seqeralabs

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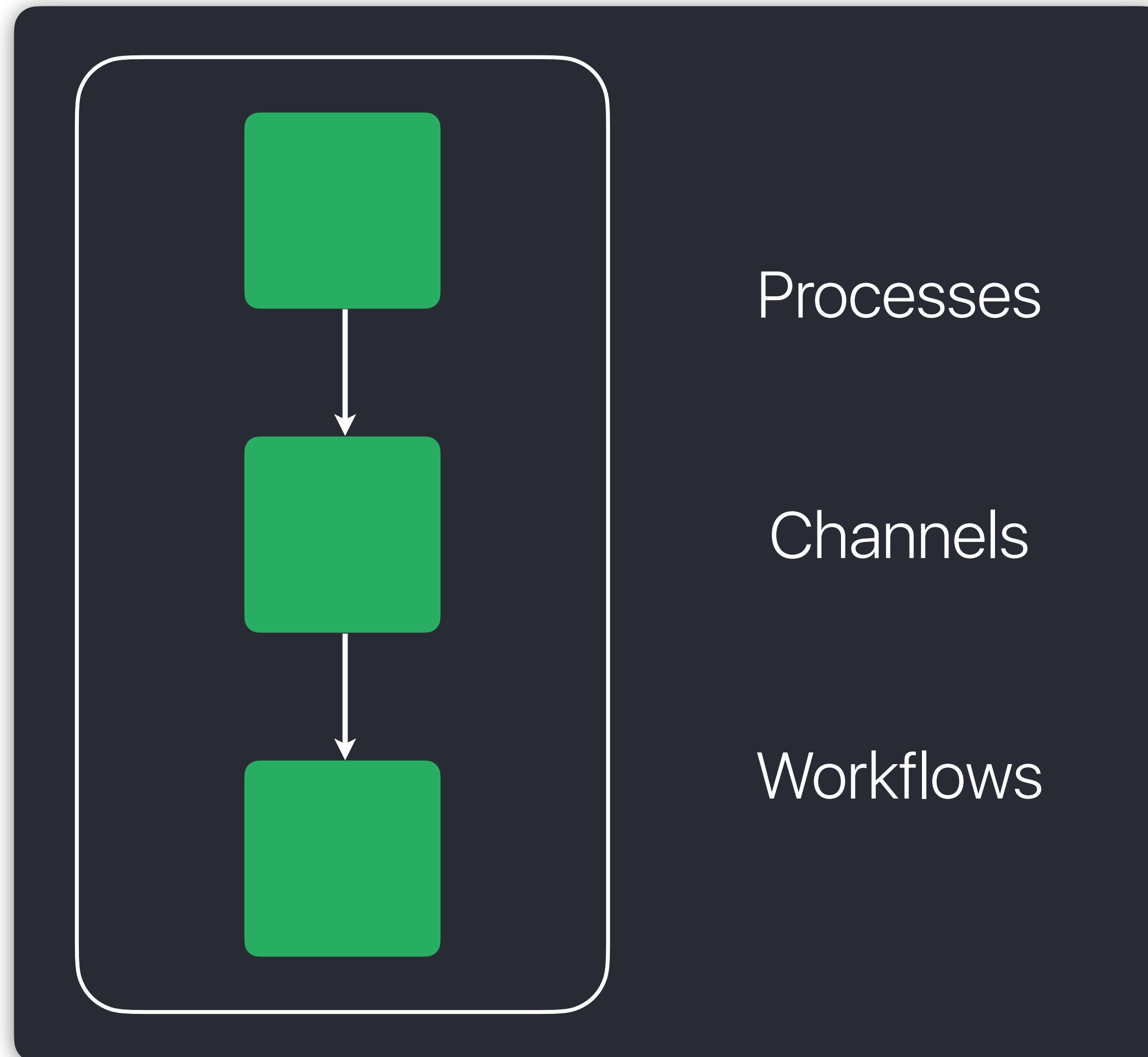Reproducible bioinformatics for everyone:

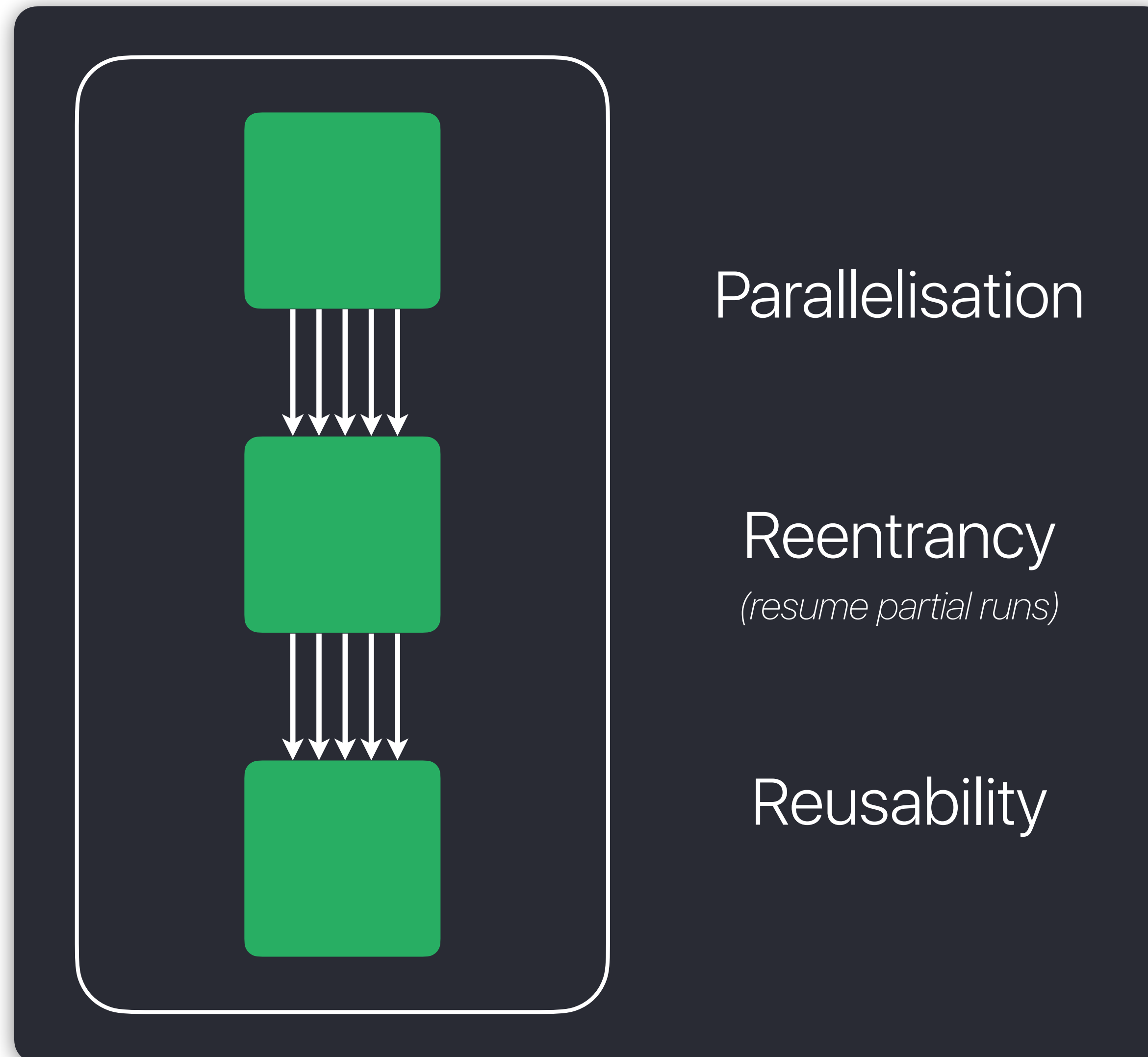# Nextflow & nf-core

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
}
```
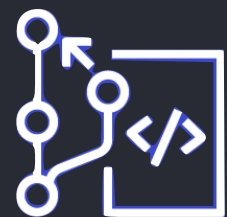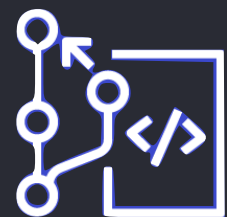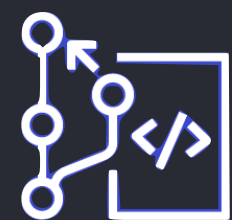
nextflow

Reproducible
Between runs

Portable
Between systems

nf-core 🍏

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

nf-core

TOOLS

Running pipelines

Writing pipelines

Testing / automation
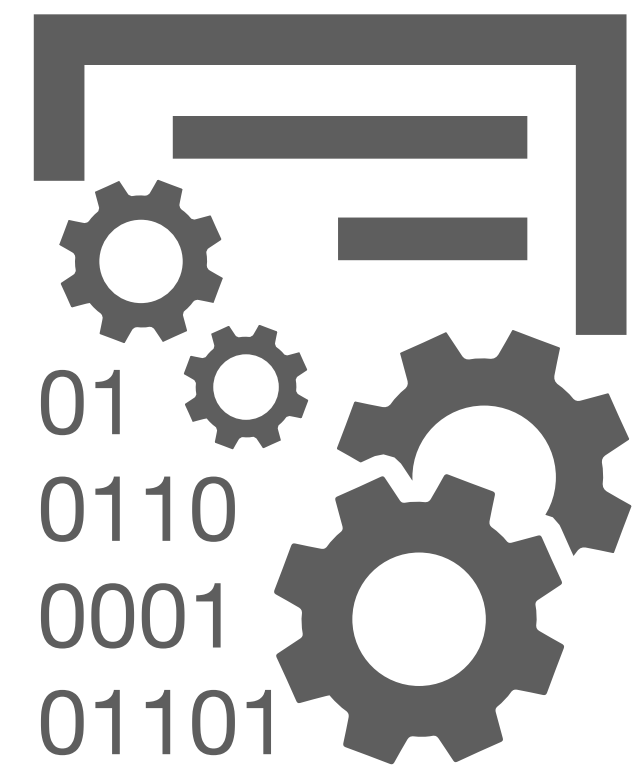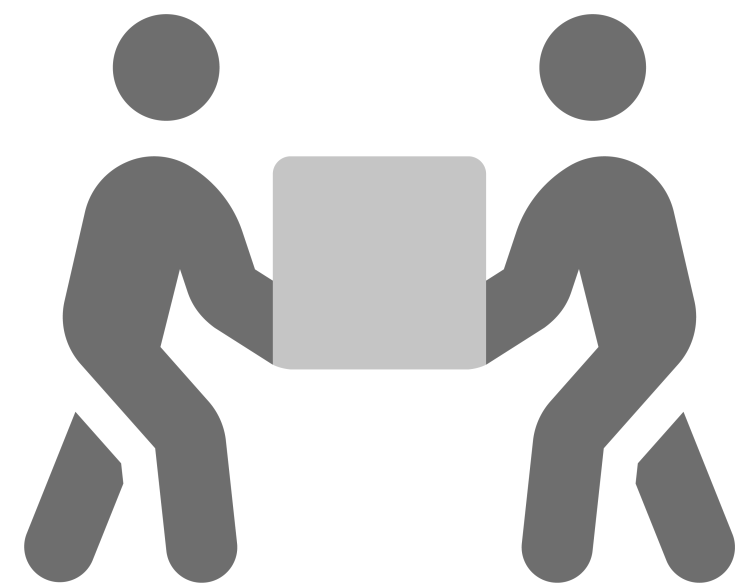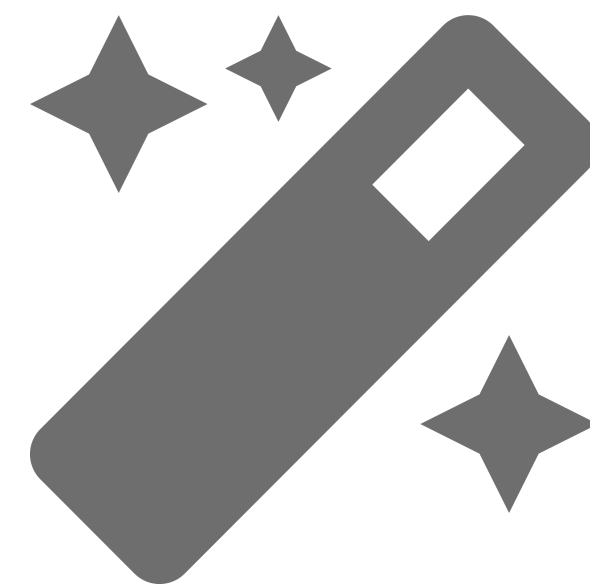
nf-core

Develop <u>with</u>
the community

Use a common
template
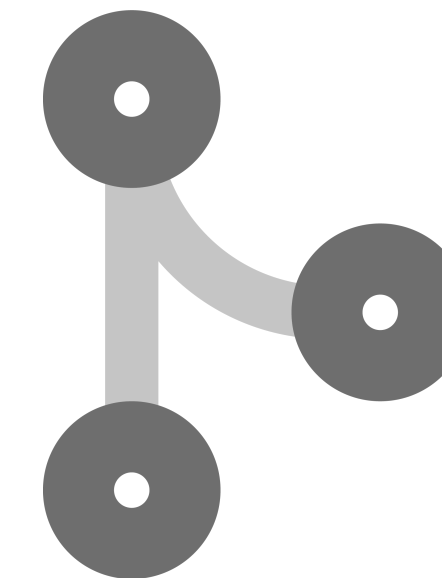
Collaborate,
don't duplicate

https://nf-co.re

nf-core

Tools are for everyone

https://nf-co.re
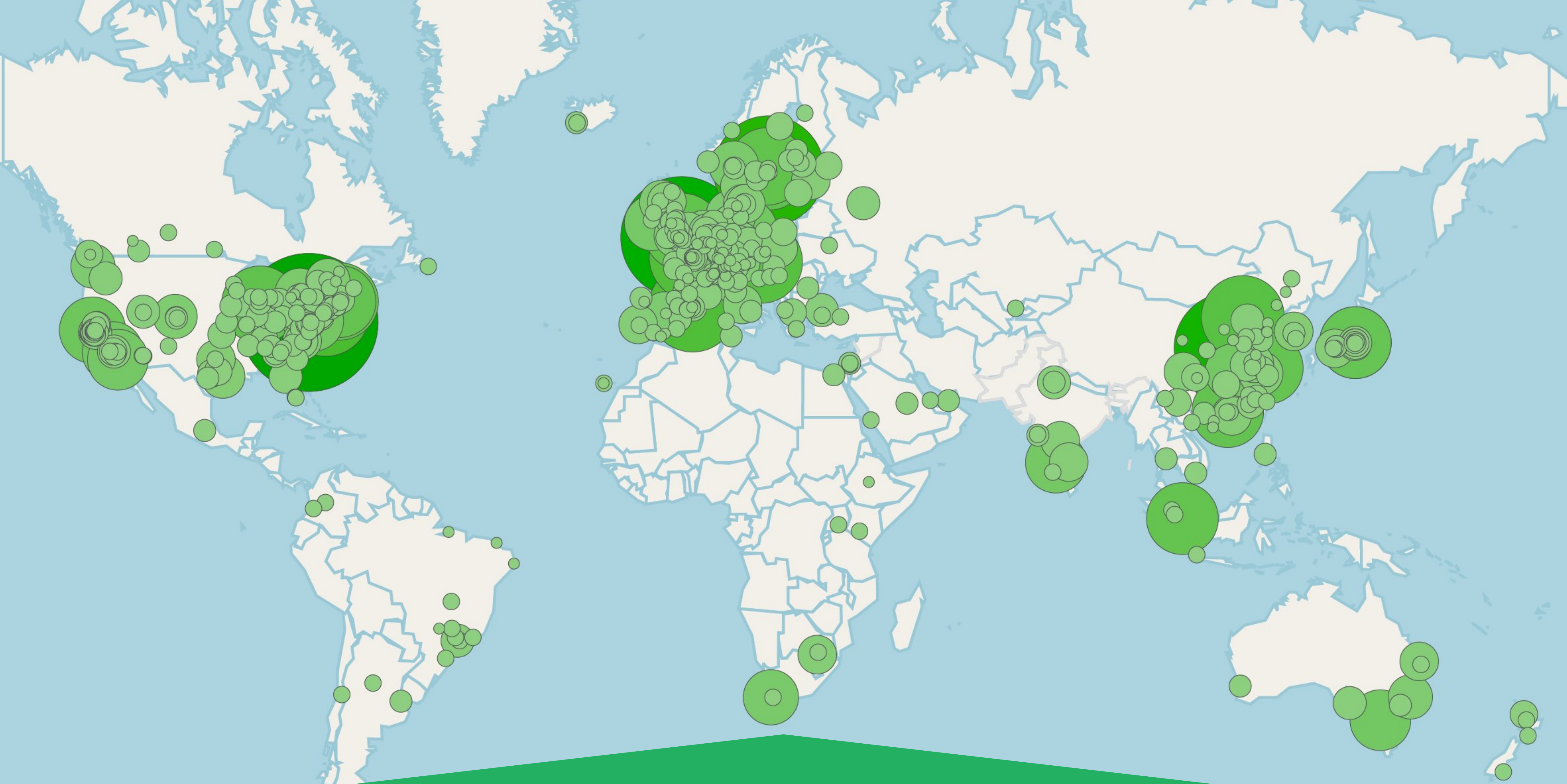
The nf-core framework for community-curated bioinformatics pipelines

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

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
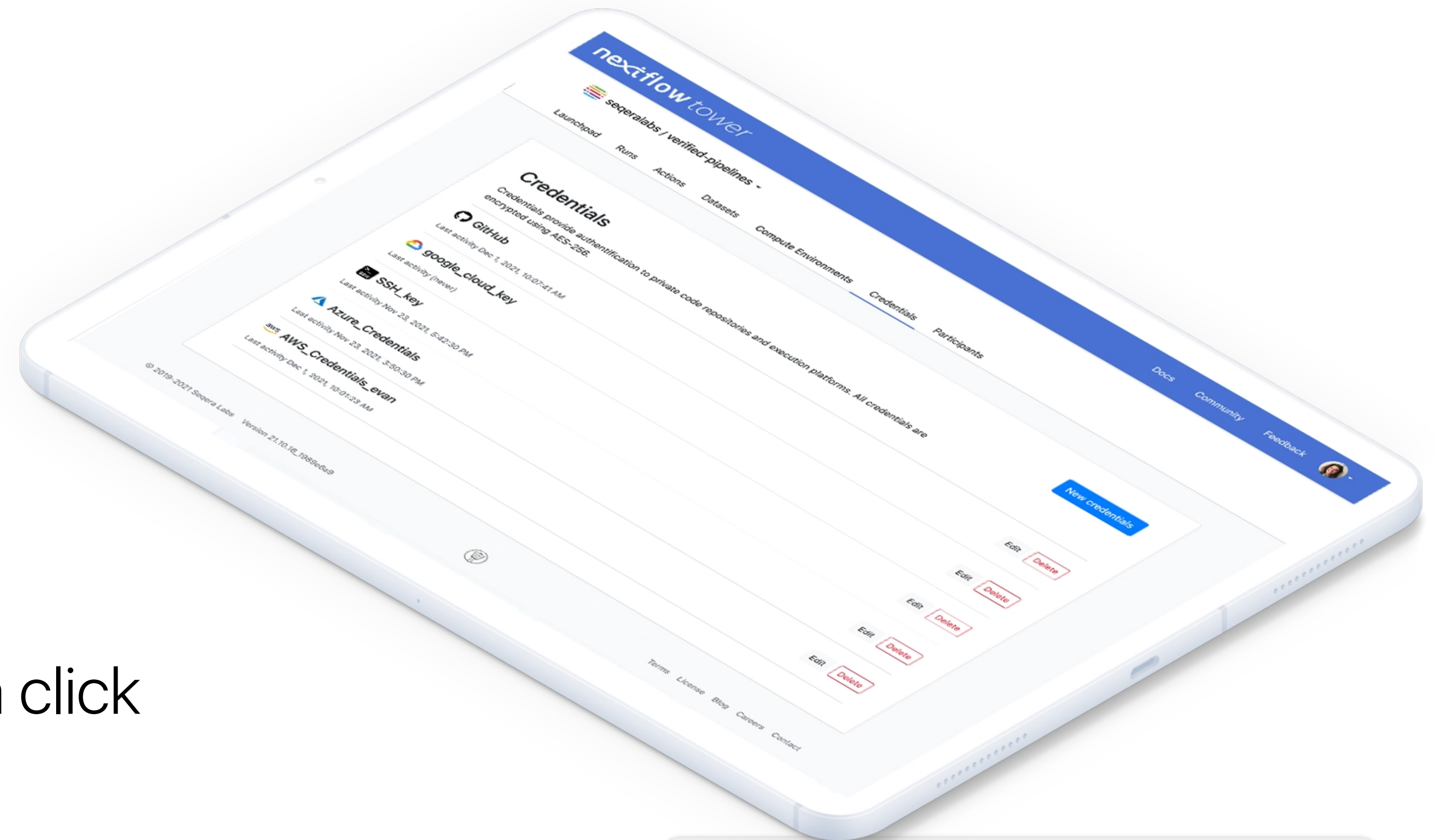
nextflow *tower*

seqeralabs
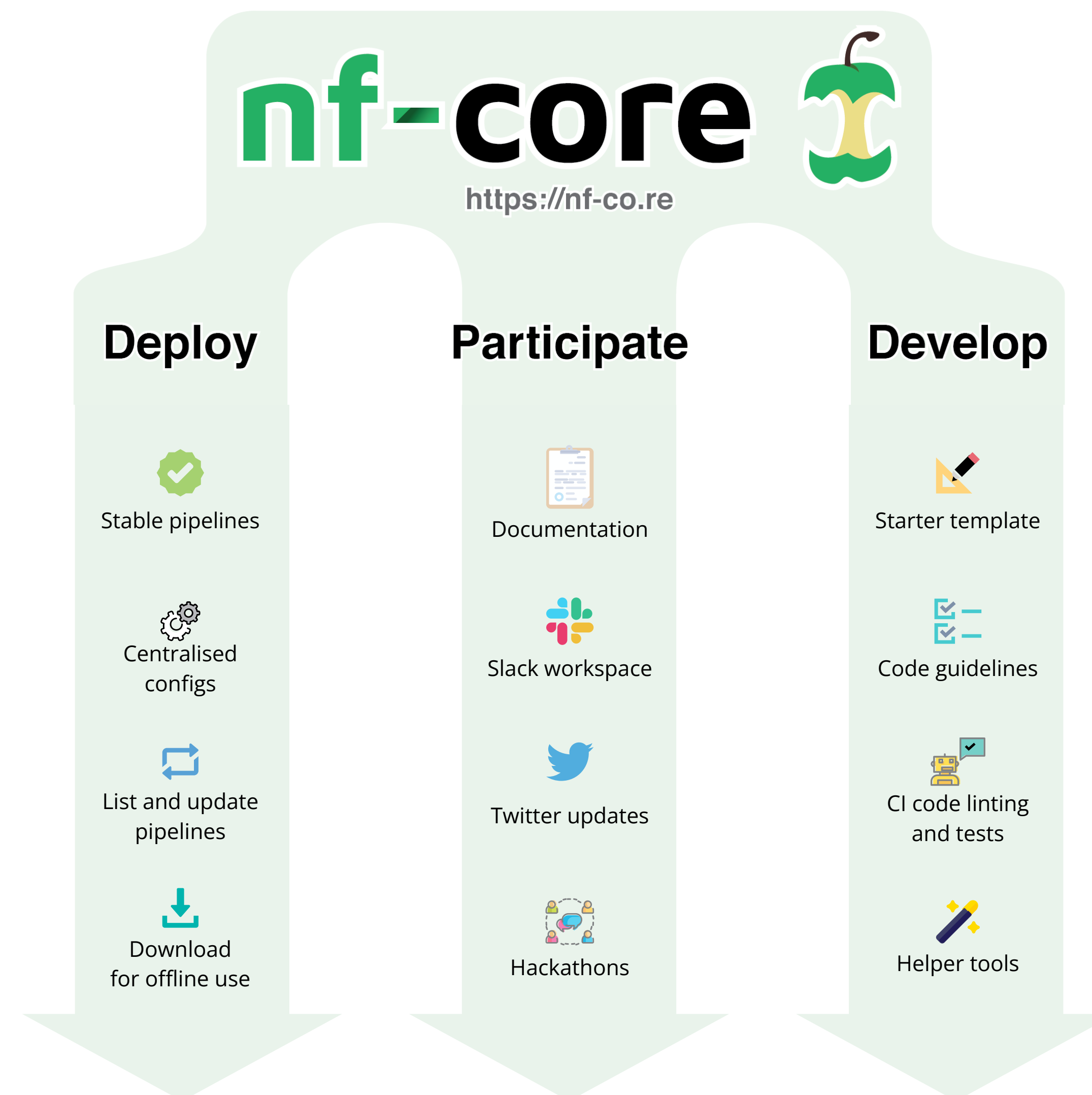
Intuitive launchpad interface

Launch, manage, and monitor

Share runs and work in teams

Create cloud infrastructure with a click

https://tower.nf

nextflow *tower*
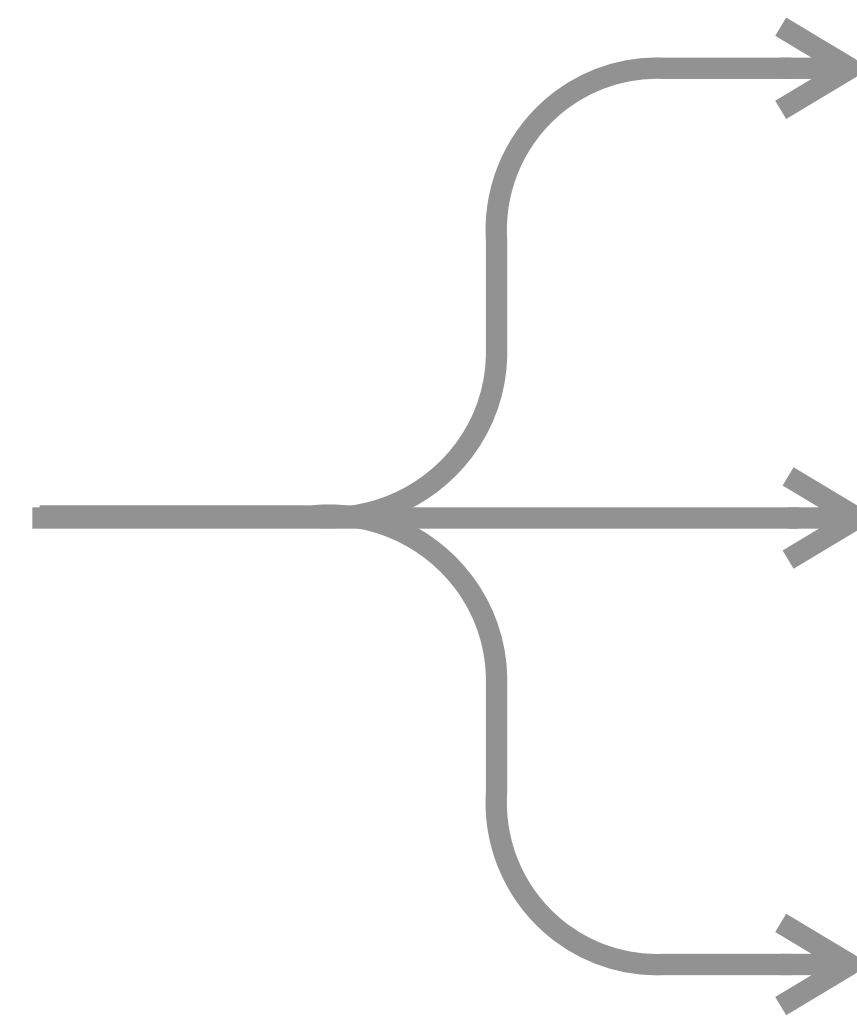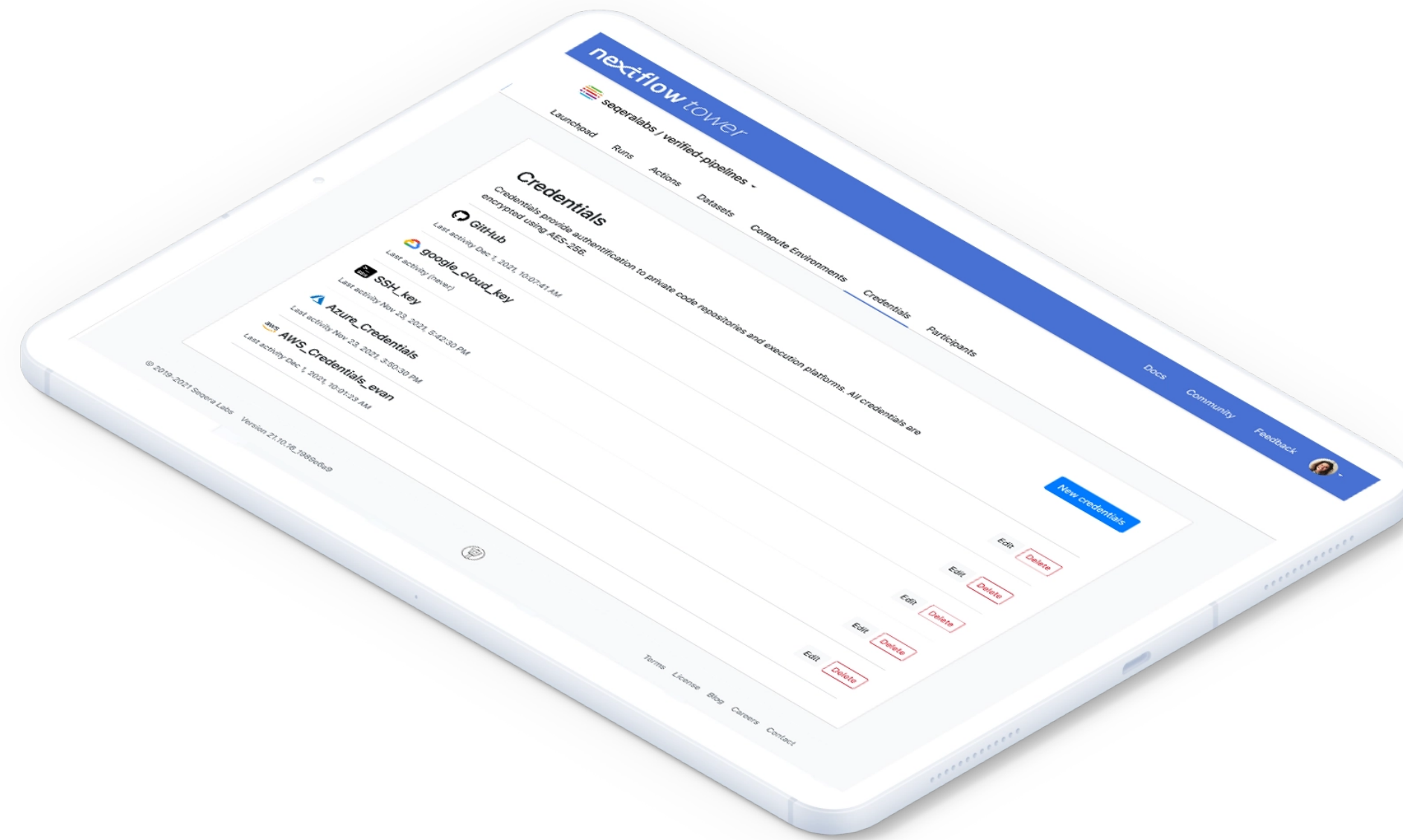
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Community: Open source

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`