Jonathan L. Golob, MD, PhD

Physician-scientist and software engineer

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With a view from the bedside, the bench and the codebase, I find what's missing, build the fix, and leave it working. I lead applied AI/ML for vaccines and infectious disease at GSK, keep a limited clinical practice, and still write the software myself.

EXPERIENCE

Director, AI/ML — Vaccines & Infectious Disease, GSK · R&D 2024 – present

Joined as Lead Engineer, AI/ML (June 2024); promoted to Director (March 2025).

- Built deep-learning models of viral evolution, infection incidence and case-accrual timing, used to guide development and lifecycle decisions for a $1B vaccine program; led their transition into maintained tools.
- Lead GSK's AI/ML and data engineering across all six Fleming Initiative Grand Challenges; GSK scientific co-lead for Antibiotics and Antifungals.
- Built and manage a specialist ML engineering team; form and direct cross-disciplinary teams of 20–30.
- Originated ViroGym, a benchmark for protein language models on viral proteins, and supervised its first author through to a NeurIPS 2026 Spotlight.

Assistant Professor, Internal Medicine / Infectious Diseases, University of Michigan 2018 – 2024

- Designed and built MaLiAmPi (senior author; patent pending) and co-led the Microbiome Preterm Birth DREAM Challenge (first author). In 2025 NSF selected the resulting dataset, one of 10 chosen in a competitive interagency process, for the NAIRR Pilot.
- Led a translational research group; protocol co-author and biomarker lead on early-phase trials; site PI for COVID-19 treatment and vaccine trials; global unblinded safety physician.
- Frontline COVID-19 critical care; co-founded the University of Michigan COVID-19 case series; early contributor to the ISARIC dataset; co-author of an early tocilizumab study.

Senior Fellow · Joel Meyers Endowment Scholar, Fred Hutchinson Cancer Center / University of Washington 2015 – 2018

Affiliate, Fred Hutchinson Cancer Center, 2018 – 2022.

- Showed that the gut microbiome predicts severe graft-versus-host disease after stem-cell transplant (first author, Clin Infect Dis 2017; Blood Advances 2019), leading to dietary intervention trials (Nature Medicine 2023).

MD–PhD, Medical Scientist Training Program, University of Washington 2001 – 2011

- PhD in Pathology on stem-cell epigenetics, with early high-throughput sequencing and a custom analysis pipeline.

Undergraduate Researcher, Johns Hopkins University School of Medicine 1997 – 2001

- In research laboratories from my first year: adenoviral and AAV vectors in Paul Kessler's laboratory, then Linzhao Cheng's laboratory, where I was second author on three papers on early lentiviral vectors for gene transfer into human blood stem cells (Stem Cells 2001; Blood 2002), work at the foundation of today's stem-cell gene therapies.

HOW I WORK: TWO EXAMPLES

Making microbiome studies comparable MaLiAmPi → harmonized DREAM Challenge dataset → NSF NAIRR Pilot selection

The problem. Microbiome studies could not be combined. Each used different laboratory and sequencing methods, so a model trained on one study failed on the next.

What was missing. A stable, shared set of features that did not depend on taxonomy or on how the samples were processed.

The fix. Designed and built MaLiAmPi, an open-source workflow that turns raw data from technically different studies into one feature set.

What it enabled. The harmonized, multi-study dataset behind the Microbiome Preterm Birth DREAM Challenge, with models validated on independent data. In 2025 NSF selected that dataset, one of 10 chosen through a competitive process with 12 federal agencies, for integration into the National Artificial Intelligence Research Resource (NAIRR) Pilot. It also supported the Stabl biomarker-discovery method (Nature Biotechnology), and the method is the subject of a pending patent.

Models that inform vaccine development decisions GSK · 2024 – present

The problem. Vaccine development and lifecycle decisions depend on how a virus will evolve and when infections will occur.

What was missing. Predictive models that decision-makers could use, with the uncertainty stated.

The fix. Built deep-learning models predicting viral evolution, infection incidence and case-accrual timing, and host–immune interactions, and led their transition into maintained tools.

What it enabled. Used to guide development and lifecycle decisions for a $1B vaccine program; related approaches supported additional programs in the $100M–$500M range.

INDEPENDENT ENGINEERING

- ChoreCode (chorecode.ai): designed and built alone; evaluates AI coding models on maintenance work with hidden tests, checks on the scorer, unsolvable tasks and cost accounting.
- Forty-plus public repositories; four packages on PyPI; one workflow maintained for eight years (github.com/jgolob).

CLINICAL

- Clinical Assistant Professor, University of Washington: limited active practice in cancer-related and transplant infections.
- Board certified, ABIM: Internal Medicine (2014), Infectious Disease (2016).

SELECTED PUBLICATIONS

78 publications, including preprints and abstracts; more than 4,100 citations (Google Scholar, November 2026).

- Zhou, **Golob**, Karimi Mamaghan, Bauer, Schwab. ViroGym. NeurIPS 2026 (Spotlight). Originated the project.
- **Golob** et al. Microbiome Preterm Birth DREAM Challenge. Cell Reports Medicine, 2023. First author.
- Minot … **Golob**. MaLiAmPi. Cell Reports Methods, 2023. Senior author.
- Riwes, **Golob** et al. Dietary intervention in stem-cell transplantation. Nature Medicine, 2023.
- Hédou et al. Stabl. Nature Biotechnology, 2024. Co-author.
- **Golob** et al. Stool microbiota predictive of severe acute GVHD. Clin Infect Dis, 2017. First author.

SKILLS

AI and evaluation: Protein and RNA language models, diffusion approaches, benchmark and evaluation design, uncertainty-aware modeling; Python, PyTorch, Nextflow, SQL.

Biology and clinical medicine: Infectious disease, oncology and transplantation; clinical trial design and safety oversight; multi-omics, organoid models, vector design.

Leading people and programs: Matrix leadership of 20–30; building specialist ML teams; build–buy–partner decisions; executive advising.

EDUCATION AND TRAINING

Transplant Infectious Diseases Fellowship, Fred Hutchinson Cancer Center, 2016–2017

Infectious Diseases Fellowship, University of Washington, 2013–2017

Internal Medicine Residency, University of Washington, 2011–2013

MD–PhD, University of Washington, 2001–2011

Dual BS degrees in Biomedical Engineering and in Computer Science, Johns Hopkins University, 1997–2001

WRITING

Science writing for The Stranger, Ars Technica and The Conversation; Delayed Critical, a stage play on nuclear safety and institutional failure (2026).