# Mapping read data

MAQ, BOWTIE2, BWA, SOAP2, SSAHA2, ELAND2, RMAP, NovoAlign, Mosaik

# Mapping read data :

# Bowtie2

http://bowtie-bio.sourceforge.net/bowtie2/index.shtml

http://bowtie-bio.sourceforge.net/bowtie2/manual.shtml

# Building genome index using Bowtie2

- bowtie2-build [options] <reference_in> <bt2_base>

| Command | What does it mean? |
| --- | --- |
| <reference_in> | A comma-separated list of files containg reference sequences |
| <bt2_base> | The basename of the index file to write (would be written in .bt2 format) |

# Using Bowtie2

- bowtie2 [options] -x <bt2-idx> {-1 <m1> -2 <m2> | -U <r> | --interleaved <i>} -S [<sam>]

| Command | What does it mean? |
|---|---|
| -x <bt2-idx> | Basename for Index file for the reference genome |
| -1 <m1> | File containing Paired end read 1 / mate 1 sequences |
| -2 <m2> | File containing Paired end read 2 / mate 2 sequences |
| -U <r> | File containing Unpaired read sequences |
| -- interleaved <i> | File containing read 1 and read 2 sequences interleaved |
| -S <sam> | Output file containing alignments in .sam format |
| -q | Reads in <m1>, <m2> , <r> are .fastq files |

# Bowtie2 : Input options

| Command | What does it mean? |
|---|---|
| -5/--trim5 <int> | Trim <int> bases from 5' (left) end of each read before alignment (default: 0). |
| -3/--trim3 <int> | Trim <int> bases from 3' (right) end of each read before alignment (default: 0). |
| --trim-to [3:\|5:]<int> | Trim reads exceeding <int> bases. Bases will be trimmed from either the 3' (right) or 5' (left) end of the read. If the read end if not specified, bowtie 2 will default to trimming from the 3' (right) end of the read. --trim-to and -3/-5 are mutually exclusive. |
| --phred33 | Input qualities are ASCII chars equal to the Phred quality plus 33. This is also called the "Phred+33" encoding, which is used by the very latest Illumina pipelines. |
| --phred64 | Input qualities are ASCII chars equal to the Phred quality plus 64. This is also called the "Phred+64" encoding. |

# Bowtie2 : Run options

| Command | What does it mean? |
|---|---|
| --end-to-end mode | Alignment from one end of the read to the other end |
| --very-fast | |
| --fast | |
| --sensitive | (default in --end-to-end mode) |
| --very-sensitive | |
| --local mode | Not entire read is required to align (soft clipping/trimming) |
| --very-fast-local | |
| --fast-local | |
| --sensitive-local | (default in --local mode) |
| --very-sensitive-local | |

# Bowtie2 : Output options

| Command | What does it mean? |
|---|---|
| --fr/--rf/--ff | The upstream/downstream mate orientations for a valid paired-end alignment against the forward reference strand. E.g., if --fr is specified and there is a candidate paired-end alignment where mate 1 appears upstream of the reverse complement of mate 2 Default: --fr (appropriate for Illumina's Paired-end Sequencing Assay). |
| --no-mixed | By default, when bowtie2 cannot find a concordant or discordant alignment for a pair, it then tries to find alignments for the individual mates. This option disables that behavior. |
| --no-discordant | By default, bowtie2 looks for discordant alignments if it cannot find any concordant alignments. A discordant alignment is an alignment where both mates align uniquely, but that does not satisfy the paired-end constraints (--fr/--rf/--ff). This option disables that behavior. |

# Bowtie2 : Output options

| Command | What does it mean? |
| --- | --- |
| -I/--minins <int> | The minimum fragment length for valid paired-end alignments. E.g. if -I 60 is specified and a paired-end alignment consists of two 20-bp alignments in the appropriate orientation with a 20-bp gap between them, that alignment is considered valid (as long as -X is also satisfied). |
| -X/--maxins <int> | The maximum fragment length for valid paired-end alignments. E.g. if -X 100 is specified and a paired-end alignment consists of two 20-bp alignments in the proper orientation with a 60-bp gap between them, that alignment is considered valid (as long as -I is also satisfied). Default: 500. |