Jacob I. Marsh, PhD

Software developer | bioinformatics | population genetics

Perth, Australia

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website: jacobimarsh.com   publications: Jacob I. Marsh

I develop and maintain software that wrangles complex molecular sequence data to make analytical predictions about population genetic evolutionary processes. I have specific expertise in Python, HPC (SLURM) and bash scripting, R/Python package development, and React/Vite programming experience.

Postdoctoral Researcher   2023 - Nov 2025

Parul Johri Lab (Population genetics), University of North Carolina, Chapel Hill

- Built [Bvalcalc] Python CLI to generate analytically predicted maps of expected diversity with custom web app to host documentation. [docs][repo]
- Tested forward-time population genetic simulations (*e.g.,* SLiM) to identify pitfalls and establish best practices [preprint][viz]
- Demographic inference testing using Ancestral Recombination Graph-based approaches for human and *Drosophila* [publication]

PhD, Plant Bioinformatics   2019-2023

David Edwards Group (Plant bioinformatics), University of Western Australia

- Designed and built [crosshap] R package for visualizing dashboard of trait mining info in local genomic region for GWAS [publication][repo]
- Found pod dehiscence (pod shatter) domestication QTL candidate in *Vigna unguiculata* (cowpea) using public databases & phylogenetics [publication]
- Haplotype mapping (SV/SNP) and GWAS for variant discovery in major soybean protein QTL [publication]

BSc (Honours)   2014-2018

Ryan Lister Lab (Epigenomics), University of Western Australia

- Single-cell transcriptomics of *A. thaliana* developing leaf using Seurat (2018)
- Genetics (Major), History (Major) (2014-2017)

References available upon request.