

Figure S1: Boxplots showing the estimated sequence divergence for the distance measures in the presence of rate variation among genes, compared to expected sequence divergence ($d = 2\tau + \theta$; dotted lines of the same colour as the boxes). Simulations were performed on a population tree with the coalescent using populations sizes of $\theta = 0.001$ (left panels) or $\theta = 0.01$ (right panels).

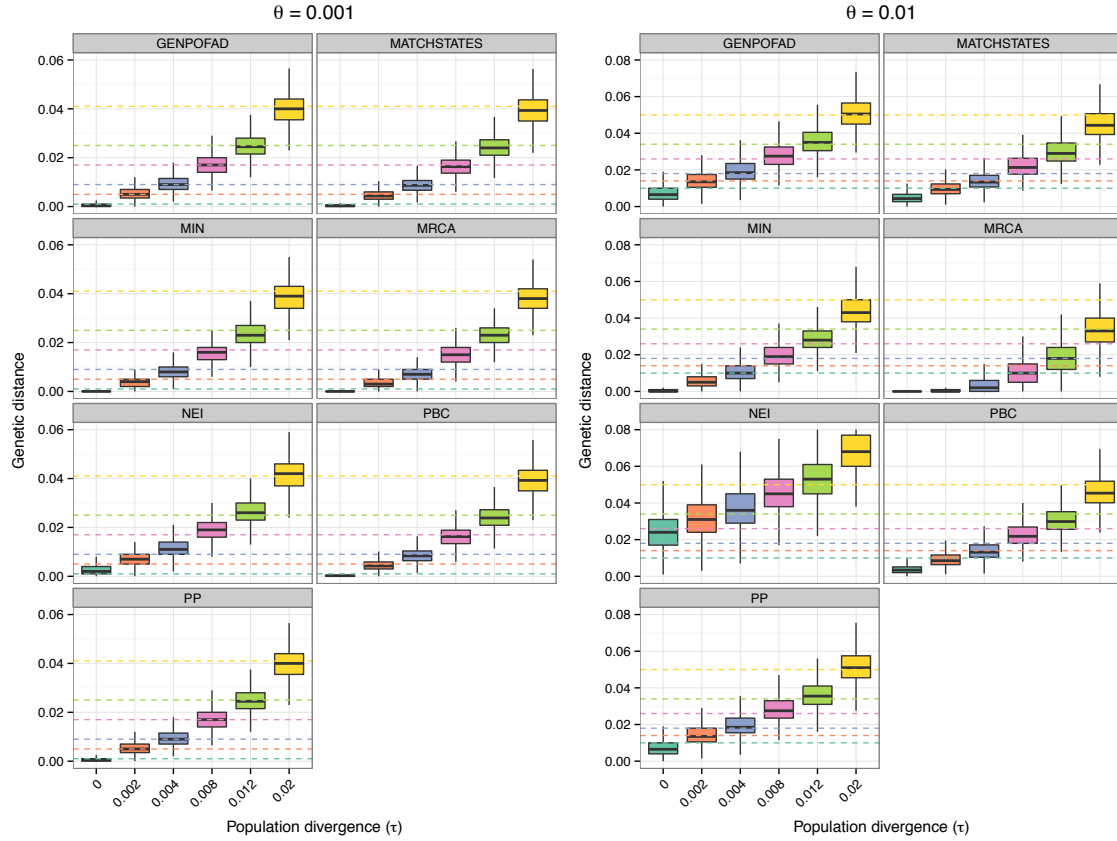


Figure S2: Boxplots showing the estimated sequence divergence for the distance measures in presence of recombination, compared to expected sequence divergence ($d = 2\tau + \theta$; dotted lines of the same colour as the boxes). Simulations were performed on a population tree with the coalescent using populations sizes of $\theta = 0.001$ (left panels) or $\theta = 0.01$ (right panels). Simulations were performed with DNA sequences of 1000 bp.