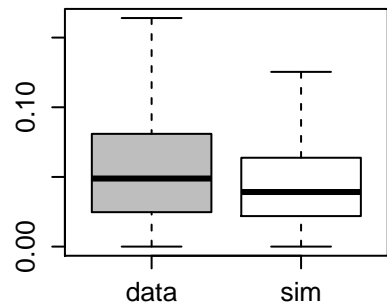
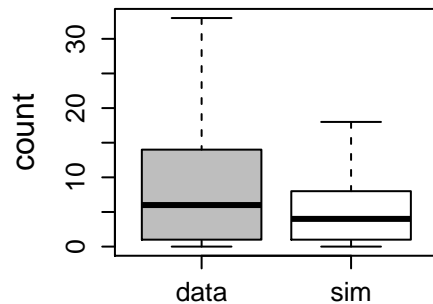


relative edit distance

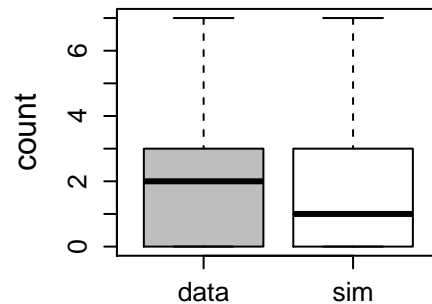
**average distance
within alignment**



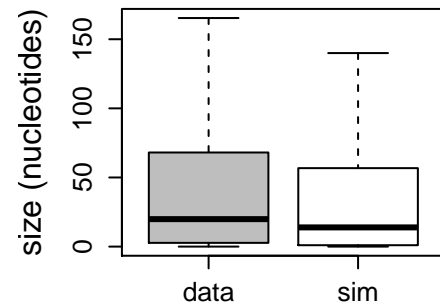
**Number of deletions
per alignment**



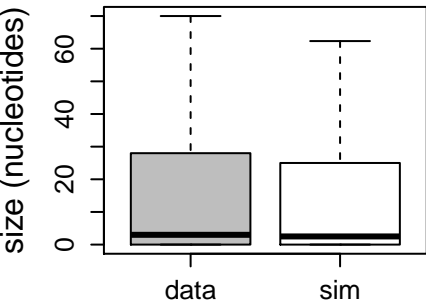
**Number of insertions
per alignment**



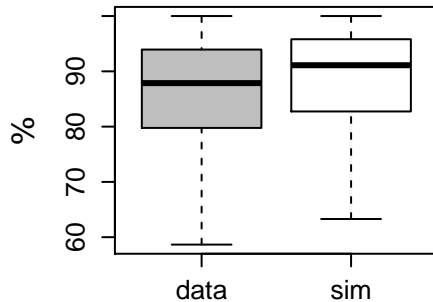
**Average size of deletions
per alignment**



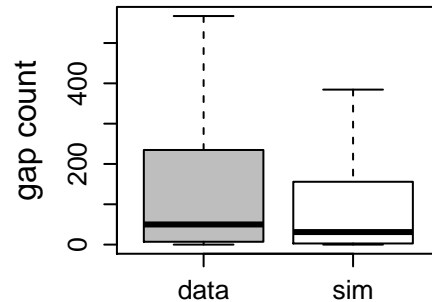
**Average size of insertions
per alignment**



**% of invariant sites
per alignment**



**Number of gaps
per sequence**



**Number of nucleotides
per sequence**

