Assistant Professor

Specialty: Physics - Biophysics

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Courses Taught:
Introductory Courses
Physics Orientation: Physics 111, 112
Survey of Physics: Physics 110

Advanced Courses
College Physics I, Physics 201
College Physics II, Physics 202
General Physics I: Physics 220
General Physics II: Physics 221
General Physics II, Physics 230

Upper Level Courses
Theoretical Solid State Physics: Physics 406
Mathematical Physics: Physics 405
Circuit Network Analysis, Physics 323
Mechanics-Statics for Engineers, Physics 307
Advanced Physics Lab, Physics 321

Graduate Level Courses
Statistical Mechanics, Physics 630

Research and/or Teaching Interests:
My research is interdisciplinary - an intersection of physics, biology and mathematics. My Ph.D. thesis research at the Wake Forest University is on mechanisms and kinetics of melting of sickle cell hemoglobin (HbS) aggregates. Dilution induced dissociation of HbS aggregate is monitored through a time-resolved extinction measurements using OLIS-1000 spectrophotometer. A stop-flow apparatus is applied for mixing the HbS sample and the phosphate buffer. Kinetic coefficients are found from the best fit of our model equations to the extinction data. I used FORTRAN and IDL for numerical computations. See my publication list for the related work.

My postdoctoral research at the University of Pittsburgh was on equilibrium motions in a protein, using Monte Carlo simulated trajectories of conformations of a coarse-grained rigid-polypeptide-plane model protein. The following questions were under investigation in my research: (a) is the stability of the coarse-grained protein model trajectory ensemble perturbed when Go-like contact potential was augmented by Ramachandran and hydrophobic propensities; (b) what is the optimal MC move (or protein fragment size) and temperature projecting the full and fast convergence of conformational trajectories; (c) do computational (Monte-Carlo, particularly) studies outline better the fluctuation profiles of equilibrium motions in a protein obtained in X-Ray or NMR experiments? I used C++ and PERL for numerical computations. See my publication list for related work.

Currently, I am working on model of protein unfolding/folding transitions (UFT): what is the machinery of protein fast memory for the precise return to single native structure from a vast pool of unfolded conformations; what are the principles, which spell out coherently an enormous information accumulated through both laboratory and computational experiments? I describe a DNA-Protein coupling perspective based model of UFT, which introduces three principles - transverse memory, virtual state, relativity of nativity. See my publication list for the related work.

I am also interested in mathematical/computational description of the sub-nuclear and intracellular DNA->RNA->Protein production machinery. See my publication list for related work.

Computation - Computer modeling of random processes using Monte-Carlo methods. In various cases of modeling and data analysis different techniques have been applied, such as the method of Maximum Likelihood and X2 , the method of Lagrange's multipliers, dimensionality analysis (method of k-nearest neighbors). Approximate analytical solutions to the kinetic (first-order nonlinear differential) equations.

University Services:

Department of Physics
Undergraduate Physics Laboratory, Dillard University
Physics Curriculum Enhancement

Division of the Natural Sciences and Public Health
Member of the News and Publication Committee

Other:
Coach of the Dillard University Algebra Undergraduate Competitions
Reviewer and Judge in the Undergraduate Research annual poster presentations at Dillard University

Professional Affiliations:

American Biophysical Society
American Physical Society
Member of the Honor Society of Sigma Pi Sigma, Wake Forest University Chapter

Selected Publications:

Aroutiounian, S., DNA-Protein coupling perspective in unfolding/folding transitions in proteins. Annual Meeting of American Biophysical Society, Boston, MA, February 28 - March 4, 2009

Aroutiounian, S., Core-Shell Model of Unfolding/Folding Transitions in Proteins, Session U40/Biomolecular computation, Annual Meeting of American Physical Society, New Orleans, LA, March 10-14, 2008

M. Ytreberg, S. Aroutiounian, D. Zuckerman "Demonstrated convergence of the equilibrium ensemble of a fast united-residue protein model", J. Chem. Theory Comput., 3 (5), 1860 -1866, 2007

S. Aroutiounian , Free Energy Landscape - Settlement of Key residues. U40/Biomolecular computation. Annual Meeting of American Physical Society, Colorado, March 2007.

Aroutiounian, S., On Matrix Operator of Exon Splicing, Proceedings of 9th Annual Conference on Computational Genomics, Baltimore, MD, October 28-31, 2006

S. Kh. Aroutiounian, "CO partial pressure dependence of the kinetics of melting of HbS aggregates studied in high concentration phosphate buffer" Abstract, SESAPS meeting, Auburn, AL, October, 2002

S. Kh. Aroutiounian, J. G. Louderback, S. K. Ballas, D. B. Kim-Shapiro, Evidence for carbon monoxide binding to sickle cell polymers during melting. Biophysical Chemistry, 91: 167-181, 2001

J. G. Louderback, S. Kh. Aroutiounian, W. C. Kerr, S. K. Ballas and D. B. Kim-Shapiro, Temperature and domain size dependence of sickle cell hemoglobin polymer melting in high concentration phosphate buffer. Biophysical Chemistry 80:21-30,1999

A. A.Chilingarian, S.Kh.Harutunyan, On the possibility of a multidimensional kinematic information analysis by means of nearest-neighbor estimations of dimensionality. Nuclear Instruments and Methods in Physics Research, A281:388-392,1989

Selected Presentations:

S. Aroutiounian, On Matrix Operator of Exon Splicing. Poster Session.
Genomes, Medicine and the Environment Conference, South Carolina, October, 2006.

S. Aroutiounian, M. Ytreberg, D. Zuckerman Fluctuations in a fast united-residue model. Poster Session. 50th Annual Meeting of Biophysics Society, Salt Lake City, UT, 2006.

S. Kh. Aroutiounian, S. Danagoulian "Fractal correlation dimensionalities and pattern formation - genomic application" 2nd Conference on Analysis and Probability on Fractals, Cornell University, NY, May, 2005

Melting of sickle cell hemoglobin fibers under different conditions. The Eighth Annual Life & Physical Science Research Symposium, NC A&T State University, April 2003

CO partial pressure dependence of the kinetics of melting of HbS aggregates studied in high concentration phosphate buffer, SESAPS meeting, Auburn, Al, October 30, 2002

Analysis of the role of carbon monoxide ligation during sickle cell hemoglobin polymer melting, Poster Session. 45th Annual Meeting of Biophysics Society, Boston, MA, 2001.

Selected Grants/Awards:

"In Search of Key Residues in a Protein on Folding/Unfolding Routes Using Single Molecule FRET". Faculty Research Incentive Grant, Dillard University, $5000.

2005-2006 Ruth L. Kirschstein NRSA Trainee. Award to the Department of Environmental and Occupational Health, University of Pittsburgh, School of Public Health.

July, 2004 Genome Scholar, Short Course on "Current Topics In Genomic Research", NHGRI / NIH, Bethesda, MD.