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 24, 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.