Workflow: ddRAD alignment and variant calling

Run Workflow

History Options

Send results to a new history

No

1: Unzip collection - Start with a paired dataset collection and unzip it into separate forward and reverse collections. (Galaxy Version 1.0.0)

Paired input to unzip *

7: Trim Galore! on collection 3: trimmed reads

2: Reference_genome

Reference_genome *

6: Mnov.GTseq.target.seqs.fasta

3: FastQC (Galaxy Version 0.72+galaxy1)

4: FastQC (Galaxy Version 0.72+galaxy1)

5: Map with BWA-MEM - Read groups set using defaults, flag unpaired reads as secondary, all other parameters at defaults (Galaxy Version 0.7.17.1)

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

Use a genome from history and build index

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

Use the following dataset as the reference sequence * required

Connected to 'output' from Step 2

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 * required

Connected to 'forward' from Step 1

Select second set of reads * required

Connected to 'reverse' from Step 1

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

Empty.

-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?

Set read groups (SAM/BAM specification)

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

Auto-assign

True

Use dataset name or collection information to automatically assign this value

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True

Use dataset name or collection information to automatically assign this value

Platform/technology used to produce the reads (PL) *

ILLUMINA

Auto-assign

True

Use dataset name or collection information to automatically assign this value

Sequencing center that produced the read (CN) - optional

Empty.

Description (DS) - optional

Empty.

Date that run was produced (DT) - optional

Empty.

ISO8601 format date or date/time, like YYYY-MM-DD

Flow order (FO) - optional

Empty.

The array of nucleotide bases that correspond to the nucleotides used for each flow of each read. Multi-base flows are encoded in IUPAC format, and non-nucleotide flows by various other characters.
Format: /*|[ACMGRSVTWYHKDBN]+/

The array of nucleotide bases that correspond to the key sequence of each read (KS) - optional

Empty.

Programs used for processing the read group (PG) - optional

Empty.

Predicted median insert size (PI) - optional

Empty.

Platform unit (PU) - optional

Empty.

Unique identifier (e.g. flowcell-barcode.lane for Illumina or slide for SOLiD)

Select analysis mode

5.Full list of options

Set algorithmic options?

Do not set

Sets -k, -w, -d, -r, -y, -c, -D, -W, -m, -S, -P, and -e options.

Set scoring options?

Set scoring options

Do not set

Sets -A, -B, -O, -E, -L, and -U options.

Set input/output options

Set

Sets -T, -h, -a, -C, -V, -Y, and -M options.

For split alignment, take alignment with smallest coordinate as primary

False

Useful for HiC data (-5)

Don't lower MAPQ for split alignment

False

By default the MAPQ score of a supplementary alignment will be lowered to the primary alignment score. (-q)

Minimum score to output *

30

-T; default=30

If there are less than THIS VALUE hits with score >80% of the max score, output them all in the XA tag *

5

-h; default=5

Output all alignments for single-ends or unpaired paired-ends

True

-a; These alignments will be flagged as secondary alignments

Append FASTA/FASTQ comment to BAM output

False

-C

Output the reference FASTA header in the XR tag

False

-C

Use soft clipping for supplementary alignments

False

-Y; By default, BWA-MEM uses soft clipping for the primary alignment and hard clipping for supplementary alignments

Mark shorter split hits of a chimeric alignment in the FLAG field as 'secondary alignment' instead of 'supplementary alignment'

True

-M; For Picard<1.96 compatibility

6: MultiQC (Galaxy Version 1.7)

7: MultiQC (Galaxy Version 1.7)

8: FreeBayes - --no-mnps --no-complex --haplotype-length 0 -kwVa Otherwise, default parameters. (Galaxy Version 1.3.1)