



**nf-core**



Community  
Updates

# nf-core 🍏

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

<https://nf-co.re>

# nf-core



70  
PIPELINES

<https://nf-co.re>

# nf-core



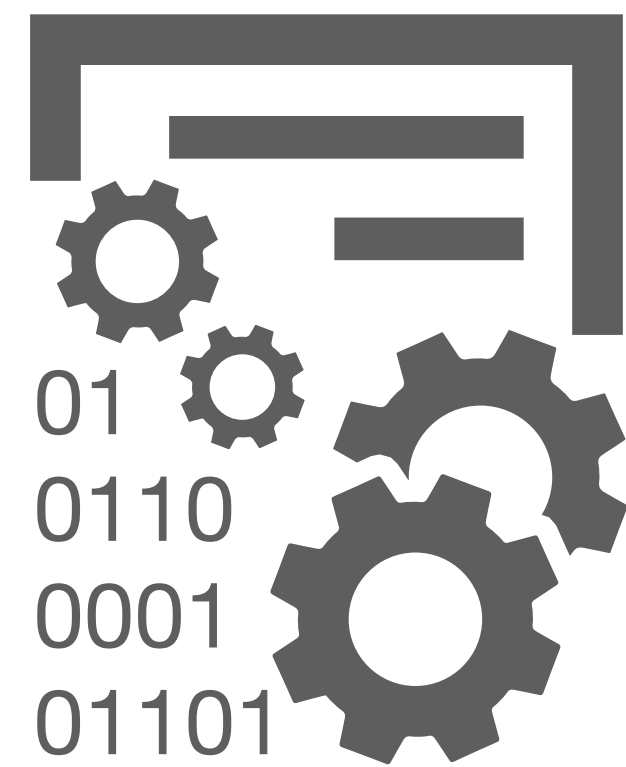
Running pipelines

Writing pipelines

Testing / automation

<https://nf-co.re>

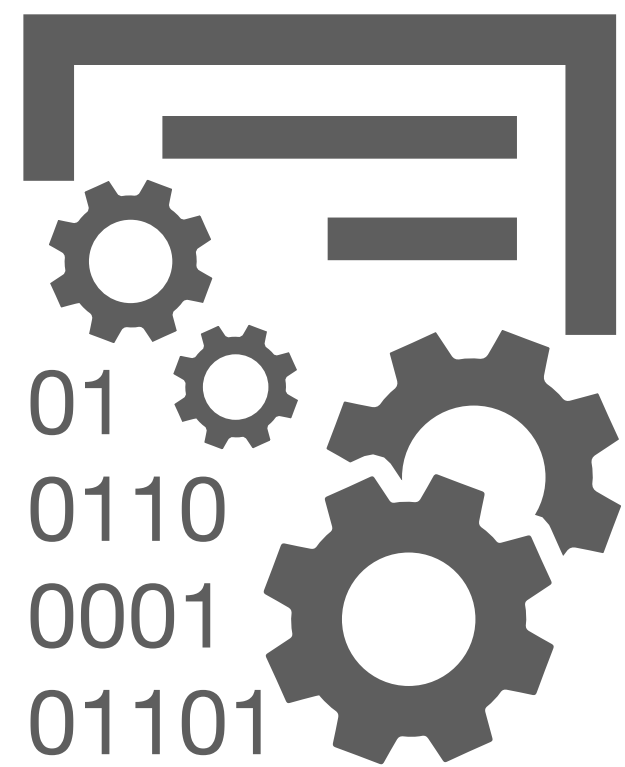
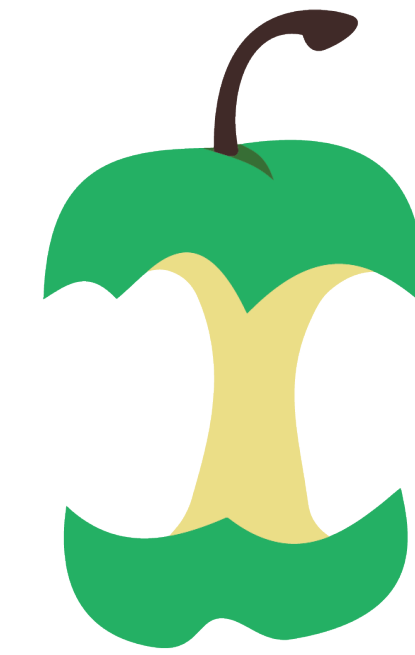
# nf-core



632  
MODULES

<https://nf-co.re>

**nf-core**



632

MODULES

11

SUB-  
WORKFLOWS

<https://nf-co.re>

# Timeline

## Community updates

2017

2018

2019

2020

2021

2022

# Timeline



2017

2018

SciLifeLab NATIONAL CTAC GENOMICS CT INFRASTRUCTURE

**Standardising Swedish genomics analyses using nextflow**

Phil Ewels @ewels @tallphil

Nextflow Meeting 2017-09-14 CRG, Barcelona

Nextflow Meeting 2017



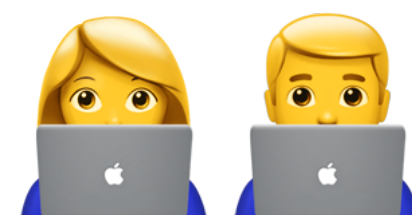
A\*STAR (Singapore) visit



QBiC (Germany) visit



# Timeline



2018

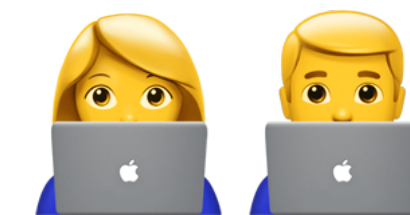
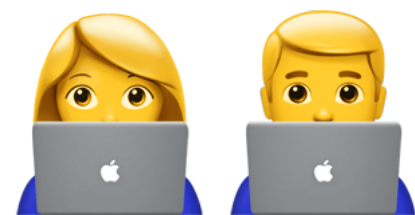


Stockholm  
hackathon



Nextflow  
Meeting 2018

# Timeline



2019

QBiC  
hackathon

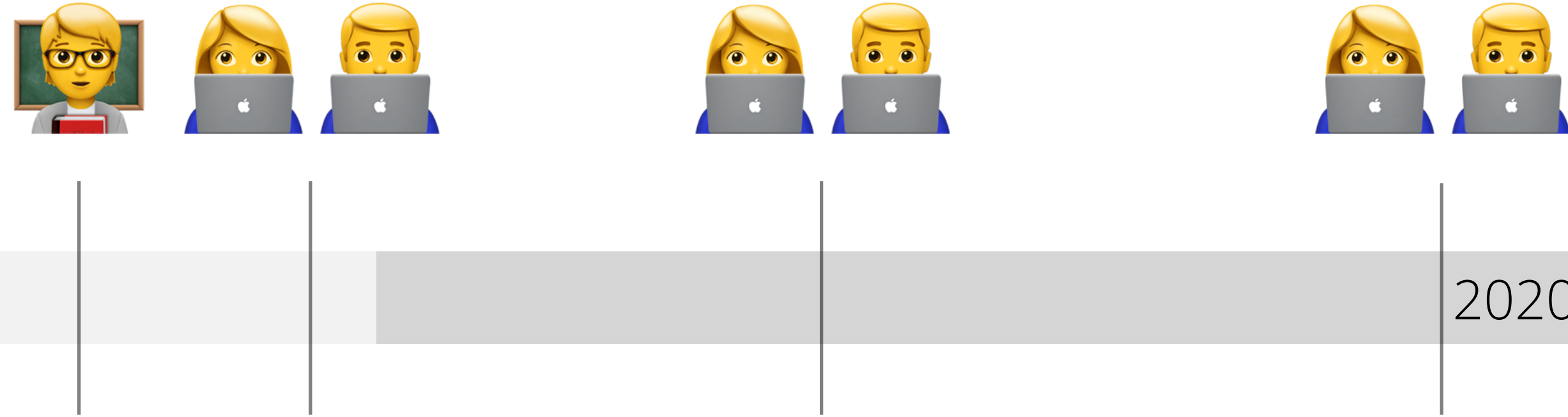


Nextflow  
Meeting 2019

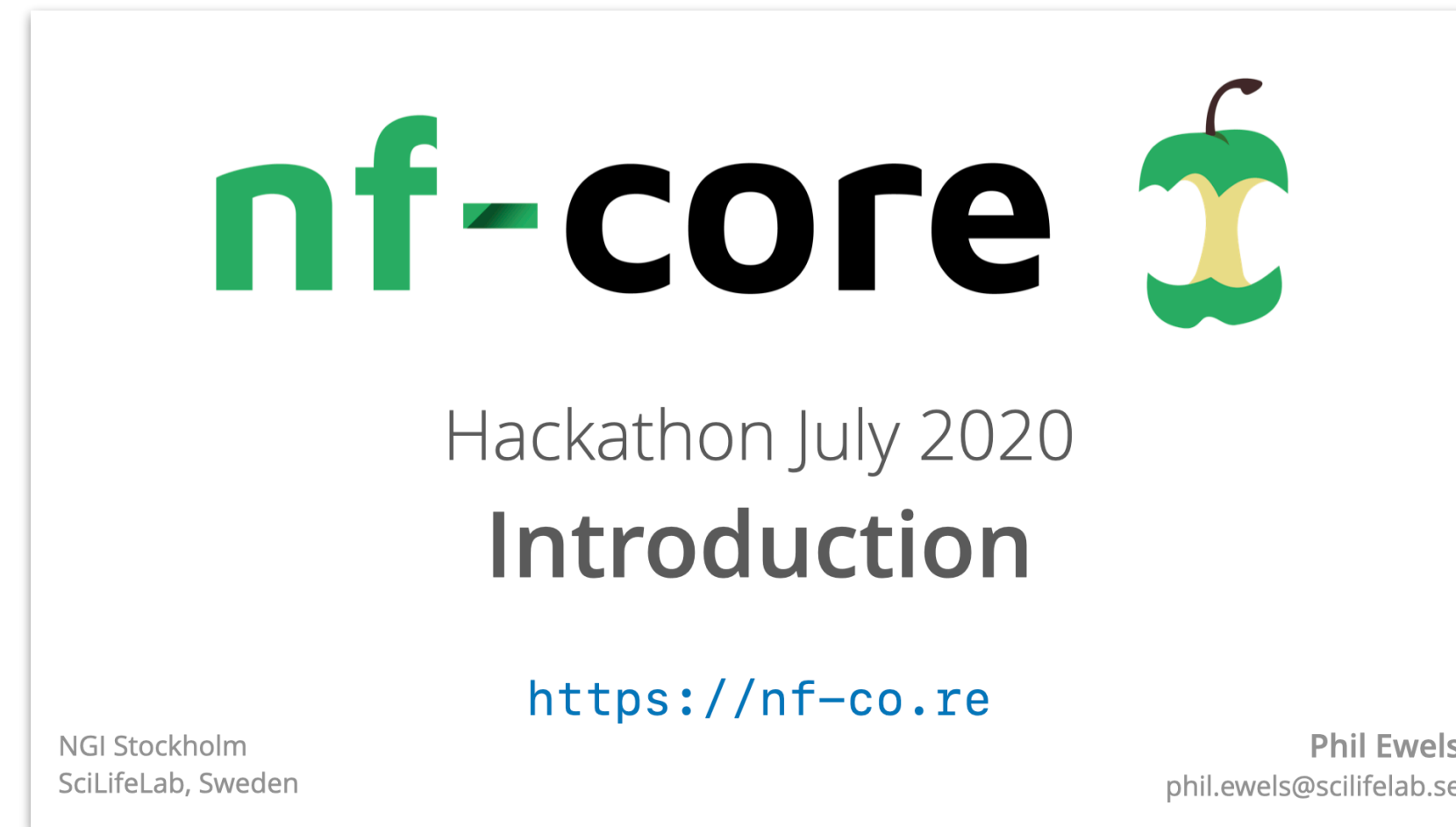


SciLifeLab  
hackathon

# Timeline

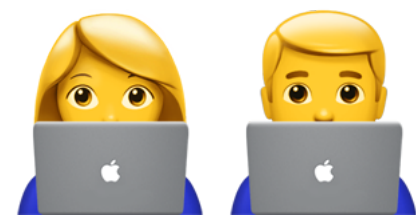
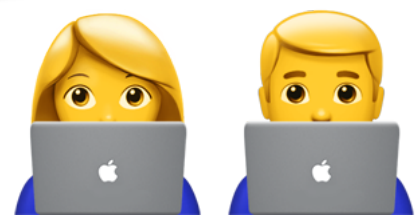


Francis Crick  
hackathon



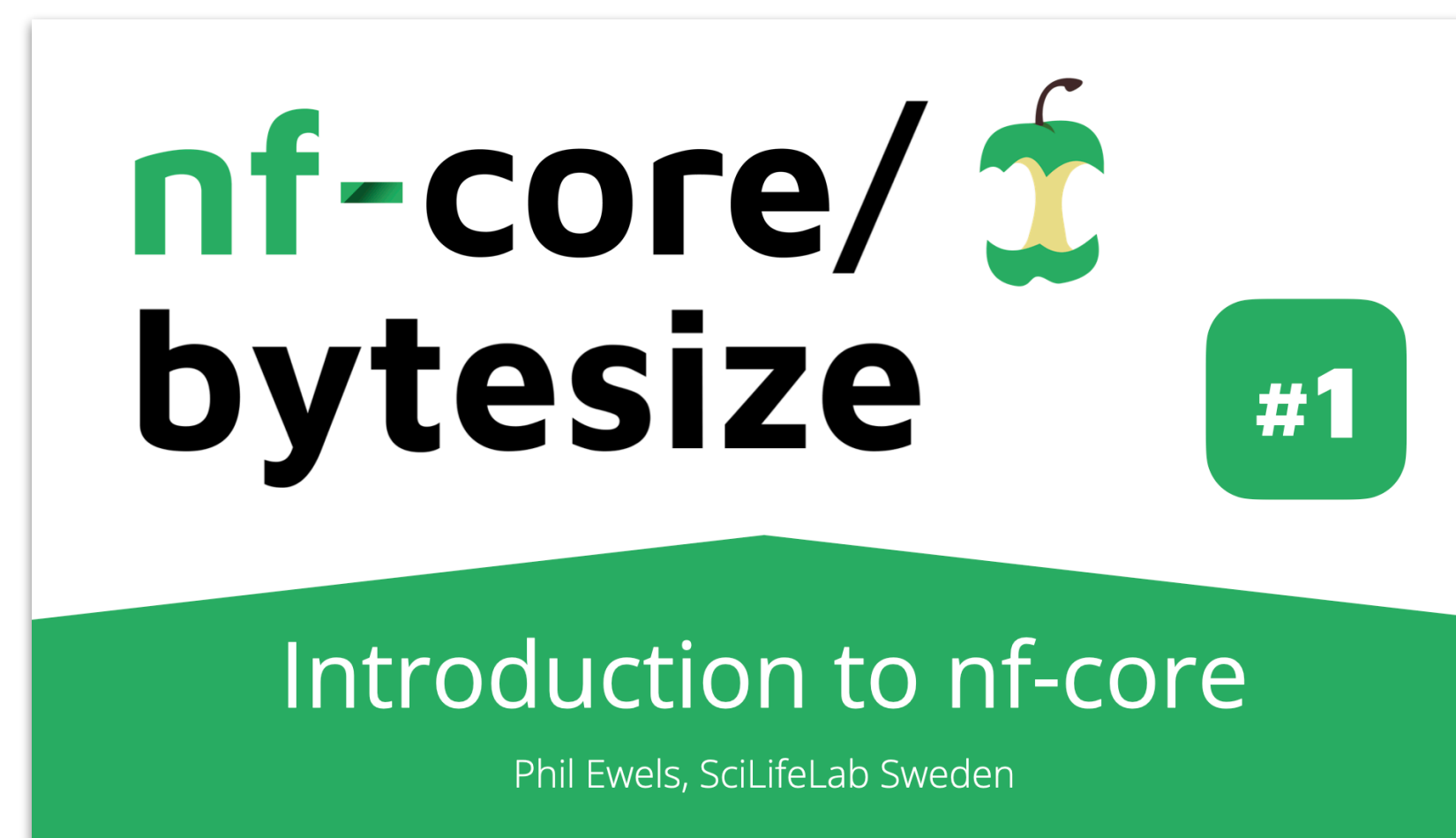
First online  
hackathon

# Timeline



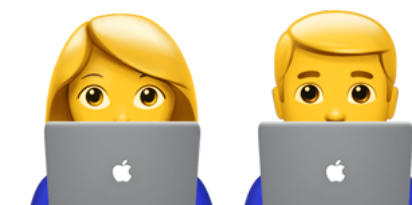
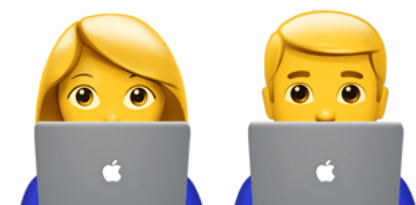
2020

CZI EOSS  
Cycle 2

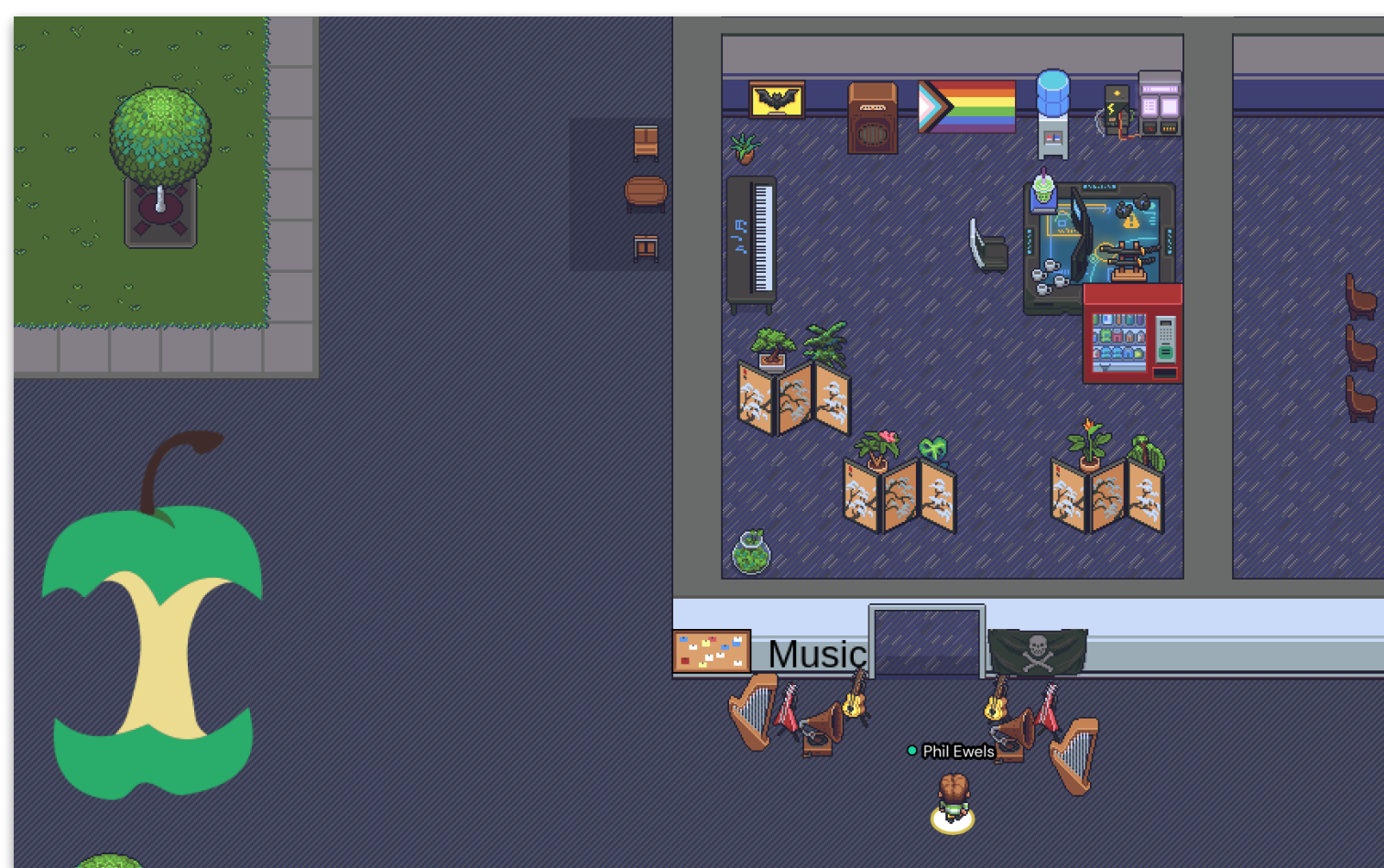


Bytesize talks  
start

# Timeline



2021



March 2021  
hackathon

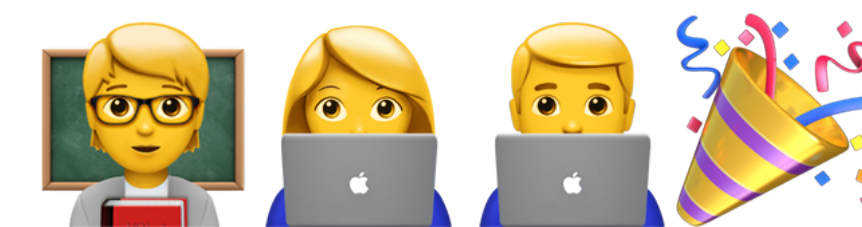
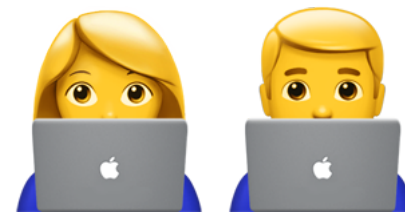
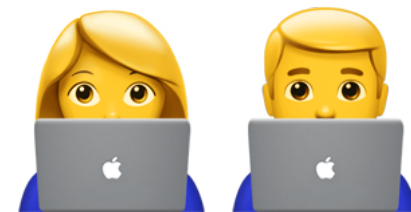
CZI EOSS  
Cycle 4

CZI EOSS  
Diversity &  
Inclusion

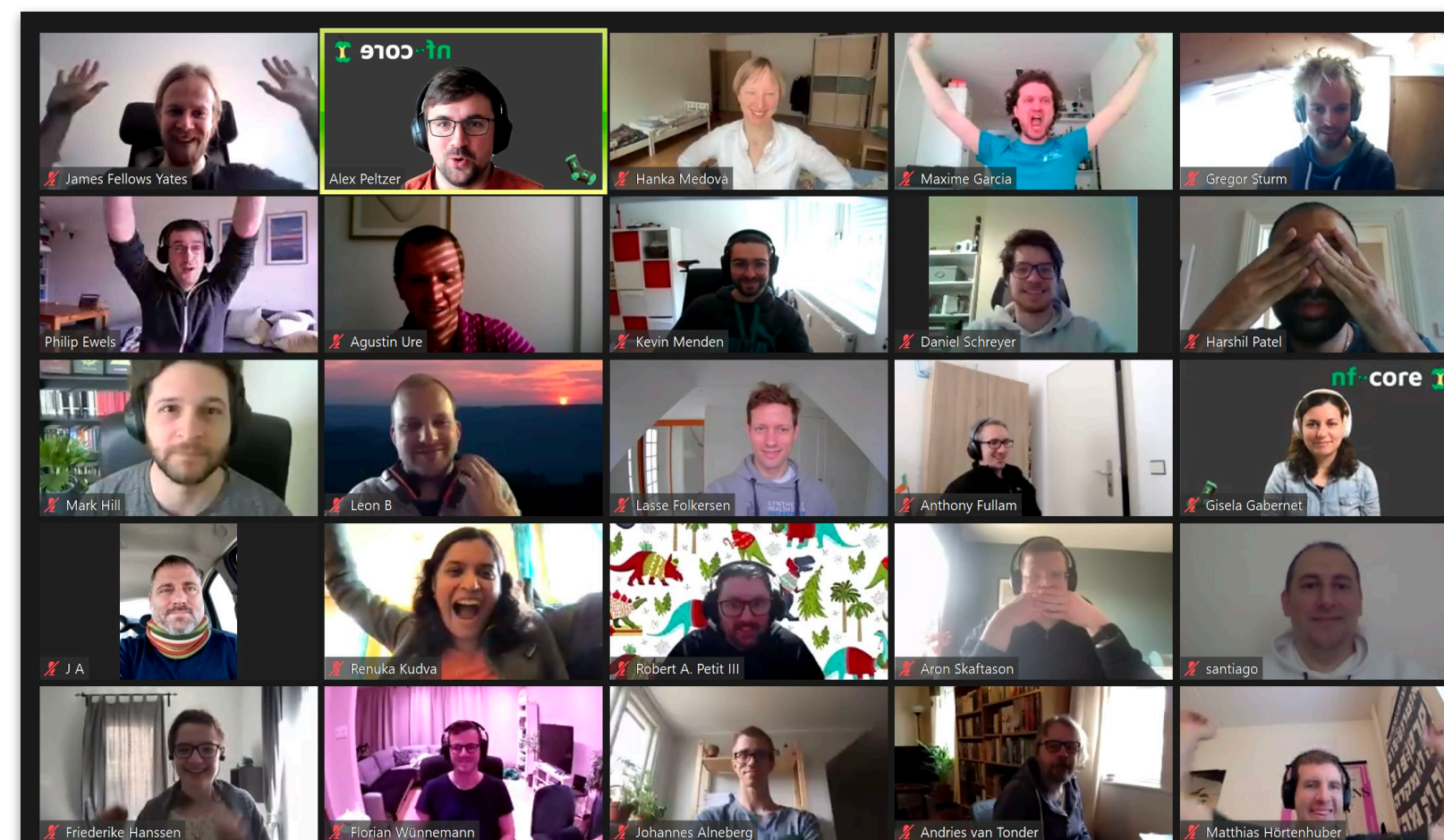


October 2021  
hackathon

# Timeline



2022



First training

October 2022  
hackathon

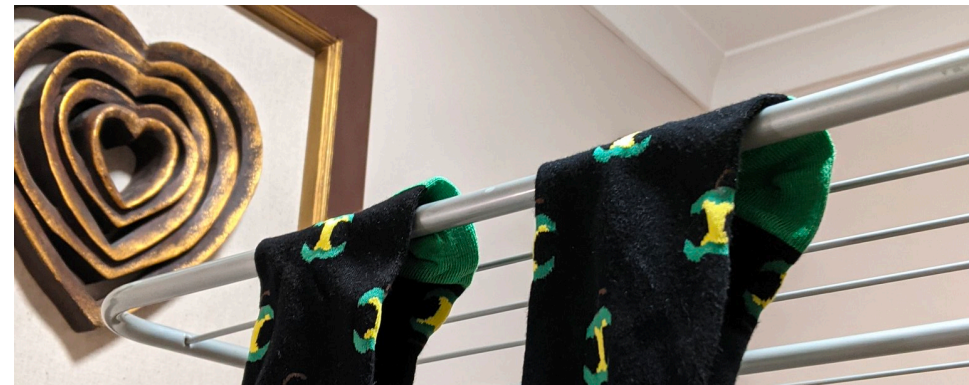
Nextflow  
Summit 2022

March 2022  
hackathon

# Community



# Community

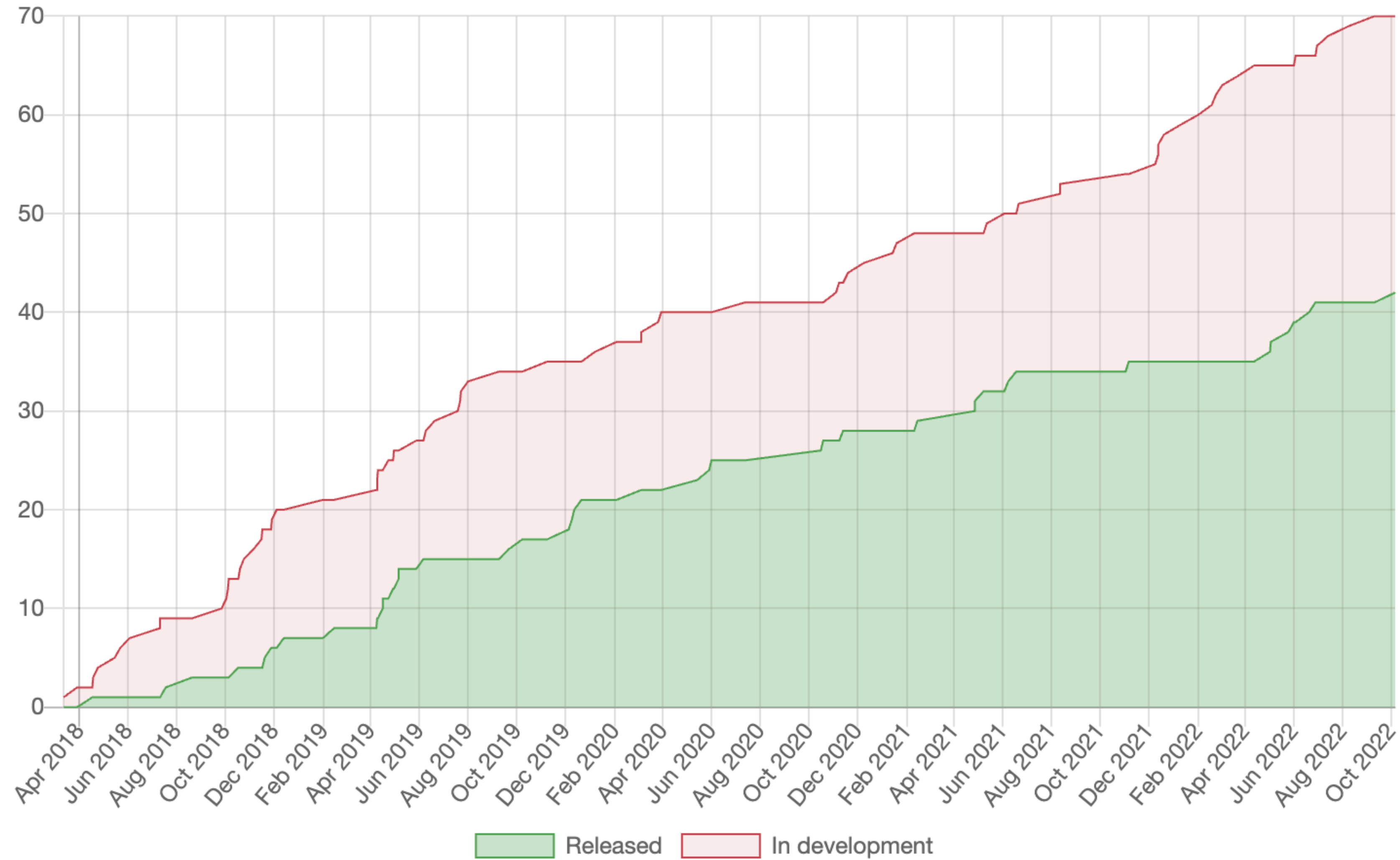




# Community



## nf-core pipeline numbers over time



# Community

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

3575

Slack users

466

GitHub organisation  
members

1475

GitHub contributors

3127

Twitter followers

86

Repositories

10.72K

Pull Requests

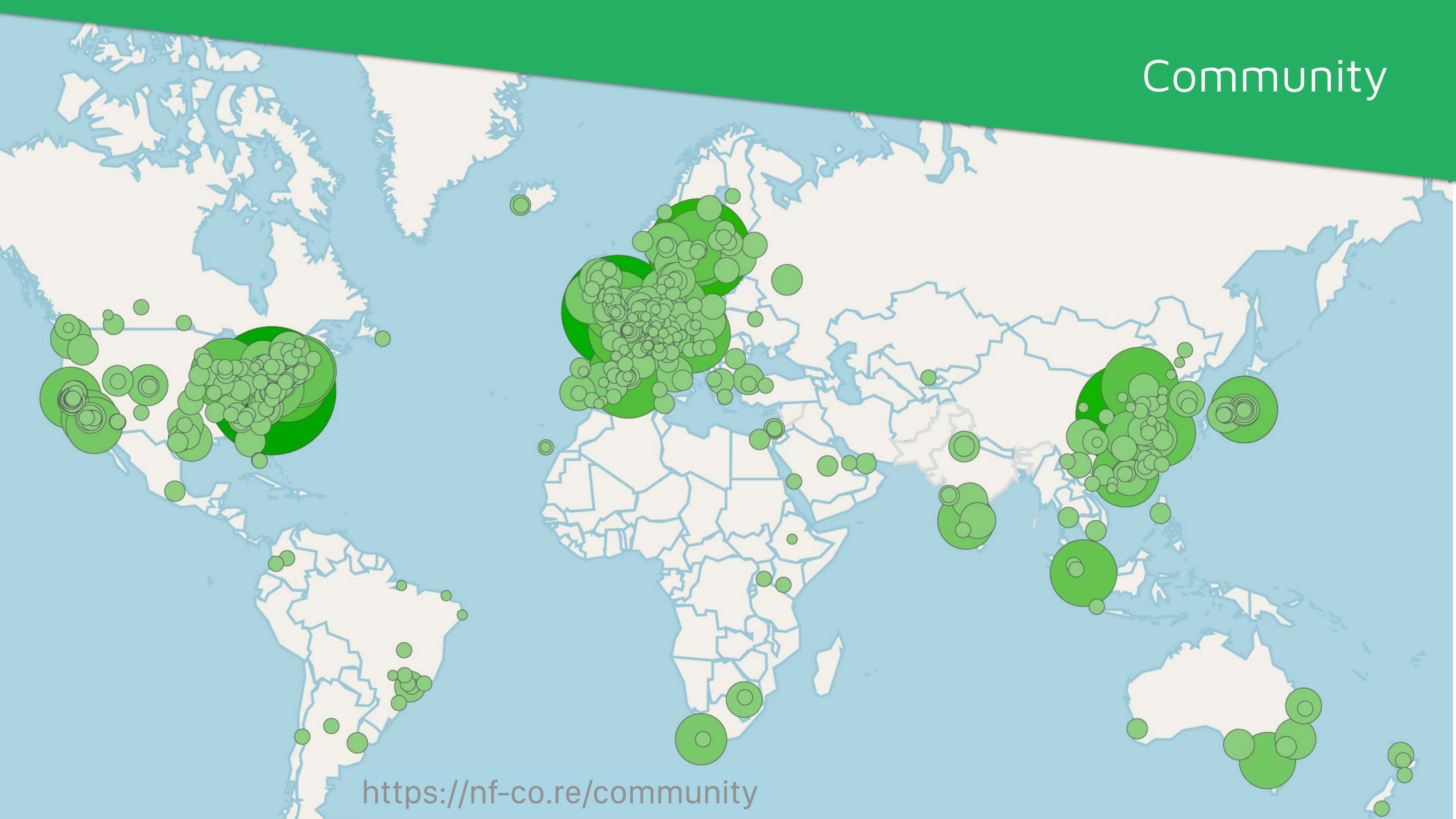
13.89K

Commits

4.73K

Issues

# Community



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

# Personnel

## Chan Zuckerberg Initiative



Phil



Marcel



Chris



Julia



Matthias



Fran

# Chan Zuckerberg Initiative



**Phil**  
EMEA



**Marcel**  
LATAM



**Chris**  
APAC



## Upcoming Events

### Bytesize: nf-core/nascent

Edmund Miller - University of Texas, USA

1<sup>st</sup> Nov 2022

 Talk

[See details](#)

 Export event 

## Past Events

### nf-core Training - October 2022

A set of global online Nextflow and nf-core training events

3<sup>rd</sup> - 5<sup>th</sup> Oct 2022 - [See details](#)

 Workshop

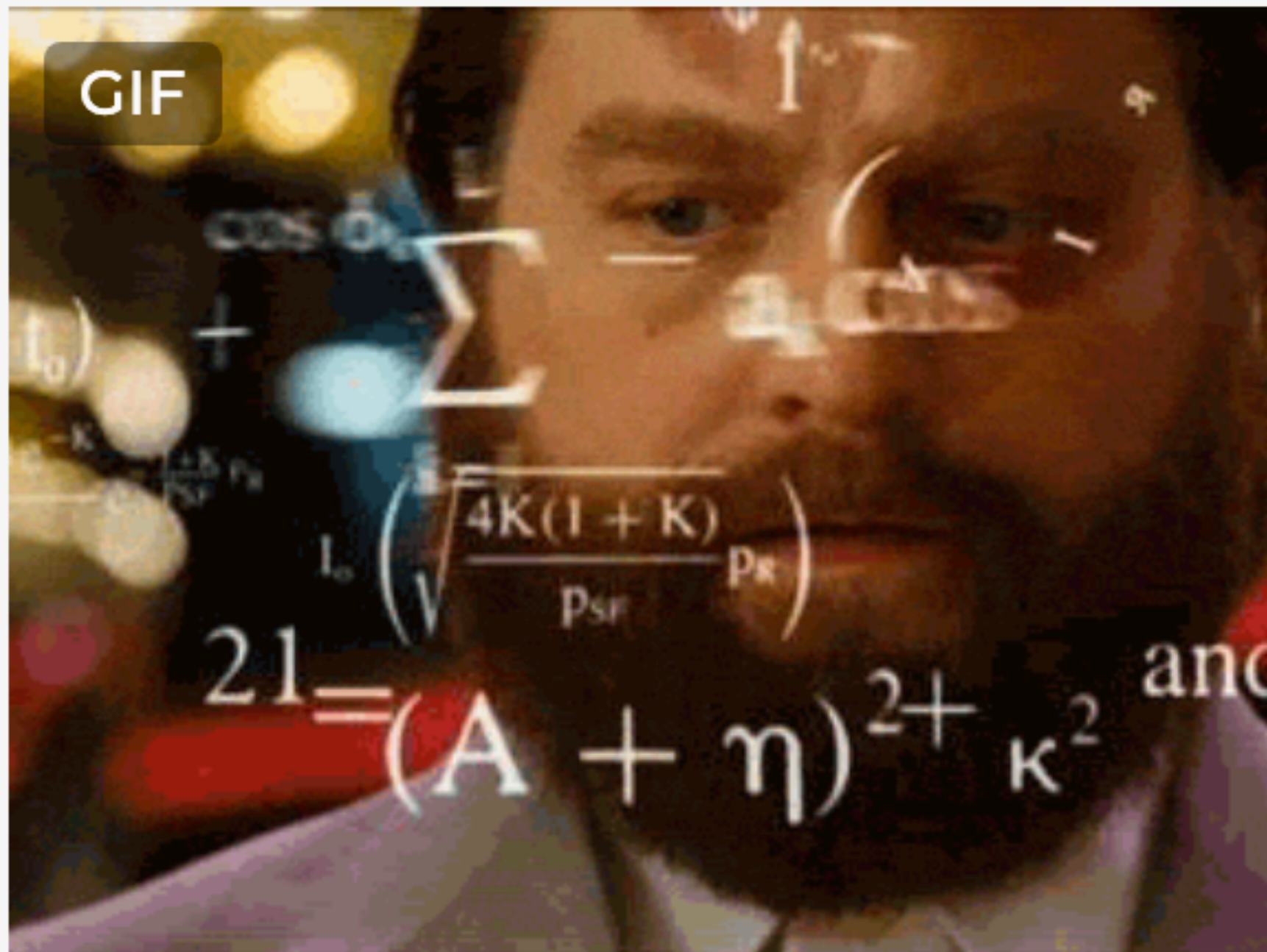
### Bytesize: community updates Sep 2022

 Talk

## Bytesize 4: GitHub contribution basics

Alexander  
23<sup>rd</sup> Feb

6 -Quiz **How many bytesize talks are currently there? (2022-10-10)**



51



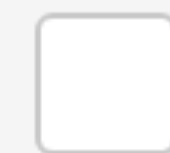
42



53



46



No answer



Byte

Gisel  
16<sup>th</sup> Feb

Byte

Maxi  
9<sup>th</sup> Feb

Byte

nf-con  
2<sup>nd</sup> Feb 2021



Mentorships

# Chan Zuckerberg Initiative



# Mentorships

# Chan Zuckerberg Initiative



Poster #16

## Nextflow and nf-core mentorships: Round 1

We look back at the success of the program so far.

nextflow

Join us on  slack



Mentorships

**Chan Zuckerberg  
Initiative**



**Mentorships Round 2 applications open!** 🎉

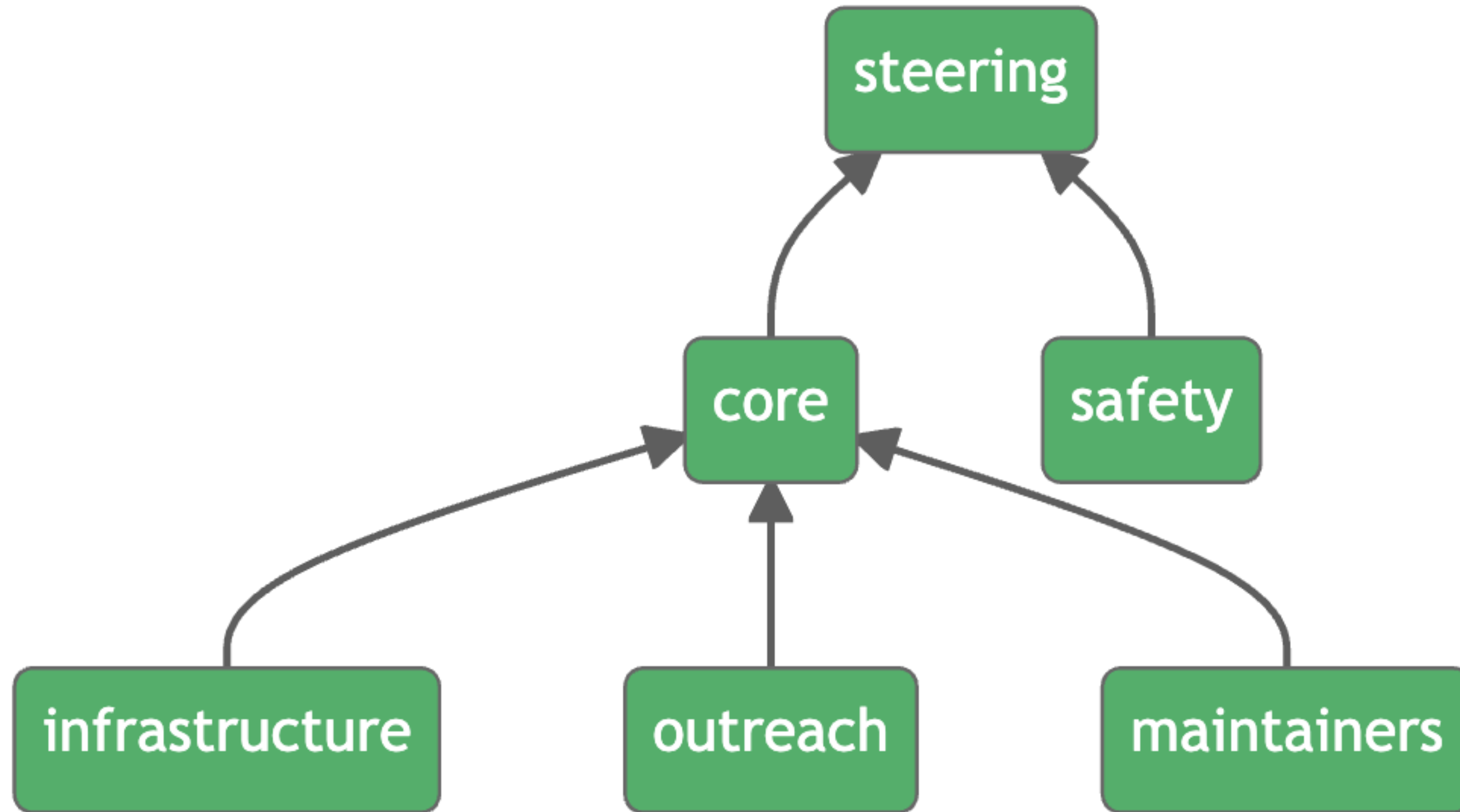
Deadline Nov 1<sup>st</sup> 2022

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

# Governance



core



# Cloud testing



nf-core / viralrecon Public Watch 16 Star 49 Fork 42

[Code](#) [Issues 9](#) [Pull requests 1](#) [Discussions](#) [Actions](#) [Security](#) [Insights](#) [Settings](#)

✓ **nf-core/viralrecon v2.1 - Lead Mink nf-core AWS full size tests #3** ⋮

[Summary](#)

Jobs

- ✓ Run AWS full tests (illumina)
- ✓ Run AWS full tests (nanopore)

Triggered via release 5 months ago	Status	Total duration	Artifacts
drpatelh published 2.1	<b>Success</b>	<b>2m 23s</b>	—

**awsfulltest.yml**  
on: release

Matrix: Run AWS full tests

✓ **2 jobs completed**  
[Show all jobs](#)

# Cloud testing



Introduction **aws Results** Usage docs Parameter docs Output docs Releases & Statistics 2.2

aws nf-core-awsmegatests / viralrecon  
/ [results-2ebae61442598302c64916bd5127cf23c8ab5611](#) / platform\_illumina Copy Bucket S3 URL

>\_ command  
`nextflow run nf-core/viralre`

↓ clones in last 2 years  
13054

stars 49 watchers 16

last release last updated  
1 month ago

open issues 9 pull requests 168

collaborators

get in touch  
[Ask a question on Slack](#)  
[Open an issue on GitHub](#)

Name	↑↓	Last Modified	↑↓	Size	↑↓
..					
<a href="#">assembly/</a>					
<a href="#">fastp/</a>					
<a href="#">fastqc/</a>					
<a href="#">kraken2/</a>					
<a href="#">multiqc/</a>					
<a href="#">pipeline_info/</a>					
<a href="#">variants/</a>					



# Cloud testing



multiqc\_report.html

Download file Copy URL Copy S3 URL

### Amplicon coverage heatmap

Export Plot

SAMPLE\_11  
SAMPLE\_07  
SAMPLE\_02  
SAMPLE\_04  
SAMPLE\_16  
SAMPLE\_18  
SAMPLE\_12  
SAMPLE\_47  
SAMPLE\_35  
SAMPLE\_42  
SAMPLE\_24  
SAMPLE\_08  
SAMPLE\_32  
SAMPLE\_48  
SAMPLE\_03  
SAMPLE\_25  
SAMPLE\_46  
SAMPLE\_17  
SAMPLE\_40  
SAMPLE\_19  
SAMPLE\_31  
SAMPLE\_21  
SAMPLE\_26

0 1 2 3 4 5

...  
nCoV-...  
nCoV-2019\_9  
nCoV-2019\_13  
nCoV-2019\_17  
nCoV-2019\_21  
nCoV-2019\_25  
nCoV-2019\_29  
nCoV-2019\_33  
nCoV-2019\_37  
nCoV-2019\_41  
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nCoV-2019\_65  
nCoV-2019\_69  
nCoV-2019\_73  
nCoV-2019\_77  
nCoV-2019\_81  
nCoV-2019\_85  
nCoV-2019\_89  
nCoV-2019\_93  
nCoV-2019\_97

Amplicon

Created with MultiQC

open issues 9 pull requests 168

collaborators

get in touch

Ask a question on Slack

Open an issue on GitHub

Toolbox

# Cloud testing



Microsoft



seqeralabs

Join the community



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

# Phil Ewels

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[phil@seqera.io](mailto:phil@seqera.io)



**seqeralabs**

<https://seqera.io>

**Chan Zuckerberg  
Initiative**



**nextflow**

**nf-core** 🍏

**nextflow** *tower*



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