200 (2006).

**Friday, October 9, 2015 at 11:30a.m.**

**Room 1400 BPS**

*Refreshments at 11:15*