Conservation efforts are rapidly incorporating genomics, from understanding the genetic diversity of natural populations to detecting hybridization between native and invasive species, understanding biology in the context of climate change, and evaluating the phylogenetic history of a species1. Researchers’ toolkit for conservation biology in the genomics era is software. For example, without software, processing—and generating—genomic data would be impossible. Thus, the use of genomics in conservation biology is dependent on advances and maintenance of software and tooling thereof.

I am a software engineer working in the field of genome sciences, with a specialty in phylogenomics, population biology, and molecular evolution. Tools I engineer have been widely adopted by the bioinformatics community, as evidenced by **over 350,000+ downloads** since 20212–9.

Here, I propose a novel algorithm