

YANA BROMBERG

Associate Professor
Department of Biochemistry and Microbiology
Rutgers University, School of Environmental and Biological Sciences
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EDUCATION

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| <i>Columbia University, New York, NY</i> Ph.D., Biomedical Informatics (Bioinformatics Track) | 2007 |
| <i>Dissertation Title: Prediction and Analysis of Effects of Non-Synonymous Single Nucleotide Polymorphisms on (Product) Protein Function</i> | |
| <i>Advisors: Burkhard Rost (Biochemistry/Molecular Biophysics), Rudolph L. Leibel (Pediatrics and Medicine/Molecular Genetics)</i> | |
| <i>Thesis Committee: David E. Shaw (Biomed. Informatics), Andrey Rzhetsky (Biomed. Informatics), Lawrence Shapiro (Biochem/Mol. Biophysics)</i> | |
| <i>Columbia University, New York, NY</i> M.Phil. Biomedical Informatics | 2004 |
| <i>State University of NY (SUNY) at Stony Brook, Stony Brook, NY</i> B.A. Biology / B.Eng. Computer Science (Magna Cum Laude) | 2001 |

APPOINTMENTS

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| <i>Institute of Advanced Studies, University of Bologna, Italy</i> Visiting Fellow | 2020 |
| <i>Rutgers University, New Brunswick, NJ</i> Associate Professor with Tenure, Dept. of Biochemistry and Microbiology | 2016-Present |
| <i>Institute for Advanced Study, Technical University of Munich, Germany</i> Hans Fischer Fellow, Dept. of Bioinformatics and Computational Biology | 2014-Present |
| <i>Rutgers University, New Brunswick, NJ</i> Adjunct Professor, Dept. of Genetics | 2013-Present |
| <i>Rutgers University, New Brunswick, NJ</i> Assistant Professor, Dept. of Biochemistry and Microbiology | 2010-2016 |
| <i>BioSof, LLC, New York, NY</i> Chief Scientific Officer (Bioinformatics Tool Development) | 2008-Present |
| <i>JPM Global, New York, NY</i> Software Developer (Natural Language Processing Tools) | 2007-2008 |
| <i>Columbia University, New York, NY</i> Post-doctoral Research Scientist, Dept. of Biochemistry and Molecular Biophysics | 2006-2010 |

HONORS

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| Visiting Fellowship at the Institute for Advanced Studies at the Alma Mater Studiorum, University of Bologna, Italy | 2020 |
| Research Excellence Award, School of Environmental and Biological Sciences, Rutgers | 2017 |
| Hans Fischer Fellowship for Outstanding Early Career Scientists, Institute of Advanced Studies at Technical University of Munich | 2014-2017 |
| NSF CAREER Award | 2016 |
| Rutgers Board of Trustees Research Fellowship for Scholarly Excellence | 2016 |
| Theobald Smith Society Young Investigator Award | 2016 |
| PhRMA Foundation Research Starter Award | 2015 |
| Brooklyn Tech Younger Alumni Recognition Award for Career Progress | 2014 |
| International Society for Computational Biology Travel Fellowship | 2008 |
| NLM Biomedical Informatics research training fellow | 2001-2005 |
| Weizmann Institute of Science, Karyn Kupciner International Science School Scholar | 2000 |
| SUNY at Stony Brook Honors Scholar | 1997-2001 |
| National Merit Scholar | 1997 |
| Guideposts Scholar | 1997 |

SCHOLARSHIP

PUBLICATIONS (67 total, in reverse publication order, advisees underlined, [BC] = book chapter, [MS] = Meeting Summary, [OR] = Original Research, [RW] = Review)

1. Wang, Y., Astrakhan, Y., Petersen, B.S., Franke, A., **Bromberg, Y.** Analysis of exome variation for association with Crohn's disease. <https://doi.org/10.1101/216432> [OR]
 2. Miller, M., Vitale, D., Rost, B., **Bromberg, Y.** fuNTRp: Identifying protein positions for variation driven functional tuning. <https://doi.org/10.1101/578757> [OR]
 3. Zhu, C., Miller, M., Lusskin, N., Mahlich, Y., Wang, Y., Zeng, Z., **Bromberg, Y.** Fingerprinting cities: differentiating subway microbiome functionality. *In press.* [OR]
 4. **Bromberg, Y.**, El-Mabrouk, N., & Radivojac, P. (2019). ISMB/ECCB 2019 Proceedings. *Bioinformatics*, 35(14), i1-i2. [MS]
 5. **Bromberg, Y.**, Capriotti, E., Carter, H. (2019) VarI-COSI 2018: a forum for research advances in variant interpretation and diagnostics. *BMC Genomics*. **20(Suppl 8)**: p.550 [MS]
 6. Miller, M., Wang, Y., **Bromberg, Y.** (2019) Elucidating the disagreement between variant effect predictions and experimental reality for the PCM1 protein. *Human Mutation* [OR]
 7. Wang, Y., Miller, M., **Bromberg, Y.** (2019) Identifying mutation-driven changes in gene functionality that lead to venous thromboembolism. *Human Mutation*. [OR]
 8. Pejaver, V., Babbi, G., Casadio, R., Folkman, L., Katsonis, P., Kundu, K., Lichtarge, O., Martelli, P.L., Miller, M., Moulton, J., Pal, L.R., Savojardo, C., Yin, Y., Zhou, Y., Radivojac, P., **Bromberg, Y.** (2019) Assessment of methods for predicting the effects of PTEN and TPMT protein variants. *Human Mutation* [OR]
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9. Hazen, R.M., **Bromberg, Y.**, Downs, R.T., Eleish, A., Flkowski, G.P., Fox, P., Giovannelli, D., Hummer, D.R., Hystad, G., Golden, J.J., Knoll, A.H., Li, C., Liu, C., Moore, E.K., Morrison, S.M., Muscente, A.D., Prabhu, A., Ralph, J., Rucker, M.Y., Runyon, S.E., Warden, L.A., Zhong, H. Chapter 21: "Deep Carbon through Deep Time: Data-Driven Insights" by *Cambridge University Press*. <https://deepcarbon.net/project/whole-earth-carbon> [BC]
 10. Performance of computational methods for the evaluation of Pericentriolar Material 1 missense variants in CAGI-5. Monzon, A.M., Carraro, M., Chiricosta, L., Reggiani, F., Han, J., Ozturk, K., Wang, Y., Miller, M., **Bromberg, Y.**, Capriotti, E., Savojardo, C., Babbi, G., Martelli, P.L., Casadio, R., Katsonis, P., Lichtarge, O., Carter, H., Kousi, M., Katsanis, N., Andreoletti, G., Moulton, J., Brenner, S.E., Ferrari, C., Leonardi, E., Tosatto, S.C.E. (2019). *Human mutation* [MS/OR].
 11. Voskanian A, (Wang, Y., **Bromberg Y.**, as part of CAGI CHEK2 challenge participants) Brenner S, Moulton J, Kann MG. (2019) Assessing the performance of in-silico methods for predicting the pathogenicity of variants in the gene CHEK2, among Hispanic females with breast cancer. *Human Mutation* [MS/OR]
 12. Honarbakhsh, M., Malta, K., Erricon, A., Zhu, C., **Bromberg, Y.**, Zhong, G., Isoherranen, N., Van Buiten, C., Raskin, I., Chikindas, M. and Breslin, P., 2019. Interaction between dietary vitamin A, gut microbes, and host vitamin A status. *The FASEB Journal*, 33(1_supplement), pp.484-7.
 13. McInnes, G., Daneshjou, R., (Wang, Y., **Bromberg, Y.**, as part of CAGI thromboembolism risk challenge participants) Moulton, J., Brenner, S., Altman, R. (2019) Predicting venous thromboembolism risk from exomes in the Critical Assessment of Genome Interpretation (CAGI) challenges. (2019) *Human Mutation* [MS/OR]
 14. Mahlich, Y., Steinegger, M., Rost, B., **Bromberg, Y.** (2018) HFSP: High speed homology-driven function annotation of proteins. *Bioinformatics* 34 (13), i304-i312 [OR]
 15. **Bromberg, Y.**, Radivojac, P. (2018) ISMB 2018 proceedings, *Bioinformatics* 34 (13), i2. [MS]
 16. Wang, S., Mandell, J.D., Kumar, Y., Sun, N., Morris, M.T., Arbelaez, J., Nasello, C., Dong, S., Duhn, C., Zhao, X., Yang, Z., Pdmanabhuni, S.S., Yu, D., King, R.A., Dietrich, A., Khalifa, N., Dahl, N., Huang, A.Y., Neale, M.B., Coppola, G., Mathews, C.A., Scharf, J.M., (**Bromberg, Y.** as part of) Tourette International Genetics Study (TIC Genetics), Tourette Syndrome Genetics Southern and Eastern Europe (TSGENESEE), Tourette Association of America International Consortium for Genetics (TAAICG), Fernandez, T.V., Buxbaum, J.D., De Rubeis, S., Grice, D.E., Xing, J., Heiman, G.A., Tischfield, J.A., Paschou, P., Willsey, A.J., State, M.W. *De novo* sequence and copy number variants are strongly associated with Tourette Disorder and implicate cell polarity in pathogenesis. *Cell Reports*, *In press* [OR]
 17. McDermott, J., **Bromberg, Y.**, Partridge, M. (2018) Ten Simple Rules for Drawing Scientific Comics. *PLoS computational biology*, 14(1), e1005845. [OR]
 18. Zhu, C., Miller, M., Marpaka, S., Vaysberg, P., Rühlemann, M.C., Wu, G., Heinsen, F.A., Tempel, M., Zhao, L., Lieb, W., Franke, A., **Bromberg, Y.** (2017) Functional sequencing read annotation for high precision microbiome analysis. *Nucleic Acids Research*, gkx1209. [OR]
 19. Zhu, C., Mahlich, Y., Miller, M., **Bromberg, Y.** (2017) fusionDB: assessing microbial diversity and environmental preferences via functional similarity networks. *Nucleic Acids Research*, 46(D1), D535-D541 [OR]
 20. Miller, M., Zhu, C., Mahlich, Y., **Bromberg, Y.** (2017) CLuBBer: removing the bioinformatics bottleneck in big data analyses. *Journal of Integrative Bioinformatics*. [OR]
 21. Daneshjou, R., Wang, Y., **Bromberg, Y.**, Bovo, S., Martelli, P. L., Babbi, G., ... & Jones, D. T. (2017). Working towards precision medicine: predicting phenotypes from exomes in the Critical Assessment of Genome Interpretation (CAGI) challenges. *Human Mutation*. [RW]
 22. Liu, J., Lopez, N., Ahn, Y. B., Goldberg, T., **Bromberg, Y.**, Kerkhof, L. J., Häggblom, M. M. (2017). Novel Reductive Dehalogenases from the Marine Sponge Associated Bacterium *Desulfoluna spongiiphila*. *Environmental Microbiology Reports*. [OR]
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23. Willsey, A. J., Abdulkadir, M., Barr, C. L. (**Bromberg, Y.** as part of) Tourette Genomics Consortium, Tischfield, J.A., State, M.W., Heiman, G.A. (2017) De Novo Coding Variants Are Strongly Associated with Tourette Disorder. *Neuron*, **94**(3): 486 - 499.e9 [OR]
 24. Mahlich, Y., Hecht, M., De Beer, T.A.P., **Bromberg, Y.**, Rost, B. (2017) Human variation has stronger functional effects than variation across species. *Nat Scientific Reports* **7**, 1608
 25. Carraro, M., Minervini, G., Giollo, M., **Bromberg, Y.**, Capriotti, E., Casadio, R., Dunbrack, R., Elefanti, L., Fariselli, P., Ferrari, C., Gough, J., Katsonis, P., Leonardi, E., Lichtarge, O., Menin, C., Martelli, P. L., Niroula, A., Pal, L. R., Repo, S., Scaini, M. C., Vihinen, M., Wei, Q., Xu, Q., Yang, Y., Yin, Y., Zaucha, J., Zhao, H., Zhou, Y., Brenner, S. E., Moulton, J., Tosatto, S. C.E. (2017), Performance of in silico tools for the evaluation of p16INK4a (CDKN2A) variants in CAGI. *Human Mutation*. 2017;00:1–9 [MS]
 26. Miller, M., **Bromberg, Y.**, Swint-Kruse, L. (2017) Variant effect prediction methods fail for rheostat positions. *Nat Scientific Reports* **7**, 41329. [OR]
 27. **Bromberg, Y.**, Hahn, M.W., Radivojac, P. (2016) Computational approaches to the understanding of evolution of molecular function. *Pac Symp Biocomput*. **22**:1-2 [RW /MS]
 28. Goldberg, T., Rost, B., **Bromberg, Y.** (2016). Computational prediction shines light on type III secretion origins. *Nat Scientific Reports*, **6**, 34516. [OR]
 29. Reeb, J., Hecht, M., Mahlich, Y., **Bromberg, Y.**, Rost, B. (2016) Predicted molecular effects tell stories about system level of disease. *PLoS Comput Biol*. **12**(8): p. e1005047. [OR]
 30. **Bromberg, Y.**, Capriotti, E., Carter, H. (2016) VarI-SIG 2015: methods for personalized medicine - the role of variant interpretation in research and diagnostics. *BMC Genomics*. **17 Suppl 2**: p. 425. [MS]
 31. Rost, B., Radivojac, P, **Bromberg, Y.** (2016) Protein function in precision medicine: deep understanding with machine learning. *FEBS Lett*. **590**(15): p. 2327-41 [RW]
 32. Bruse, S., Xing, J., Moreau, M., **Bromberg, Y.**, Jang, J., Wang, N., Picchi, M., Lin, Y., Langley, R., Qualls, C., Klensney-Tait, J., Zabner, J., Mao, J., Belinsky, S., Tesfaigzi, Y., Nyunoya T. (2016) Whole exome sequencing in severe COPD. *Human Genomics*. **10**(1):1-12. [OR]
 33. Greene, C.S., Foster, J.A., Stanon, B.A., Hogan, D.A., **Bromberg, Y.** (2016) Computational approaches to study microbes and microbiomes. *Pac Symp Biocomput* 2016. :557-567 [RW]
 34. Zhu, C., Delmont, T.O., Vogel, T.M., **Bromberg, Y.** (2015) Functional basis of microorganism classification. *PLoS Comput Biol*. **11**(8): e1004472. [OR]
 35. **Bromberg, Y.** and Capriotti, E. (2015) VarI-SIG 2014: from SNPs to variants: interpreting different types of genetic variants. *BMC Genomics*. **16**(Suppl 8):I1. [MS]
 36. Hecht, M., **Bromberg, Y.**, Rost, B. (2015) Better prediction of functional effects for sequence variants. *BMC Genomics*. **16**(Suppl 8):S1. [OR]
 37. **Bromberg, Y.** and Capriotti E. (2015) SNP-SIG 2013: the state of the art of genomic variant interpretation. *Bioinformatics*. **31**(3): 449-450. [MS]
 38. Yachdav, G., Kloppmann, E., Kajan, L., Hecht, M., Goldberg T., Hamp, T., Hönigschmid, P., Schafferhans, A., Roos, M., Bernhofer, M., Richter, L., Ashkenazy, H., Punta, M., Schlessinger, A., **Bromberg, Y.**, Schneider, R., Vriend, G., Sander, C., Ben-Tal, N., Rost, B. (2014) PredictProtein--an open resource for online prediction of protein structural and functional features. *Nucleic Acids Res*. **W1**: W337-W343 [OR]
 39. Harel, A., **Bromberg, Y.**, Falkowski, P.G., Bhattacharya, D. (2014) Evolutionary history of redox metal-binding domains across the tree of life. *Proc Natl Acad Sci U S A*. **111**(19):7042-7047. [OR]
 40. **Bromberg, Y.**, Capriotti, E. (2014) SNP-SIG 2013: from coding to non-coding - new approaches for genomic variant interpretation. *BMC Genomics*. **15**(Suppl 4):S1 [MS]
 41. Senn, S., Nanda, V., Falkowski, P.G., **Bromberg, Y.** (2014). Function-based assessment of structural similarity measurements using metal co-factor orientation. *Proteins*.**82**:648-656 [OR]
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42. de Ridder, J., **Bromberg, Y.**, Michaut, M., Satagopam, V.P., Corpas, M., MacIntyre, G., Alexandrov, T. (2013). The young PI buzz: learning from the organizers of the Junior Principal Investigator Meeting at ISMB-ECCB 2013. *PLoS Comput Biol.* **9**: e1003350. [MS]
 43. Ren, X., Graham, J.C., Jing, L., Mikheev, A.M., Gao, Y., Lew, J.P., Xie, H., Kim, A.S., Shang, X., Friedman, C., Vail, G., Fang, M.Z., **Bromberg, Y.**, Zarbl, H. (2013). Mapping of Mcs30, a new mammary carcinoma susceptibility quantitative trait locus (QTL30) on rat chromosome 12: identification of fry as a candidate Mcs gene. *PLoS One.* **8**: e70930. [OR]
 44. **Bromberg, Y.** (2013). Building a genome analysis pipeline to predict disease risk and prevent disease. *J Mol Biol.* **425**: 3993-4005. [RW]
 45. **Bromberg, Y.**, Kahn, P. C., Rost, B. (2013) Neutral and weakly nonneutral sequence variants may define individuality. *Proc Natl Acad Sci U S A.* **110**: 14255-14260 [OR]
 46. **Bromberg Y.** (2013) Disease Gene Prioritization. *PLoS Comput Biol.* **9**(4): e1002902. [BC]
 47. Ellinghaus, D., Zhang, H., Zeissig, S., Lipinski, S., Till, A., Jiang, T., Stade, B., **Bromberg, Y.**, Ellinghaus, E., ... & Franke, A. (2013) Association Between Variants of PRDM1 and NDP52 and Crohn's Disease, Based on Exome Sequencing and Functional Studies. *Gastroenterology.* **145**: 339-347 [OR]
 48. Hecht, M., **Bromberg, Y.**, Rost, B. (2013). News from the protein mutability landscape. *J Mol Biol.* **425**: 3937-3948. [OR]
 49. **Bromberg, Y.**, Capriotti, E. (2013) Thoughts from SNP-SIG 2012: future challenges in the annotation of genetic variations. *BMC Genomics.* **14**(Suppl 3): S1 [MS]
 50. Capriotti, E., Altman, R. B., **Bromberg, Y.** (2013) Collective judgment predicts disease-associated single nucleotide variants. *BMC Genomics.* **14**(Suppl 3): S2 [OR]
 51. **Bromberg, Y.**, Capriotti, E. (2012). SNP-SIG Meeting 2011: identification and annotation of SNPs in the context of structure, function, and disease. *BMC Genomics* 13 Suppl 4, S1. [MS]
 52. Schaefer, C., Meier, A., Rost, B., **Bromberg, Y.** (2012) SNPdbe: constructing an nsSNP functional impacts database. *Bioinformatics.* **28**: 601-602 [OR]
 53. Schaefer, C., **Bromberg, Y.**, Achten, D., Rost, B. (2012) Disease-related mutations predicted to impact protein function. *BMC Genomics.* **13**(Suppl 4): S11 [OR]
 54. Rawat, S. R., Mannisto, M. K., **Bromberg, Y.**, Haggblom, M. M. (2012) Comparative genomic and physiological analysis provides insights into the role of Acidobacteria in organic carbon utilization in Arctic tundra soils. *FEMS Microbiol Ecol.* **82**: 341-355 [OR]
 55. Harel, A., Falkowski, P., **Bromberg, Y.** (2012) TrAnsFuSE refines the search for protein function: oxidoreductases. *Integr Biol (Camb).* **4**: 765-777 [OR]
 56. Capriotti, E., Nehrt, N. L., Kann, M. G., **Bromberg, Y.** (2012) Bioinformatics for personal genome interpretation. *Brief Bioinform.* **13**: 495-512 [RW]
 57. Wainreb, G., Ashkenazy, H., **Bromberg, Y.**, Starovolsky-Shitrit, A., Haliloglu, T., Ruppin, E., Avraham, K. B., Rost, B., Ben-Tal, N. (2010) MuD: an interactive web server for the prediction of non-neutral substitutions using protein structural data. *Nucleic Acids Res* **38**: W523-528[OR]
 58. Zaghoul, N. A., Liu, Y., Gerdes, J. M., Gascue, C., Oh, E. C., Leitch, C. C., **Bromberg, Y.**, Binkley, J., Leibel, R. L., Sidow, A., Badano, J. L., Katsanis, N. (2010) Functional analyses of variants reveal a significant role for dominant negative and common alleles in oligogenic Bardet-Biedl syndrome. *Proc Natl Acad Sci U S A.* **107**: 10602-10607 [OR]
 59. Sester, M., Koebernick, K., Owen, D., Ao, M., **Bromberg, Y.**, May, E., Stock, E., Andrews, L., Groh, V., Spies, T., Steinle, A., Menz, B., Burgert, H. G. (2010) Conserved amino acids within the adenovirus 2 E3/19K protein differentially affect downregulation of MHC class I and MICA/B proteins. *J Immunol.* **184**: 255-267 [OR]
 60. **Bromberg, Y.**, Yachdav, G., Ofran, Y., Schneider, R., Rost, B. (2009) New in protein structure and function annotation: hotspots, single nucleotide polymorphisms and the 'Deep Web'. *Curr Opin Drug Discov Devel:* **12**: 408-419 [RW]
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61. **Bromberg, Y.**, Overton, J., Vaisse, C., Leibel, R. L., Rost, B. (2009) In silico mutagenesis: a case study of the melanocortin 4 receptor. *FASEB J.* **23**: 3059-3069 [OR]
 62. Calton, M. A., Ersoy, B. A., Zhang, S., Kane, J. P., Malloy, M. J., Pullinger, C. R., **Bromberg, Y.**, Pennacchio, L. A., Dent, R., McPherson, R., Ahituv, N., Vaisse, C. (2009) Association of functionally significant Melanocortin-4 but not MC-3 receptor mutations with severe adult obesity in a large North American case-control study. *Hum Mol Genet.* **18**: 1140-1147 [OR]
 63. **Bromberg, Y.**, Rost, B. (2009) Correlating protein function and stability through the analysis of single amino acid substitutions. *BMC Bioinformatics.* **10**(Suppl 8): S8 [OR]
 64. **Bromberg, Y.**, Yachdav, G., Rost, B. (2008) SNAP predicts effect of mutations on protein function. *Bioinformatics.* **24**, 2397-2398 [OR]
 65. **Bromberg, Y.**, Rost, B. (2008) Comprehensive in silico mutagenesis highlights functionally important residues in proteins. *Bioinformatics.* **24**: i207-212 [OR]
 66. Dokmanovic-Chouinard, M., Chung, W. K., Chevre, J. C., Watson, E., Yonan, J., Wiegand, B., **Bromberg, Y.**, Wakae, N., Wright, C. V., Overton, J., Ghosh, S., Sathe, G. M., Ammala, C. E., Brown, K. K., Ito, R., LeDuc, C., Solomon, K., Fischer, S. G., Leibel, R. L. (2008) Positional cloning of "Lisch-Like", a candidate modifier of susceptibility to type 2 diabetes in mice. *PLoS Genet.* **4**: e1000137 [OR]
 67. **Bromberg, Y.**, Rost, B. (2007) SNAP: predict effect of non-synonymous polymorphisms on function. *Nucleic Acids Res.* **35**: 3823-3835 [OR]
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INVITED TALKS (108 total, in reverse order)

Keynotes and Plenary

1. Rutgers Annual ENIGMA Astrobiology Symposium, New Brunswick, NJ. *Increasing Complexity of Nanomachines in Microbial Ancestors.* May 8, 2019.
 2. TedX Rutgers "Pale Blue Dot" conference, New Brunswick, NJ. *What makes us human? People, microbes, and the "stuff" of life.* February 23, 2019.
 3. 4D-Workshop (Deep-time Data Driven Discovery), Washington, DC. *Deep learning from deep time: computational techniques for mapping protein structure-function relationships to evolutionary time-scales.* June 4, 2018
 4. The molecular basis of diseases: can we infer phenotypes from protein variant analysis? FEBS 2018 Advanced Course, Bologna, Italy. *Labeling tune-able protein positions for evaluating variation effects.* May 24, 2018
 5. VIB Applied Bioinformatics in Life Sciences Conference 2018, Leuven, Belgium. *Deeper understanding of microbiomes as a benefit of forgetting microbial names.* March 8, 2018.
 6. International Symposium on Molecular Evolution and Medicine. Philadelphia, PA. *Improving variant effect prediction: function, disease, and evolution of "normal."* September 16, 2017
 7. Goldschmidt Conference 2017, Geobiology in the Time of Big Data session, Paris, France. *Food and Dating Proteins: Assessing Origins of Biological Electron Transfer.* August 14, 2017.
 8. Joint Genome Informatics Workshop (GIW) and International Conference on Bioinformatics (InCoB), GIW/INCOB 2015 conference, Tokyo, Japan. *Cracking the disease code: large-scale genomic data analysis unveils pathogenesis pathways.* September 9, 2015.
 9. MidSouth Computational Biology and Bioinformatics Society (MCBIOS) annual conference. Little Rock, AR. *Interpreting genomic data to inform pathogenesis pathways.* March 13, 2015.
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Conference presentations

1. Second Workshop on Microbiomics, Metagenomics, and Metabolomics @ ACM-BCB'2019. Niagara Falls, NY. **TBD**. Sept 8, 2019
 2. Meaning of Life Symposium. MIT, Cambridge, MA. **42, or if I HAD TO formalize my thoughts**. March 13, 2019.
 3. US-Serbia/West Balkan Data Science Workshop, Belgrade, Serbia. **Deeper understanding of microbiomes as a benefit of forgetting microbial names**. August 28, 2018
 4. CAGI'18 meeting, Chicago, IL. **CAGI 2018: PTEN and TPMT challenges, the state of the art in evaluating variant effects**. July 5, 2018.
 5. Microbiology at Rutgers Symposium, Rutgers University, New Brunswick, NJ. **Deeper understanding of microbiomes as a benefit of forgetting microbial names**. February 2, 2018
 6. i3D retreat, Rutgers University, Newark, NJ. **Understanding molecular function and malfunction**. October 25, 2017
 7. Principles of gene circuit design workshop. Oaxaca, Mexico. **Predicting modifiable protein residues for more effective analysis of exonic variation**. September 11, 2017
 8. American Chemical Society (ACS) Symposium Fall meeting, Washington, D.C. **Don't forget to set the function to low: predicting modifiable protein residues and effects of their variation**. August 21, 2017.
 9. LabRoots Genetics and Genomics Virtual Event. **Not all variants are created equal: what went wrong in the prediction of functional effects of exomic variation**. May 10, 2017
 10. Computational BioMedicine - From genes to networks to biomarkers. University of Southern Denmark (SDU), Odense, Denmark. **Not all variants are created equal: what went wrong in the prediction of functional effects of exomic variation**. January 18, 2017.
 11. The Theobald Smith Society (NJ American Society for Microbiology) meeting. Rutgers University, New Brunswick, NJ. **Tell me what you do and I'll tell you who you are: functional basis of microorganism and microbiome annotation**. November 14, 2016
 12. ISMB Junior Principal Investigator Meeting. Orlando, Florida. **Climbing the tenure ladder: strategic decisions for promotion**.
<https://www.slideshare.net/secret/nuUow4umogGYQQ> July 10, 2016
 13. Gordon Research Conference on Human SNPs & Disease, Understanding the Mechanisms of Variant Effects in the Era of Genome Sequencing. Mount Holyoke College, South Hadley, MA. **Interpreting genomics data to infer pathogenesis pathways**. June 14, 2016
 14. Keck-RPI Science Day Meeting. Rensselaer Polytechnic Institute, Troy, NY. **Food and Dating Proteins: Assessing Origins of Biological Electron Transfer**. June 8^t, 2016.
 15. Humboldt Technische Universität München Institute for Advanced Study (TUM-IAS) General Assembly, Garching, Germany. **Functional Basis of Microorganism Classification**. April 28, 2016
 16. Pacific Symposium on Biocomputing (PSB 2016) "Computational approaches to study microbes and microbiomes" workshop. Kona, HI. **Functional basis of microorganism classification**. January 5, 2016.
 17. Basel Computational Biology Conference ([BC]2 2015). Basel, Switzerland. **Functional basis of microorganism classification**. June 8, 2015.
 18. Great Lakes Bioinformatics Conference (GLBio 2015) conference. **Functional basis of microorganism classification**. May 19, 2015.
 19. Great Lakes Bioinformatics Conference (GLBio 2015) conference. **Personalized Medicine Tutorial**. May 18, 2015.
 20. GIW/ISCB-Asia 2014 conference, Tokyo, Japan. **The last straw did not break the camel's back: searching for causative variants of polygenic disease disregards individual predisposing genomic differences**. December 16, 2014.
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21. IAS Fellows Meeting. Technical University of Munich, Garching, Germany. *Tell me what you do and I'll tell you who you are: exploring functional basis of microorganism classification*. October 2, 2014.
 22. Gordon Research Conference on Human SNPs & Disease, Discussion leader, Easton, MA. *Genetics of personalized medicine and rare diseases*. August 7th, 2014
 23. Intelligent Systems in Molecular Biology (ISMB'2014) conference, Career Development for Women in Science meeting, Boston, MA. *What makes a job candidate stand out: Perspectives from young group leaders and the people who hire them*. July 15, 2014
 24. BioIT conference, Clinical Genomics Track, Boston, MA. *Mapping Disease Risk to The Human Variome*. April 30, 2014.
 25. Critical Assessment of Genome Interpretation (CAGI 2013) meeting, Discussion leader, Berlin, Germany. *Structure vs. evolution for variant interpretation*. July 18, 2013
 26. 2013 Summit on Translational Bioinformatics, San Francisco, CA. *Future challenges in the annotation of genetic variation*. March 18, 2013
 27. VarI-SIG 2012 Meeting, Long Beach, CA. *Noise in Biology*. July 14, 2012.
 28. 107 Statistical Mechanics Conference, Rutgers, NJ. *Differentiating SNP-mediated function disruption from disease*. May 6, 2012.
 29. Critical Assessment of Genome Interpretation (CAGI 2011) meeting, Berkeley, CA. *Evaluating (Crohn's) Disease Predisposition From Exome Data*. December 9, 2011
 30. Critical Assessment of Genome Interpretation (CAGI 2011) meeting, Berkeley, CA. *Divining P53 recovery mutants*. December 9, 2011.
 31. Meeting of the Society for Bioinformatics in the Nordic Countries, Helsinki, Finland. *Identifying protein functional sites using in silico mutagenesis*. May 5, 2011
 32. High Performance Computing Symposium, Lehigh University, Bethlehem, PA. *Identifying protein functional sites using in silico mutagenesis*. April 15, 2011
 33. Symposium on Microbiology, Rutgers, New Brunswick, NJ. *Identifying protein functional sites using in silico mutagenesis*. February 4, 2011
 34. Critical Assessment of Genome Interpretation (CAGI 2010) meeting, Berkeley, CA. *Evaluating SNPs using SNAP*. December 10, 2010.
 35. Humboldt Technische Universität München Institute for Advanced Study (TUM-IAS) General Assembly, Lake Starnberg, Germany. *Annotating protein function via mutation analysis: a SNAPpy approach*. April 12, 2010.
 36. European Conference on Computational Biology, Cagliari, Italy. *Comprehensive in silico mutagenesis highlights functionally important residues in proteins*. September 25, 2008
 37. NLM trainee meeting, Bethesda, MD. *Predicting functional effects of nsSNPs: a Neural Network approach*. July 11, 2005.
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Invited talks

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1. Princeton University Biological Sciences Society dinner series, Princeton, NJ. TBD. September 2019
 2. Microbiome Center Seminar Series, Penn State University, University Park, PA. **Forget their names: understanding the microbiome without focusing on individual microbes**. March 15, 2019.
 3. Dept. of Biology, Emory University, Atlanta, GA. **Forget their names: understanding the microbiome without focusing on individual microbes**. November 8, 2018.
 4. Computational Genomics seminar series, Icahn School of Medicine at Mount Sinai, New York, NY. **Cracking the disease code: analyzing genomic variation to identify pathogenesis pathways and predict disease**. October 22, 2018
 5. NAI Kickoff Meeting, Rutgers University, New Brunswick, NJ. **Evolution of Nanomachines**. May 21, 2018
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6. Green Brook Middle School, Teen Talk club, Greenbrook, NJ. **Adventures in science and life.** April 20, 2018
 7. School of Informatics, Computing, & Engineering Research Seminar, Indiana University, Bloomington, IN. **Hiding in plain sight: finding new knowledge at the intersection of big data and precision medicine.** April 6, 2018
 8. MIT Math & CSAIL Bioinformatics seminar, Cambridge, MA. **Deeper understanding of microbiomes as a benefit of forgetting microbial names.** April 4, 2018
 9. Nature International Journal of Science Research seminar, New York, NY. **Cracking the disease code: analyzing genomic variation to identify pathogenesis pathways and predict disease.** April 3, 2018
 10. Carnegie Institution Geophysical Laboratory seminar series, Washington, DC. **Timing evolution of biological redox via structural similarity network analysis.** March 25, 2018
 11. Center for Bioinformatics Research series, Indiana University, Bloomington, IN. **Functional basis of microbiome annotation: theory to practice.** December 7, 2017
 12. IBD Genetics Consortium Cycle IV meeting, Bethesda, MD. **Functional basis of microbiome annotation in disease: theory to practice.** November 30, 2017
 13. Genomic Instability & Cancer Genetics Research Program Meeting, Rutgers Cancer Institute, New Brunswick, NJ. **Hiding in plain sight: finding new knowledge at the intersection of big data and precision medicine.** November 9, 2017
 14. Epidemiology colloquium, Medical center of the university of Munich, LMU, Munich, Germany. *Functional basis of microbiome annotation: theory to practice.* July 11, 2017
 15. Peking Union Medical College Hospital and Chinese Academy of Medical Sciences joint seminar, Beijing, China. *Functional basis of microbiome analysis.* May 16, 2017
 16. State Key Laboratory of Microbial Metabolism seminar, Shanghai Jiao Tong University, Shanghai, China. *Functional basis of microbiome analysis.* May 15, 2017
 17. Henan Provincial People's Hospital Seminar, Zhengzhou, China. *Functional basis of microbiome analysis.* May 13, 2017
 18. Systems Biology seminar at Boston University, Boston, MA. **Functional basis of microorganism and microbiome annotation.** April 14, 2017.
 19. Department of Computer Science Seminar Series, NJIT, Newark, NJ. *Not all variants are created equal: what went wrong in the prediction of functional effects of exomic variation.* February 21, 2017.
 20. Department of Computational Biology Seminar Series, University of Lausanne, Switzerland. *Functional basis of microbiome annotation.* January 26, 2017.
 21. Computational Biology Group, Department of Computational Biology, University of Lausanne, Switzerland. *Not all variants are created equal: what went wrong in the prediction of functional effects of exomic variation.* January 23, 2017.
 22. Helmholtz Zentrum Seminar. Munich, Germany. *Functional Bases of Microorganism Classification.* May 23, 2016.
 23. European Bioinformatics Institute (EBI), European Molecular Biology Laboratory (EMBL), Hinxton, England. *Extracting molecular function patterns from microbial genomes and metagenomes.* April 10, 2016
 24. University College London, Department of Structural & Molecular Biology, London, England. *Extracting molecular function patterns from microbial genomes and metagenomes.* April 5, 2016
 25. Randall Seminar Series, Dept. of Biological Sciences. University of Idaho, Moscow, ID. *Functional Bases of Microorganism Classification.* March 11, 2016.
 26. How Proteins Became the Catalysts of Life Workshop. Rutgers, Piscataway, NJ. *Food and Dating Proteins: Assessing Origins of Biological Electron Transfer.* January 28th, 2016
 27. Frontiers in Bioinformatics and Systems Biology Colloquium. UCSD, Sand Diego, CA. *Mapping genomic variation to complex diseases.* January 14, 2016.
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28. New York Genome Center Five Points Lecture. New York Genome Center, New York, NY. *Mapping genomic variation to complex diseases*. December 2, 2015.
 29. Rutgers University Center for Proteomics Research (CIPR) workshop on Advances in Computational and Data Science for Investigative Discovery in Biology and Medicine. New Brunswick, NJ. *Does a computer dream of sheep genes, proteins, and functions?* October 22, 2015.
 30. Brooklyn Technical High School Invited speaker series, New York, NY. *Curiouser and curiouser: getting involved in bioinformatics research*. October 21, 2015.
 31. Joint research retreat of the Rutgers School of Environmental and Biological Sciences (SEBS, New Brunswick) and the Rutgers Center for Computational and Integrative Biology (CCIB, Camden). Camden, NJ. *"Function" in biology: a computational analysis*. October 9, 2015.
 32. Rutgers Child Health Institute (CHI) Science Seminar Series meeting. New Brunswick, NJ. *Interpreting genomic data to inform pathogenesis pathways*. September 28, 2015.
 33. Microbiome Working Group meeting, Columbia University Medical Center (CUMC), New York, NY. *Tell me what you do and I'll tell you who you are: functional basis of microorganism classification*. September 14, 2015
 34. Dept. of Biomedical Informatics, Columbia University, New York, NY. *Interpreting genomic data to inform pathogenesis pathways*. April 21, 2015.
 35. Dept. of Biomedical and Health Informatics, The Children's Hospital of Pennsylvania, Philadelphia, PA. *Interpreting genomic data to inform pathogenesis pathways*. April 8, 2015.
 36. Dept. of Biological Sciences, Seton Hall University, South Orange, NJ. *Functional Bases of Microorganism Classification*. March 26, 2015
 37. Dept. of Biochemistry and Molecular Biology, University of Kansas Medical Center, Kansas City, KS. *The last straw did not break the camel's back: searching for causative variants of polygenic disease disregards individual predisposing genomic differences*. October 31, 2014.
 38. Basel Computational Biology Center (BC2), Basel University Biozentrum / Swiss Institute for Bioinformatics, Basel, Switzerland. *The last straw did not break the camel's back: searching for causative variants of polygenic disease disregards individual predisposing genomic*. October 6, 2014.
 39. Fermentation Club Seminar, Rutgers, New Brunswick, NJ. *Functional Bases of Microorganism Classification*. September 12, 2014
 40. Interactive Group on Human Genetics, UMDNJ, Piscataway, NJ. *Exome analysis for disease gene prioritization*. March 11, 2014.
 41. Computing Seminar Series, Oklahoma Medical Research Foundation, Oklahoma City, OK. *Functional basis of microorganism classification*. October 3, 2013
 42. Research Seminar Series, Oklahoma Medical Research Foundation, Oklahoma City, OK. *Noise in the (human) machine: functionally neutral variants, individuality, and disease*. October 3, 2013
 43. Dept. of Biomedical Informatics retreat, *Invited presentation and panel discussion*, Columbia University, NY. **Adventures in Bioinformatics**. September 10, 2013
 44. Dept. of Genetics Adjunct Professor Seminar, Rutgers, NJ. *Noise in biology or how neutral variants define individuality*. February 25, 2013
 45. Ecology and Evolution Membership Seminar, Rutgers, NJ. *Computing prokaryotic diversity using functional similarity*. October 25, 2012
 46. Environmental Microbial Genomics Group, Ecole Centrale de Lyon, Université de Lyon, France. *Computing prokaryotic diversity using functional similarity*. October 1, 2012
 47. Buck Institute for Research on Aging, Novato, CA. *Noise in Biology*. July 6, 2012.
 48. Institute of Clinical Molecular Biology, Christian-Albrechts-University, Kiel, Germany. *CAGI 2011: Critical Assessment of Genome Interpretation: SNAP results*. March 9, 2012.
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49. Dept. of Biochemistry and Molecular Biology, The George S Wise Faculty of Life Sciences, Tel Aviv University, Tel Aviv, Israel. *Identifying protein functional sites using in silico mutagenesis*. July 21, 2011
 50. Center for Biotechnology and Medicine, Rutgers, New Brunswick, NJ. *Defining “functional effects” in mutation databases*. June 9, 2011.
 51. Joint European Molecular Biology Laboratory (EMBL) and Technische Universitat Munchen (TUM) retreat, Schliersee, Germany. *Identifying protein functional sites using in silico mutagenesis*. April 2, 2011
 52. Buck Institute for Research on Aging, Novato, CA. *Identifying protein functional sites using in silico mutagenesis*. March 18, 2011
 53. Environmental and Occupational Health Sciences Institute, Rutgers, New Brunswick, NJ. *Identifying protein functional sites using in silico mutagenesis*. February 17, 2011
 54. Center for Computational and Integrative Biology, Rutgers, Camden, NJ. *Annotating protein function via mutation analysis: a SNAPpy approach*. November 22, 2010
 55. Genentech, San Francisco, CA. *Predicting functional effects of nsSNPs using SNAP: Screening for Non-Acceptable Polymorphisms*. February 17, 2010
 56. Fermentation Club seminar, Rutgers, NJ. *Annotating protein function via mutation analysis: a SNAPpy approach*. January 29, 2010.
 57. Monsanto, St. Louis, MO. *Predicting functional effects of nsSNPs using SNAP: Screening for Non-Acceptable Polymorphisms*. April 21, 2009
 58. European Molecular Biology Laboratories (EMBL), Heidelberg, Germany. *Protein function in terms of mutation*. March 11, 2009.
 59. Basel University Biozentrum / Swiss Institute for Bioinformatics, Basel, Switzerland. *Protein function in terms of mutation*. March 9, 2009.
 60. Dept. of Structural & Molecular Biology, United College of London, London, UK. *Protein function in terms of mutation*. December 19, 2008
 61. GeneCards meeting, Crown Human Genome Center, Weizmann Institute, Rehovot, Israel. *Comprehensive in silico mutagenesis highlights functionally important residues in proteins*. September 10, 2008.
 62. Dissertation Defense, Columbia University, NY. *SNAP: Screening for Non-Acceptable Polymorphisms*. December 5, 2006.
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FUNDING

ACTIVE

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|---|-------------------|
| <p>CAN8- NASA Astrobiology Institute (Falkowski, PI) National Aeronautics and Space Administration (NASA) <i>ENIGMA: Evolution of Nanomachines In Geospheres and Microbial Ancestors</i> Building computational tools to understand the (early life on Earth) evolution of protein structures necessary for biological electron transfer.</p> | 04/2018 – 04/2023 |
| <p>1 R01 MH115958 01 (Heiman, PI) National Institutes of Mental Health (NIMH) <i>1/7 Collaborative Genomic Studies of Tourette Disorder</i> Optimizing computational pipeline (AVA,Dx) for identifying Tourette genes from genome variation data.</p> | 04/2018 – 04/2023 |
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| NSF CAREER Award: 1553289 (Bromberg, PI) Advances in Biological Informatics (National Science Foundation) <i>Molecular functional diversity of microbes and microbiomes</i> Developing tools for functional analysis and classification of bacteria, with applications to microbiome (community) analysis. | 04/2016 – 04/2021 |
| 1 U01 GM115486 01 (Bromberg, PI) National Institutes of General Medical Sciences (NIGMS) <i>AVA,Dx: Analysis of Variation for Association with Disease</i> Building a computational pipeline (AVA,Dx) for identifying disease genes and annotating disease predisposition from genome variation data. | 09/2015 – 05/2020 |
| COMPLETED | |
| Alfred P. Sloan Foundation workshop grant (Hazen, PI) <i>The 4-D Workshop: Deep-Time Data-Driven Discovery and the Evolution of earth</i> | 11/2017 – 06/2018 |
| Hans Fischer Fellowship (Bromberg, PI) Institute of Advanced Studies at the Technische Universitat Munchen <i>FuSiON: Functional Basis of Microorganism Classification.</i> | 07/2014 – 10/2018 |
| 5 U24 MH068457 12 (Tischfield, PI) National Institutes of Mental Health (NIMH) <i>Center for Genomic Studies on Mental Disorders</i> | 06/2013 – 05/2018 |
| Informatics Research Starter Grant (Bromberg, PI) PhRMA Foundation <i>Analysis of Variation for Association with Disease.</i> | 01/2015 – 12/2015 |
| GBMF2807 (Falkowski, PI) Gordon and Betty Moore Foundation <i>Evolutionary map of life's electron transfer reactions.</i> | 04/2011 – 04/2014 |
| R43-LM010156-01 (Bromberg, PI) National Library of Medicine (NLM), SBIR Phase 1 <i>Improved Manuscript Search Through PubSeq</i> | 06/2009 – 03/2011 |

TEACHING

COURSES (primary audience and % responsibility)

Rutgers University, New Brunswick, NJ

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|--|---------------------|
| 11:126:485/16:765:585 <i>Bioinformatics</i> (Grad/Undergrad, 100%) | 2011-Present |
| A 13-week lecture/computational lab series developed by Dr. Bromberg. Curriculum requirement for the Biotechnology major, and a well-attended elective for other majors. | |
| 16:682:550 Special Topics in Microbial Biology: Bioinformatics Journal Club (Grad, 50%) | 2015-2017 |
| 11:115:201 <i>Contemporary issues in Biochemistry</i> (Undergrad, 5%) | 2014-Present |
| Douglas Project SUPER <i>Introduction to Scientific Research</i> (Undergrad, 8%) | 2014-Present |

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| 16:215:601 Seminar in Ecology (Grad, 8%) | 2014-2016 |
| 11:115:404/504 General Biochemistry (Undergrad, 5%) | 2013-Present |
| 11:115:301 Introduction to Biochemistry (Undergrad, 10%) | 2012-2013 |
| 16:682:521 Seminars in Microbiology (Grad, 8%) | 2010-Present |
| 11:115:428/16:115:616 Homology Modeling of Proteins (Grad/Undergrad, 10%) | 2011-2012 |

Technical University of Munich, Munich, Germany

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| Protein Prediction for Computer Scientists (Undergrad, Guest Lectures) | 2015-Present |
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University of Bologna, Italy

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|---|-----------|
| Mapping genomes to disease (Intensive graduate course, 100%) | 2015-2018 |
| A 20-hour lecture and practical applications series newly developed by Dr. Bromberg for students in University of Bologna International Masters Bioinformatics program. | |

STUDENTS AND POST-DOCS (Rutgers, unless otherwise specified; IAS=Institute for Advanced Study, TUM=Technische Universität München, SDU=U of Southern Denmark)

Post-Docs (5 current of 9 total)

| | |
|---------------------------|-------------------|
| 1. Dr. Ariel Aptekmann | 04/2019 – present |
| 2. Dr. Adrienne Hoarfrost | 04/2019 – present |
| 3. Dr. Kenneth McGuinness | 09/2018 – present |
| 4. Dr. Maximilian Miller | 03/2018 – present |
| 5. Dr. Chengsheng Zhu | 04/2017 – present |
| 6. Dr. Anton Molyboha | 02/2017 – 02/2018 |
| 7. Dr. Wenfeng Kang | 05/2014 – 09/2014 |
| 8. Dr. Stefan Senn | 03/2012 – 03/2014 |
| 9. Dr. Arye Harel | 09/2010 – 04/2014 |

Ph.D. Students (2 current of 6 total)

| | | |
|---------------------------|---|-------------------|
| 1. Zishou Zeng | Quantitative Biomedicine | 09/2017 – present |
| 2. Carl Maximilian Miller | TUM Bioinformatics and Computational Biology | 11/2015 – 03/2017 |
| 3. Yanran Wang | Microbiology and Molecular Genetics | 04/2015 – present |
| 4. Yannick Mahlich | TUM Bioinformatics and Computational Biology, IAS student | 11/2014 – 07/2019 |
| 5. Tatyana Goldberg | TUM Bioinformatics and Computational Biology, co-advisor | 01/2012 – 05/2016 |
| 6. Chengsheng Zhu | Microbiology and Molecular Genetics | 04/2011 – 04/2017 |

Graduate Students, non-PhD thesis advisement (8 total)

| | | |
|----------------------|--|-------------------|
| 1. Jan Siess | Quantitative Biomedicine, Rotation | 09/2018 – 12/2018 |
| 2. Arnav Pondicherry | Rutgers-RWJMS medical school, Independent Research | 10/2017 – 01/2018 |
| 3. Alexandra Pushkar | Quantitative Biomedicine, Rotation | 09/2016 – 07/2017 |

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|----|----------------------|---|--------------------------|
| 4. | Nidia Obscura Acosta | <i>University of Helsinki, Mathematics and Computer Science. Masters thesis</i> | 05/2016 – 05/2017 |
| 5. | Lisheng Zhou | <i>Microbiology and Molecular Genetics, Rotation</i> | 01/2012 – 03/2012 |
| 6. | Ben Jelen | <i>Environmental Sciences, Project supervisor</i> | 08/2011 – 12/2013 |
| 7. | Maximilian Hecht | <i>TUM Bioinformatics and Computational Biology, Project supervisor</i> | 01/2011 – 05/2015 |
| 8. | Christian Schaefer | <i>TUM Bioinformatics and Computational Biology, Project supervisor</i> | 01/2010 – 11/2012 |

Thesis Committees (advisor, 8 total)

| | | | |
|----|-------------------|---|----------------|
| 1. | Yuanchao Zhang | <i>Microbiology and Molecular Genetics (Dr. Deanne Taylor)</i> | TBA |
| 2. | Nicole Koribanics | <i>Environmental Microbiology (Dr. Lee Kerkhof)</i> | 06/2017 |
| 3. | Christian Wiwie | <i>SDU Dept. of Mathematics and Computer Science (Dr. Jan Baumbach)</i> | 01/2017 |
| 4. | Nora Lopez | <i>Environmental Microbiology (Dr. Lee Kerkhof)</i> | 12/2016 |
| 5. | Ashley DeNegre | <i>Ecology and Evolution (Dr. Nina Fefferman)</i> | 11/2015 |
| 6. | Guy Yachdav | <i>TUM Bioinformatics and Computational Biology (Dr. Burkhard Rost)</i> | 07/2015 |
| 7. | Omar Haq | <i>Molecular Biophysics and Computational Biology (Dr. Ronald M Levy)</i> | 05/2012 |
| 8. | Mauro Lapelosa | <i>Molecular Biophysics and Computational Biology (Dr. Ronald M Levy)</i> | 10/2011 |

Undergraduate Students (IR = Independent Research; 18 total)

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|----|--|-------------------------------------|
| 1. | Shon Shmushkevich (<i>Molecular Biology, Hunter College</i>) <i>Microbial functionality in marine sediments</i> | IR: Sum'19 |
| 2. | Anusha Siddaramanna (<i>Computer Science</i>) <i>Optimizing scoring of variation-disrupted genes</i> | IR: Sum'19 |
| 3. | Alexis Faulborn (<i>Plant Biotechnology and Biochemistry</i>) <i>Predicting position-driven non-synonymous variant functional effects</i> | IR: S'19, Sum'19 |
| 4. | Revanth Korrapolu (<i>Computer Science</i>) <i>Optimizing large-scale sequence alignments</i> | IR: F'18, S'19 |
| 5. | Chahna Patel (<i>Biomedical Engineering</i>) <i>Differentiating eukaryotic and prokaryotic origins of sequencing reads</i> | IR: S'18, Sum'18, F'18, S'19 |
| 6. | Nicholas Lusskin (<i>Biotechnology</i>) <i>Differentiating microbiome environments by read functional analysis</i> | IR: F'17, S'18, F'18, S'19 |
| 7. | Daniel Vitale (<i>Biology</i>) <i>Differentiating toggles and rheostats in variant effect predictions</i> | IR: S'17 |

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| 8. Riva Patel (<i>Biochemistry</i>) <i>Annotating oxygen requirements of oxidoreductases</i> | IR: F'15, S'16 |
| 9. Srinayani Marpaka (<i>Genetics, Computer Science</i>) <i>Extracting metagenome function from read data</i> | IR: S'15, F'15 |
| 10. Akash Mitra (<i>Genetics, Biotechnology</i>) <i>Analysis of functional effect of synonymous variants</i> | IR: S'15 |
| 11. Linda Cook (<i>Computer Science</i>) <i>Evolution of metal-binding folds for electron transfer</i> | Aresty Summer Science program, Sum'14, IR: S'15 |
| 12. Manfred Roos (<i>Computational Biology and Bioinformatics, TUM</i>) <i>Prediction of active sites from protein sequence</i> | Bachelor Thesis, 2012-2014 |
| 13. Pavel Vaysberg (<i>Biotechnology</i>) <i>Extracting metagenome function from read data.</i> | IR: S'14, F'14 |
| 14. Remy Koch (<i>Biotechnology</i>) <i>Automated annotation of protein catalytic sites</i> | IR: S'14 |
| 15. Catherine Plotts (<i>Nutritional Sciences</i>) <i>MeSH term-based identification of disease-related publications</i> | IR: F'12, S'13 |
| 16. Sean Bryan (<i>Biotechnology</i>) <i>Automated annotation of protein sequence sites of importance.</i> | IR: Sum'12, F'12, S'13 |
| 17. Steven Yen (<i>Biotechnology</i>) <i>Disease-gene identification using NLP</i> | IR: Sum'12 |
| 18. Chris Rusnak (<i>Mathematics, Biology</i>) <i>Sequence analysis for active site identification in proteins.</i> | DIMACS REU Sum'11, IR: from F'11 to S'13 |

High School Students (4 total)

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|--------------------|---------------------------------------|------------------------|
| 1. Jeffrey Yang | <i>Westfield High School</i> | 05/2018-01/2019 |
| 2. Alexander Chong | <i>Brooklyn Technical High School</i> | 06/2013-09/2013 |
| 3. Eva Justo | <i>Brooklyn Technical High School</i> | 06/2013-09/2013 |
| 4. Brian Okonski | <i>Brooklyn Technical High School</i> | 06/2013-09/2013 |

SERVICE

ABBREVIATIONS: *ECCB* = European Conference on Computational Biology, biannually joint with ISMB; *GRC* = Gordon Research Conference, *IEEE* = Institute of Electrical and Electronics Engineers, *ISCB* = International Society for Computational Biology; *ISMB* = Intelligent Systems in Molecular Biology, flagship conference of ISCB; *PSB* = Pacific Symposium on Biocomputing; *VarI-COSI/-SIG* = Variation Interpretation Community of Special Interest / Satellite Interest Group Meeting

Professional Activities

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| Chair, GRC Human Single Nucleotide Polymorphisms & Disease | 2020 |
| Vice-Chair, GRC Human Single Nucleotide Polymorphisms & Disease | 2018 |

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| Organizer , Computational and Translational Methods for Cancer Genomics Workshop | 2018 |
| Chair , Proceedings, ISCB-Latin America conference | 2018 |
| Chair , 4-D Workshop for Deep-Time Data Driven Discovery | 2018 |
| Member , Informatics Advisory Committee for the PhRMA Foundation | 2018-Present |
| Member , ISMB Awards and Keynote Selection Committee | 2017-Present |
| Program Chair , IEEE International Conference on Bioinformatics and Biomedicine (BIBM) | 2017 |
| Chair , Computational Approaches to Understanding the Evolution of Molecular Function, PSB | 2017 |
| Chair , Proceedings track, joint ISMB/ECCB conference | 2017-Present |
| Chair , Computational Approaches to Study Microbes and Microbiomes workshop, PSB | 2016 |
| Director, Board of Directors , ISCB | 2016-Present |
| Chair , Proteins Theme, ISCB-Latin America conference | 2016 |
| Organizer , GRC Power Hour (women in science) | 2016 |
| Chair , Disease Theme, joint ISMB/ECCB conference | 2015-2016 |
| Guest Associate Editor , PLoS Computational Biology | 2013-Present |
| Organizer , Junior PI Meeting, ISMB/ECCB | 2013-2015 |
| Editor , BMC Genomics, Proceedings of the VarI-SIG special issue | 2011-Present |
| Chair (and VarI-COSI representative since 2014), VarI-SIG | 2011-Present |
| Organizer , Grant Writing Workshop and Tutorial, ISMB/ECCB | 2011-2012 |
| Chair , ISMB/ECCB Poster and Short Talks Sessions | 2010-2015 |

Grant Proposal Review

Panels: PhRMA foundation, NIH BDMA (National Institutes of Health Biodata Management and Analysis), NIH *ad hoc* panels, NSF BIO and CISE (National Science Foundation Biological Sciences AND Computer and Information Science and Engineering) directorate panels, DOE *ad hoc* panels

External: European Research Council (ERC), Swiss National Science Foundation (SNSF), Polish National Academy of Sciences (NCN), French National Institute of Health and Medical Research (INSERM), KU Leuven (University of Leuven, Belgium) Research Council

Selected Reviewer Appointments: Journals, Awards, and Conference Proceedings

Nature Journals: Communications, Scientific Reports

PLoS Journals: Computational Biology, One, Genetics, Proteins, Protein Science

BMC Journals: Bioinformatics, Genomics

Cell, Proceedings of the National Academy of Sciences (PNAS), Bioinformatics, Biomedical Informatics, DATABASE: Journal of Biological Databases and Curation, Journal of Molecular Biology, Human Molecular Genetics, Human Mutation, IEEE ACM Transactions on Computational Biology & Bioinformatics

American Medical Informatics Association (AMIA) Translational Bioinformatics Proceedings, BioOntologies Special Interest Group Proceedings, ISMB Killer App Award

Membership and affiliations

| | |
|---|--------------|
| Chair, Dept. of Biochemistry and Microbiology and Dept. of Marine and Coastal Sciences joint faculty search committee | 2017 |
| Member, ISCB Representative, FASEB Science Research Conferences Advisory Committee | 2016-2017 |
| Founding Member, IQB (Institute for Quantitative Biomedicine) Graduate program, Rutgers | 2015-Present |
| Member, Center for Digestive Health in the New Jersey Institute for Food, Nutrition, and Health (IFNH) faculty search committee | 2015 |
| Member, Eveleigh Fenton endowed chair Biochemistry and Microbiology faculty search committee | 2015 |
| Member, Rutgers Discovery Informatics Institute Internal Advisory Board | 2014-Present |
| Member, ASM: American Society for Microbiology | 2014-2017 |
| Member, Theobald Smith Society | 2014-2017 |
| Member, Human Genetics Institute of NJ | 2012-Present |
| Member, Ecology and Evolution Graduate Program, Rutgers | 2012-Present |
| Member, University Physical Facilities and Space Committee | 2012-2013 |
| Associate Clinical Member, the Cancer Institute of New Jersey (CINJ) | 2011-Present |
| Member, Microbiology and Molecular Genetics Program, Rutgers | 2011-Present |
| Research Experience for Undergraduates (REU) Mentor | 2011-2013 |
| Member (and 2014 Chair), Admissions and Academic Standards Committee of the Microbial Biology Graduate Program, Rutgers | 2011-2014 |
| Member, Microbial Biology Program, Rutgers | 2010-Present |
| Member, Interview Committee, SEBS General Honors Program | 2010-Present |
| Member, American Medical Informatics Association (AMIA) | 2003-2007 |
| Member, ISCB | 2003-Present |
| Member, Phi Beta Kappa Society | 2001-Present |
