



Community updates

Major projects and initiatives
from the past 12 months.

Modern software engineering - for science

Empowering
scientists with
modern software
engineering

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

Its fluent syntax simplifies the implementation and deployment of complex parallel and reactive workflows on any cloud or cluster.

 **nextflow**
workflow management

 **nextflow**

Modern software engineering - for science

A community
collaborating on
pipeline
development

Pipelines follow best-practices to ensure maximum portability and reproducibility. The large community makes the pipelines exceptionally well tested and easy to run.

Extensive documentation covering installation, usage and description of output files ensures that you won't be left in the dark.

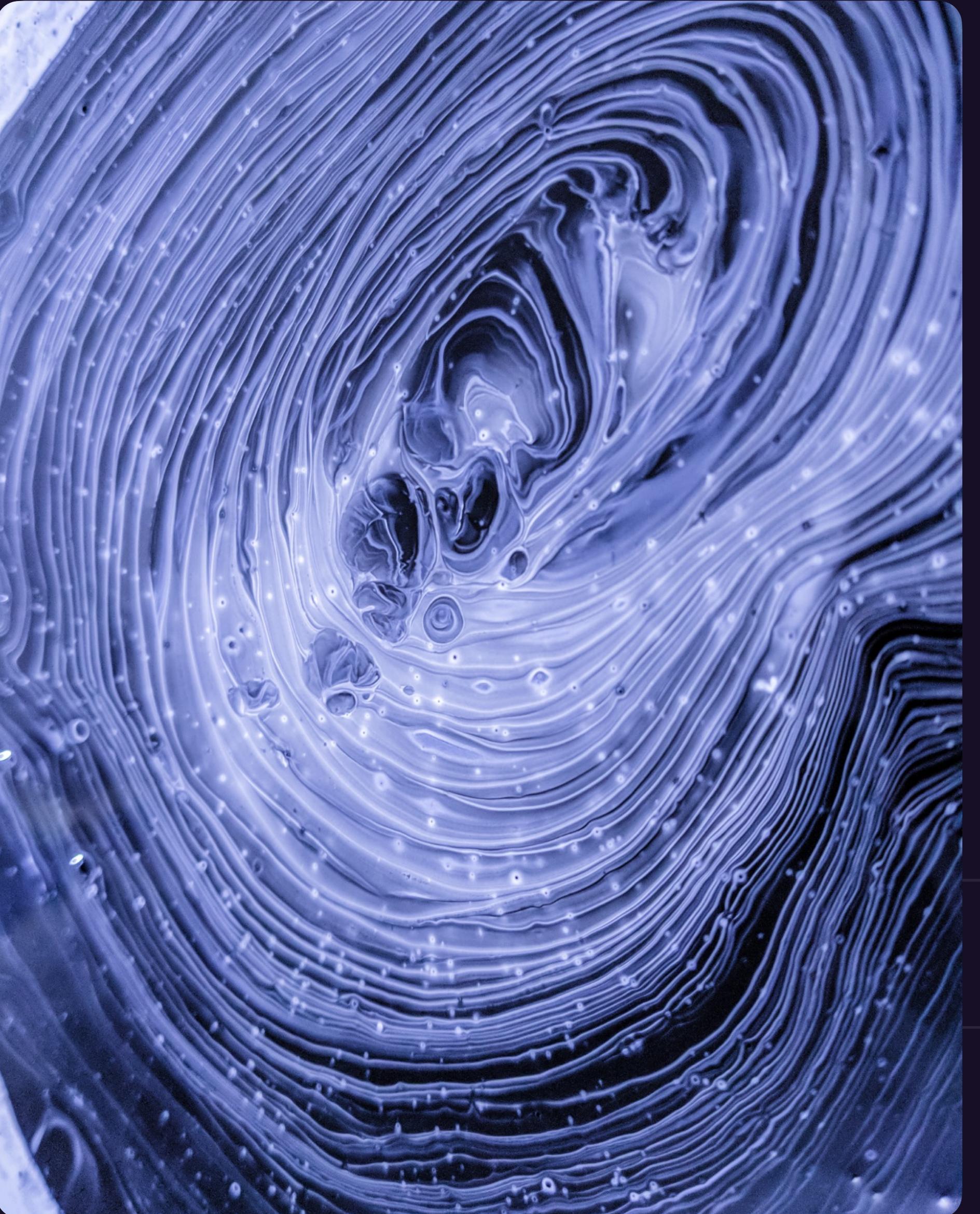
 **nextflow**
workflow management

nf-core 



Community growth

Where we are in numbers





708

Developers committing to nf-core GitHub repositories



708

X 8,848

People following for Nextflow + nf-core X (twitter) accounts



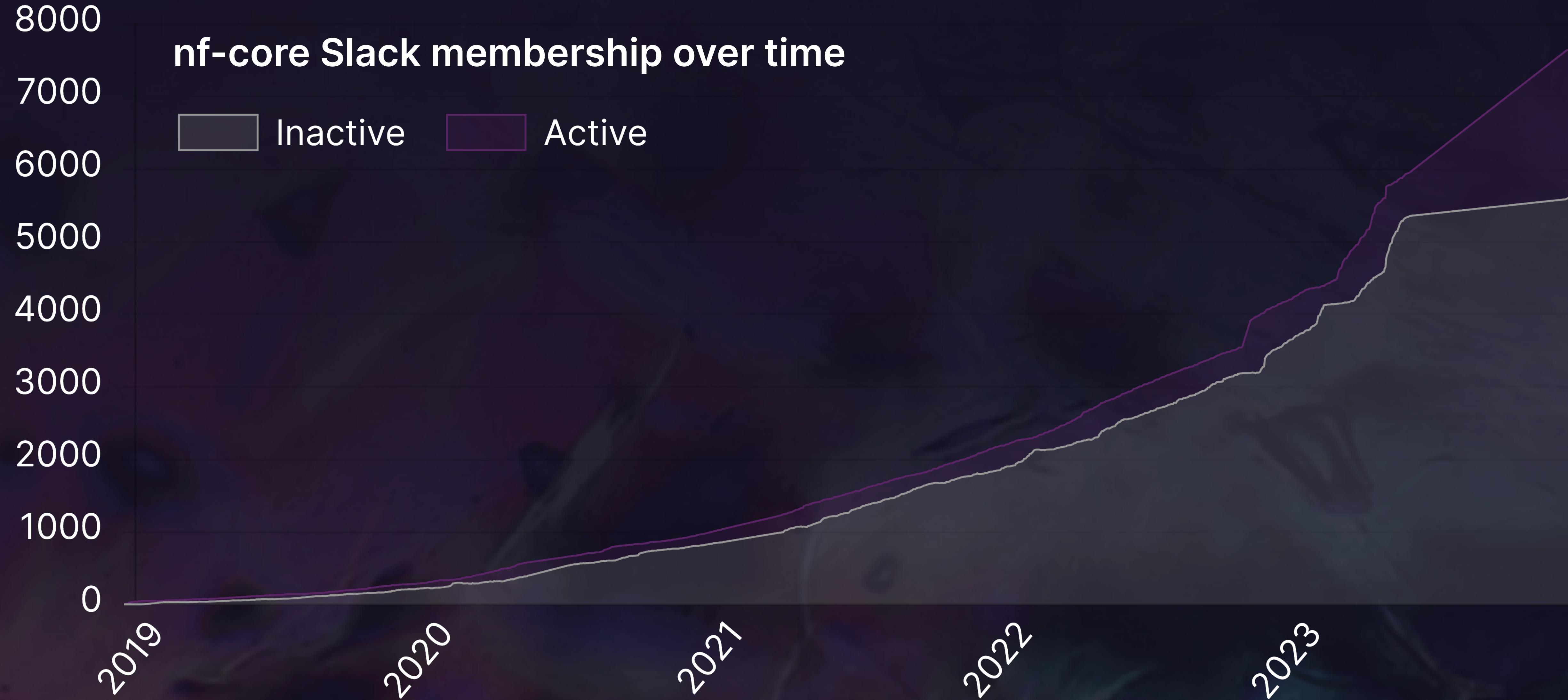
708

X 8,848

10,790

Users on Nextflow + nf-core Slack Organisations

Slack members



Active Slack members



Nov
2018

Jun
2019

Feb
2020

Sep
2020

May
2021

Dec
2021

Jul
2022

Mar
2023



Nov
2018

Jun
2019

Feb
2020

Sep
2020

May
2021

Dec
2021

Jul
2022

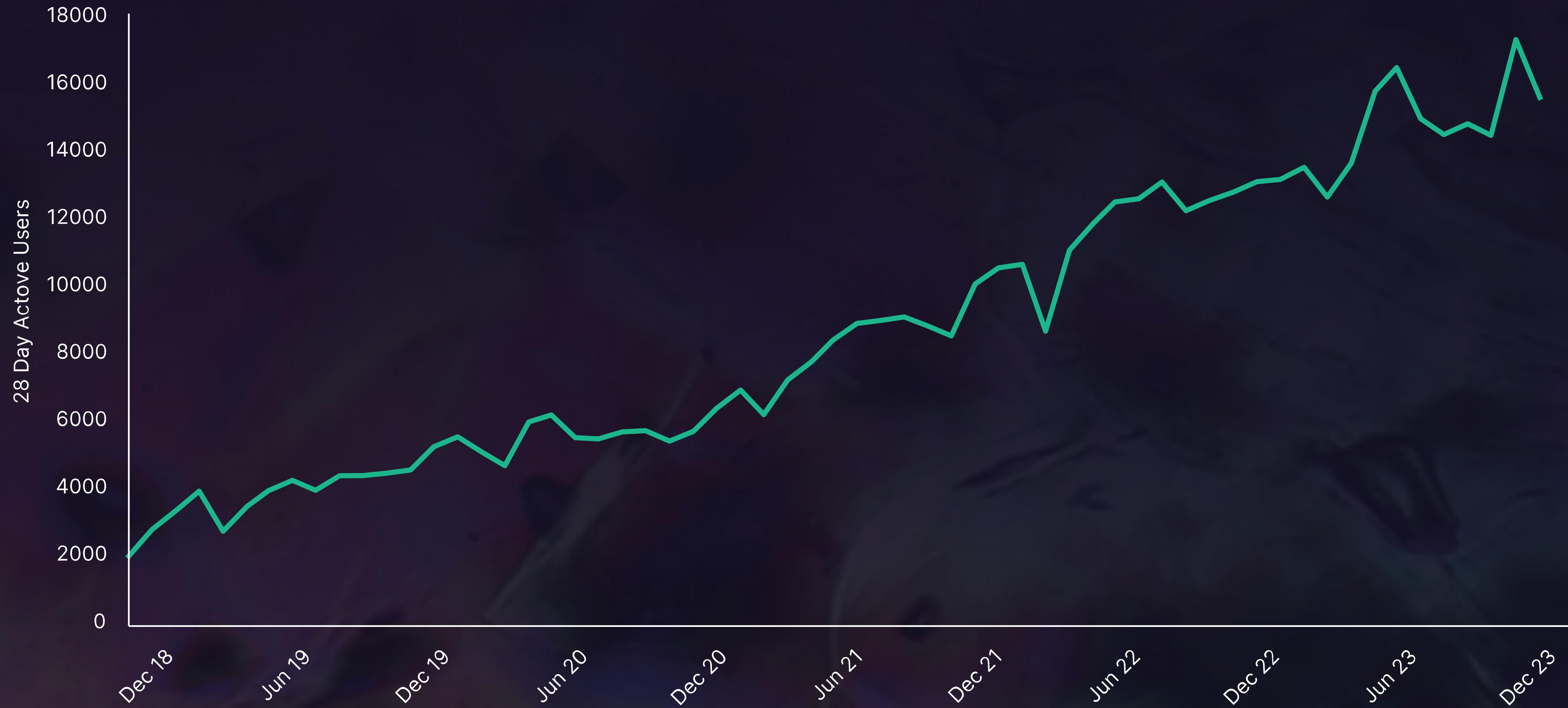
Mar
2023

15 March 2023 - 1.5k active users —
Community training

Weekly active members

Members who posted

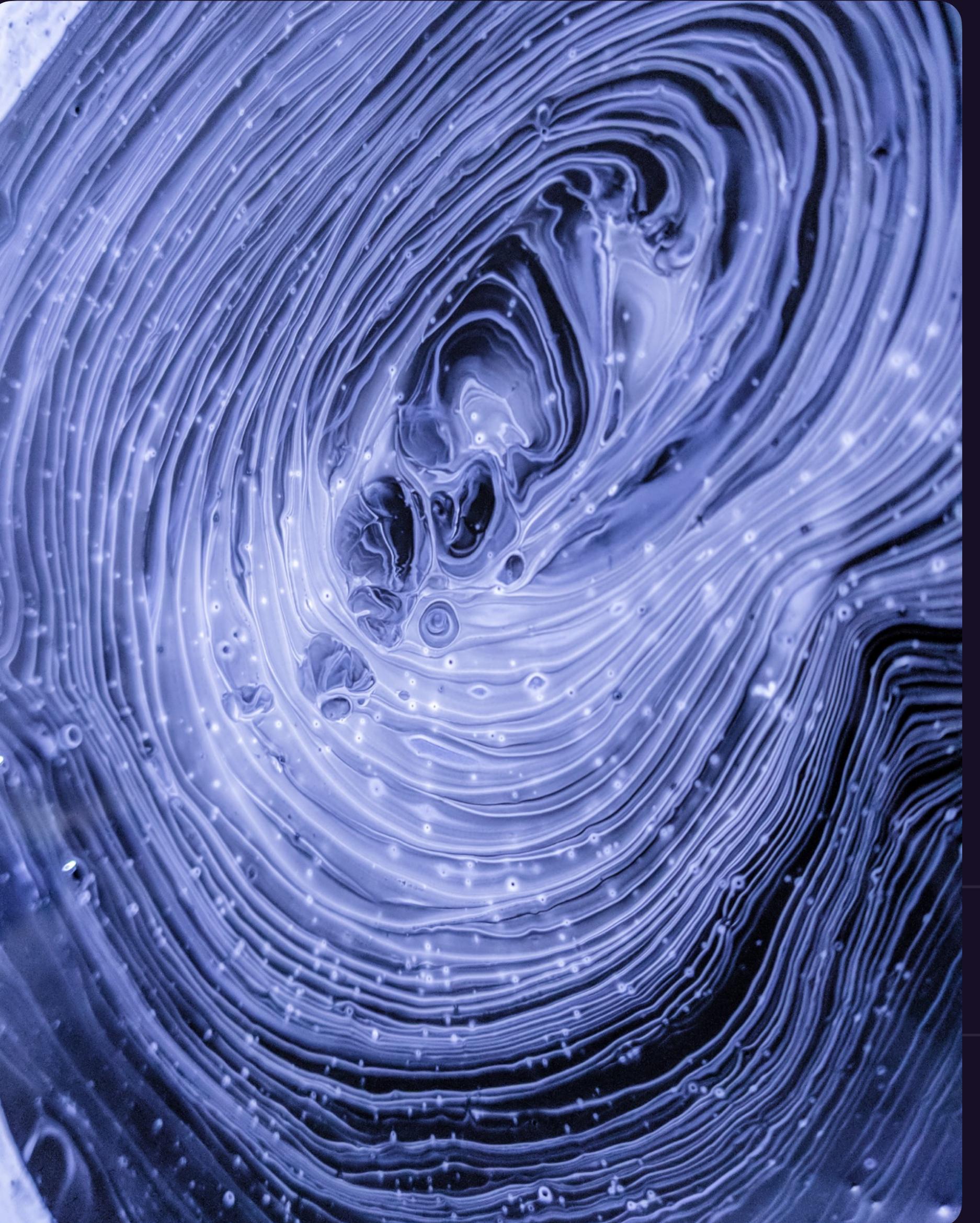
Nextflow Docs - Unique IPs





Building with nf-core

Using nf-core tooling and
resources



nf-core modules + subworkflows

Pipeline

Pipeline parameters
Resource requests
Tool arguments
Input channels

Subworkflow

Channels
Pipeline logic

Module

Module

Module

nf-core resources

93

Pipelines

nf-core 

Ready-to-use pipelines, covering most techniques in genomics.

Increasingly: proteomics, imaging and more.

nf-core resources

54

Subworkflows

nf-core 

Shared subworkflows for common analysis pathways

nf-core resources

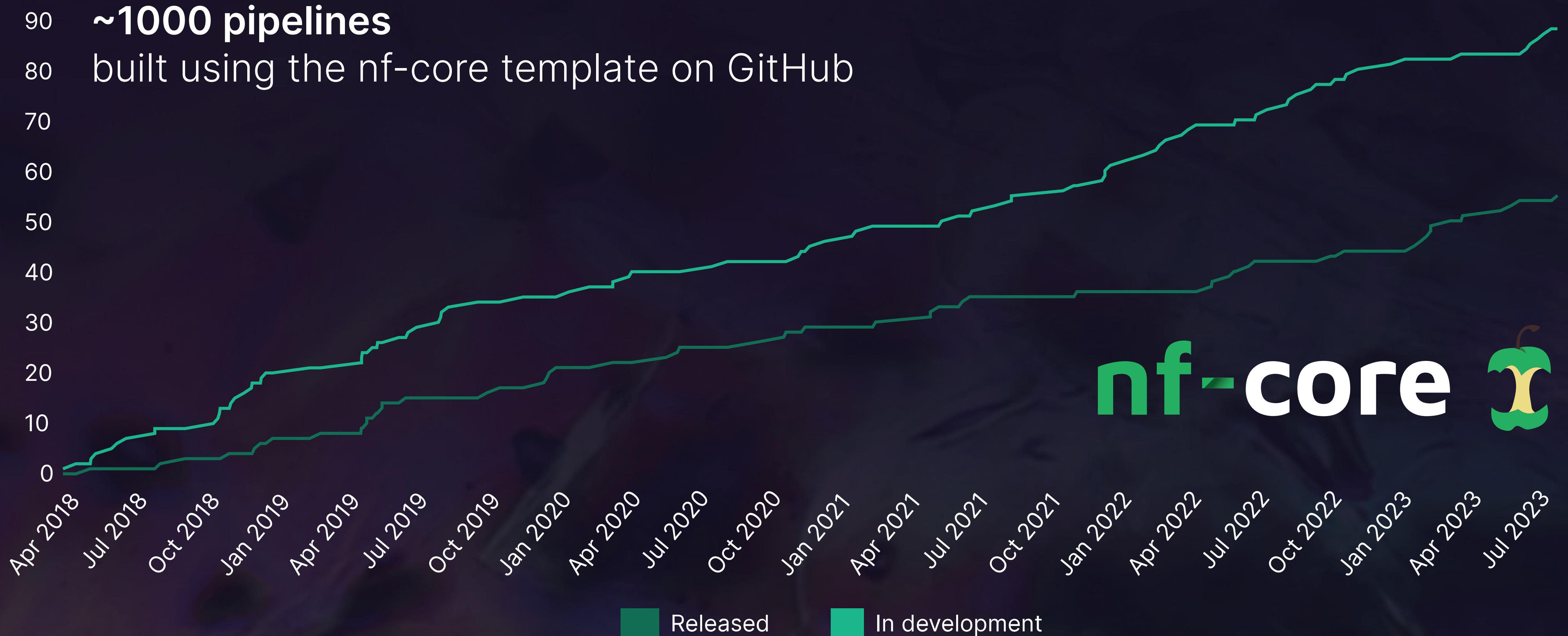
1,078

Modules

nf-core 

Tool process wrappers, with bundled software
and continuous-integration testing

nf-core pipelines



nf-core/tools

nf-core --help

nf-core/tools

For users

- List
- Launch
- Download
- Params

For developers

- Create
- Lint
- Modules
- Subworkflows
- Schema

nf-core/tools

For users

For developers

For everyone

nf-core modules + subworkflows

Custom



Pipeline

Pipeline parameters

Resource requests

Tool arguments

Input channels

Subworkflow

Channels

Pipeline logic

Module

Module

Module

nf-core modules + subworkflows

Custom



Pipeline

Pipeline parameters

Resource requests

Tool arguments

Input channels

Subworkflow

Channels

Pipeline logic

Module

Module

Module

nf-core modules + subworkflows

Custom

nf-core 

Pipeline

Pipeline parameters

Resource requests

Tool arguments

Input channels

Subworkflow

Channels

Pipeline logic

Module

Module

Module

nf-core modules + subworkflows

Custom



Pipeline

Pipeline parameters

Resource requests

Tool arguments

Input channels

Subworkflow

Channels

Pipeline logic

Module

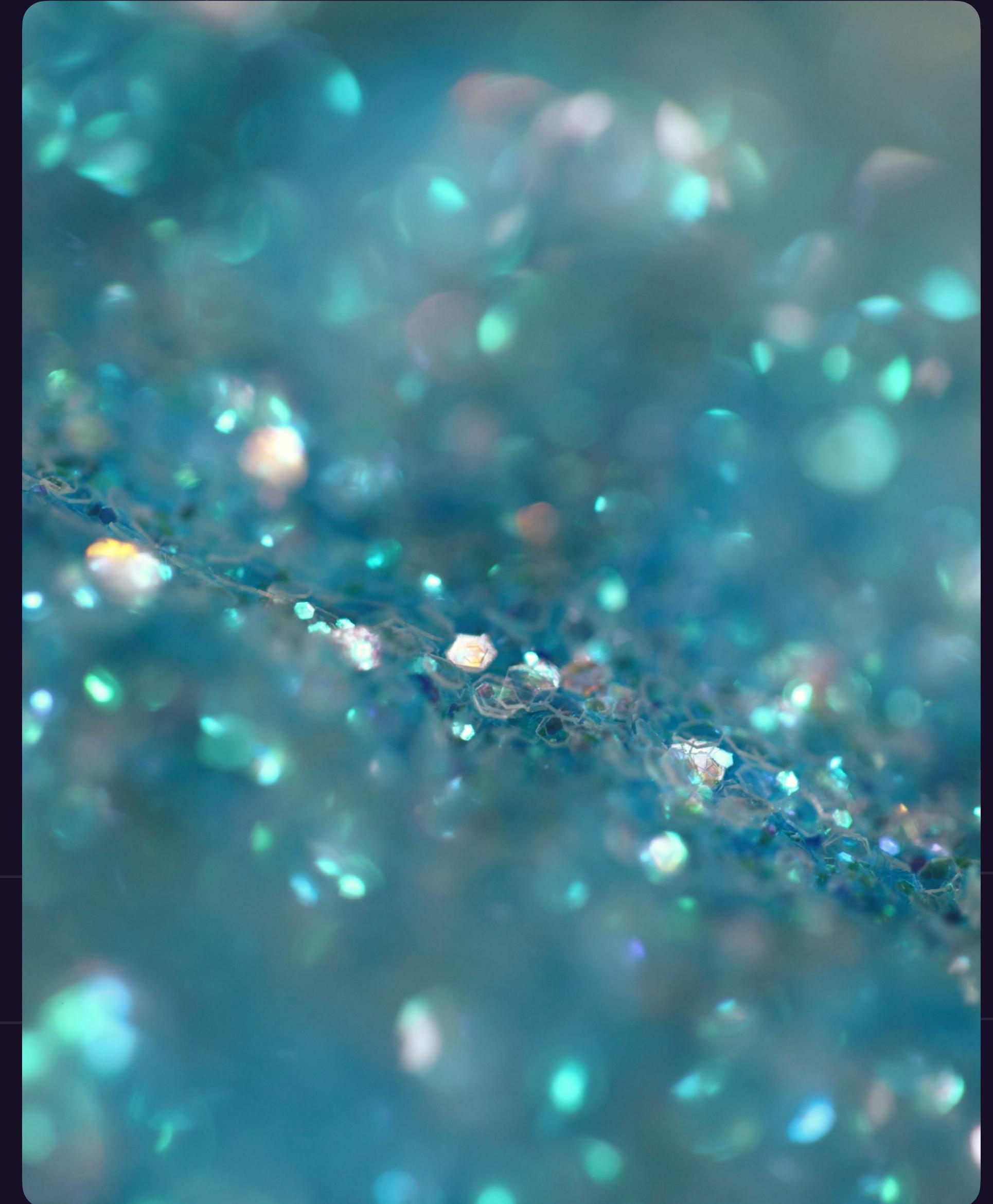
Module

Module



Community projects

New infrastructure to support
users and developers



A testing framework for Nextflow pipelines



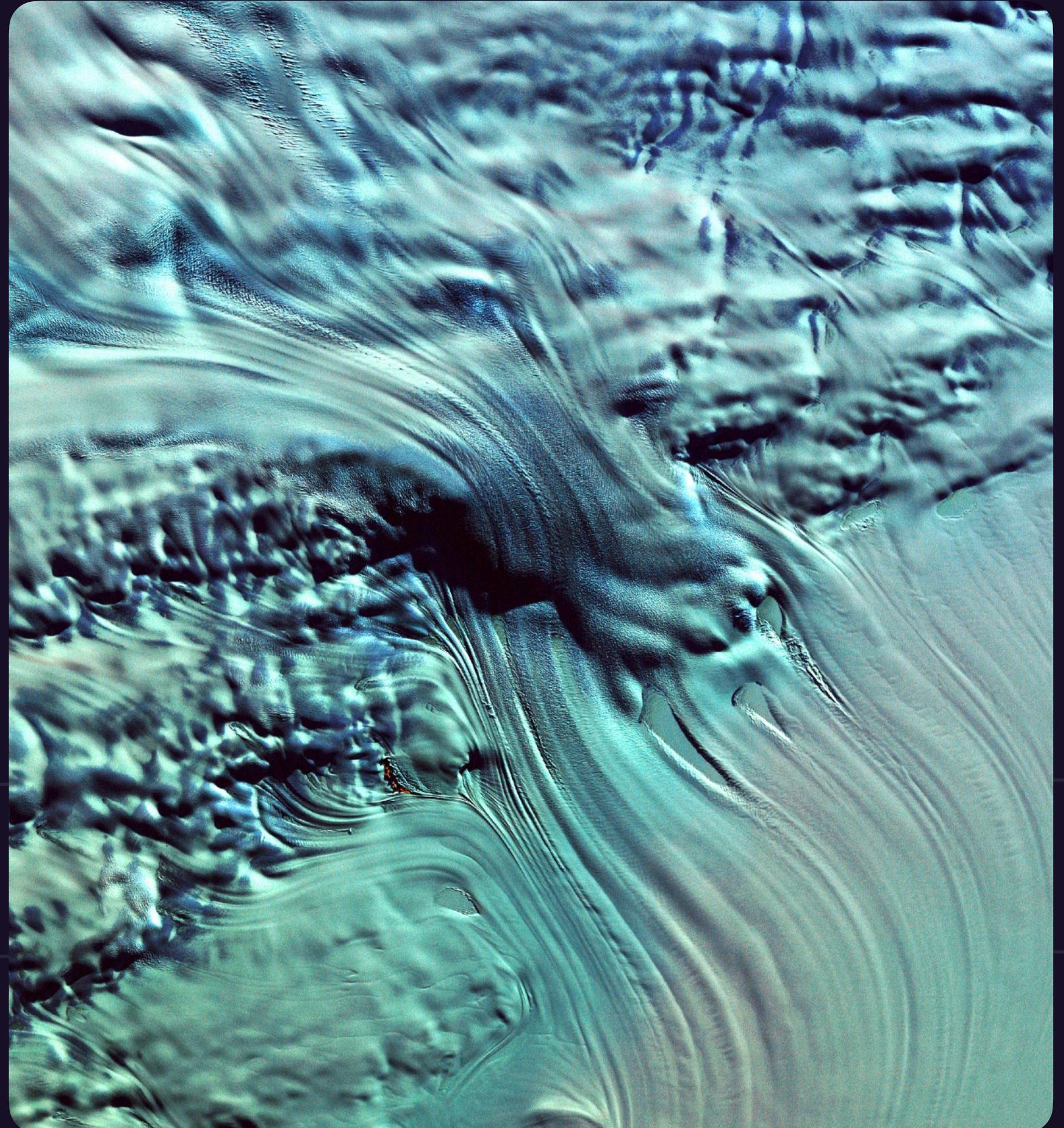
nf-test

Lukas Forer
Sebastian Schönherr



Ensuring code quality through CI

- A testing DSL, similar to Nextflow itself
- Uses snapshots to capture expected states
- Built in assertion types and functionality, suited to Nextflow use-cases



A testing framework for Nextflow pipelines



nf-test

Lukas Forer
Sebastian Schönherr



Ensuring code quality through CI

- A testing DSL, similar to Nextflow itself
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```
nextflow_pipeline {  
  
    name "Test Hello World"  
    script "nextflow-io/hello"  
  
    test("hello world example should start 4 processes") {  
        expect {  
            with(workflow) {  
                assert success  
                assert trace.tasks().size() == 4  
                assert "Ciao world!" in stdout  
                assert "Bonjour world!" in stdout  
                assert "Hello world!" in stdout  
                assert "Hola world!" in stdout  
            }  
        }  
    }  
}
```

code.askimed.com/nf-test/ >

nextflow

Nextflow plugins ecosystem

nf-validation

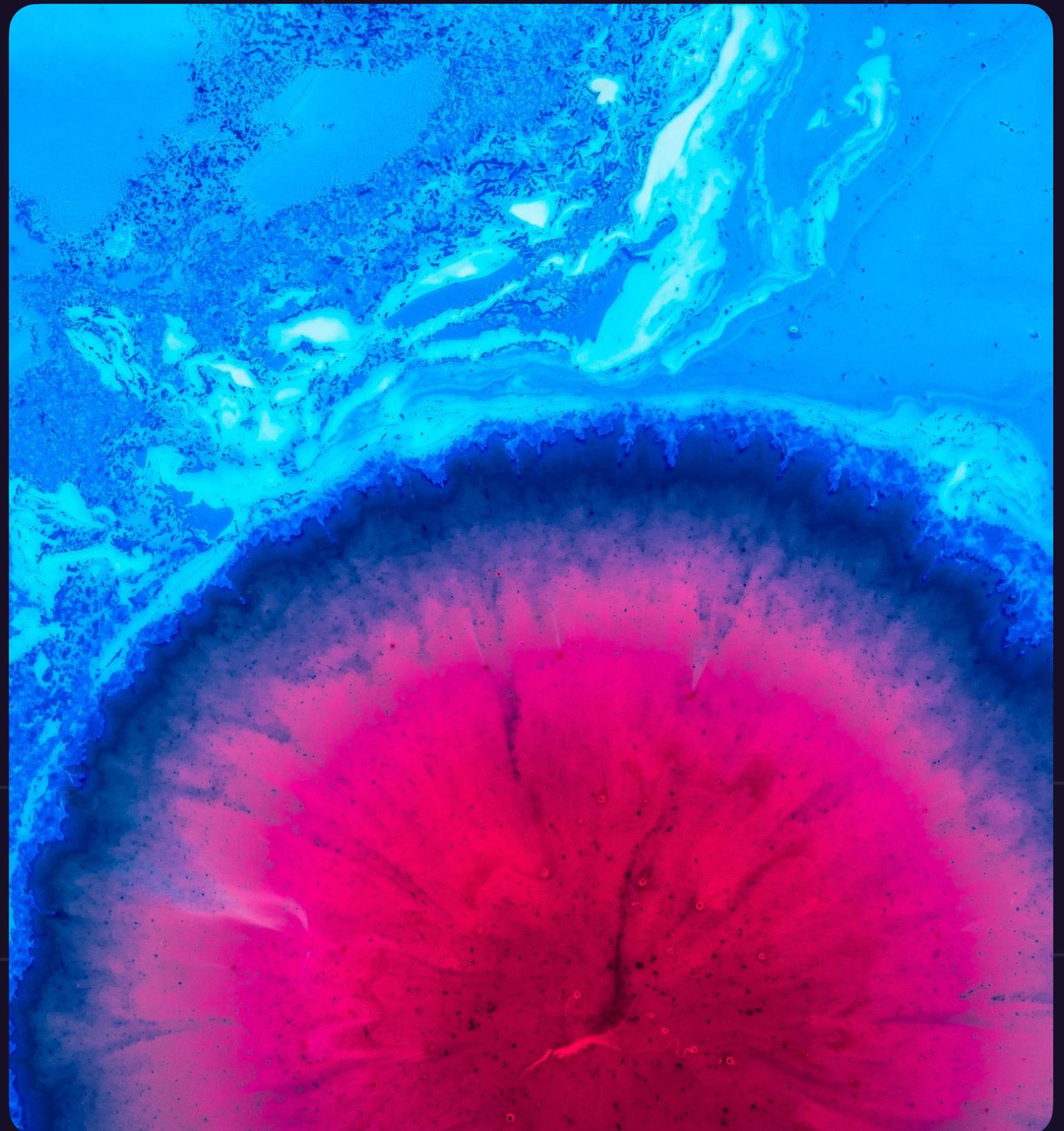
Validate parameters
Create channels from sample sheets

nf-prov

Provenance reporting
BioCompute Objects / RO-Crates

nf-co2footprint

Report on energy consumption and
CO₂ emissions, suggest improvements.



Nextflow plugins ecosystem

nf-float

Adds a new Nextflow executor
for working with MemVerge



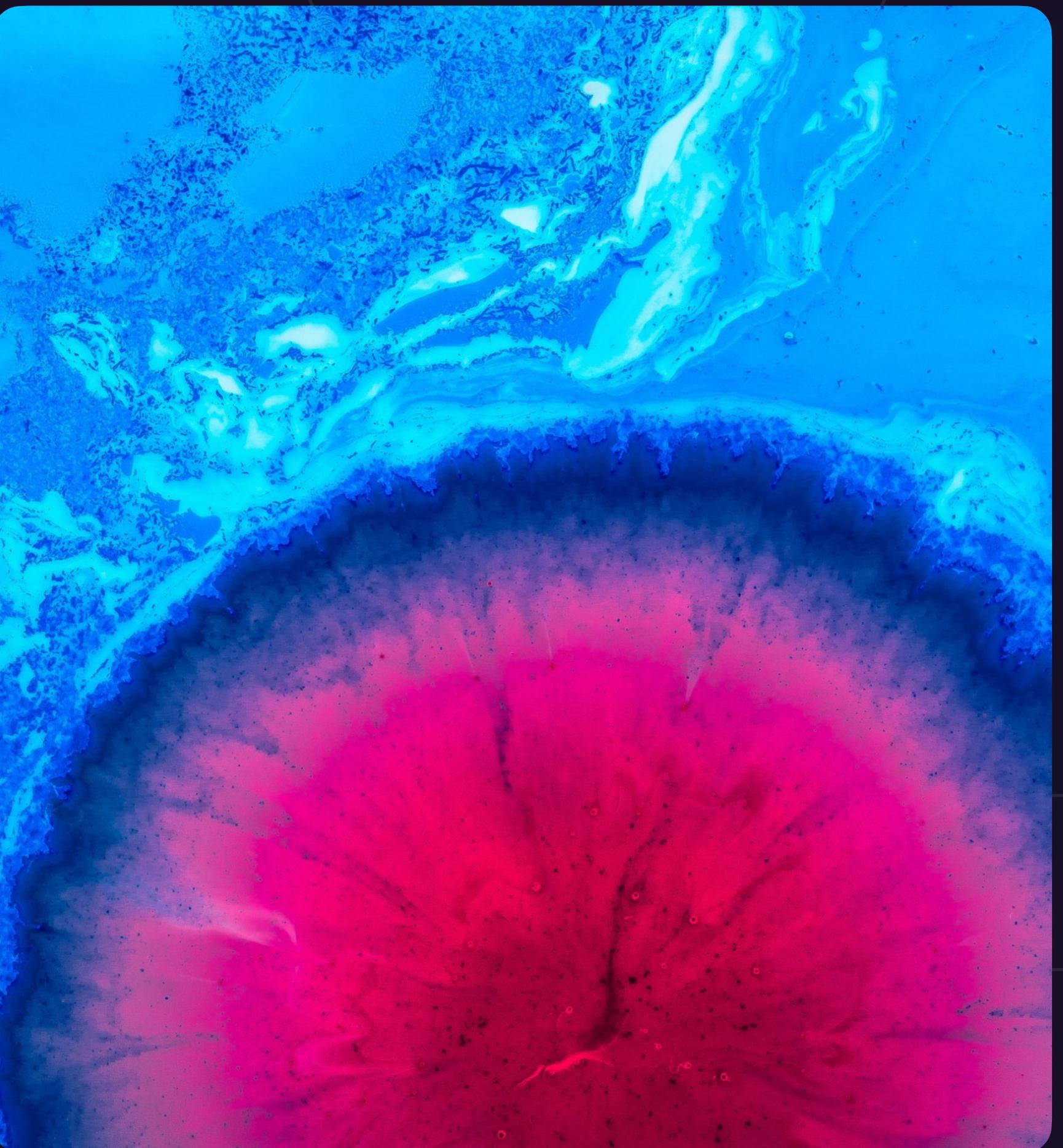
nf-quilt

Automatically publish pipeline
results to Quilt packages



Announcing Java-Native nf-quilt: versioned and
verified data inputs and outputs for Nextflow

Ernie Prabhakar
Thurs Nov 30, 4:45 PM



Collaboration on accreditation (FDA / IVDR / ISO)

#regulatory and #benchmarking

- Many nf-core pipelines being used in healthcare / accredited settings.
- Nextflow helps with provenance reporting
- MultiQC logs software versions and QC outputs
- New page listing known public documentation

Please let us know if you've done any related work with an nf-core pipeline!



New nf-core website

Rebuilt from the ground up

- Site-wide search!
- Deployment previews
- Support for MDX, markdown extensions
- Markdown front-matter schema
- New hosting

 astro



 nextflow

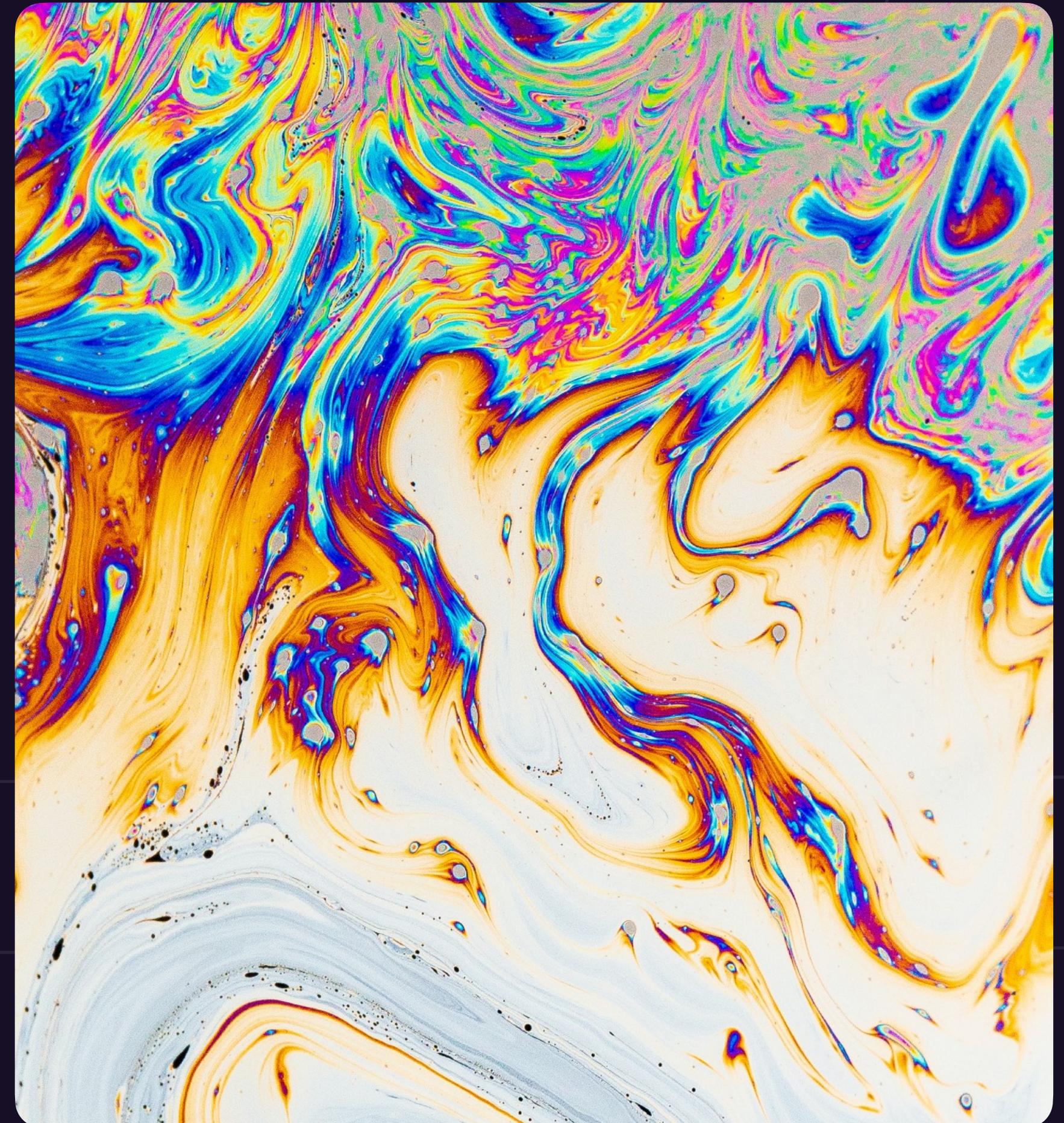
nf-core tools

Helper tools for users & developers

- Improved download capability
- More fine-grained control of pipeline creation from the nf-core template
- Helper tools for subworkflows & nf-test support

Coming soon..

- Rewritten launch and schema tooling
- User friendly terminal app, using Textual





```
nf-core pipelines create
```

```
> nf-core pipelines create
```

```
py3.10  ~/GitHub/nf-core/tools/demo  textual-create •  python3.10 -zsh
```

Channels: The Nextflow Podcast



New podcast for developers!

- New episodes every second Monday
- Technical deep dives with Nextflow developers
- Interviews with leaders in the field
- 24 episodes so far, each 30 mins - 1 hour
- Join us on Spotify, Apple Music, YouTube, Twitter (X)



CHANNELS
the **nextflow** podcast

Channels: The Nextflow Podcast



New podcast for developers!

- Ep20: Tower CLI, infrastructure as code and some Seqera road map previews
- Ep21: Live debugging Nextflow / Ambassadors
- Ep22: Better error messages
- Ep23: Clever containers: Wave & Wavelit
- Ep24: Requesting resources
- Ep25: Interview: Geraldine Van der Auwera
- Ep26: Community interviews



Ep. 25 November 6, 2023

Interview | Geraldine Van der Auwera

Developer Advocate @ Seqera



Ep. 26 November 21, 2023

Interviews

Code & community at the 2023 nf-core hackathon

Raquel Manzano | Edmund Miller

Rieke Hanssen | Francesco Lescai



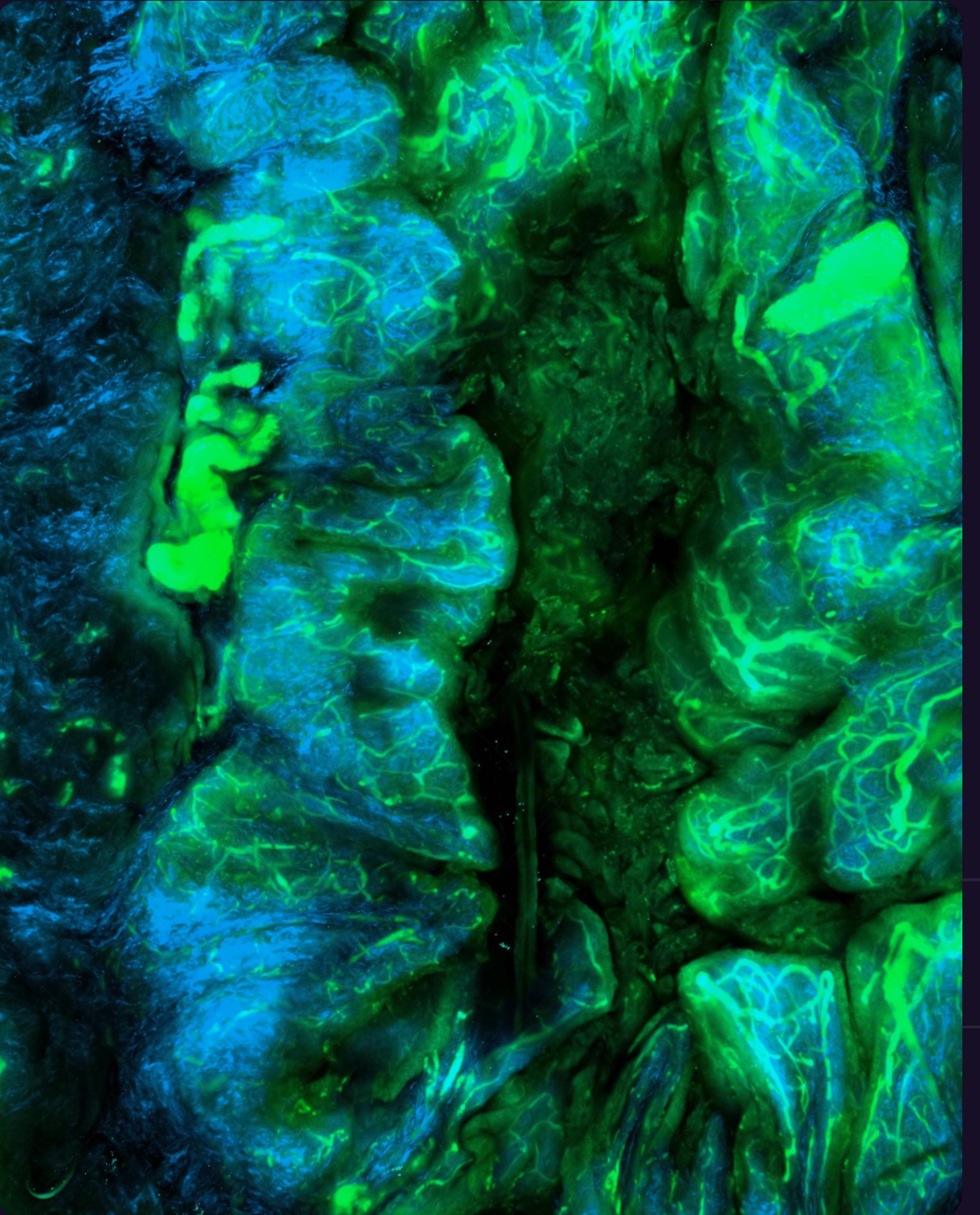
supported by seqera

Geraldine
VdA



Community initiatives

New projects for the community



Nextflow Ambassadors

Introducing the Nextflow Ambassador Program – an initiative designed to foster **collaboration, knowledge sharing, and community growth**

Nextflow Ambassadors

What you get

Help to shape and grow the Nextflow and nf-core communities



What you do

Receive training and get access to our content library



Access a travel fund for conferences; get support for local events



Get recognition for your work, as well as exclusive swag!



How to apply



Nextflow Ambassadors

What you get

What you do

How to apply

Engage with the local, national, and international Nextflow community



Speak about Nextflow and nf-core at meetings and events



Running local events such as user groups, hackathons, and workshops



Writing or sharing tweets, blogs, articles, and technical docs



Nextflow Ambassadors

What you get

What you do

How to apply

nextflow.io/ambassadors >

We're looking for people who:

- Joined the Nextflow and nf-core community at least 6-months ago
- Share our information reliably and appropriately
- Have already participated in some of our events and/or initiatives
- Are willing to actively support the community as an ambassador for at least one year

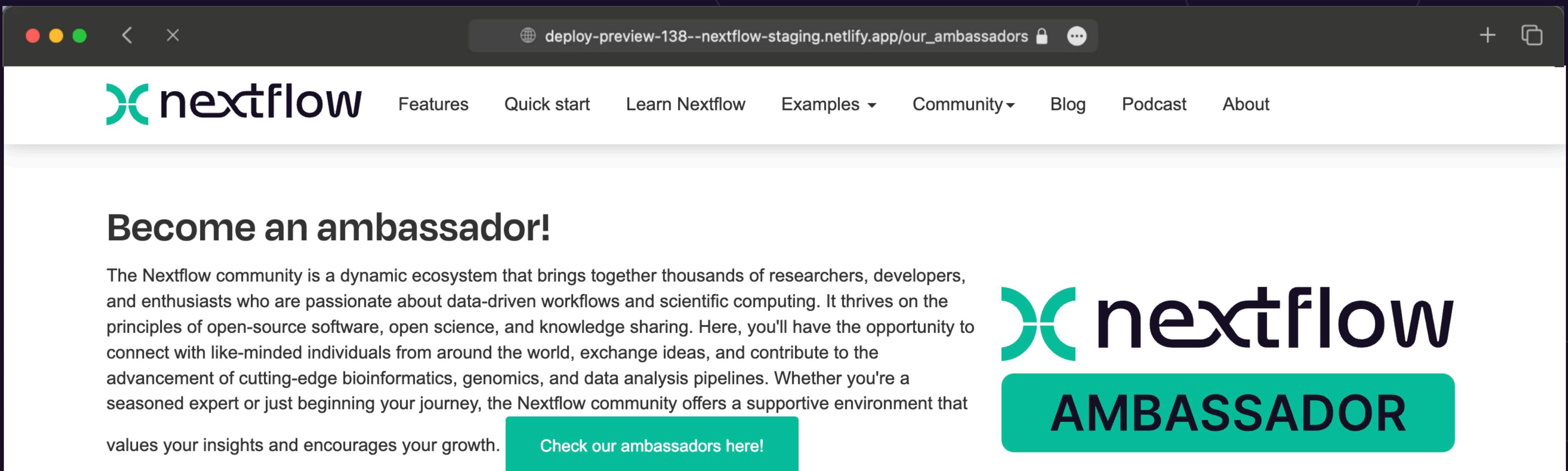


Nextflow Ambassadors

What you get

What you do

How to apply



The screenshot shows a web browser window with the Nextflow website. The URL in the address bar is `deploy-preview-138--nextflow-staging.netlify.app/our_ambassadors`. The page features a navigation bar with links for Features, Quick start, Learn Nextflow, Examples, Community, Blog, Podcast, and About. The main content area has a heading "Become an ambassador!" followed by a paragraph describing the Nextflow community and its ambassador program. A teal button at the bottom right of this section says "Check our ambassadors here!". To the right of the main content, there is a large Nextflow logo with the word "AMBASSADOR" overlaid on it.

Become an ambassador!

The Nextflow community is a dynamic ecosystem that brings together thousands of researchers, developers, and enthusiasts who are passionate about data-driven workflows and scientific computing. It thrives on the principles of open-source software, open science, and knowledge sharing. Here, you'll have the opportunity to connect with like-minded individuals from around the world, exchange ideas, and contribute to the advancement of cutting-edge bioinformatics, genomics, and data analysis pipelines. Whether you're a seasoned expert or just beginning your journey, the Nextflow community offers a supportive environment that values your insights and encourages your growth.

Check our ambassadors here!

Why become a Nextflow Ambassador?

The Nextflow ambassador program is a unique and exciting initiative designed to empower passionate individuals within the Nextflow community to play a more active role in fostering collaboration, knowledge sharing, and engagement. As a Nextflow Ambassador, you will have the opportunity to amplify the reach and impact of Nextflow by promoting its adoption, organizing community events, sharing your expertise through presentations and tutorials, and assisting fellow community members with their questions and challenges. This program is a way to recognise the dedicated volunteers that contribute their time, enthusiasm, and expertise to help grow and strengthen the Nextflow ecosystem. By becoming a Nextflow Ambassador, you'll not only enhance your own skills and network but also contribute to the advancement of scientific

Nextflow Ambassadors

What you get

What you do

How to apply

The screenshot shows a web browser window displaying the 'Our Ambassadors' page of the Nextflow website. The page features a header with the Nextflow logo and navigation links for Features, Quick start, Learn Nextflow, Examples, Community, Blog, Podcast, and About. Below the header, the title 'Nextflow Ambassadors' is centered. The main content area displays a grid of ambassador profiles in cards. Each card contains a circular profile picture, the ambassador's name, and social media icons. The cards are arranged in two rows. The first row contains four cards: Abhinav Sharma, Adam Talbot, Alex Peltzer, and Anabella Trigila. The second row contains three cards: Bhargava Morampalli, I., and OW. The card for Anabella Trigila is highlighted with a green border.

nextflow

Features Quick start Learn Nextflow Examples Community Blog Podcast About

Nextflow Ambassadors

Abhinav Sharma

Adam Talbot

Alex Peltzer

Anabella Trigila

Bhargava Morampalli

I.

OW

Nextflow Ambassadors

What you get

What you do

How to apply

nextflow.io/ambassadors >

Read more in our blog post on [nextflow.io!](#)



**Nextflow
ambassador
handbook**

September 2023

Community Forum

A new home for the community across all Seqera tools, built with Discourse – brings **public access, scales with the community and fosters better structured discussion**

Community Forum

community.seqera.io

Sign Up Log In

Welcome to the community!

We're happy to have you here. If you need help, please search before you post.

Search

all categories ► all tags ► Categories Latest Top

Category Topics Latest

Seqera Platform (Tower) 0

Collaborative data analysis at scale, on-premises or in any cloud.

>Welcome to Seqera Community! 1
7 Aug

Random

Community Forum



**Introducing
community.seqera.io**

Learn more

community.seqera.io >

Read more in our blog post on [nextflow.io!](#)

Geraldine Van de Auwera

New Seqera Lead Developer Advocate!

- Formerly worked at the Broad Institute with GATK, WDL, terra.bio
- Wrote the O'Reilly book "Genomics in the Cloud"
- Lives in Boston, USA 🇺🇸

Please get in touch if you'd like to work together on training, collaborative blog posts, podcasts, anything Nextflow related!



Thank you



Phil Ewels, PhD

Product Manager for Open Source
phil.ewels@seqera.io

