Adam D Schuyler, PhD

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Education

Ph.D.	Johns Hopkins University, Baltimore, MD Mechanical Engineering – Dr. Gregory S Chirikjian	2006
B.A.	Williams College, Williamstown, MA Mathematics with Honors – Dr. Thomas A Garrity	2000

Professional Experience

- Assistant Professor — 2013-*present*
  UConn Health, Department of Molecular Biology and Biophysics
- Postdoctoral Fellow — 2009-2013
  UConn Health, Department of Molecular Biology and Biophysics
  Structural Biology – Dr. Jeffrey C Hoch
- Postdoctoral Fellow — 2007-2009
  University of Michigan
  Neurology – Dr. Eva L Feldman
  Biophysics – Dr. Heather A Carlson
- NIH Cancer Research Training Award Fellowship — 2003
  Structural Glycobiology Section, LECB, NCI, NIH – Dr. Pradman K Qasba
- NIH Cancer Research Training Award Fellowship — 2001
  Molecular Structure Section, LECB, NCI, NIH – Dr. Robert L Jernigan

Honors and Affiliations

- NMRbox: National Center for Biomolecular NMR Data Processing and Analysis — 2015-*present*
  Senior Staff, Co-Director of Platform Development, and Director of Training
- Molecular, Microbial and Structural Biology Department Retreat – Best Poster — 2011
- Sinai Medical Staff Foundation Fellowship — 2006-2009
- Graduate Teaching Assistant — 2004
  Johns Hopkins University, Department of Mechanical Engineering
- Reviewer: PROTEINS, PLoS Comp Bio, PLoS ONE, Digital Signal Processing, — 2003-*present*
  Journal of Physical Chemistry, Royal Society Open Science, Concepts in Magnetic Resonance A, Physical Biology, Metallomics
- Abel Wolman Fellowship, Johns Hopkins University — 2000-2001
  Outstanding first-year doctoral candidate in Whiting School of Engineering.
- Sigma Xi, The Scientific Research Society – inducted — 2000

Journal Publications

$*$ denotes corresponding author status for ADS

(1) J Masison, PJ Michalski, LM Loew, and **AD Schuyler*** (2018). mol2sphere: Spherical Decomposition of Multi-Domain Molecules for Visualization and Coarse Grained Spatial Modeling. *bioRxiv*.

(2) MA Zambrello, **AD Schuyler**, MW Maciejewski, F Delaglio, I Bezsonova, and JC Hoch (2018). Nonuniform Sampling in Multidimensional NMR for Improving Spectral Sensitivity. *Methods 138-9*, 62–68.

(3) MW Maciejewski, **AD Schuyler**, MR Gryk, II Moraru, PR Romero, EL Ulrich, HR Eghbalnia, M Livny, F Delaglio, and JC Hoch (2017). Another barrier to reproducibility. *Science 354*, (eLetter), 1240–1241.

(4) MW Maciejewski, **AD Schuyler**, MR Gryk, II Moraru, PR Romero, EL Ulrich, HR Eghbalnia, M Livny, F Delaglio, and JC Hoch (2017). NMRbox: A Resource for biomolecular NMR computation. *Biophysical Journal 112*, 1529–1534.

(5) H Monajemi, DL Donoho, JC Hoch, and **AD Schuyler** (2017). Incoherence of Partial-Component Sampling in multidimensional NMR. *arXiv*.

(6) MA Zambrello, MW Maciejewski, **AD Schuyler**, G Weatherby, and JC Hoch (2017). Robust and Transferable Quantification of NMR Spectral Quality using IROC Analysis. *Journal of Magnetic Resonance*.

(7) **AD Schuyler***, MW Maciejewski, AS Stern, and JC Hoch (2015). Nonuniform sampling of hypercomplex multidimensional NMR experiments: Dimensionality, quadrature phase and randomization. *Journal of Magnetic Resonance 254*, 121–130.

(8) JC Hoch, MW Maciejewski, M Mobli, **AD Schuyler**, and AS Stern (2014). Nonuniform Sampling and Maximum Entropy Reconstruction in Multidimensional NMR. *Accounts of chemical research 47*, 708–717.

(9) **AD Schuyler***, MW Maciejewski, AS Stern, and JC Hoch (2013). Formalism for hypercomplex multidimensional NMR employing partial-component subsampling. *Journal of Magnetic Resonance 227*, 20–24.

(10) MW Maciejewski, M Mobli, **AD Schuyler**, AS Stern, and JC Hoch (2012). Data Sampling in Multidimensional NMR: Fundamentals and Strategies. *Topics in Current Chemistry 316*, ed. by V Orekhov, and M Billeter, 49–78.

(11) M Mobli, MW Maciejewski, **AD Schuyler**, AS Stern, and JC Hoch (2012). Sparse sampling methods in multidimensional NMR. *Physical Chemistry Chemical Physics 14*, 10835–10843.

(12) MW Maciejewski, M Fenwick, **AD Schuyler**, AS Stern, V Gorbatyuk, and JC Hoch (2011). Random phase detection in multidimensional NMR. *Proceedings of the National Academy of Sciences of the United States of America 108*, 16640–16644.

(13) **AD Schuyler**, MW Maciejewski, H Arthanari, and JC Hoch (2011). Knowledge-based nonuniform sampling in multidimensional NMR. *Journal of Biomolecular NMR 50*, 247–262.

(14) **AD Schuyler***, HA Carlson, and EL Feldman (2011). Computational methods for identifying a layered allosteric regulatory mechanism for ALS-causing mutations of Cu-Zn superoxide dismutase 1. *Proteins: Structure, Function, and Bioinformatics 79*, 417–427.

(15) J Hur, KA Sullivan, **AD Schuyler**, Y Hong, M Pande, DJ States, HV Jagadish, and EL Feldman (2010). Literature-based discovery of diabetes- and ROS-related targets. *BMC Medical Genomics 3*, 49–49.

(16) J Hur, **AD Schuyler**, DJ States, and EL Feldman (2009). SciMiner: Web-based literature mining tool for target identification and functional enrichment analysis. *Bioinformatics 25*, 838–840.

(17) SA Sakowski, **AD Schuyler**, and EL Feldman (2009). Insulin-like growth factor-I for the treatment of amyotrophic lateral sclerosis. *Amyotroph Lateral Sclerosis 10*, 63–73.

(18) **AD Schuyler**, RL Jernigan, PK Qasba, B Ramakrishnan, and GS Chirikjian (2009). Iterative cluster-NMA: A tool for generating conformational transitions in proteins. *Proteins: Structure, Function, and Bioinformatics 74*, 760–776.

(19) **AD Schuyler***, HA Carlson, and EL Feldman (2009). Computational Methods for Predicting Sites of Functionally Important Dynamics. *Journal of Physical Chemistry B 113*, 6613–6622.

(20) AM Vincent, SA Sakowski, **A Schuyler**, and EL Feldman (2008). Strategic approaches to developing drug treatments for ALS. *Drug Discovery Today 13*, 67–72.

(21) S Assaf, LC Chen, T Cheslack-Postava, B Cooper, A Diesl, T Garrity, M Lepinski, and **A Schuyler** (2005). A Dual Approach to Triangle Sequences: A Multidimensional Continued Fraction Algorithm. *INTEGERS: The Electronic Journal of Combinatorial Number Theory 5*, A8.

(22) **AD Schuyler**, and GS Chirikjian (2005). Efficient determination of low-frequency normal modes of large protein structures by cluster-NMA. *Journal of Molecular Graphics and Modelling 24*, 46–58.

(23) **AD Schuyler**, G Chirikjian, JQ Lu, and H Johnson (2005). Random-walk statistics in moment-based $\mathcal{O}(N)$ tight binding and applications in carbon nanotubes. *Physical Review E 71*, 046701.

(24) **AD Schuyler**, and GS Chirikjian (2004). Normal mode analysis of proteins: a comparison of rigid cluster modes with C_α coarse graining. *Journal of Molecular Graphics and Modelling 22*, 183–193.

Book Chapters

(1) MW Maciejewski, **AD Schuyler**, and JC Hoch In *Protein NMR: Methods and Protocols*; Springer: 2018, pp 341–352.

(2) JC Hoch, MW Maciejewski, M Mobli, **AD Schuyler**, and AS Stern In *Encyclopedia of Magnetic Resonance*; John Wiley & Sons, Ltd: 2012.

Talks

- UConn Health - Molecular Biology and Biophysics ◇ Farmington, CT 2017
  "Taking a swing at ALS"
- UConn Health - Center for Cell Analysis and Modeling ◇ Farmington, CT 2016
  "A computational model of allosteric activation: insights into SOD1-linked ALS"
- Chicago Area NMR Discussion Group Meeting ◇ Milwaukee, WI 2016
  "Nonuniform sampling: theory and NMRbox tools"
- New York Structural Biology Center ◇ New York, NY 2015
  "Partial-Component Nonuniform Sampling"
- Experimental Nuclear Magnetic Resonance Conference ◇ Boston, MA 2014
  "Hypercomplex Multidimensional NMR Employing Partial-Component Nonuniform Sampling"
- University of Connecticut Health Center ◇ Molecular, Microbial and Structural Biology 2013
  "Molecular Modeling Reveals Molecular Function"
- University of Connecticut Health Center ◇ Molecular, Microbial and Structural Biology 2009
  "Computational Models of Allostery: Potential Mechanisms for Disease Control"
- Biophysical Society Annual Meeting ◇ Boston, MA 2009
  "Computational Methods for Predicting Sites of Functionally Important Dynamics"
- Boston University ◇ Physiology and Biophysics 2009

"Computational Models of Allostery: Potential Mechanisms for Disease Control"

- Johns Hopkins University ◇ Mechanical Engineering – Bio Seminar Series 2004
  "Biological function determined by cluster-NMA on very large structures"

- Joint Meetings of the MAA and AMS ◇ Providence, RI 1999
  "A Dual Approach to Triangle Sequences: A Multidimensional Continued Fraction Algorithm", T Cheslack-Postava, A Diesl, T Garrity, M Lepinski and A Schuyler

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Selected Conference Posters

- Experimental Nuclear Magnetic Resonance Conference ◇ Pacific Grove, CA 2017
  DL Craft and **AD Schuyler**. "nus-tool: A utility for generating, analyzing, and converting NUS sample schedules."

- Experimental Nuclear Magnetic Resonance Conference ◇ Pittsburgh, PA 2016
  AD Schuyler, K Baskaran, VB Chen, H Eghbalnia, O Gorbatyuk, MR Gryk, D Jones, MW Maciejewski, D Maziuk, II Moraru, PR Romero, EL Ulrich, G Weatherby, JR Wedell, and JC Hoch. "NMRbox: National Center for Biomolecular NMR Data Processing and Analysis."

- Biophysical Society Meeting ◇ Los Angeles, CA 2016
  AD Schuyler, K Baskaran, VB Chen, H Eghbalnia, O Gorbatyuk, MR Gryk, D Jones, MW Maciejewski, D Maziuk, II Moraru, PR Romero, EL Ulrich, G Weatherby, JR Wedell, and JC Hoch. "NMRbox: NATIONAL CENTER FOR BIOMOLECULAR NMR DATA PROCESSING AND ANALYSIS."

- GRC: Computational Aspects of Biomolecular NMR ◇ Lucca, Italy 2015
  AD Schuyler, J Wagner and JC Hoch. "Ring Current Shifts: A geometric characterization and survey of the BMRB".

- Upstate NY NMR Symposium ◇ Troy, NY 2013
  AD Schuyler, MW Maciejewski, AS Stern and JC Hoch. "Characterizing Sensitivity for Hypercomplex Multidimensional NMR Employing Partial-Component Subsampling".

- GRC: Computational Aspects of Biomolecular NMR ◇ Mount Snow, VT 2013
  AD Schuyler, MW Maciejewski, AS Stern and JC Hoch. "Characterizing Sensitivity for Hypercomplex Multidimensional NMR Employing Partial-Component Subsampling".

- Experimental Nuclear Magnetic Resonance Conference ◇ Pacific Grove, CA 2011
  AD Schuyler, MW Maciejewski and JC Hoch. "Improved Metrics for Predicting Performance of Nonuniformly Sampled Schedules".

- Biophysical Society Annual Meeting ◇ Baltimore, MD 2011
  AD Schuyler. "Binding Profiles Based on Normal Mode Analysis as a Foundation for a Unified Approach to Allosteric Activation of Prolactin Receptor".
  Biophysical Journal, 2011, 100(3) Supplement 1, 550a.

- Experimental Nuclear Magnetic Resonance Conference ◇ Daytona Beach, FL 2010
  M Mobli, AS Stern, W Bermel, GF King, MW Maciejewski, **AD Schuyler** and JC Hoch. "Nonuniform sampling for improving resolution in multidimensional NMR".

- Biophysical Society Annual Meeting ◇ San Francisco, CA 2010
  AD Schuyler and JC Hoch. "Characterization and Optimization of Nonuniform Sampling for Multidimensional NMR Experiments".
  Biophysical Journal, 2010, 98(3) Supplement 1, 175a.

- American Neurological Association Annual Meeting ◇ Salt Lake City, UT 2008
  AD Schuyler, HA Carlson and EL Feldman. "Computational Analysis of Familial Amyotrophic Lateral Sclerosis Causing Mutations of Cu-Zn Superoxide Dismutase".
  Annals of Neurology, 2008, 64(S12), S44-S45.

- Biophysical Society Annual Meeting ◇ Long Beach, CA 2008
  AD Schuyler, HA Carlson and EL Feldman. "Normal Mode Directed Exploration of Conformation Space as a Tool for Studying Macromolecular Interactions".
  Biophysical Journal, 2008, 94, Supplement, 235-Pos.
- Biophysical Society Annual Meeting ◇ Baltimore, MD 2007
  AD Schuyler and EL Feldman. "Iterative Cluster Normal Mode Analysis (icNMA): A Tool for Traversing the Conformation Energy Landscape with an Application to ALS".
  Biophysical Journal, 2007, Supplement, LB3-Pos.
- Biophysical Society Annual Meeting ◇ Baltimore, MD 2004
  AD Schuyler and GS Chirikjian. "Efficient determination of low-frequency modes on large protein structures by cluster-NMA".
  Biophysical Journal, 2004, 86, Supplement, 2597-Pos.
- Institute for Biophysical Research Annual Meeting ◇ Linthicum Heights, MD 2003
  AD Schuyler and GS Chirikjian. "Cluster-NMA: A Computationally Efficient, Rigid-Body-Based, Normal Mode Analysis Tool".
- The 7^{th} Johns Hopkins Folding Meeting ◇ Berkeley Springs, WV 2003
  MK Kim, **AD Schuyler** and GS Chirikjian. "Protein Dynamics Modeling".