

Andrew Josef Severin

CURRICULUM VITAE

Contact

Home:
5558 North Dakota Avenue.
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Social

Twitter://isugif
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website://Bioinformaticsworkbook.org

Education

Ph.D. Biophysics
Iowa State University
2003-2009

B.S. Biotechnology
North Dakota State University
1998-2001

Interests

Science Fiction Writing
Drawing
Coding in Swift
Hiking/camping/exploring

Summary

I am a broadly trained biologist with 18 years of experience in molecular biology, genomics, and bioinformatics in a wide range of species. My research interests include using high-throughput sequencing data from multi-omic experiments to investigate emergent properties in biological systems. In addition, I have managed the Genome Informatics Facility (GIF) since its founding in 2011, which serves as a centralized resource of expertise on the application of sequencing technologies and open source software to biological systems. I developed its mission to integrate bioinformatic expertise into tutorials and workflows that are easy to understand and use by faculty, staff and students to enable the transformation of 'big data' into data that dramatically accelerates our understanding of biology and evolutionary processes.

Experience

Iowa State University
Manager Research
Adjunct Assistant Professor in Ecology,
Evolution and Organismal Biology
Scientist I
Associate Scientist

Iowa State University
Postdoctoral Research Associate

Iowa State University
Graduate Student Research Assistant

North Dakota University
Undergraduate Research Assistant

Office Of Biotechnology, GIF
2020-Present
2012-Present

2014-2019
2011-2014

Randy Shoemaker, Advisor
2009-2011

Amy Andreotti, Advisor
2003-2009

David Horvath, Advisor
USDA,ARS,Northern Crops Science Lab.
Fargo, ND

Online Resources and Products

Iowa State University
Bioinformatics Workbook

Genome Informatics Facility
2017-present

Education

Ph.D. Biophysics
B.S. Biotechnology

2009
2001

Iowa State University
North Dakota State University

Ames, Iowa
Fargo, North Dakota

Publications

36. Estefanía González-Alvarez M, Severin A, Sayadi M, Keating AF. PFOA-induced ovotoxicity differs between lean and obese mice with impacts on ovarian reproductive and DNA damage sensing and repair proteins. *Toxicological Sciences*. 2022 Dec;190(2):173-88. [Impact Factor 3.703] Effort 10% I provided guidance on the data analysis and input to the manuscript.
35. Novbatova G, Timme K, **Severin A** , Sayadi M, Keating AF. Pre-conceptional exposure to glyphosate affects the maternal hepatic and ovarian proteome. *Toxicological Sciences*. 2022 Dec;190(2):204-14. [Impact Factor = 3.703] Effort 10% I provided guidance on the data analysis and input to the manuscript.
34. Sahoo DK, Borcharding DC, Chandra L, Jergens AE, Atherly T, Bourgois-Mochel A, Ellinwood NM, Snella E, **Severin AJ** , Martin M, Allenspach K. Differential transcriptomic profiles following stimulation with lipopolysaccharide in intestinal organoids from dogs with inflammatory bowel disease and intestinal mast cell tumor. *Cancers*. 2022 Jul 20;14(14):3525. [Impact Factor = 6.639] Effort 15% I performed the data analysis, methods and results.
33. Ploessl D, Zhao Y, Cao M, Ghosh S, Lopez C, Sayadi M, Chudalayandi S, **Severin AJ** , Huang L, Gustafson M, and Shao Z, 2022. A repackaged CRISPR platform unlocks the utility of non-homologous end joining in microbial factory engineering *Nat. Chem. Biol.* Accepted. [Impact Factor = 12.59] Effort 10%. I provided guidance on the data analysis and input to the manuscript.
32. Zhao, J., Qi, Y., Liu, P., **Severin, A.** , Sayadi, M., Paetau-Robinson, I., White, W. 2022. Prebiotic Effects of a Cranberry Beverage in a Randomized, Placebo-Controlled, Crossover Clinical Trial. *Current Developments in Nutrition*, 5(Supplement_2), 1190-1190. [Impact Factor = 2.91] Effort 15%. I performed the non-statistical analyses and provided methods/results text.
31. Masonbrink RE, Alt D, Bayles DO, Boggiatto P, Edwards W, Tatum F, Williams J, Wilson-Welder J, Zimin A, **Severin AJ** and Olsen S, 2021. A pseudomolecule assembly of the Rocky Mountain elk genome. *Plos one*, 16(4), p.e0249899. [Impact Factor = 3.24] Effort 15%. I guided the analyses and contributed to the writing/editing of the paper.
30. Murugan K, Suresh SK, Seetharam AS, **Severin AJ** and Sashital DG, 2021. Systematic in vitro specificity profiling reveals nicking defects in natural and engineered CRISPR–Cas9 variants. *Nucleic acids research*, 49(7), pp.4037-4053. . [Impact Factor = 16.97] Effort 10%. I generated the counts table for the frequency of each sequence variant in the pool of reads and contributed to the editing of the paper.
29. Shell WA, Steffen MA, Pare HK, Seetharam AS, **Severin AJ** , Toth AL. and Rehan SM, 2021. Sociality sculpts similar patterns of molecular evolution in two independently evolved lineages of eusocial bees. *Communications biology*, 4(1), pp.1-9. [Impact Factor = 6.268] Effort 10% I provided guidance on the data analysis and input on the editing of the manuscript.
28. Wu, H, Gontarek BC, Yi,G, Beall BD, Neelakandan AK, Adhikari B, Chen R, McCarty DR, **Severin AJ** and Becraft PW, 2020. The thick aleurone1 gene encodes a NOT1 subunit of the CCR4-NOT complex and regulates cell patterning in endosperm. *Plant Physiology*, 184(2), pp.960-972. [Impact Factor = 6.902] Effort 3%. I Identified the likely region for the NOT1 gene using BSRSeq and contributed to the editing of the manuscript.
27. Bagheri H, **Severin AJ** and Rajan H, 2020. Detecting and correcting misclassified sequences in the large-scale public databases. *Bioinformatics*, 36(18), pp.4699-4705. [Impact Factor = 6.937] Effort 30%. I conceived the application of the SDSI to genomics, guided the analysis and wrote/edited a large portion of the manuscript.
26. Murugan K, Seetharam AS, **Severin AJ** and Sashital DG, 2020. CRISPR-Cas12a has widespread off-target and dsDNA-nicking effects: EDITORS' PICK: Cas12a nickase activities. *Journal of Biological Chemistry*, 295(17), pp.5538-5553. [Impact Factor = 5.157] Effort 10%. I performed data curation and guided some of the analyses, contributed to the editing of the paper.
25. Redweik GA, Daniels K, **Severin AJ** , Lyte M and Mellata M, 2020. Oral treatments with probiotics and live Salmonella vaccine induce unique changes in gut neurochemicals and microbiome in chickens. *Frontiers in microbiology*, 10, p.3064. [Impact Factor = 4.076] Effort 15%. I performed the data analysis, provided methods/results text and provided input on the editing of the manuscript.
24. Masonbrink RE, Maier TR, Muppurala U, Seetharam AS, Lord E, Juvale PS, Schmutz J, Johnson NT, Korkin D, Mitchum, MG, Mimee B, Eves-van den Akker S, Hudson M, **Severin AJ** , and Baum, TJ, 2019. The genome of the soybean cyst nematode (*Heterodera glycines*) reveals complex patterns of duplications involved in the evolution of parasitism genes. *BMC genomics*, 20(1), pp.1-14. [Impact Factor = 3.969] Effort 15%. I was integral to the conception of the project, performed some analyses, guided the remaining bioinformatic analyses, contributed to the writing and editing of the paper.

23. Bagheri H, Muppirala U, Masonbrink RE, **Severin AJ** and Rajan H, 2019. Shared data science infrastructure for genomics data. *BMC bioinformatics*, 20(1), pp.1-13. [Impact Factor = 3.242] Effort 25%. I conceived the application of the SDSI to genomics, guided the analysis and wrote/edited a large portion of the manuscript.
22. Sommer-Lassa MM, Reecy J, **Severin AJ**, Somwarpet-Seetharam A and Mayes MS, 2019. 69 The effects of feeding a novel *Saccharomyces cerevisiae* feed additive on the prevalence and abundance of antimicrobial resistance genes in the microbiome (s) of receiving beef calves. *Journal of Animal Science*, 97(Supplement_2), pp.40-41. [Impact Factor = 3.159] Effort 10%. I provided guidance on the data analysis and input on the editing of the manuscript.
21. Barnes SN, Masonbrink RE, Maier TR, Seetharam A, Sindhu AS, **Severin AJ** and Baum TJ, 2019. *Heterodera glycines* utilizes promiscuous spliced leaders and demonstrates a unique preference for a species-specific spliced leader over *C. elegans* SL1. *Scientific reports*, 9(1), pp.1-11. [Impact Factor = 4.379] Effort 5%. I provided guidance on the data analysis and input on the editing of the manuscript.
20. Masonbrink RE, Purcell CM, Boles SE, Whitehead A, Hyde JR, Seetharam AS. and **Severin AJ**, 2019. An annotated genome for *Haliotis rufescens* (red abalone) and resequenced green, pink, pinto, black, and white abalone species. *Genome biology and evolution*, 11(2), pp.431-438. [Impact Factor = 3.462] Effort 65%. I conceived the project, guided the analysis and wrote most of the manuscript.
19. Masonbrink R, Maier TR, Seetharam AS, Juvalle PS, Baber L, Baum TJ. and **Severin AJ**, 2019. SCNBase: a genomics portal for the soybean cyst nematode (*Heterodera glycines*). *Database*, 2019. [Impact Factor = 3.451] Effort 40%. I conceived the project, guided the analysis and edited the manuscript.
18. Purcell CM, Seetharam AS, Snodgrass O, Ortega-García S, Hyde JR. and **Severin AJ**, 2018. Insights into teleost sex determination from the *Seriola dorsalis* genome assembly. *BMC genomics*, 19(1), pp.1-11. [Impact Factor = 3.969] Effort 65%. I conceived the project, performed or guided the analysis, wrote and edited most of the manuscript.
17. Srivastava R, Li, Z, Russo G, Tang J, Bi, R, Muppirala U, Chudalayandi S, **Severin AJ**, He, M, Vaitkevicius SI. and Lawrence-Dill CJ, 2018. Response to persistent ER stress in plants: a multiphasic process that transitions cells from prosurvival activities to cell death. *The Plant Cell*, 30(6), pp.1220-1242. [Impact Factor = 11.28] Effort 5%. I provided guidance on the data analysis and input to the manuscript.
16. Abdelrahman H, ElHady M, Alcivar-Warren A, Allen S, Al-Tobasei R, Bao L, Beck B, Blackburn H, ..., **Severin AJ**, Bosworth B, Buchanan J and Chappell J, 2017. Aquaculture genomics, genetics and breeding in the United States: current status, challenges, and priorities for future research. *BMC genomics*, 18(1), pp.1-23. [Impact Factor = 3.969] Effort 1%. This was the collective effort of the participants of an aquaculture meeting. I provided input and content for the paper but was not a major driver of its composition.
15. Cao M, Seetharam AS, **Severin AJ** and Shao Z, 2017. Rapid isolation of centromeres from *Scheffersomyces stipitis*. *ACS synthetic biology*, 6(11), pp.2028. [Impact Factor = 5.571] Effort 5%. I provided guidance on the data analysis and input on the writing of the manuscript.
14. Johnson TA, Looft T, **Severin AJ**, Bayles DO, Nasko DJ, Wommack KE, Howe A and Allen HK, 2017. The in-feed antibiotic carbadox induces phage gene transcription in the swine gut microbiome. *MBio*, 8(4). [Impact Factor = 6.784] Effort 30%. I performed the metagenomics analyses, provided methods and results text and edited the manuscript.
13. Purcell C, **Severin AJ**, Sylvia P, Wegner N and Hyde J, 2017. Improving Aquaculture Production in *Haliotis* Species through the Development of a Genomic Toolkit. *Bull. Jap. Fish. Res. Edu. Agen.* No, 45, pp.21-27. [Impact Factor = NA] Effort 35%. I collaborated in the conception of the project along with the analysis and writing of the paper.
12. Purcell C, **Severin AJ**, Buonaccorsi V, Drawbridge M, Stuart, K and Hyde, J 2017. Exploring Transcriptomic Patterns in Slow-and Fast-growing *Seriola dorsalis* Larvae. *Bull. Jap. Fish. Res. Edu. Agen.* No, 45, pp.47-55. [Impact Factor = NA] Effort 35%. I collaborated in the conception of the project along with the analysis and writing of the paper.
11. Masonbrink R, **Severin AJ** and Seetharam AS, 2017. Comparative genomics of soybean and other legumes. In *The Soybean Genome* (pp. 83-93). Springer Cham. [Impact Factor = NA] Effort 20%. I provided guidance on how to write a book chapter and provided input and revision to the chapter.
10. Mou KT, Clark TA, Muppirala UK, **Severin AJ** and Plummer PJ, 2017. Methods for genome-wide methylome profiling of *Campylobacter jejuni*. In *Campylobacter jejuni* (pp. 199-210). Humana Press New York NY. [Impact Factor = 1.17] Effort 5%. I provided guidance on the data analysis and input to the manuscript.
9. Standage DS, Berens AJ, Glastad KM, **Severin AJ**, Brendel VP. and Toth AL, 2016. Genome, transcriptome and methylome sequencing of a primitively eusocial wasp reveal a greatly reduced DNA methylation system in a social insect. *Molecular ecology*, 25(8), pp.1769-1784. [Impact Factor = 6.185] Effort 15%. I provided guidance on the data analysis and input on the writing of the manuscript.

8. Lin T, Lashbrook CC, Cho SK, Butler NM, Sharma P, Muppirala U, **Severin AJ**, Hannapel DJ 2015. Transcriptional analysis of phloem-associated cells of potato. *BMC genomics* 16 (1), 1. [Impact Factor = 3.969] Effort 10%. I provided guidance on the data analysis and input on the writing of the manuscript.
7. Seetharam A, Gomez A, Purcell CM, Hyde JR, Blood PD, **Severin AJ**, 2015. NCBI-BLAST programs optimization on Extreme Science and Engineering Discovery Environment resources for sustainable aquaculture. *Proceedings of the 2015 Extreme Science and Engineering Discovery Environment Conference*. [Impact Factor = NA] Effort 60%. I conceived the project, guided analysis, wrote and edited most of the manuscript.
6. Seetharam AS, Kawaler E, Du ZQ, Rothschild MF, **Severin AJ**, 2015. Microbiome analyses of pacific white shrimp (*Litopenaeus vannamei*) collected from disparate geographical locations. *Genomics data* 6, 67-69. [Impact Factor = 1.99] Effort 60%. I conceived how to utilize the data for project, guided analysis, wrote and edited most of the manuscript.
5. Xue C, Seetharam AS, Musharova O, Severinov K, Brouns SJJ, **Severin AJ**, Sashital DG, 2015. CRISPR interference and priming varies with individual spacer sequences. *Nucleic acids research* 43 (22), 10831-10847. [Impact Factor = 16.97] Effort 10%. I provided guidance on the data analysis and input on the writing of the manuscript.
4. Lanubile A, Muppirala UK, **Severin AJ**, Marocco A, and Munkvold GP 2015. Transcriptome profiling of soybean (*Glycine max*) roots challenged with pathogenic and non-pathogenic isolates of *Fusarium oxysporum*. *BMC genomics* 16 (1), 1. [Impact Factor = 3.969] Effort 5%. I guided the analysis, provided training to the postdoc and rewrote methods as needed.
3. Pilcher CM Jones CK, Schroyen M, **Severin AJ**, Patience JF, Tuggle CK and Koltes JE, 2015. Transcript profiles in longissimus dorsi muscle and subcutaneous adipose tissue: A comparison of pigs with different post-weaning growth rates. *Journal of Animal Science*, 93 (5), 2134-2143. [Impact Factor = 3.159] Effort 15%. I performed the RNA-Seq analysis and explored different models with Koltes.
2. Mou KT, Muppirala U, **Severin AJ**, Clark T, Boitano M, Plummer PJ, 2015. A comparative analysis of methylome profiles of *Campylobacter jejuni* sheep abortion isolate and gastroenteric strains using PacBio data. *Frontiers in Microbiology*, 5, p.782. [Impact Factor = 5.64] Effort 10%. I guided the analysis, wrote and edited the bioinformatics methods.
1. Solin SL, Wang Y, Mauldin J, Schultz LE, Lincow DE, Brodskiy PA, Chou HH, **Severin AJ**, Sakaguchi D and McGrail M 2014. Molecular and Cellular Characterization of a Zebrafish Optic Pathway Tumor Line Implicates Glia-Derived Progenitors in Tumorigenesis. *PLoS ONE*, 9(12), p.e114888. [Impact Factor = 2.74] Effort 10% I identified the location of the transgene and performed the RNA-Seq data analysis used in the paper.

Grants and Contracts

Grants: Total: \$6,222,989 [To ISU: \$3,555,644] (To Severin: \$1,510,648)				
Role (writing effort)	Period of Performance	Funding Source	Title (Authors)	Total Amount [to ISU] (to Severin)
Co-PI (30%)	2018-2022	National Science Foundation	The roles of exaptive and adaptive co-option in eye evolution (Serb J, Andrew AJ)	\$969,410 [\$969,410] (\$110,919)
Senior Personnel † (5%)	2021	North Central Soybean Research Program	An integrated approach to enhance durability of SCN resistance for long-term, strategic SCN management (Phase III) (Scaboo A, Baum T, Tylka G, Mitchum M Ngyuen H, Hudson M Diers B)	\$675,062 [\$273,741] (\$86,615)
Co-PI (5%)	2018-2021	North Central Soybean Research Program	An integrated approach to enhance durability of SCN resistance for long-term, strategic SCN management (Phase II) (Scaboo A, Baum T, Severin AJ Tylka G, Mitchum M Ngyuen H, Hudson M Diers B)	\$1,677,089 [\$588,874] (\$227,370)
PI (90%)	2016	Extreme Science and Engineering Discovery Environment	Genome Assembly and Annotation of Red Abalone Yellowtail, Soybean Cyst Nematode and Spiny Softshell Turtle	\$50,680 [\$50,680] (\$50,680)
PI (70%)	2015-2017	National Oceanic and Atmospheric Administration Saltonstall-Kennedy	Development of a genomic toolkit to guide broodstock selection and culture practices for <i>Seriola lalandi</i> and <i>Seriola rivoliana</i>	\$298,859 [\$298,859] (\$298,859)
PI (70%)	2015-2017	National Oceanic and Atmospheric Administration Saltonstall-Kennedy	Development of a genomic toolkit for <i>Haliotis</i> species to guide broodstock selection and endangered species restoration (Severin AJ, Drawbridge M)	\$282,852 [\$282,852] (\$282,852)
Co-PI (12%)	2015-2018	North Central Soybean Research Program	An integrated approach to enhance durability of SCN resistance for long-term, strategic SCN management (Baum T, Severin AJ Tylka G, Mitchum M Ngyuen H, Hudson M Diers B)	\$1,787,766 [\$609,957] (\$241,218)

Grants and Contracts Continued

Co-PI (40%)	2015-2016	National Science Foundation CAMTech Center	Development of a genomic toolkit to explore genetic diversity of soybean cyst nematode populations (Baum T, Severin AJ)	\$155,000 [\$155,000] (\$48,000)
PI (90%)	2014	Extreme Science and Engineering Discovery Environment	Genomic Resource Development of Yellow Tail Teosinte, Soybean and Steptochaeta	\$111,158 [\$111,158] (\$111,158)
Co-PI (50%)	2014-2015	United Soybean Board	The effect of rotations of host resistance genes (Rps) on pathogen avirulence genes (Avr) in the soybean-Phytophthora sojae pathosystem (Robertson A, Severin AJ)	\$157,857 [\$157,857] (\$39,620)
Co-PI (10%)	2014	ISU College of Human Sciences	Immune mediated mechanisms of insulin resistance in obese African Americans (Kohut M, Ackermann M, Severin AJ)	\$24,355 [\$24,355] (\$2,500)
Co-PI (35%)	2012	ISU LASCAC	Bioinformatic infrastructure & training (Toth A, Severin AJ Luecke G)	\$32,901 [\$32,901] (\$10,857)

NOTE: Only funds specifically for bioinformatics support or personnel/equipment cost/equivalent equipment cost specifically for GIF are included in the "to Severin" calculation.

† In June of 2019, Office of Biotechnology policy changed and Facility Managers are not be listed as principal investigators. The grant is listed here to indicate writing effort provided and funds written into the proposal for bioinformatic services performed by Genome Informatics Facility

RSAs and NACAs for bioinformatics Services with GIF				\$2,109,826
Role (writing effort)	Period of Performance	Funding Source	Title (Authors)	Award Amount (to GIF)
Senior Personnel ‡ (40%)	2021-2024	United States Department of Agriculture Non-Assistance Cooperative Agreement	Agricultural Research Using High Performance Computing for Big Data, including Geospatial Analytics Bioinformatics, and Other Related Technologies (Coyle J, Peters D)	\$1,241,418.00 (\$1,241,418.00)
Senior Personnel ‡ (100%)	2020	United States Department of Agriculture Research Service Agreement	Bioinformatics analysis of bison genome (Serb J, Olsen S)	\$29,700 (\$29,700)
Senior Personnel ‡ (40%)	2019	United States Department of Agriculture Non-Assistance Cooperative Agreement	Agricultural Research Using High Performance Computing for Big Data, including Geospatial, Analytics, Bioinformatics, and Other Related Technologies (Coyle J, Peters D)	\$410,000 (\$410,000)
Senior Personnel ‡ (50%)	2017-2022	United States Department of Agriculture Non-Assistance Cooperative Agreement	Computational analysis of host, bacteria and microbiome for development of strategies to enhance health and food safety (Serb J, Loving C)	\$428,708 (\$428,708)

‡ In the Office of Biotechnology, all Research Service Agreements (RSAs) and Non-Assistance Cooperative Agreement (NACAs) are run through the director or equivalent representative in accordance with Facility Managers not being listed as principal investigators. The RSAs and NACAs listed here indicate writing effort provided and funds written into the proposal for bioinformatic services performed by Genome Informatics Facility or supports staff in the Genome Informatics Facility.

Grants and Contracts Continued

Government Contracts		\$313,936.75		
Role (writing effort)	Period of Performance	Funding Source	Title	Award Amount
subcontractor (100%)	2021	Southwest Fisheries Science Center	Advancing genomic resources for abalone and <i>Seriola</i> species	\$47,725
subcontractor (100%)	2020	Southwest Fisheries Science Center	GBS analysis of Thermal tolerance on 150 F2 <i>Seriola dorsalis</i>	\$10,925
subcontractor (100%)	2019	Southwest Fisheries Science Center	Genome assembly of White and green abalone using nanopore/Hi-C and resequencing analysis of red-green abalone hybrid	\$40,020
subcontractor (100%)	2018	Southwest Fisheries Science Center	GBS analysis for data from <i>Seriola dorsalis</i> thermal tolerance and abalone sex determination	\$10,000
subcontractor (100%)	2018	Southwest Fisheries Science Center	Resequencing of 15 white abalone to explore heterozygosity	\$21,750
subcontractor (100%)	2018	Southwest Fisheries Science Center	Resequencing of 35 Almaco Jack (<i>Seriola rivoliana</i>)	\$27,728.75
subcontractor (100%)	2016	Southwest Fisheries Science Center	Resequencing of pinto abalone and white cultured and wild abalone	\$27,000.
subcontractor (100%)	2015	Southwest Fisheries Science Center	Pacific Albacore Genome Assembly and Sex Determining Marker Development	\$39,999
subcontractor (100%)	2014	Southwest Fisheries Science Center	<i>Seriola dorsalis</i> Sex Determining and Regional Marker Development	\$52,398
subcontractor (100%)	2012	Southwest Fisheries Science Center	Genome Assembly of <i>Seriola dorsalis</i> and RNA-Seq Analysis of Growth heterogeneity	\$36,491.

Awards, and Recognition

- Professional and Scientific Citation Award 2019
- PS Staff Excellence award April 2017
- Roy J Carver Biotechnology Fellowship Award Recipient at ISU, 2007-2008
- Biotechnology Graduate Fellowship Award at ISU, 2003-2007
- Departmental Graduate Student Teaching Award at ISU, 2006.
- National Science Foundation GraSUS Fellow at NDSU, 2002
- ND EPSCoR Science Bound Program Fellow at NDSU, 2001
- Research Experience for Undergraduates, fellow at NDSU, 1998

Invited Seminars

- 2019 "Transforming big data into informative data to accelerate scientific discovery" University of Iowa, Iowa City IA
- 2016 *Seriola* "genomics and the knowledge repository" Serioladb.org United States-Japan National Resources Panel on Aquaculture, Seattle WA
- 2015 "Lessons learned: the story of a genome informatics facility's strategies for Organizing Biological Data Analysis" NYU Lagone Medical Center, New York NY
- 2014 "Lessons learned: the story of a genome informatics facility's strategies for transparency, reproducibility and education" ABRF MadSci Conference, Baltimore Md.
- 2011 "Application of RNA-Seq in Soybean Crop Improvement" Crop Science Society of America, San Antonio Texas.
- 2011 "RNA-Sequencing and the Soybean Genome" Plant and Animal Genome Conference, San Diego California.
- 2010 "Applications of Next Generation Sequencing to Glycine max" (Massimo Delledonne), University of Verona Italy.
- 2010 "A Guide to the Soybean Transcriptome" Post Doctoral Research day Iowa State University, Ames Iowa.

Teaching Experience

- 2017-present An online living workbook on bioinformatics. <https://bioinformaticsworkbook.org>
- 2016-2019 Instructor Iowa State University Intro to Linux and HPC, GEN 542 (1 credit)
- 2017 Instructor Iowa State University Introduction to Next-Generation Sequencing BCB 660 (spring) (3 credit)
- 2014 Instructor Iowa State University Introduction to Next-Generation Sequencing BCB 660 (fall) (3 credit)
- 2014 Big-Data Biology and DNA, LAS 103D (Spring) (1 credit) Independent study BIOL 499 (spring) (2 credit)

2013 Instructor Iowa State University Independent study BIOL 499, (fall) (2 credit)
2012 Co-Instructor with Amy Toth, Iowa State University (3 credit) Introduction to Next-Generation Sequencing BCB 660 (fall)
2006 Graduate Teaching Assistant Department of Biochemistry Biophysics and Molecular Biology Iowa State University, BBMB 412
Experimental lab techniques in Molecular Biophysics and Structural Biology
2005 Graduate Teaching Assistant Department of Biochemistry Biophysics and Molecular Biology Iowa State University BBMB 411
Techniques in Biochemical Research
2002 National Science Foundation Graduate Teaching Fellows in K-12 Education GraSUS, North Dakota State University, High School
Mathematics
2001 Instructor North Dakota State University, Elementary Algebra (Spring Fall)

Guest Lectures

2022 GRST 565 section on the topic of Data Management Practice, Silvina Arias
2021 GRST 565 section on the topic of Data Management Practice, Silvina Arias

Mentorship

Undergraduate research students (6)

- Jeffrey Haltom (2012-2015)
- Chad Soenksen (2012-2014)
- Steve Hernandez (2012-2014)
- Kristen McKibben (2013-2014)
- Andrew Meyer (2013-2014)
- Kevin Buchik (2011-2013)

Postdoctoral Associates (5)

- Dr. Jennifer Chang (2020 – present)
- Dr. Sathesh-Kuma Sivasankaran (2020 – present)
- Dr. Rick Masonbrink (2016)
- Dr. Arun Seetharam (2014-2016)
- Dr. Usha Muppirala (2014-2016)

Employees (5)

- Dr. Arun Seetharam (2016-2020)
- Dr. Usha Muppirala (2016-2017)
- Dr. Rick Masonbrink (2017-present)
- Dr. Siva Chudalayandi (2017-present)
- Dr. Maryam Sayadi (2018-2021)

Graduate Committee Member for: (6)

- Jeffrey Haltom (PI Xun Gu: ISU) 2018-present PHD (BCB)
- Jeffrey Haltom (PI Maura Mcgrail: ISU) 2017-2018 Masters (BCB)
- Urminder Singh (PI Eve Wurtele: ISU) 2017-2021 PHD (BCB)
- Shofi Andari (PIs Eve Wurtele/Karin Dorman: ISU) 2021- 2022 PHD (BCB)
- Cameron Fay (PI Amy Toth: ISU) 2021- 2022 Masters (IGG)
- Paulina Mejia Ruiz (PI Ricardo Perez Enriquez: Av. Instituto Politécnico Nacional) 2017- 2022 PHD (Acuicultura)
- Mudith Ekanayake (PI Dennis Lavrov EEOB: ISU) 2022 - Present)

Outreach

- Bioinformatics workbook (2017-present)
- Extreme Science and Engineering Discovery Environment Campus Champion for Iowa State University (2014-present)
- Bioinformatics undergraduate club advisor Iowa State University (2013)
- Co-Hosted the Seriola Symposium (January 2016)
- Chair of American Society of Agronomy bioinformatics community, (2013)

James Coyle, Ph.D

Director of the High Performance Computing Facility
IT Services Academic Technologies
Iowa State University, Ames, Iowa.
Email: jjc@iastate.edu
Phone: (515) 294-2099

Context: Over the last ten years, Jim and I have developed a strong collaboration. At first it involved purchasing into and testing the shared super computing resources. More recently, we have collaborated on several RSA and NACA agreements with the USDA to provide HPC services and bioinformatic expertise.

Catherine Purcell, Ph.D

Aquaculture Geneticist/Genomicist
Southwest Fisheries Science Center, La Jolla, California
Email: catherine.purcell@noaa.gov
Phone: (858) 546-7189

Context: Catherine and I have collaborated on projects to improve genomic resources for several aquaculture species (red Abalone, green abalone, black abalone, white abalone, *Seriola dorsalis*, *Seriola rivoliana* and Albacore). Over the last nine years, this collaboration has culminated in several published papers and many successful grant proposals.

Jeanne Serb, Ph.D.

Associate Professor of Ecology, Evolution and Organismal Biology
Directory of the Office of Biotechnology
Iowa State University, Ames, Iowa.
Email: serb@iastate.edu
Phone: (515) 294-7479

Context: Jeanne and I started writing grants together in 2016 and we were funded by National Science Foundation in 2018. The Genome Informatics Facility I manage is a part of the Office of Biotechnology, which In 2018, Jeanne became the director.

Amy Toth, Ph.D.

Professor of Ecology, Evolution and Organismal Biology and Entomology
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Context: I have known Amy since my second week as the manager of the Genome Informatics Facility. We continue to collaborate on many projects together including genome assembly, annotation and differential expression in wasps and bees, written a successful LASCAC proposal for teaching compute nodes, co-taught BCB660 "Introduction to Next-Generation Sequencing" and published several papers together. She has deepened my appreciation and love for all insects including the ones with pointy posteriors.