Jacob I. Marsh, PhD

Bioinformatics | software developer

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website: jacobimarsh.com   publications: Jacob I. Marsh

I develop software to wrangle, visualise and make sense of complex molecular variation. I have specific expertise in population genetics/genomics, as well as R package development, bash/Python scripting, and tech stack experience.

Postdoctoral Researcher   2023-2025

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

- Built Python CLI to generate maps of expected diversity and building web app to host documentation, query-able SQLite database and D3.js viz [please enquire to view private repo and test CLI, expected May 2025]
- 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]
- 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.