

Galaxy for virologist training Exercise 6: Illumina Variant Calling 101

Title	Galaxy
Training dataset:	PRJEB43037 - In August 2020, an outbreak of West Nile Virus affected 71 people with meningoencephalitis in Andalusia and 6 more cases in Extremadura (south-west of Spain), causing a total of eight deaths. The virus belonged to the lineage 1 and was relatively similar to previous outbreaks occurred in the Mediterranean region. Here, we present a detailed analysis of the outbreak, including an extensive phylogenetic study. This is one of the outbreak samples.
Questions:	<ul style="list-style-type: none"> • What is variant calling? • What is a vcf file? • How can I inspect a variant in a bam file to look for false positives? • How can I make a consensus genome based on a variant calling process?
Objectives:	<ul style="list-style-type: none"> • Understand variant calling concept • Learn how to interpret a vcf file • Learn how to make a reference consensus genome. • Learn how to visualize mapping and variant calling results
Estimated time:	2h

1. Description

After mapping, when we have a re-sequencing experiment, the next step usually comprises the variants calling step. Variant calling software tries to identify variants, positions that differ in our reads compared to a reference genome. We may want to have a consensus genome as well, which is obtained by including the variants we just identified in the published reference genome. We are going to address this type of analysis in this tutorial.

2. Upload data to galaxy

Training dataset

- Experiment info: PRJEB43037, WGS, Illumina MiSeq, paired-end
- Fastq R1: [ERR5310322_1](ftp://ftp.sra.ebi.ac.uk/vol1/fastq/ERR531/002/ERR5310322/ERR5310322_1.fastq.gz) - url :
ftp://ftp.sra.ebi.ac.uk/vol1/fastq/ERR531/002/ERR5310322/ERR5310322_1.fastq.gz
- Fastq R2: [ERR5310322_2](ftp://ftp.sra.ebi.ac.uk/vol1/fastq/ERR531/002/ERR5310322/ERR5310322_2.fastq.gz) url :
ftp://ftp.sra.ebi.ac.uk/vol1/fastq/ERR531/002/ERR5310322/ERR5310322_2.fastq.gz

- Reference genome NC_009942.1: [fasta](#) -- [gff](#)

Create new history

- Click the **+** icon at the top of the history panel and create a new history with the name **variant calling 101 tutorial** as explained [here](#)

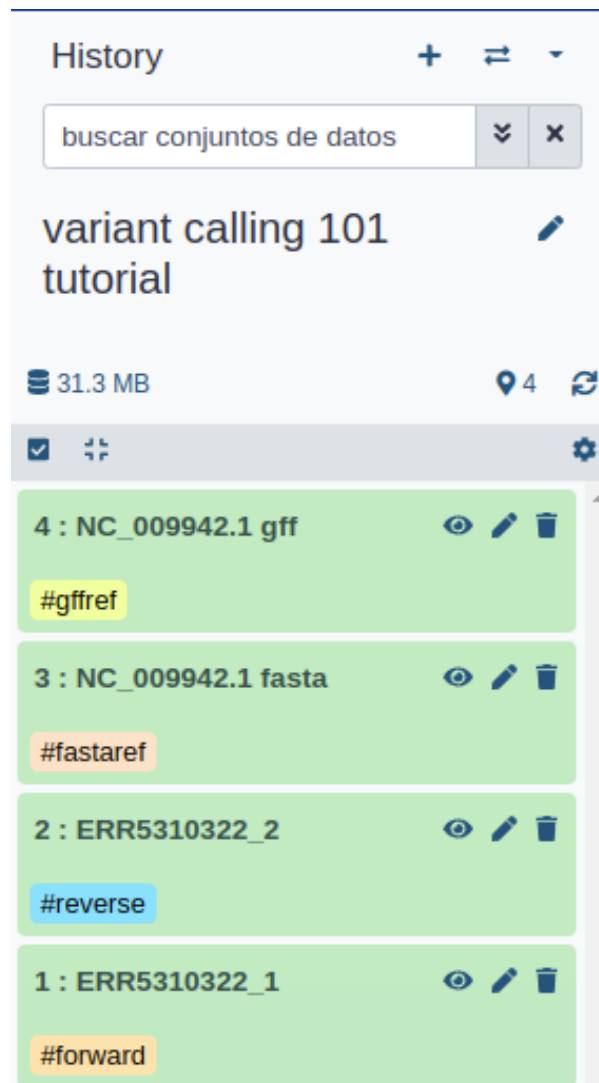
Upload data

Follow the same instructions [here](#)

```
ftp://ftp.sra.ebi.ac.uk/vol1/fastq/ERR531/002/ERR5310322/ERR5310322_1.fastq.gz
ftp://ftp.sra.ebi.ac.uk/vol1/fastq/ERR531/002/ERR5310322/ERR5310322_2.fastq.gz
https://ftp.ncbi.nlm.nih.gov/genomes/all/GCF/000/875/385/GCF_000875385.1_ViralProj30293/GCF_000875385.1_ViralProj30293_genomic.fna.gz
https://ftp.ncbi.nlm.nih.gov/genomes/all/GCF/000/875/385/GCF_000875385.1_ViralProj30293/GCF_000875385.1_ViralProj30293_genomic.gff.gz
```

Rename the data as follows:

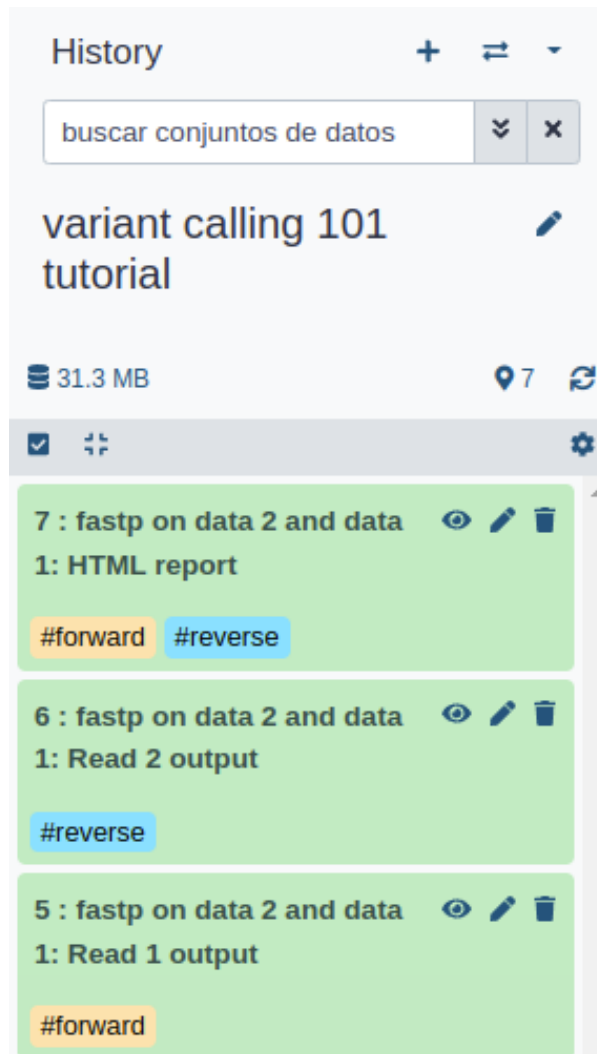
- **ERR5310322_1.fastq.gz** to **ERR5310322_1** with tag **#forward**
- **ERR5310322_2.fastq.gz** to **ERR5310322_2** with tag **#reverse**
- **GCF_000875385.1_ViralProj30293_genomic.fna.gz** to **NC_009942.1 fasta** with tag **#fastaref**
- **GCF_000875385.1_ViralProj30293_genomic.gff.gz** to **NC_009942.1 gff** with tag **#gffref**



3. Preprocess our reads.

Follow instructions [here](#)

Then, fix fastp tags on the output data to be as follows:



4. Map trimmed reads against the reference genome.

Follow:

1. Is this single or paired library: paired.
2. FASTA/Q file #1 : fastp Read 1 output #forward
3. FASTA/Q file #2 : fastp Read 2 output #reverse
4. Will you select a reference genome from your history or use a built-in index? : Use a genome from the history and build index.
5. Do you want to use presets? : Very sensitive local. This setting will hugely affect the mapping results, depending on the dataset/experiment must be tweaked (read [bowtie2 manual](#))
6. Save the bowtie2 mapping statistics to the history

Galaxy Europe

Flujo de Trabajo

Visualizar

Datos Compartidos ▾

Ayuda ▾

Usuario ▾

Using 0%

Herramientas

☆ ▾

bowtie2

x

Cargar Datos

Show Sections

Bowtie2 - map reads against reference genome

SALSA scaffold long read assemblies with Hi-C

bamPEFragmentSize Estimate the predominant cDNA fragment length from paired-end sequenced BAM/CRAM files

Extract the marker sequences and metadata from the MetaPhlAn database

TB-Profiler Profile Infer strain types and drug resistance markers from sequences

HUMANNn to profile presence/absence and abundance of microbial pathways and gene families

MetaPhlAn to profile the composition of microbial communities

MaxBin2 clusters metagenomic contigs into bins

InStrain Profile Creates an inStrain profile (microdiversity analysis) from a mapping file

hicBuildMatrix create a contact matrix

Man with miniman? A fast pairwise

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: 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 result in dramatic changes in runtime. See help below to understand effects of these presets.

Do you want to tweak SAM/BAM Options?

No

See "Output Options" section of Help below for information

Save the bowtie2 mapping statistics to the history

Yes

Email notification

No

Send an email notification when the job completes.

✓ Execute

Bowtie2 Overview

History

+ − ▾

buscar conjuntos de datos

▾ x

variant calling 101 tutorial

✎

31.3 MB

📍 🔗 ⚙️

7 : fastp on data 2 and data 1:

👁 ✎ 🗑

HTML report

#forward #reverse

6 : fastp on data 2 and data 1:

👁 ✎ 🗑

Read 2 output

#reverse

5 : fastp on data 2 and data 1:

👁 ✎ 🗑

Read 1 output

#forward

4 : NC_009942.1 gff

👁 ✎ 🗑

#gffref

3 : NC_009942.1 fasta

👁 ✎ 🗑

#fastaref

2 : ERR5310322_2

👁 ✎ 🗑

#reverse

1 : ERR5310322_1

👁 ✎ 🗑

Samtools mpileup

- 5 / 12

- 6. Disable BAQ (per-Base Alignment Quality), see below: Yes
- 7. Do not discard anomalous read pairs: Yes
- 8. max per-file depth; avoids excessive memory usage: 0
- 9. Minimum base quality for a base to be considered: 20
- 10. Click execute and wait.

Herramientas

mpileup1

Show Sections

VarScan mpileup for variant detection

bctools mpileup Generate VCF or BCF containing genotype likelihoods for one or multiple alignment (BAM or CRAM) files

Samtools mpileup multi-way pileup of variants2

WORKFLOWS

Todos los flujos de trabajo

Samtools mpileup multi-way pileup of variants (Galaxy Version 2.1.7)

Run Tool

Tool Parameters

BAM file(s) *3

accepted formats switch to column select

Use a reference sequence4

Use a genome/index from the history

Reference *5

3: GCF_000875385.1_ViralProj30293_genomic.fna.gz

accepted formats

Set advanced options6

Advanced

Set filter by flags

Do not filter

Select regions to call

Do not limit

Select read groups to exclude

Do not exclude

(-f)

(-R/--exclude-RG)

Samtools mpileup multi-way pileup of variants (Galaxy Version 2.1.7)

Run Tool

7

Disable read-pair overlap detection

Yes

(-x/--ignore-overlaps)

Do not discard anomalous read pairs

Yes

(-A/--count-orphans)

Disable BAQ (per-Base Alignment Quality), see below

Yes

(-B/--no-BAQ)

Coefficient for downgrading mapping quality for reads containing excessive mismatches *

0

Given a read with a phred-scaled probability q of being generated from the mapped position, the new mapping quality is about $\sqrt{q}(\text{INT-}q/\text{INT})^{\text{INT}}$. A zero value disables this functionality; if enabled, the recommended value for BWA is 50 (-C/--adjust-MQ)

max per-file depth; avoids excessive memory usage *8

0

(-d/--max-depth)

Recalculate BAQ on the fly

No

Ignore existing BQ tags (-E/--redo-BAQ)

Minimum mapping quality for an alignment to be used *

0

(-q/--min-MQ)

Minimum base quality for a base to be considered *9

20

(-t2/--min-BQ)

quality is in the Illumina-1.3+ encoding

No

(-6/--illumina1.3+)

Output options

Default

Additional Options

Email notification

No

Send an email notification when the job completes.

Run Tool10

11. Click the :eye: icon on the history and inspect the mpileup output.

VarScan

1. Search **VarScan Mpileup** in the search toolbox.
2. Samtools pileup dataset: samtools mpileup output
3. Minimum read depth: 10
4. Minimum supporting reads: 5
5. Minimum base quality at a position to count a read: 20
6. Minimum variant allele frequency threshold: 0,75
7. Default p-value threshold for calling variants: 0,05
8. Click execute and wait

Herramientas

VarScan Mpileup

WORKFLOWS

Todos los flujos de trabajo

VarScan Mpileup for variant detection

VarScan Mpileup for variant detection (Galaxy Version 2.4.3.1)

Tool Parameters

Samtools pileup dataset *

17: Samtools mpileup on data 3 and data 15

accepted formats

Analysis type *

single nucleotide variation

Minimum coverage *

10

Minimum depth at a position to make a call (i-min-coverage)

Minimum supporting reads *

5

Minimum number (default: 2) of variant-supporting reads at a position required to make a call (i-min-reads)

Minimum base quality *

20

The minimum base quality at the variant position required to use a read for calling (i-min-avg-qual)

Minimum variant allele frequency *

0,75

Minimum variant allele frequency (default: 0,8) required for calling a variant (i-min-var-freq)

Minimum homozygous variant allele frequency *

0,75

Minimum homozygous variant allele frequency (default: 0,8) required for calling a variant (i-min-hom-var-freq)

Default p-value threshold for calling variants *

0,05

Ignore variants with >99% support on one strand *

no

sample_names

Separate sample names by comma; leave blank to use default sample names.

Additional Options

Email notification

☐ No

Send an email notification when the job completes.

Run Tool

1. Click the :eye: icon and inspect the vcf file.

VCF stats

1. Search **bcftools stats** in the search toolbox.
2. VCF/BCF Data: varscan vcf output.
3. Click execute and wait.
4. Click the :eye: icon and inspect the stats.

► How many variants do we have in our vcf file?

Ivar variants

1. Search **ivar variants** in the search toolbox.
2. Select **ivar variants Call variants from aligned BAM file**
3. Bam file: bowtie bam output
4. Reference: NC_009942.1
5. Minimum quality score threshold to count base: 20
6. Minimum frequency threshold: 0.75
7. Output format: Both tabular and vcf

8. In VCF only output variants that PASS all filters > Yes
9. Click execute and wait.

Herramientas

ivar

Cargar Datos

Show Sections

ivar remove reads from trimmed BAM file

ivar variants Call variants from aligned BAM file

ivar consensus Call consensus from aligned BAM file

ivar get masked Detect primer mismatches and get primer indices for the amplicon to be masked

ivar filter variants Filter variants across replicates or multiple samples aligned using the same reference

ivar trim Trim reads in aligned BAM

Freyja: Call variants and get sequencing depth information

Freyja: Bootstrapping method

Freyja: Aggregate and visualize demixed results

Freyja: Demix lineage abundances

Multivariate PCA, PLS and OPLS

Univariate Univariate statistics

FLUJOS DE TRABAJO

Todos los flujos de trabajo

ivar variants Call variants from aligned BAM file (Galaxy Version 1.3.1+galaxy2)

Bam file

8: Bowtie2 on data 3, data 6, and data 5: alignments

Aligned reads, to trim primers and quality

Reference

3: NC_009942.1 fasta (as fasta)

Minimum quality score threshold to count base

20

(-q)

Minimum frequency threshold

0,75

(-t)

Output format

Both Tabular and VCF

In VCF only output variants that PASS all filters

☒ Yes

(--pass_only)

Email notification

☐ No

Send an email notification when the job completes.

ivar uses the output of the samtools mpileup command to call variants - single nucleotide variants(SNVs) and indels. In order to call variants correctly, the reference file used for alignment must be passed to iVar using the -r flag. The output of samtools pileup is piped into ivar variants to generate a .tsv file with the variants. There are two parameters that can be set for variant calling using ivar - minimum quality(Default: 20) and minimum frequency(Default: 0.03). Minimum quality is the minimum quality

Lofreq

Insert indel qualities

1. Search **Insert indel qualities** in the search toolbox. Select **Insert indel qualities into a BAM file**
2. Reads: bowtie2 bam output.
3. Click execute and wait.




Insert indel qualities into a BAM file (Galaxy
Version 2.1.5+galaxy0)

☆ Favorite



🔄 Versions

▼ Options

Reads



7: Bowtie2 on data 3, data 5, and data 4: alignments ▼



Indel calculation approach

Uniform ▼

Indel quality to add

30

Should probably not be left at the default value

Separate deletion quality

Leave blank to use the same values for insertions and deletions

Call variants

1. Search **lofreq** in the search toolbox. Select Call variants with lofreq.
2. Input reads in BAM format: indel qualities bam output.
3. Choose the source for the reference genome: History. NC_009942.1
4. Types of variants to call: SNVs and INDELs
5. Variant calling parameters: Configure settings
6. Minimal coverage: 10
7. Minimum baseQ: 20
8. Minimum baseQ for alternate bases: 20
9. Click execute and wait.

Herramientas

lofreq

Show Sections

Lofreq filter called variants posteriorly

Add Lofreq alignment quality scores to aligned read SAM/BAM records

Call variants with Lofreq

Realign reads with Lofreq viterbi

WORKFLOWS

Todos los flujos de trabajo

Call variants with Lofreq (Galaxy Version 2.1.5+galaxy3)

Run Tool

Tool Parameters

Input reads in BAM format *

22: Add indel qualities to data 15

Choose the source for the reference genome

History

Reference *

3: GCF_000875385.1_ViralProj30293_genomic.fna.gz (as fasta)

Call variants across

Whole reference

Types of variants to call *

SNVs and indels

Variant calling parameters

Configure settings

Coverage

Minimal coverage *

10

Coverage cap *

1000000

Base-calling quality

Minimum baseQ *

20

Minimum baseQ for alternate bases *

20

Base quality to use for alternate bases

Use original base qualities

Base alignment quality

Mapping quality

Source quality

Joint quality

Variant filter parameters

Preset filtering on QUAL score + coverage + strand bias (lofreq call default)

Additional Options

Email notification

No

Run Tool

Compare vcfs among callers

Visualize datasets

1. Search upSet diagram in the search toolbox.

2. Select input files for which to produce intersections: select vcf from varscan, vcf from lofreq filter and vcf from ivar variants.

3. Click execute and wait.

4. Click the :eye: icon and check the diagram.

Compare vcfs among callers

Visualize datasets

1. Search upSet diagram in the search toolbox.

2. Select input files for which to produce intersections: select vcf from varscan, vcf from lofreq filter and vcf from ivar variants.

3. Click execute and wait.

4. Click the :eye: icon and check the diagram.

- How many variants differ among the vcfs?

7. Consensus genome

Bcftools consensus

1. Search **bcftools consensus** in the search toolbox.
2. VCF/BCF Data: varscan vcf output.
3. Choose a reference genome: use genome/reference from history. Select NC_009942.1.
4. Click execute and wait.

bcftools consensus Create consensus sequence by applying VCF variants to a reference fasta file (Galaxy Version 1.9+galaxy1)

☆ Favorite

🔄 Versions

▼ Options

VCF/BCF Data

📄 📄 📁

18: VarScan mpileup on data 16 ▼

⬆️ 📁

Choose the source for the reference genome

Use a genome from the history ▼

Reference genome

📄 📄 📁

3: NC_009942.1 (as fasta) ▼

⬆️ 📁

Note: for this example we are not going to mask any position with low coverage, this will be addressed in the exercise 8, with a real example.

Ivar Consensus

1. Search **ivar consensus** in the search toolbox.
2. Bam file: bowtie bam output.
3. Use N instead of - for regions with less than minimum coverage: Yes

ivar consensus

Call consensus from aligned BAM file (Galaxy Version 1.3.1+galaxy0)

☆ Favorite

🔄 Versions

▼ Options

Bam file

7: Bowtie2 on data 3, data 5, and data 4: alignments

Aligned reads, to trim primers and quality

Minimum quality score threshold to count base

20

(-q)

Minimum frequency threshold

0

0 - Majority or most common base

0.2 - Bases that make up atleast 20% of the depth at a position

0.5 - Strict or bases that make up atleast 50% of the depth at a position

0.9 - Strict or bases that make up atleast 90% of the depth at a position

1 - Identical or bases that make up 100% of the depth at a position. Will have highest ambiguities (-t)

Minimum depth to call consensus

10

Here is the galaxy history for this exercise: <https://usegalaxy.eu/u/smonzon/h/variant-calling-101-tutorial-1>