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:

```
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.

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 and use BAM output. For example:

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