

Gene tree correction methods benchmark on simulated datasets

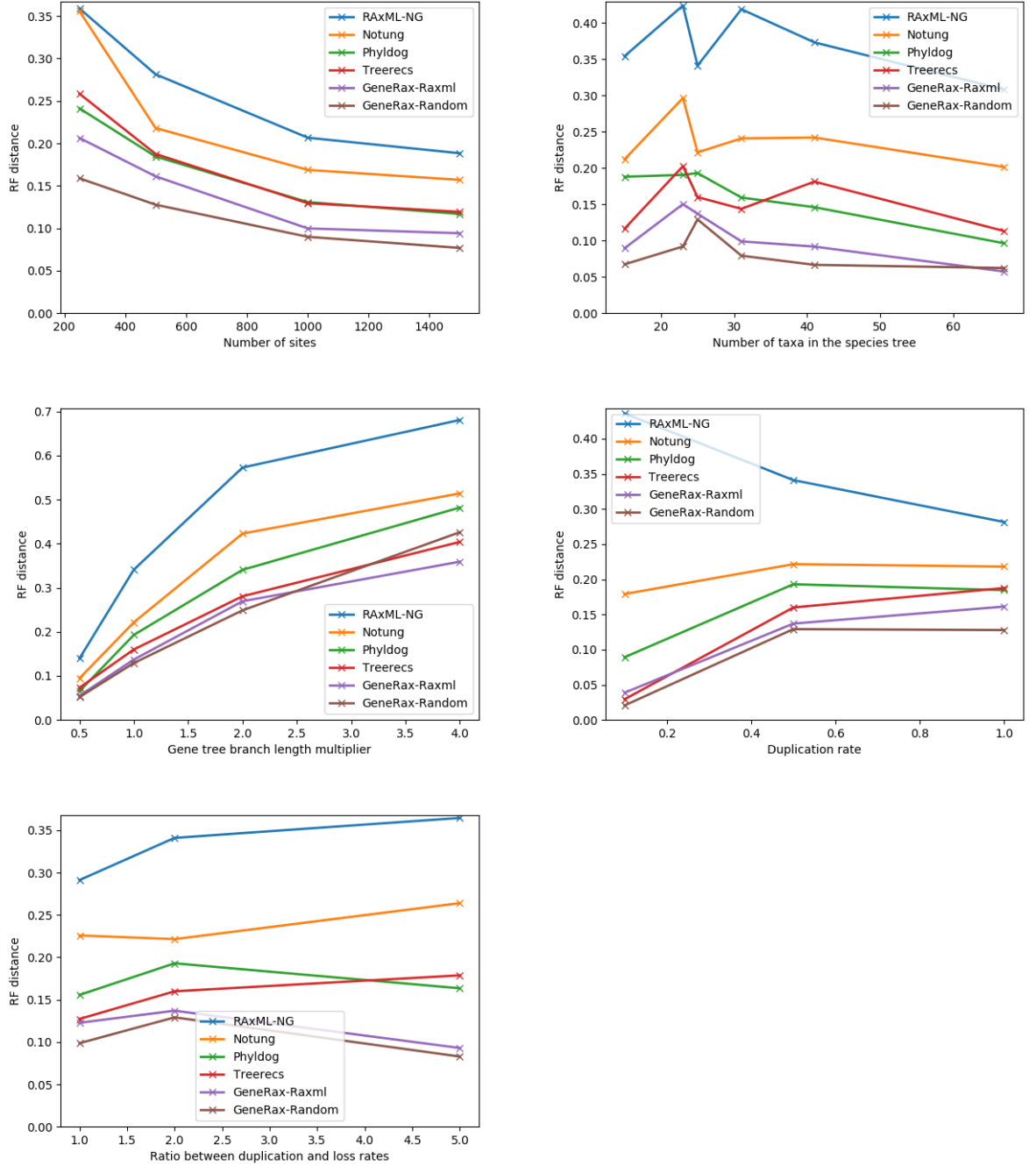


Figure 1: On each plot, one parameter varies while the other ones are fixed. Notung, Phyldog, Treerecs and GeneRax-Raxml start from the RAXML-NG tree. RAXML-NG was ran from 10 starting random trees. GeneRax-Random starts from a random tree. Notung and Treerecs need support values: we generated them with RAXML-NG and 100 bootstrap trees