DNA sequences from a population has an unobservable genealogical history. In analyzing such data, a crucial stepping stone is to be able to integrate over evolutionary histories according their probability according to a model and given the data. Doing this has been the focus of research for more than 2 decades. Doing this has been the focus of research for more than 2 decades. The basic probability model for genealogical histories with recombination was given Watterson (1975) and Kingman (1982). Until 1994 (Griffiths and Tavare), this was solely used as a tool for simulating genealogical histories without knowing the content (mutational configuration) of the sequences. Since late 90s there has been a string of attempts to apply stochastic integration methods (Importance Sampling, MCMC,..) to do this. In the absence of recombination it is a hard, but doable problem. Due to the enormous increase in DNA sequences from populations and the importance of this problem in genetic mapping, the problem remains as important as ever.

Recursions (Ethier and Griffiths, 1987) can be written to calculate the likelihood of a data set in terms of possible ancestral configurations (Song, Lyngsø and Hein, 2006). The number of ancestral configurations grows as a function of number of sampled sequences and segregating sites but also depends on the exact configuration of segregating sites. Griffiths and Marjoram (1996) and Fearnhead and Donnelly (2001) devised importance samplers to intergrate of histories. Lyngsø, Song and Hein (2008) used a branch and bound algorithm to analyze a model with recombination. Presently there exists no satisfactory method to do this for decent data sizes.