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| **aln** | bwa aln [-n maxDiff] [-o maxGapO] [-e maxGapE] [-d nDelTail] [-i nIndelEnd] [-k maxSeedDiff] [-l seedLen] [-t nThrds] [-cRN] [-M misMsc] [-O gapOsc] [-E gapEsc] [-q trimQual] <in.db.fasta> <in.query.fq> > <out.sai>  Find the SA coordinates of the input reads. Maximum *maxSeedDiff* differences are allowed in the first *seedLen* subsequence and maximum *maxDiff* differences are allowed in the whole sequence.  **OPTIONS:**   |  | | --- | |  | |  | | **-n***NUM* | Maximum edit distance if the value is INT, or the fraction of missing alignments given 2% uniform base error rate if FLOAT. In the latter case, the maximum edit distance is automatically chosen for different read lengths. [0.04] | | **-o***INT* | Maximum number of gap opens [1] | | **-e***INT* | Maximum number of gap extensions, -1 for k-difference mode (disallowing long gaps) [-1] | | **-d***INT* | Disallow a long deletion within INT bp towards the 3’-end [16] | | **-i***INT* | Disallow an indel within INT bp towards the ends [5] | | **-l***INT* | Take the first INT subsequence as seed. If INT is larger than the query sequence, seeding will be disabled. For long reads, this option is typically ranged from 25 to 35 for ‘-k 2’. [inf] | | **-k***INT* | Maximum edit distance in the seed [2] | | **-t***INT* | Number of threads (multi-threading mode) [1] | | **-M***INT* | Mismatch penalty. BWA will not search for suboptimal hits with a score lower than (bestScore-misMsc). [3] | | **-O***INT* | Gap open penalty [11] | | **-E***INT* | Gap extension penalty [4] | | **-R***INT* | Proceed with suboptimal alignments if there are no more than INT equally best hits. This option only affects paired-end mapping. Increasing this threshold helps to improve the pairing accuracy at the cost of speed, especially for short reads (~32bp). | | **-c** | Reverse query but not complement it, which is required for alignment in the color space. (Disabled since 0.6.x) | | **-N** | Disable iterative search. All hits with no more than *maxDiff* differences will be found. This mode is much slower than the default. | | **-q***INT* | Parameter for read trimming. BWA trims a read down to argmax\_x{\sum\_{i=x+1}^l(INT-q\_i)} if q\_l<INT where l is the original read length. [0] | | **-I** | The input is in the Illumina 1.3+ read format (quality equals ASCII-64). | | **-B***INT* | Length of barcode starting from the 5’-end. When *INT* is positive, the barcode of each read will be trimmed before mapping and will be written at the **BC** SAM tag. For paired-end reads, the barcode from both ends are concatenated. [0] | | **-b** | Specify the input read sequence file is the BAM format. For paired-end data, two ends in a pair must be grouped together and options **-1** or **-2** are usually applied to specify which end should be mapped. Typical command lines for mapping pair-end data in the BAM format are:  bwa aln ref.fa -b1 reads.bam > 1.sai  bwa aln ref.fa -b2 reads.bam > 2.sai  bwa sampe ref.fa 1.sai 2.sai reads.bam reads.bam > aln.sam | | **-0** | When **-b** is specified, only use single-end reads in mapping. | | **-1** | When **-b** is specified, only use the first read in a read pair in mapping (skip single-end reads and the second reads). | | **-2** | When **-b** is specified, only use the second read in a read pair in mapping. | |