

Julian Stamp

Providence, RI 02906

Email: julian.d.stamp@gmail.com | [Website](#)

SUMMARY

I am a researcher with a strong technical and statistical background, bringing **5+ years of experience** in both academic research and professional consulting. My expertise includes **Python, R, and C++**, with a strong focus on **machine learning** algorithms and **statistical modeling**. I am the **author and maintainer** of multiple **open-source statistical software** packages.

EDUCATION

Brown University

Ph.D. in Computer Science & Computational Biology

Providence, RI, USA

2021 – 2025

- **Thesis:** Statistical and Computational Advances for Detecting Nonlinear Contributions to Complex Traits

Ludwig Maximilian University of Munich

M.S. in Physics

Munich, BY, Germany

2016 – 2018

University of Konstanz

B.S. in Physics

Konstanz, Germany

2012 – 2016

TECHNICAL SKILLS

Languages : Python, R, C++, Groovy, Matlab

Frameworks : PyTorch, TensorFlow, ScikitLearn, Numpy, Scipy, Pandas

Dev Tools : Git, Github, Bitbucket, OpenShift, Jenkins, Docker

Other : Statistics, Research, Genetics, Biology, Physics, Project Management, HPC, Slurm, OpenMP, Software Automation

RESEARCH AND INDUSTRY EXPERIENCE (3/6)

Ph.D. Candidate

Brown University

Jan. 2021 – Nov. 2020

Providence, RI, USA

- Identified open scientific questions, **mathematical problems** and **algorithmic challenges** in studying human disease.
- Developed **statistical models** and **machine learning algorithms** capable to analyze large human data **improving power by up to 80%** compared to state of the art models.
- Developed open-source **software implementations** of the machine learning algorithms that run **10× to 90× faster** than comparable state of the art algorithms.

Software Consultant

TNG Technology Consulting GmbH

May 2019 – Nov. 2020

Munich, BY, Germany

- Worked in **cross-functional teams**, collaborating with developers, DevOps engineers, and stakeholders of a global insurance company to **align technical solutions with business objectives**.
- **Collaboratively** developed targets and road maps for the **cloud migration and automation** of the **software build infrastructure**.
- Developed software **build & testing automation** and **cloud deployment infrastructure & automation** for testing and production environments.

Research Assistant

Max Planck Institute for Neurobiology

Mar. 2017 – Dec. 2017

Munich, Germany

- Independently **reviewed scientific literature** to learn algorithms to **process 2-dimensional images** to **reconstruct a 3-dimensional anatomical representation** of a mouse brain.
- Developed software for **image alignment** and **3-dimensional reconstruction** of anatomical images.

PUBLICATIONS

- [1] **Stamp, J.**, Pattillo Smith, S., Weinreich, D., & Crawford, L. (2025). Sparse modeling of interactions enables fast detection of genome-wide epistasis in biobank-scale studies. *bioRxiv*, 2025–2001.
- [2] Kim, I. E., Jr, Oduor, C., **Stamp, J.**, Luftig, M. A., Moormann, A. M., Crawford, L., & Bailey, J. (2025). Incorporation of Epstein–Barr viral variation implicates significance of Latent Membrane Protein 1 in survival prediction and prognostic subgrouping in Burkitt lymphoma. *International Journal of Cancer*
- [3] **Stamp, J.**, Crawford, L. (2025). Discovery of Epistasis in cardiac traits. *Nature Cardiovascular Research - News and Views* article (soon to be published)
- [4] Smith, S. P., Darnell, G., Udwin, D., **Stamp, J.**, Harpak, A., Ramachandran, S., & Crawford, L. (2024). Discovering non-additive heritability using additive GWAS summary statistics. *Elife*, 13, e90459.
- [5] Li, K., Chaguza, C., **Stamp, J.**, Chew, Y. T., Chen, N. F. G., Ferguson, D., ... Others. (2024). Genome-wide association study between SARS-CoV-2 single nucleotide polymorphisms and virus copies during infections. *PLOS Computational Biology*, 20(9), e1012469.
- [6] Balvert, M., Cooper-Knock, J., **Stamp, J.**, Byrne, R. P., Mourragui, S., van Gils, J., ... Others. (2024). Considerations in the search for epistasis. *Genome Biology*, 25(1), 296.
- [7] **Stamp, J.**, DenAdel, A., Weinreich, D., & Crawford, L. (2023). Leveraging the genetic correlation between traits improves the detection of epistasis in genome-wide association studies. *G3: Genes, Genomes, Genetics*, 13(8), jkad118.
- [8] Edeleva, E., Salditt, A., **Stamp, J.**, Schwintek, P., Boekhoven, J., & Braun, D. (2019). Continuous nonenzymatic cross-replication of DNA strands with in situ activated DNA oligonucleotides. *Chemical Science*, 10(22), 5807–5814.

SOFTWARE

- [1] **Stamp, J.**, Crawford, L. (2025). smer: Sparse Marginal Epistasis Test. *R package version 0.0.1*, <https://github.com/lcrawlab/sme>.
- [2] **Stamp, J.**, Crawford, L. (2024). mvMAPIT: Multivariate Genome Wide Marginal Epistasis Test. *R package version 2.0.3*, <https://github.com/lcrawlab/mvMAPIT>.
- [3] **Stamp, J.**, Crawford, L. (2025) cphMAPIT: Cox Proportional Hazards Marginal Epistasis Test. *R package (to be published)*, <https://github.com/jdstamp/cphmapit>.

PRESENTATIONS & INVITED LECTURES

- [1] **Stamp, J.** (2023) Leveraging the Genetic Correlation between Traits Improves the Detection of Epistasis in Genome-wide Association Studies. *Intelligent Systems for Molecular Biology*. Lyon, France
- [2] **Stamp, J.** (2023) Partitioning the Non-additive Variation of Complex Traits. *A Multidisciplinary Approach to Epistasis Detection*. Lorentz Center, Leiden University, Leiden, Netherlands

FELLOWSHIPS

Vartan Gregorian Fellowship <i>Brown University</i>	2021-2022 <i>Providence, RI</i>
Erasmus Stipend <i>Ludwig Maximilian University</i>	2018 <i>Munich, Germany</i>
PROMOS Stipend <i>University of Konstanz</i>	2016 <i>Konstanz, Germany</i>

COMMUNITY SERVICE

Educator (Volunteering) <i>Orphanage for boys, Fundación Alalay</i>	Jun. & Jul. 2015 <i>La Paz, Bolivia</i>
Educator (Volunteering) <i>Pre-school, École Perceval</i>	2011 – 2012 <i>Chatou, France</i>