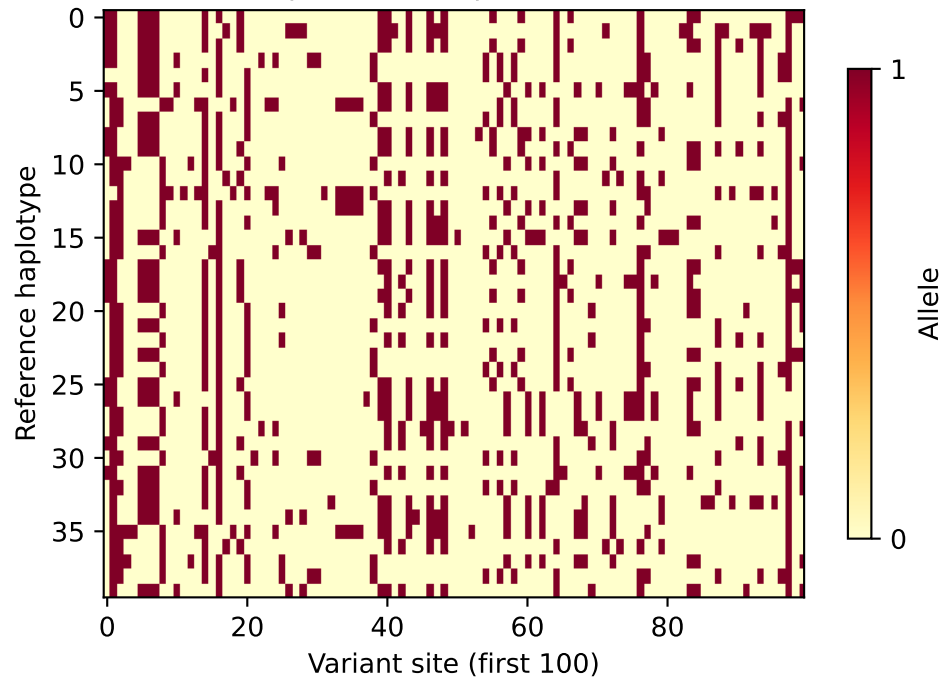
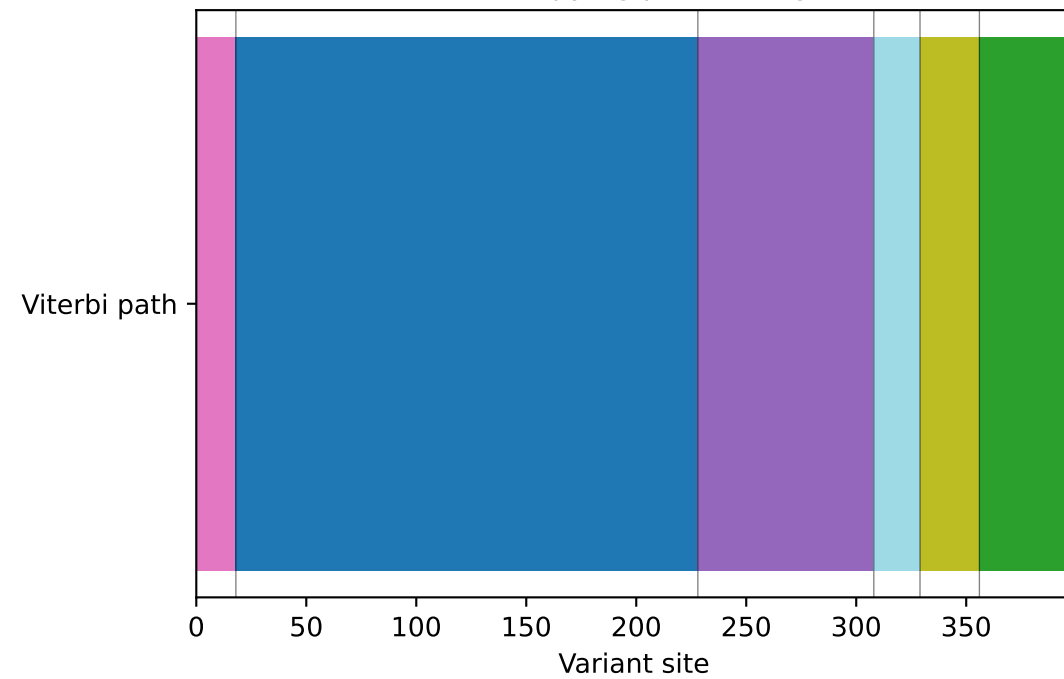


# Demo: Li & Stephens HMM on msprime-simulated Haplotypes (500 kb)

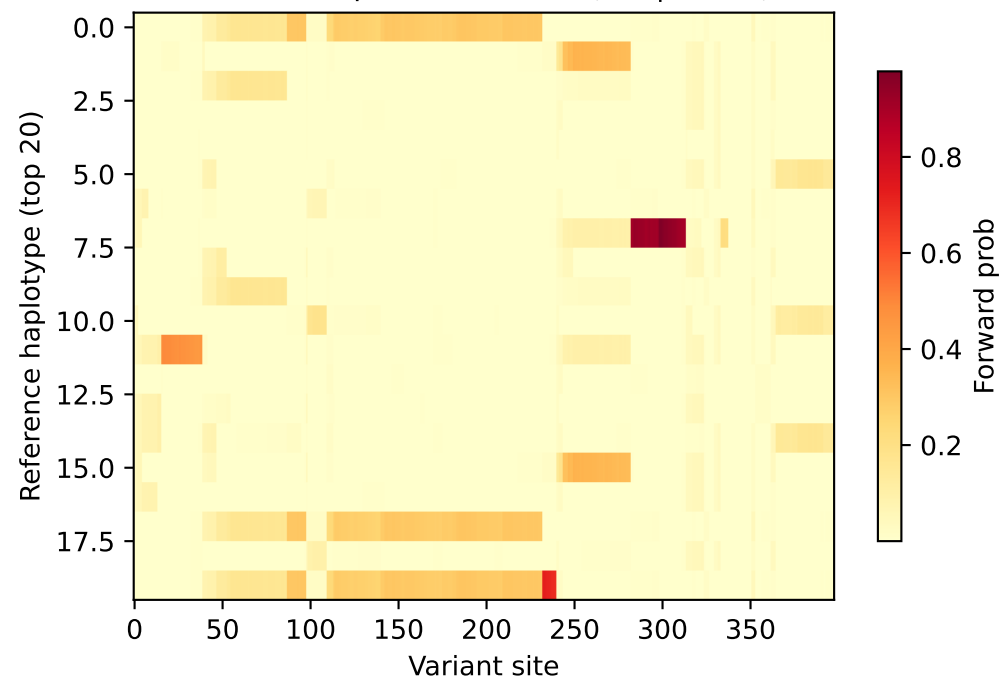
A. Reference panel (40 haps, 398 sites from VCF)



B. Inferred copying path (6 segments)



C. Forward probabilities  $P(Z_\ell = k | \text{data}_{1:\ell})$



D. Posterior decoding (top 5 sources)

