

# Adam R. Rivers, PhD

United States Department of Agriculture  
Agricultural Research Service  
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## EDUCATION

- Ph.D. Biological Oceanography, Massachusetts Institute of Technology / Woods Hole Oceanographic Institution. 2009
- B.A. Biology/Chemistry, New College of Florida, 2001

## PROFESSIONAL APPOINTMENTS

- 2023– United States Department of Agriculture, Agricultural Research Service  
Acting Research Leader, Geospatial and Environmental Epidemiology Research Unit
- Started the new research unit and developed a budget and cooperative agreements with Mississippi State University
  - Initiated a computational internship program with Mississippi State University
  - Oversee agreement for the operation of the Cray CS500 High Performance Computer, Atlas
  - Led a scoping workshop for the unit's 5-year plan
- 2017– United States Department of Agriculture, Agricultural Research Service  
Biologist, Computational Bioinformatics, Genomics and Bioinformatics Research Unit  
Courtesy Faculty, University of Florida, Dept. of Microbiology and Cell Science  
Member, University of Florida, Emerging Pathogens Institute
- Led the Scientific Advisory Committee for SCINet, the USDA's scientific computing Initiative for 4 years and served on the Executive Committee for Scinet, making operational decisions
  - Established ARS Artificial Intelligence Center of Excellence
  - Conduct research in a wide range of microbiome fields
  - Conduct research in volatile organic compound chemometrics
  - Develop computer-vision-based systems for animal disease prediction and allergy diagnostics
  - Plan in-person training workshops in artificial intelligence and microbiome science
- 2016–17 US Department of Energy, Joint Genome Institute  
Metagenome Program Head

Research Scientist, Environmental Genomics and Systems Biology, Lawrence Berkeley National Laboratory

- Led one of 5 science programs at the Joint Genome Institute (JGI) sequencing 25 terabases a year of microbial and plant-microbe metagenome and multi-omic data
- Initiated all new metagenomics research brought to JGI by users (scientists applying to sequencing grant programs) as well as reviewed research plans, proposals, and publications for computational and statistical design
- Developed and implemented new bioinformatic and computational methods in genomics including a machine learning-based taxonomic classifier
- Developed data processing pipelines that used both high-performance computing environments and cloud-based big-data environments like Apache Spark on Mesos or Yarn/Hadoop. For example, iTagger, a pipeline and database system for processing 10,000 amplicon samples per year)

2014–16 US Department of Energy, Joint Genome Institute  
Research Scientist

- Developed new statistical methods for genomics using multinomial logistic regression, Bayesian network inference, and generalized linear models
- Train user scientists in genomics, teach at the biannual “Microbial Genomics and Metagenomics” workshop, and developed a community workshop on bioinformatics for microbial ecosystem engineering

2009–14 University of Georgia  
Postdoctoral Research Associate, Department of Marine Science

- Led research developing metatranscriptomics methods to determine role of microbes in degrading subsurface oil and gas from the Deepwater Horizon oil spill
- Published articles on genomics methods and modeling of nutrient use and photosynthesis
- Published a reannotated genome of model microbe *Ruegeria pomeroyi*
- Developed and applied computational methods for genome-wide small RNA studies

## RESEARCH AREAS

Microbial ecology and Microbiome science in plants, animals, fungi, aquatic, and soil systems

Applied machine learning: genomic, metagenomic, and chemometric data

Bioinformatics software development and high-performance computing

## ARTICLES IN PEER-REVIEWED JOURNALS AND PREPRINTS

- Foxx, A. J., Einarsson, S. V., Franco Meléndez, K. P., and Rivers, A. R. (2025). Exploring the influence of seed bacteria and fungi on seed germination and seedling traits in brachypodium congeners. *Symbiosis*, pages 1–14
- Foxx, A. J. and Rivers, A. R. (2025). A cautionary tale of batch corrections on confounded microbiome community profiles. *iMetaOmics*, page e70025
- Swientoniewski, L. T., Rambo, I. M., Nesbit, J. B., Cheng, H., Gipson, S. A., Jones, S. M., Doan, D. T., Dreskin, S. C., Mustafa, S. S., Smith, S. A., et al. (2025). Linear and conformational epitopes of vicilin-buried peptides as a model for improved nut allergy diagnostics. *Frontiers in Allergy*, 6:1648262
- Gorman, Z., Liu, H., Sorg, A., Grissett, K. S., Yactayo-Chang, J. P., Li, Q.-B., Rivers, A. R., Basset, G. J., Rering, C. C., Beck, J. J., et al. (2025). Flood-induced insect resistance in maize involves flavonoid-dependent salicylic acid induction. *Plant, Cell & Environment*
- Einarsson, S. V. and Rivers, A. R. (2024). Itsxpress version 2: software to rapidly trim internal transcribed spacer sequences with quality scores for amplicon sequencing. *Microbiology Spectrum*, 12(12):e00601–24
- Page, C. A., Simpson, S., D’Souza, C. B., Pérez-Díaz, I. M., and Rivers, A. R. (2024a). Whole-genome sequences of fermentative and spoilage-associated lactic acid bacteria, *Lysinibacillus capsici* and a *Serratia marcescens* isolated from commercial cucumber fermentations. *Microbiology Resource Announcements*, 13(12):e00910–24
- Franco Meléndez, K., Schuster, L., Donahey, M. C., Kairalla, E., Jansen, M. A., Reisch, C., and Rivers, A. R. (2024). MicroMPN: methods and software for high-throughput screening of microbe suppression in mixed populations. *Microbiology Spectrum*, pages e03578–23
- Page, C. A., Simpson, S., Pérez-Díaz, I. M., and Rivers, A. R. (2024b). Annotated whole-genome sequences of fermentative and spoilage associated *Bacilli* and proteobacteria autochthonous to commercial cucumber fermentation. *Microbiology Resource Announcements*, pages e00926–23
- Ray, C. L., Abernathy, J. W., Green, B. W., Rivers, A. R., Schrader, K. K., Rawles, S. D., McEntire, M. E., Lange, M. D., and Webster, C. D. (2024). Effect of dietary phytase on water and fecal prokaryotic and eukaryotic microbiomes in a hybrid tilapia (*Oreochromis aureus* x *O. niloticus*) mixotrophic biofloc production system. *Aquaculture*, 581:740433
- Rambo, I., Rivers, A., McBride, J., Swientoniewski, L., Cheng, H., Simon, R., Ryan, R., Nesbit, J., Hurlburt, B., and Maleki, S. (2023). Changes in ige and igg4 epitopes of peanut allergens following peanut oral immunotherapy. *Journal of Allergy and Clinical Immunology*, 151(2):AB33
- Rambo, Ian M., Kronfel, Christina M., Rivers, Adam R., Swientoniewski, Lauren T., McBride, Jane K., Cheng, Hsiaopo, Simon, Reyna J., Ryan, Robert, Tilles, Stephen A., Nesbit, Jacqueline, Kulis, Micheal D., Hurlburt, Barry K., and Maleki, Soheila J. (2023). IgE and IgG4 epitopes of the peanut allergens shift following oral immunotherapy. *Frontiers in Allergy*, 4
- Valles, S. M., Zhao, C., Rivers, A. R., Iwata, R. L., Oi, D. H., Cha, D. H., Collignon, R. M., Cox, N. A., Morton, G. J., and Calcaterra, L. A. (2023). RNA virus discoveries in the electric ant, *Wasmannia auropunctata*. *Virus Genes*, pages 1–14

- Mejia, C., Trujillo Rodriguez, L., Poudel, R., Ellington, A., Rivers, A. R., and Reisch, C. (2022). An arrayed transposon library of *Ruegeria pomeroyi* DSS-3. *bioRxiv*, pages 2022–09
- Vaughn, J. N., Branham, S. E., Abernathy, B., Hulse-Kemp, A. M., Rivers, A. R., Levi, A., and Wechter, W. P. (2022). Graph-based pangenomics maximizes genotyping density and reveals structural impacts on fungal resistance in melon. *Nature Communications*, 13(1):7897
- Poudel, R., Rodriguez, L. T., Reisch, C. R., and Rivers, A. R. (2022). Guidemaker: Software to design crispr-cas guide RNA pools in non-model genomes. *GigaScience*, 11
- Coatsworth, H., Bozic, J., Carrillo, J., Buckner, E. A., Rivers, A. R., Dinglasan, R. R., and Mathias, D. K. (2022). Intrinsic variation in the vertically transmitted core virome of the mosquito *Aedes aegypti*. *Molecular Ecology*, 31(9):2545–2561
- Rivers, A. R., Grodowitz, M. J., Miles, G. P., Allen, M. L., Elliott, B., Weaver, M., Bon, M.-C., Rojas, M. G., and Morales-Ramos, J. (2022). Gross morphology of diseased tissues in *Nezara viridula* (hemiptera: Pentatomidae) and molecular characterization of an associated Microsporidian. *Journal of Insect Science*, 22(2):4
- Foxx, A. J., Franco Meléndez, K. P., Hariharan, J., Kozik, A. J., Wattenburger, C. J., Godoy-Vitorino, F., and Rivers, A. R. (2021). Advancing equity and inclusion in microbiome research and training. *Msystems*, 6(5):e01151–21
- Guard, J., Rivers, A. R., Vaughn, J. N., Rothrock, M. J., Oladeinde, A. H., and Shah, D. H. (2021). At homopolymer strings in *Salmonella enterica* subspecies i contribute to speciation and serovar diversity. *Microorganisms*, 9(10):2075
- Fernandez-baca, C. P., Rivers, A. R., Maul, J. E., Kim, W., Poudel, R., McClung, A. M., Roberts, D. P., Reddy, V. R., and Barnaby, J. Y. (2021). Rice plant-soil microbiome interactions driven by root and shoot biomass. *Diversity*, 13(3):125
- Fernandez-Baca, C. P., Rivers, A. R., Kim, W., Iwata, R., McClung, A. M., Roberts, D. P., Reddy, V. R., and Barnaby, J. Y. (2021). Changes in rhizosphere soil microbial communities across plant developmental stages of high and low methane emitting rice genotypes. *Soil Biology and Biochemistry*, 156:108233
- Peters, D. P. C., Rivers, A., Hatfield, J. L., Lemay, D. G., Liu, S., and Basso, B. (2020). Harnessing AI to Transform Agriculture and Inform Agricultural Research. *IT Professional*, 22(3):16–21
- Sudduth, K. A., Woodward-Greene, M. J., Penning, B. W., Locke, M. A., Rivers, A. R., and Veum, K. S. (2020). AI Down on the Farm. *IT Professional*, 22(3):22–26
- Boyles, S. M., Mavian, C. N., Finol, E., Ukhanova, M., Stephenson, C. J., Hamerlinck, G., Kang, S., Baumgartner, C., Geesey, M., Stinton, I., Williams, K., Mathias, D. K., Prosperi, M., Mai, V., Salemi, M., Buckner, E. A., Lednicky, J. A., Rivers, A. R., and Dinglasan, R. R. (2020). Under-the-Radar Dengue Virus Infections in Natural Populations of *Aedes aegypti* Mosquitoes. *mSphere*, 5(2)
- Bolyen, E., Rideout, J. R., Dillon, M. R., Bokulich, N. A., Abnet, C. C., Al-Ghalith, G. A., Alexander, H., Alm, E. J., Arumugam, M., Asnicar, F., Bai, Y., Bisanz, J. E., Bittinger, K., Brejnrod, A., Brislawn, C. J., Brown, C. T., Callahan, B. J., Caraballo-Rodríguez, A. M., Chase, J., Cope, E. K., Da Silva, R., Diener, C., Dorrestein, P. C., Douglas, G. M., Durall, D. M., Duvallet, C., Edwardson, C. F., Ernst,

- M., Estaki, M., Fouquier, J., Gauglitz, J. M., Gibbons, S. M., Gibson, D. L., Gonzalez, A., Gorlick, K., Guo, J., Hillmann, B., Holmes, S., Holste, H., Huttenhower, C., Huttley, G. A., Janssen, S., Jarmusch, A. K., Jiang, L., Kaehler, B. D., Kang, K. B., Keefe, C. R., Keim, P., Kelley, S. T., Knights, D., Koester, I., Kosciulek, T., Kreps, J., Langille, M. G. I., Lee, J., Ley, R., Liu, Y.-X., Loftfield, E., Lozupone, C., Maher, M., Marotz, C., Martin, B. D., McDonald, D., McIver, L. J., Melnik, A. V., Metcalf, J. L., Morgan, S. C., Morton, J. T., Naimey, A. T., Navas-Molina, J. A., Nothias, L. F., Orchanian, S. B., Pearson, T., Peoples, S. L., Petras, D., Preuss, M. L., Priesse, E., Rasmussen, L. B., Rivers, A., Robeson, M. S., Rosenthal, P., Segata, N., Shaffer, M., Shiffer, A., Sinha, R., Song, S. J., Spear, J. R., Swafford, A. D., Thompson, L. R., Torres, P. J., Trinh, P., Tripathi, A., Turnbaugh, P. J., Ul-Hasan, S., van der Hooft, J. J. J., Vargas, F., Vázquez-Baeza, Y., Vogtmann, E., von Hippel, M., Walters, W., Wan, Y., Wang, M., Warren, J., Weber, K. C., Williamson, C. H. D., Willis, A. D., Xu, Z. Z., Zaneveld, J. R., Zhang, Y., Zhu, Q., Knight, R., and Caporaso, J. G. (2019). Reproducible, interactive, scalable and extensible microbiome data science using QIIME 2. *Nature Biotechnology*, 37(8):852–857
- Smith, M. W., Herfort, L., Rivers, A. R., and Simon, H. M. (2019). Genomic signatures for sedimentary microbial utilization of phytoplankton detritus in a fast-flowing estuary. *Frontiers in Microbiology*, 10:2475
- Valles, S. M. and Rivers, A. R. (2019). Nine new RNA viruses associated with the fire ant *Solenopsis invicta* from its native range. *Virus Genes*, 55(3):368–380
- Rivers, A. R., Weber, K. C., Gardner, T. G., Liu, S., and Armstrong, S. D. (2018). ITSxpress: Software to rapidly trim internally transcribed spacer sequences with quality scores for marker gene analysis. *F1000Research*, 7:1418
- Bowers, R. M., Kyrpides, N. C., Stepanauskas, R., Harmon-Smith, M., Doud, D., Reddy, T. B. K., Schulz, F., Jarett, J., Rivers, A. R., Elie-Fadrosh, E. A., Tringe, S. G., Ivanova, N. N., Copeland, A., Clum, A., Becraft, E. D., Malmstrom, R. R., Birren, B., Podar, M., Bork, P., Weinstock, G. M., Garrity, G. M., Dodsworth, J. a., Yooseph, S., Sutton, G., Glöckner, F. O., Gilbert, J. A., Nelson, W. C., Hallam, S. J., Jungbluth, S. P., Ettema, T. J. G., Tighe, S., Konstantinidis, K. T., Liu, W.-T., Baker, B. J., Rattei, T., Eisen, J. A., Hedlund, B. P., McMahon, K. D., Fierer, N., Knight, R., Finn, R. D., Cochrane, G., Karsch-Mizrachi, I., Tyson, G. W., Rinke, C., Kyrpides, N. C., Schriml, L., Garrity, G. M., Hugenholtz, P., Sutton, G., Yilmaz, P., Meyer, F., Glöckner, F. O., Gilbert, J. A., Knight, R., Finn, R. D., Cochrane, G., Karsch-Mizrachi, I., Lapidus, A., Meyer, F., Yilmaz, P., Parks, D. H., Eren, A. M., Schriml, L., Banfield, J. F., Hugenholtz, P., Woyke, T., Doud, D., Reddy, T. B. K., Jarett, J., Rivers, A. R., Elie-Fadrosh, E. A., Tringe, S. G., Ivanova, N. N., Copeland, A., Clum, A., Becraft, E. D., Malmstrom, R. R., Birren, B., Schriml, L., Podar, M., Bork, P., Weinstock, G. M., Banfield, J. F., Garrity, G. M., Hugenholtz, P., Parks, D. H., Tyson, G. W., Rinke, C., Dodsworth, J. a., Yooseph, S., Sutton, G., Yilmaz, P., Glockner, F. O., Meyer, F., Gilbert, J. A., Nelson, W. C., Hallam, S. J., Jungbluth, S. P., Ettema, T. J. G., Tighe, S., Konstantinidis, K. T., Liu, W.-T., Baker, B. J., Rattei, T., Eisen, J. A., Hedlund, B. P., McMahon, K. D., Fierer, N., Knight, R., Finn, R. D., Karsch-Mizrachi, I., Eren, A. M., and Woyke, T. (2017). Minimum information about a single amplified genome (MISAG) and a metagenome-assembled genome (MIMAG) of bacteria and archaea. *Nature Biotechnology*, in press(8):725–731
- Lamit, L. J., Romanowicz, K. J., Potvin, L. R., Rivers, A. R., Singh, K., Lennon, J. T., Tringe, S. G., Kane, E. S., and Lilleskov, E. A. (2017). Patterns and drivers of fungal community depth stratification in

Sphagnum peat. *FEMS microbiology ecology*, 93(7)

- Paez-Espino, D., Chen, I. M. A., Palaniappan, K., Ratner, A., Chu, K., Szeto, E., Pillay, M., Huang, J., Markowitz, V. M., Nielsen, T., Huntemann, M., Reddy, T. B., Pavlopoulos, G. A., Sullivan, M. B., Campbell, B. J., Chen, F., McMahon, K., Hallam, S. J., Denef, V., Cavicchioli, R., Caffrey, S. M., Streit, W. R., Webster, J., Handley, K. M., Salekdeh, G. H., Tsesmetzis, N., Setubal, J. C., Pope, P. B., Liu, W. T., Rivers, A. R., Ivanova, N. N., and Kyrpides, N. C. (2017). IMG/VR: A database of cultured and uncultured DNA viruses and retroviruses. *Nucleic Acids Research*, 45(D1):D457–D465
- Rivers, A. R., Burns, A. S., Chan, L.-K., and Moran, M. A. (2016). Experimental Identification of Small Non-Coding RNAs in the Model Marine Bacterium *Ruegeria pomeroyi* DSS-3. *Frontiers in Microbiology*, 7
- Beier, S., Rivers, A. R., Moran, M. A., and Obernosterer, I. (2015b). The transcriptional response of prokaryotes to phytoplankton-derived dissolved organic matter in seawater. *Environmental Microbiology*, 17(10):3466–3480
- Beier, S., Rivers, A. R., Moran, M. A., and Obernosterer, I. (2015a). Phenotypic plasticity in heterotrophic marine microbial communities in continuous cultures. *The ISME journal*, 9(5):1141–51
- Kemp, D. W., Rivers, A. R., Kemp, K. M., Lipp, E. K., Porter, J. W., and Wares, J. P. (2015). Spatial Homogeneity of Bacterial Communities Associated with the Surface Mucus Layer of the Reef-Building Coral *Acropora palmata*. *PloS one*, 10(12):e0143790
- Rivers, A. R., Smith, C. B., and Moran, M. A. (2014). An Updated genome annotation for the model marine bacterium *Ruegeria pomeroyi* DSS-3. *Standards in genomic sciences*, 9(1):11
- Moran, M. A., Satinsky, B., Gifford, S. M., Luo, H., Rivers, A., Chan, L.-K., Meng, J., Durham, B. P., Shen, C., Varaljay, V. A., Smith, C. B., Yager, P. L., and Hopkinson, B. M. (2013). Sizing up metatranscriptomics. *The ISME journal*, 7(2):237–43
- Rivers, A. R., Rose, A. L., and Webb, E. A. (2013a). An online calculator for marine phytoplankton iron culturing experiments. *Journal of Phycology*, 49(5):1017–1021
- Rivers, A. R., Sharma, S., Tringe, S. G., Martin, J., Joye, S. B., and Moran, M. A. (2013b). Transcriptional response of bathypelagic marine bacterioplankton to the Deepwater Horizon oil spill. *The ISME journal*, 19(1):1–15
- Rivers, A. R., Jakuba, R. W., and Webb, E. A. (2009). Iron stress genes in marine *Synechococcus* and the development of a flow cytometric iron stress assay. *Environmental Microbiology*, 11(2):382–396
- Teske, A., Edgcomb, V., Rivers, A. R., Thompson, J. R., de Alvin, V. G., Molyneaux, S. J., Wirsén, C. O., de Vera Gomez, A., Molyneaux, S. J., and Wirsén, C. O. (2009). A molecular and physiological survey of a diverse collection of hydrothermal vent *Thermococcus* and *Pyrococcus* isolates. *Extremophiles : life under extreme conditions*, 13(6):905–15
- Mcintyre, P. B., Michel, E., France, K., Rivers, A., Hakizimana, P., and Cohen, A. S. (2005). Individual- and Assemblage-Level Effects of Anthropogenic Sedimentation on Snails in Lake Tanganyika. *Conservation Biology*, 19(1):171

## GRANTS AND AWARDS

### Awards and Honors

- 2012 Innocentive challenge winner: Heat Stable Prevention of Flavan3-ol -iron (II) complexes (\$25,000).

### Grants and Fellowships

- 2023 The detection of bovine mastitis by thermography and machine learning (\$140,000). ARS Administrator Funded Postdoctoral Research Associate Program. PI
- 2022 Biologically-inspired detection of odors guided by machine learning. ARS Geospatial and Environmental Epidemiology panel. Co-PI with Auburn University.
- 2022 Xenosurveillance of flies in wet markets to monitor for the emergence and spillover potential of viral, bacterial, and parasitic pathogens. (\$431,085). ARS Geospatial and Environmental Epidemiology panel. Co-PI.
- 2022 Developing tools for the real-time monitoring and query of all the world's publicly available sequence data (\$270,000 to ORISE). USDA-ARS SCINet Fellowship program. PI.
- 2021 The Real-time Pen-side Detection of Bovine Respiratory Disease by Chemical Analysis (\$127,000). Foundation for Food and Agriculture Research. ICASATWG-0000000032. PI.
- 2021 Applying artificial intelligence to reduce antimicrobial use in livestock (\$85,000) University of Florida Research Foundation. UF-ROSF2021. Co-PI.
- 2019 Salmonella typing and phenotypic prediction from genomes and metagenomes using population genomics and machine learning (\$455,993). National Institute of Food and Agriculture AFRI, Food and Agriculture Cyberinformatics and Tools Initiative. NIFA 2019-67021-29924. PI.
- 2019 Sex determination of eggs by high-speed volatile compound mass spectrometry and machine learning (\$396,763). Foundation for Food and Agriculture Research, Eggtech Prize. EggTech-0000000017. PI.
- 2019 Developing probabilistic graphical models and analysis software to integrate multi-omics data (User facility exometabolite analysis). DOE Joint Genome Institute New Investigator Grant. JGI 505422. PI.
- 2019 Tools to rationally engineer microbial consortia for beneficial outcomes in crops. (\$140,000). ARS Administrator Funded Postdoctoral Research Associate Program. PI
- 2018 Applied Agricultural Genomics and Bioinformatics Research (\$3,334,520 ). ARS In-house appropriated research ARS 6066-21310-005-00D . Co-PI.
- 2018 Ecology and biogeochemical impacts of DNA and RNA viruses throughout the global oceans ( \$1,052,917) National Science Foundation NSF-1829831. Collaborator.
- 2017 Microbiomes from pre-antibiotic era poultry. A grant supplement to the CRIS titled: Characterizing Antimicrobial Resistance in Poultry Production Environments ( \$107,000) ARS 6040-32000-010-00D. Collaborator.

## INTELLECTUAL PROPERTY

- 2024 Rivers, A.R. A system and method for determining the sex and viability of poultry eggs prior to hatching. ]  
US Patent 12,085,549. Issued September 10, 2024.
- 2014 Licensed a tangible biological (a biotinylated small RNA ladder) to Kerafast

## INVITED TALKS

- 2024 “Engineering Microbial Consortia”. American Society for Microbiology Microbe, Atlanta, GA June 14.
- 2023 “Novel Phenotyping with Machine Learning and High-speed, Volatile Organic Compound Profiling” USDA-ARS Grape Industry Workshop. Beltsville, MD November 7
- 2023 “Ecological controls of methane emission in rice”. Tsukuba Conference for Future Shapers. Tsukuba, Japan. September 25.
- 2023 “Methane inhibitors for genetic engineering of rice”. Inception Workshop on Reducing Methane Emissions in Rice. International Rice Research Institute. Los Baños, Philippines. July 10.
- 2022 “Determining the sex of chicken eggs by machine learning and high-speed volatiles mass spectrometer”. American Chemical Society, Spring meeting, San Diego, CA. March 20.
- 2020 “USDA’s efforts to advance AI Applications in Agriculture” IBM Research Almaden Forum Talk. San Jose, CA, March 3.
- 2019 “AI, ML, Oh My: An overview of methods and software” AI and Machine Learning SCINet Conference: Current Uses and Potential to Solve Complex Problems in Agriculture, Beltsville, MD, September 20.
- 2019 “Deep Learning for Agriculture” AI and Machine Learning SCINet Conference: Current Uses and Potential to Solve Complex Problems in Agriculture, Beltsville, MD, September 20.
- 2019 “Microbiome data are compositional: What this means and how to deal with it” International Workshop on the Fruit Microbiome, Leesburg, VA, September 12.
- 2014 “The ecological response of microbes to Deepwater Horizon.” Skidaway Institute of Oceanography.
- 2013 “The ecological response of bathypelagic microbes to Deepwater Horizon.” New College of Florida.
- 2011 “Harvesting Our Future: Environmental Challenges for our Fisheries. New College of Florida.” Invited Panel Discussion.



## CONFERENCE ACTIVITY

### Conference Presentations

- 2022 Rivers, A.R. Determining the sex of chicken eggs by machine learning and high-speed volatiles mass spectrometry. American Chemical Society Spring 2022 Conference. San Diego, CA.
- 2019 Rivers, A.R. ITSxpress: software to trim internally transcribed spacers with quality scores for sequence variant analysis. Third Workshop on Statistical and Algorithmic Challenges in Microbiome Data Analysis at The Simons Foundation , New York, NY April 1.
- 2018 Rivers, A.R. Vica: Software to classify highly divergent viruses. ISME Congress. Leizig Germany.
- 2015 Rivers, A.R. , Tringe, S.G. Discovering viruses in metagenomes and metatranscriptomes. NSF HAB response workshop. Bowling Green, OH.
- 2015 Beier, S., Rivers, A.R., Moran, M.A., Obernosterer, I. The transcriptional response of prokaryotes to the addition of phytoplankton-derived DOM in seawater. Marine Microbes Gordon Research Conference.
- 2015 Rivers, A.R., Sharma, S., Lindquist, E., Tringe, S., Joye, S.B., Moran, M.A. Transcriptional responses of deep water Bacteria and Archaea to hydrocarbon contamination from the Deepwater Horizon spill. ASLO Ocean Sciences.
- 2010 Rivers, A.R., Sharma, S., Chan, L., Moran, M.A. Methods for identifying small non-coding RNAs and quantitatively measuring small RNA abundance by pyrosequencing. International Society for Microbial Ecology Meeting.
- 2010 Newton, R.J., Chan, L.K., Rivers, A.R., Sharma, S., Moran, M.A. Gene expression profiles for a marine roseobacter grown with different phosphorus sources. International Society for Microbial Ecology Meeting.
- 2009 Rivers, A.R. From Genes to ecosystems: understanding how the ocean's most abundant photosynthetic organisms use iron. University of Alabama, Birmingham, School of Public Health.
- 2009 Rivers, A.R. and Webb, E.A. 2007. Light induced DFB toxicity: decoupling the normal iron stress response. Center for Environmental Bioinorganic Chemistry Symposium, Princeton University.
- 2005 Rivers, A.R., Trowbridge, N. and Webb, E.A. 2005. The location of IdiA in marine Synechococcus and development of a whole cell labeling and flow cytometry assay for detection of iron stress. ASLO Ocean Sciences.

## TEACHING EXPERIENCE

### USDA Agricultural Research Service

USDA/University of Florida machine learning workshop, Gainesville, Florida

USDA microbiome training workshop, Beltsville, Maryland

**University of Georgia**

Field Studies in oceanography and marine methods, Mo'orea, French Polynesia

**New College of Florida**

Microbes in hosts and the Environment, Sarasota, FL

**Massachusetts Institute of Technology**

Graduate Resident Tutor

**SERVICE****Journal Peer Review**

*Frontiers in Microbiology*

*Bioinformatics*

*mSystems*

*Microorganisms*

*F1000 Research*

*Environmental Microbiology*

*BMC Genomics*

*Phytobiomes*

*Nature Scientific Data*

**Funding Agency Peer Review**

USDA National Institute of Food and Agriculture

Genomes British Columbia

US Department of Energy Joint Genome Institute

**Service to Field**

Chair, SCINet Advisory Committee (USDA scientific computing initiative)

Member, SCINet Executive Committee (USDA scientific computing initiative)

Organizer, USDA Artificial Intelligence Center of Excellence

Editorial Advisory Board, ACS Agricultural Science and Technology

**PROFESSIONAL AFFILIATIONS**

American Society for Microbiology

## PROFESSIONAL EXPERIENCE

- 2008–09 Massachusetts Institute of Technology  
Intern, Technology Licensing Office
- 2001–03 BESTechnologies, Inc, Sarasota, FL  
Microbiologist

## SELECTED MEDIA COVERAGE

- 2016 *Inventology* by Pagan Kennedy. Featured in a book about open innovation.
- 2010 *Good Morning America*. “Deepwater Horizon Oil Spill” May 27.
- 2010 *New York Times*. “A Proliferation of Plumes? (Deepwater Horizon Oil Spill)” June 2.

## TECHNICAL SKILLS

### Statistical and Computational Methods

Python package development and deployment. Machine learning (Scikit-learn, Tensorflow, Keras), Statistical modeling (R and Python Statsmodels). Probabilistic graphical models (Bayesian networks). Web application development, (Backends: MongoDB, PostgreSQL, MySQL, Frameworks: Eve, Flask, VueJS, React components, Visualization: Plotly, Dash, Streamlit, Leaflet, Static template rendering: Jekyll.)

### Bioinformatics

Development and operation of complex workflows for production-scale sequencing with workflow managers like Nextflow and Cromwell. Deployment of workflow managers for metagenomic assembly, metatranscriptomics and statistical analysis. Application of compositional data methods. I developed and maintained the QIIME 2 plugin ITSxpress.

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