

Reproducible bioinformatics for everyone:

Nextflow & nf-core



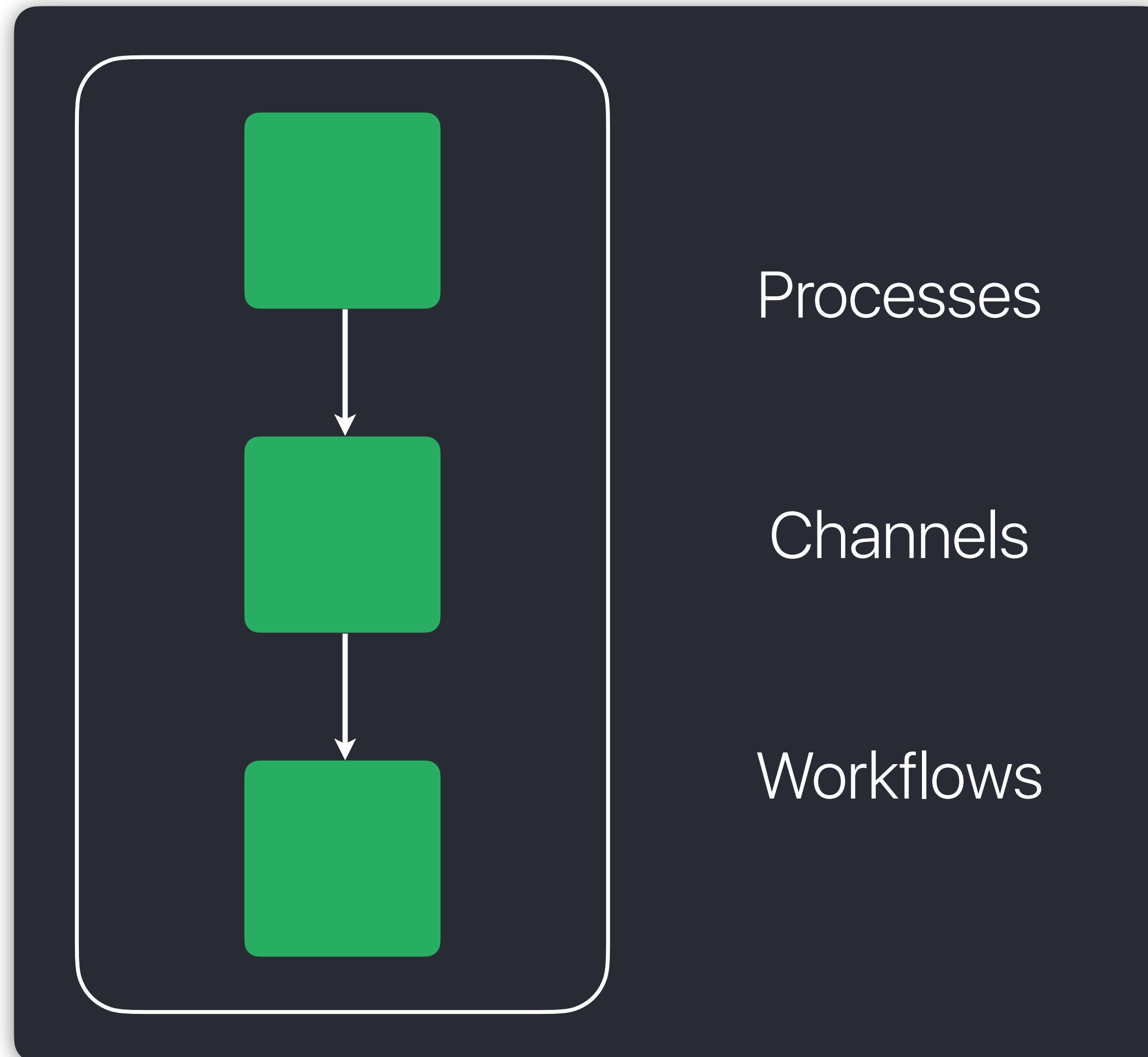
nextflow



nextflow

Language

nextflow



nextflow

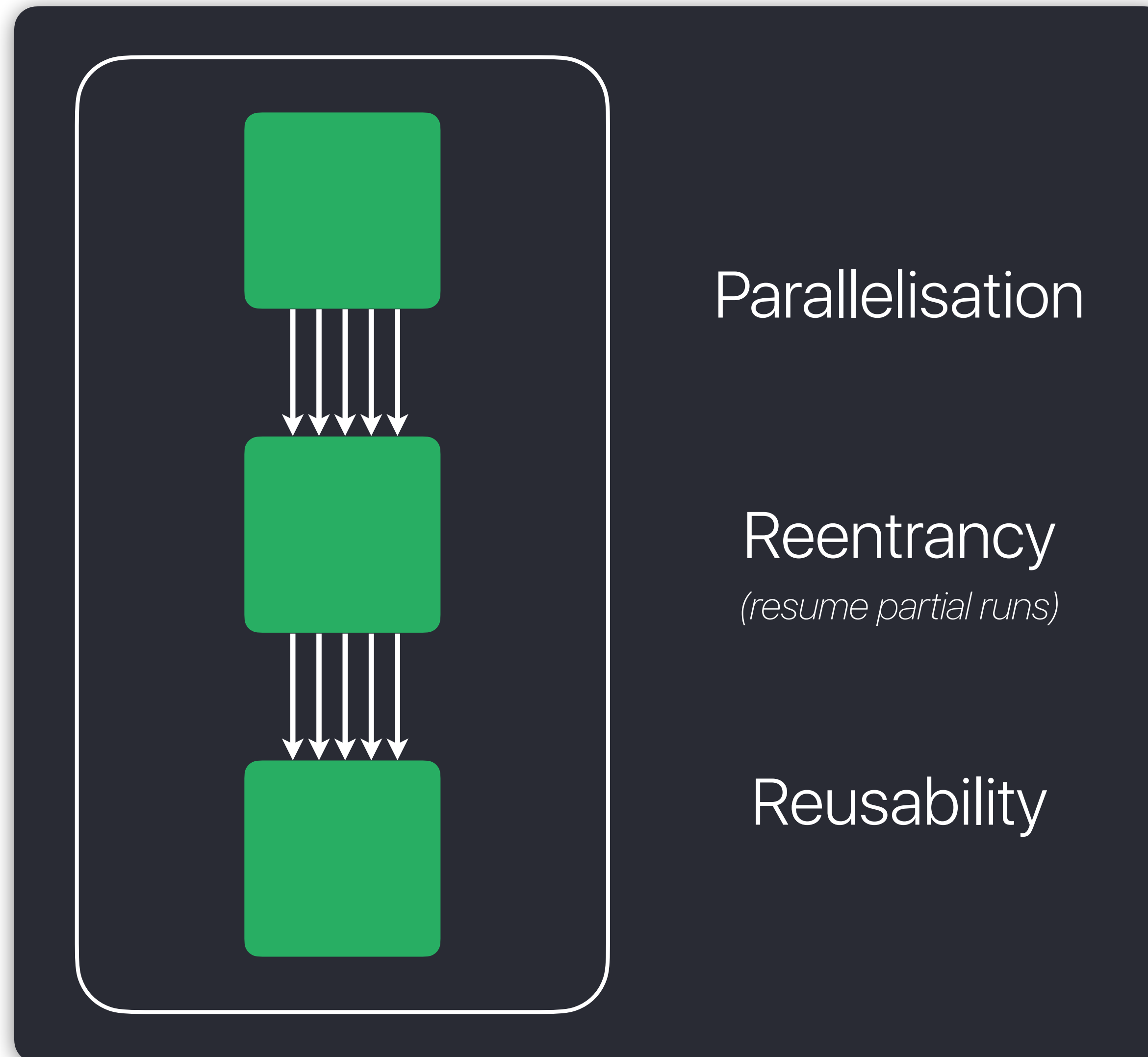
```
#!/usr/bin/env nextflow
process fastqc {
    input:
    path input

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

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

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

nextflow



nextflow

Language

Software

Compute

nextflow



git



GitHub



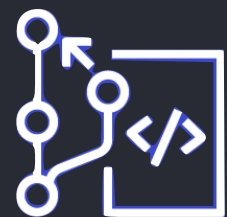
Bitbucket



GitLab



Gitea



AWS CodeCommit



Azure Repos

Software

Compute

nextflow



git



GitHub



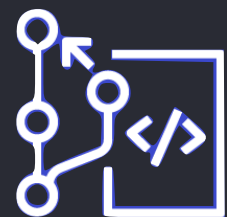
Bitbucket



GitLab



Gitea



AWS CodeCommit



Azure Repos



docker



Singularity



CONDA

Compute

nextflow



git



GitHub



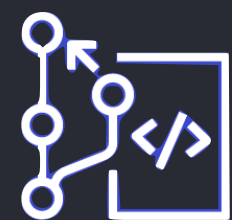
Bitbucket



GitLab



Gitea



AWS CodeCommit



Azure Repos



docker



Singularity



CONDA

SGE



Microsoft Azure



slurm

workload manager



openstack



aws

LSF

PBS



Google Cloud



kubernetes

nextflow

Reproducible

Between runs

Portable

Between systems

nextflow



nextflow

nf-core 



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>

nf-core



TOOLS

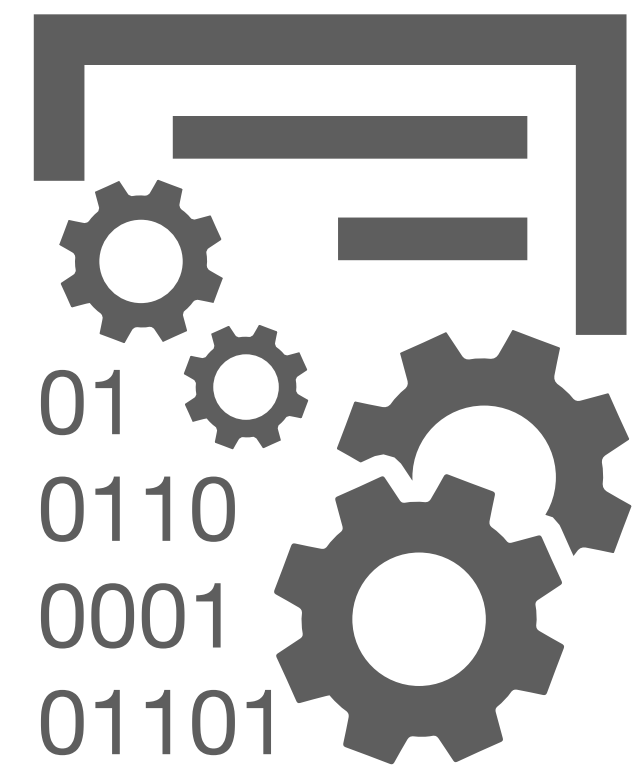
Running pipelines

Writing pipelines

Testing / automation

<https://nf-co.re>

nf-core



708

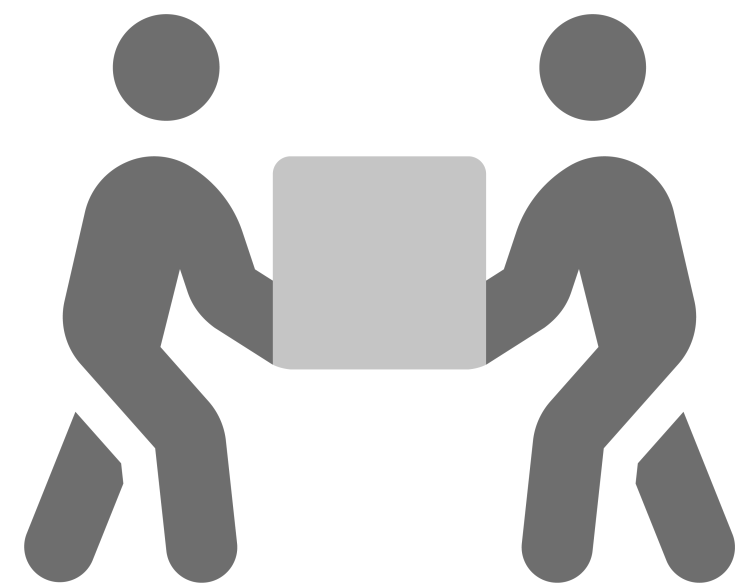
MODULES

24

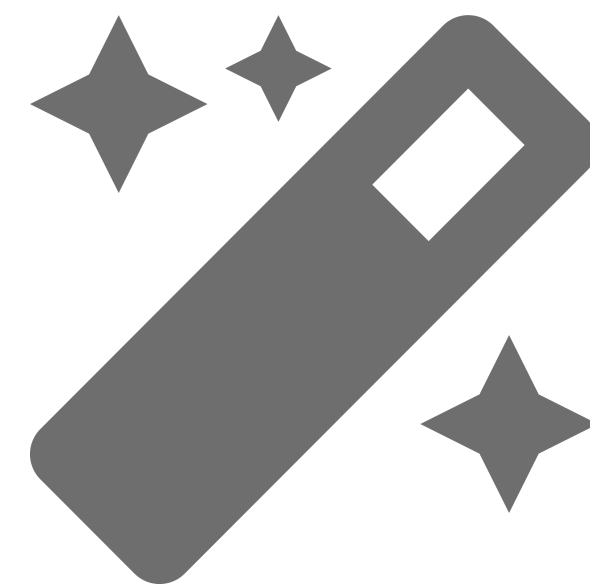
SUB-WORKFLOWS

<https://nf-co.re>

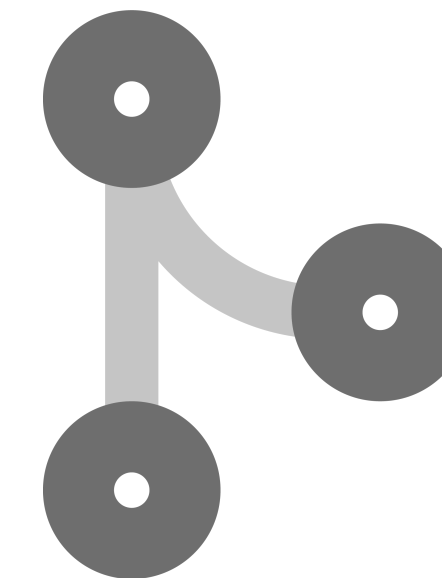
nf-core



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>

nf-core 

Tools are for everyone

<https://nf-co.re>

4135

Slack users

527

GitHub organisation
members

1583

GitHub contributors

3294

Twitter followers

90

Repositories

11.61K

Pull Requests

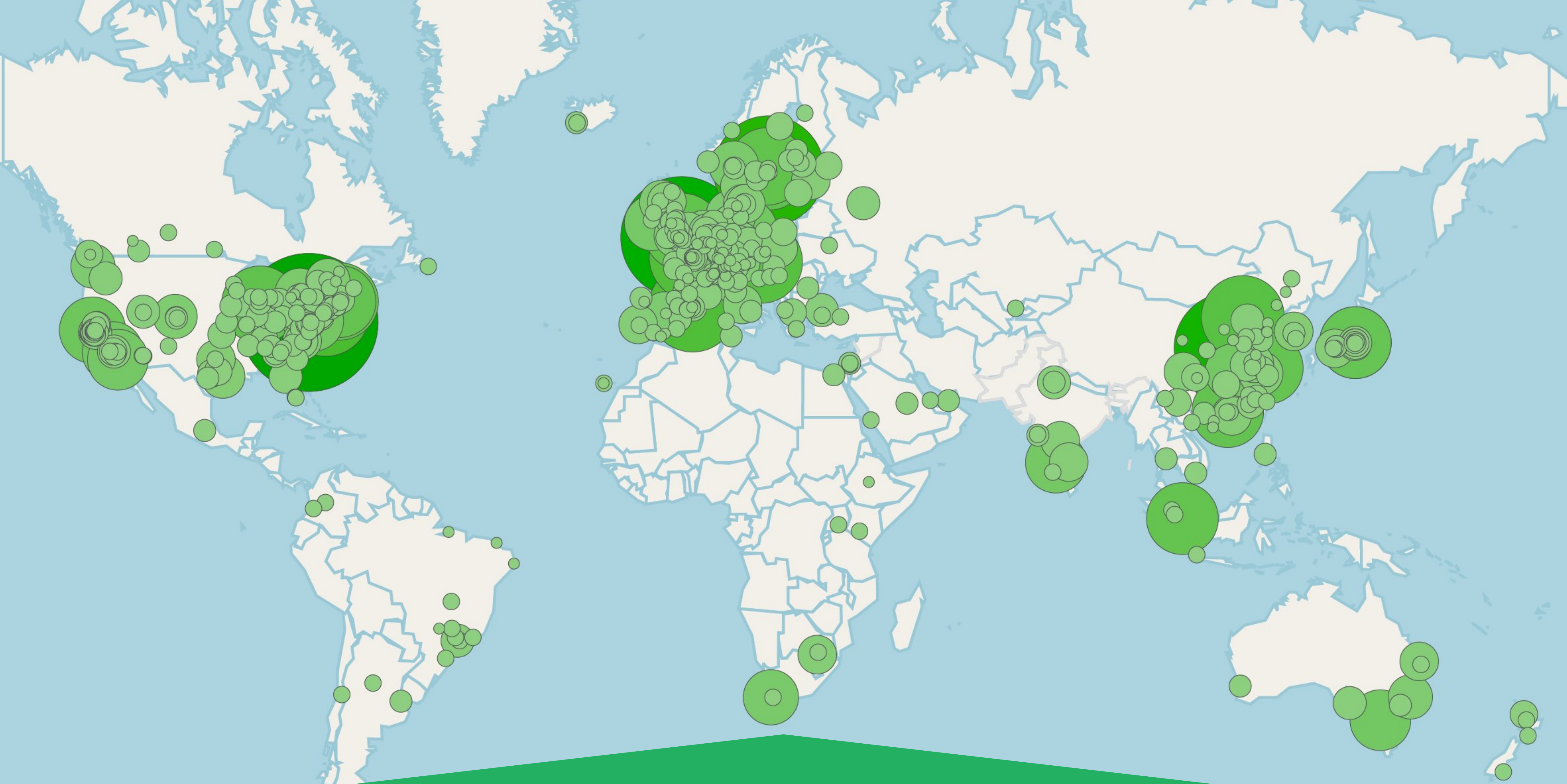
32.37K

Commits

5.21K

Issues


<https://nf-co.re>



<https://nf-co.re>

Correspondence | Published: 13 February 2020

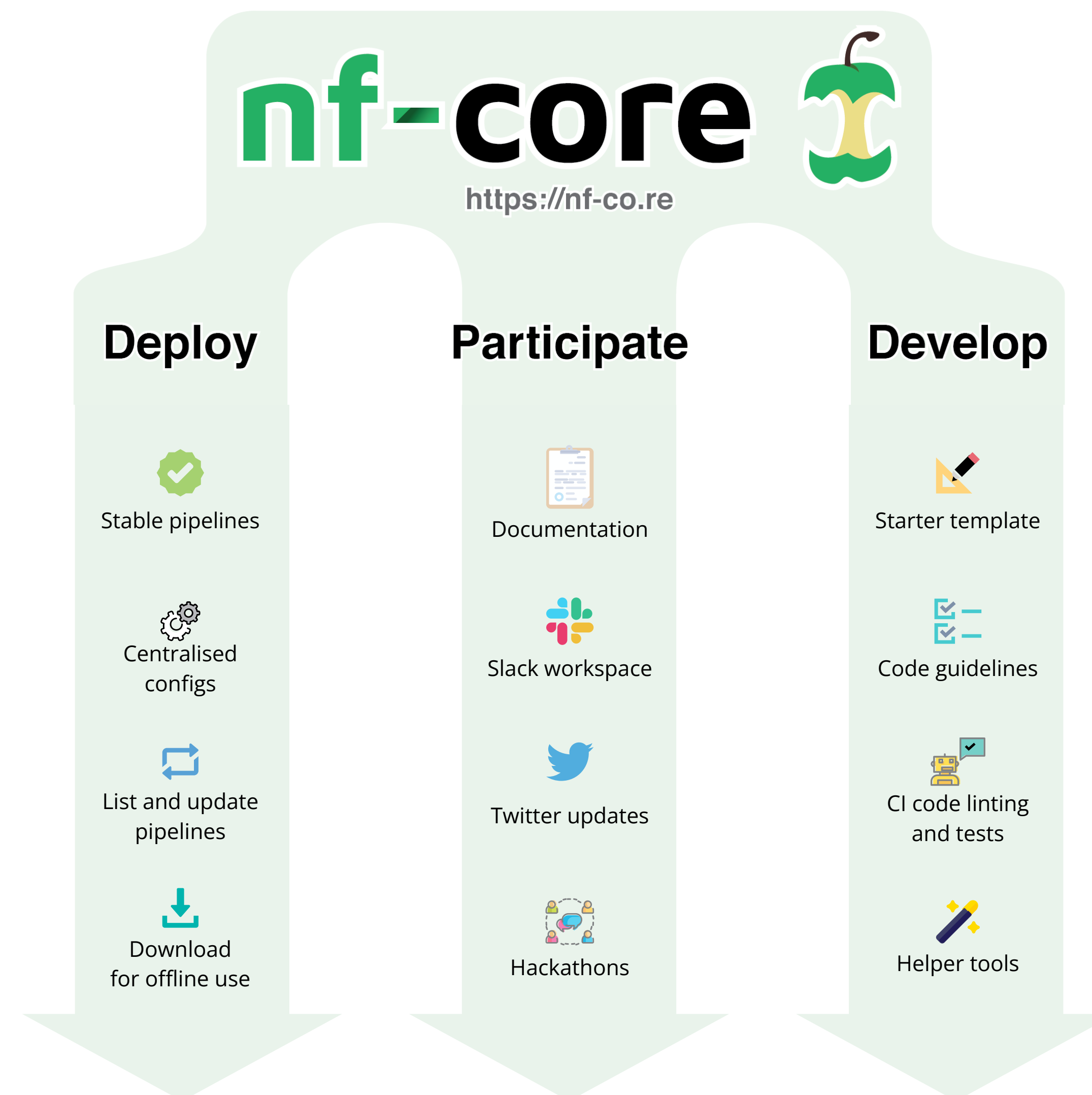
The nf-core framework for community-curated bioinformatics pipelines

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*



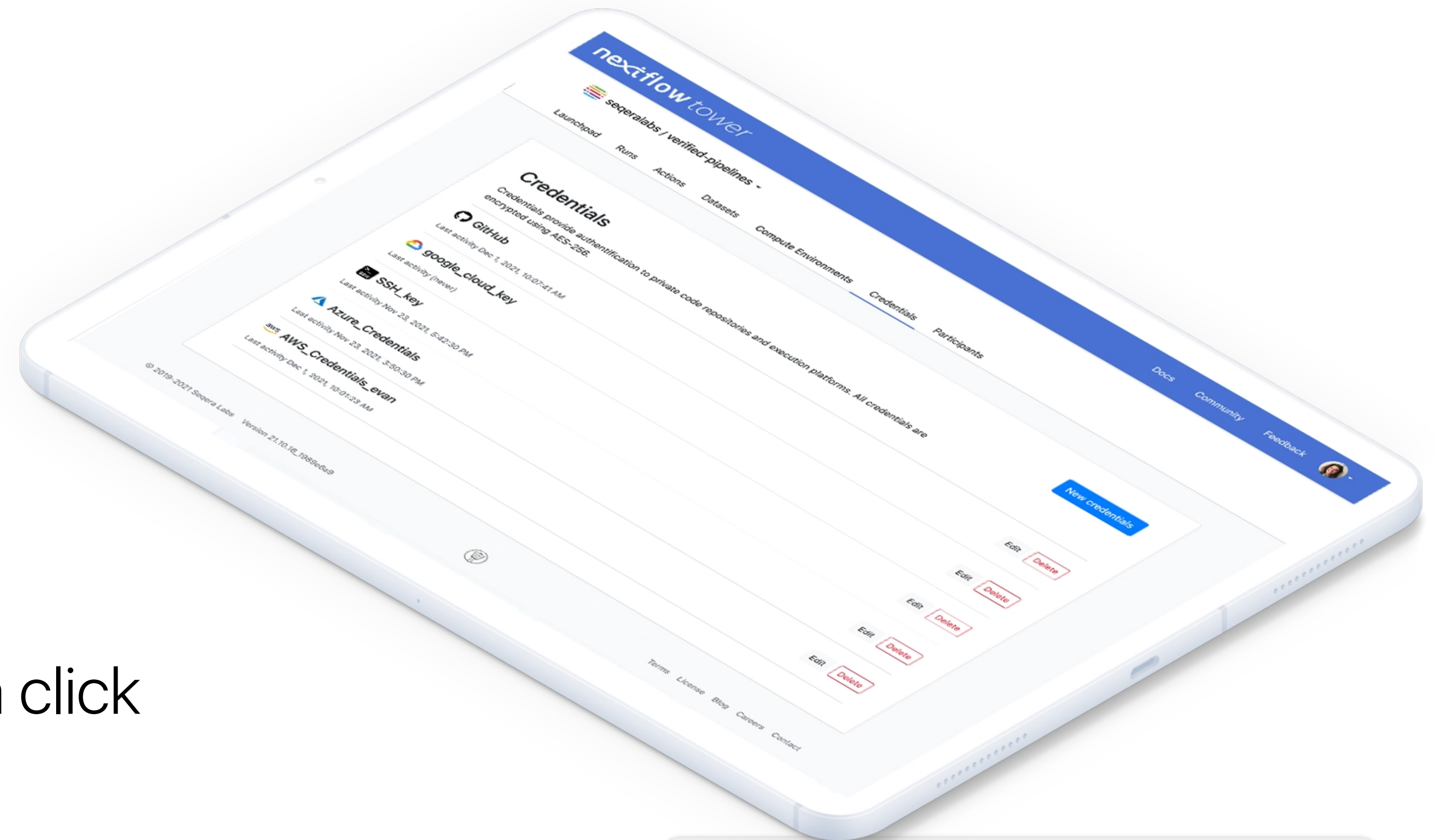


Intuitive launchpad interface

Launch, manage, and monitor

Share runs and work in teams

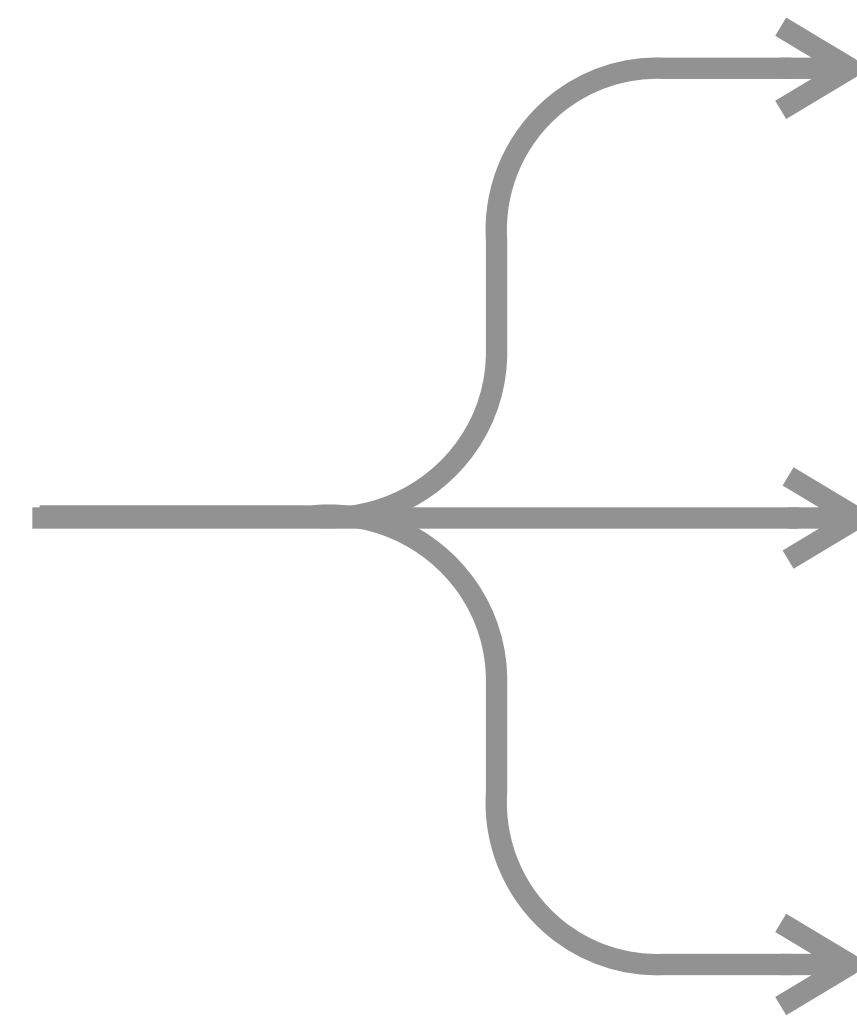
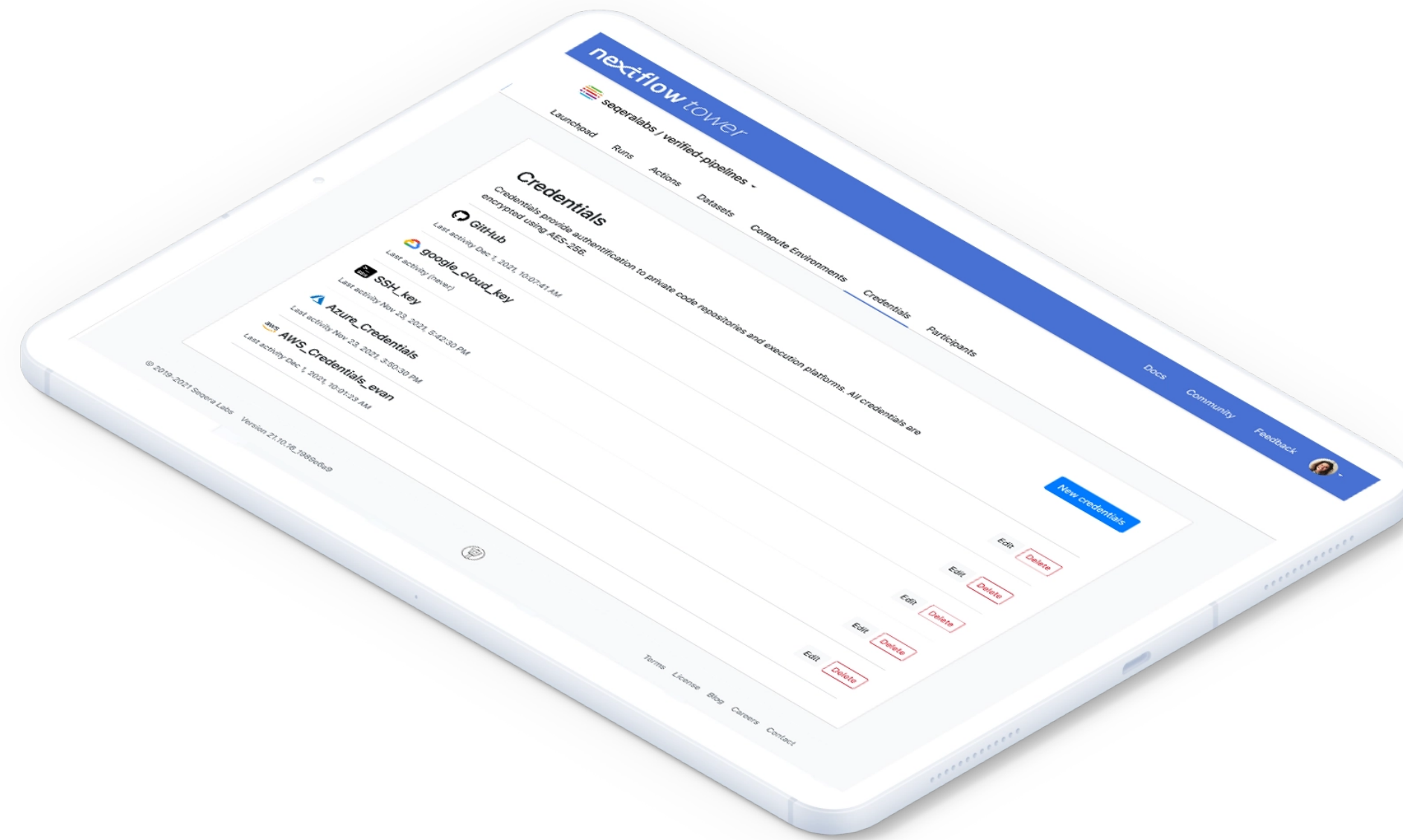
Create cloud infrastructure with a click



<https://tower.nf>



nextflow tower



Community: Open source

Cloud: Free & paid tiers

Enterprise: Commercial

<https://tower.nf>



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**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>