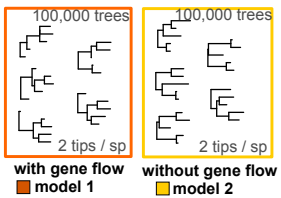
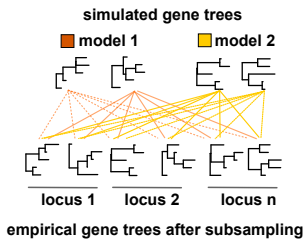


(1a) Simulate gene trees

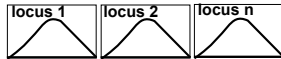


(2) Calculate distances between simulated and empirical gene trees

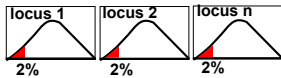


(3) Rejection

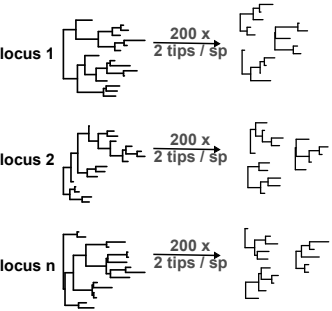
Build a distribution of gene tree distances including all models



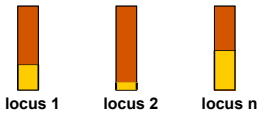
Retain gene tree distances within the 2% of distribution



(1b) Subsample empirical gene trees



(4) Calculate the relative frequency of each model in the retained distances



(5) Calculate total support of each model across all loci

