

# Julian Stamp

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## SUMMARY

I am a researcher with a strong technical and statistical background, and experience in both **academic research** and **professional software development**. My work focuses on **machine learning** and **statistical modeling**, using **Python, R, and C++**. 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 (expected)

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

## RESEARCH AND INDUSTRY EXPERIENCE (3/6)

### Ph.D. Candidate

*Brown University*

Jan. 2021 – 2025 (expected)

*Providence, RI, USA*

- Identified open scientific questions, **mathematical problems** and **algorithmic challenges** in **genome-wide association studies of human traits**.
- 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*

- **Reviewed scientific literature** to identify 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

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- [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) Epistasis in cardiac traits. *Nat Cardiovasc Res (News & Views)*.
- [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

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- [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

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- [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

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

## COMMUNITY SERVICE

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