

Ravin Poudel

Computational Biologist with 6 years of experience in computational and statistical genomics. Machine-learning and graphical-model enthusiast.

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EXPERIENCE

Computational Biologist, Artizan Biosciences

Dec2019-Present

- Developed workflows for 16S, and metagenomics analyses, and analysed over 2000 biological samples from mouse and human model of IBD.
- Retrieved and analyzed publicly available datasets for bacterial genes/genome of interest.
- Developed and implemented tools to evaluate the association between bacterial communities and strains with disease model phenotypes.

Computational Biologist, University of Florida /USDA-ARS(GBRU)

Aug2018-Dec2019

- Curated several bioinformatics pipelines to support batch processing of sequence and metadata for local and high-performance automated analyses.
- Built a novel Trait-Associated OTU-Wide Network (TAOWN) analysis based on random forest and association-based network models.
- Developing probabilistic graphical models and analysis software to integrate multi-omics data [Based on python and BayesiaLab].
- Developing bioinformatics and statistical tools to investigate gene function and essentiality using Transposon Sequencing (TnSeq) method [Based on python].
- Developed python based program to identify gRNA in any small genome [Based on python].

Graduate Research Assistant, University of Florida

Aug2013-Aug2018

- 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

Nov2012-May2013

- Implemented assays to identify markers associated with cancer-initiating stem cells.

Summer Undergraduate Research, University of Pittsburgh

Jun2011-Jul2011

- 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

Aug2008-May2012

- 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 & Network Modeling). University of Florida
- 2008- 2012 B.S., Biology with honors. Truman State University

Grants

- Developing probabilistic graphical models and analysis software to integrate multi-omics data. [2019] CO-PI - Funded through JGI.

SKILLS

Programming

- R / Bioconductor
- Python/Jupyter
- SAS
- SQL
- HPC / AWS
- UNIX/Linux
- BayesiaLab
- Conda/Docker

Bioinformatics

- Quality check
FastQC, BBtools
- Alignment/ Mapper
BLAST, Bowtie
- Assembly
SPAdes, Megahit
- Tools/ Pipelines
GATK, QIIME2, Galaxy
- Annotation
Prodigal, Kaiju
- Classifier
Kraken, Kaiju
- Databases
KEGG, COGs, Pfam, VFDB, other

Statistical Analyses

- Network analysis
- Bayesian statistics
- Machine learning
- Parameter optimization
- GWAS-Phenotype prediction

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. 2019. Integration of system phenotypes in microbiome networks to identify candidate synthetic communities: a study of the grafted tomato rhizobiome. bioRxiv.

• 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"]

• Garrett, K. A., Alcalá-Briseño, 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.

• Karen A Garrett, RI Alcalá-Briseño, Kelsey F Andersen, Jeremy Brawner, RA Choudhury, Erik Delaquis, Joubert Fayette, Ravin Poudel, Duncan Purves, Jennifer Rothschild, IM Small, Sara Thomas-Sharma, Yanru Xing. 2020. Effective altruism as an ethical lens on research priorities. Phytopathology.