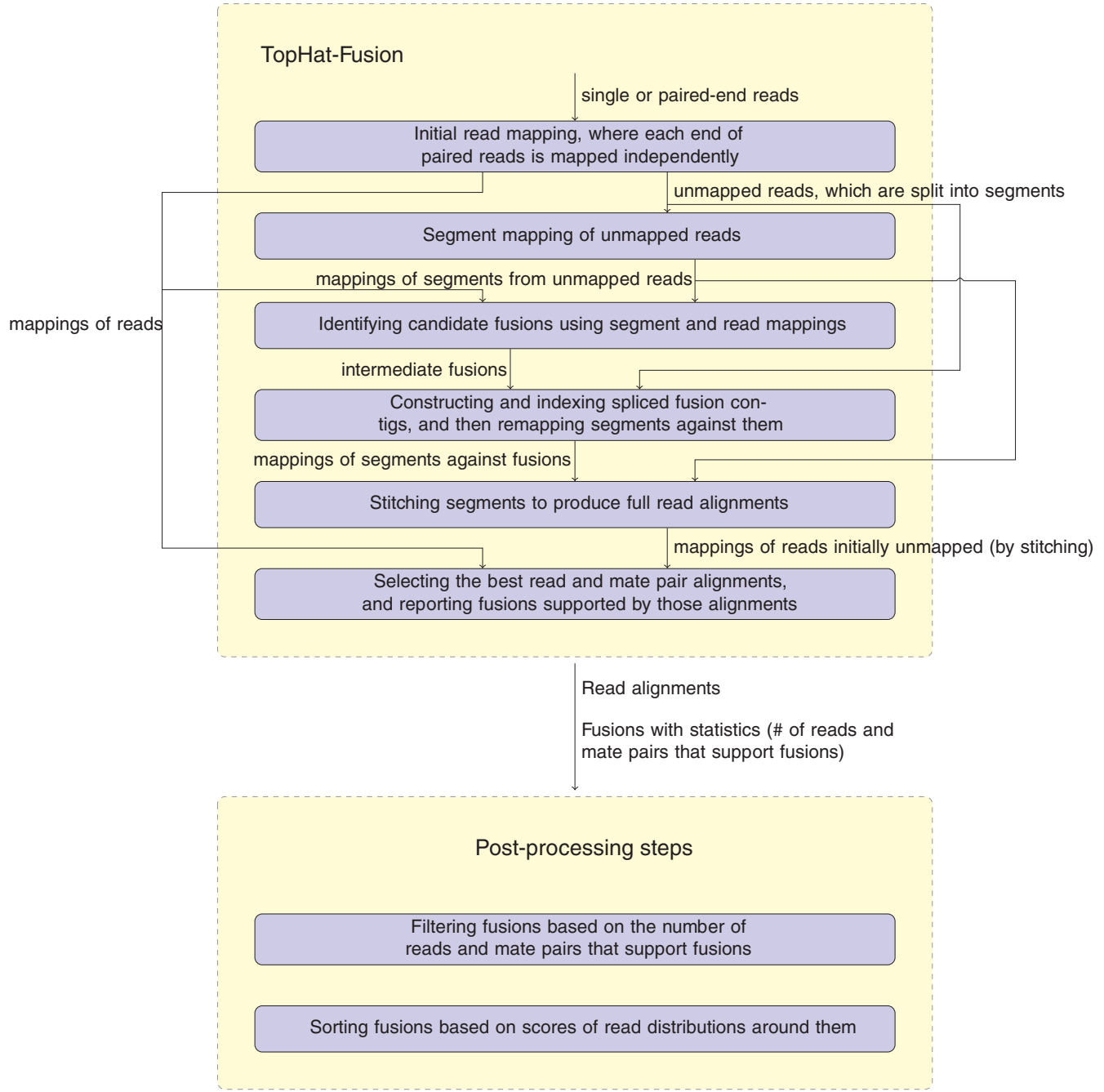
TopHat-Fusion
single or paired-end reads
Initial read mapping, where each end of paired reads is mapped independently
unmapped reads, which are split into segments
Segment mapping of unmapped reads
mappings of segments from unmapped reads
mappings of reads
Identifying candidate fusions using segment and read mappings
intermediate fusions
Constructing and indexing spliced fusion contigs, and then remapping segments against them
mappings of segments against fusions
Stitching segments to produce full read alignments
mappings of reads initially unmapped (by stitching)
Selecting the best read and mate pair alignments, and reporting fusions supported by those alignments
Read alignments
Fusions with statistics (# of reads and mate pairs that support fusions)
Post-processing steps
Filtering fusions based on the number of reads and mate pairs that support fusions
Sorting fusions based on scores of read distributions around them