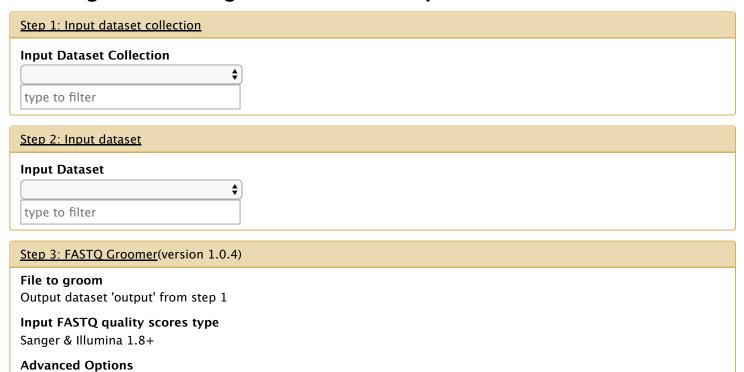
Running workflow "gatk-variant-call-paired-datasets-collection"



Step 4: Bowtie2(version 2.2.6.2)

Is this single or paired library

Paired-end Dataset Collection

FASTQ Paired Dataset

Hide Advanced Options

Output dataset 'output_file' from step 3

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

Not available.

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

Not available.

Do you want to set paired-end options?

Yes

Set the minimum fragment length for valid paired-end alignments

Not available.

Set the maximum fragment length for valid paired-end alignments

500

Select the upstream/downstream mate orientations for a valid paired-end alignment against the forward reference strand

--fr

Disable no-mixed behavior

Not available.

Disable no-discordant behavior

Not available.

Allow mate dovetailing

Not available.

Disallow one mate alignment to contain another

Not available.

Disallow mate alignments to overlap

Not available.

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

Use a genome from the history and build index

Select reference genome

Output dataset 'output' from step 2

Set read groups information?

Set read groups (SAM/BAM specification)

Auto-assign

Not available.

Read group identifier (ID)

group_id

Auto-assign

Not available.

Read group sample name (SM)

group_sample_name

Platform/technology used to produce the reads (PL)

ILLUMINA

Auto-assign

Not available.

Library name (LB)

Not available.

Sequencing center that produced the read (CN)

Not available.

Description (DS)

Not available.

Date that run was produced (DT)

Not available.

Flow order (FO)

Not available.

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

Not available.

Programs used for processing the read group (PG)

Not available.

Predicted median insert size (PI)

Not available.

Platform unit (PU)

Not available.

Select analysis mode

1: Default setting only

Do you want to use presets?

No, just use defaults

Save the bowtie2 mapping statistics to the history

Not available.

Step 5: Realigner Target Creator(version 2.8.0)

Choose the source for the reference list

History

BAM file

Output dataset 'output' from step 4

Using reference file

Output dataset 'output' from step 2

Known Variants

Basic or Advanced GATK options

Basic

Basic or Advanced Analysis options

Basic

Step 6: Indel Realigner(version 2.8.0)

Choose the source for the reference list

History

BAM file

Output dataset 'output' from step 4

Using reference file

Output dataset 'output' from step 2

Restrict realignment to provided intervals

•

Known Variants

LOD threshold above which the realigner will proceed to realign

5.0

Use only known indels provided as RODs

Not available.

Basic or Advanced GATK options

Basic

Basic or Advanced Analysis options

Basic

Step 7: Unified Genotyper(version 2.8.0)

Choose the source for the reference list

History

BAM files

BAM file 1

BAM file

Output dataset 'output_bam' from step 6

Using reference file

Output dataset 'output' from step 2

Provide a dbSNP Reference-Ordered Data (ROD) file

Set dbSNP

dbSNP ROD file

\$

dbsnp ROD name

dbsnp

Genotype likelihoods calculation model to employ

ROTH

The minimum phred-scaled confidence threshold at which variants not at 'trigger' track sites should be called 30.0

The minimum phred-scaled confidence threshold at which variants not at 'trigger' track sites should be emitted (and filtered if less than the calling threshold)

30.0

Basic or Advanced GATK options

Basic

Basic or Advanced Analysis options

Basic

Step 8: SnpEff(version 4.0.0)

Sequence changes (SNPs, MNPs, InDels)

Output dataset 'output_vcf' from step 7

Input format

VCF

Output format

VCF (only if input is VCF)

Genome source

Named on demand

Snpff Genome Version Name (e.g. GRCh38.76)

hg19

Upstream / Downstream length

5000 bases

Set size for splice sites (donor and acceptor) in bases

2 bases

Annotation options

Nothing selected.

Use custom interval file for annotation

Selection is Optional \$

Only use the transcripts in this file.

Selection is Optional **♦**

Filter output

Nothing selected.

Filter out specific Effects

No

Chromosomal position

Use default (based on input type)

Text to prepend to chromosome name

Not available.

Produce Summary Stats

True

Do not report usage statistics to server

True

Send results to a new history

tools used in this workflow:

```
"tool_id": null,
"tool_id": null,
"tool_id": "toolshed.g2.bx.psu.edu/repos/devteam/fastq_groomer/fastq_groomer/1.0.4",
"tool_id": "toolshed.g2.bx.psu.edu/repos/devteam/bowtie2/bowtie2/2.2.6.2",
"tool_id": "toolshed.g2.bx.psu.edu/repos/iuc/gatk2/gatk2_realigner_target_creator/2.8.0",
"tool_id": "toolshed.g2.bx.psu.edu/repos/iuc/gatk2/gatk2_indel_realigner/2.8.0",
"tool_id": "toolshed.g2.bx.psu.edu/repos/iuc/gatk2/gatk2_unified_genotyper/2.8.0",
"tool_id": "toolshed.g2.bx.psu.edu/repos/iuc/snpeff/snpEff/4.0.0",
```