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Agricultural Research Service
Genomics and Bioinformatics Research Unit
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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

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
Affiliate Scientist, Lawrence Berkeley National Laboratory

2016–17 US Department of Energy, Joint Genome Institute
Metagenome Program Head
Research Scientist, Environmental Genomics and Systems Biology, Lawrence Berkeley
National Laboratory

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

2019–14 University of Georgia
Postdoctoral Research Associate, Department of Marine Science

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

PUBLICATIONS

Articles in Peer-Reviewed Journals

- 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 Hoof, 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., Tsismetzis, 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

- 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

- 2019 Provisional US Patent Application 62/947,681 A system and method for determining the sex and viability of poultry eggs prior to hatching
- 2014 Licensed a tangible biological (a biotinylated small RNA ladder) to Kerafast

INVITED TALKS

- 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

- 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

F1000 Research

Environmental Microbiology

BMC Genomics

Phytobiomes

Nature Scientific Data

Funding Agency Peer Review

USDA National Institute of Food and Agriculture

Genome 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)

PROFESSIONAL AFFILIATIONS

International Society for Microbial Ecology

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, Spark MLlib), Statistical modeling (R and Python Statsmodels). Probabilistic graphical models (Bayesian networks). Web application development, (Backends: MongoDB, PostgreSQL, MySQL, Frameworks: Eve, Flask, VueJS, Visualization: Datatables, Plotly, Dash, Leaflet, Static template rendering: Jekyll.)

Bioinformatics

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

Updated May 2020