

# Geoffrey D Hannigan, PhD

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<http://microbiology.github.io/>

## Summary

Solutions-oriented digital leader with eight years experience in the biotech and pharma industry, and almost 15 years scientific experience. In my current role I drive both scientific innovation internally by leading research as a principal computational biologist, as well as drive external digital innovation as lead for the Merck Digital Sciences Studio startup accelerator. My scientific expertise is in computational biology, data science, systems biology, machine learning, and drug discovery. I have experience working with business development teams, and most notably I led a \$2M research deal with a startup. I have broad experience across business value streams including drug discovery, drug development and manufacturing, business development, and organizational leadership, and have led many successful programs and teams in these areas.

## Education

University of Pennsylvania – PhD, Cell & Molecular Biology, 2015

University of Minnesota Duluth – BS, Cell & Molecular Biology, 2011

## Relevant Experience

### **EXECUTIVE DIRECTOR & CO-FOUNDER, MERCK DIGITAL SCIENCES STUDIO – 2022 - PRESENT**

Executive lead and co-founder of Merck Digital Sciences Studio, a startup accelerator program focused on digital enablement of drug discovery & development. Leverage both scientific and business acumen to accelerate startups toward success, including fostering engagements between Merck and startups.

### **PRINCIPAL SCIENTIST, MERCK RESEARCH LABS – 2020 - PRESENT**

Computational biologist and people manager leading and contributing to discovery research which blends computational, genetics, systems biology, machine learning, and molecular approaches. Led external partnership to establish a large observational clinical study for drug discovery. Led internal design and development of a GxP platform to improve manufacturing and commercialization.

### **ASSOCIATE PRINCIPAL SCIENTIST, MERCK RESEARCH LABS – 2017 - 2020**

Computational biologist and founding team member that co-developed the DeepBGC algorithm for using deep learning to identify synthetic biology signatures for drug and biomarker discovery. Established a flexible and scalable microbiome analysis platform for use on-prem as well as on cloud compute resources.

### **SCIENTIFIC ADVISOR, SMARTPHAGE – 2015 - 2017**

Scientific advisory board member for SmartPhage, a biotech focused on the development of effective, precise therapies based on modern disease models. Contributed to facilitating academic collaborations, exploring grant and other funding opportunities, and providing insight into future scientific directions of the company.

### **RESEARCH FELLOW, UNIVERSITY OF MICHIGAN – 2015 - 2017**

Led research in both computational and molecular biology, which focused on building and leveraging advanced analytical technologies (including systems biology, machine learning, and network analysis) to identify biomarkers and prognostic models in oncology and infectious disease. Also performed basic research to understand biological mechanisms of human disease in oncology and infectious disease.

## Professional Development & Certifications

Duke University – Corporate Education Certificate, Business Leadership Program, 2020

Howard Hughes Medical Institute – Certificate, Med Into Grad Scholar, 2015

## Skills

Scientific Skills: R, Python, Julia, MySQL, Neo4j/Cypher, GNU Make, Nextflow, AWS, Unix/Linux, Machine Learning, Microbiome Processing, Genomic Processing, RNA-seq Processing & Analysis, Cell Culture, Illumina Next Generation Sequencing, PCR, Western Blot, In Vivo Models

Business/Leadership Skills: Team Management, Organizational Management, Organizational Strategy, Business Development, Budgeting, Contracting, Program Administration, Negotiations, Alliance Management

## Select Publications

Total of 16 publications: 2 senior author publications and 10 first author publications.

Gokul Swaminathan, et al, **Geoffrey D Hannigan**. 2021. Vaccine Hyporesponse Induced by Individual Antibiotic Treatment in Mice and Non-Human Primates Is Diminished upon Recovery of the Gut Microbiome. *Vaccines*.

David Prihoda, et al, **Geoffrey D Hannigan**. 2021. The application potential of machine learning and genomics for understanding natural product diversity, chemistry, and therapeutic translatability. *Natural Product Reports*.

**Geoffrey D Hannigan**, et al. 2019. A Deep Learning Genome-Mining Strategy For Biosynthetic Gene Cluster Prediction. *Nucleic Acids Research*.

**Geoffrey D Hannigan**, et al. 2018. Biogeography and Environmental Conditions Shape Bacteriophage-Bacteria Networks Across the Human Microbiome. *PLOS Computational Biology*.

**Geoffrey D Hannigan**, et al. 2018. Diagnostic Potential & the Interactive Dynamics of the Colorectal Cancer Virome. *mBio*.

**Geoffrey D Hannigan**, et al. 2015. The human skin dsDNA virome: Topographical and temporal diversity, genetic enrichment, and its dynamic associations with the host microbiome. *mBio*. 6(5):e01578-15.

## Patents

**Geoffrey D Hannigan**, Prihoda D, Soukup J, Woelk CH, Bitton DA. 2018. Identifying Biosynthetic Gene Clusters. 62/779.697

## Software Publications

**Geoffrey D Hannigan**, Loesche MA, Hodgkinson BP, Mehta S and Grice EA. **Creator** (cre), **Author** (aut). patPRO: Visualizing Temporal Microbiome Data. <http://CRAN.R-project.org/package=patPRO>

Oksanen J, et al. **Contributor** (ctb). Vegan: R Package for Community Ecologists. <http://CRAN.R-project.org/package=vegan>