Useful and Usable
Map with Bowtie for Illumina

Will you select a reference genome from your history or use a built-in index?:
- Use a built-in index

Built-ins were indexed using default options

Select a reference genome:
- ce6

if your genome of interest is not listed - contact Galaxy team

Is this library mate-paired?:
- Single-end

FASTQ file:
- 1: Pasted Entry

Must have Sanger-scaled quality values with ASCII offset 33

Bowtie settings to use:
- Commonly used

For most mapping needs use Commonly used settings. If you want full control use Full parameter list

Suppress the header in the output SAM file:
- Checkmark

Bowtie produces SAM with several lines of header information by default

Execute
Bowtie settings to use:

- Full parameter list
- For most mapping needs use Commonly used settings. If you want full control use full parameter list

Skip the first n reads (-s):

- 0

Only align the first n reads (-u):

- 1 for off

Trim n bases from high-quality (left) and of each read before alignment (-5):

- 0

Trim n bases from low-quality (right) end of each read before alignment (-3):

- 0

Maximum number of mismatches permitted in the seed (-n):

- 2

May be 0, 1, 2, or 3

Maximum permitted total of quality values at mismatched read positions (-e):

- 70

Seed length (-l):

- 28

Minimum value is 5

Whether or not to round to the nearest 10 and saturating at 30 (-nomaaround):

- Round to nearest 10

Number of mismatches for SOAP-like alignment policy (-v):

- 1

-1 for default MAQ-like alignment policy

Whether or not to try as hard as possible to find valid alignments when they exist (-y):

- Do not try hard

Tryhard mode is much slower than regular mode

Report up to n valid alignments per read (-k):

- 1

Whether or not to report all valid alignments per read (-a):

- Do not report all valid alignments

Suppress all alignments for a read if more than n reportable alignments exist (-m):

- 1

-1 for no limit

Whether or not to make Bowtie guarantee that reported singleton alignments are 'best' in terms of stratum and in terms of the quality values at the mismatched positions (-best):

- Do not use best

Removes all stratum bias. Only affects which alignments are reported by Bowtie. Runs slower with best option

Maximum number of backtracks permitted when aligning a read (-maxbts):

- 125

Override the offset of the index to n (-o):

- 1

-1 for default

Seed for pseudo-random number generator (-seed):

- 1

-1 for default

Suppress the header in the output SAM file:

- Bowtie produces SAM with several lines of header information by default

Execute
Bowtie settings to use:
- Full parameter list
- For most mapping needs use Commonly used settings. If you want full control use Full parameter list
- Skip the first n reads (-s): 0
- Only align the first n reads (-u): -1
  -1 for off
- Trim n bases from high-quality (left) end of each read before alignment (-S): 0
- Trim n bases from low-quality (right) end of each read before alignment (-L): 0
- Maximum number of mismatches permitted in the seed (-n): 2
  - May be 0, 1, 2, or 3
- Maximum permitted total of quality values at mismatched read positions (-o): 7D
- Seed length (-l): 28
- Minimum value is 5
- Whether or not to round to the nearest 10 and saturating at 30 (-nomaground): Round to nearest 10
  - C
- Whether or not to try as hard as possible to find valid alignments when they exist (-y): Do not try hard
  - C
- Try hard mode is much slower than regular mode
- Report up to n valid alignments per read (-k): 1
- Whether or not to report all valid alignments per read (-a): Do not report all valid alignments
  - C
- Suppress all alignments for a read if more than n reportable alignments exist (-m): -1
  - C
  -1 for no limit
- Whether or not to make Bowtie guarantee that reported singleton alignments are "best" in terms of stratum and in terms of the quality values at the mismatched positions (-best): Do not use best
  - C
  - Removes all stratum bias. Only affects which alignments are reported by Bowtie. Runs slower with best option
- Maximum number of backtracks permitted when aligning a read (-maxback): 125
- Override the offset of the index to n (-o): -1
  - C
  -1 for default
- Seed for pseudo-random number generator (-seed): -1
  - C
  -1 for default
- Suppress the header in the output SAM file:
  - X
  - Bowtie produces SAM with several lines of header information by default

Execute
Bowie settings to use:
- Full parameter list
- For most mapping needs use Commonly used settings. If you want full control use Full parameter list

Skip the first n reads (-s):
- 0

Only align the first n reads (-u):
- 1
- 0 for off

Trim n bases from high-quality (left) end of each read before alignment (-5):
- 0

Trim n bases from low-quality (right) end of each read before alignment (-3):
- 0

Maximum number of mismatches permitted in the seed (-n):
- 2
- May be 0, 1, 2, or 3

Maximum permitted total of quality values at mismatched read positions (-e):
- 7

Seed length (-l):
- 28

Minimum value is 5

Whether or not to round to the nearest 10 and saturating at 30 (-noground):
- Round to nearest 10

Number of mismatches for SOAP-like alignment policy (-v):
- 1
- -1 for default MAQ-like alignment policy

Whether or not to try as hard as possible to find valid alignments when they exist (-v):
- Do not try hard

Report up to n valid alignments per read (-k):
- 1

Whether or not to report all valid alignments per read (-o):
- Do not report all valid alignments

Suppress all alignments for a read if more than n reportable alignments exist (-m):
- -1
- -1 for no limit

Whether or not to make Bowtie guarantee that reported singleton alignments are ‘best’ in terms of stratum and in terms of the quality values at the mismatched positions (-best):
- Do not use best

Maximum number of backtracks permitted when aligning a read (-maxhts):
- 125

Override the offset of the index to n (-o):
- 1
- -1 for default

Seed for pseudo-random number generator (--seed):
- 1
- -1 for default

Suppress the header in the output SAM file:
- 

Bowtie produces SAM with several lines of header information by default:
- "Execute"
Bowtie settings to use:

For most mapping needs use Commonly used settings. If you want full control use Full parameter list.

Skip the first n reads (-s):

-1

Only align the first n reads (-u):

-1 for off

Trim n bases from high-quality (left) end of each read before alignment (-5):

0

Trim n bases from low-quality (right) end of each read before alignment (-3):

0

Maximum number of mismatches permitted in the seed (-n):

2

May be 0, 1, 2, or 3

Maximum permitted total of quality values at mismatched read positions (-e):

7D

Seed length (-l):

28

Minimum value is 5

Whether or not to round to the nearest 10 and saturating at 30 (-nomaxground):

Round to nearest 10

Number of mismatches for SOAP-like alignment policy (-v):

-1

-1 for default MAQ-like alignment policy

Whether or not to try as hard as possible to find valid alignments when they exist (-y):

Do not try hard

Try hard mode is much slower than regular mode

Report up to n valid alignments per read (-k):

1

Whether or not to report all valid alignments per read (-a):

Do not report all valid alignments

Suppress all alignments for a read if more than n reportable alignments exist (-m):

-1

-1 for no limit

Whether or not to make Bowtie guarantee that reported singleton alignments are ‘best’ in terms of stratum and in terms of the quality values at the mismatched positions (-best):

Do not use best

Removes all stratum bias. Only affects which alignments are reported by Bowtie. Runs slower with best option

Maximum number of backtracks permitted when aligning a read (-maxbackts):

125

Override the off rate of the index to n (-e):

-1

-1 for default

Seed for pseudo-random number generator (-seed):

-1

-1 for default

Suppress the header in the output SAM file:

Yes

Bowtie produces SAM file with several lines of header information by default.

Execute
Override the offrate of the index with `<int>`. If `<int>` is greater than the offrate used to build the index, then some row markings are discarded when the index is read into memory. This reduces the memory footprint of the aligner but requires more time to calculate text offsets. `<int>` must be greater than the value used to build the index.
Library:
1: Pasted Entry

Reference database:
Select from list of available databases

Available database:
dm3 (whole genome)

Max. number of mismatches allowed in the entire read:
0

Multi-mappers limit:
10
Multi-mappers mapping more than this number of times will be discarded.

Find reads matching:
Both strands

Execute
## Mapping results for ag42fa

### Summary Statistics

<table>
<thead>
<tr>
<th>Category</th>
<th>Sequences</th>
<th>%_seq</th>
<th>Reads</th>
<th>%_reads</th>
<th>%_reads</th>
</tr>
</thead>
<tbody>
<tr>
<td>Input</td>
<td>1,010,128</td>
<td>100.00</td>
<td>14,196,384</td>
<td>100.00</td>
<td></td>
</tr>
<tr>
<td>non Mappers</td>
<td>297,178</td>
<td>29.42</td>
<td>3,625,468</td>
<td>25.54</td>
<td></td>
</tr>
<tr>
<td>maxed-out Mappers</td>
<td>64,467</td>
<td>6.38</td>
<td>2,624,179</td>
<td>18.48</td>
<td></td>
</tr>
<tr>
<td>All Mappers</td>
<td>648,463</td>
<td>64.2</td>
<td>7,946,737</td>
<td>55.98</td>
<td>100.00</td>
</tr>
<tr>
<td>Unique Mappers</td>
<td>604,348</td>
<td>93.19</td>
<td>6,453,910</td>
<td>81.21</td>
<td></td>
</tr>
<tr>
<td>multi Mappers</td>
<td>44,135</td>
<td>6.81</td>
<td>1,492,827</td>
<td>18.79</td>
<td></td>
</tr>
</tbody>
</table>

### Mapping Parameters

<table>
<thead>
<tr>
<th>Parameter</th>
<th>Value</th>
</tr>
</thead>
<tbody>
<tr>
<td>bowtie_params</td>
<td>-k 10 -m 10 -v 2</td>
</tr>
<tr>
<td>database</td>
<td>/data/hannon/gordon/databases/bowtie/dm3_genome/dm3_genome</td>
</tr>
<tr>
<td>input_filename</td>
<td>/datafc/hannon/gordon/bowtie.dataset_79015.fa.tm7Pu6y2VJMd/input/dataset_79015.fa</td>
</tr>
<tr>
<td>mapping_starttime</td>
<td>Thu May 13 23:46:44 2010</td>
</tr>
<tr>
<td>project_name</td>
<td>ag42fa</td>
</tr>
</tbody>
</table>
### Custom Tracks

<table>
<thead>
<tr>
<th>Track Type</th>
<th>Example</th>
<th>Track Definition</th>
</tr>
</thead>
<tbody>
<tr>
<td>Bam(color-strand)</td>
<td><img src="image1" alt="Bam(color-strand) Example" /></td>
<td>track name=&quot;ag42fa&quot; color=&quot;red&quot; bamColorMode=strand type=bigWig visibility=2 bigDataUrl=&quot;/bh/datafc/hannon/gordon/bowtie.dataset_79015.fa.tr/mapping/results.mappers.bam&quot;</td>
</tr>
<tr>
<td>Bam(color-tag)</td>
<td><img src="image2" alt="Bam(color-tag) Example" /></td>
<td>track name=&quot;ag42fa&quot; color=&quot;purple&quot; bamColorMode=tag type=bigWig visibility=2 bigDataUrl=&quot;/bh/datafc/hannon/gordon/bowtie.dataset_79015.fa.tr/mapping/results.mappers.bam&quot;</td>
</tr>
<tr>
<td>Coverage (by strand)</td>
<td><img src="image3" alt="Coverage (by strand) Example" /></td>
<td>track name=&quot;ag42fa&quot; color=&quot;blue&quot; type=bigWig visibility=2 bigDataUrl=&quot;/bh/datafc/hannon/gordon/bowtie.dataset_79015.fa.tr/mapping/results.positiveCoverage.bam&quot;</td>
</tr>
</tbody>
</table>

**Legend:**
- **Positive Strand (blue)**
- **Negative Strand (red)**
- **Multi-Mapper**
- **Unique Mappers**
<table>
<thead>
<tr>
<th>File</th>
<th>Details</th>
<th>Path (on Bluehelix)</th>
</tr>
</thead>
<tbody>
<tr>
<td>Input File</td>
<td>The file used for the mapping process (from Galaxy).</td>
<td><code>/datafc/hannon/gordon/bowtie.dataset_79015.fa.tm7Pu6y2VJMd/input/79015.fa</code></td>
</tr>
<tr>
<td>All Mappers</td>
<td>FASTA file with all sequences which mapped to the reference database.</td>
<td><code>/datafc/hannon/gordon/bowtie.dataset_79015.fa.tm7Pu6y2VJMd/mapping/mappers.fa</code></td>
</tr>
<tr>
<td>Non Mappers</td>
<td>FASTA file with all sequences which did not map to the reference database.</td>
<td><code>/datafc/hannon/gordon/bowtie.dataset_79015.fa.tm7Pu6y2VJMd/mapping/nonmappers.fa</code></td>
</tr>
<tr>
<td>Maxed-out mappers</td>
<td>FASTA file with all sequences which mapped more than the maximum mapping limit.</td>
<td><code>/datafc/hannon/gordon/bowtie.dataset_79015.fa.tm7Pu6y2VJMd/mapping/maxmappers.fa</code></td>
</tr>
<tr>
<td>Mapping Directory</td>
<td>The directory containing all mapping results.</td>
<td><code>/datafc/hannon/gordon/bowtie.dataset_79015.fa.tm7Pu6y2VJMd/mapping</code></td>
</tr>
<tr>
<td>Mapping results (Intervals)</td>
<td>A BED-like text file containing the mapped sequences (after filtering)</td>
<td><code>/datafc/hannon/gordon/bowtie.dataset_79015.fa.tm7Pu6y2VJMd/mapping/results.mappers.txt</code></td>
</tr>
<tr>
<td>Mapping results (SAM)</td>
<td>A SAM file containing the mapping results (after filtering)</td>
<td><code>/datafc/hannon/gordon/bowtie.dataset_79015.fa.tm7Pu6y2VJMd/mapping/results.mappers.sam</code></td>
</tr>
<tr>
<td>Unfiltered results (SAM)</td>
<td>A SAM file containing the unfiltered (raw) mapping results</td>
<td><code>/datafc/hannon/gordon/bowtie.dataset_79015.fa.tm7Pu6y2VJMd/mapping/results.raw.sam</code></td>
</tr>
<tr>
<td>SAM Headers</td>
<td>SAM format headers, needed for some samtools programs</td>
<td><code>/datafc/hannon/gordon/bowtie.dataset_79015.fa.tm7Pu6y2VJMd/mapping/header.sam</code></td>
</tr>
</tbody>
</table>
Usable Tools

Usable Data
“Good design is [...] an act of communication between the designer and the user”

Donald A. Norman
The Design of Everyday Things