

Ravin Poudel

Postdoctoral researcher with 6 years of experience in computational and statistical genomics. Expert in microbiome analytics and network analysis.

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EXPERIENCE

Computational Biologist, University of Florida /USDA-ARS(GBRU) Aug 2018 – present

- Curated several bioinformatics pipelines to support batch processing of sequence and metadata for local and high-performance automated analyses; accommodated issues associated with complex installation and dependencies, and time-intensive and parameter-heavy steps; offered effective figures and summary statistics for visualizing progress and quality control. Significantly reduced processing time via automation and boosted R&D.
- Built a novel Trait-Associated OTU-Wide Network (TAOWN) analysis based on random forest and association-based network models. Implemented the model to identified optimal parameters (OTUs) predictive of host-performance (Yield) in the grafted and the non-grafted tomato systems.
- Analyzed high-resolution (temporal) root-associated fungal and bacterial sequence data associated with the disease-resistance and the disease-susceptible tomato plants of bacterial wilt disease caused by the *Ralstonia solanacearum* to develop constraint-based dynamic Bayesian network (DBN). Applied Least Absolute Shrinkage and Selection Operator (LASSO) to infer inductive causations and feature (OTU) selection; developed tools to support engineering of effective synthetic communities for the biological usages.

Graduate Research Assistant, University of Florida Aug 2013 - Aug 2018

- Characterized shifts in the microbial community interactions, composition, and diversity associated with grafted tomato.
- Developed an analytical and theoretical framework to support the selection of candidate taxa for biological usages by using network models and Simulated Annealing (SA) algorithm.
- Performed ML algorithms, including graph models and Random Forest to optimize feature selection for building trait-based microbiome networks.
- Organized and taught R, network analysis, and statistical analyses courses in the university, student organizations, and at the international meetings.

Research Assistant, Harvard University Nov 2012-May 2013

- Implemented assays to identify markers associated with cancer-initiating stem cells.
- Investigated efficacy of monoclonal antibodies to suppress cancer and cancer-initiating stem cells.

Summer Undergraduate Research, University of Pittsburgh Jun 2011-Jul 2011

- Performed in-vivo and in-vitro molecular quantitative assays to understand the efficacy of combinatorial drug therapy (with Dasatinib and dendritic cell) against melanoma growth.

Undergraduate Research Student, Truman State University Aug 2008-May 2012

- Investigated primer design tools (eg. Primer 3, Primer-BLAST) to design OTU- specific primer and bench-marked the primers for further usages.
- Performed end-to-end analyses of Sanger Sequence and NGS in Genious and Sequencher for environmental samples, and curated pipeline for submitting sequences to NCBI.
- Characterized shifts in the root-associated fungal endophytes composition and diversity associated from the environmental samples collected across the large geographic areas in USA.

EDUCATION

- 2013- 2018 Ph.D., Plant Pathology (Microbial Ecology). University of Florida
- 2008- 2012 B.S., Biology with honors. Truman State University

RECENT COURSES

- Machine Learning, Stanford University - MOOC
- Probabilistic Graphical Models, Stanford University - MOOC
- Bayesian Data Analysis, Duke University - MOOC

OTHER

- I have given over 20 presentations at the national and international meetings.
- I was one of four graduate students awarded to present in the I. E. Melhus Graduate Student Symposium at the American Phytopathological Society meeting, 2017.
- Selected to participate in the 1st symposium for the Society of Young Network Scientists at the NetSci meeting, 2017.
- Received a travel award to participate in the training course at the CABI- UK, funded via United States Culture Collection Network.

SKILLS

Programming

- R / Bioconductor
- Python
- BioPython
- Octave
- SAS
- SQL
- HPC and cloud computing
- UNIX/Linux
- Git
- Tableau

Bioinformatics

- **Quality check / Statistics**
FastQC, BBtools, Quast, CheckM, Trimmomatic
- **Alignment/ Mapper**
BLAST, Bowtie, V/USEARCH, Diamond, HMMER, MEGAN, GraphMap
- **Assembly**
SPAdes, Megahit
- **Tools/ Pipelines**
GATK, Samtools, Mash, MetaBat, CONCOCT, QIIME, DADA2, Anvio, Galaxy
- **Annotation**
Prodigal, Kaiju, prokka, GHOST KOALA
- **Classifier**
Kraken, Kaiju, SILVA, RDP, Greengenes
- **Databases**
KEGG, COGs, Pfam, Interpro

Computational Biology

- Amplicon-Metagenomics
- Shotgun- Metagenomics
- RNAseq Analysis
- SNP and Variant Discovery

Statistical Analyses

- Network analysis
- GIS
- Bayesian statistics
- Machine learning
- Parameter optimization
- Multivariate statistics
- Community analyses

PUBLICATIONS

Full list at ravinpoudel.github.io/publication/

- Poudel, R., Jumpponen, A., Kennelly, M. M., Rivard, C. L., Gomez-Montano, L., and Garrett, K. A. 2018. Rootstocks shape the rhizobiome: Rhizosphere and endosphere bacterial communities in the grafted tomato system. *Appl Environ Microbiol*.
- Poudel, R., Jumpponen, A., Schlatter, DC, Paulitz, TC, McSpadden Gardener, BB, Kinkel, LL, and Garrett, KA. Microbiome networks: A systems framework for identifying candidate microbial assemblages for disease management. *Phytopathology* 106:1083-1096, 2016. [The most downloaded papers published in [phytopathology-2016](https://doi.org/10.1093/phytopathology-2016-7)]
- Garrett, K. A., Alcalá-Briseno, R. I., Andersen, K. F., Buddenhagen, C. E., Choudhury, R. A., Fulton, J. C., Nopsa, J. F. H., Poudel, R., and Xing, Y. 2018. Network analysis: A systems framework to address grand challenges in plant pathology. *Annu. Rev. Phytopathol.* 56.