Curriculum Vitae Jasper Götting

I set out to become a zoologist but got massively derailed by impact-oriented cost–benefit analyses. After finishing my virology Ph.D. and exploring and evaluating technical biosecurity interventions, I now focus on making the AI/biotech intersection safe.

Experience

Since 05/2024 **Research Scientist AI+Bio** *at SecureBio*

Part of the *AI and Biotechnology Risks* team, working on AI capability evaluations. First author of the Virology Capabilities Test (VCT). Leading the development of SecureBio's biology evaluation dashboard and next-generation GPAI evaluations.

09/2022 – 10/2024 **Research Fellow** *at Convergent Research*

Roadmapping biosecurity interventions with a focus on far-UV air disinfection; including organizing academic workshops, writing reports and recommendations, and interfacing with scientists, funders, and policymakers.

05/2024 – 09/2024 **Research Contractor** *for Ellison Institute of Technology Oxford*

Research on clinical MGS host nucleic acid depletion for EIT's Pathogen Mission.

09/2018 – 07/2022 **Virology Ph.D.** *at the Schulz Lab in the Institute of Virology, Hannover Biomedical Research School*

Thesis: "DNA viral diversity data for epidemiological and diagnostic studies"
Summa cum laude (with distinction) and awarded the Infection Biology Ph.D. Thesis Prize
Also served as the student representative of the Infection Biology Ph.D. program

02/2018 – 04/2018 **The Data Incubator** *at Data Reply, Munich*

8-week Data Science boot camp covering: SQL, Web-scraping, (un)supervised Machine Learning, Deep Learning, NLP, Time Series, MapReduce, and Spark
Capstone project: Identification of roof solar panels on satellite imagery using CNNs

Education

10/2014 – 02/2017 **M.Sc. Biomedical Science** *at the Hannover Medical School*

Thesis at the Institute for Biophysics, University Osnabrück

10/2011 – 09/2014 **B.Sc. Biology** *at the Leibniz University Hannover*

Teaching assistant in physiology and field assistant for a mouse lemur population study in northern Madagascar
Thesis at the Neuroanatomy Institute, Hannover Medical School

Skills

Laboratory- and Related Skills

High-throughput sequencing (Illumina SBS, Nanopore Sequencing) workflows

Various bioinformatics CLI tools and software suits (e.g., CLC, Geneious Prime) around sequencing data analysis and phylogenetics

Gene Technology, Biosafety and Biosecurity – State Approved Course §15 GenTSV for Project Leaders and Responsible Persons for Biosafety

Machine Learning Skills and Courses

Intermediate programming and scripting: Python, R, Bash, SQL

Large language model evaluations using Inspect AI or CLI

Machine Learning in R (*University of Cambridge, UK)*, Machine Learning *(Stanford University on Coursera)*, Bayesian Statistics: From Concept to Data Analysis *(UC Santa Cruz on Coursera)*

Other Skills

Public Speaking (EAGx talks, podcasts, academic conferences, general audiences)

Alumnus of the Center For Applied Rationality (CFAR) programme

Languages:	German (native), English (fluent), Mandarin (basic knowledge), Latin (Intermediate Latin certificate)

Other Engagements and Personal Interests

- Member of the European Leadership Network's *New European Voices on Existential Risk* (NEVER) project
- Board member of *Effective Altruism Germany*
- Member of the Pandemic Preparedness & Biosecurity working group at the *Global Health Hub Germany*
- Former Pandemics course facilitator for *BlueDot Impact*
- Science communication and high school student engagement with *I'm a Scientist*
- Specialist and mentor for *80,000 Hours* and *HI-Med* advisees
- Former Outreach Support & Speaker for the *Effective Altruism Foundation*, Berlin
- Co-founder of the *Effective Altruism chapters* Osnabrück and Hannover
- Member of *Mensa International*
- Former member of the *animal rights student group* Osnabrück

Gamemastering for TTRPG groups, hiking, and drumming to/exploring weird music on the recreational side.

Publications

- **Götting, J.***, Medeiros, P.*, Sanders, J. G.*, Li, N., Phan, L., Elabd, K., ... & Donoughe, S. (2025). Virology Capabilities Test (VCT): A Multimodal Virology Q&A Benchmark. arXiv e-prints, https://arxiv.org/abs/2504.16137.
- **Götting, J.** (2022). DNA viral genomic diversity data for epidemiologic and diagnostic studies (Doctoral dissertation, Dissertation, Hannover, Medizinische Hochschule Hannover, 2022).
- **Götting, J.**, Cordes, A. K., Steinbrück, L., & Heim, A. (2022). Molecular phylogeny of human adenovirus type 41 lineages. Virus Evolution, 8(2), veac098.
- **Götting, J.**, Baier, C., Panagiota, V., Maecker-Kolhoff, B., Dhingra, A., & Heim, A. (2022). High genetic stability of co-circulating human adenovirus type 31 lineages over 59 years. Virus Evolution, 8(2), veac067.
- Rahman Siregar, A., Gärtner, S., **Götting, J.**, Stegen, P., Kaul, A., Schulz, T. F., ... & Winkler, M. (2022). A Recombinant System and Reporter Viruses for Papiine Alphaherpesvirus 2. Viruses, 14(1), 91.
- Sogkas, G., Dubrowinskaja, N., Schütz, K., Steinbrück, L., **Götting, J.**, Schwerk, N., ... & Atschekzei, F. (2022). Diagnostic yield and therapeutic consequences of targeted next-generation sequencing in sporadic primary immunodeficiency. International Archives of Allergy and Immunology, 183(3), 337-349.
- Bühler, M., Runft, S., Li, D., **Götting, J.**, Detje, C. N., Nippold, V., ... & Gerhauser, I. (2022). IFN-**β** deficiency results in fatal or demyelinating disease in C57BL/6 mice infected with Theiler's murine encephalomyelitis viruses. Frontiers in immunology, 13, 786940.
- Rovai, A., Chung, B., Hu, Q., Hook, S., Yuan, Q., Kempf, T., **...** & Ott, M. (2022). In vivo adenine base editing reverts C282Y and improves iron metabolism in hemochromatosis mice. Nature Communications, 13(1), 5215.
- **Götting, J.**, Lazar, K., Suárez, N. M., Steinbrück, L., Rabe, T., Goelz, R., ... & Ganzenmueller, T. (2021). Human cytomegalovirus genome diversity in longitudinally collected breast milk samples. Frontiers in cellular and infection microbiology, 11, 664247.
- Dhingra, A.*, **Götting, J.***, Varanasi, P. R., Steinbrueck, L., Camiolo, S., Zischke, J., ... & Ganzenmueller, T. (2021). Human cytomegalovirus multiple-strain infections and viral population diversity in haematopoietic stem cell transplant recipients analysed by high-throughput sequencing. Medical Microbiology and Immunology, 210, 291-304.
- Fritz, A., Bremges, A., Deng, Z. L., Lesker, T. R., **Götting, J.**, Ganzenmueller, T., ... & McHardy, A. C. (2021). Haploflow: strain-resolved de novo assembly of viral genomes. Genome biology, 22, 1-19.
- Deng, Z. L., Dhingra, A., Fritz, A., **Götting, J.**, Münch, P. C., Steinbrück, L., ... & McHardy, A. C. (2021). Evaluating assembly and variant calling software for strain-resolved analysis of large DNA viruses. Briefings in bioinformatics, 22(3), bbaa123.
- Krooss, S. A., Dai, Z., Schmidt, F., Rovai, A., Fakhiri, J., Dhingra, A., **...** & Ott, M. (2020). Ex vivo/in vivo gene editing in hepatocytes using "all-in-one" CRISPR-adeno-associated virus vectors with a self-linearizing repair template. Iscience, 23(1).
- Chukhno, E., Gärtner, S., Rahman Siregar, A., Mehr, A., Wende, M., Petkov, S., **...** & Winkler, M. (2019). A Fosmid-Based System for the Generation of Recombinant Cercopithecine Alphaherpesvirus 2 Encoding Reporter Genes. Viruses, 11(11), 1026.