



Introduction to nf-core



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



Guidelines



Tools



Pipelines

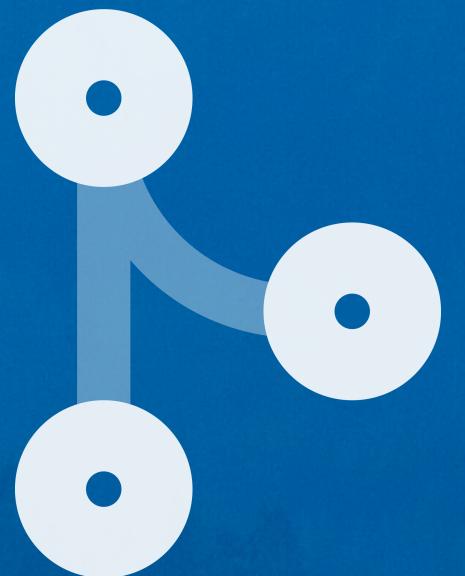
nf-core



Develop with
the community



Start from the
template



Collaborate,
don't duplicate

nf-core



23

UNDER DEVELOPMENT



6

ARCHIVED

Available Pipelines

Can you think of another pipeline that would fit in well? [Let us know!](#)

Search keywords

Filter:

Released 25

Under development 14

Archived 3

Sort:

Last Release

Alphabetical

Stars

Display:



nf-core/viralrecon ✓

☆ 18

amplicon assembly covid-19 covid19 illumina metagenomics

sars-cov-2 variant-calling viral virus

Assembly and intrahost/low-frequency variant calling for viral samples

Version 1.1.0

Published 7 days ago

nf-core/imcyto ✓

☆ 5

cytometry image-analysis image-processing image-segmentation

Image Mass Cytometry analysis pipeline

Version 1.0.0

Published 1 month ago

nf-core/coproid ✓

☆ 2

adna ancient-dna coprolite microbiome

Genomic data classification pipeline

nf-core/sarek ✓

☆ 49

cancer germline somatic variant-calling

Analysis pipeline to detect germline or somatic variants from WGS / targeted sequencing

Version 2.6.1

Published 1 week ago

nf-core/slamseq ✓

☆ 3

differential-expression quantseq slamseq transcriptomics

SLAMSeq processing and analysis pipeline

Version 1.0.0

Published 2 months ago

nf-core/mhcquant ✓

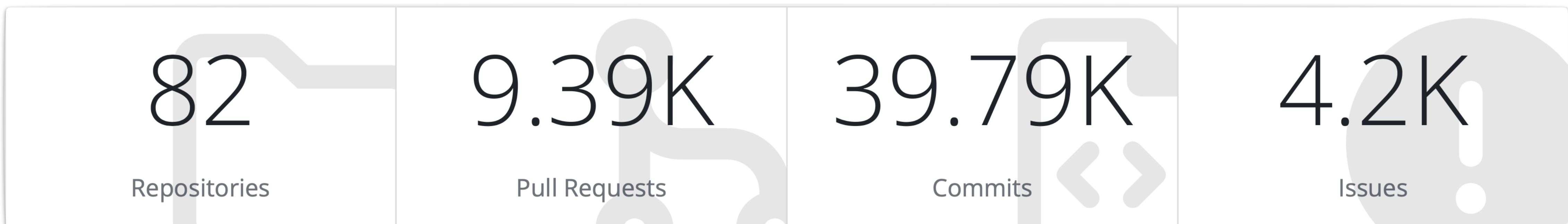
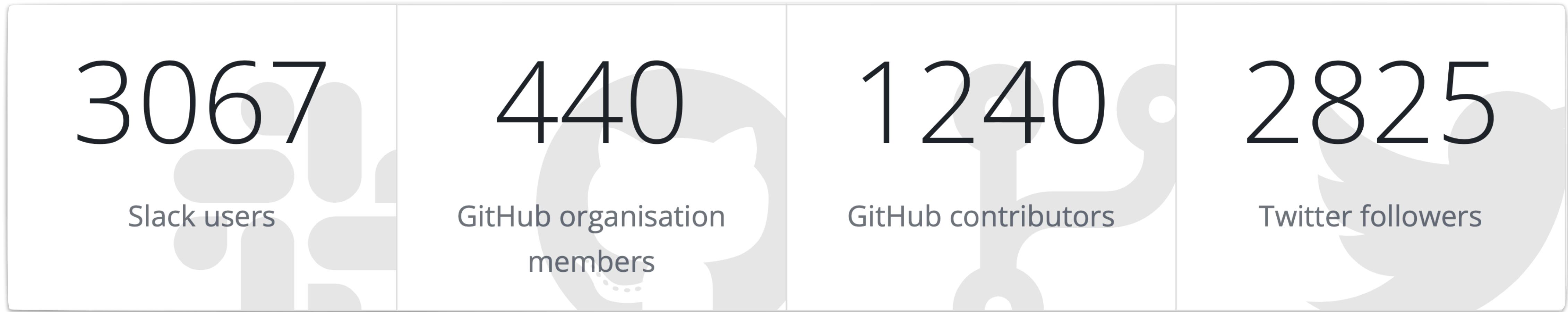
☆ 12

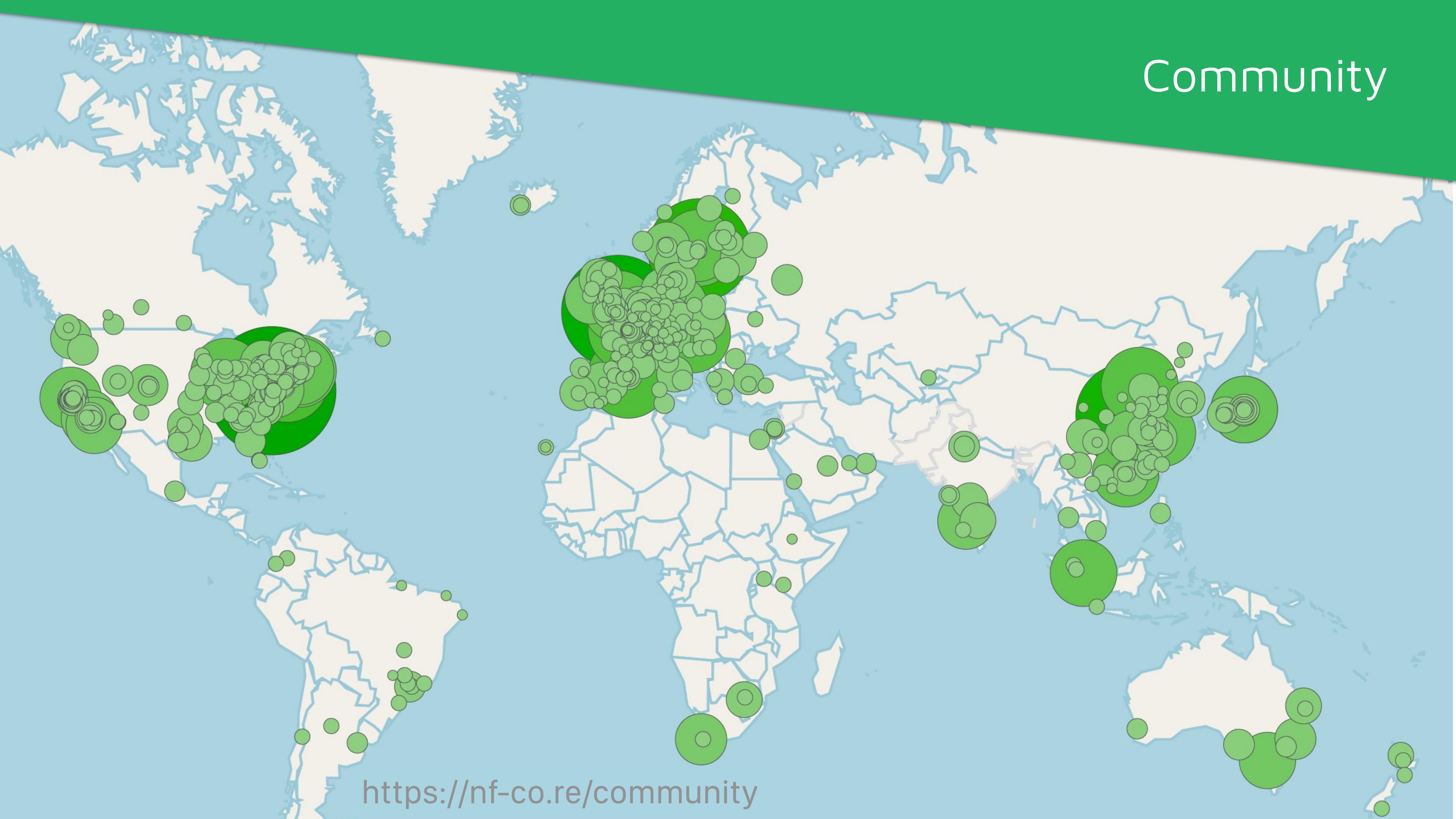
mass-spectrometry mhc peptides

Identify and classify MHC ligand peptides from mass-spectrometry

Community

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





Community

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

Correspondence | Published: 13 February 2020

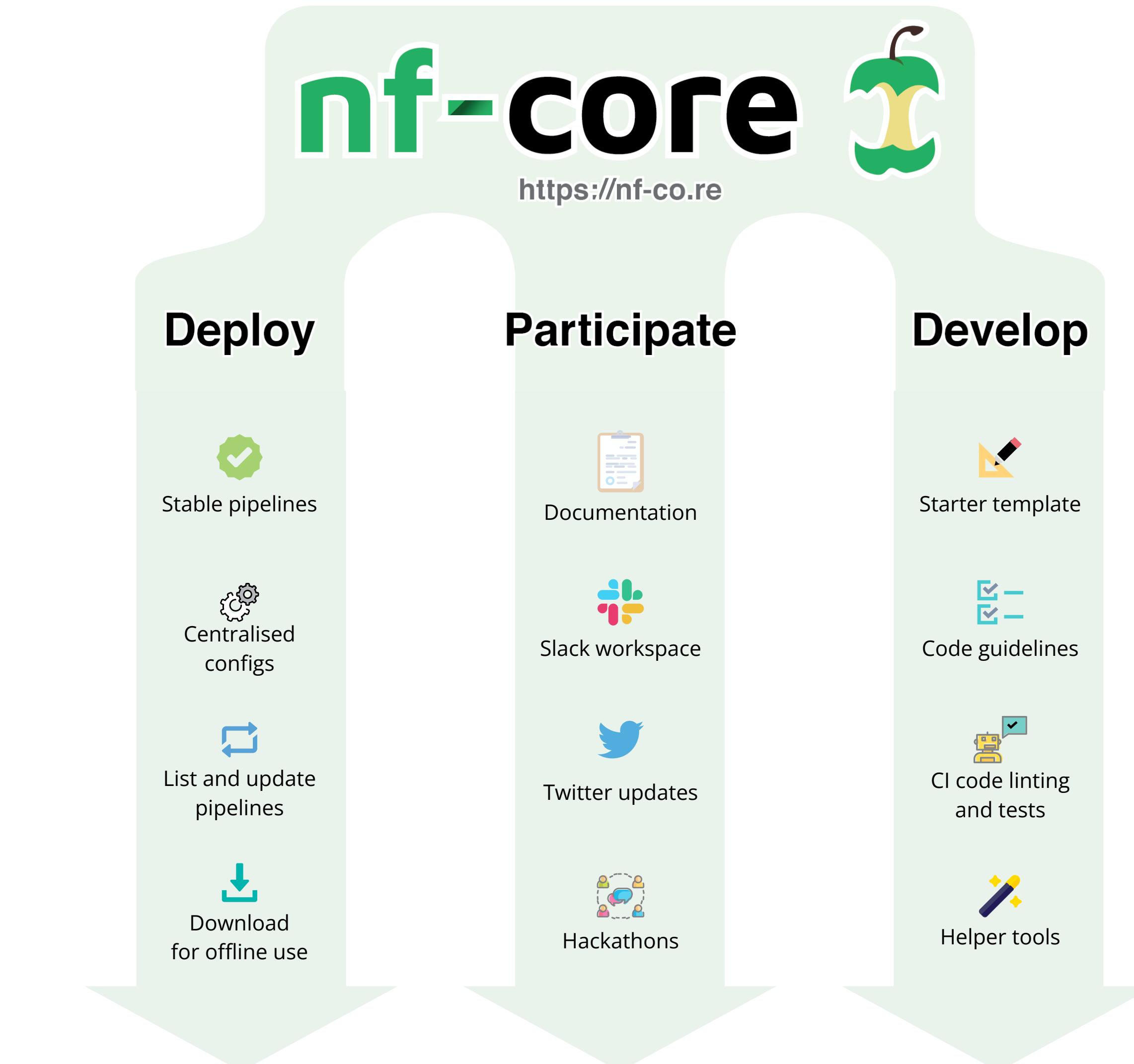
The nf-core framework for community-curated bioinformatics pipelines

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.

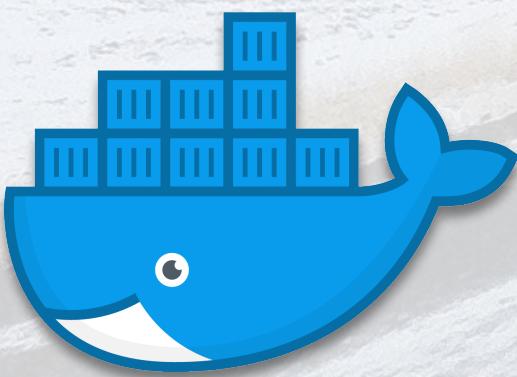


Requirements

1

nextflow

2



docker®

or



or

CONDA

3

nf-core/tools



Introduction  Results Usage docs **Parameter docs** Output docs Releases & Statistics  3.4 

Parameters

> Input/output options

Define where the pipeline should find input data and save output data.

 <code>--input</code>	Path to comma-separated file containing information about the samples in the experiment.	 Help
 <code>--outdir</code>	Path to the output directory where the results will be saved.	default: './results'
 <code>--email</code>	Email address for completion summary.	 Help
 <code>--multiqc_title</code>	MultiQC report title. Printed as page header, used for filename if not otherwise specified.	
 <code>--save_merged_fastq</code>	Save FastQ files after merging re-sequenced libraries in the results directory.	

 **UMI options**

Options for processing reads with unique molecular identifiers

On this page

Parameters

- > Input/output options
- UMI options
- Read filtering options
- Reference genome options
- Read trimming options
- Alignment options
- Process skipping options

 Show all help  Show hidden params

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Launch wizard

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

Read trimming options

`--save_trimmed` True False

Save the trimmed FastQ files in the results directory.

[?](#)

[Launch](#)

Alignment options

Options to adjust parameters and filtering criteria for read alignments.

 `--aligner` star_salmon

Specifies the alignment algorithm to use - available options are 'star_salmon', 'star_rsem' and 'hisat2'.

 `--pseudo_aligner` [Select an option]

Specifies the pseudo aligner to use - available options are 'salmon'. Runs in addition to '--aligner'.

 `--bam_csi_index` True False

Create a CSI index for BAM files instead of the traditional BAI index. This will be required for genomes with larger chromosome sizes.

 `--star_ignore_sjdbgtf` True False

When using pre-built STAR indices do not re-extract and use splice junctions from the GTF file.

On this page

Nextflow command-line flags

>_ Input/output options

|||| UMI options

||| Read filtering options

|| Reference genome options

☒ Read trimming options

≠ Alignment options

▶ Process skipping options

 Show hidden params

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▶ `--salmon_quant_libtype`

?

Launch wizard

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

```
nf-core launch --id 1637063024_d92e0f1632c2
```

```
nextflow run nf-core/rnaseq -params-file nf-params.json
```

Running in the cloud

nextflow



Google Cloud



Microsoft
Azure

Running in the cloud

<https://github.com/nf-core/viralrecon>

 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** ...

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

Summary

Jobs

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

awsfulltest.yml
on: release

Matrix: Run AWS full tests

 **2 jobs completed**

Show all jobs

Running in the cloud

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

aws nf-core-awsmegatests / viralrecon / [results-2ebae61442598302c64916bd5127cf23c8ab5611](#) / platform_illumina

[Copy Bucket S3 URL](#)

Name	Last Modified	Size
..		
assembly/		
fastp/		
fastqc/		
kraken2/		
multiqc/		
pipeline_info/		
variants/		

→ command
`nextflow run nf-core/viralrecon`

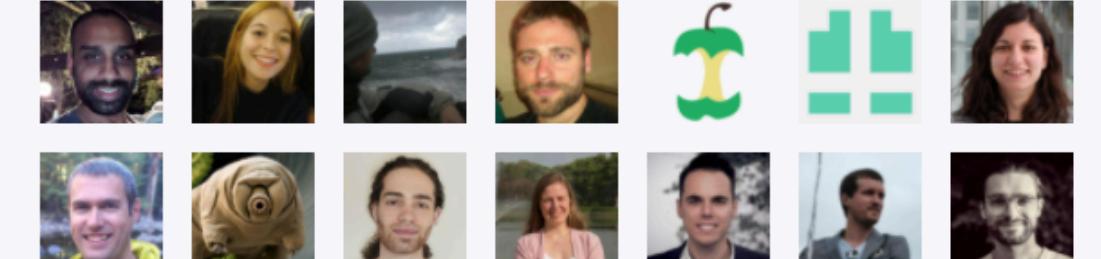
↓ clones in last 2 years
13054

stars 49 watchers 16

last release last updated
1 month ago

open issues pull requests
9 168

collaborators



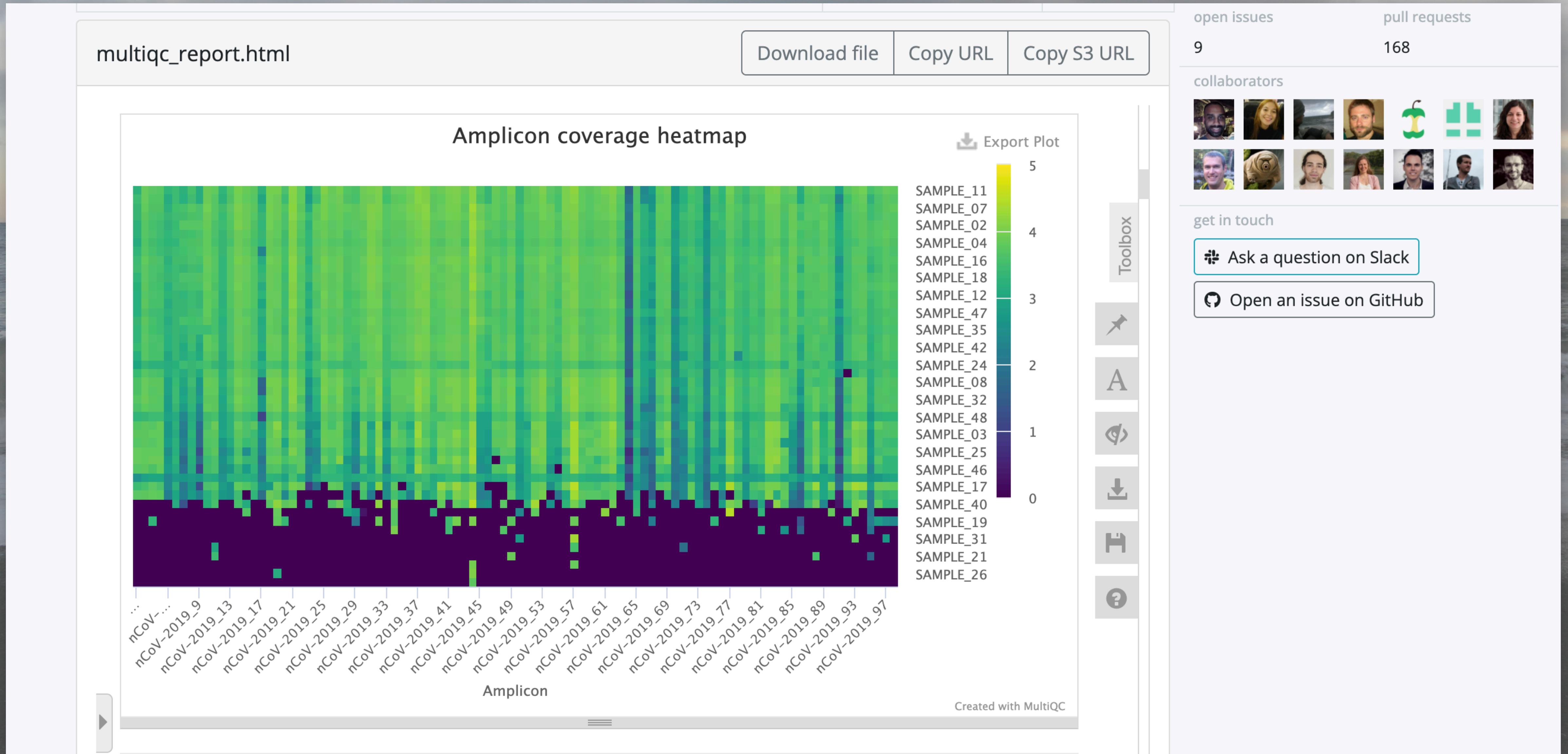
get in touch

[Ask a question on Slack](#)

[Open an issue on GitHub](#)

Running in the cloud

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



Join the community



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

nf-core



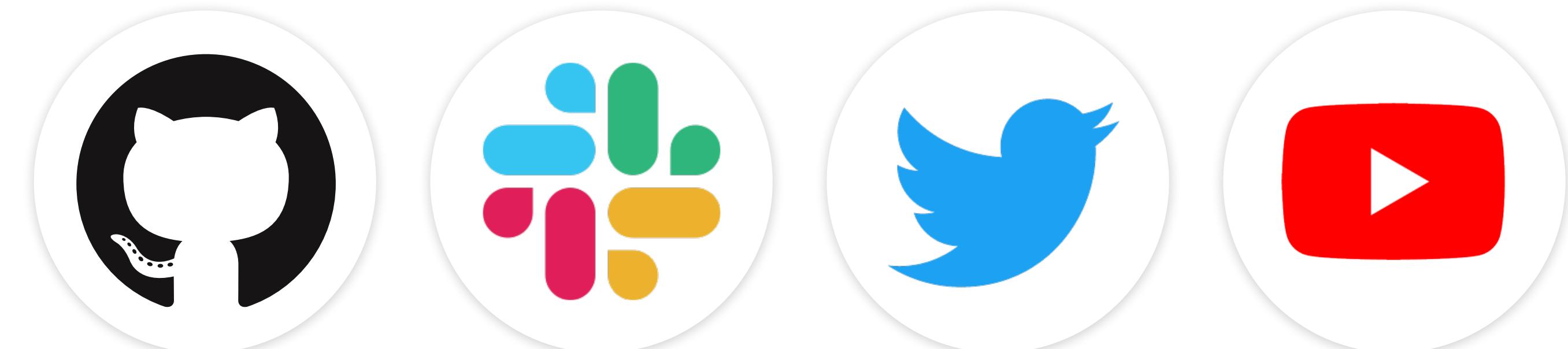
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<https://nf-co.re/join>