

SARS-COV-2 NEXTFLOW PIPELINE



Reproducible pipelines with Nextflow

```
nextflow.enable.dsl=2

process sayHello {
    input:
        val cheers
    output:
        stdout

    """
    echo $cheers
    """
}

workflow {
    channel.of('Ciao','Hello','Hola') | sayHello | view
}
```

Nextflow

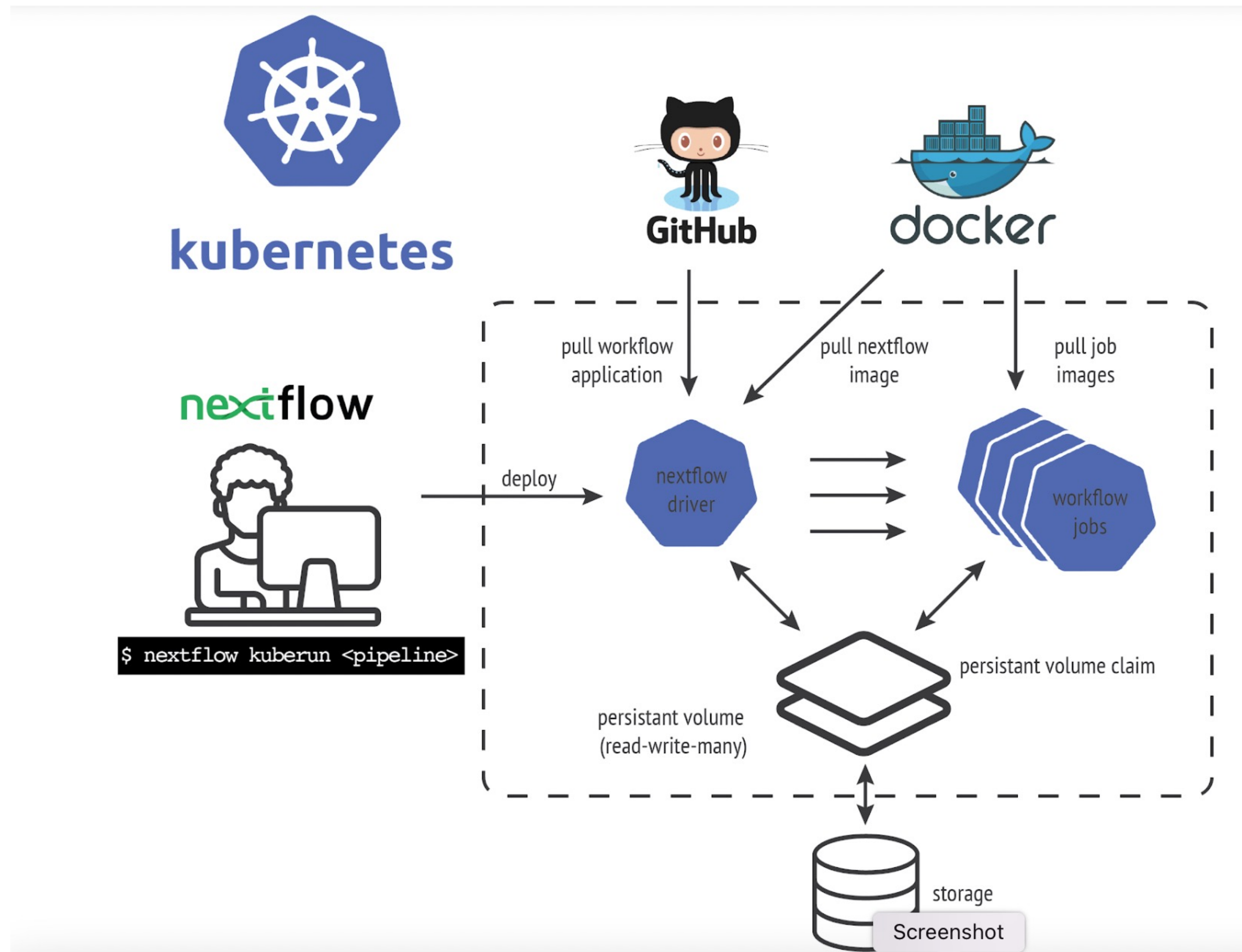
Data-driven computational pipelines

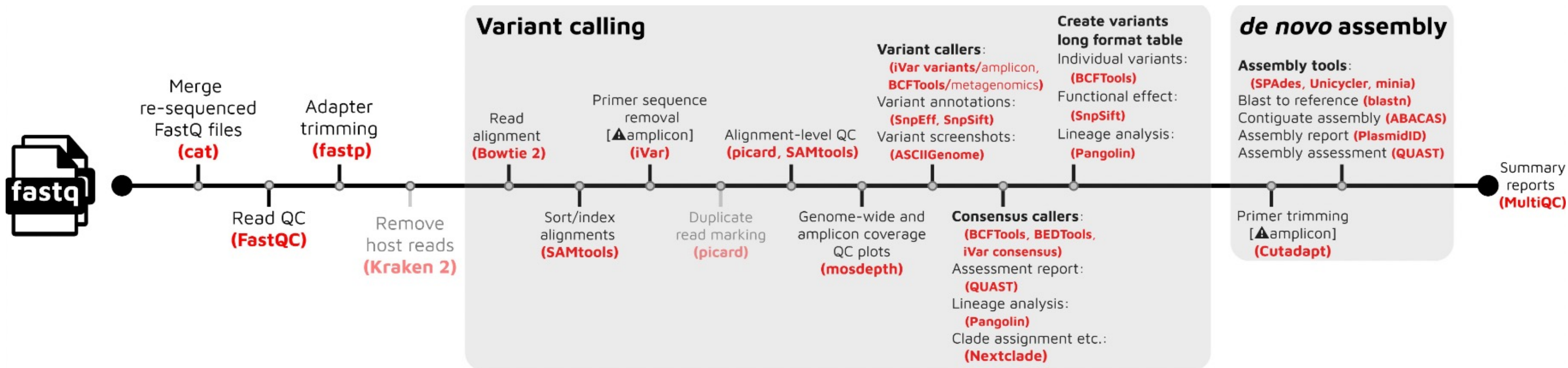
Nextflow enables scalable and reproducible scientific workflows using software containers. It allows the adaptation of pipelines written in the most common scripting languages.

Its fluent DSL simplifies the implementation and the deployment of complex parallel and reactive workflows on clouds and clusters.

[Find out more](#)

Allows for reproducible results

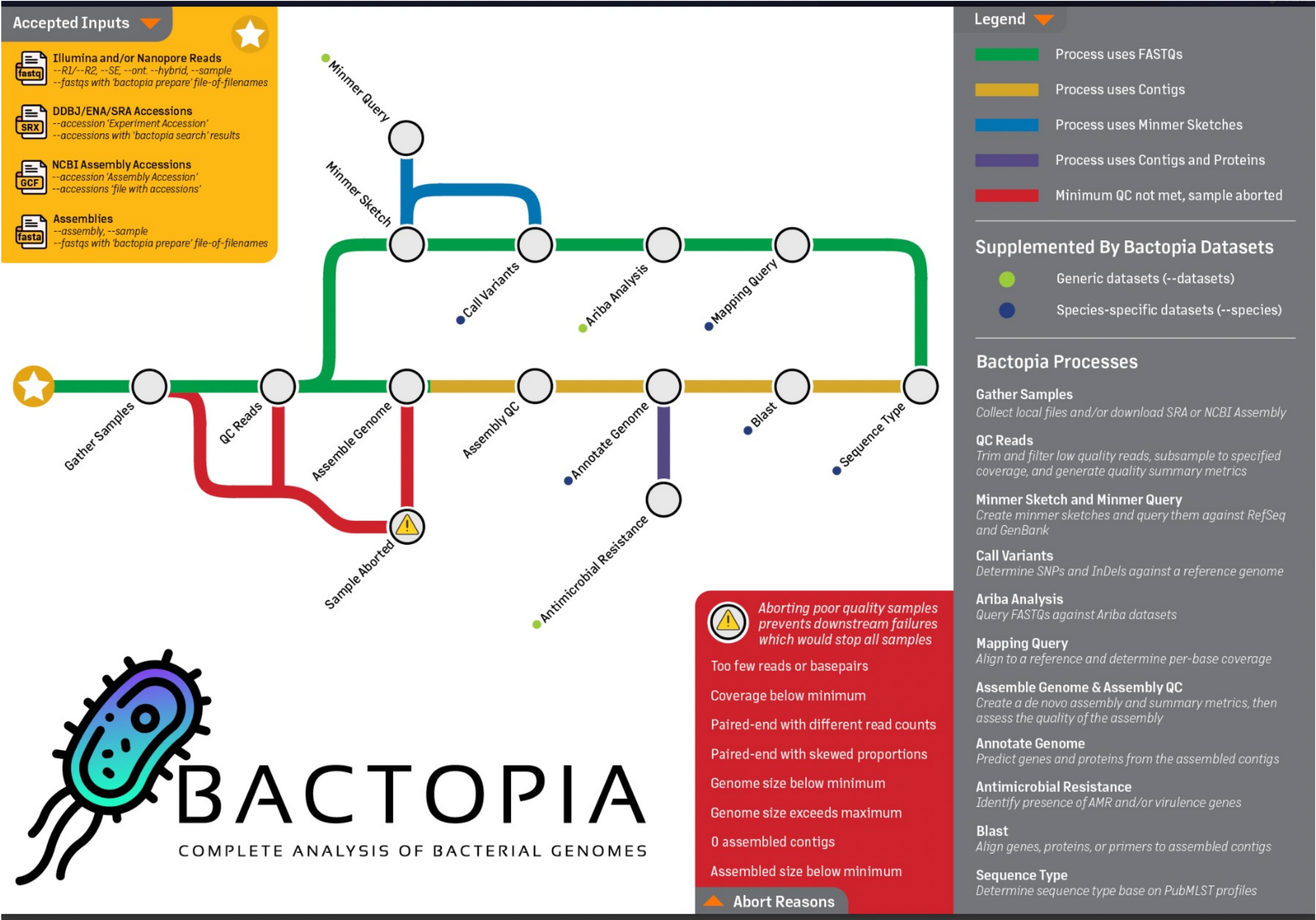




nf-core  **/ viralrecon v2.4.1**

Assembly and intrahost/low-frequency variant calling for viral samples

There are many different nextflow pipelines



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nf-core/
mycosnp

nextflow DSL2 **≥21.10.3**  run with **conda**  run with **docker** run with **singularity**

Introduction

nf-core/mycosnp is a bioinformatics best-practice analysis pipeline for MycoSNP is a portable workflow for performing whole genome sequencing analysis of fungal organisms, including *Candida auris*. This method prepares the reference, performs quality control, and calls variants using a reference. MycoSNP generates several output files that are compatible with downstream analytic tools, such as those for used for phylogenetic tree-building and gene variant annotations..

Questions?