PathogenSurveillance

nf-core 1

Standardize and download input

custom R script, entrez eutils

Fast initial ID

bbmap sendsketch

Select and download references

NCBI datasets

Trim adapters

fastp

Assemble genomes

spades, flye

Sketch assemblies and references

sourmash sketch

Compare all sketches

sourmash compare

Select contextual references

Custom R script

Annotate genomes

bakta

Identify shared orthologs

pirate

Align shared orthologs

mafft

Infer phylogeny

iqtree2

Select mapping reference

Custom R script

Align reads

Variant calling

and

SNP

bwa mem

Call variants

graphtyper, picard

Filter variants

vcflib

Infer phylogeny

iqtree2

Select contextual references

Input data:

Sequence data

References (optional)

Metadata

Custom R script

Extract BUSCO genes

busco

Align BUSCO genes

mafft

Infer phylogeny

igtree2

Make quality control reports multiqc, fastqc, quast

Make main report

Custom Quarto script, psminer

Output data:

Interactive reports Static reports Intermediate files

