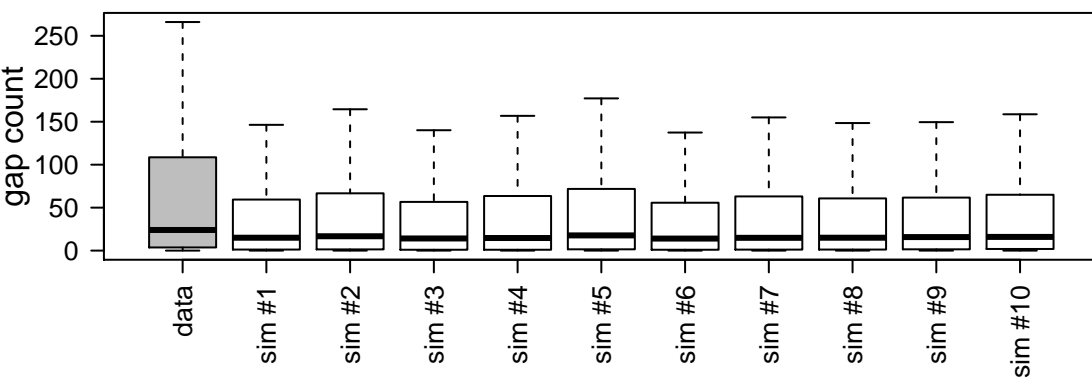
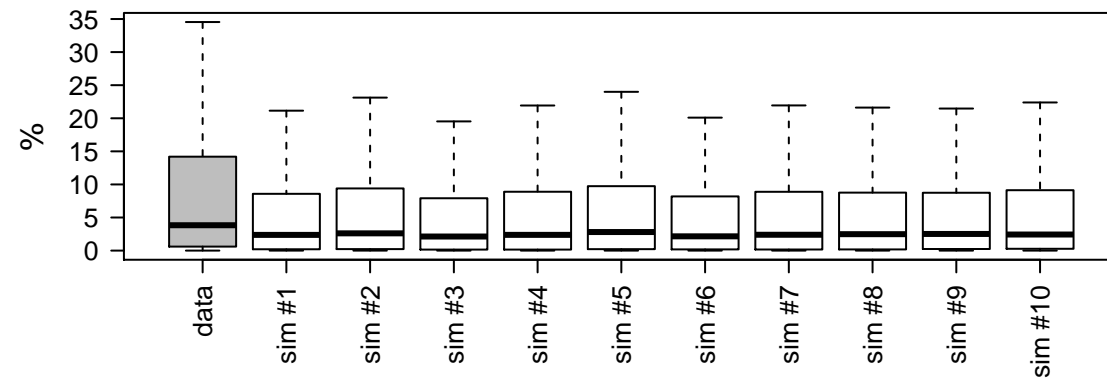


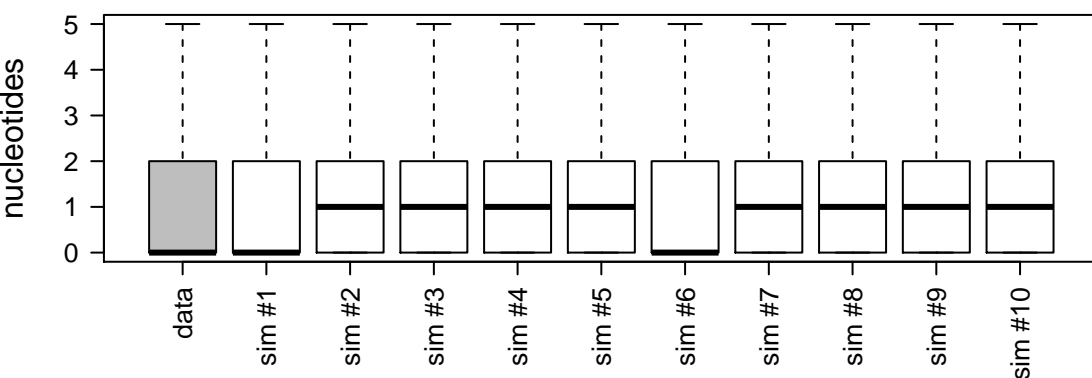
Number of gaps per sequence



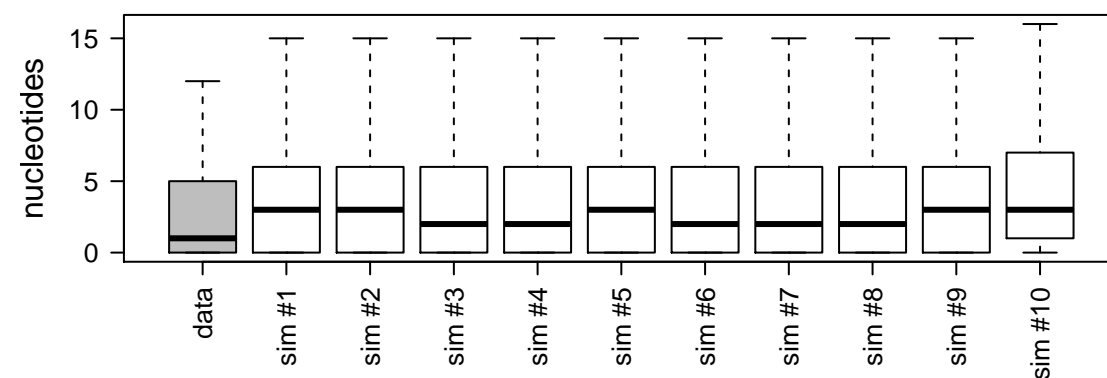
% gaps per sequence



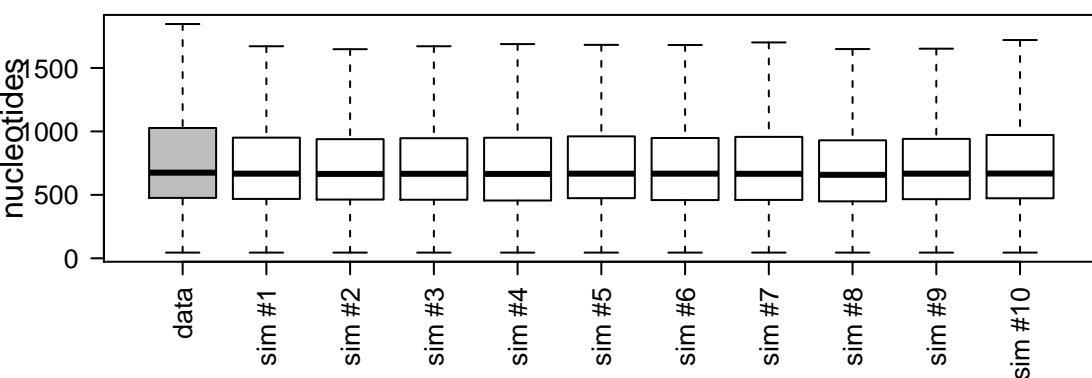
Number of insertions per alignment



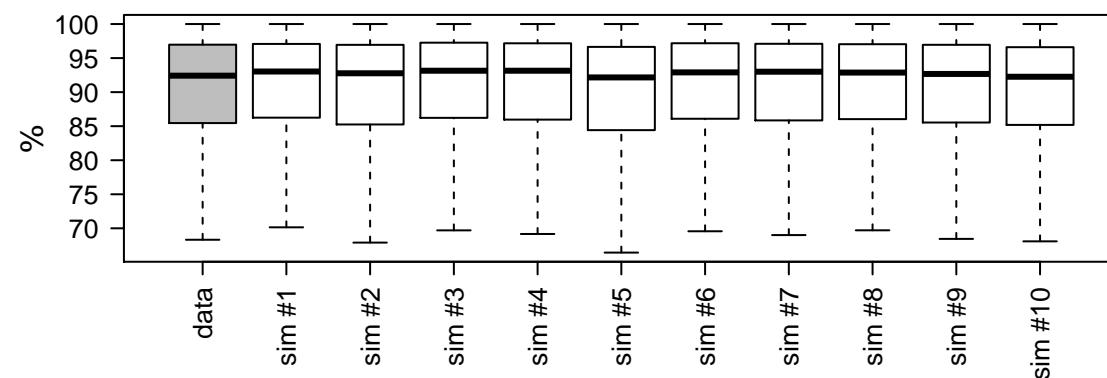
Number of deletions per alignment



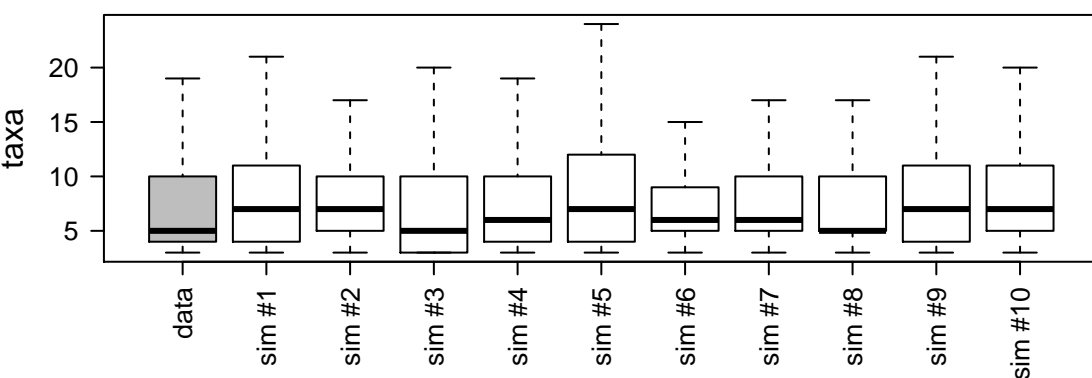
Number of nucleotides per sequence



% of invariant sites per alignment



Number of taxa per alignment



Number of alignments per taxon

