



**Stony Brook
University**

College of Arts and Sciences
Department of Ecology & Evolution
*Institute for Advanced Computational
Science*

Life Sciences Building
Room 610
E jackie.weissman@stonybrook.edu
<https://microbialgamut.com/>



**Postdoctoral Associate
Metagenomic Trait Prediction and/or Modeling Microbial Systems
Stony Brook University**

The Microbial Genomes And Metagenomes to Unravel Traits Lab (mGAMUT Lab; PI: JL Weissman) at Stony Brook University (<https://microbialgamut.com/>) has openings for **two** postdoctoral researchers to begin in January 2027 (start date negotiable). We seek researchers interested in (1) building trait prediction models capable of resolving complex microbial traits from genomes and metagenomes, and/or (2) building mathematical models of microbial community dynamics using a trait-based framework. These positions are part of our recently funded NIH R35 to use trait-based approaches to model the dynamics of the human microbiome (read more [here](#)). This position will be for one year initially, and may be renewable throughout the grant period dependent on continuing applicant contributions to the project (project running through August 2031).

Our lab develops new computational tools to infer what microbes are doing and can do directly from genomic and metagenomic data (e.g., <https://github.com/jlw-ecoevo/gRodon2>). We aim to develop a mechanistic, trait-based understanding of microbial dynamics, asking whether differences in the predicted growth strategies and environmental preferences of individual organisms in a community can be used to inform ecological models of bacterial community dynamics in response to perturbation. Our group is actively engaged in this research on three primary fronts. First, we are working to develop methods for (meta)genomic trait inference to determine the distribution of complex microbial traits in a community directly from sequencing data. Second, we are using our trait-inference approaches to identify natural structuring of microbial communities to inform model development for host-associated microbiomes. Third, we are integrating our taxon-specific inferences of growth strategies into dynamic models of community succession that can be ground-truthed against microbiome time-series data. Ultimately, we will apply our mechanistic metagenomes-to-dynamics approach to generate predictive models of community dynamics that can be applied to large, publicly available metagenomic time series to provide insight into assembly processes of the human microbiome in response to environmental perturbations.

The successful applicant should have or will shortly obtain a PhD in Computational Biology, Biology, Ecology & Evolution, Computer Science, Mathematics, or Physics, or a closely related field, with research experience using computational approaches to answer biological questions. We seek candidates with a strong quantitative preparation.

Our lab is committed to creating a collaborative, equitable, and inclusive working environment, and we welcome candidates who share those goals. You can find out more about the lab, including our code of conduct, on our [website](#). Our lab is located in the [Institute for Advanced Computational Science](#) and in the [Department of Ecology & Evolution](#) at Stony Brook University.

**FAR
BEYOND**

Applications will be accepted until October 11, 2026. Applicants must submit materials electronically through the SBU Jobs system: <https://stonybrook.taleo.net/careersection/2/jobdetail.ftl?job=2603237> [position number 2603237]

- a resume/CV that documents all applicable required and preferred qualifications,
- a representative publication (e.g., a peer-reviewed paper, submitted manuscript, or dissertation), and
- a cover letter (1-2 pages; optional) that briefly (1) describes their relevant training and research accomplishments, (2) explains their reasons for applying for this specific position, and (3) clarifies any of the required or preferred job qualifications listed on the official posting that the candidate may meet but are not clearly indicated on their CV

The official posting and online application can be found at

<https://stonybrook.taleo.net/careersection/2/jobdetail.ftl?job=2603237>.

Queries regarding this position can be made by email to: jackie.weissman@stonybrook.edu

The anticipated annual salary range for this position is \$72,000-\$76,000

Job Description

Required Qualifications: Doctoral Degree (or foreign equivalent) in Computational Biology, Biology, Ecology and Evolution, Computer Science, Mathematics, or Physics, or closely related field degree in hand by the start of the position. For those with degrees that are not explicitly computational (e.g., Biology), a record of coursework and research in quantitative areas must be shown. For those with degrees not explicitly related to biology (e.g., Mathematics), a record of coursework and research concerning biological questions must be shown.

Preferred Qualifications:

- Experience analyzing genomic and/or metagenomic data using computational methods.
- Experience developing new approaches for the analysis of biological data beyond the application of established pipelines OR experience developing mathematical or statistical models of biological systems.
- A record of publishing computational biology (broadly defined), bioinformatics, or theoretical ecology (modeling) research in peer-reviewed scientific journals
- Experience in programming in R, Python, or a similar programming language.
- A demonstrated commitment to open-science, to team-science, and to fostering an inclusive and equitable research environment.
- Experience working in microbial systems, specifically to answer questions in
- microbial ecology and evolution.
- Experience with population genetics.
- Experience developing R packages.
- Experience applying or developing machine learning tools.
- Strong scientific writing skills.