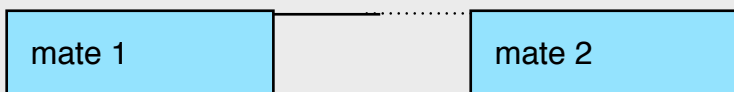


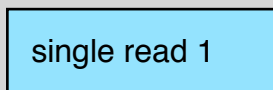


Pairs that align concordantly to the same contig with a MAPQ above the threshold (default =10) are **counted as one alignment to Contig A**

Pairs that aligning to the different contigs are **not counted as one alignment to any contig**



Pairs that align uniquely but discordantly (alignments violate expected insert size or orientation) to the same contig with a MAPQ above the threshold (default =10) are **counted as one alignment to Contig A**



Single ends that align uniquely with a MAPQ above the threshold (default =10) are **counted as one alignment to Contig A**



Pairs that with only one mate aligning with a MAPQ above the threshold (default =10) and the other mate aligning non-uniquely or not aligning at all are **counted as one alignment to Contig A**

