C u r r i c u l u m   V i t a e

Iddo Friedberg, M.Sc. Ph.D.

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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 2014).

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
Member-elect, board of directors, the International Society for Computational Biology. (Appointment starts January 2016)

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 Method*s 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. **JAFA: 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, <u>Friedberg I</u> (2006) **Ten Simple Rules for Selecting a Postdoctoral Position**. *PLoS Comp Biol* 2(11): e1

2. <u>Friedberg I</u>., 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 <u>Friedberg I</u>. **The 2006 Automated Function Prediction Meeting BMC Bioinformatics** 8 (2007) (S8)

4. <u>Friedberg I</u> **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 <u>Friedberg I</u> **The automated function prediction SIG looks back at 2013 and prepares for 2014** (2014) *Bionformatics* 10.1093/bioinformatics/btu117

6. <u>Friedberg I,</u> Wass M, Mooney SD, Radivojac P **Ten Simple Rules for a Community Computational Challenge** (2015) *PLoS Comp Biol* 11(4):e1004150

Book chapters

1. <u>Friedberg I</u> **IPRStats, overview** in *Encyclopedia of Metagenomics* Ed. Karen Nelson, Publisher: Springer (2012)

2. Radivojac P and <u>Friedberg I</u> **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, <u>Friedberg</u> 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, Ruttenberg 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, <u>Friedberg</u> 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) S*tand. Genomic Sci*. 3(3):232-4

3. Field D, <u>Friedberg I</u>, 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) 8th 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 20th 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)

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

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

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/

<u>Other Academic Service Activities</u>
Editorial board memberships:
PloS ONE; BMC-Bioinformatics; Database (Oxford University Press); Microbial Informatics and Experimentation (BMC)
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 (Universityof 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)

Miami University: Mitchell Balish, Rachael Morgan-Kiss, Xiao-Wen Cheng, Chun Liang, Dhananjai Rao Miami University: (co-advisor of a graduate student), Yoshinori Tomayaso.

At Iowa State University: Carolyn Lawrence-Dill, Baskar Ganapathysubramanian , Jonathan Kelly, Greg Phillips