

CURRICULUM VITAE

May 2023

Alice Rebecca Wattam, Research Associate Professor
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RESEARCH INTERESTS

Comparative genomics, Microbiology, Antimicrobial resistance, Vaccine analysis

EDUCATION

1994-2000 University of Arizona, Tucson, AZ, Postdoctoral Research Fellow
1992-1994 University of Arizona, Tucson, AZ, MacArthur Postdoctoral Research Fellow
1988-1992 University of Wisconsin, Madison, WI, Ph.D. Entomology and Veterinary Science
Advisors Bruce Christensen (Veterinary Science) and Walter Goodman
Entomology)
1985-1987 University of New Mexico, Albuquerque, NM, M.S. Biology
Advisor Eric S. Loker
1978-1983 University of New Mexico, Albuquerque, NM, B.S. Biology

PROFESSIONAL EXPERIENCE

2018-present Research Associate Professor, University of Virginia, Charlottesville, VA
2014-2018 Research Assistant Professor, Virginia Tech, Blacksburg, VA
2012-2018 Project Director, Virginia Bioinformatics Institute, Virginia Tech, Blacksburg, VA
2008-2012 Research Scientist/Computational Biology Scientist, Virginia Bioinformatics Institute, Virginia Tech, Blacksburg, VA
2005-2008 Senior Computational Biologist, Virginia Bioinformatics Institute, Virginia Tech, Blacksburg, VA
2002-2005 Affiliated Faculty, Virginia Bioinformatics Institute, Virginia Tech, Blacksburg, VA
2001-2003 Project Analyst, Buscom Communications Inc., Wellesley, MA
1994-2000 Postdoctoral Research Fellow, Department of Ecology and Evolutionary Biology, University of Arizona, Tucson, AZ
1992-1994 MacArthur Postdoctoral Research Fellow, University of Arizona, Tucson, AZ
1987-1992 Graduate Research Assistant, Department of Veterinary Science, University of Wisconsin, Madison, WI
1985-1987 Graduate Teaching Assistant, Department of Biology, University of New Mexico, Albuquerque, NM

PUBLICATIONS

Refereed Journals

50. Scholz HC, Heckers KO, Appelt S, Geier-Dömling D, Schlege P, **Wattam AR**. Isolation of *Brucella inopinata* from a White's Tree Frog (*Litoria caerulea*): Pose exotic frogs a potential risk to human health? 2023. Accepted. *Frontiers in Microbiology*.

49. Viana MVC, Galdino JH, Profeta R, Oliveira M, Tavares L, de Castro Soares S, Carneiro P, **Wattam AR**, Azevedo V. Analysis of *Corynebacterium silvaticum* genomes from Portugal reveals a single cluster and a clade suggested to produce diphtheria toxin. 2023 PeerJ. 9;11:e14895. doi: 10.7717/peerj.14895. PMID: 36919166
48. Olson RD, Brettin T, Conrad N, Cucinell C, Davis JJ, Dempsey DM, Dickerman A, Dietrich EM, Kenyon RW, Kuscuoglu M, Lefkowitz E, Lu J, Machi D, Macken C, Mao C, Niewiadomska A, Nguyen M, Olsen GJ, Overbeek JC, Overbeek R, Parrello B, Parrello V, Porter J, Pusch GD, Shukla M, Singh I, Stewart L, Tan G, Thomas C, VanOeffelen M, Vonstein V, Wallace ZS, Warren AS, **Wattam AR**, Xia F, Yoo H, Zhang Y, Zmasek C, Scheuermann RH, Stevens RL. Introducing the Bacterial and Viral Bioinformatics Resource Center: a resource combining PATRIC, IRD, and ViPR. 2023. Nucleic Acids Res. 2023 Jan 6;51(D1):D678-D689. doi: 10.1093/nar/gkac1003. PMID: 36350631
47. Huang C, Guo F, Wang H, Olivares J, Dalton Iii J, Belyanina O, **Wattam AR**, Cucinell CA, Dickerman AW, Qin QM, Han A, de Figueiredo P. An automated system for interrogating the evolution of microbial endosymbiosis. 2022. Lab Chip. 2022 Oct 13. doi: 10.1039/d2lc00602b.
46. Yang J, Eslami M, Chen YP, Das M, Zhang D, Chen S, Roberts AJ, Weston M, Volkova A, Faghihi K, Moore RK, Alaniz RC, **Wattam AR**, Dickerman A, Cucinell C, Kendziorowski J, Coburn S, Paterson H, Obanor O, Maples J, Servetas S, Dootz J, Qin QM, Samuel JE, Han A, van Schaik EJ, de Figueiredo P. Phenotype-Based Threat Assessment. Proc Natl Acad Sci U S A. 2022 Apr 5;119(14):e2112886119. doi: 10.1073/pnas.2112886119. Epub 2022 Apr 1. PMID: 35363569.
45. Canário Viana MV, Profeta R, Cerqueira JC, Wattam AR, Barh D, Silva A, Azevedo V. Evidence of episodic positive selection in *Corynebacterium diphtheriae* complex of species and its implementations in identification of drug and vaccine targets. PeerJ. 2022 Feb 16;10:e12662. doi: 10.7717/peerj.12662. PMID: 35190783; PMCID: PMC8857904.
43. VanOeffelen M, Nguyen M, Aytan-Aktug D, Brettin T, Dietrich EM, Kenyon RW, Machi D, Mao C, Olson R, Pusch GD, Shukla M, Stevens R, Vonstein V, Warren AS, **Wattam AR**, Yoo H, Davis JJ. 2021. A genomic data resource for predicting antimicrobial resistance from laboratory-derived antimicrobial susceptibility phenotypes. Brief Bioinform. 2021 Aug 11:bbab313. doi: 10.1093/bib/bbab313.
43. Riojas MA, Frank AM, Greenfield SR, King SP, Meehan CJ, Strong M, **Wattam AR**, Hazbón MH. 2021. Identification and Characterization of Mycobacterial Species Using Whole-Genome Sequences. Methods Mol Biol. 2314:399-457. doi: 10.1007/978-1-0716-1460-0_19.
21. Viana MVC, Profeta R, da Silva AL, Hurtado R, Cerqueira JC, Ribeiro BFS, Almeida MO, Morais-Rodrigues F, Soares SC, Oliveira M, Tavares L, Figueiredo H, **Wattam AR**, Barh D, Ghosh P, Silva A, Azevedo V. 2020. Taxonomic classification of strain PO100/5 shows a broader geographic distribution and genetic markers of the recently described *Corynebacterium silvaticum*. PLoS One 15(12):e0244210. doi: 10.1371/journal.pone.0244210. eCollection 2020.
41. Madin J, Nielsen D, Brbic M, Corkrey R, Danko D, Edwards K, Engqvist M, Fierer N, Geoghegan J, Gillings M, Kyrpides N, Litchman E, Mason C, Moore L, Nielsen S, Paulsen I, Price N, Reddy TBK, Richards M, Rocha E, Schmidt T, Shaaban H, Shukla M, Supek F, Tetu S, Vieira-Silva S, **Wattam AR**, Westfall D, Westoby M. 2020. A synthesis of bacterial and archaeal phenotypic trait data. Sci Data. Jun 5;7(1):170. doi: 10.1038/s41597-020-0497-4.
40. Gagetti P, Errecalde L, **Wattam AR**, De Belder D, Ojeda Saavedra M, Corso A, Rosato AE. 2020. Characterization of the First *mecA*-Positive Multidrug-Resistant *Staphylococcus pseudintermedius* Isolated from an Argentinian Patient. Microb Drug Resist. doi: 10.1007/s12250-020-0040-4.
40. Gagetti P, Wattam AR, Giacoboni G, De Paulis A, Bertona E, Corso A, Rosato AE. 2019. Identification and molecular epidemiology of methicillin resistant *Staphylococcus*

- pseudintermedius strains isolated from canine clinical samples in Argentina. BMC Vet Res. 15(1):264. doi: 10.1186/s12917-019-1990-x. PMID: 31351494
39. Ibrahim IC, Parise MTD, Parise D, Sfeir MZT, de Paula Castro TL, **Wattam AR**, Ghosh P, Barh D, Souza EM, Góes-Neto A, Gomide ACP, Azevedo V. 2019. Transcriptome profile of *Corynebacterium pseudotuberculosis* in response to iron limitation. BMC Genomics. 20(1):663. doi: 10.1186/s12864-019-6018-1. PMID: 31429699 Free PMC article.
 38. Saranathan R, Levi MH, **Wattam AR**, Malek A, Asare E, Behin DS, Pan DH, Jacobs WR Jr, Szymczak WA. 2020. *Helicobacter pylori* Infections in the Bronx, New York: Surveying Antibiotic Susceptibility and Strain Lineage by Whole-Genome Sequencing. J Clin Microbiol. 58(3). pii: e01591-19. doi: 10.1128/JCM.01591-19.
 37. Davis JJ, **Wattam AR**, Aziz RK, Brettin T, Butler R, Butler RM, Chlenski P, Conrad N, Dickerman A, Dietrich EM, Gabbard JL, Gerdes S, Guard A, Kenyon RW, Machi D, Mao C, Murphy-Olson D, Nguyen M, Nordberg EK, Olsen GJ, Olson RD, Overbeek JC, Overbeek R, Parrello B, Pusch GD, Shukla M, Thomas C, VanOeffelen M, Vonstein V, Warren AS, Xia F, Xie D, Yoo H, Stevens R. 2020. The PATRIC Bioinformatics Resource Center: Expanding Data and Analysis Capabilities. 2020. Nucleic Acids Res. 2020 Jan 8;48(D1):D606-D612. doi: 10.1093/nar/gkz943. PMID: 31667520
 36. Banerjee K, Sekar P, Krishnan P, **Wattam AR**, Roy S, Hays JP, Menezes GA. 2018. Whole genome sequence analysis of NDM-1, CMY-4, and SHV-12 coproducing *Salmonella enterica* serovar Typhimurium isolated from a case of fatal burn wound infection. Infection and Drug Resistance 11:2491—2495.
 35. Viana MVC, Sahm A, Góes Neto A, Figueiredo HCP, **Wattam AR**, Azevedo V. 2018. Rapidly evolving changes and gene loss associated with host switching in *Corynebacterium pseudotuberculosis*. PLoS One 12;13(11):e0207304
 34. Imchen M, Kumavath R, Barh D, Vaz A, Góes-Neto A, Tiwari S, Ghosh P, **Wattam AR**, Azevedo V. 2018. Comparative mangrove metagenome reveals global prevalence of heavy metals and antibiotic resistome across different ecosystems. Sci Rep. 2018 8(1):11187. doi: 10.1038/s41598-018-29521-4.
 33. Oliverira A, Folador EL, Cybelle AP, Neto AG, Azevedo V, **Wattam AR**. 2017. Cell Division in genus *Corynebacterium*: protein-protein interaction and molecular docking of SepF and FtsZ in the understanding of cytokinesis in pathogenic species. Annals of the Brazilian Academy of Sciences, 90(2 suppl 1):2179-2188.
 32. Oliveira A, Oliveira LC, Aburjaile F, Benevides L, Tiwari S, Jamal SB, Silva A, Figueiredo HCP, Ghosh P, Portela RW, De Carvalho Azevedo VA, **Wattam AR**. 2017. Insight of Genus *Corynebacterium*: Ascertainning the Role of Pathogenic and Non-pathogenic Species. Front Microbiol. 8:1937. doi: 10.3389/fmicb.2017.01937.
 31. Antonopoulos DA, Assaf R, Aziz RK, Brettin T, Bun C, Conrad N, Davis JJ, Dietrich EM, Disz T, Gerdes S, Kenyon RW, Machi D, Mao C, Murphy-Olson DE, Nordberg EK, Olsen GJ, Olson R, Overbeek R, Parrello B, Pusch GD, Santerre J, Shukla M, Stevens RL, VanOeffelen M, Vonstein V, Warren AS, **Wattam AR**, Xia F and Yoo H. 2017. PATRIC as a unique resource for studying antimicrobial resistance. Briefings in Bioinformatics, doi: 10.1093/bib/bbx083.
 30. Imchen M, Kumavath R, Barh D, Azevedo V, Ghosh P, Viana M and **Wattam AR**. 2017. Searching for signatures across microbial communities: Metagenomic analysis of soil samples from mangrove and other ecosystems. Scientific Reports 7, Article number: 8859
 29. Viana MVC, Figueiredo H, Ramos R, Guimarães LC, Pereira FL, Dorella FA, Selim SAK, Salaheldean M, Silva A, **Wattam AR**, Azevedo V. 2017. Comparative genomic analysis between *Corynebacterium pseudotuberculosis* strains isolated from buffalo. PLoS One. 12(4): e0176347.

28. Al Dahouk S, Köhler S, Occhialini A, Jiménez de Bagüés MP, Hammerl JA, Eisenberg T, Vergnaud G, Cloeckaert A, Zygmunt MS, Whatmore AM, Melzer F, Drees KP, Foster JT, **Wattam AR**, Scholz HC. 2017. *Brucella* spp. of amphibians comprise genomically diverse motile strains competent for replication in macrophages and survival in mammalian hosts. *Nature Scientific Reports*, 7: 44420.
27. Canário Viana MV, **Wattam AR**, Batra DG, Boisvert S, Brettin TS, Frace M, Xia F, Azevedo V, Tiller R, Hoffmaster AR. 2017. Genome sequences of two *Brucella suis* strains isolated from the same patient, 8 years apart. *Genome Announcements* 5(9): e01687-16.
26. Canário Viana MV, **Wattam AR**, Batra DG, Boisvert S, Brettin TS, Frace M, Xia F, Azevedo V, Tiller R, Hoffmaster AR. 2017. Genome sequences of three *Brucella canis* strains isolated from humans and a dog. *Genome Announcements*. 5(8): e01688-16
25. **Wattam AR**, Davis JJ, Assaf R, Boisvert S, Brettin T, Bun C, Conrad N, Dietrich EM, Disz T, Gabbard JL, Gerdes S, Henry CS, Kenyon RW, Machi D, Mao C, Nordberg EK, Olsen GJ, Murphy-Olson DE, Olson R, Overbeek R, Parrello B, Pusch GD, Shukla M, Vonstein V, Warren A, Xia F, Yoo H, Stevens RL. 2017. Improvements to PATRIC, the all-bacterial Bioinformatics Database and Analysis Resource Center. *Nucleic Acids Research* 45(D1): D535-D542.
24. Davis JJ, Boisvert S, Brettin T, Kenyon RW, Mao C, Olson R, Overbeek R, Santerre J, Shukla M, **Wattam AR**, Will R, Xia F, Stevens R. 2016. Antimicrobial Resistance Prediction in PATRIC and RAST. *Sci Rep*. 14;6: 27930
23. Davis JJ, Gerdes S, Olsen GJ, Olson R, Pusch GD, Shukla M, Vonstein V, **Wattam AR**, Yoo H. 2016. PATtyFams: Protein Families for the Microbial Genomes in the PATRIC Database. *Front Microbiol*. 7:118.
22. Saadeh B, Caswell CC, Chao Y, Berta P, **Wattam AR**, Roop RM 2nd, O'Callaghan D. 2015 Transcriptome-Wide Identification of Hfq-Associated RNAs in *Brucella suis* by Deep Sequencing. *J Bacteriol*.198(3):427-35.
21. Tufariello J, Kerantzas C, Vilcheze C, Clader B, Nordberg N, Fischer J, Hartman T, Yang E, Driscoll T, Cole L, Sebra R, Maqbool S, **Wattam AR**, Jacobs W. 2015. The complete genome sequence of the emerging pathogen *Mycobacterium haemophilum* explains its unique culture requirements. *MBio*, 6: e01313-15.
20. Brettin T, Davis JJ, Disz T, Edwards RA, Gerdes S, Olsen GJ, Olson R, Overbeek R, Parrello B, Pusch GD, Shukla M, Thomason JA 3rd, Stevens R, Vonstein V, **Wattam AR**, Xia F. 2015. RASTtk: a modular and extensible implementation of the RAST algorithm for building custom annotation pipelines and annotating batches of genomes. *Sci Rep*.5:8365
19. Warren AS, Aurrecochea C, Brunk B, Desai P, Emrich S, Giraldo-Calderón GI, Harb O, Hix D, Lawson D, Machi D, Mao C, McClelland M, Nordberg E, Shukla M, Vosshall LB, **Wattam AR**, Will R, Yoo HS, Sobral B. 2015. RNA-Rocket: an RNA-Seq analysis resource for infectious disease research. *Bioinformatics* 31(9):1496-8.
18. Mao C, Abraham D, **Wattam AR**, Wilson MJ, Shukla M, Yoo HS, Sobral BW. 2014. Curation, integration and visualization of bacterial virulence factors in PATRIC. *Bioinformatics*. 31(2):252-8.
17. Panas MW, Jain P, Yang H, Mitra S, Biswas D, **Wattam AR**, Letvin NL, Jacobs WR. 2014. Noncanonical SMC protein in *Mycobacterium smegmatis* restricts maintenance of *Mycobacterium fortuitum* plasmids. *Proceedings of the National Academy of Sciences, USA*. 111:13264-71
16. Faria JP, Disz TL, Hausmann A, Henry CS, Olson R, Overbeek RA, Pusch GD, Shukla M, Vonstein V, **Wattam, AR**. 2014. Enabling comparative modeling of closely related genomes: Example Genus *Brucella*. *3 Biotech*.

15. **Wattam AR**, Foster JT, Mane SP, Beckstrom-Sternberg SM, Beckstrom-Sternberg JM, Dickerman AW, Keim P, Pearson T, Shukla M, Ward DV, Williams KP, Sobral BW, Tsolis RM, Whatmore AM, O'Callaghan D. 2014. Comparative phylogenomics and evolution of the brucellae: A path to virulence. *Journal of Bacteriology*, 196(5): 920-30.
14. Overbeek R, Olson R, Pusch GD, Olsen GJ, Davis JJ, Disz TL, Edwards, R, Gerdes, S, Parrello B, Shukla M, Vonstein V, **Wattam AR**, Xia F, Stevens RL. 2014. The SEED and the Rapid Annotation of microbial genomes using Subsystems Technology (RAST). *Nucleic Acids Research*, N42 (D1): D206-D214.
13. **Wattam AR**, Abraham D, Dalay O, Disz TL, Driscoll T, Gabbard JL, Gillespie JJ, Gough R, Hix D, Kenyon R, Machi D, Mao C, Nordberg EK, Olson Overbeek R, Pusch GD, Shukla M, Schulman J, Stevens RL, Sullivan DE, Vonstein V, Warren A, Will R, Wilson MJC, Yoo HS, Zhang C, Zhang Y, Sobral BW. 2014. PATRIC, the Bioinformatics Resource Center for bacterial data. *Nucleic Acids Research*, 42 (D1): D581-D591.
12. Rajasekaran P, Alexander JC, Seleem MN, Jain N, Sriranganathan N, **Wattam AR**, Setubal JC, Boyle SM. 2013. Peptide nucleic acids inhibit growth of *Brucella suis* in pure culture and in infected murine macrophages. *Int J Antimicrob Agents*. 2013 41(4): 358-62
11. **Wattam AR**, Inzana T, Williams KP, Mane SM, Shukla M, Almeida N, Dickerman AW, Mason S, Moriyón I, O'Callaghan D, Whatmore AM, Sobral BW, Tiller RV, Hoffmaster AR, Frace MA, De Castro C, Molinaro A, Boyle SM, De BK, Setubal JC. 2012. Comparative genomics of early-diverging *Brucella* strains reveals a novel lipopolysaccharide biosynthesis pathway. *MBio* 3(5): e00246-12
10. Gillespie JJ, **Wattam AR**, Cammer SA, Gabbard J, Shukla M., Dalay O, Driscoll T, Hix D, Mane SP, Mao C, Nordberg EK, Scott M, Schulman JR, Snyder EE, Sullivan DE, Wang C, Warren A, Williams KP, Xia T, Yoo HS, Zhang C, Zhang Y, Will R, Kenyon RW, Sobral BW. 2011. PATRIC: The Comprehensive Bacterial Bioinformatics Resource with a Focus on Human Pathogenic Species. *Infect Immun*. 79(11): 4286-98
9. **Wattam AR**, Williams KP, Snyder EE, Almeida NF, Shukla M, Dickerman, AW, Crasta OR, Kenyon R, Lu J, Yoo H, Ficht TA, Tsolis RM, Munk C, Tapia R, Han CS, Detter JC, Bruce D, Brettin TS, Sobral BW, Boyle SM and Setubal JC. 2009. Analysis of ten *Brucella* genomes reveals evidence for horizontal gene transfer despite preferred intracellular lifestyle. *Journal of Bacteriology*. 191(11): 3569-79.
8. Gillespie JJ, Williams K, Shukla M, Snyder EE, Nordberg E, Ceraul SM, Dharmanolla C, Rainey D, Soneja J, Vishnubhat ND, **Wattam AR**, Purkayastha A, Shallom JM, Czar M, Crasta O, Setubal J, Azad A, Sobral B. (2008) *Rickettsia* phylogenomics: unwinding the intricacies of obligate intracellular life. *PLoS One* 3(4):e2018.
7. He Y., Vines RR. **Wattam AR.**, Abramochikin GV., Dickerman AW., Eckart JD., Sobral BW. 2005. PIML: the Pathogen Information Markup Language. *Bioinformatics* 21 (1): 116-21.
6. Kidwell MG, **Wattam AR**. 1998. An important step forward in the genetic manipulation of mosquito vectors of human disease. *Proceedings of the National Academy of Sciences, USA* 95: 3349-3350.
5. **Wattam AR**, Christensen BM. 1992. Further evidence that the genes controlling susceptibility of *Aedes aegypti* to filarial parasites function independently. *The Journal of Parasitology* 78: 1092-1095.
4. **Wattam AR**, Christensen BM. 1992. Variation in *Aedes aegypti* mRNA populations related to strain, sex, and development. *The American Journal of Tropical Medicine and Hygiene* 47: 702-707.
3. **Wattam AR**, Christensen BM. 1992. Induced polypeptides associated with filarial worm refractoriness in *Aedes aegypti*. *Proceedings of the National Academy of Sciences, USA* 89: 6502-6505.

2. Duszynski DW, **Wattam AR**. 1987. Coccidian parasites (Apicomplexa: Eimeriidae) from Insectivores. IV. Four new species in *Talpa europaea* from England. *Journal of Protozoology* 35: 55-59.
1. Duszynski DW, **Wattam AR**. 1987. Coccidian parasites (Apicomplexa: Eimeriidae) from Insectivores. V. Ten forms from the moles of Japan (*Euroscaptor*, *Mogera* spp.). *Journal of Protozoology* 35: 60-62.

Refereed Conference and Workshop Publications

1. Zhao, J, Xue T, Yang B, Williams K, **Wattam AR**, Will R, Sharp B, Kenyon R, Crasta O, Sobral BW. 2006. Genome Annotation and Comparison System. The 2006 International Conference on Bioinformatics & Computational Biology (BIOCOMP), June 2006, Las Vegas, NV, USA

Book Chapters

6. Singh P, Tufariello JM, **Wattam AR**, Gillis TP, Jacobs Jr WR. Genomics Insights into the Biology and Evolution of Leprosy Bacilli. International Textbook of Leprosy, DM Scollard and TP Gillis eds. Rhetoric & Scientific & Technical Communication. 2018
5. Setubal JC, Almeida N, **Wattam AR**. Comparative Genomics for Prokaryotes. *Methods in Molecular Biology*, 2018;1704:55-78.
4. **Wattam AR**, Brettin T, Davis JJ, Gerdes S, Kenyon R, Machi D, Mao C, Olson R, Overbeek R, Pusch GD, Shukla MP, Stevens R, Vonstein V, Warren A, Xia F, Yoo H. Assembly, Annotation, and Comparative Genomics in PATRIC, the All Bacterial Bioinformatics Resource Center. *Methods in Molecular Biology*, 2018;1704:79-101
3. **Wattam AR**, Gabbard JL, Shukla M, Sobral BW. 2014. Comparative Genomic Analysis at the PATRIC, A Bioinformatic Resource Center. *Methods Mol Biol.* 1197:287-308.
2. Sobral BW, **Wattam AR**. 2012. Comparative genomics and phylogenomics of the *Brucella*. In *Brucella: Molecular microbiology and Genetics*. I. López-Goñi & D. O'Callaghan (eds.). intricacies of obligate intracellular life. *PLoS ONE* 3: e2018.
1. Sriranganathan N, MN Seleem, SC Olsen, LE Samartino, AM Whatmore, B Bricker, D O'Callaghan, SM Halling, OR Crasta, **AR Wattam**, et al. 2007. Genome sequencing and bioinformatics resources. *Animal associated microbes. Genome Mapping in Animals and Microbes* C. Cole and V. Nene, Springer. 8. Horizon Scientific Press, Jan 2012.

Technical Reports

1. Specialty Water Treatment Chemicals: What's Ahead? 2003. Buscom Communications Inc., 240 pp.

INVITED SEMINARS (since 2012)

- 2016- TWAS-ROESEAP Biotechnology Workshop of Food Technology. Bangkok, Thailand. Raw reads to full scale analysis: The virtual integration of private and public data in the Pathosystems Resource Integration Center.
- 2016- Computational Biology and Genomics Research Center, Universidade Federal de Minas Gerais. Minas Gerais, Brazil. Patterns in Metagenomic Data From Diverse Biomes: Computational Challenge Analyzing Large Environmental Sequence Data.
- 2016- GENÉTICA 2016, Brazilian-International Congress of Genetics. Caxambu, Brazil. Patterns in Metagenomic Data From Diverse Biomes: Computational Challenges Analyzing Large Environmental Sequence Data.

2016- Computational Biology and Genomics Research Center, University of São Paulo. São Paulo, Brazil. Patterns in Metagenomic Data From Diverse Biomes: Computational Challenge Analyzing Large Environmental Sequence Data.

2015- 68th Annual Brucellosis Research Conference. Chicago, IL. “Changes at RefSeq and how they impact the *Brucella* researcher”

2015 -Margaret Kidwell Speaker Series Symposium. University of Arizona, Tucson AZ. “Evolution of a pathogen results in corresponding evolution of a bioinformatics resource center.”

2014-NSF-VT REU:Microbiology (Microbiology in the Post-Genome Era) symposium, Virginia Tech, Blacksburg, VA. “PATRIC: A resource for infectious disease research.”

2012-Wadsworth Center, Albany, NY. “PATRIC: A resource for infectious disease research. Real-life examples used to drive software development.”

2012-65th Annual Brucellosis Research Conference, Chicago, IL. “A practical overview of PATRIC for *Brucella* researchers.”

2012-St. Jude Children's Research Hospital, Memphis TN. “PATRIC, a bioinformatics resource for pathogen researchers.”

SCIENTIFIC COMMUNITY ACTIVITIES

Memberships

American Association for the Advancement of Science
American Society of Microbiologists

Review Editor

Frontiers in Microbiology
Frontiers in Genetics

Reviewer

Bioinformatics
BioMed Research International
BMC Bioinformatics
BMC Genomics
Frontiers in Microbiology
Frontiers in Genetics
Infection Genetics and Evolution
International Journal of Microbiology
International Journal of Systemic and Evolutionary Microbiology
Genome Biology and Evolution
Journal of Veterinary Medicine and Animal Health
Journal of Theoretical Biology
Molecular Phylogenetics and Evolution
Msystems
Nucleic Acids Research

Oxford Database
PLoS Computational Biology
PLoS Neglected Tropical Diseases
PLoS One
Science of the Total Environment
Trends in Food Science & Technology

Special Topic Workshops

2023

- University of Virginia, Charlottesville, Virginia (April 2023)
- NIAID meeting Understanding Immune Evasion in Tickborne Diseases – online BV-BRC demo (May 2023)
- Argonne National Lab, Lemont, Illinois (June 2023)
- 25th Biennial Evergreen Phage Meeting, Olympia, Washington (August 2023)

2022 (11)

- Texas A&M University, College Station, Texas (March 2022).
- NIAID Tick-borne pathogens, Tick endosymbionts – online BV-BRC demo (March 2022)
- NIAID Tick-borne pathogens, Metagenomic analysis of tick samples – online BV-BRC demo (April 2022)
- NIAID Tick-borne pathogens, Comparative genomics of tick-transmitted bacteria– online BV-BRC demo (May 2022)
- American Society of Microbiology, Washington D.C. (June 2022)
- NIAID Tick-borne pathogens, RNA-Seq and SNP analysis of bacteria transmitted by ticks – online BV-BRC demo (June 2022)
- Argonne National Lab, Lemont, Illinois (July 2022)
- University of Virginia, Charlottesville, Virginia (August 2022)
- Brazilian Veterinary Students – BV-BRC demo (October 2022)
- Microbial Genomics Workshop – BV-BRC demo (online) for Ukrainian students (December 2022)
- Argonne National Lab, Lemont Illinois (December 2022)

2021 (1)

- 24th Biennial Evergreen Phage Meeting, Olympia, Washington (August 2021)

2020 (1)

- Bacterial Bioinformatics (Massive Open Online Course), Coursera (launched 01 October 2020)

2019 (8)

- DuPont, Madison, Wisconsin (August 2019)
- Bacteriophage Meeting, Evergreen State College, Olympia, Washington (August 2019)
- Seattle Children’s Hospital, Seattle, Washington. PATRIC Bioinformatics Resource Center Workshop” (June 2019)
- Argonne National Labs, Lemont, Illinois. “PATRIC Bioinformatics Resource Center Workshop” (April 2019)

- Odense University Hospital, Odense, Denmark. "PATRIC Bioinformatics Resource Center Workshop" (March 2019).
- Explora Biotech, Mestre, Italy "PATRIC Workshop 2019" (March 2019).
- University of Pittsburgh, Pittsburgh, Pennsylvania. "PATRIC Bioinformatics Resource Center Workshop" (February, 2019).
- Albert Einstein Medical College, New York, New York. "PATRIC Bioinformatics Resource Center Workshop" (January 2019).

2018 (11)

- National Cancer Institute, Fort Detrick, Maryland. "PATRIC Bioinformatics Resource Center Workshop" (December 2018)
- Argonne National Labs, Lemont, Illinois. "PATRIC Bioinformatics Resource Center Workshop" (October 2018)
- University of California-Los Angeles, Los Angeles, California. "PATRIC Bioinformatics Resource Center Workshop" (August 2018)
- Midwestern University, Glendale, Arizona. "PATRIC Bioinformatics Resource Center Workshop" (August 2018)
- American Type Culture Collection (ATCC), Manassas, Virginia. "PATRIC Bioinformatics Resource Center Workshop" (July 2018)
- Virginia Tech, Blacksburg, Virginia. "Analysis of sequencing data-Using PATRIC as part of the downstream analysis." Host: Stan Hefta. Taught as part of a summer course for honors students at Virginia Tech. (June 2018)
- ASM Microbe Meeting, Atlanta, Georgia. "Assemble, annotate and analyze your own genome using PATRIC, the all bacterial bioinformatics resource center." (June 2018)
- Argonne National Labs, Lemont, Illinois. "PATRIC Bioinformatics Resource Center Workshop" (May 2018)
- University of Chicago Center in Beijing, Beijing, China. "Machine Learning, Bioinformatics and Antimicrobial Resistance." (April 2018)
- Baylor College of Medicine, Houston, Texas. "PATRIC Bioinformatics Resource Center Workshop" (March 2018)
- University of California, San Diego, California. "PATRIC Bioinformatics Resource Center Workshop" (January 2018)

2017 (8)

- Argonne National Labs, Lemont, Illinois. "PATRIC Bioinformatics Resource Center Workshop" (Nov 2017)
- Translational Health Science and Technology Institute (THSTI), Delhi, India. "Indo-US Workshop on Genomics and Bioinformatics to Explore Human Microbial Ecology in Health and Disease" (Sept 2017) 25 participants
- Argonne National Labs, Lemont, Illinois. "PATRIC Bioinformatics Resource Center Workshop" (August 2017)
- University of Michigan, Ann Arbor, Michigan. "Assemble, annotate and analyze your own genome using PATRIC, the all bacterial bioinformatics resource center."
- Virginia Tech, Blacksburg, Virginia. "Isolation, sequencing and analysis of metagenomics data-Using PATRIC as part of the downstream analysis." Host: Stan Hefta. Taught as part of a summer course for honors students at Virginia Tech
- ASM Microbe Meeting, New Orleans, Louisiana. "Assemble, annotate and analyze your own genome using PATRIC, the all bacterial bioinformatics resource center."

- New York City, New York. Host: Joao Xavier at the Sloan Kettering Cancer center. "PATRIC Bioinformatics Resource Center Workshop"
- Chicago, Illinois, Host: Great Lakes Bioinformatics Consortium 2017. "PATRIC Bioinformatics Resource Center Workshop"

2016 (7)

- Bangkok, Thailand, Host: 2016 TWAS-ROESEAP Biotechnology Workshop of Food Technology.
- Gainesville, Florida, Host: Valerie de Crecy. "PATRIC Bioinformatics Resource Center Workshop"
- Sanford Burnham Presby Institute, San Diego, California. Host: Andrei Osterman. "PATRIC Bioinformatics Resource Center"
- Virginia Tech, Blacksburg, VA. Host: Fralin Institute. "2016 Biotechnology Educators Conference" Four individual workshops conducted over two days.
- Argonne National Labs, Lemont, Illinois. "PATRIC Bioinformatics Resource Center Workshop"
- ASM Microbe Meeting, Boston, Massachusetts. "Assemble, annotate and analyze your own genome using PATRIC, the all bacterial bioinformatics resource center."
- University of Nebraska Medical Center Workshop, Omaha, Nebraska. "PATRIC Bioinformatics Resource Center Workshop"

2015 (9)

- University of Chicago, Chicago, Illinois. "PATRIC for the Brucellosis Researcher"
- Mayo Clinic, Rochester, Minnesota. Host: Nicholas Chia. "PATRIC Bioinformatics Resource Center Workshop"
- Gainesville, Florida, Host: Valerie de Crecy. "PATRIC Bioinformatics Resource Center Workshop"
- Virginia Tech, Blacksburg, VA. Host: Fralin Institute. "2015 Biotechnology Educators Conference" Four individual workshops conducted over two days.
- Shanghai, China. Host: Shanghai Jiaotong University. "PATRIC Bioinformatics Resource Center Workshop"
- Shanghai, China. Host: Institute of Antibiotics, Fudan University. "PATRIC Bioinformatics Resource Center Workshop"
- Beijing, China. Host: Juan Li at National Institute for Communicable Disease Control and Prevention. "PATRIC Bioinformatics Resource Center Workshop"
- Lemont, IL. Host: Argonne National Labs. "PATRIC Bioinformatics Resource Center Workshop"
- Arlington, VA. Host: Virginia Tech. "PATRIC workshop of High School and Community College Educators."

2014 (7)

- Universidade Federal de Minas Gerais. Belo Horizonte, Brazil (ISCB-Latin America X-Meeting). "PATRIC Bioinformatics Resource Center Workshop"
- Virginia Tech, Blacksburg, VA. Host: NSF-VT REU:Microbiology (Microbiology in the Post-Genome Era). "PATRIC Bioinformatics Resource Center Workshop"
- University of Chicago, Chicago, IL. Host: Rick Stevens. "PATRIC Bioinformatics Resource Center Workshop"
- University of Montpellier, Montpellier, France. Host: David O'Callaghan. "PATRIC Bioinformatics Resource Center Workshop"

- Nestle Corporation, Lausanne, Switzerland. Hosts: Stéphane Duboux and Wilbert Sybesma. "PATRIC Bioinformatics Resource Center Workshop"
- Cornell Medical School, New York, NY. Host: Dirk Schnappinger. "PATRIC Bioinformatics Resource Center Workshop"
- Albert Einstein College of Medicine, Bronx, NY. Host: Bill Jacobs Jr. "PATRIC Bioinformatics Resource Center Workshop"

2013 (9)

- KwaZulu-Natal Research Institute for Tuberculosis and HIV (K-RITH), Durban, South Africa. Host: William Bishai. "Bioinformatics of Infectious Diseases: Comparative Genomics of M. tuberculosis"
- Centers for Disease Control, Atlanta, GA. Host: Alex Hoffmaster. "PATRIC Bioinformatics Resource Center Workshop"
- Colorado State University, Fort Collins, CO. Host: Patrick Brennan. "PATRIC Bioinformatics Resource Center Workshop"
- National Institute of Health, Bethesda, MD. Host: Karlynn Noble. "PATRIC Bioinformatics Resource Center Workshop"
- Johns Hopkins University, Baltimore, MD. Host: Gyanu Lamichhane. "PATRIC Bioinformatics Resource Center Workshop"
- Pacific Northwest National Laboratory, Richland, WA. Hosts: Charles Ansong and Josh Adkins. "PATRIC Bioinformatics Resource Center Workshop"
- Seattle BioMed, Seattle, WA. Hosts: David Sherman and Tige Rustad. "PATRIC Bioinformatics Resource Center Workshop"
- Virginia Tech, Blacksburg, VA. Host: Biswarup Mukhopadhyay. "Bioinformatics Workshop for Bacterial Data Analysis"
- Louisiana State University, Baton Rouge, LA. Host: National Hansen's Disease Programs and LSU School of Veterinary Medicine. "Bioinformatics Workshop for Bacterial Data Analysis"

2012 (4)

- Albert Einstein College of Medicine, Bronx, NY. Host: Bill Jacobs Jr. "PATRIC Bioinformatics Resource Center Workshop"
- Texas A&M University, College Station, Texas. Host: Jim Samuels. "PATRIC Bioinformatics Resource Center Workshop"
- Joint Workshop with Duke University and the University of North Carolina, Raleigh, NC. Hosts: David Tobin and Miriam Braunstein. "PATRIC Bioinformatics Resource Center Workshop"
- International 3-day Webinar with participants from India, South Africa, Moldova and US. Host: Antonino Catanzaro. "PATRIC Bioinformatics Resource Center Workshop"

2011 (4)

- INTA Castelar, Centro de Ciencias Veterinarias y Agronomicas, Buenos Aires, Argentina. Host: Luis Sanmartino "Analysis tools for *Brucella* and other Bacterial Pathogens"
- University of California, Davis, CA Host: Rene Tsolis. "PATRIC Website Overview and Navigation"
- Office of Cyber Infrastructure and Computational Biology, Bethesda, MD. Host: NIAID. "PATRIC Website Overview and Navigation"
- Virginia Tech, Blacksburg, VA. Host: Virginia Tech's Genetics, Bioinformatics and Computational Biology Program. "PATRIC Bioinformatics Resource Center Workshop"

Review Committee

- Department of Energy Office of Science - SFA projects for KBase Applications (July 2021)

FUNDING

Current

- Project Title: Bacterial and viral bioinformatics resource center (BV-BRC)
PI: Ron Kenyon
Co-PI: Rebecca Wattam
Source of Support: National Institutes of Health – National Institute of Allergy and Infectious diseases (NIH-NIAID)
Total Award Period Covered: 9/15/2019-9/14/2024
- Project Title: iSENTRY: An integrated microfluidics-enabled system for phenotypic detection of biothreat agents
PI: Rebecca Wattam
Source of Support: Defense Advanced Research Projects Agency (DARPA)
Total Amount Awarded: \$629,946
Total Award Period Covered: : 12/01/2018 – 06/30/2023
Effort: 2.4 months cy (20%)

Prior

- Project Title: Bacterial and viral bioinformatics resource center (BV-BRC)
PI: Ron Kenyon
Co-PI: Rebecca Wattam
Source of Support: National Institutes of Health – National Institute of Allergy and Infectious diseases (NIH-NIAID)
Total Award Period Covered: 9/15/2019-9/14/2024
- Project Title: Integrative Genomics Approach to Computational Assessment of Threats (IGACAT)
PI: Stephen Eubank
Source of Support: Intelligence Advanced Research Projects Activity (IARPA)
Total Amount Awarded: \$10,278,788 (Rebecca Wattam Portion: \$6,262,344)
Total Award Period Covered: 4/1/2017-9/30/2020
Effort: 0.6 months cy (5%)

Effort: 9 months cy (75%)
- Project Title: Synthetic Information Systems for Better Informing Public Health Policymakers - Supplement 1
PI: Stephen Eubank
Source of Support: National Institutes of Health - National Institute of General Medical Sciences (NIH-NIGMS)
Total Amount Awarded: \$95,128 (Rebecca Wattam Portion: \$4,696)
Total Award Period Covered: 10/1/2016-8/31/2018
Effort: 0.45 months cy
- Project Title: Pathosystems Resource Integration Center - BRC for Bacterial Diseases PATRIC 3
PI: Ron Kenyon

Source of Support: University of Chicago (National Institutes of Health - National Institute of Allergy and Infectious Diseases (NIH-NIAID))

Total Amount Awarded: \$9,234,930 (Rebecca Wattam Portion: \$8,734,352)

Total Award Period Covered: 9/15/2014-9/14/2019

- Project Title: Genomic and Proteomic Architecture of Atherosclerosis.
PI: Herrington
Co-PI: AR Wattam. 10% credit

ACADEMIC SUPERVISION

PhD Students Advised or Co-advised

- Daniel E. Sullivan, PhD, GBCB Program, Virginia Tech, Blacksburg, VA. Supervised May 2013 to May 2016.
- Marcus Vinicius Canário Viana, PhD candidate, Laboratório de Genética Celular e Molecular, Universidade Federal de Minas Gerais, Belo Horizonte, Minas Gerais, Brazil. Supervised September 2015 until present.
- Alberto Fernandes de Oliveira Junior, PhD, Laboratório de Genética Celular e Molecular, Universidade Federal de Minas Gerais, Belo Horizonte, Minas Gerais, Brazil. Supervised September 2015 until May 2017.

MS & PhD Students – Committee Member

- Eric K. Nordberg, PhD, GBCB Program, Virginia Tech, Blacksburg, VA. Supervised Sept 20, 2013 to Nov 11, 2015
- Hyseung Yoo, PhD candidate, Industrial and Systems Engineering, Virginia Tech, Blacksburg VA. Supervised Sept 2013 to October 2015
- Marcus Viana, PhD candidate, Universidade Federal de Minas Gerais, Minas Gerais, Brazil. Supervised September 2015 to present
- Alberto de Olivera, PhD candidate, Universidade Federal de Minas Gerais, Minas Gerais, Brazil. Supervised September 2015 to May 2017
- Ingrid Wei Yun Hsu, MPH, Virginia Tech, Blacksburg VA. Supervised May 2016 to August 2017