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CURRICULUM VITAE

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Bristow, VA 20110   mmasso@gmu.edu

Education:

2006	**PhD Bioinformatics**, George Mason University, Fairfax, VA
2001	**Professional Certificate in Bioinformatics**, University of California at Santa Cruz, CA
1993	**ABD Mathematics**, University of Delaware, Newark, DE
1990	**MS Mathematics**, University of Delaware, Newark, DE
1985	**BS Mathematics**, Physics Minor, University of Delaware, Newark, DE

Publications:

1. Masso, M., Bansal, A., Bansal, A., Henderson, A., and Vaisman, I.I. Structure-Based Functional Analysis of BRCA1 RING Domain Variants: Concordance of Computational Mutagenesis, Experimental Assay, and Clinical Data, Biophys Chem 266 (2020) 106442.
2. Masso, M. Functional Analysis of BRCA1 RING Domain Variants: Computationally Derived Structural Data Can Improve Upon Experimental Features for Training Predictive Models, Integr Biol 12 (2020) 233-239.
3. Masso, M. Accurate and Efficient Structure-Based Computational Mutagenesis for Modeling Fluorescence Levels of *Aequorea victoria* Green Fluorescent Protein Mutants, Protein Eng Des Sel 33 (2020) gzaa022.
4. Masso, M. Active Participation in Current Faculty Research Inspires Student Achievement, PRIMUS (2020) Published online November 29, 2020.
5. Masso, M., Bansal, A., Prem, P., Gajjala, A., and Vaisman, I.I. Fitness of Unregulated Human Ras Mutants Modeled by Implementing Computational Mutagenesis and Machine Learning Techniques, Heliyon 5 (2019) e01884.
6. Masso, M., Rao, N., and Pyarasani, P. Modeling Transcriptional Activiation Changes to Gal4 Variants via Structure-Based Computational Mutagenesis, PeerJ 6 (2018) e4844.
7. Masso, M. All-Atom Four-Body Knowledge-Based Statistical Potential to Distinguish Native Tertiary RNA Structures from Nonnative Folds, J Theor Biol 453 (2018) 58-67.
8. Masso, M. All-Atom Four-Body Knowledge-Based Statistical Potentials to Distinguish Native Protein Structures from Nonnative Folds, Biomed Res Int 2017 (2017) 5760612.
9. Masso, M. Sequence-Based Predictive Models of Resistance to HIV-1 Integrase Inhibitors: An n-Grams Approach to Phenotype Assessment, Current HIV Research 13 (2015) 497-502.
10. Masso, M. Modeling Functional Fhanges to *Escherichia coli* Thymidylate Synthase Upon Single Residue Replacements: A Structure-Based Approach, PeerJ 3 (2015) e721.
11. Masso, M. and Vaisman, I.I. AUTO-MUTE 2.0: A Portable Framework With Enhanced Capabilities for Predicting Protein Functional Consequences Upon Mutation, Advances in Bioinformatics 2014 (2014) 278385.
12. Masso, M., Chuang, G., Hao, K., Jain, S., and Vaisman, I.I. Structure-Based Predictors of Resistance to the HIV-1 Integrase Inhibitor Elvitegravir, Antiviral Research 106 (2014) 5-12.
13. Masso, M. Four-Body Atomic Potential for Modeling Protein-Ligand Binding Affinity: Application to Enzyme-Inhibitor Binding Energy Prediction, BMC Structural Biology 13(Suppl 1) (2013) S1.
14. Masso, M. and Vaisman, I.I. Sequence and Structure Based Models of HIV-1 Protease and Reverse Transcriptase Drug Resistance, BMC Genomics 14(Suppl 4) (2013) S3.
15. Masso, M. Fast and Accurate Structure-Based Prediction of Resistance to the HIV-1 Integrase Inhibitor Raltegravir, Proc ACM Conf. Bioinformatics, Comput. Biology, and Biomedical Informatics (2013) 736-741.
16. Masso M. Knowledge-Based Scoring Function Derived from Atomic Tessellation of Macromolecular Structures for Prediction of Protein-Ligand Binding Affinity, Proc IEEE BIBMW (2012) 17-21.
17. Masso M. Prediction of Human Immunodeficiency Virus Type 1 Drug Resistance: Representation of Target Sequence Mutational Patterns via an n-Grams Approach, Proc IEEE BIBM (2012) 173-178.
18. Masso M. Generation of Atomic Four-Body Statistical Potentials Derived from the Delaunay Tessellation of Protein Structures, Proc 34th Annual International Conference of the IEEE Engineering in Medicine and Biology Society (2012) 6321-6324.
19. Masso M. A Multibody Atomic Statistical Potential for the Prediction of Enzyme-Inhibitor Binding Energy, Proc 34th Ann. Int'l Conference of the IEEE Engineering in Medicine and Biology Society (2012) 5526-5529.

20. Masso M. and Vaisman I.I. A Structure-Based Computational Mutagenesis Elucidates the Spectrum of Stability-Activity Relationships in Proteins, Proc 33rd Annual International Conference of the IEEE Engineering in Medicine and Biology Society (2011) 3225-3228.
21. Masso M. and Vaisman I.I. Structure-Based Prediction of Protein Activity Changes: Assessing the Impact of Single Residue Replacements, Proc 33rd Annual International Conference of the IEEE Engineering in Medicine and Biology Society (2011) 3221-3224.
22. Masso M. Sequence-Based Prediction of HIV-1 Coreceptor Usage: Utility of n-Grams for Representing gp120 V3 Loops, Proc ACM Conf. on Bioinformatics, Computational Biology, and Biomedicine (2011) 309-314.
23. Masso M. and Vaisman I.I. Modeling Cell Proliferation Activity of Human Interleukin-3 Upon Single Residue Replacements, Proc BIOSTEC BIOINFORMATICS (2011) 93-101.
24. Ravich V., Masso M., and Vaisman I.I. A Combined Sequence-Structure Approach for Predicting Resistance to the Non-nucleoside HIV-1 Reverse Transcriptase Inhibitor Nevirapine, Biophys Chem 153 (2011) 168-172.
25. Masso M. Overcoming the Curse of Dimensionality in a Statistical Geometry Based Computational Protein Mutagenesis, Proc IEEE ICDM BioDM Workshop (2010) 719-725.
26. Masso M. Improving Prediction Accuracy via Subspace Modeling in a Statistical Geometry Based Computational Protein Mutagenesis, Int J Knowl Disc Bioinformatics 1 (2010) 54-68.
27. Masso M. and Vaisman I.I. Structure-Based Machine Learning Models for Computational Mutagenesis, in Introduction to Protein Structure Prediction: Methods and Algorithms (eds: H. Rangwala and G. Karypis), Wiley Book Series on Bioinformatics, December 2010. ISBN: 9780470470596 (Textbook)
28. Masso M. and Vaisman I.I. Accurate and Efficient gp120 V3 Loop Structure Based Models for the Determination of HIV-1 Co-receptor Usage, BMC Bioinformatics 11 (2010) 494.
29. Masso M. and Vaisman I.I. Knowledge-Based Computational Mutagenesis for Predicting the Disease Potential of Human Non-Synonymous Single Nucleotide Polymorphisms, J Theor Biol 266 (2010) 560-568.
30. Masso M. and Vaisman I.I. AUTO-MUTE: Web-Based Tools for Predicting Stability Changes in Proteins Due to Single Amino Acid Replacements, Protein Eng Des Sel 23 (2010) 683-687.
31. Masso M., Mathe E., Parvez N., Hijazi K., and Vaisman I.I. Modeling the Functional Consequences of Single Residue Replacements in Bacteriophage f1 Gene V Protein, Protein Eng Des Sel 22 (2009) 665-671.
32. Masso M., Alsheddi T., and Vaisman I.I. Accurate Prediction of Stability Changes in Bacteriophage T4 Lysozyme Upon Single Amino Acid Replacements, Proc IEEE BIBM (2009) 26-30.
33. Masso M., Mathe E., Parvez N., Hijazi K., and Vaisman I.I. Structure Based Functional Analysis of Bacteriophage f1 Gene V Protein, Proc IEEE BIBM (2008) 402-406.
34. Masso M., Hijazi K., Parvez N., and Vaisman I.I. Computational Mutagenesis of *Lac* Repressor: Insight Into Structure-Function Relationships and Accurate Prediction of Mutant Activity, Proc ISBRA 2008, Lecture Notes in Bioinformatics 4983 (2008) 390-401.
35. Masso M. and Vaisman I.I. Accurate Prediction of Stability Changes in Protein Mutants by Combining Machine Learning with Structure Based Computational Mutagenesis, Bioinformatics 24 (2008) 2002-2009.
36. Barenboim M., Masso M., Vaisman I.I., and Jamison D.C. Statistical Geometry Based Prediction of Non-Synonymous SNP Functional Effects Using Random Forest and Neuro-Fuzzy Classifiers, Proteins 71 (2008) 1930-1939.
37. Masso M. and Vaisman I.I. Accurate Prediction of Enzyme Mutant Activity Based on a Multibody Statistical Potential, Bioinformatics 23 (2007) 3155-3161.
38. Masso M. and Vaisman I.I. A Novel Sequence-Structure Approach for Accurate Prediction of Resistance to HIV-1 Protease Inhibitors, IEEE Proc 7th BIBE Vol. II (2007) 952-958.
39. Masso M., Lu Z., and Vaisman I.I. Computational Mutagenesis Studies of Protein Structure-Function Correlations, Proteins 64 (2006) 234-245.
40. Jagota A. and Masso M. Computational Methods in Phylogenetic Analysis. Sunnyvale: Bioinformatics By the Bay Press, 2005. ISBN: 0970029764 (Textbook).
41. Masso M. DC-SIGN Points the Way to a Novel Mechanism for HIV-1 Transmission, Medscape General Medicine 5 (2), May 23, 2003.
42. Masso M. and Vaisman I. Comprehensive Mutagenesis of HIV-1 Protease: A Computational Geometry Approach, Biochem Biophys Res Comm 305 (2003) 322-326.
43. Masso M. Differential Equations Computer Lab Manual, Brookdale Community College, 1994 (Textbook).

Selected Scientific Presentations:

Lectures

1. Active Participation in Current Faculty Research Inspires Student Achievement, AMS-MAA Joint Mathematics Meetings, Baltimore Convention Center, Baltimore, MD, Jan. 16-19, 2019.

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2. Predicting Drug Resistance: Probability and Statistics Meet the Building Blocks of Proteins, AMS-MAA Joint Mathematics Meetings, Baltimore Convention Center, Baltimore, MD, Jan. 15-18, 2014.
3. Fast and Accurate Structure-Based Prediction of Resistance to the HIV-1 Integrase Inhibitor Raltegravir, Computational Structural Biology Workshop (CSBW), ACM Conference on Bioinformatics, Computational Biology, and Biomedical Informatics (ACM BCB), Bethesda, MD, Sept. 22-25, 2013.
4. An Atomic Four-Body Potential for the Prediction of Protein-Ligand Binding Affinity, Computational Structural Biology Workshop (CSBW), IEEE International Conference on Bioinformatics and Biomedicine (BIBM 2012), Philadelphia, PA, Oct. 4-7, 2012.
5. Prediction of Human Immunodeficiency Virus Type 1 Drug Resistance: Representation of Target Sequence Mutational Patterns via an n-Grams Approach, IEEE International Conference on Bioinformatics and Biomedicine (BIBM 2012), Philadelphia, PA, Oct. 4-7, 2012.
6. Generation of Atomic Four-Body Statistical Potentials Derived from the Delaunay Tessellation of Protein Structures, 34th Annual International Conference of the IEEE Engineering in Medicine and Biology Society (EMBC 2012), San Diego, CA, Aug. 28-Sept. 1, 2012.
7. Atomic Four-Body Statistical Potential for Macromolecular Structure Analysis, Annual Meeting of the Society for Mathematical Biology, Knoxville, Tennessee, July 25-28, 2012.
8. A Structure-Based Computational Mutagenesis Elucidates the Spectrum of Stability-Activity Relationships in Proteins, 33rd Annual International Conference of the IEEE Engineering in Medicine and Biology Society (EMBC 2011), Boston, MA, Aug. 30-Sept. 3, 2011.
9. Structure-Based Prediction of Protein Activity Changes: Assessing the Impact of Single Residue Replacements, 33rd Annual International Conference of the IEEE Engineering in Medicine and Biology Society (EMBC 2011), Boston, MA, Aug. 30-Sept. 3, 2011.
10. Sequence-Based Prediction of HIV-1 Coreceptor Usage: Utility of n-Grams for Representing gp120 V3 Loops, ACM Conf. on Bioinformatics, Comput. Biology, and Biomedicine (ACM BCB), Chicago, IL, Aug. 1-3, 2011.
11. Modeling Cell Proliferation Activity of Human Interleukin-3 Upon Single Residue Replacements, International Conference on Bioinformatics Models, Methods, and Algorithms (BIOSTEC BIOINFORMATICS 2011), Rome, Italy, Jan. 26-29, 2011.
12. Overcoming the Curse of Dimensionality in a Statistical Geometry Based Computational Protein Mutagenesis, IEEE International Conference on Data Mining (ICDM 2010) Workshop on Biological Data Mining and its Applications in Healthcare (BioDM), Sydney, Australia, Dec. 14-17, 2010.
13. Using Biology to Teach Geometry: Protein Structure Tessellations in Matlab, Annual Summer Meeting of the Mathematical Association of America (MathFest 2010), Pittsburgh, Pennsylvania, August 5-7, 2010.
14. Applied Knowledge-Based Computational Mutagenesis, George Mason Univ., Invited Lecture, Feb. 23, 2010.
15. Accurate Prediction of Stability Changes in Bacteriophage T4 Lysozyme Upon Single Amino Acid Replacements, IEEE International Conference on Bioinformatics and Biomedicine (BIBM 2009), Bethesda, MD, Nov. 1-4, 2009.
16. Novel Pedagogical Resources Based on Protein Structure Analysis, Annual Summer Meeting of the Mathematical Association of America (MathFest 2009), Portland, Oregon, August 6-8, 2009.
17. Novel Pedagogical Resources Based on Protein Structure Analysis, Annual Meeting of the Society for Mathematical Biology, University of British Columbia, Vancouver, Canada, July 27-30, 2009.
18. Novel Pedagogical Resources Based on Protein Structure Analysis, MD-DC-VA Section Meeting of the Mathematical Association of America, University of Mary Washington, Fredericksburg, VA, April 17-18, 2009.
19. Computational Mutagenesis for Analysis of Protein Functional Changes Upon Mutation, AMS-MAA Joint Mathematics Meetings, Washington, DC, Jan. 5-8, 2009.
20. Delaunay Tessellation for the Elucidation of Protein Structure-Function Relationships, MD-DC-VA Section Meeting of the Mathematical Association of America, Hood College, Frederick, MD, Nov. 7-8, 2008.
21. Structure Based Functional Analysis of Bacteriophage f1 Gene V Protein, IEEE International Conference on Bioinformatics and Biomedicine (BIBM 2008), Philadelphia, PA, Nov. 3-5, 2008.
22. Computational Mutagenesis in Analysis of Protein Stability and Function: Effects of Hydration, 6th Congress of the International Society for Theoretical Chemical Physics (ISTCP-VI), Vancouver, Canada, July 19-24, 2008.
23. Functional Analysis of the *Escherichia coli Lac* Repressor: A Computational Mutagenesis Approach, Fourth Int'l Symposium on Bioinformatics Research and Applications (ISBRA 2008), Atlanta, GA, May 6-9, 2008.
24. Computational Mutagenesis for Predicting Functional Consequences of Amino Acid Replacements in Proteins, George Mason University, Manassas, VA, Invited Lecture, Nov. 27, 2007.
25. A Novel Sequence-Structure Approach for Accurate Prediction of Resistance to HIV-1 Protease Inhibitors, IEEE 7th International Conference on Bioinformatics and Bioengineering (BIBE 2007), Harvard Medical School Conference Center, Boston, MA, Oct. 14-17, 2007.

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26. A Statistical Geometry Approach for the Functional Analysis of Protein Mutants, Universidad Central del Caribe, Bayamon, Puerto Rico, Invited Lecture, Nov. 6, 2006.
27. A Novel Approach for Accurate Prediction of HIV-1 Drug Resistance Mutations, Ninth Annual Computational Genomics Conference, Baltimore, MD, Oct. 28-31, 2006.
28. A Novel Approach for Accurate Prediction of HIV-1 Drug Resistance Mutations, Joint SIAM-SMB Conference on the Life Sciences, Raleigh, NC, July 31-Aug. 4, 2006.
29. Analysis of Proteins Using Statistical Geometry, Annual Summer Meeting of the Mathematical Association of America (MathFest 2004), Rhode Island Convention Center, Providence, RI, Aug. 12-14, 2004.
30. Functional Analysis of HIV-1 Protease Using a Four-Body Statistical Potential, Annual Meeting of the Society for Mathematical Biology, University of Michigan, Ann Arbor, MI, July 25-28, 2004.
31. Protein Mutational Analysis Using Statistical Geometry Methods, James Madison University, Harrisonburg, VA, Invited Lecture, Nov. 21, 2003.
32. Protein Mutational Analysis Using Statistical Geometry Methods, St. Mary's College of Maryland, St. Mary's City, MD, Invited Lecture, Nov. 19, 2003.
33. A Statistical Geometry Approach to the Study of Protein Structure, Annual Summer Meeting of the Mathematical Association of America (MathFest 2003), Univ. of Colorado, Boulder, CO, July 29-Aug. 2, 2003.
34. A Statistical Geometry Approach to the Study of Protein Structure, MD-DC-VA Section Meeting of the Mathematical Association of America, Norfolk State University, Norfolk, VA, April 11-12, 2003.
35. Insights into Differential Equations via Derive, The Seventh Annual International Conference on Technology in Collegiate Mathematics (ICTCM), Walt Disney World Dolphin, Orlando, FL, Fall 1994.
36. Differential Equations Meets Derive, MAA/MATYCNJ Joint Meeting, Union County College, NJ, Fall 1994.

Posters

37. Masso, M., Bansal, A., Prem, P., Gajjala, A., and Vaisman, I.I. Cancer-ML: Modeling Fitness of Unregulated Ras Mutants Using Computational Mutagenesis and Machine Learning, 63rd Biophysical Society Meeting, Baltimore, MD, March 2-6, 2019.
38. Masso, M., Bansal, A., Prem, P., Gajjala, A., and Vaisman, I.I. Modeling Fitness of Ras Mutants Using Computational Mutagenesis and Machine Learning, American Association for the Advancement of Science (AAAS), Washington, DC, Feb. 14-17, 2019.
39. Masso, M. Structure-Based Modeling of Fluorescence Levels in Green Fluorescent Protein from *Aequorea victoria* upon Single and Multiple Amino Acid Substitutions, Protein Society 32nd Annual Symposium, Boston, Massachusetts, July 9-12, 2018.
40. Masso, M. An Atomic Four-Body Statistical Potential to Distinguish Native RNA Structures from Nonnative Folds, 62nd Biophysical Society Meeting, SF, CA, Feb. 17-21, 2018.
41. Masso, M. An Accurate and Efficient Atomic Four-Body Knowledge-Based Potential to Distinguish Native Protein Structures from Non-Native Folds, Protein Society 31st Annual Symposium, Montreal, Canada, July 24-27, 2017.
42. Masso, M., Rao, N., and Pyarasani, P. Modeling Variant Gal4 Transcriptional Activation: A Structure-based Approach, American Association for the Advancement of Science (AAAS), Washington, DC, Feb. 11-15, 2016.
43. Masso, M., Chuang, G., Jain, S., Hao, K., and Vaisman, I.I. Structure-Based Predictors of Resistance to the HIV-1 Integrase Inhibitor Elvitegravir, 58th Biophysical Society Meeting, SF, CA, Feb. 15-19, 2014.
44. Masso, M. A Multibody Atomic Statistical Potential for the Prediction of Enzyme-Inhibitor Binding Energy, 57th Biophysical Society Meeting, Philadelphia Convention Center, Philadelphia, PA, Feb. 2-6, 2013.
45. Masso, M. A Multibody Atomic Statistical Potential for the Prediction of Enzyme-Inhibitor Binding Energy, 34th Annual International Conference of the IEEE Engineering in Medicine and Biology Society (EMBC), San Diego, CA, Aug. 28-Sept. 1, 2012.
46. Masso M. and Vaisman I.I. Modelling Structure-Function Relationships in DNA Processing Enzymes Using Computational Mutagenesis, 4th EU-USA Conference on DNA Base Damage and Repair, Holmenkollen, Oslo, Norway, May 18-22, 2011.
47. Masso M. and Vaisman I.I. Modeling HIV-1 Protease Functional Consequences Upon Mutation: Structure Based Prediction of Enzymatic Activity Change and Inhibitor Susceptibility, Annual Meeting of the Society for Mathematical Biology (SMB), University of British Columbia, Vancouver, Canada, July 27-30, 2009.
48. Masso M. and Vaisman I.I. Modeling HIV-1 Protease Functional Consequences Upon Mutation: Structure Based Prediction of Enzymatic Activity Change and Inhibitor Susceptibility, HIV Protease and Beyond: The Past, Present and Future of HIV Structural Biology, National Cancer Institute, Frederick, MD, Jan. 30-31, 2009.
49. Masso M. and Vaisman I.I. Accurate Prediction of Stability Changes in Protein Mutants Using Four-Body Contact Potential and Machine Learning Techniques, Joint ISMB/ECCB, Vienna, Austria, July 21-25, 2007.

50. Masso M. and Vaisman I.I. Accurate Prediction of Stability Alterations in Single-Site Protein Mutants Based on a Novel Computational Mutagenesis, 51st Biophysical Society Meeting, Baltimore, MD, March 3-7, 2007.
51. Masso M. and Vaisman I.I., Accurate Prediction of Enzyme Mutant Activity Based on a Multibody Statistical Potential, ECCB, Eilat, Israel, Jan. 21-24, 2007.
52. Masso M. and Vaisman I.I. Modeling Functional Consequences of Amino Acid Replacements in Proteins, Joint SIAM-SMB Conference on the Life Sciences, Raleigh, NC, July 31-Aug. 4, 2006.
53. Masso M. and Vaisman I.I. Modeling Functional Consequences of Amino Acid Replacements in Proteins, DIMACS - Comput. Approaches to Protein Defects in Human Disease, Rutgers University, April 20, 2006.
54. Masso M. and Vaisman I.I. Functional Prediction of Protein Mutants Using a Four-Body Potential, ISMB, Detroit, MI, June 25-29, 2005.
55. Masso M. and Vaisman I.I. Automated Functional Inference of Enzyme Mutants Utilizing a Four-Body Statistical Potential, The Ninth Annual International Conference on Research in Computational Molecular Biology (RECOMB), Cambridge, MA, May 14-18, 2005.
56. Masso M. and Vaisman I.I. Functional Prediction of Protein Mutants Using a Four-Body Potential, American Association for the Advancement of Science (AAAS), Washington, DC, Feb. 17-21, 2005.
57. Masso M. and Vaisman I.I. Comprehensive Mutagenesis of HIV-1 Protease: A Statistical Geometry Approach, European Conference on Computational Biology (ECCB), Paris, France, Sept. 27-30, 2003.
58. Masso M. and Vaisman I.I. Analyzing Protein Structure-Function Correlations Using Statistical Geometry, Intelligent Systems for Molecular Biology (ISMB), Brisbane, Australia, June 29-July 3, 2003.
59. Masso M. and Vaisman I.I. Comprehensive Mutational Analysis of HIV-1 Protease Using Four-Body Statistical Potentials, Frontiers in Bioinformatics Symposium, Buffalo, NY, June 6-8, 2003.
60. Masso M. and Vaisman I.I. Comprehensive Mutagenesis of HIV-1 Protease: A Computational Geometry Approach, BIO-IT Coalition, Tysons Corner, VA, April 29-30, 2003.
61. Masso M. and Vaisman I.I. Computational Mutagenesis Analysis of HIV-1 Protease: A Statistical Geometry Approach, Discreet Mathematics and Theoretical Computer Science (DIMACS) Workshop on Protein Domains: Identification, Classification and Evolution, Rutgers University, Feb. 27-28, 2003.
62. Jagota A., Masso M., and van Osdol W.W. Quantifying the Discrimination Power of Various Conditions in the Yeast Data Set, Critical Assessment of Microarray Data Analysis (CAMDA), Duke Univ, Dec. 18-19, 2000.

Professional Experience:

2006 – Present **Bioinformatics and Computational Biology, George Mason University** **Fairfax, VA**
Affiliate Faculty, Research Associate
- Conduct research in computational mutagenesis and machine learning.
- Mentor bioinformatics students with research projects.
- Instructor for a graduate Introduction to Bioinformatics course.
- Guest instructor for a graduate Protein Structure Analysis course.

2002 – 2006 **Bioinformatics and Computational Biology, George Mason University** **Fairfax, VA**
Instructor, Graduate Teaching and Research Assistant
- Instructor and assistant for graduate Introduction to Bioinformatics course.
- Mentored students working on projects that incorporate computational mutagenesis and machine learning.

1993 – 1995 **Mathematics Department, Brookdale Community College** **Lincroft, NJ**
Tenure-Track Faculty Instructor
- Taught a full load of courses, ranging from remedial arithmetic to calculus and differential equations, incorporating computer software at all levels.
- Awarded a course development grant to prepare a computer lab component for the differential equations course.
- Gave presentations at local and national conferences.
- Participated in numerous departmental and college-wide committees.

Summer 1993 **Delaware Technical and Community College** **Wilmington, DE**
Adjunct Faculty Instructor
- Algebra and precalculus instructor for the Upward Bound Math/Science Initiative summer program.
- Provided academic guidance to minority high school students with an interest in math and science.

1988 – 1993 **Department of Mathematical Sciences, University of Delaware** **Newark, DE**

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Instructor, Graduate Teaching Assistant
- Taught courses in college algebra, statistics, precalculus, and computer-aided calculus I and II for matriculating students.
- Recruited to teach five special sections of the above courses for the Division of Continuing Education, RISE program (minority engineers), and Academic Advancement program (pre-freshman minority students).
- Ran problem sessions for business calculus courses and computer lab sessions for differential equations courses.

Fall 1992   **Widener University, University College**   **Wilmington, DE**
Adjunct Faculty Instructor
- Taught calculus I, with emphasis on business and economics applications; students were adults working on conferring business degrees part-time.

Selected Honors, Scholarships, and Awards:

- NSF Travel Award to attend IEEE International Conference on Bioinformatics and Biomedicine (2009, 2012).
- Registration fee grant to attend BIOSTEC BIOINFORMATICS 2011.
- NSF Travel Award to attend IEEE International Conference on Data Mining (ICDM 2010).
- Faculty of 1000 Biology: evaluations for Masso M. & Vaisman I.I. Bioinformatics 2007 Dec 1 23 (23): 3155-61 http://www.f1000biology.com/article/id/1098693/evaluation
- Erdös number 2 (me ← Arun Jagota ← Paul Erdös), Erdös Number Project http://www.oakland.edu/enp/
- NSF Travel Award to attend 7th IEEE BIBE, 2007.
- Landahl Student Travel Awards, Society for Mathematical Biology (SMB), 2004, 2006, 2009, and 2012.
- Workshop Travel Awards, DIMACS, 2003 and 2006.
- Graduate Teaching Assistant, George Mason University, School of Computational Sciences, 2004-2006.
- Navachat Tongvichit Memorial Fellowship for Excellence in Bioinformatics, George Mason University, 2005.
- ECCB, ISMB, and RECOMB Travel Awards, Int'l Society for Computational Biology (ISCB), 2003 and 2005.
- Graduate Research Assistant, George Mason University, School of Computational Sciences, 2002-2004.
- Graduate Student Travel Fund Scholarships for MAA MathFest, George Mason University, 2003 and 2004.
- Fellow, Biostatistics Department, UCLA, Eugene Cota Robles Award, 1998-1999.
- Math/Science Division Differential Equations Course Development Grant, Brookdale Comm. College, 1994.
- Graduate Teaching Assistant, University of Delaware, Department of Mathematical Sciences, 1988-1993.
- Fellow, University of Delaware, Department of Mathematical Sciences, 1992.
- Baxter-Sloyer Excellence in Teaching Award, University of Delaware, 1991.
- University of Delaware Departmental Teaching Awards, Department of Mathematical Sciences, 1990 and 1991.

Professional Development:

- Recurring program committee member and referee, BIOSTEC BIOINFORMATICS and International Conference on Physiological Computing Systems (PhyCS).
- Mentor, Aspiring Scientists Summer Internship Program (ASSIP), George Mason University, 2013, 2015, 2018.
- Invited referee: Nucleic Acids Research, PeerJ, PloS ONE, Amino Acids, BMC Cancer, CBE--Life Sciences Education, Journal of Theoretical Biology, International Journal of Data Mining and Bioinformatics, Journal of Diabetes Research, HIV/AIDS - Research and Palliative Care, Future Microbiology, Physical Chemistry Chemical Physics, Molecular Genetics and Metabolism, International Journal of Peptide Research and Therapeutics, BioMed Research International.
- Panelist, Bioinformatics Education Workshop, BIBM 2009, Bethesda, MD, Nov. 1-4, 2009.
- Tutorial co-presenter: Knowledge-Based Study of Protein Structure-Function Correlations Using Computational Geometry, IEEE Int'l Conf. on Bioinformatics and Biomedicine (BIBM 2009), Bethesda, MD, Nov. 1-4, 2009.
- Chair, Session on Undergraduate Education, Annual Meeting of the Society for Mathematical Biology, University of British Columbia, Vancouver, Canada, July 27-30, 2009.
- Chair, AMS Session on Biology II, Joint AMS/MAA Mathematics Meetings, Washington, DC, Jan. 5-8, 2009.
- Tutorial co-presenter: Statistical Geometry of Protein Structure and Computational Mutagenesis, IEEE International Conference on Bioinformatics and Biomedicine (BIBM 2008), Philadelphia, PA, Nov. 3-5, 2008.
- Program committee member and referee, ISIBM International Joint Conferences on Bioinformatics, Systems Biology and Intelligent Computing, August 3-6, 2009, Shanghai, China.
- Invited referee, International Journal of Computational Biology and Drug Design, 2008 – Present.
- Presented 2-hour lecture on statistical machine learning at Computational Methods in Molecular and Solid-State Systems Student Workshop (http://proteins.gmu.edu/cmmsss.html), George Mason University, May 16, 2008.

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- Developing the AUTO-MUTE (http://proteins.gmu.edu/automute) suite of web servers for predicting functional consequences of amino acid mutations in proteins, March 2007 – Present.
- Presented a 4-hour workshop in statistical machine learning for the College of Science faculty and graduate students at George Mason University, Nov. 3, 2006.
- Invited referee, 2007 ACM Symposium on Applied Computing, Bioinformatics Track.
- Research project advisor for graduate and undergraduate students in the fields of computational mutagenesis and machine learning, George Mason University, Bioinformatics and Computational Biology, 2005-Present.
- Grant Proposal Reviewer, Aids Fonds Netherlands, Keizersgracht 390, 1016 GB Amsterdam, 2004 – 2007.
- Participant, Mammalian Bioinformatics Teaching and Learning Workshop, BioQUEST Curriculum Consortium, BEDROCK Project, The Jackson Laboratory, Bar Harbor, Maine, Nov. 3-6, 2004.

Affiliations:

- Biophysical Society (BPS)
- American Association for the Advancement of Science (AAAS)
- The Protein Society (PS)
- Institute of Electrical and Electronics Engineers (IEEE)
- International Antiviral Society-USA (IAS-USA)
- American Mathematical Society (AMS)
- Mathematical Association of America (MAA)