samtools

> Tools for handling high-throughput sequencing (genomics) data.
> Used for reading/writing/editing/indexing/viewing of data in SAM/BAM/CRAM format.

- Convert a SAM input file to BAM stream and save to file:

```
samtools view -S -b {{input.sam}} > {{output.bam}}
```

- Take input from stdin (-) and print the SAM header and any reads overlapping a specific region to stdout:

```
{{other_command}} | samtools view -h - chromosome:start-end
```

- Sort file and save to BAM (the output format is automatically determined from the output file's extension):

```
samtools sort {{input}} -o {{output.bam}}
```

- Index a sorted BAM file (creates {{sorted_input.bam.bai}}):

```
samtools index {{sorted_input.bam}}
```

- Print alignment statistics about a file:

```
samtools flagstat {{sorted_input}}
```

- Count alignments to each index (chromosome / contig):

```
samtools idxstats {{sorted_indexed_input}}
```

- Merge multiple files:

```
samtools merge {{output}} {{input_1}} [{{input_2}}...]
```

- Split input file according to read groups:

```
samtools split {{merged_input}}
```