

Reproducible bioinformatics for everyone:

Nextflow & nf-core



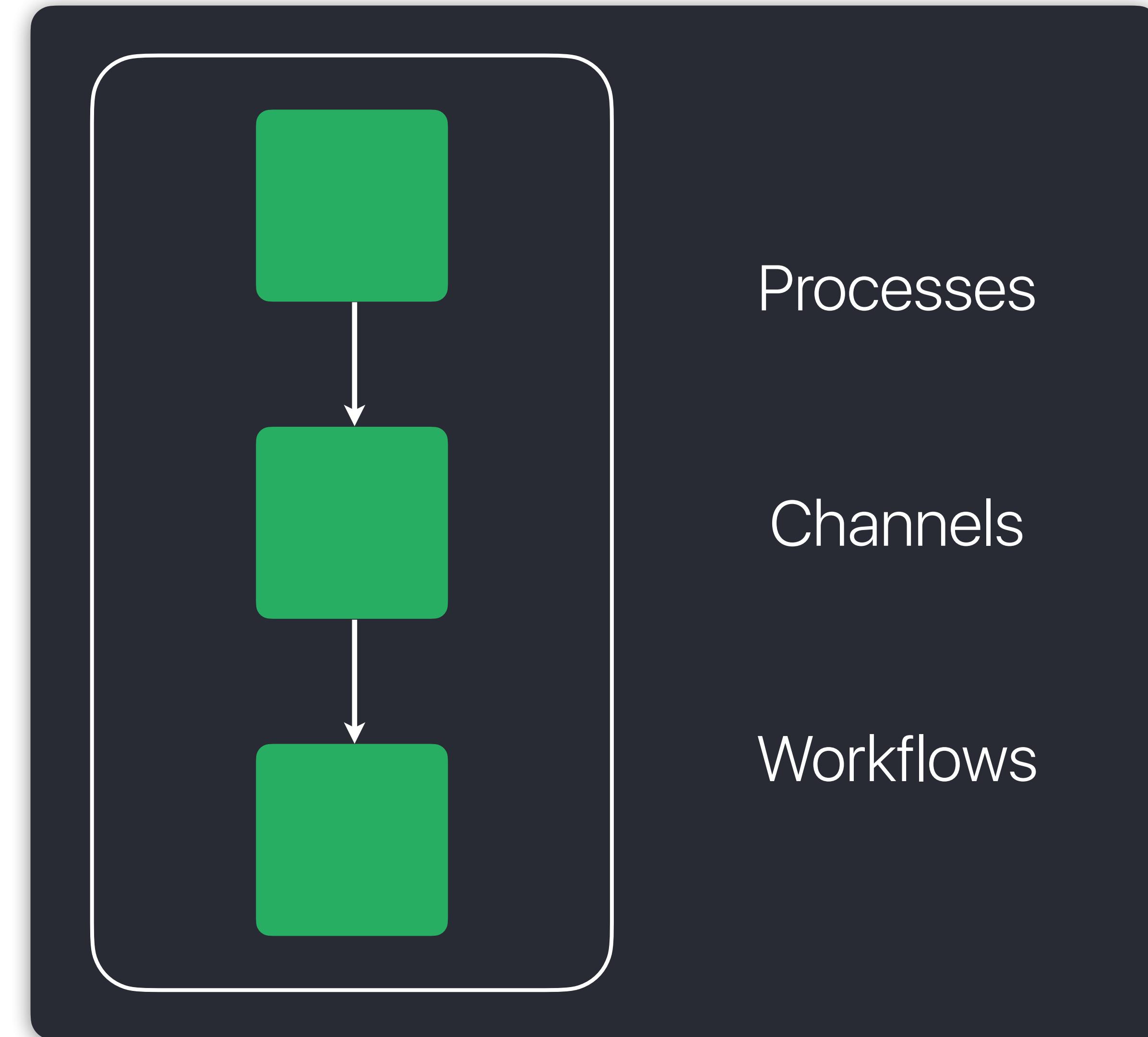
nextflow





Language

nextflow



nextflow

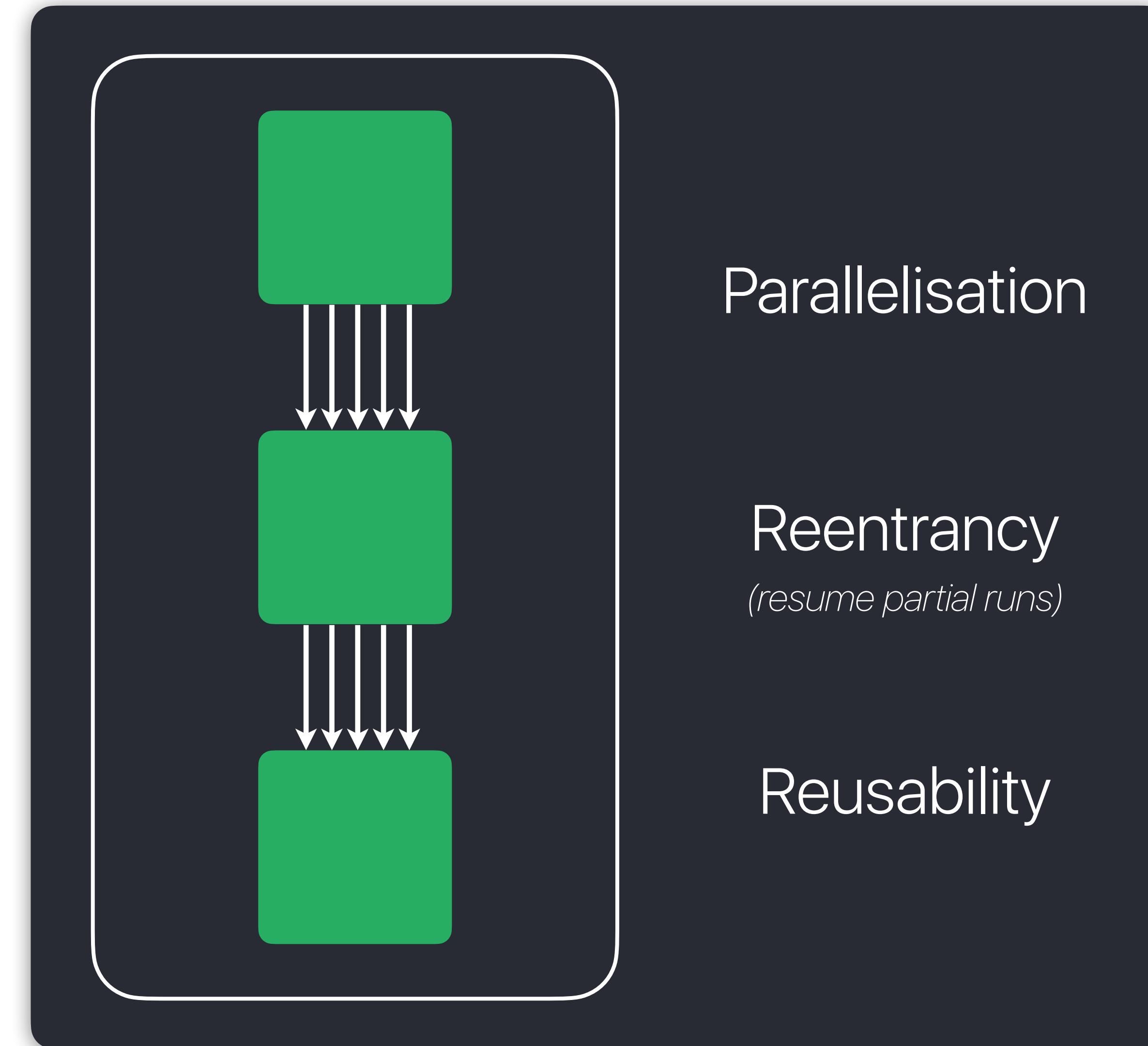
```
#!/usr/bin/env nextflow
process fastqc {
    input:
    path input

    output:
    path "*_fastqc.{zip,html}"

    script:
    """
    fastqc -q $input
    """
}

workflow {
    Channel.fromPath("*.fastq.gz") | fastqc
}
```

nextflow





Language

Software

Compute

nextflow



git



GitHub



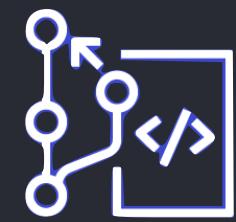
Bitbucket



GitLab



Gitea



AWS CodeCommit



Azure Repos

Software

Compute

nextflow



git



GitHub



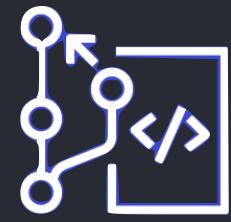
Bitbucket



GitLab



Gitea



AWS CodeCommit



Azure Repos



docker®



Singularity



CONDA

Compute

nextflow



git



GitHub



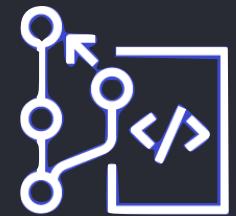
Bitbucket



GitLab



Gitea



AWS CodeCommit



Azure Repos



docker®



Singularity



aws



slurm
workload manager

LSF

PBS



Google Cloud



kubernetes



Microsoft Azure

nextflow

```
#!/usr/bin/nextflow
process fastqc {
    container "biocontainers/fastqc" ←
        input:
        path input

        output:
        path "*_fastqc.{zip,html}"

        script:
        """
        fastqc -q $input
        """
}

workflow {
    Channel.fromPath("*.fastq.gz") | fastqc
}
```

```
docker {
    enabled = true
}
```



```
nextflow run main.nf -c ~/mylocal.conf
```

nextflow

```
#!/usr/bin/nextflow
process fastqc {
    container "biocontainers/fastqc"

    input:
    path input

    output:
    path "*_fastqc.{zip,html}"

    script:
    """
    fastqc -q $input
    """
}

workflow {
    Channel.fromPath("*.fastq.gz") | fastqc
}
```

```
process {
    executor = 'slurm'
}
singularity {
    enabled = true
}
```



Singularity

```
nextflow run main.nf -c ~/myhpc.conf
```

nextflow

```
#!/usr/bin/nextflow
process fastqc {
    container "biocontainers/fastqc"
    input:
        path input
    output:
        path "*_fastqc.{zip,html}"
    script:
        """
        fastqc -q $input
        """
}
workflow {
    Channel.fromPath("*.fastq.gz") | fastqc
}
```

```
process {
    executor = 'slurm'
    queue = { task.time < 3.h ? 'short' : 'long' }
    beforeScript = "module load singularity"
}
singularity {
    enabled = true
    cacheDir = "/resources/nxf/singularity"
}
params {
    max_cpus = 24
    max_memory = 240.GB
    max_time = 168.h
}
```

```
nextflow run main.nf -c ~/myhpc.conf
```

nextflow

```
#!/usr/bin/nextflow
process fastqc {
    container "biocontainers/fastqc"

    input:
    path input

    output:
    path "*_fastqc.{zip,html}"

    script:
    """
        fastqc -q $input
    """

}

workflow {
    Channel.fromPath("*.fastq.gz") | fastqc
}
```

```
process {
    executor = 'awsbatch'
    queue = 'my-batch-queue'
}
aws {
    region = 'us-east-1'
}
```



```
nextflow run main.nf -c ~mycloud.conf
```

nextflow

```
#!/usr/bin/nextflow
process fastqc {
    container "biocontainers/fastqc"

    input:
    path input

    output:
    path "*_fastqc.{zip,html}"

    script:
    """
        fastqc -q $input
    """

}

workflow {
    Channel.fromPath(params.input) | fastqc
}
```

```
params {
    input = "*.fastq.gz"
}
```

```
nextflow run main.nf --input "data/input*.fq"
```



Reproducible

Between runs

Portable

Between systems

nextflow



nextflow

nf-core





A community effort to collect a curated set
of analysis pipelines built using Nextflow.

<https://nf-co.re>

nf-core



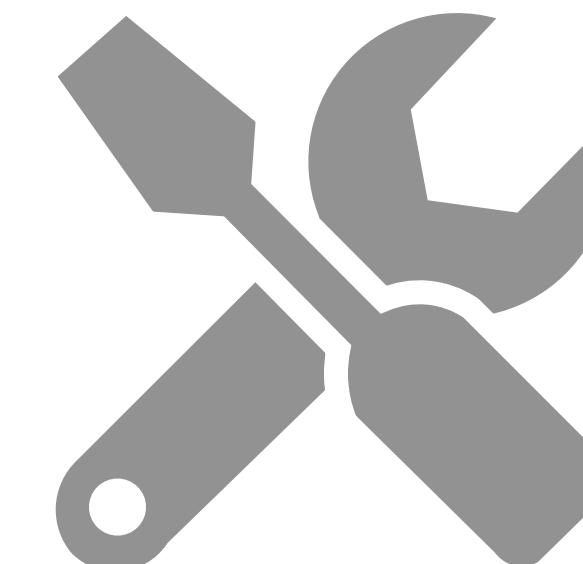
73

PIPELINES

<https://nf-co.re>



TOOLS



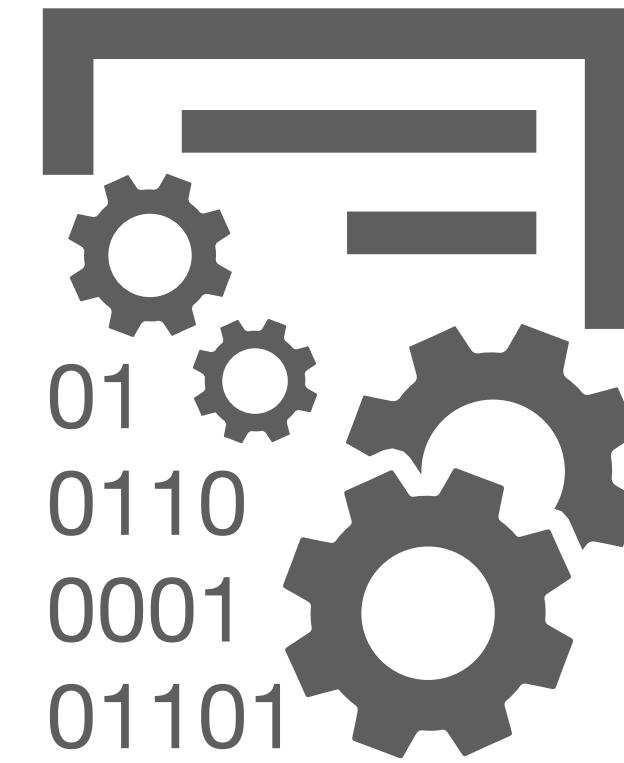
Running pipelines

Writing pipelines

Testing / automation

<https://nf-co.re>

nf-core



708

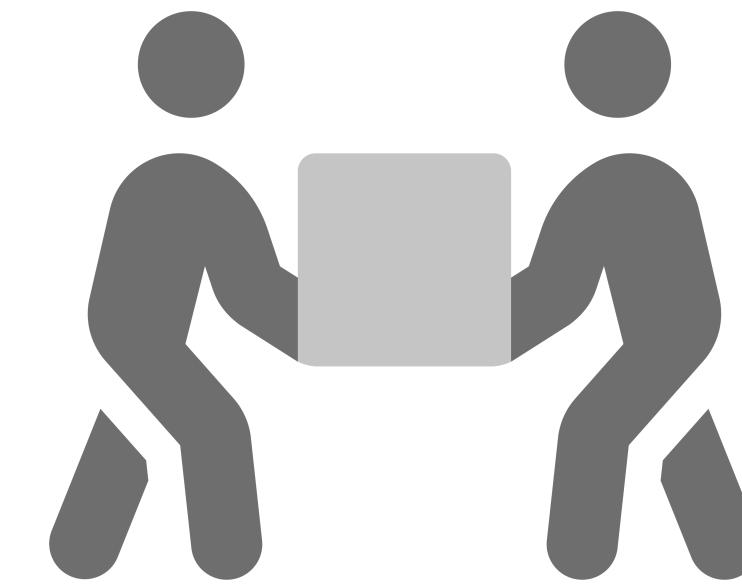
MODULES

24

SUB-WORKFLOWS

<https://nf-co.re>

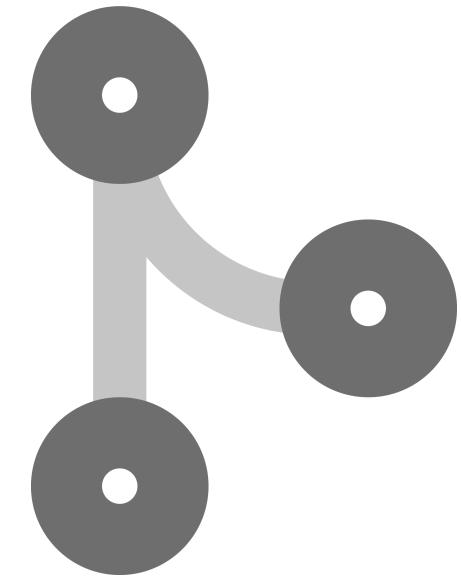
nf-core



Develop with
the community



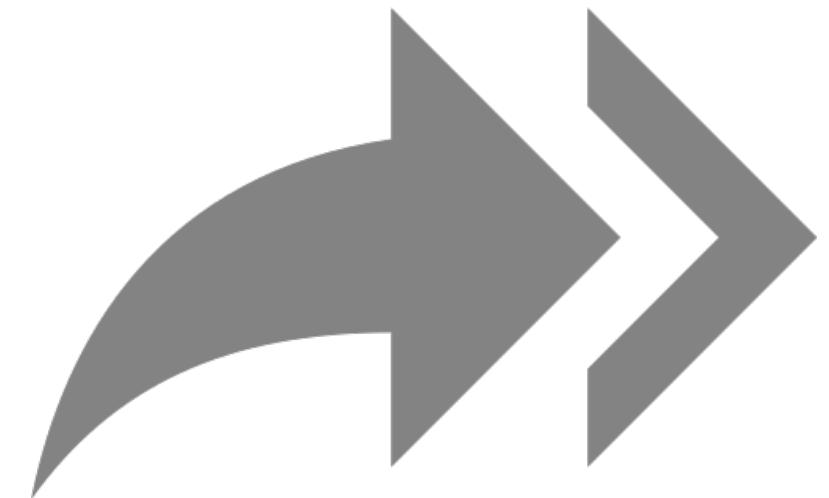
Use a common
template



Collaborate,
don't duplicate

<https://nf-co.re>

nf-core



Tools built for
everyone



Works with any
Nextflow pipeline



Collaborate on
components

<https://nf-co.re>

4135

Slack users

527

GitHub organisation
members

1583

GitHub contributors

3294

Twitter followers

90

Repositories

11.61K

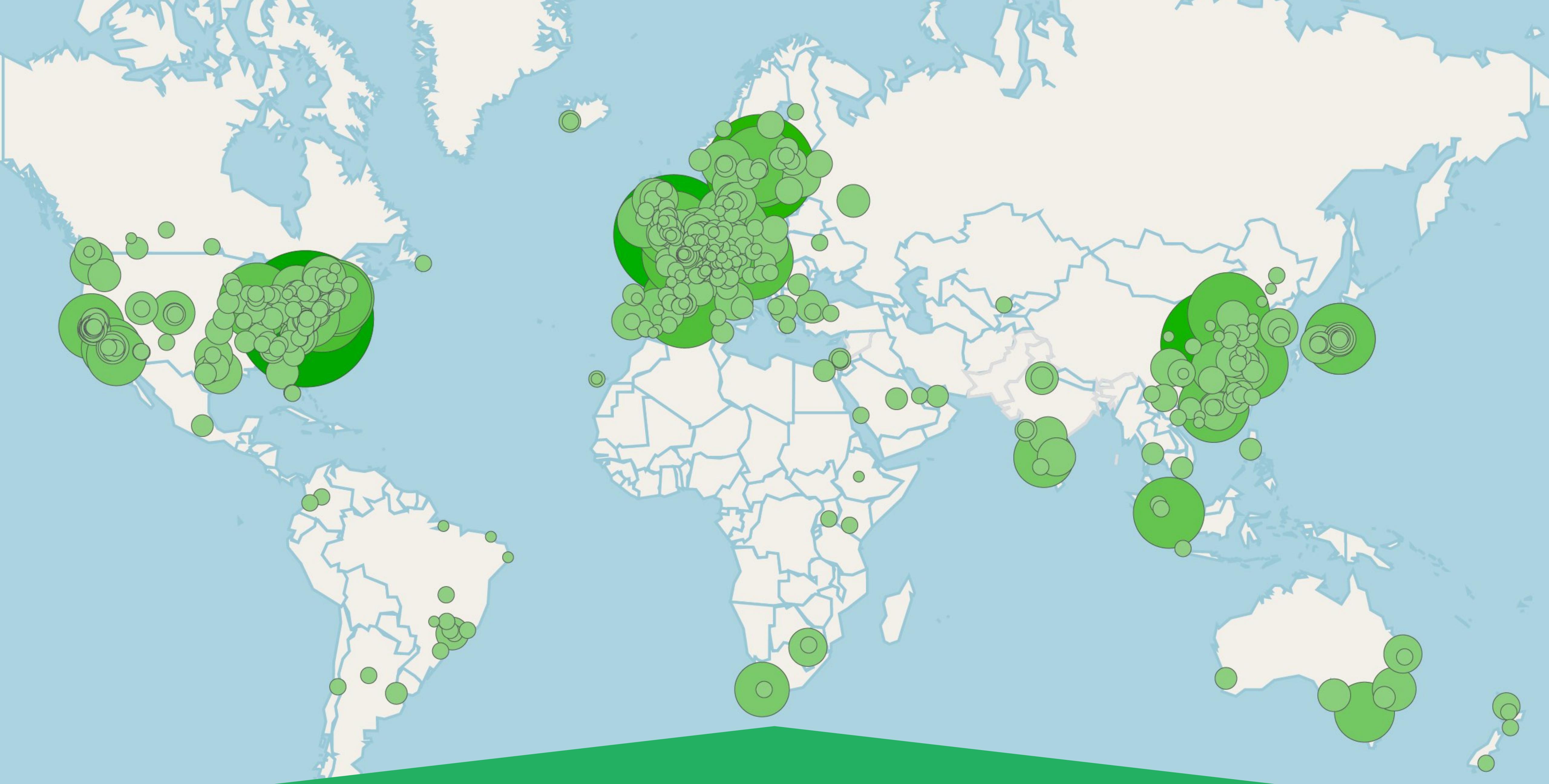
Pull Requests

32.37K

Commits

5.21K

Issues



<https://nf-co.re>

Correspondence | Published: 13 February 2020

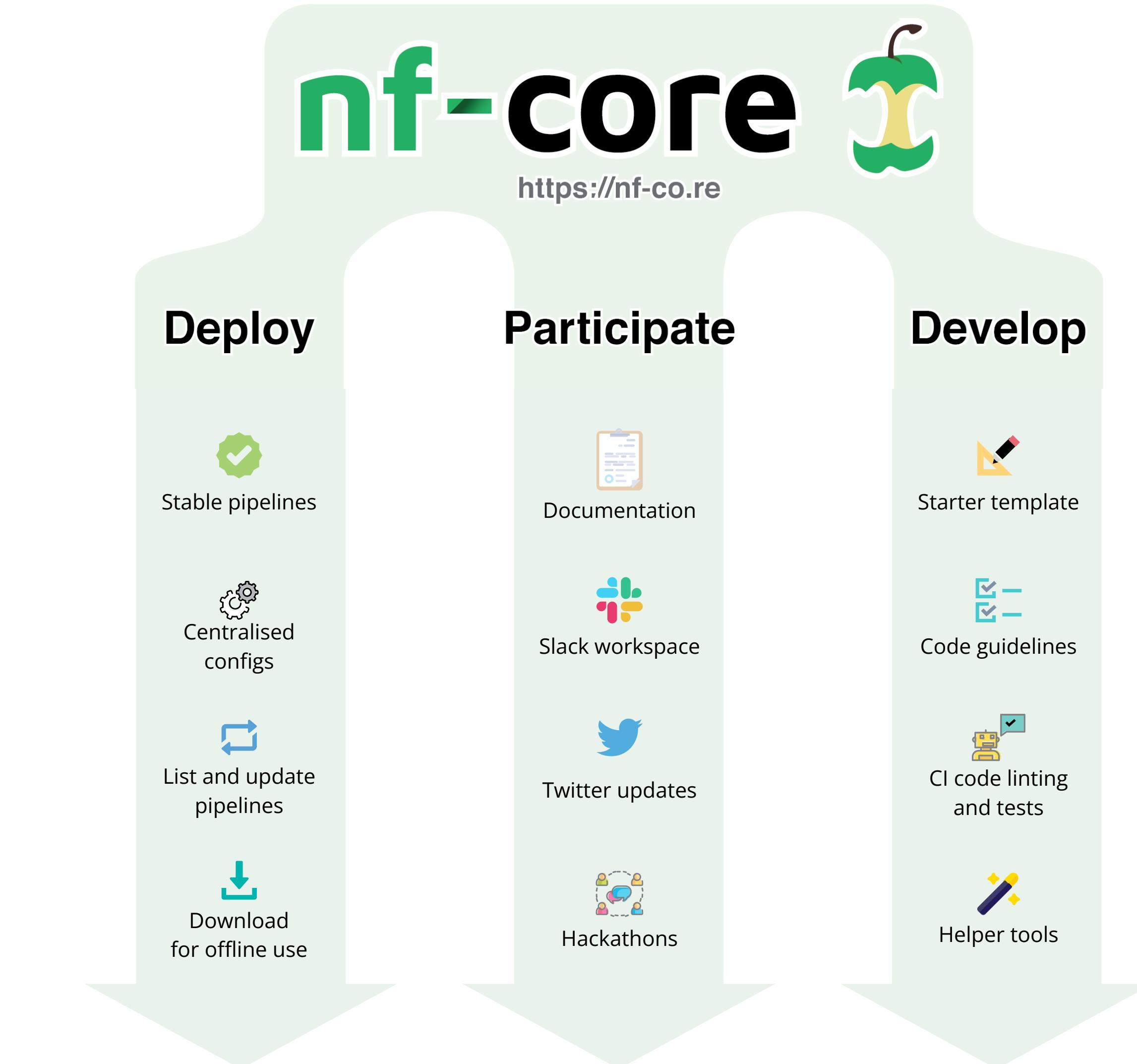
The nf-core framework for community-curated bioinformatics pipelines

Philip A. Ewels, Alexander Peltzer, Sven Fillinger, Harshil Patel, Johannes Alneberg,
Andreas Wilm, Maxime Ulysse Garcia, Paolo Di Tommaso & Sven Nahnsen 

Nature Biotechnology 38, 276–278(2020) | Cite this article

3253 Accesses | 3 Citations | 172 Altmetric | Metrics

To the Editor — The standardization, portability and reproducibility of analysis pipelines are key issues within the bioinformatics community. Most bioinformatics pipelines are designed for use on-premises; as a result, the associated software dependencies and execution logic are likely to be tightly coupled with proprietary computing environments. This can make it difficult or even impossible for others to reproduce the ensuing results, which is a fundamental requirement for the validation of scientific findings. Here, we introduce the nf-core framework as a means for the development of collaborative, peer-reviewed, best-practice analysis pipelines (Fig. 1). All nf-core pipelines are written in Nextflow and so inherit the ability to be executed on most computational infrastructures, as well as having native support for container technologies such as Docker and Singularity. The nf-core community (Supplementary Fig. 1) has developed a suite of tools that automate pipeline creation, testing, deployment and synchronization. Our goal is to provide a framework for high-quality bioinformatics pipelines that can be used across all institutions and research facilities.



Join the community



<https://nf-co.re/join>



nextflow tower



nextflow tower

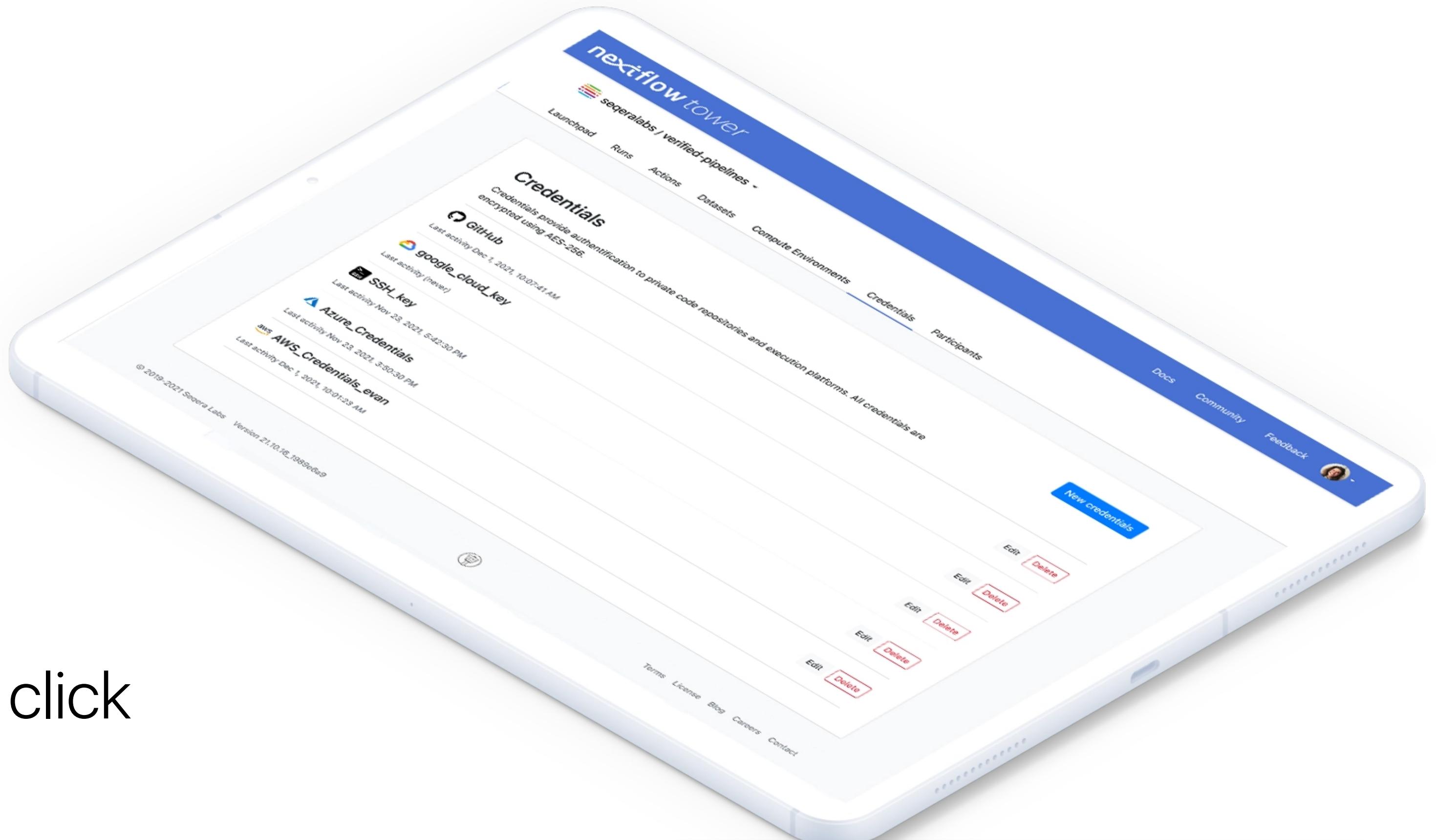
 seqera labs

Intuitive launchpad interface

Launch, manage, and monitor

Share runs and work in teams

Create cloud infrastructure with a click

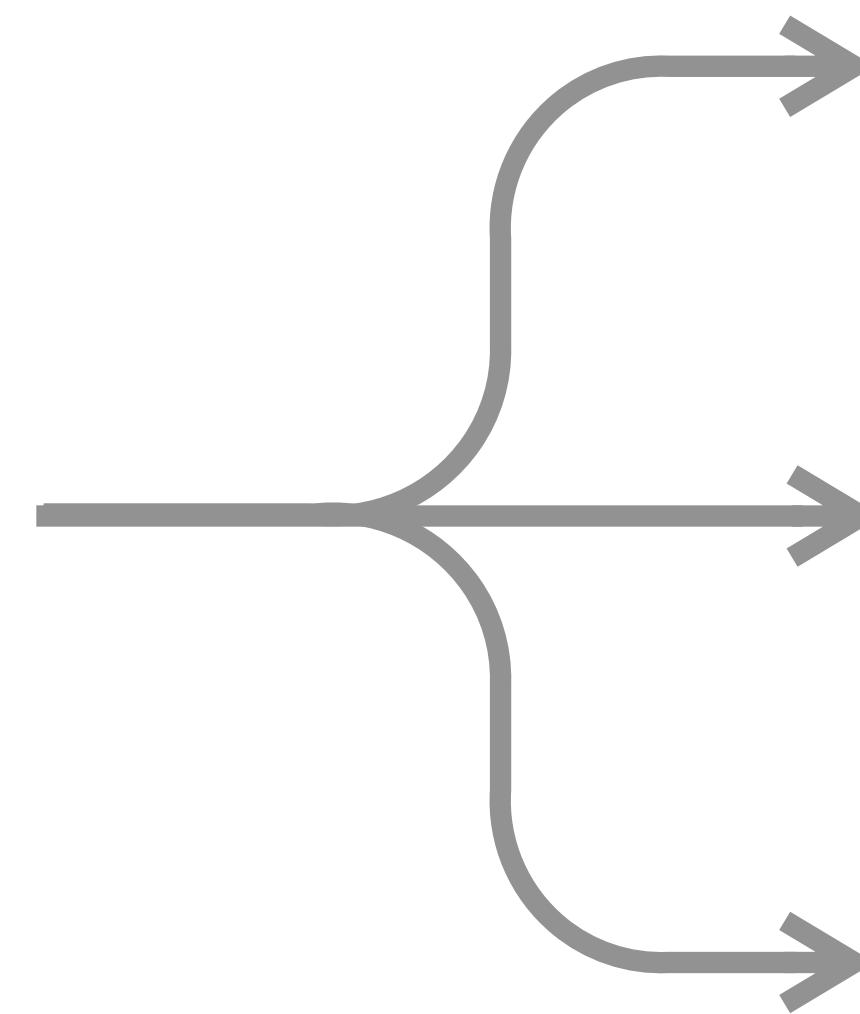
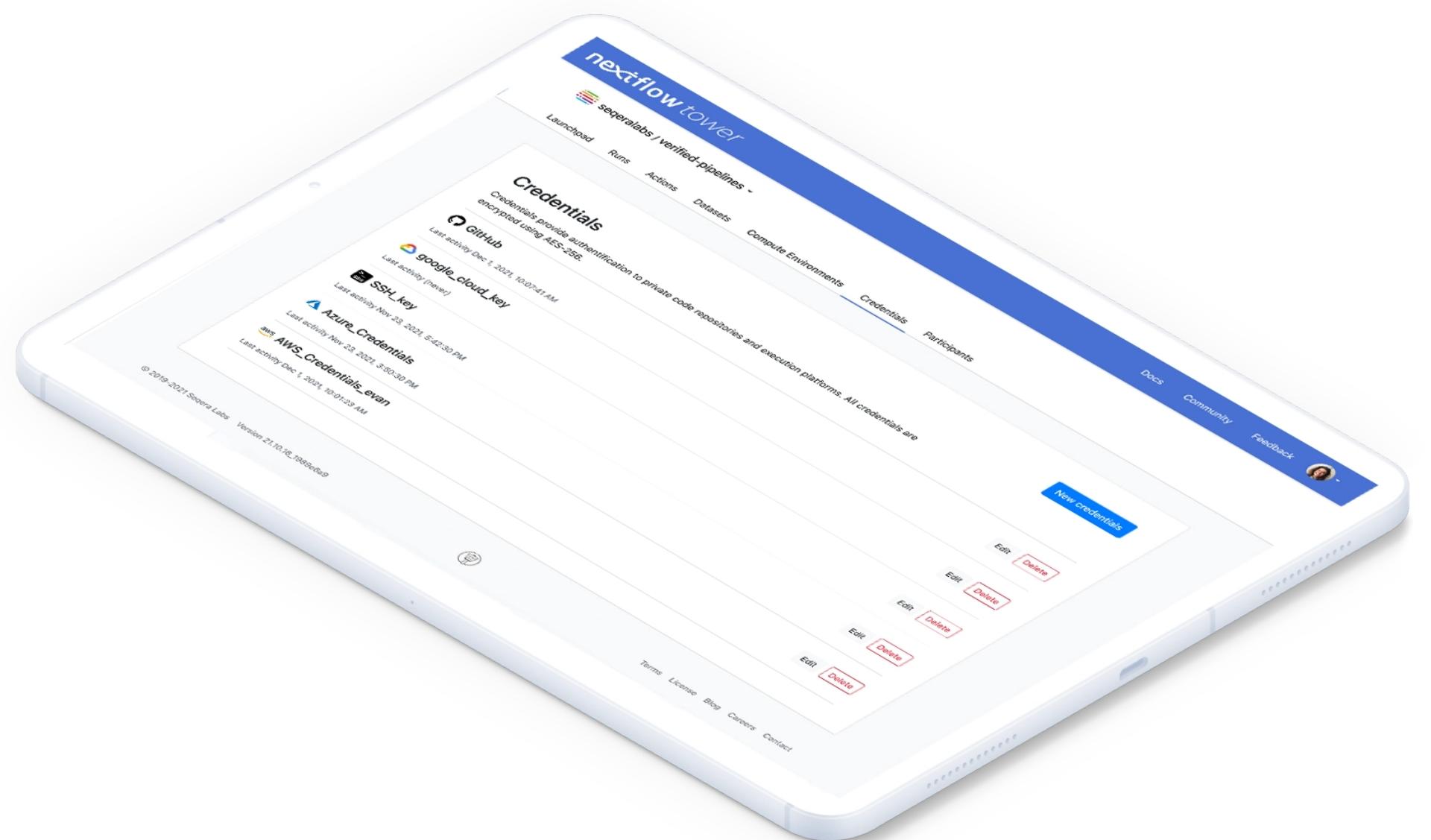


<https://tower.nf>



nextflow tower

 seqera labs



Community: Open source



Cloud: Free & paid tiers



Enterprise: Commercial

<https://tower.nf>

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 ewels



seqeralabs

<https://seqera.io>

**Chan Zuckerberg
Initiative**



nextflow SUMMIT 2022

<https://summit.nextflow.io>

Nextflow / nf-core training

6-10 March 2023

nf-core hackathon

20-24 March 2023

<https://nf-co.re>

<https://nextflow.io>