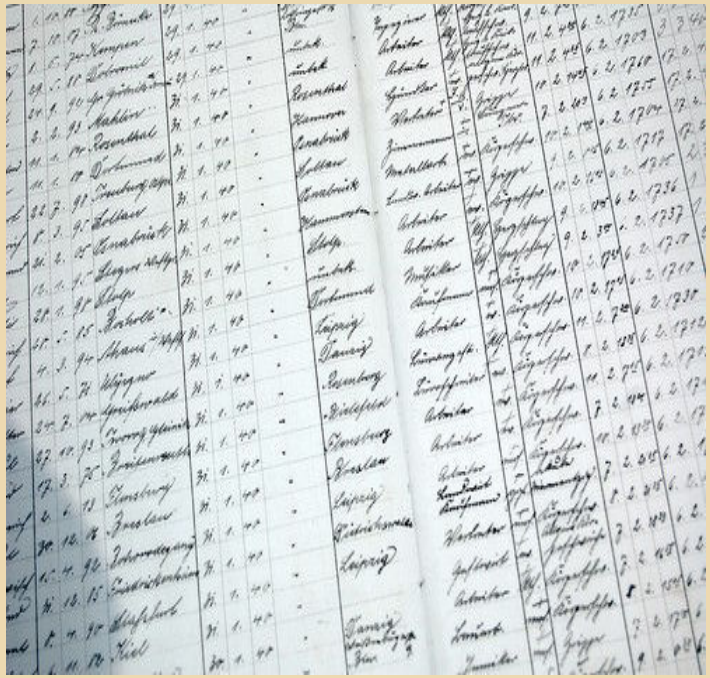
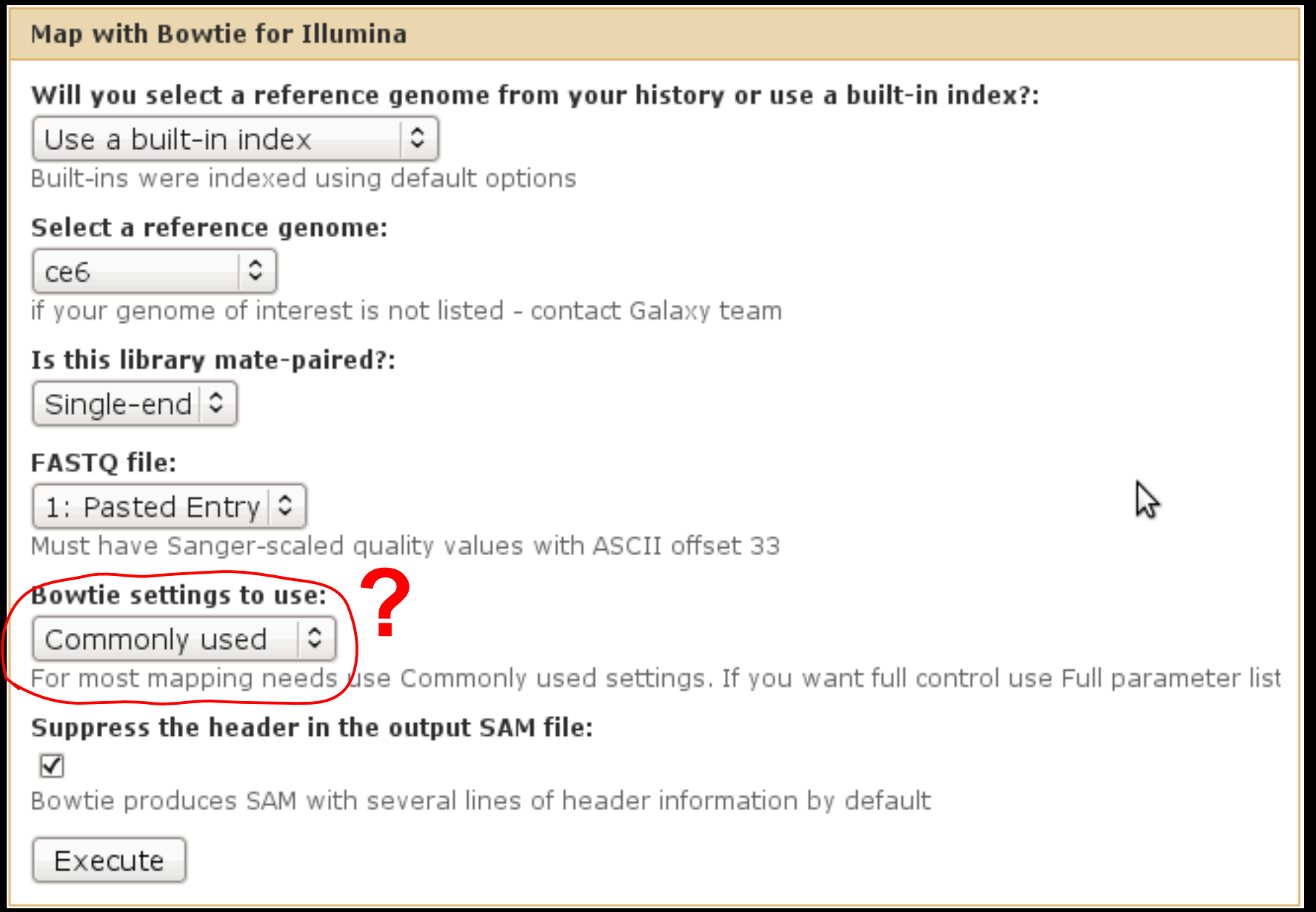
Useful and Usable

Assaf Gordon
Hannon Lab, CSHL

Usable Tools

Usable Data




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:
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 (-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 (--nomaqround):

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 strand 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 offrate 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 (-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

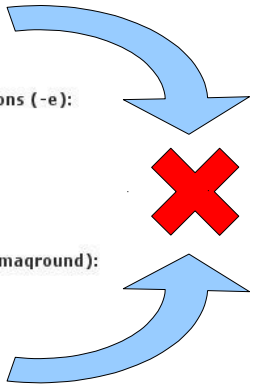
Maximum permitted total of quality values at mismatched read positions (-e):

70

Seed length (-l):

28

Minimum value is 5



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

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 strand 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 offrate 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 (-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 (--nomaqround):

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 strand 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 offrate of the index to n (-o):

-1

-1 for default

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

-1

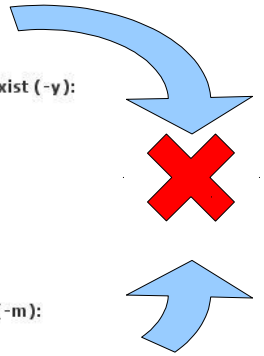
-1 for default

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 (-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 (--nomaqround):

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 strand 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 offrate 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 (-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 (--nomaqround):

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 strand 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 offrate of the index to n (-o):

-1

-1 for default

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

-1

-1 for default

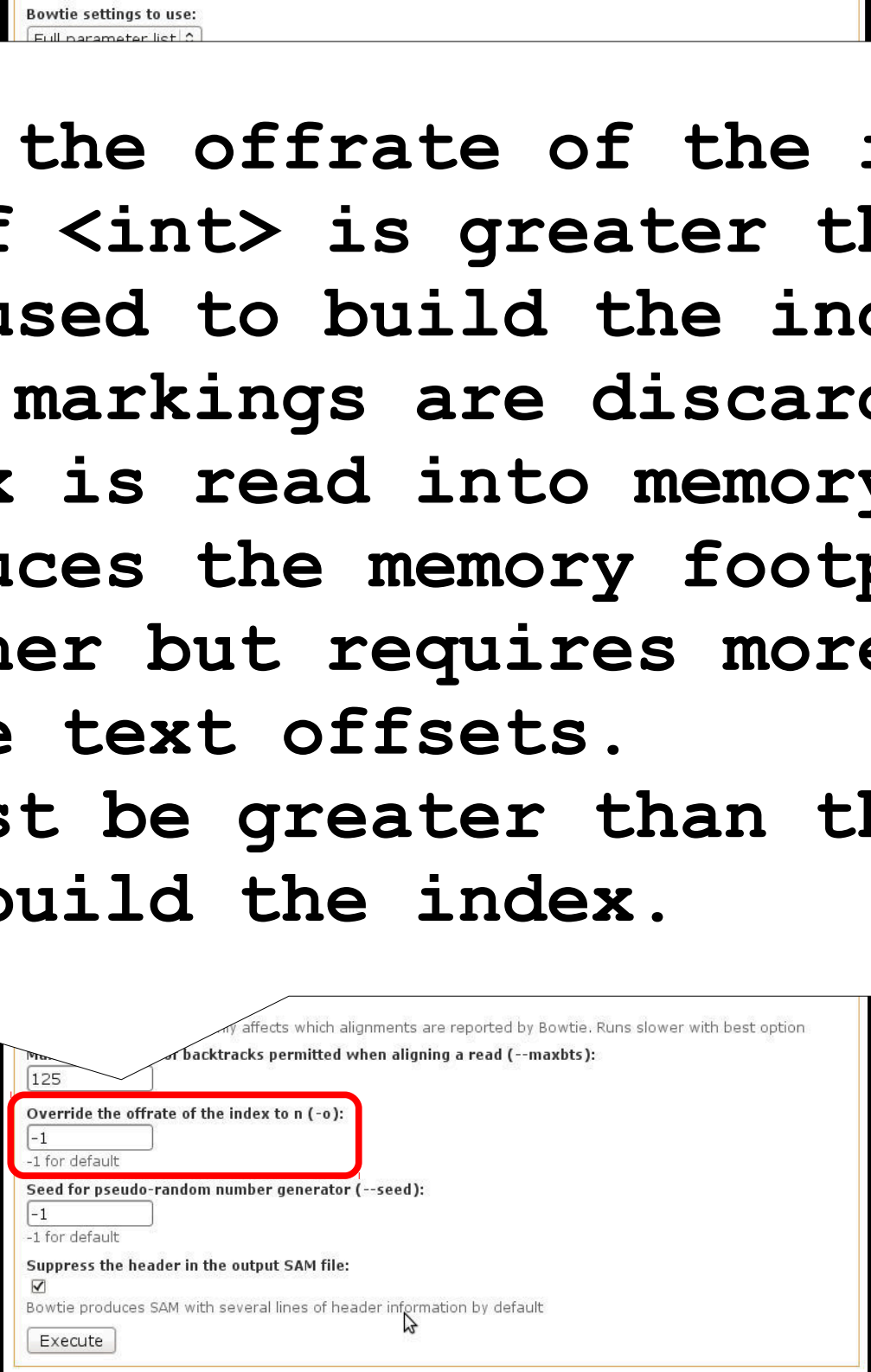
Suppress the header in the output SAM file:

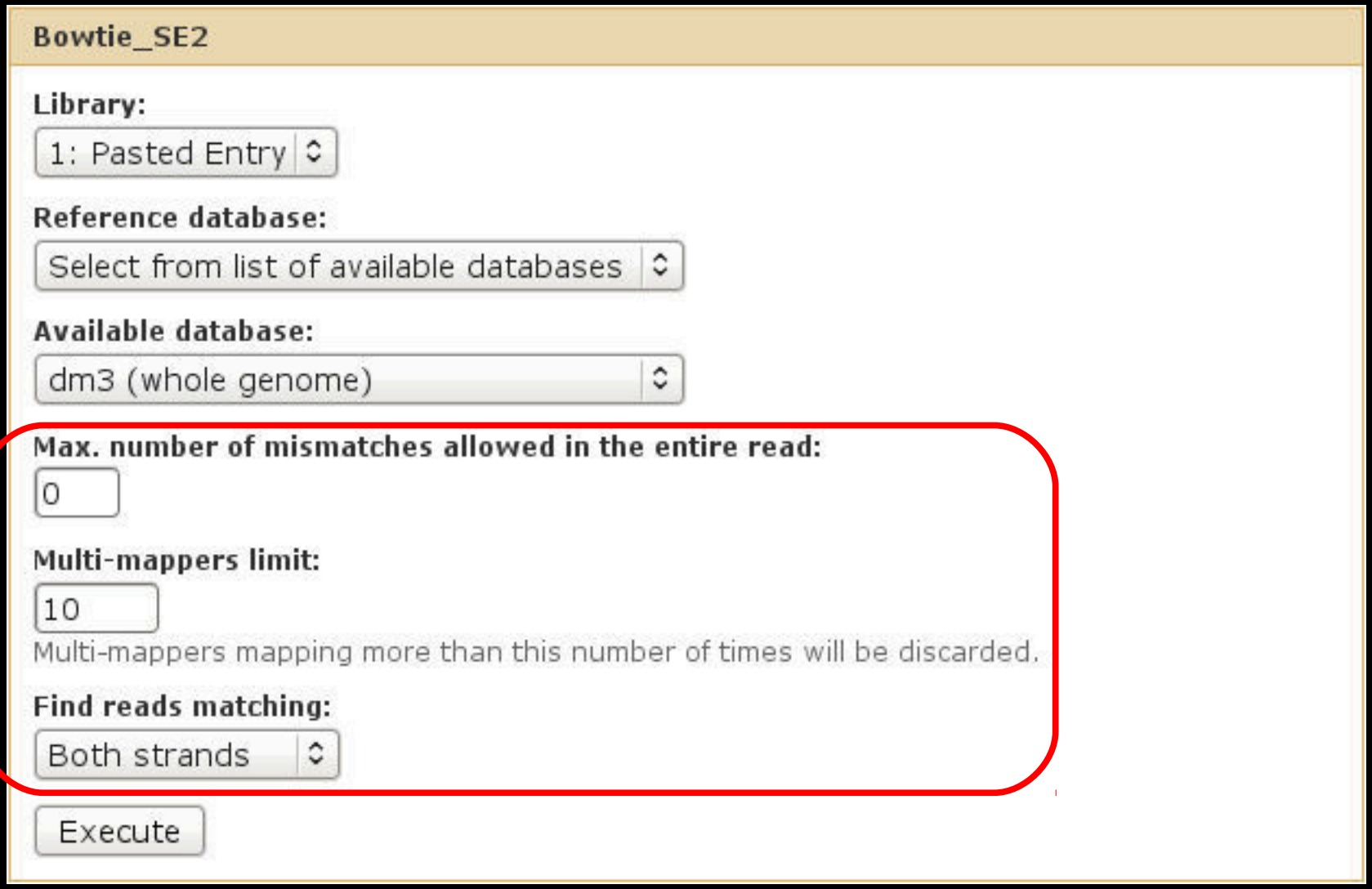
☑

Bowtie produces SAM with several lines of header information by default

Execute

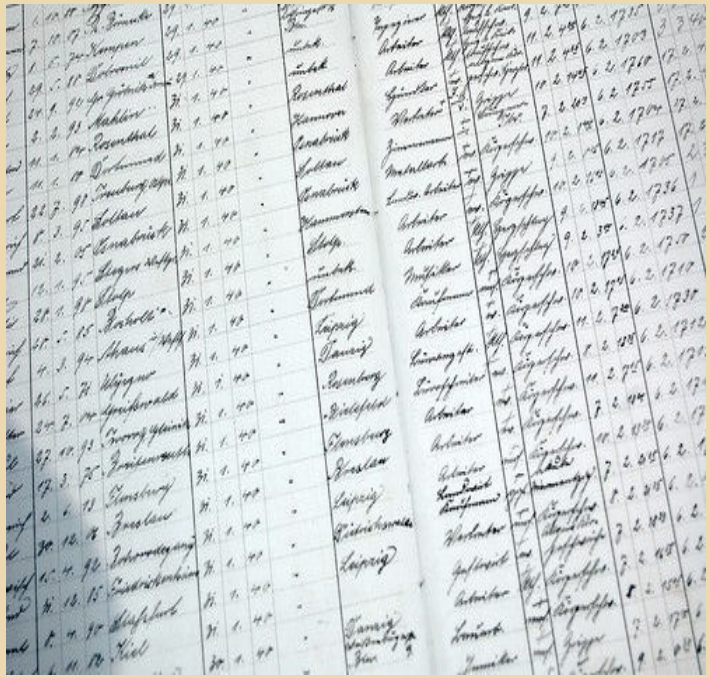
Override the offrate of the index with <int>. If <int> is greater than the offrate used to build the index, then some row markings are discarded when the index is read into memory.
This reduces the memory footprint of the aligner but requires more time to calculate text offsets.
<int> must be greater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

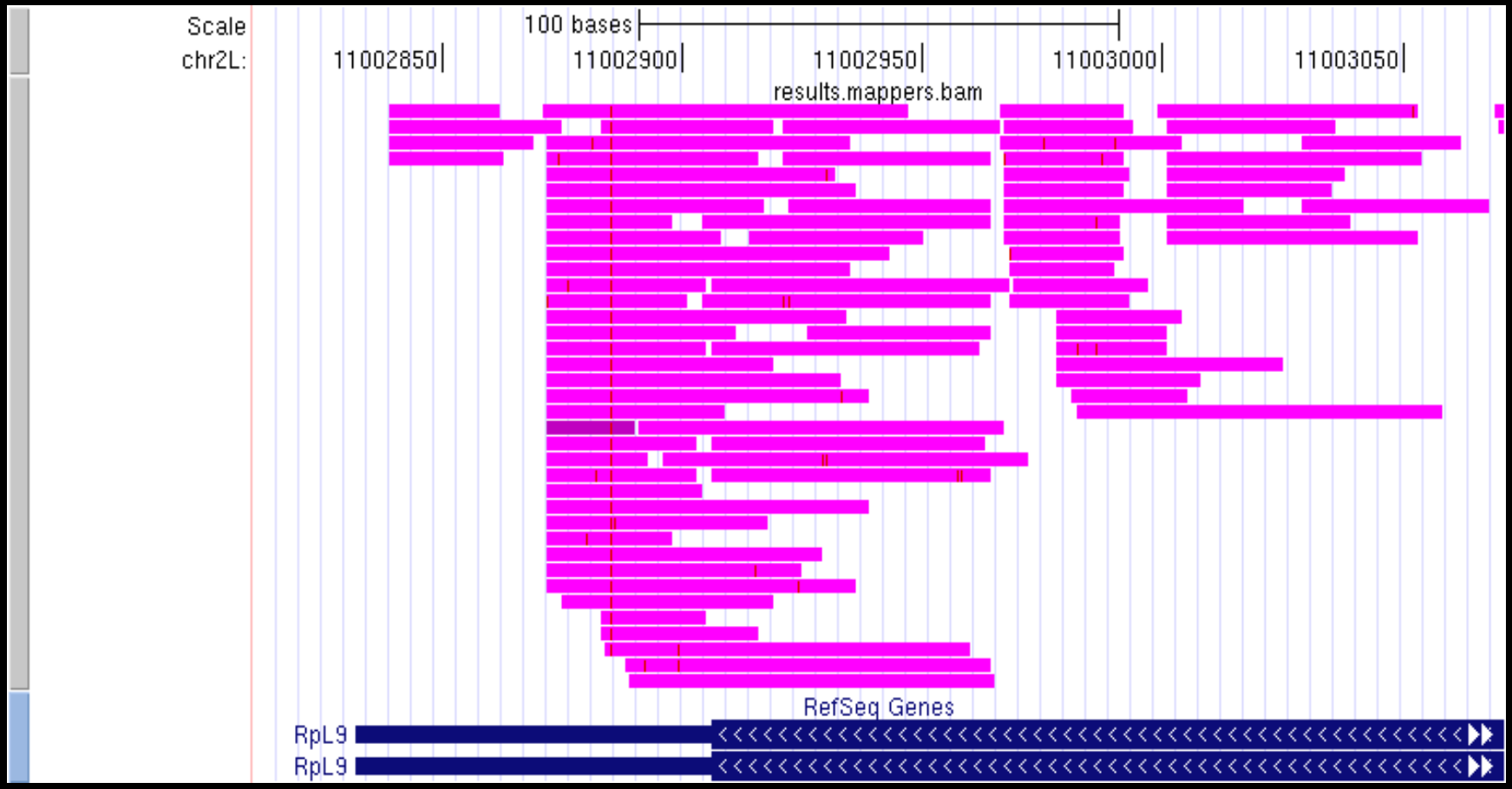


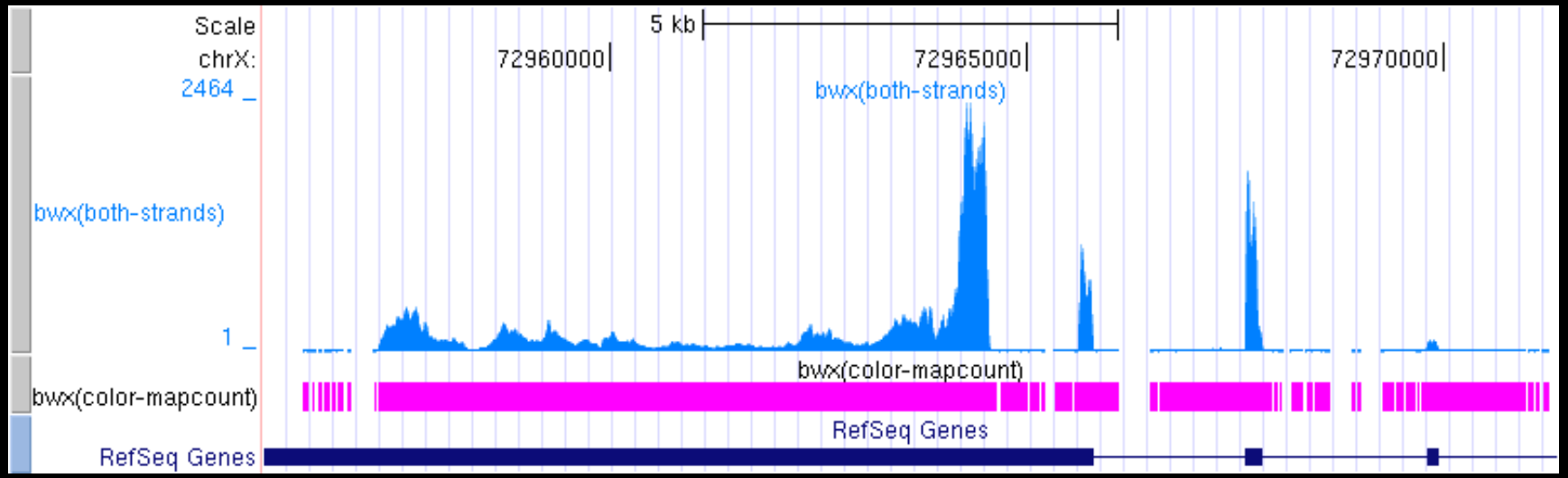

Bowtie_SE2
Library:
1: Pasted Entry
Reference database:
Select from list of available databases
Available database:
dm3 (whole genome)
Max. number of mismatches allowed in the entire read:
0
Multi-mappers limit:
10
Multi-mappers mapping more than this number of times will be discarded.
Find reads matching:
Both strands
Execute

Usable Tools

Usable Data

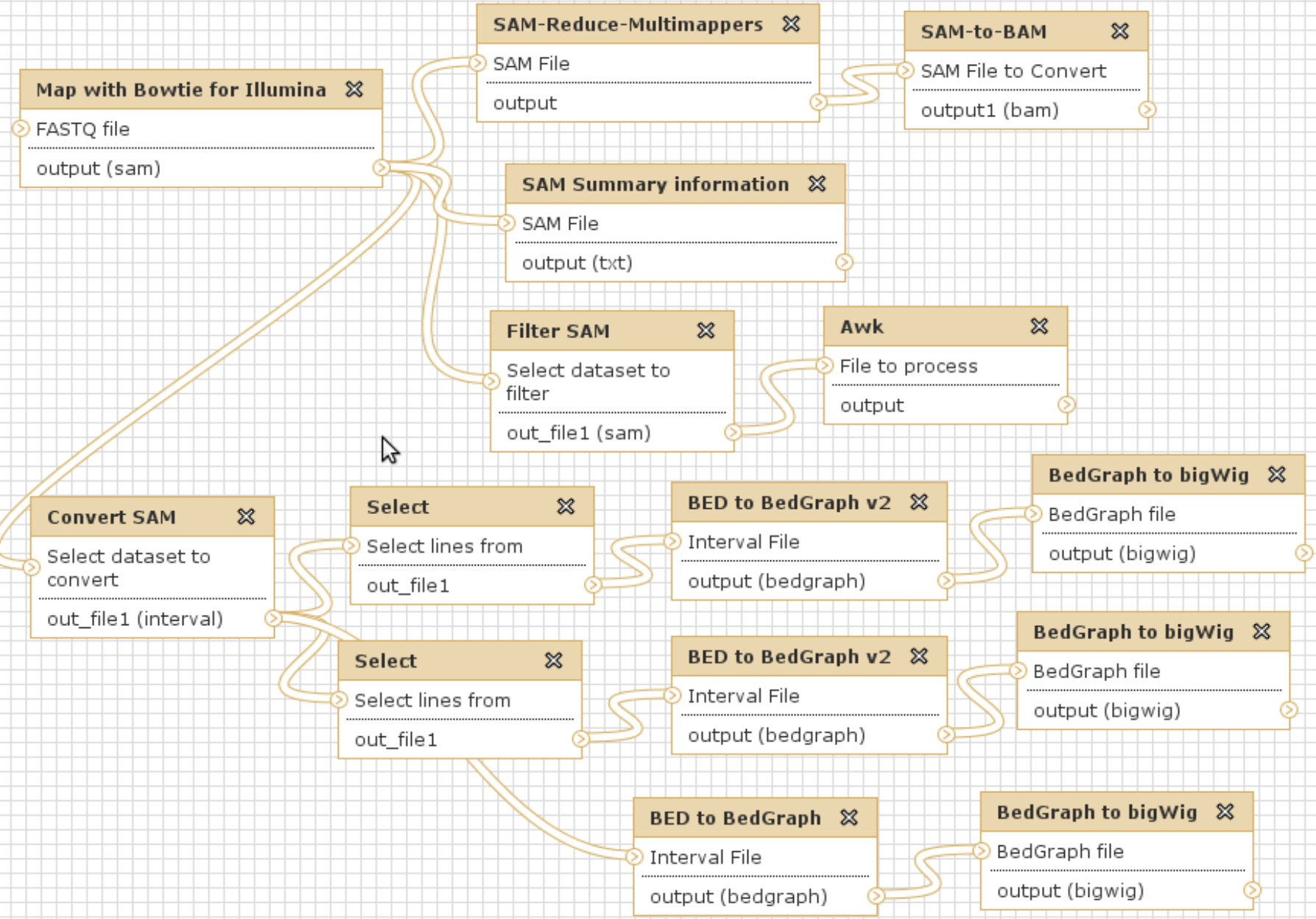


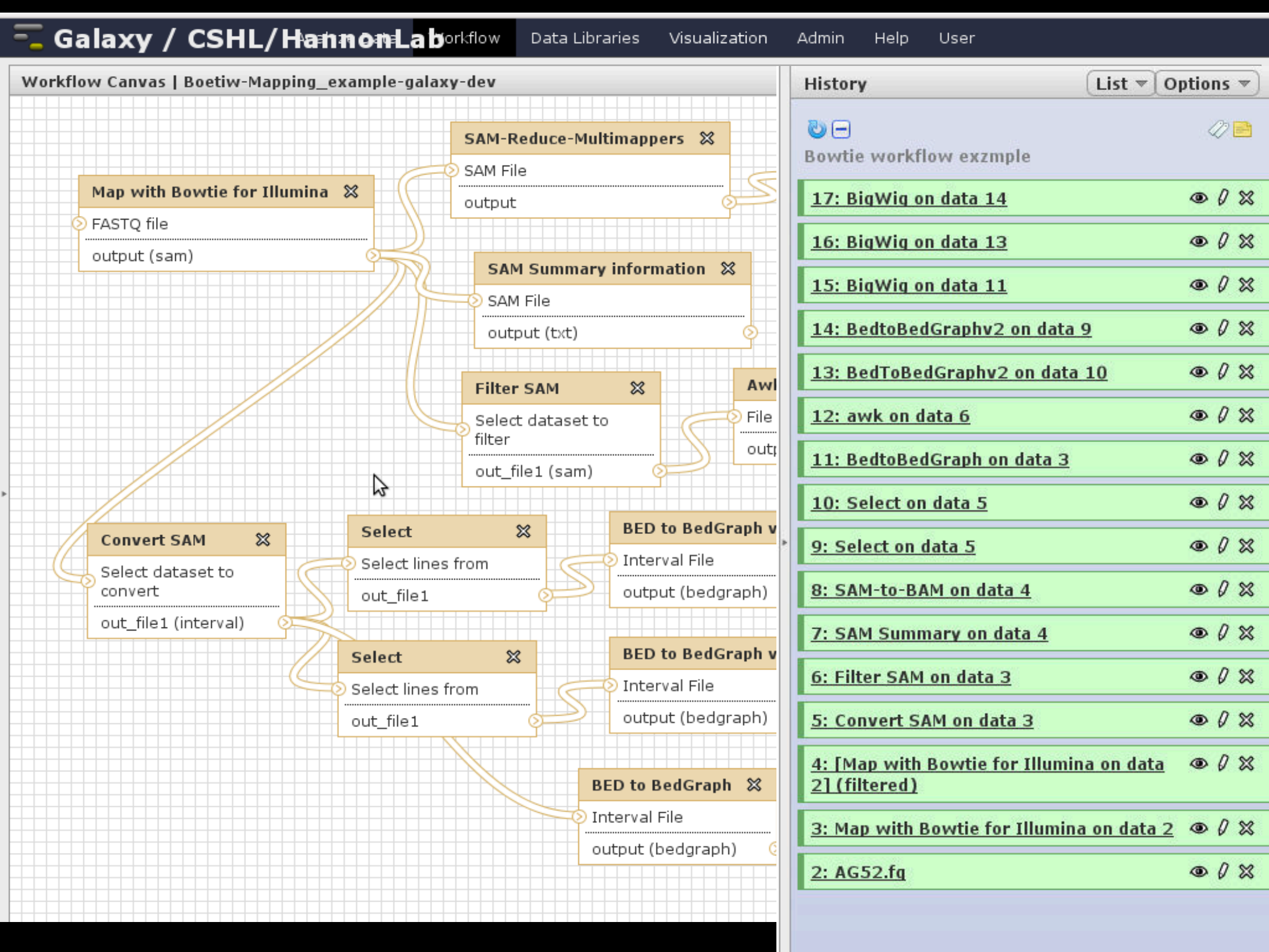

Scale
chr2L:
100 bases
11002850
11002900
11002950
11003000
11003050
results.mappers.bam
RefSeq Genes
RpL9
RpL9


Scale
chrX:
5 kb
72960000
72965000
72970000
2464
bwx(both-strands)
bwx(both-strands)
1
bwx(color-mapcount)
bwx(color-mapcount)
RefSeq Genes
RefSeq Genes

Workflow Canvas | Boetiw-Mapping_example-galaxy-dev

Options




Galaxy / CSHL/HannonLab
Workflow
Data Libraries
Visualization
Admin
Help
User
Workflow Canvas | Boetiw-Mapping_example-galaxy-dev
SAM-Reduce-Multimappers
SAM File
output
Map with Bowtie for Illumina
FASTQ file
output (sam)
SAM Summary information
SAM File
output (txt)
Filter SAM
Select dataset to filter
out_file1 (sam)
Awl
File
outp
Convert SAM
Select dataset to convert
out_file1 (interval)
Select
Select lines from
out_file1
BED to BedGraph v
Interval File
output (bedgraph)
Select
Select lines from
out_file1
BED to BedGraph v
Interval File
output (bedgraph)
BED to BedGraph
Interval File
output (bedgraph)
History
List
Options
Bowtie workflow exzmple
17: BigWig on data 14
16: BigWig on data 13
15: BigWig on data 11
14: BedtoBedGraphv2 on data 9
13: BedToBedGraphv2 on data 10
12: awk on data 6
11: BedtoBedGraph on data 3
10: Select on data 5
9: Select on data 5
8: SAM-to-BAM on data 4
7: SAM Summary on data 4
6: Filter SAM on data 3
5: Convert SAM on data 3
4: [Map with Bowtie for Illumina on data 2] (filtered)
3: Map with Bowtie for Illumina on data 2
2: AG52.fq

Mapping results for ag42fa

Summary Statistics

Category	Sequences	%_seq	%_seq	Reads	%_reads	%_reads
Input	1,010,128	100.00		14,196,384	100.00	
non Mappers	297,178	29.42		3,625,468	25.54	
maxed-out Mappers	64,467	6.38		2,624,179	18.48	
All Mappers	648,483	64.2	100.00	7,946,737	55.98	100.00
Unique Mappers	604,348		93.19	6,453,910		81.21
multi Mappers	44,135		6.81	1,492,827		18.79

Mapping Parameters

Parameter	Value
bowtie_params	-k 10 -m 10 -v 2
database	/data/hannon/gordon/databases/bowtie/dm3_genome/dm3_genome
input_filename	/datafc/hannon/gordon/bowtie.dataset_79015.fa.tm7Pu6y2VJMd/input/dataset_79015.fa
mapping_starttime	Thu May 13 23:46:44 2010
project_name	ag42fa

History List Options

Bowtie-SE test dm3

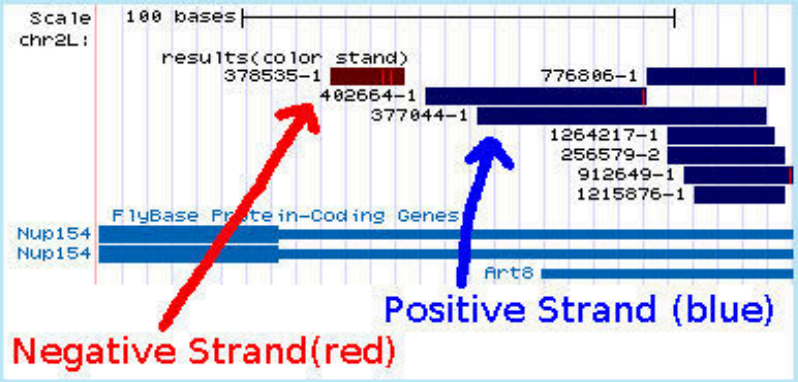
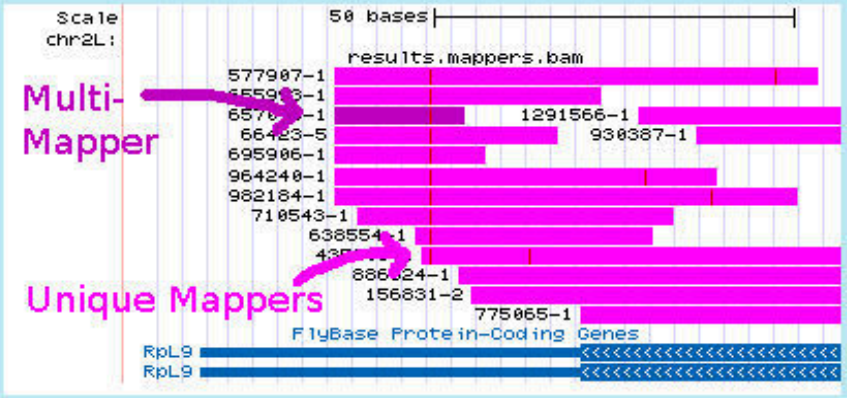
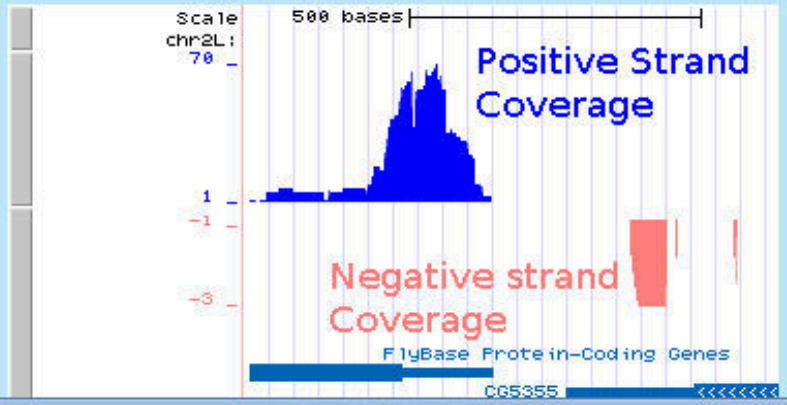
5: Exon Junctions Mapping [ag42.fa]

4: Genome Mapping [ag42.fa]

2: Genome Mapping [ag42.fa]

1: ag42.fa

Custom Tracks

Track Type	Example	Track Definition
Bam(color-strand)		track name="ag42fa(color-s bamColorMode=strand type=ba visibility=3 bigDataUrl=/re /bh//datafc/hannon/gordon /bowtie.dataset_79015.fa.tr /mapping/results.mappers.ba
Bam(color-tag)		track name="ag42fa(color-ma bamColorMode=tag type=bam visibility=3 bigDataUrl=/re /bh//datafc/hannon/gordon /bowtie.dataset_79015.fa.tr /mapping/results.mappers.ba
Coverage (by strand)		track name="ag42fa(positive color=0,0,255 type=bigWig visibility=2 bigDataUrl=bluehelix:/data /gordon /bowtie.dataset_79015.fa.tr /mapping/results.positive.b track name="ag42fa(negative color=255,0,0 type=bigWig visibility=2 bigDataUrl=bluehelix:/data /gordon /bowtie.dataset_79015.fa.tr

History List Options

Bowtie-SE test dm3

- 5: Exon Junctions Mapping [ag42.fa]
- 4: Genome Mapping [ag42.fa]
- 2: Genome Mapping [ag42.fa]
- 1: ag42.fa

Mapping result Files

File	Details	Path (on Bluehelix)
Input File	The file used for the mapping process (from Galaxy).	/datafc/hannon/gordon /bowtie.dataset_79015.fa.tm7Pu6y2VJMd/input /dataset_79015.fa
All Mappers	FASTA file with all sequences which mapped to the reference database.	/datafc/hannon/gordon /bowtie.dataset_79015.fa.tm7Pu6y2VJMd/mapping /mappers.fa
Non Mappers	FASTA file with all sequences which did not map to the reference database.	/datafc/hannon/gordon /bowtie.dataset_79015.fa.tm7Pu6y2VJMd/mapping /nonmappers.fa
Maxed-out mappers	FASTA file with all sequences which mapped more than the maximum mapping limit.	/datafc/hannon/gordon /bowtie.dataset_79015.fa.tm7Pu6y2VJMd/mapping /maxmappers.fa
Mapping Directory	The directory containing all mapping results.	/datafc/hannon/gordon /bowtie.dataset_79015.fa.tm7Pu6y2VJMd/mapping
Mapping results (Intervals)	A BED-like text file containing the mapped sequences (after filtering)	/datafc/hannon/gordon /bowtie.dataset_79015.fa.tm7Pu6y2VJMd/mapping /results.mappers.txt
Mapping results (SAM)	A SAM file containing the mapping results (after filtering)	/datafc/hannon/gordon /bowtie.dataset_79015.fa.tm7Pu6y2VJMd/mapping /results.mappers.sam
Unfiltered results (SAM)	A SAM file containing the unfiltered (raw) mapping results	/datafc/hannon/gordon /bowtie.dataset_79015.fa.tm7Pu6y2VJMd/mapping /results.raw.sam
SAM Headers	SAM format headers, needed for some samtools programs	/datafc/hannon/gordon /bowtie.dataset_79015.fa.tm7Pu6y2VJMd/mapping /header.sam

History List Options

Bowtie-SE test dm3

5: Exon Junctions Mapping [ag42.fa]

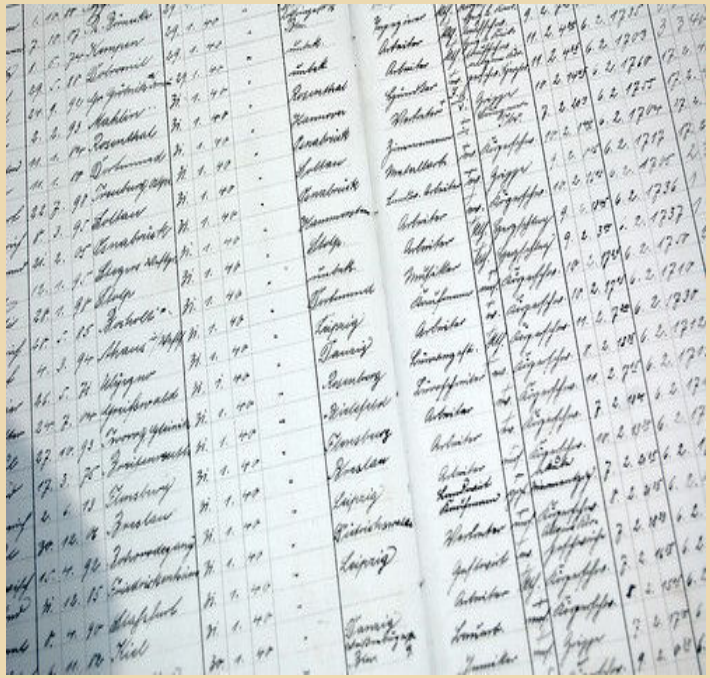
4: Genome Mapping [ag42.fa]

2: Genome Mapping [ag42.fa]

1: ag42.fa

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