Alignment with bowtie2

Tools

bowtie2

Alignment

Bowtie2 - map reads against reference genome

Bowtie2 - map reads against reference genome (Galaxy Version 2.2.6.2) Options

Is this single or paired library

Paired-end

FASTQ file #1

18: HG0101_clean_1.fastq

Must be of datatype "fastqsanger"

FASTQ file #2

19: HG0101_clean_2.fastq

Must be of datatype "fastqsanger"

Write unaligned reads (in fastq format) to separate file(s)

Yes No

--un/--un-conc; This triggers --un parameter for single reads and --un-conc for paired reads

Write aligned reads (in fastq format) to separate file(s)

Yes No

--al/--al-conc; This triggers --al parameter for single reads and --al-conc for paired reads

Do you want to set paired-end options?

No

See "Alignment Options" section of Help below for information

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

Use a genome from the history and build index

Built-ins were indexed using default options. See `Indexes` section of help below

GRCh37_region1.fasta

150 000nt, chr20

31: Bowtie2 on data 1, data 19, and data 18: aligned reads (sorted BAM)

31: HG0101_bowtie2.bam

Save the bowtie2 mapping statistics to the history

Yes No

Alignment with BWA

Tools

BWA

Alignment

Map with BWA - map short reads (< 100 bp) against reference genome

Map with BWA-MEM - map medium and long reads (> 100 bp) against reference genome

Map with BWA-MEM - map medium and long reads (> 100 bp) against reference genome (Galaxy Version 0.7.12.1)

Options

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

Use a genome from history and build index

Use the following dataset as the reference sequence

1: GRCh37_region1.fasta

You can upload a FASTA sequence to the history and use it as reference

Algorithm for constructing the BWT index

Auto. Let BWA decide the best algorithm to use

(-a)

Single or Paired-end reads

Paired

Select between paired and single end data

Select first set of reads

10: HG0101_clean_1.fastq

Specify dataset with forward reads

Select second set of reads

11: HG0101_clean_2.fastq

Specify dataset with reverse reads

Enter mean, standard deviation, max, and min for insert lengths.

-I; This parameter is only used for paired reads. Only mean is required while sd, max, and min will be inferred. Examples: both "250" and "250,25" will work while "250,,10" will not. See below for details.

Set read groups information?

Do not set

Specifying read group information can greatly simplify your downstream analyses by allowing combining multiple datasets.

Select analysis mode

1.Simple Illumina mode

Execute

33: Map with BWA-MEM on data 11, data 10, and data 1 (mapped reads in BAM format)

33: HG0101_BWA.bam

Playing with options of Bowtie2

Read file: tweak_single_end.fq

Three reads, single-end

Same reference: GRCh37_region1.fasta

Default parameters

Is this single or paired library

Single-end

How many alignments do you find ?

Option -a (all alignments)

Select analysis mode

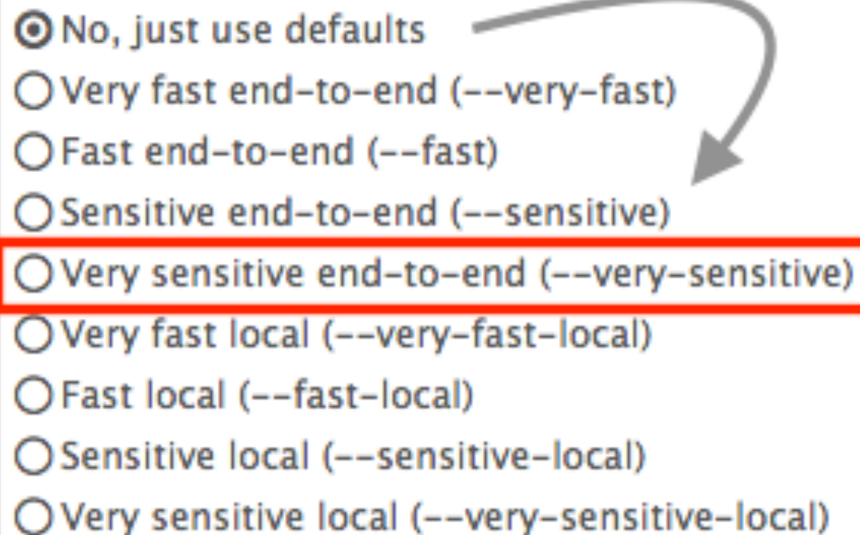
2: Full parameter list

Do you want to use -a or -k options

Set -a option

Make sure you understand implications of setting -k and -a.
a options

Sensitivity



End-to-endmode versus local mode

Select analysis mode

1: Default setting only

Do you want to use presets?

- (•) No, just use defaults
- ( ) Very fast end-to-end (--very-fast)
- ( ) Fast end-to-end (--fast)
- ( ) Sensitive end-to-end (--sensitive)
- ( ) Very sensitive end-to-end (--very-sensitive)
- ( ) Very fast local (--very-fast-local)
- ( ) Fast local (--fast-local)
- ( ) Sensitive local (--sensitive-local)
- ( ) Very sensitive local (--very-sensitive-local)

Allow selecting among several preset parameter settings. Choosing between these will
understand effects of these presets.

Concordant/discordant (paired reads)

concordant_discordant1.fq

concordant_discordant2.fq

Read 1 (2x180nt): 19861 + / 20161 +

Read 2 (2x180nt): 29341 + / 29641 -

Read 3 (2x180nt): 42301 + / 50401 -

Read4 (2x180nt): / 149341 +