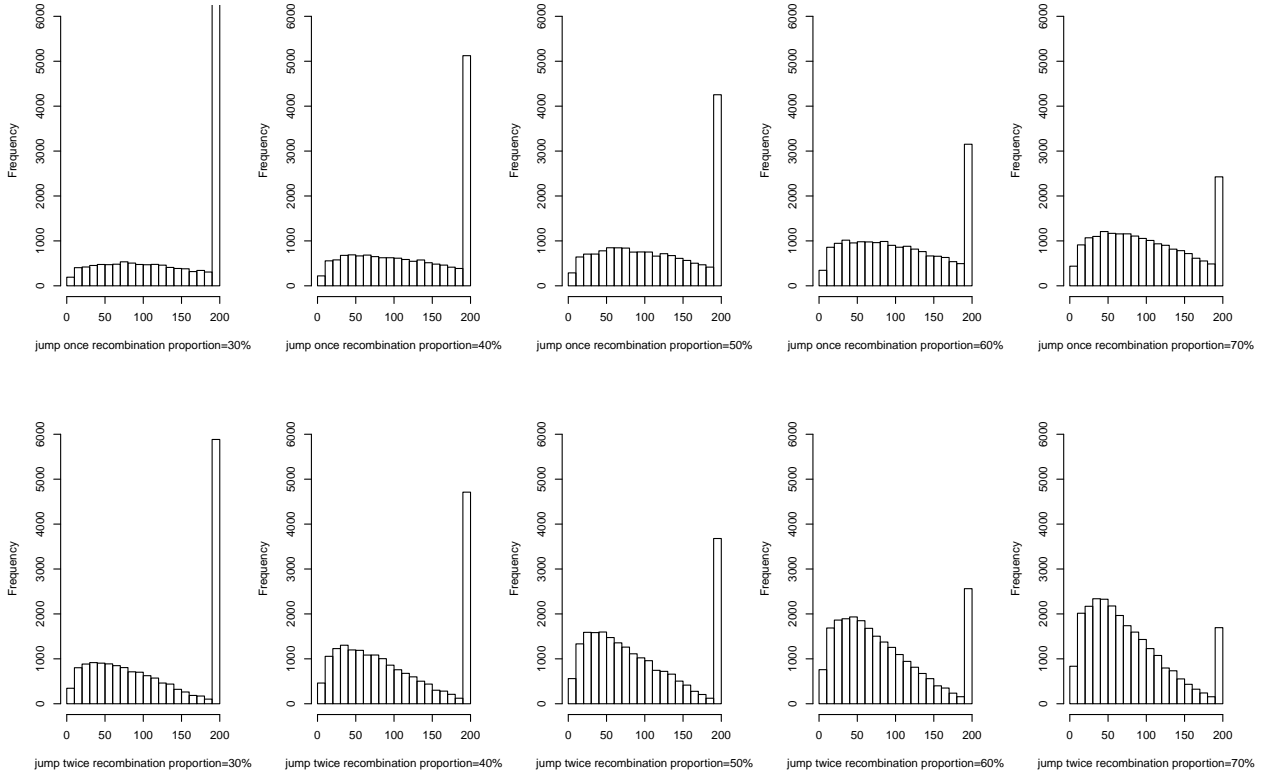


The distribution of contributing donor lengths in partial alignments calculated by JHMM

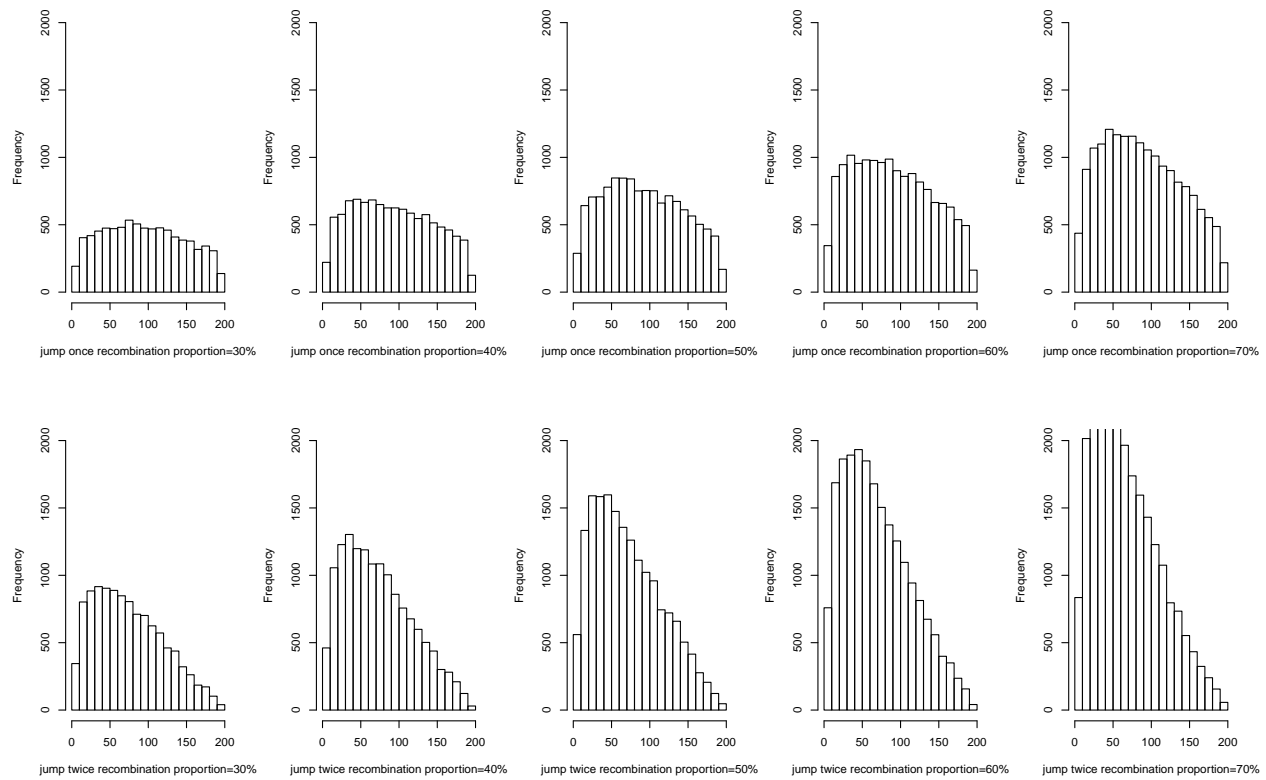
Qian Feng

22/08/2019

Let us firstly look at the distributions from simulated dataset. Following each plot is the histogram of contributing donor lengths when recombination proportion increases from 30% to 70% at both jump once and jump twice case.



Since some target sequence is fully aligned to another donor sequence, so we just temporarily ignore the whole segment length = 200 sequences. This leads to the pictures below. It turns out 10 amino acids is a good threshold for decreasing artefacts.



Lastly, this is the contributing donor lengths distribution from Ghana pilot real data.

