

Julian Stamp

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SUMMARY

I am a Researcher with a strong technical and statistical background, **5+ years experience** in industry and research working with **Python, R, and C++** as well as **machine learning** algorithms. I am the **author and maintainer** of multiple **open-source statistical software** packages.

EDUCATION

Brown University <i>Ph.D. in Computer Science & Computational Biology</i>	Providence, RI, USA 2025 (expected)
<ul style="list-style-type: none">• Thesis: Statistical and Computational Advances for Detecting Nonlinear Contributions to Complex Traits	
Ludwig Maximilian University of Munich <i>M.S. in Physics</i>	Munich, BY, Germany 2018
University of Konstanz <i>B.S. in Physics</i>	Konstanz, Germany 2016

TECHNICAL SKILLS

Languages	: Python, R, C++, Groovy, Matlab
Frameworks	: PyTorch, TensorFlow, ScikitLearn
Dev Tools	: Git, Github, Bitbucket, OpenShift, Jenkins, Docker, JetBrains IDEs
Other	: Statistics, Machine Learning, Project Management, Research, HPC, Slurm, OpenMP

RESEARCH AND ENGINEERING EXPERIENCE

Ph.D. Candidate <i>Brown University</i>	Jan. 2021 – Nov. 2020 Providence, RI, USA
<ul style="list-style-type: none">• 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× – 90× faster than comparable state of the art algorithms.	
Software Consultant <i>TNG Technology Consulting GmbH</i>	May 2019 – Nov. 2020 Munich, BY, Germany
<ul style="list-style-type: none">• Collaboratively developed targets and road maps for the cloud migration and automation of the software build infrastructure of a global insurance company.• Developed software build & testing automation and cloud deployment infrastructure & automation for testing and production environments.	
Research Assistant <i>Max Planck Institute for Neurobiology</i>	Mar. 2017 – Dec. 2017 Munich, Germany
<ul style="list-style-type: none">• 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. (2024). Incorporation of Epstein-Barr viral variation implicates significance of LMP1 in survival prediction and prognostic subgrouping in Burkitt lymphoma. *bioRxiv*, 2024–2005.
- [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>