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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 Dates 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

SELECTED MACHINE LEARNING APPLICATIONS

1. Vica: A workflow for identifying highly divergent viruses in metagenomes. Training Data:
   Refseq 2TB of string data. Preprocessing: balanced tree sampling, and multiple feature
   extraction (short kmers, codon usage, protein domains, minhash signatures) converted to
   TFrecords. Model: Tensorflow DNN linear classifier 2 layer, regularized with dropout and batch

normalized. Personally wrote code. Project transferred to graduate student to improve by controlling for prior probability shift `https://github.com/USDA-ARS-GBRU/vica`.

2. Salmonella genotyping and phenotype prediction from partially missing metagenomic data. Training data 200,000, 4MB Salmonella genomes. Preprocessing: selection of core Single nucleotide polymorphisms in core genome and approximate nearest neighbor search by Hierarchical Navigable Small World Graph. Personally wrote code. Funded to develop: A disentangled variational autoencoder for reduced representations of genomes. Training of regularized feed-forward neural network for multiclass label serotype and MLST prediction. Training of regularized feed-forward neural network for antimicrobial resistance. Development of active learning/ screening system for prediction of sanitizer resistance with minimal new data.

3. Prediction of the sex of day-old eggs from from high-speed volatiles mass spectrometry. Developed model on pilot data that used univariate feature selection and L1 regularized logistic regression to predict sex. Personally wrote code. Funded to develop: Larger scale system for prediction across breeds/sites. Preprocessing: Topological persistence data transformation, finial model form will depend on complexity of large scale data. Semisupervised learning planned for field-deployed instruments to improve deployed models.

4. Probabilistic graphical models for building microbiome-plant-disease interaction. Integration of exometabolomics data and metagenomic data to create boolean Bayesian models of microbe-disease networks. Applications include the selection of microbial consortia for bioaugmentation. Coding done by postdoc.

5. Multi-promoter optimization for increased biosynthetic yield. Development of a coupled robotic-ML system. Univariate promoter response curves are fit to logistic model and a random initialization set is selected. Personally wrote code. Funded to develop: Constraint programming (OR-tools CP-CATS solver) used to robotically set up reactions. Bayesian global optimization is used to efficiently select new promoter concentrations until optimal parameters are determined

PUBLICATIONS

Articles in Peer-Reviewed Journals

Journal Article Manuscripts Under Review

2019   Boyles, S. M. et al. "Under-the-radar dengue virus infections in natural populations of *Aedes aegypti* mosquitoes."

2020   Sudduth K.A et al. "AI Down On the Farm"

2020   Liu S. et al. "AI Applications in Agriculture"

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 metatransciptomes. 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, Fench 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, PosgreSQL, 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 February 2020