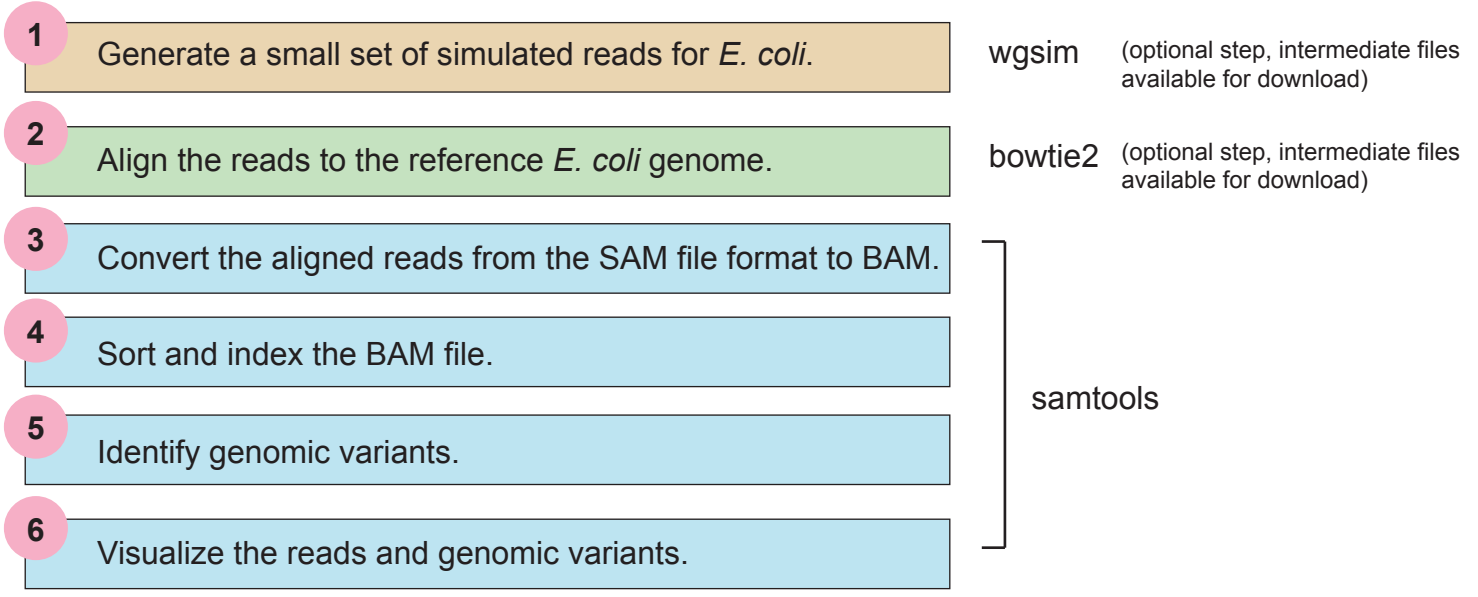
1
Generate a small set of simulated reads for E. coli.
wgsim
(optional step, intermediate files available for download)
2
Align the reads to the reference E. coli genome.
bowtie2
(optional step, intermediate files available for download)
3
Convert the aligned reads from the SAM file format to BAM.
4
Sort and index the BAM file.
5
Identify genomic variants.
6
Visualize the reads and genomic variants.
samtools