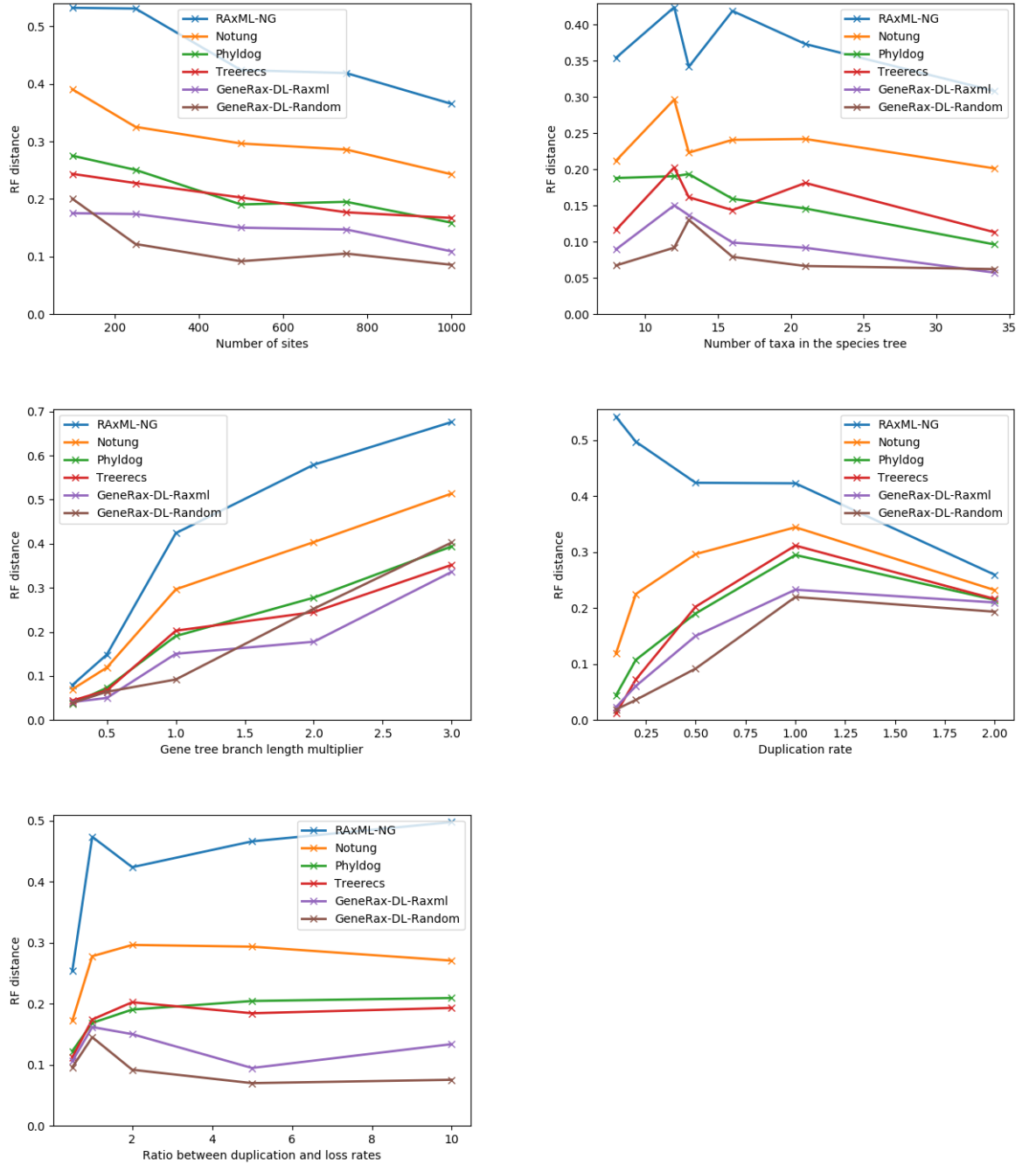# Gene tree correction methods benchmark on simulated datasets



**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.