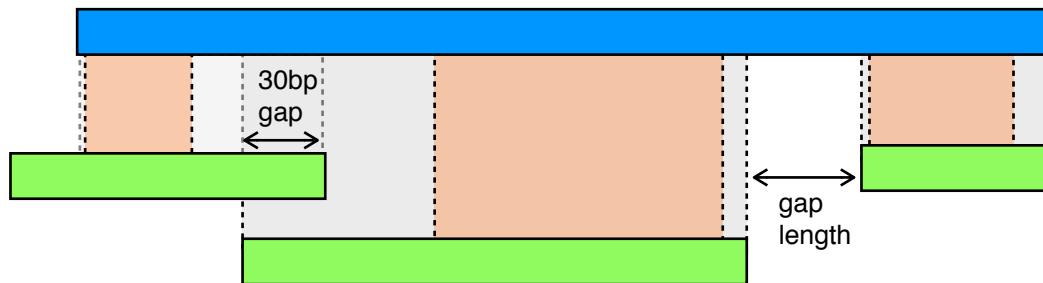


If the filters for minimum percent of the possible alignment ( $f\_align$  and  $s\_align$ ) were set to 30 and 90 the first alignment would be discarded and the second alignment would be kept in the filtered XMAPs and super-scaffolded fasta.



If the potential alignments of to scaffolds, their footprints, overlap each other in the XMAP they are separated by a 30 bp gap of n's in the super-scaffold fasta. If they do not overlap, a gap the length is the distance between the scaffold's footprints.



Assembled scaffolds

BioNano assembled molecule maps



Potential length of the alignment

Actual length of the alignment