

SNAP Quick Start

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If you received SNAP as a compressed file, first decompress it with `gunzip`. Then use the following commands:

To build an index into a new directory named `index-dir`:

```
snap-aligner index reference.fa index-dir
```

You can also give the `-s` option to set seed size. The seed size is the minimum size of a perfect match between the read and the reference for a given alignment. The default is 27, but you might want to choose a smaller size if have short reads (say, less than 100 bases). Seed sizes below 20 are not recommended due to poor performance and false positives.

For a human genome reference, we recommend at least 64GB of memory. However, it will work with only 48GB, but when you build the index you need to specify the `-sm` (“small memory”) switch, which will trade speed of index build for memory footprint. If you do not have enough memory to build the index with `-sm` then you probably do not have enough memory to align reads with that index. `-sm` only affects the speed of index building; the indices built with it are the same as without it.

```
snap-aligner index reference.fa index-dir -sm
```

To align unpaired reads:

```
snap-aligner single index-dir reads.fq -o output.sam
```

To align paired-end reads:

```
snap paired index-dir read1.fq read2.fq -o output.sam
```

SNAP will also take input in SAM and BAM format, and will produce output in BAM format. It will determine the file type by the file extension (“`.sam`” or “`.bam`” or “`.fastq`” for example).

If you want to sort, mark duplicates and index the output (thus skipping the need for several pipeline stages commonly used with other aligners), include the `-so` flag. For example:

```
snap-aligner paired index-dir read1.fq read2.fq -so -o output.bam
```

By default, SNAP will use one thread per core on your machine, so there is ordinarily no need to tell it how many to use.