Margaret E. Johnson

Johns Hopkins University
School of Arts & Sciences
110 Jenkins Hall
Baltimore, MD 21218

margaret.johnson@jhu.edu
Work: (410) 516-2376
Cell: (646) 326-5132
Office: 121C Mergenthaler

Education:

University of California, Berkeley 2004-2009
Ph.D in Bioengineering, Thesis Adviser: Teresa Head-Gordon
Thesis title: *Understanding the interplay of structure and dynamics in liquids using coarse-grained models and experiment*

Columbia University 2000-2004
B.S. in Applied Math *Magna Cum Laude*
Minor in Bioengineering

Professional Experience:

Assistant Professor, Department of Biophysics, Johns Hopkins University. 2013-Present

National Institutes of Health (NIH) 2009-2013
Postdoctoral Researcher, Laboratory of Chemical Physics. Research Adviser: Dr. Gerhard Hummer

Research Support:

Current:
NIH R00 Pathway to Independence Award R00GM098371 *Modeling the nucleation of clathrin coated vesicles at the membrane*. $249,000/year. 2013-2016

Prior:
NIH K99 Pathway to Independence Award: *Modeling the nucleation of clathrin coated vesicles at the membrane*. 2011-2013

Publications:

Holland, D.O., Shapiro, B.H., Xue, P., & **Johnson, M.E.*** Positive selection for scale-free protein networks from motifs in protein binding interface networks. *In preparation* (2016).

Yogurtcu, O.N. & **Johnson, M.E.*** Theory of bi-molecular association dynamics in 2D for accurate model and experimental parameterization of binding rates. *J. Chem. Phys.* **143**, 084117 (2015).

Johnson, M.E.* & Hummer, G. Free propagator reweighting integrator for single-particle dynamics in reaction-diffusion models of heterogeneous protein-protein interaction systems. *Phys. Rev. X* **4,** 031037 (2014). PMC4440698, PMID: 26005592.

Johnson, M.E. & Hummer, G. Evolutionary pressure on the topology of protein interface interaction networks. *J. Phys. Chem. B* **117,** 13098-13106 (2013). PMC3808520 PMID: 23701316

Johnson, M.E.* & Hummer, G. Interface resolved network of protein-protein interactions. *PLoS Comput Biol.* **9,** e1003065 (2013). PMC3656101 PMID: 23701316

Johnson, M.E. & Hummer, G. Characterization of a Dynamic string method for the construction of transition pathways in molecular systems. *J. Phys. Chem. B* **116,** 8573-8583 (2012). PMC3406241 PMID: 22616575

Johnson, M.E. & Hummer, G. Nonspecific binding limits the number of proteins in a cell and shapes their interaction networks. *Proc. Nat. Acad. Sci. USA*. **108**, 603-608 (2011). PMC3021073 PMID: 21187424

Ponder, J.W., Wu, C.J., Ren, P.Y., Pande, V.S., Chodera, J.D., Schnieders, M.J., Haque, I., Mobley, D.L., Lambrecht, D.S., DiStasio, R.A., Head-Gordon, M., Clark, G.N.I., **Johnson, M.E.**, Head-Gordon, T. Current status of the AMOEBA polarizable force field. *J. Phys. Chem. B.* **114,** 2549-2564 (2010). PMC2918242 PMID: 20136072

Johnson, M.E.*, Malardier-Jugroot, C. & Head-Gordon, T*. Effects of co-solvents on peptide hydration water structure and dynamics. *Phys. Chem. Chem. Phys.* **12,** 393-405 (2010).

Malardier-Jugroot, C., Bowron, D.T., Soper, A.K., **Johnson, M.E**., & Head-Gordon, T. Structure and water dynamics of aqueous peptide solutions in the presence of co-solvents. *Phys. Chem. Chem. Phys.* **12,** 382-392 (2010).

Johnson, M.E. & Head-Gordon, T. Assessing thermodynamic-dynamic relationships for waterlike liquids. *J. Chem. Phys.* **130,** 214510 (2009).

Johnson, M.E., Malardier-Jugroot, C., Murarka, R.K. & Head-Gordon, T. Hydration water dynamics near biological interfaces. *J. Phys. Chem. B.* **113,** 4080-4092 (2009).

Malardier-Jugroot, C., **Johnson, M.E**., Murarka, R.K. & Head-Gordon, T. Aqueous peptides as experimental models for hydration water dynamics near protein surfaces. *Phys. Chem. Chem. Phys*. **10**, 4903-4908 (2008).

Johnson, M.E., Head-Gordon, T. & Louis, A.A. Representability problems for coarse-grained water potentials. *J. Chem. Phys.* **126,** 144509 (2007).

Head-Gordon, T. & **Johnson, M.E**. Tetrahedral Structure or chains for liquid water. *Proc. Nat. Acad. Sci. USA* **103**, 7973-7977 (2006).

***Corresponding Author**

Pubmed link:
http://www.ncbi.nlm.nih.gov/sites/myncbi/1XCwaYfWsal5f/bibliography/46177854/public/?sort=date&direction=ascending
Google Scholar:
https://scholar.google.com/citations?user=PWWKcAMAAAAJ&hl=en&oi=pll

Awards and Honors:

NIH K99/R00 Pathway to Independence Award: *Modeling the nucleation of clathrin coated vesicles at the membrane*	2011
Mini Statistical Mechanics Meeting, Berkeley, CA: Grand Prize Poster Award	2011
NIH Fellows Award for Research Excellence (FARE)	2010
American Chemical Society Conference San Francisco, CA: Physical Chemistry Outstanding Poster Award	2006
Nominated by Columbia Dept. of Applied Math and Physics for George Vincent Wendell Memorial Award	2004

Teaching Experience:

Johns Hopkins University

Undergraduate teaching: Models and Algorithms in Biophysics. AS 250.302, Spring semester.	2015-Present

Graduate teaching: Biophysics Graduate Program Introductory Computer Bootcamp. Organizer and instructor, Fall semester. 2014

Previous teaching experience

Creator and co-leader of Biophysics journal club for summer undergraduate researchers, Bethesda, NIH. 2012

Graduate Student Instructor, UC Berkeley, Computational Methods in Biophysics BE243/143 2007

Graduate Student Instructor, UC Berkeley, Freshman Physics 7A 2005

Leadership and Service:

NIMBioS Working Group, "Improving Tools for Spatially-Realistic Cell Simulations". PIs: Robert F Murphy, CMU and James Faeder, Univ. Pittsburgh 2015-2017

Faculty mentor, STEM Achievement for Baltimore Elementary Schools (SABES). Johns Hopkins NSF Funded program. 2014-2015

Workshop Chair, Artificial Cells: Understanding and Engineering, Biophysical Society Meeting, Baltimore. 2015

Graduate Board Oral exam committee, Program in Molecular Biophysics 2014, 2016

Thesis Committee member, Biology Department, Chemical and Biological Engineering Department. 2014-2015

Judge for NIH-NIDDK Fellows retreat 2011-2013

Judge for NIH Graduate student research symposium 2012

Invited Seminars:

"*Mechanisms of protein assembly at the membrane: Insights from theory and reaction-diffusion simulation*" Center for Cell Analysis and Modeling, University of Connecticut Health Center, Farmington, CT. May 2016

"*Modeling protein interactions and assembly at the cell-scale*" NIMBioS Working Group on "Improving Tools for Spatially Realistic Cell Simulations", Knoxville, TN. Mar. 2016 & Dec. 2015

(Declined-Maternity) CECAM Workshop on Molecular and Chemical Kinetics, Free University, Berlin, Germany. — Sept. 2015

"*Optimizing protein interactions for the crowded cell*" Telluride Science Research Center, Workshop on Macromolecular Crowding, Telluride, CO. — June 2015

"*Modeling protein interactions and assembly at the cellular length and timescales*" Department of Computational and Systems Biology, Univ. of Pittsburgh, Pittsburgh, PA. — March 2015

"*Modeling protein interactions and assembly with single particle reaction diffusion and multi-scale methods*" Krasnow Institute for Advanced Study, George Mason University, VA. — Feb. 2015

"*Free-propagator reweighting integrator (FPR) for single particle reaction diffusion in solution and on the membrane"* Banff International Research Station workshop on Single Particle Reaction Diffusion Methods, Banff, Canada. — Nov. 2014

"*Modeling protein interactions and assembly processes in the cell*" IBR Retreat, Johns Hopkins University, Baltimore, MD. — Sept. 2013

"*Connecting protein network topology to specificity and regulation in protein-protein interactions"* School of Public Health, Johns Hopkins Univ. Baltimore, MD. — March 2013

"*Connecting protein network topology to specificity and regulation in protein-protein interactions"* NIDDK Fellows Retreat, NIH, Bethesda, MD. — March 2013

"*Evolutionary pressure on interface-interface topology in protein interaction networks"* Laboratory of Chemical Physics, NIH, Bethesda, MD. — Nov 2012

"*Evolutionary pressure on interface-interface topology in protein interaction networks"* NIDDK Fellows Retreat, NIH, Bethesda, MD. — April 2012

"*Refining protein interaction networks with interface structure and protein expression levels"* Laboratory of Chemical Physics, NIH, Bethesda, MD. — Feb. 2012

"*Refining protein interaction networks with interface structure and protein expression levels"* Biophysical Society Meeting platform presentation, San Diego, CA. — Feb. 2012

"*How nonspecific binding between proteins shapes their interaction networks and expression levels"* Biophysics Department, Johns Hopkins — Jan. 2012

University, Baltimore, MD.

"*Nonspecific binding limits the number of proteins in a cell and shapes their interaction topology"* Chemistry Department, University of Chicago, Chicago, IL. Jan. 2012

"*How nonspecific binding between proteins shapes their interaction networks and expression levels"* Stadtman Seminar, NIH, Bethesda, MD. Dec. 2011

"*Nonspecific binding limits the number of proteins in a cell and shapes their interaction topology"* NHLBI Systems Biology research seminar, NIH, Bethesda, MD. Oct. 2011

"*Nonspecific binding limits the number of proteins in a cell and shapes their interaction topology"* Gordon Research Conference: Cellular Systems Biology. Davidson, NC July 2011

"*Nonspecific binding limits the number of proteins in a cell and shapes their interaction topology"* NIDDK Fellows Retreat, NIH, Bethesda, MD. April 2011

"*Nonspecific binding limits the number of proteins in a cell and shapes their interaction topology"* Biophysical Society Meeting platform presentation, Baltimore, MD. March 2011

"*How many proteins are too many?"* Laboratory of Chemical Physics, NIH, Bethesda, MD. 2010

"*Assessing theories of liquid dynamics"* Prof. Ken Dill Research Group, UCSF, San Francisco, CA. 2008

"*Evaluating theories of liquid dynamics"*Prof. Jhih-Wei Chu Research Group, UC Berkeley, Berkeley, CA. 2008

Recent Contributed Talks/Posters:

"Governing principles of multiprotein complex formation on the cell membranes" Biophysical Society Meeting, Los Angeles, CA Feb 2016

"*Computational investigation of membrane adaptor proteins under different cellular conditions*" Biophysical Society Meeting, Baltimore, MD Feb 2015

"*Modeling reaction-diffusion processes in 2D and 3D with a novel single-particle integrator"* GRC on Stochastic Physics in Biology, Ventura, CA Jan 2015

"*Modeling reaction-diffusion processes in 2D and 3D with a novel single-particle integrator"* Berkeley Mini Statistical Mechanics Meeting, Berkeley, CA — 2007-2015

"*Multi-scale modeling of protein assembly in clathrin-mediated endocytosis"* Biophysical Society Thematic Meeting, Modeling of Biomolecular Systems Interactions, Istanbul, Turkey — Nov 2014

"*Multi-scale modeling of protein assembly in clathrin-mediated endocytosis"* GRC on Lysosomes and Endocytosis, Andover, NH — June 2014

"*Free propagator reweighting algorithm for reaction-diffusion simulations of heterogeneous protein systems"* Biophysical Society Meeting, San Francisco, CA — Feb 2014

Advisees:

David Holland: Graduate student in Biomedical Engineering, Johns Hopkins University. October 2013-Present.

Osman Yogurtcu, PhD: Post-doctoral fellow. December 2013-Present.

Dariush Mohammadyani, PhD: Post-doctoral fellow. May 2016-Present.

Benjamin Shapiro, MS: Undergraduate then Master's student in Applied Math, Johns Hopkins University. 2014-May 2016.

Raza Ul-Haq, PhD: Post-doctoral fellow, March 2015-Feb 2016.

Undergraduate Researchers:

Rohan Tilva: Johns Hopkins University, 2015-Present.

Athena Chen: Biophysics and Mathematics, Johns Hopkins University, 2015-Present.

Pei Xue: Biophysics, Johns Hopkins University, 2014-2015.