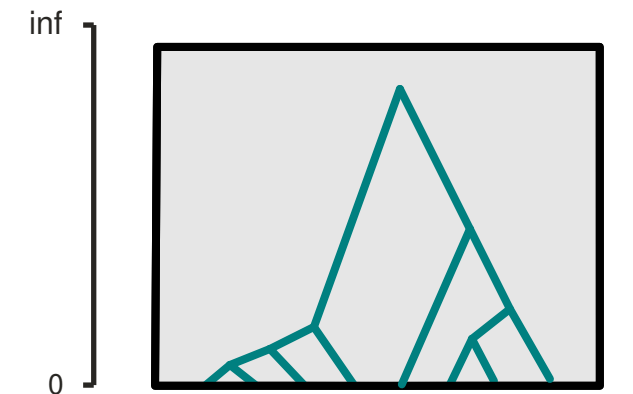


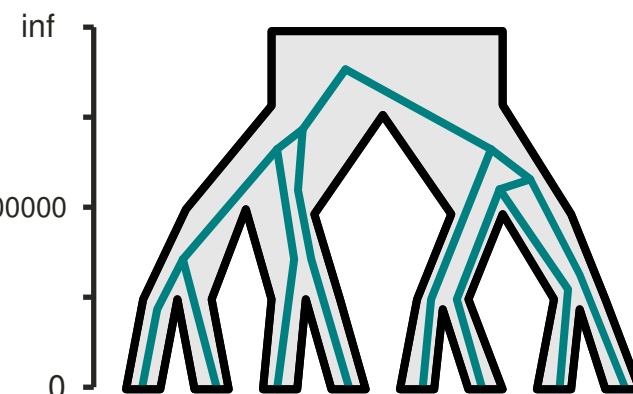
(a) Constant N_e Models



Single-population Model

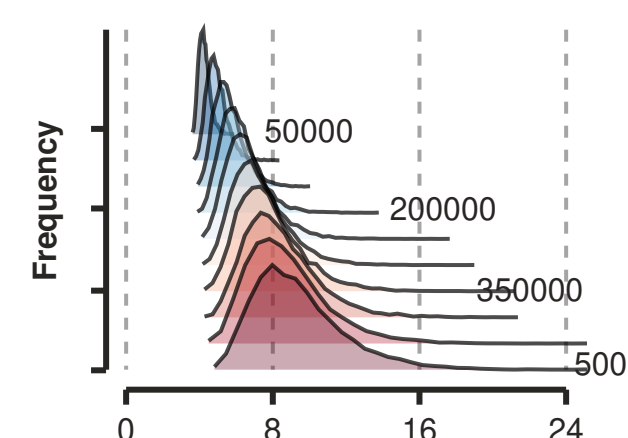
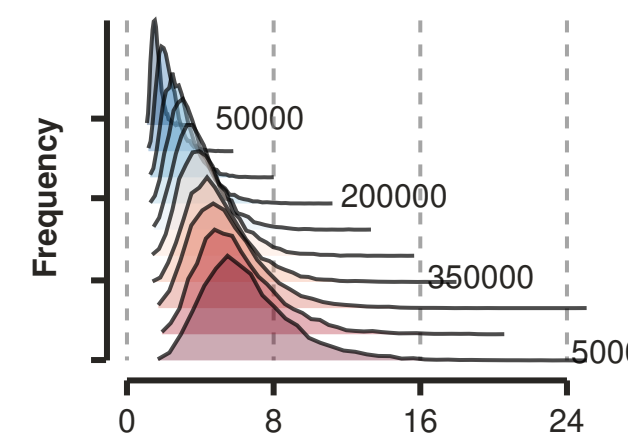
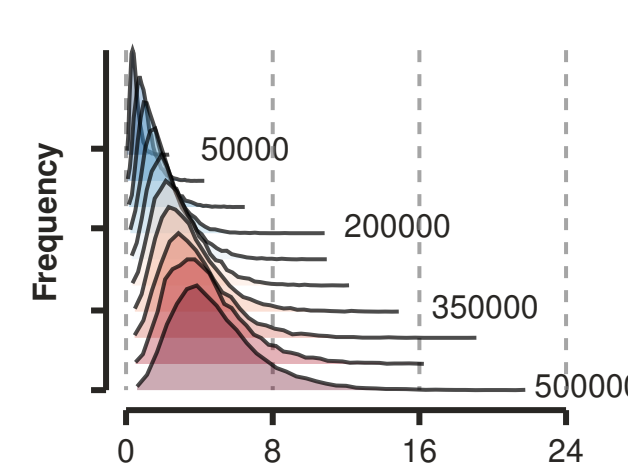


Two-population Model



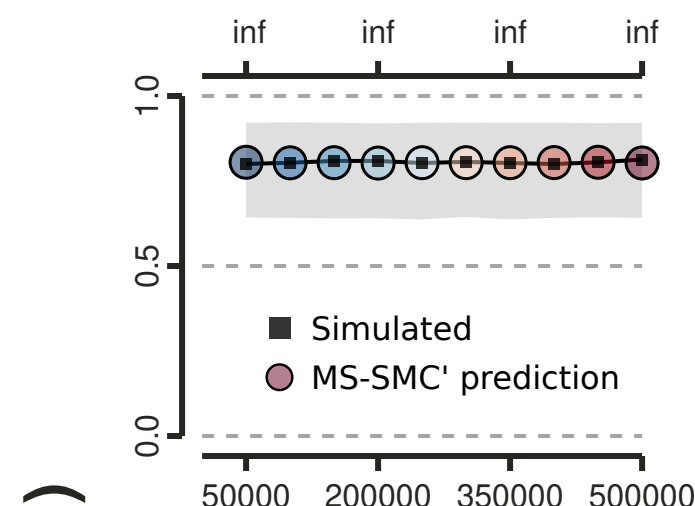
Phylogeny Model

(b) Sum Genealogy Edge Length distribution $\times N_e$

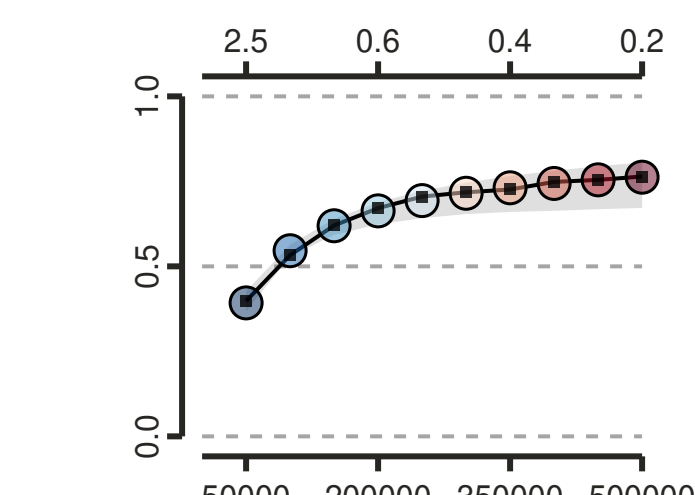
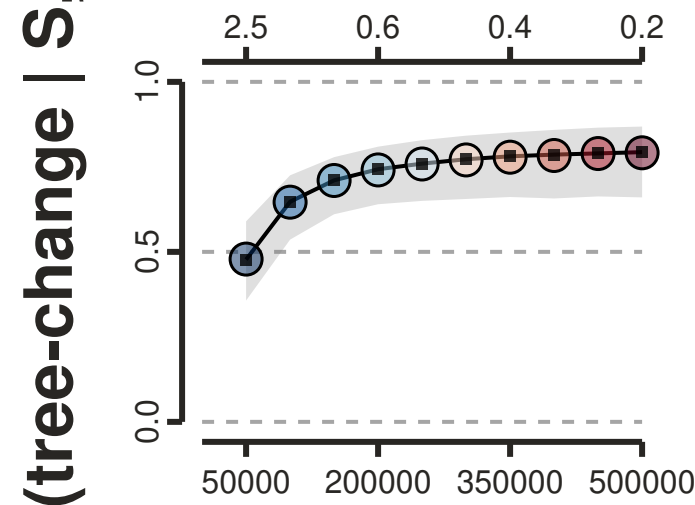


Genealogy sum length ($\times 10^6$)

(c) Model Edge Length ($\times 1/2N_e$)

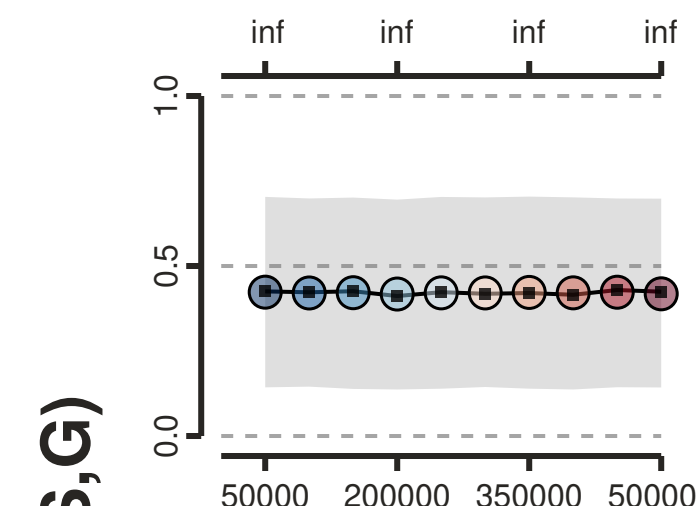


P(tree-change | S,G)

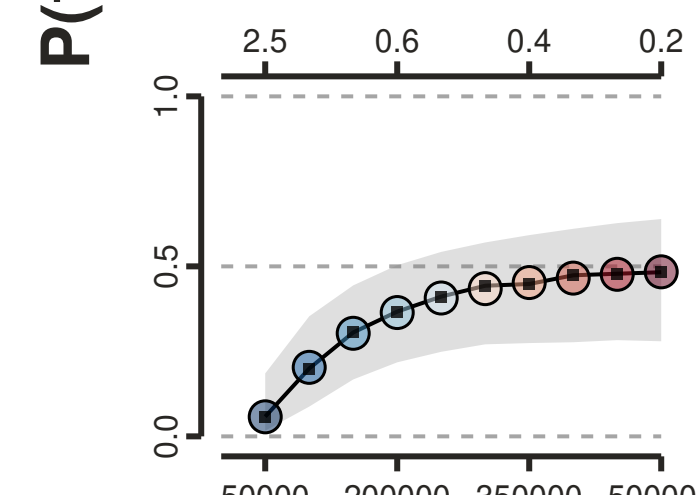
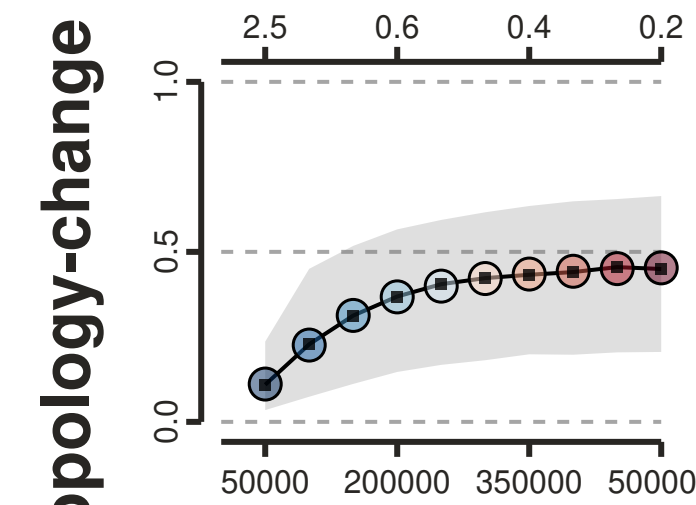


Effective population size (N_e)

(d) Model Edge Length ($\times 1/2N_e$)

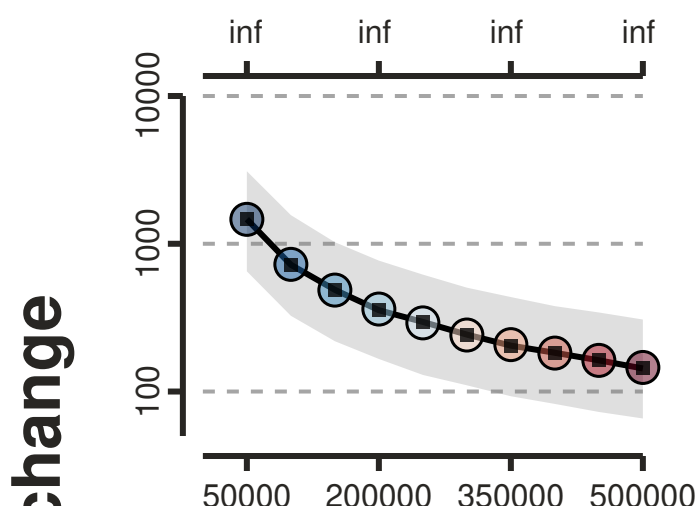


P(topology-change | S,G)

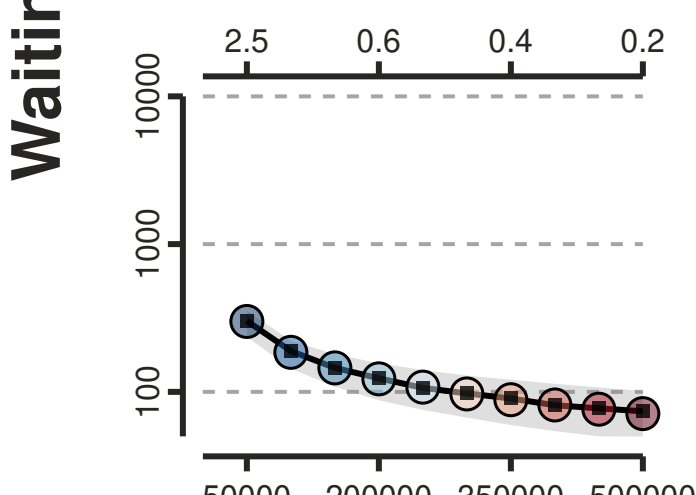
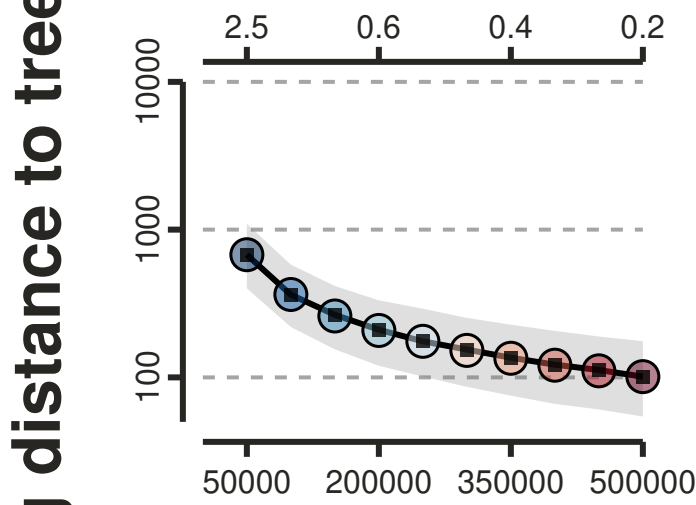


Effective population size (N_e)

(e) Model Edge Length ($\times 1/2N_e$)

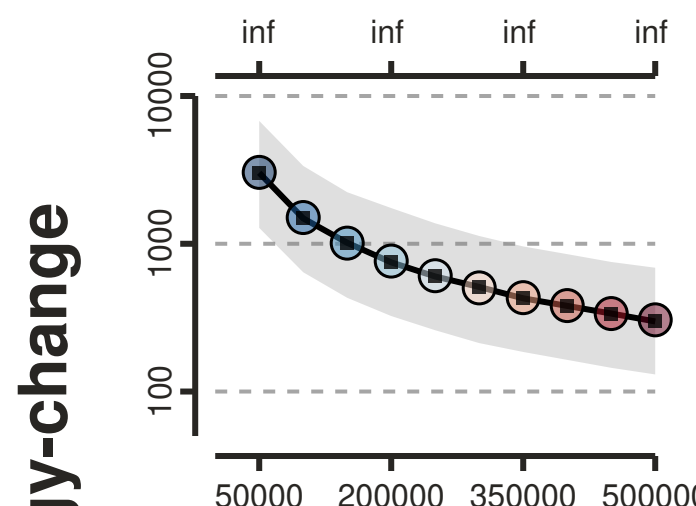


Waiting distance to tree-change

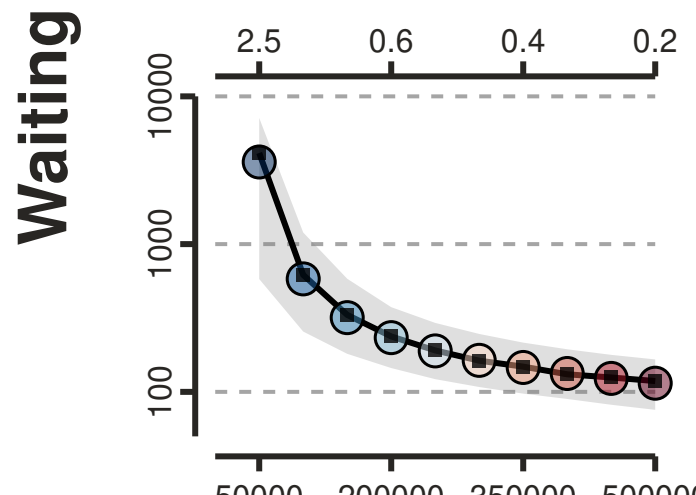
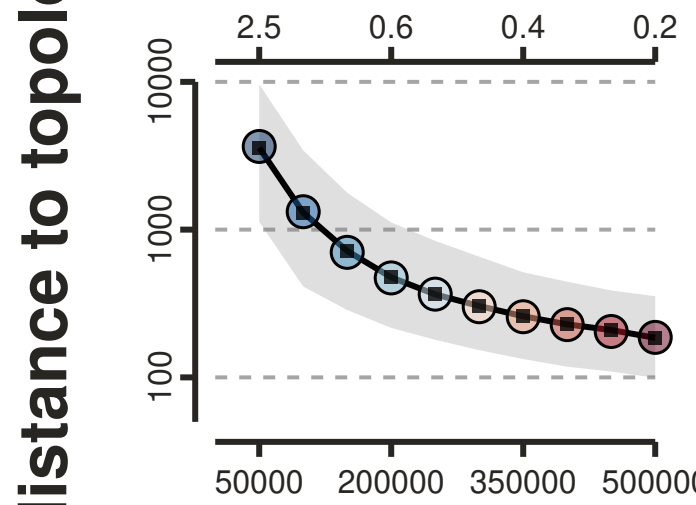


Effective population size (N_e)

(f) Model Edge Length ($\times 1/2N_e$)



Waiting distance to topology-change



Effective population size (N_e)