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Engineering & Scientific Consulting

Aman Gill, Ph.D.

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Professional Profile

Dr. Gill relies on broad industry experience in consulting and research and development roles across therapeutics, synthetic biology, and diagnostics companies, combined with deep expertise in functional and population genomics as a PhD and postdoc in Ecology and Evolution. Focal areas in his work have spanned environmental and host-associated microbiomes, gene editing tools including RNAi and CRISPR-like systems, and AI-enabled enzyme engineering. As a seasoned computational biologist and bioinformatician, Dr. Gill has led projects to devise custom computational pipelines for a host of needs including taxonomic, functional, and multi-omic profiling of genomes and metagenomes, AI and machine learning model development, bioinformatics workflows for clinical and regulatory analyses, and data mining.

Dr. Gill utilizes his experience in functional and predictive genomics, community ecology, and population-level variation to enhance risk assessment for ecotoxicology and off-target effects of gene silencing and editing technologies like RNAi and CRISPR. Prior to Exponent, he used co-analysis of metagenomic sequence and environmental data to understand how Green Infrastructure installations for stormwater management shape the diversity and function of soil microbial communities with respect to nutrient cycling and pollution degradation pathways. More recently, Dr. Gill used large language models (LLMs) trained on protein sequences and in silico binding assays to discover and engineer enzymes for therapeutics and bioeconomy applications, including DNA detection and editing, plastic degradation, and greenhouse gas capture and conversion. His experience with in vitro diagnostics includes curation of comprehensive pathogen genomic databases, target identification and off-target analysis, and FDA regulatory analyses for analytical sensitivity and specificity. He also has extensive experience conducting gene expression studies using RNA-seq and RT-qPCR, and epigenetic analysis using Oxford Nanopore sequencing.

Academic Credentials & Professional Honors

Ph.D., Ecology & Evolution, Stony Brook University, 2014

B.A., History, University of California, Berkeley, 2003

B.A., Integrative Biology, University of California, Berkeley, 2003

Academic Appointments

Visiting Assistant Professor, Department of Mathematics and Science, Pratt Institute, 2013-2016

NSF Postdoctoral Fellow, UC Berkeley, Department of Environmental Science & Policy Management, 2016-2019

Prior Experience

Consultant, DeepStack Bio, 2023 – present

Associate Director of Computational Biology, Proof Diagnostics, 2021 – 2023

Bioinformatics Staff Scientist, Twist Biosciences, 2021

Bioinformatics Scientist, Assembly Biosciences, 2019-2021

Patents

WIPO WO2023170535. Novel Nucleic Acid-Guided Nucleases and Use Thereof, September 2023 (Maamar, Hedia; Gill, Aman).

WIPO WO2023170534. Methods and Compositions for Diagnosing Diseases. September 2023 (Maamar, Hedia; Gill, Aman).

Publications

Silver, A., Perez, S., Gee, M., Xu, B., Garg, S., Will, K. and Gill, A., 2021. Persistence of the ground beetle (Coleoptera: Carabidae) microbiome to diet manipulation. PLoS One, 16(3), p.e0241529.

Attygalle, A.B., Xu, S., Moore, W., McManus, R., Gill, A. and Will, K., 2020. Biosynthetic origin of benzoquinones in the explosive discharge of the bombardier beetle Brachinus elongatulus. The Science of Nature, 107, pp.1-11.

Gill, A.S., Purnell, K., Palmer, M.I., Stein, J. and McGuire, K.L., 2020. Microbial composition and functional diversity differ across urban green infrastructure types. Frontiers in Microbiology, 11, p.912.

Gill, A.S., et al. A practical guide for functional transcriptomics: A case study in RNA interference and qPCR to understand the explosive chemistry of Brachinus bombardier beetles (Coleoptera: Carabidae). In: Transcriptomics in Entomology Research, CABI publishing: Wallingford, UK. 2019.

Brodsky, O.L., Shek, K.L., Dinwiddie, D., Bruner, S.G., Gill, A.S., Hoch, J.M., Palmer, M.I. and McGuire, K.L., 2019. Microbial communities in bioswale soils and their relationships to soil properties, plant species, and plant physiology. Frontiers in microbiology, 10, p.452890.

Lee, J.M., Tan, J., Gill, A.S. and McGuire, K.L., 2019. Evaluating the effects of canine urine on urban soil microbial communities. Urban Ecosystems, 22, pp.721-732.

Hoch, J.M., Rhodes, M.E., Shek, K.L., Dinwiddie, D., Hiebert, T.C., Gill, A.S., Salazar Estrada, A.E., Griffin, K.L., Palmer, M.I. and McGuire, K.L., 2019. Soil microbial assemblages are linked to plant community composition and contribute to ecosystem services on urban green roofs. Frontiers in Ecology and Evolution, 7, p.198.

Gill, A.S., Lee, A. and McGuire, K.L., 2017. Phylogenetic and functional diversity of total (DNA) and expressed (RNA) bacterial communities in urban green infrastructure bioswale soils. Applied and Environmental Microbiology, 83(16), pp.e00287-17.

Will, K.W., Gill, A.S., Lee, H. and Attygalle, A.B., 2010. Quantification and evidence for mechanically metered release of pygidial secretions in formic acid-producing carabid beetles. Journal of insect science, 10(1), p.12.

Will, K.W. and Gill, A.S., 2008. Phylogeny and classification of Hypherpes auctorum (Coleoptera: Carabidae: Pterostichini: Pterostichus). Annals of Carnegie Museum, 77(1), pp.93-127.

Presentations

Organizer. Phylogenetic approaches in microbiome research, Hennig Society meeting, 2019. UC Berkeley. Invited speaker. Revelations from insect transcriptomics, Entomology Society of America meeting, Nov. 2017.

Project Experience

Led efforts to integrate population-level genetic differentiation and local adaptation patterns into ecotoxicology risk assessment. Assisted regulatory ecological risk assessment for an environmental RNAi product.

Prior to exponent:

Managed a project to discover, characterize, and screen novel RNA-programmable nuclease and nickase enzyme systems, resulting in two provisional patents.

Developed a computational strategy and workflow to identify microbial antigens suitable for targeting for antibody affinity.

Conducted a metagenomic & environmental survey to characterize microbial diversity and functional potential in Green Infrastructure soils for stormwater management.