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GENOMIC FILE MANIPULATION
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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 *

7194: data 7192, data 982, and others (discarded)

2: Reference_genome

Reference_genome *

1926: GCA_004329385.1_megNov1_genomic.fna.gz (as 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)

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)

Choose the source for the reference genome

History

Run in batch mode?

Merge output VCFs

Selecting individual mode will generate one VCF dataset for each input BAM dataset. Selecting the merge option will produce one VCF dataset for all input BAM datasets

BAM dataset(s) * required

Connected to 'bam_output' from Step 5

Use the following dataset as the reference sequence * required

Connected to 'output' from Step 2

Limit variant calling to a set of regions?

Do not limit

Sets --targets or --region options

Read coverage

Use defaults

Sets --min-coverage, --limit-coverage, and --skip-coverage

Choose parameter selection level

5. Full list of options

Select how much control over the freebayes run you need

Additional inputs

Do not provide additional inputs

Sets --samples, --populations, --cnv-map, --trace, --failed-alleles, --variant-input, --only-use-input-alleles, --haplotype-basis-alleles, --report-all-haplotype-alleles, --report-monomorphic options, --observation-bias, and --contamination-estimates

Reporting options

Use defaults

Sets -P --pvar option

Population model options

Use defaults

Sets --theta, --ploidy, --pooled-discrete, and --pooled-continuous options

Reference allele options

History
search datasets
Mnov GTSEEK 2022 FreeBayes
FreeBayes analysis of Mnov GTseq data generated in 2022
9.18 GB | 12 | 425 | 7511
7947 : data 7192, data 7188, and others (discarded)
a list with 573 bam datasets
7373 : BAMs for gt.20000 reads data 7192, data 7188, and others (filtered)
a list with 178 bam datasets
7194 : data 7192, data 982, and others (discarded)
a list with 573 fastq.gz pairs
7193 : data 7192, fastqs gt.20000 reads data 982, and others (filtered)

Use defaults

Sets --use-reference-allele and --reference-quality options

Allelic scope options

Set alleic scope options

Sets -I, i, -X, -u, -n, --haplotype-length, --min-repeat-size, --min-repeat-entropy, and --no-partial-observations options

Ignore SNP alleles

False

(--no-snps)

Ignore indels alleles

False

(--no-indels)

Ignore multi-nucleotide polymorphisms, MNPs

True

(--no-mnps)

Ignore complex events (composites of other classes)

True

(--no-complex)

How many best SNP alleles to evaluate *

0

Alleles are ranked by the sum of supporting quality scores. Set to 0 to evaluate all (--use-best-n-alleles)

Allow haplotype calls with contiguous embedded matches of up to (nucleotides) *

0

(--haplotype-length)

When assembling observations across repeats, require the total repeat length at least this many bp *

5

(--min-repeat-size)

To detect interrupted repeats, build across sequence until it has entropy > (bits per bp) *

1

(--min-repeat-entropy)

Exclude observations which do not fully span the dynamically-determined detection window

False

By default, FreeBayes uses all observations, dividing partial support across matching haplotypes when generating haplotypes (--no-partial-observations)

Turn off left-alignment of indels

False

(--dont-left-align-indels)

Input filters

No input filters (default)

Sets -4, -m, -q, -R, -Y, -Q, -U, -z, -$, -e, -0, -F, -C, -3, -G, and -! options

Population and mappability priors

Set population and mappability priors

Sets -k, -w, -V, and -a options

No population priors

True

Equivalent to --pooled-discrete --hwe-priors-off and removal of Ewens Sampling Formula component of priors (--no-population-priors)

Disable estimation of the probability of the combination arising under HWE given the allele frequency as estimated by observation frequency

True

(--hwe-priors-off)

Disable incorporation of prior expectations about observations

True

Uses read placement probability, strand balance probability, and read position (5"-3") probability (--binomial-obs-priors-off)

Disable use of aggregate probability of observation balance between alleles as a component of the priors

True

(--allele-balance-priors-off)

Genotype likelihood options

Use defaults

Sets --base-quality-cap, --experimental-gls, and --prob-contamination options

Algorithmic features

Use defaults

Sets --report-genotypes-likelihood-max, -B, --genotyping-max-banddepth, -W, -N, S, -j, -H, -D, -= options