

## Curriculum Vitae

Iddo Friedberg, M.Sc. Ph.D.

### **Present Address:**

Iddo Friedberg  
2118 Vet Med  
Iowa State University  
Ames, IA 50011 USA  
Tel: +1 515 294 5959  
email: idoerg@iastate.edu

URL: <http://iddo-friedberg.net>

Google scholar: <http://is.gd/exikel>

### **Research Interests**

Evolution of protein function  
Evolution of operons and gene neighborhoods  
Protein structure-function relationships  
Metagenomics, host-microbiome interactions  
Computational protein function prediction  
Dynamics and construction of biological databases and biocuration

### **Academic Employment**

**2015-** Associate Professor, Veterinary Microbiology and Preventive Medicine, Iowa State University.

**2009-2015** Assistant Professor, Departments of Microbiology and Computer Science & Software Engineering (affiliate) Miami University Oxford, Ohio USA. Research in my lab deals with the evolution of bacterial gene clusters, computational metagenomics, and prediction of protein function. Teaching: I developed and taught an upper-division bioinformatics course, and an undergraduate minor bioinformatics program; undergraduate seminar; graduate seminar; Lab: four graduate students, one scientific programmer, five undergraduate students (as of 2015).

**2007- 2009** Research Associate, bioinformatics core, marine microbial ecology, California Institute for Telecommunications and Information Technology, University of California, San Diego. Research in metagenomic data. Develop new methods for functional classification and analysis of metagenomes. Locate and analyze functional clusters of genes on metagenomic assemblies. I also lead a four person team implementing the acquisition of metagenomic data and metadata into a semantic

database.

**2002-2007** Postdoctoral associate at Adam Godzik's lab. Program in Bioinformatics and Systems Biology, Sanford-Burnham Institute, La Jolla, CA, USA. Research in structural bioinformatics, including protein classification, function prediction and function based target selection for structural genomics.

**1997-2002** Teaching assistant. Faculty of Medicine, The Hebrew University of Jerusalem, Israel. Taught a lab course in introductory bioinformatics for advanced undergraduate and graduate students.

### **Education**

**1997-2002** Ph.D student at Dr. Hanah Margalit's lab, Dept. of Molecular Genetics and Biotechnology, The Hebrew University - Hadassah Medical School, Jerusalem. I investigated proteins displaying a low pairwise identity, but a high overall structural similarity. Finding the structural parameters for such a phenomenon, and investigating its evolutionary implications in various protein families were the two chief goals of my research. Thesis title: "Sequence-Structure Relationship in Proteins: a Computational Analysis of Proteins that Differ in Sequence but Share the Same Fold".

**1995-1996** M.Sc. studies in Structural & Molecular Biochemistry at the Biological Chemistry dept., Institute of Life-Sciences, The Hebrew University, Jerusalem, Israel. Advisors: Prof. Joseph Orly & Dr. Aryeh Weiss. Graduated January 1997, *Magna cum Laude*. Thesis subject: "Immunofluorescent Quantitative Protein Analysis of Cultured Cells: Use of a Digital Microscopy Workstation".

**1991-1994** B.Sc. in Biology, The Hebrew University, Jerusalem, Israel. Graduated 1994, *Magna cum Laude*.

### **Memberships**

International Society of Computational Biology  
International Society of Biocuration

### **Honors**

Director, the International Society for Computational Biology.  
Senior member, the International Society for Computational Biology

### **Publications**

Highly cited publications marked with a \*

Impact statistics (Google Scholar): *h*-index: 20; Citations: 3726.

Peer-reviewed, published or accepted:

1. Morton JT, Freed SD, Lee SW, and Friedberg I **A large scale prediction of bacteriocin gene blocks suggests a wide functional spectrum for bacteriocins** (2015) *BMC Bioinformatics* **16**:381
2. Pope WH, Bowman CA, Russell DA *et al* **Whole genome comparison of a large collection of mycobacteriophages reveals a continuum of phage genetic diversity** (2015) *eLife* **4**:e06416
3. Ream DC, Bankapur AR, Friedberg I **An Event-Driven Approach for Studying Gene Block Evolution in Bacteria** (2015) *Bioinformatics* 10.1093/bioinformatics/btv128
4. Jiang Y, Clark W, Friedberg I and Radivojac P **The impact of incomplete knowledge on the evaluation of protein function prediction: a structured-output learning perspective** (2014) *Bioinformatics* **1**:30 i609-616
5. Ream DC, Murakami ST, Schmidt, EE, Huang GH, Liang C , Friedberg I and Cheng XW **Comparative analysis of error-prone replication mononucleotide repeats across baculovirus genomes** (2013) *Virus Research* **2**(26) 217-225
6. Anton BP, Chang Y..., Friedberg I, ..., Roberts RJ, Steffen M and Kasif S. **The COMBREX Project: Design, Methodology, and Initial Results** (2013) *PLoS Biology* Aug;11(8):e1001638
7. Oberlin AT, Jurkovic DA, Balish MF and Friedberg I **Biological Database of Images and Genomes: tools for community annotations linking image and genomic information** (2013) *Database* <http://dx.doi.org/10.1093/database/bat016>
8. Schnoes AM, Ream DC, Thorman AW, Babbitt PC, Friedberg I **Biases in the Experimental Annotations of Protein Function and their Effect on Our Understanding of Protein Function Space** (2013) *PLoS Computational Biology* **9**(5)e1003063
9. \*Radivojac P, Clark WT, Oron TR, Schnoes AM, Wittkop T, Sokolov A, Graim K, Funk C, Verspoor K, Ben-Hur A, Pandey G, Yunes JM, Talwalkar AS, Repo S, Souza ML, Piovesan D, Casadio R, Wang Z, Cheng J, Fang H, Gough J, Koskinen P, Törönen P, Nokso-Koivisto J, Holm L, Cozzetto D, Buchan DW, Bryson K, Jones DT, Limaye B, Inamdar H, Datta A, Manjari SK, Joshi R, Chitale M, Kihara D, Lisewski AM, Erdin S, Venner E, Lichtarge O, Rentzsch R, Yang H, Romero AE, Bhat P, Paccanaro A, Hamp T, Kaßner R, Seemayer S, Vicedo E, Schaefer C, Achten D, Auer F, Boehm A, Braun T, Hecht M, Heron M, Hönigschmid P, Hopf TA, Kaufmann S, Kiening M, Krompass D, Landerer C, Mahlich Y, Roos M, Björne J, Salakoski T, Wong A, Shatkay H, Gatzmann F, Sommer I, Wass MN, Sternberg MJ, Skunca N, Supek F, Bošnjak M, Panov P, Džeroski S, Smuc T, Kourmpetis YA, van Dijk AD, Braak CJ, Zhou Y, Gong Q, Dong X, Tian W, Falda M, Fontana P, Lavezzo E, Di

- Camillo B, Toppo S, Lan L, Djuric N, Guo Y, Vucetic S, Bairoch A, Linial M, Babbitt PC, Brenner SE, Orengo C, Rost B, Mooney SD and Friedberg I **A Large-Scale Assessment of Protein Function Annotations** (2013) *Nature Methods* 10(3):221-7 (64 citations in Google Scholar)
10. Donovan SM, Wang M, Li M, Friedberg I, Schwartz SL, Chapkin RS. **Host-microbe interactions in the neonatal intestine: role of human milk oligosaccharides.** (2012) *Advances in Nutrition* 3(3):450S-455S
  - 11.\* Schwartz S, Friedberg I, Ivanov IV, Davidson LA, Goldsby JS, Dahl DB, Herman D, Wang M, Donovan SM, Chapkin RS. **A metagenomic study of diet-dependent interaction between gut microbiota and host in infants reveals differences in immune response.** (2012) *Genome Biology* Apr 30;13(4):r32 (35 citations, rated “Highly Accessed” in Genome Biology).
  12. Bielewicz S, Bell E, Kong W, Friedberg I, Priscu JC, Morgan-Kiss RM **Protist diversity in a permanently ice-covered Antarctic lake during the polar night transition** (2011) *ISME Journal* 3/2011
  13. Kelly RJ, Vincent DE and Friedberg I **IPRStats: visualization of the functional potential of an InterProScan run** (2010) *BMC Bioinformatics* 1(Suppl2):S13
  - 14.\* Wooley JC, Godzik A and Friedberg I **A Primer on Metagenomics** *PLoS Computational Biology* (2010) (Review article; 232 citations in Google Scholar).
  15. Cock PJ, Antao T, Chang JT, Chapman BA, Cox CJ, Dalke A, Friedberg I, Hamelryck T, Kauff F, Wilczynski B, de Hoon MJ. **Biopython: freely available Python tools for computational molecular biology and bioinformatics** *Bioinformatics* (2009) Mar 20
  16. Godzik A., Jambon M. and Friedberg I. **The Assessment of Protein Function Predictions** *Cellular and Molecular Life Sciences* (2007) (19-20)2505-11
  17. Friedberg Ilan, Nika K., Tautz L., Saito K., Cerignoli F., Friedberg Iddo, Godzik A. and Mustelin T **Identification and characterization of Dusp27, a novel dual-specific protein phosphatase** (2007) *FEBS Letters* May 29;581(13):2527-33
  18. Friedberg I and Godzik A. **Functional Differentiation of Proteins: Implications for Structural Genomics** (2007) *Structure* 15(4):405-415
  19. Friedberg I, Harder T., Kolodny R., Sitbon E., Li Z. and Godzik A. **Using an alignment of fragment strings for comparing protein structures** *Bioinformatics* (2007) 23: e219-e224
  - 20.\* Friedberg I. **Automated Function Prediction: the Genomic Challenge** *Briefings in Bioinformatics* (2006) Sep;7(3):225-42 (Invited Review, 246 citations in Google Scholar)
  21. Friedberg I, Harder T. and Godzik A. **JAJA: a Protein Function Annotation Meta-**

- Server** *Nucleic Acids Research* (2006) Jul 1;34:W379-80
22. Friedberg I. and Godzik, A. **Connecting the Protein Structure Universe by Using Sparse Recurring Fragments** *Structure (Camb.)* (2005) Aug;13(8):1213-24
23. Friedberg I. and Godzik A. **Fragnostic: walking through protein structure space** *Nucleic Acids Research* (2005) 33:W249-W251
24. Friedberg I., Jaroszewski L., Ye Y. and Godzik A. **The interplay of fold recognition and experimental structure determination in structural genomics** *Current Opinion in Structural Biology* (2004) 14:307-312 1
25. Alonso A., Sasin J., Bottini N., Friedberg I., Friedberg I., Osterman A., Godzik A., Hunter T., Dixon J., and Mustelin T. **Protein Tyrosine Phosphatases in the Human Genome** *Cell* (2004) Jun 11;117(6):699-711
26. Bourne P.E., Allerston C.K.J., Krebs W., Li W., Shindyalov I.N., Godzik, A., Friedberg I., Liu T., Wild D., Hwang S., Gharamani Z., Chen L., and Westbrook J. **The Status of Structural Genomics Defined through the Analysis of Current Targets and Structures** *Pac. Sym. Biocomp.* (2004) 375-386
27. Friedberg I. and Margalit H: **PeCoP: automatic determination of persistently conserved positions in protein families** (2002) *Bioinformatics* 18 (9):1276-1277
28. Friedberg I. and Margalit H.: **Persistently Conserved Positions in Structurally-Similar, Sequence Dissimilar Proteins: Roles in Preserving Protein Fold and Function** (2002) *Protein Science* 11(2):350-360
29. Friedberg I., Kaplan T, and Margalit H: **Evaluation of PSI-BLAST alignment Accuracy in Comparison to Structural Alignments.** (2000) *Protein Science*, Nov;9(11):2278-84
30. Friedberg I., Kaplan T. and Margalit H.: **Glimmers in the Midnight Zone: Characterization of Aligned Identical Residues in Sequence-Dissimilar Proteins Sharing a Common Fold** (2000) *Proc. Int. Sys. Comp. Biol.* 2000: 162-170 (Now *Bioinformatics*)
31. Cherradi N, Rossier MF, Vallotton MB, Timberg R, Friedberg I., Orly J, Wang XJ, Stocco DM, Capponi AM: **Submitochondrial distribution of three key steroidogenic proteins (steroidogenic acute regulatory protein and cytochrome p450scc and 3beta-hydroxysteroid dehydrogenase isomerase enzymes) upon stimulation by intracellular calcium in adrenal glomerulosa cells.** *J. Biol. Chem.* 1997 Mar 21;272(12):7899-7907

**Editorials and opinion pieces in scientific journals:**

1. Bourne PE, Friedberg I (2006) **Ten Simple Rules for Selecting a Postdoctoral Position.** *PLoS Comp Biol* 2(11): e1
2. Friedberg I., Jambon M. and Godzik A. **New Avenues in Protein Function Prediction** *Protein Science* (2006) Jun;15(6):1527-9
3. Rodrigues A, Grant B, Godzik A and Friedberg I. **The 2006 Automated Function Prediction Meeting** *BMC Bioinformatics* 8 (2007) (S8)
4. Friedberg I **Book review: "Data Mining Techniques for the Life Sciences"** *The Quarterly Review of Biology* (2011) 86:336-337
5. Wass MN, Mooney SD, Linial M, Radivojac P and Friedberg I **The automated function prediction SIG looks back at 2013 and prepares for 2014** (2014) *Bioinformatics* 10.1093/bioinformatics/btu117
6. Friedberg I. Wass M, Mooney SD, Radivojac P **Ten Simple Rules for a Community Computational Challenge** (2015) *PLoS Comp Biol* 11(4):e1004150

### **Book chapters**

1. Friedberg I **IPRStats, overview** in *Encyclopedia of Metagenomics* Ed. Karen Nelson, Publisher: Springer (2012)
2. Radivojac P and Friedberg I **Community based Evaluation of Computational Function Prediction** in *The Gene Ontology Handbook* Eds: Dessimoz C and Skunca N Publisher: Springer (2016) (accepted)

### **Other Publications**

1. Field D, Sansone S, Delong EF, Sterk P, Friedberg I, Gaudet P, Lewis S, Kottmann R, Hirschman L, Garrity G, Cochrane G, Wooley J, Meyer F, Hunter S, White O, Bramlett B, Gregurick S, Lapp H, Orchard S, Rocca-Serra P, Ruttenger A, Shah N, Taylor C, Thessen A. **Meeting Report: BioSharing at ISMB 2010.** (2010) *Stand Genomic Sci.* 3(3):232-4
2. Field D, Sansone S, Delong EF, Sterk P, Friedberg I, Kottmann R, Hirschman L, Garrity G, Cochrane G, Wooley J, Meyer F, Hunter S, White O. **Meeting Report: Metagenomics, Metadata and MetaAnalysis (M3) at ISMB 2010.** (2010) *Stand. Genomic Sci.* 3(3):232-4
3. Field D, Friedberg I, Sterk P, Kottmann R, Glöckner FO, Hirschman L, Garrity GM, Cochrane G, Wooley J, Gilbert J **Meeting Report: "Metagenomics, Metadata and Meta-analysis" (M3) Special Interest Group at ISMB 2009.** (2009) *Stand. Genomic Sci.* 1(3):278-82

### **Select Conference Publications and Invited Talks (>80 presentations since 1997)**

1. **Glimmers in the Midnight Zone** (Lecture) 8<sup>th</sup> Intelligent Systems in Computational

- Biology conference, San Diego, CA USA (2000)
2. **Generation and Use of Substitution Matrices in Biopython.** Bioinformatics Open Source Conference (BOSC) 2001, Copenhagen, poster & lecture: **Friedberg I & Chapman B.**
  3. **Use of Fragments for Mapping Protein Structure Space (Lecture)**  
University of California, San Diego, Weizmann Institute of Science, Israel 8/2004, Tel Aviv University 8/2004, Ben Gurion University, Israel 8/2004, Compugen, Israel 8/2004
  4. **The Assessment of Function Prediction Servers (Lecture)**  
First Automated Function Prediction Special Interest Group meeting 7/2005.
  5. **Using an alignment of fragment strings for comparing protein structures**  
European Conference for Computational Biology 2006 (Lecture. Declined due to last minute travel cancellation).
  6. **Structural Biology as a Data Rich Science (Lecture)**  
University of California, Riverside; University of California, Merced; University of Virginia; George Mason University
  7. **Function Based Target Selection for Structural Genomics (Lecture)**  
ISMB/ECCB 2007 (August 2007)  
2008: Technion, Israel, Hebrew University Jerusalem, Israel; Tel Aviv University, Israel; Texas A&M University, TX USA; University of Kansas, KS USA; Ontario Institute for Cancer Research, ON Canada
  8. **Protein Function Differentiation: Structural Genomics and Metagenomics Connections (Lecture)**  
Computational Systems Bioinformatics 2007, La Jolla California
  9. **Visualization of the Functional Potential of Metagenomes (Lecture)**  
Ohio Collaborative Conference on Bioinformatics (OCCBIO) 2010
  10. **Assessing Functional Predictions, Critical Assessment for Function Annotations (Lecture)** 18th Microbial Genomics Meeting, Lake Arrowhead, CA September 2010
  11. **Handling the Metagenomic Data Deluge (Lecture)**  
Texas A&M, October 2010
  12. **Assessing Functional Predictions (Lecture)** Critical Assessment of Genome Interpretation, University of California Berkeley, CA December 2010
  13. **Metagenomic Networks: an invited tutorial**  
MITACS Workshop on Biological Networks and Systems Biology, Simon Fraser University Harbor Center, Vancouver January, 2011
  14. **The Event-Driven Model of Operon Evolution (Lecture)**  
Annual meeting of the Ohio Chapter of the American Society of Microbiology, March 2011.
  15. **Future directions for CAGI and Genome Interpretation** (Invited panelist) ISMB

2011

- 16. The Human gut Ecosystem: Gut Microbiome and Host Transcriptome in Breast-fed vs. Formula-fed Infants (Lecture)** ISMB 2011 (late breaking research track).
- 17. The Mycoplasma Online Genome Database, Microscopy & Genomics (Lecture)**  
Ontario Institute for Cancer Research, Toronto. 2011
- 18. The Critical Assessment of Function Annotations (Lecture)** Cold Spring Harbor Symposium on Genome Informatics 2011, University of California San Diego, CA 2012, Great Lakes Bioinformatics Conference, 2013
- 19. The Human Gut Ecosystem: Gut Microbiome and Host Transcriptome in Breast-fed vs. Formula-fed Infants (Lecture)** (Columbia University NY, Ohio State University OH, Scripps Research Institute, CA) 2012
- 20. Invited lecture: Big Data in Bioinformatics** 20<sup>th</sup> Annual Midwest Microbial Pathogenesis Conference (Columbus OH) 2013
- 21. Handling the biological data deluge** (University of Cincinnati 2013, Colorado State University 2013, Iowa State University) 2014
- 22. An event-driven approach for studying gene block evolution in bacteria** (Intelligent Systems in Molecular Biology, Dublin, Ireland 2015)
- 23. An event-driven approach for studying gene block evolution in bacteria** (The ACM Conference on Bioinformatics, Computational Biology, and Health Informatics Atlanta, GA) 2015
- 24. A large scale prediction of bacteriocin gene blocks suggests a wide functional spectrum for bacteriocins** (Genome Informatics, Cold Spring Harbor Laboratory, NY 2015
- 25. Handling Biological Big Data** University of Notre Dame, Department of Biology, invited speaker 2015

## **Grants**

### **Funded:**

Miami University Shoupp Award for Industry / Academia collaboration. “Applying Workflows to Field Programmable Gate Array Technology” (2009) \$5,000 (awarded)  
Miami University College of Arts & Science Summer Research Award (\$5,000) 2010  
Miami University Committee on Faculty Research grant (\$20,000) (PI) 2009-2010  
US Department of Energy “**Critical Assessment of Function Annotation Conference**” \$5,000 (PI) 2010-2011  
NIH R13 “**Conference: Critical Assessment of Function Annotation**” (Co investigator, PI: Predrag Radivojac, Indiana University) (\$20,000) 2010-2011  
NSF/ABI “**ABI Innovation: Analysis of Operon Evolution Using an Event Driven**



**Approach**” (\$642,729) (PI) 2012-2016

NSF/ABI “**Bilateral BBSRC-NSF/BIO Collaborative Research: ABI Development: A Critical Assessment of Protein Function Annotation**” (\$506,490) (PI) 2015-2018

PI: Friedberg. Co-PI’s: Predrag Radivojac (Indiana University), Sean D Mooney (University of Washington), Casey Greene (University of Pennsylvania), Claire O’Donovan, Maria J Martin (European Bioinformatics Institute) Funding agencies: Joint NSF & BBSRC (UK) Total funding: \$1.5M Funding to PI: \$500,000, 9/2015-8/2018

### **Teaching**

#### **Undergraduate & Graduate courses:**

##### **2009-2015:**

*BMZ 115:* Introductory Biology. I teach a microbiology module to undergraduates (freshmen/sophomores)

*MBI/BOT/ZOO 485/585* Principles of Bioinformatics (developed by me; seniors / graduate students). The course aims to teach the theory and practice of common genome analysis tools that are used by experimental biologists. Students learn the theory and practice of sequence alignment, genetic distance, phylogenetic trees, sequence assembly and genomic comparisons.

*MBI 690* Graduate Seminar

*MBI 224* Phage genomics. This is the second of a two-semester course given under the auspices of HHMI. In the first part (which I do not teach), the students isolate environmental mycobacteriophages. Those are sequence and assembled extramurally. In the second part of the course, which I co-teach, the students learn the basics of genome annotations, and annotate the phage genomes they isolated in the first semester. So far we have annotated four genomes in two years, and have generated three GenBank genomic entries for novel phages.

*MBI 490* Senior Seminar

### **Student Mentoring**

**2015-** Huy Nguyen (PhD, Computer Science), Md Nafiz Hamid (PhD, Bioinformatics and Computational Biology)

**2009-2015:** I engaged fifteen undergraduate students in independent studies. Six of the students were engaged in an inter-institutional competition organized by Texas A&M university. The competition involved rigorous annotation of protein sequences in UniProtKB, and taught the students detailed reading of scientific papers, the proper use of Gene Ontology based annotation, and application of critical thinking and detail-oriented skills towards protein annotation. Three students have received Summer Research Appointment fellowships to research in my lab. Three (Ryan Kelly, David Vincent, Alexander Thorman) are co-authors on published papers. One undergraduate student

received an NSF Graduate Research Fellowship (James Morton).

**2009-2015** Mentored one PhD candidate in the Microbiology Program (David Ream) one master's student (Ashwani Kumar), three master's students at the Computer Science program of Miami University (Jake Gregg, Andrew Oberlin, Osama Jomaa)

**2005-2006** While I was a postdoc, I tutored an exchange graduate student in part of his thesis project. Mr. Tim Harder and I co-authored two papers in the publications list.

### **Other teaching**

**2012:** Co-designed the bioinformatics undergraduate minor at Miami University

**1999-2002** Teaching assistant, *Bioinformatics: computational sequence analysis of biological macromolecules*. Undergraduate senior/post graduate course, The Hebrew University, Jerusalem

**1996** GNA-VSNS Biocomputing course. Contributed instructional software to one of the first distance learning course in bioinformatics, coordinated at the University of Bielefeld, Germany. <http://www.techfak.uni-bielefeld.de/bcd/welcome.html>

**1996-1997** GNA-VSNS Principles of Protein Structure course: structural biology and bioinformatics distance learning course from Birkbeck College, London, UK. <http://www.cryst.bbk.ac.uk/PPS/>

### **Other Academic Service Activities**

#### **Editorial board memberships:**

*PloS ONE*; *BMC-Bioinformatics*; *Database (Oxford University Press)*;

**2015-2016** Chair, poster session, Intelligent Systems in Molecular Biology (Dublin, Ireland 2015, Orlando, FL, USA 2016)

**2013-2014** Organizing Committee, Annual meeting of the International Biocuration Society; session chair in annual meeting (Toronto, April 2014).

**2012** Program committee member, European Conference on Computational Biology

**2012** Served on a special emphasis panel study, NIH/NIGMS

**2012** Breakout session moderator: Bioinformatics for Metagenomics and Core Facilities, as part of the Drexel University Microbiome workshop, Philadelphia, PA

**2010** Developed assessment methods for the Critical Assessment of Genome Interpretation Experiment led by Steven E. Brenner, University of California Berkeley. (Manuscript in preparation). <http://genomeinterpretation.org>

**2009** Grant reviewer, Binational Science Foundation

**2008** Grant reviewer, National Science Foundation Plant Genome Research Program

**2008** Guest Editor, *PLoS Computational Biology*

**2007** Book proposal reviewer for CRC press

**2007** Guest editor *BMC Bioinformatics* special section on automated function prediction, published May, 2007

**2007** Organizer and co-chair, metagenomics workshop, Computational Systems Bioinformatics conference 2007, La Jolla, California

**2006, 2007, 2013** Program committee member, Pacific Symposium of Biocomputing.

**2006** Guest editor, *Protein Science* special section on automated protein function prediction. June, 2006.

Program committee member, Intelligent Systems in Molecular Biology (ISMB) 2003, 2005, 2006

**2005- present: Founder, co-organizer and co-chair of the Automated Function**

**Prediction meetings** <http://BioFunctionPrediction.org> This activity has been funded by the NIH (\$20,000) and US-DOE (\$5,000). The meeting now hosts a biannual community-driven critical assessment experiment in which research teams are evaluated for their ability to predict the function of proteins given their sequence.

**2002-present** Manuscript referee for the following publications: *PNAS*, *Bioinformatics*; *Proteins: structure function and bioinformatics*; *Nucleic Acids Research*; *BMC Bioinformatics*; *BMC Genomics*; *Protein Science*; *PLoS Computational Biology*; *PLoS One*; *Genome Biology*; *Drug Discovery Today*; *Trends in Genetics*; *Journal of Molecular Biology*;

### **Other activities**

**2009 – present** I am the author of a popular science blog, Byte Size Biology (<http://bytesizebio.net>). Posts have been published in two editions of the Open Laboratory book (2009 & 2010), competitively selected from hundreds of submissions worldwide. Blog posts were also used in K-12 teaching. The blog receives over 10,000 unique views per month.

**2005:** Project coordinator Biopython. As project coordinator, I was responsible for monitoring software versioning system deposits, coordination among developers (see below), and compiling a version release.

**2000-** I have been involved as a programmer with several open-source bioinformatics projects. Most notably the Biopython (<http://biopython.org>) project aiming at providing basic tools for bioinformatics in the Python programming language.

### **Major Collaborators**

Predrag Radivojac (Indiana University), Sean Mooney (University of Washington), Shaun Lee (University of Notre Dame), Robert Chapkin (Texas A&M University), Sharon Donovan (University of Illinois, Urbana-Champaign), Patricia Babbitt (University of California, San Diego), Claire O'Donovan, Maria Martin (European Bioinformatics Institute)

*At Iowa State University:* Carolyn Lawrence-Dill, Baskar Ganapathysubramanian ,  
Jonathan Kelly, Bradley Blitvich

(January, 2016)