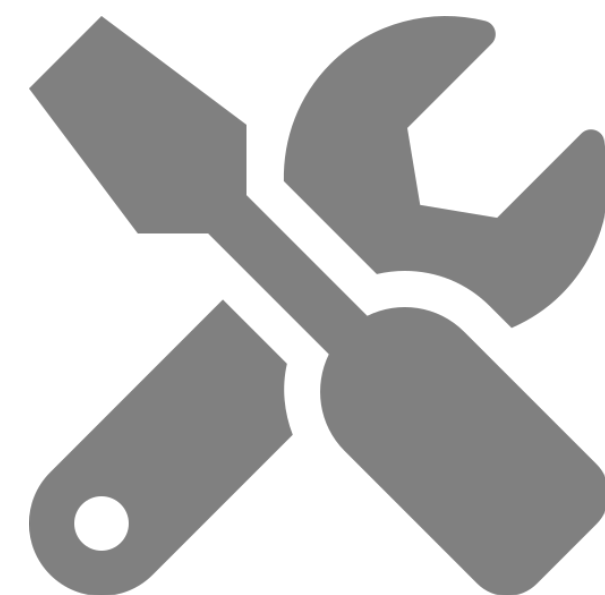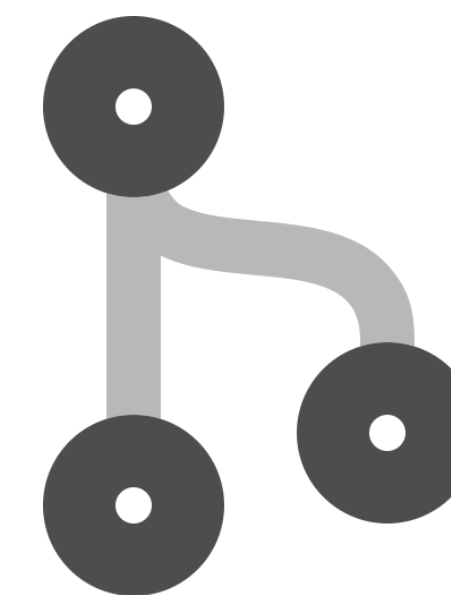Guidelines

Tools

Pipelines

nf-core

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/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 🍏

24

RELEASED

16

UNDER DEVELOPMENT

4

ARCHIVED

nf-core

Community

https://nf-co.re/stats

Community

https://nf-co.re/stats
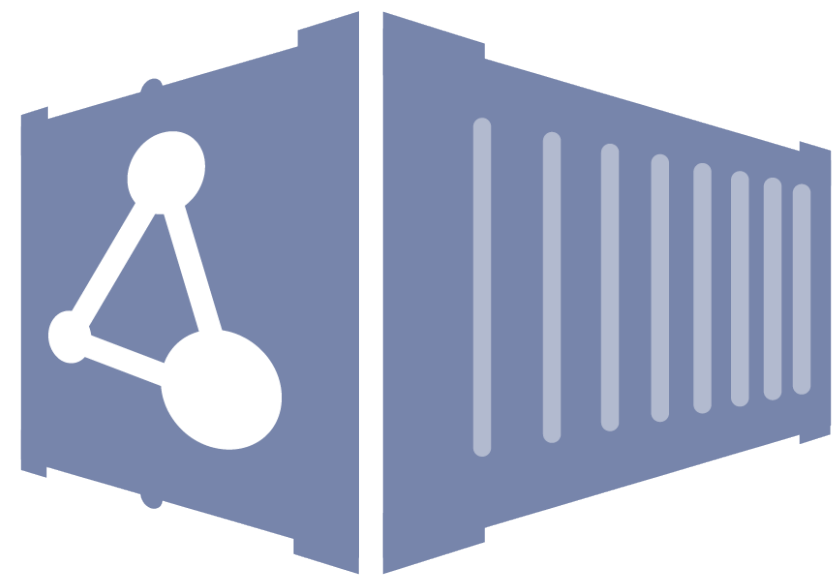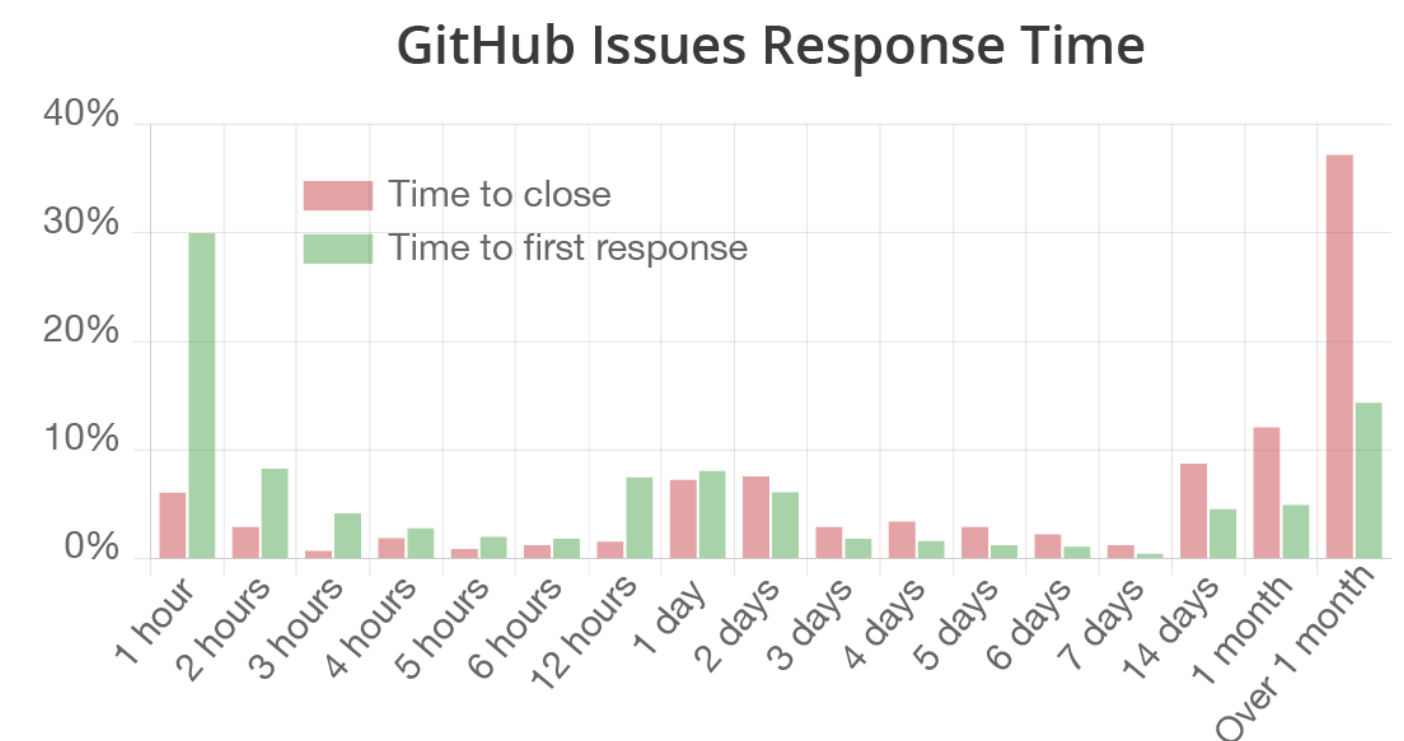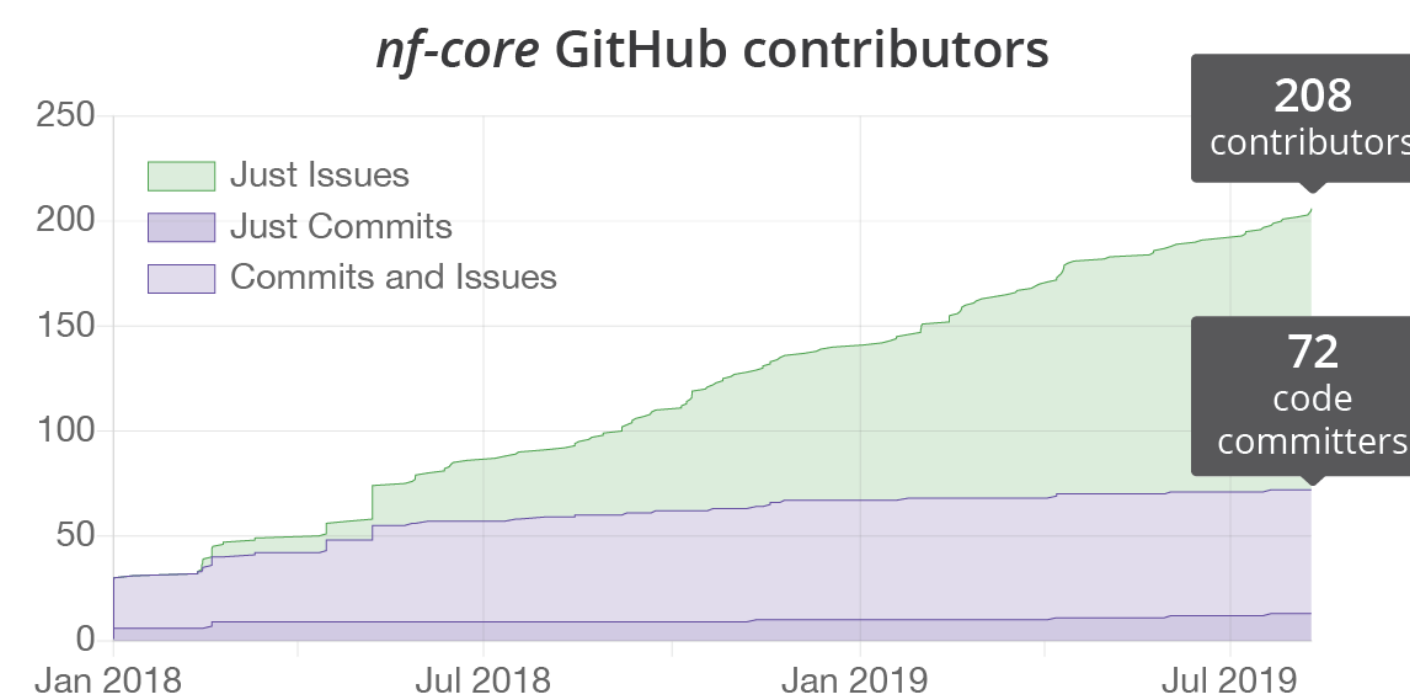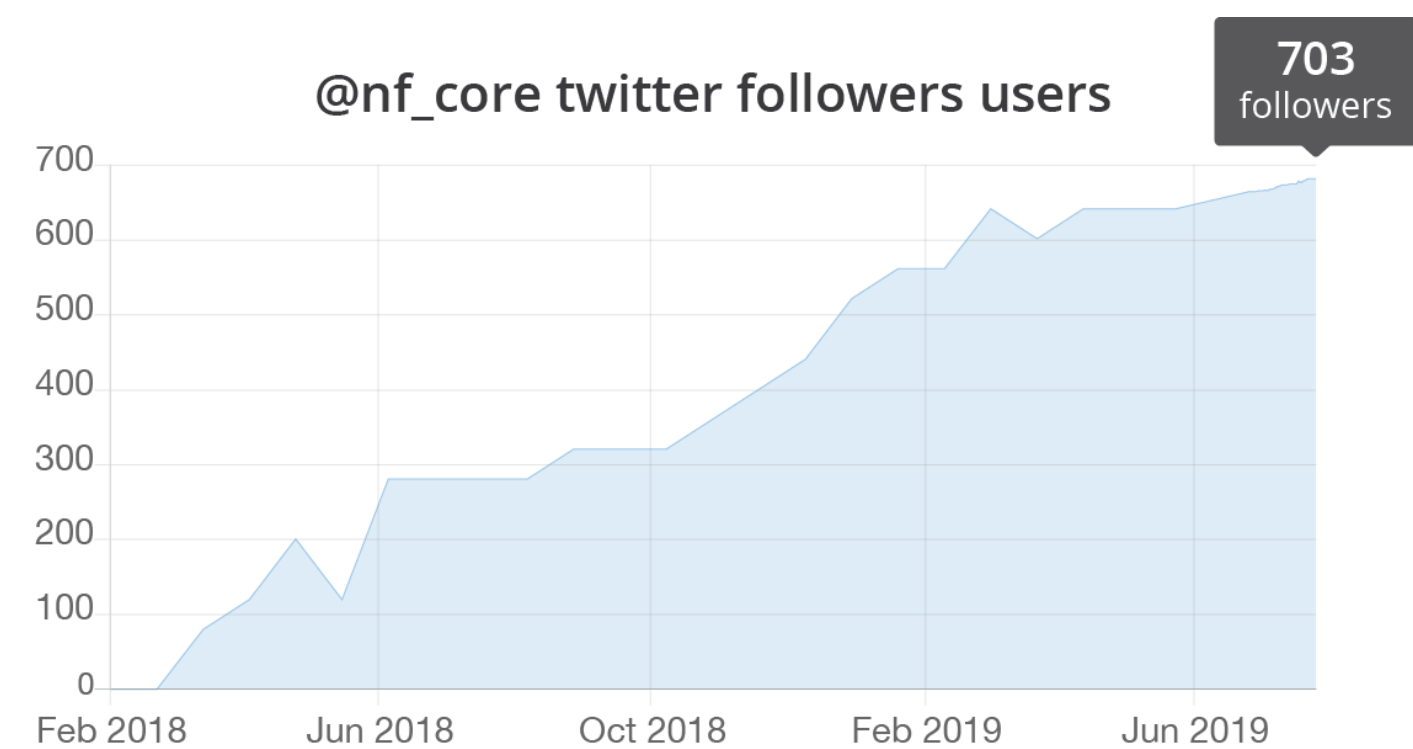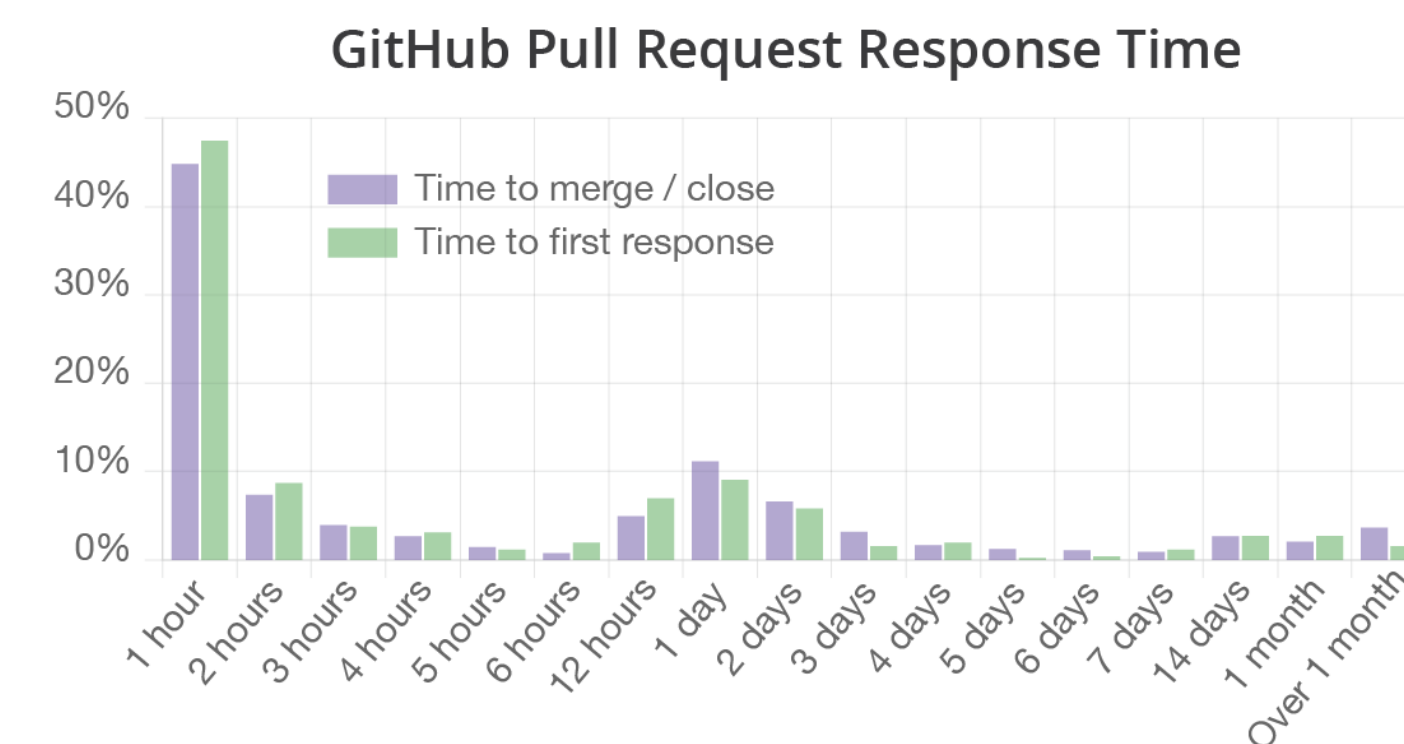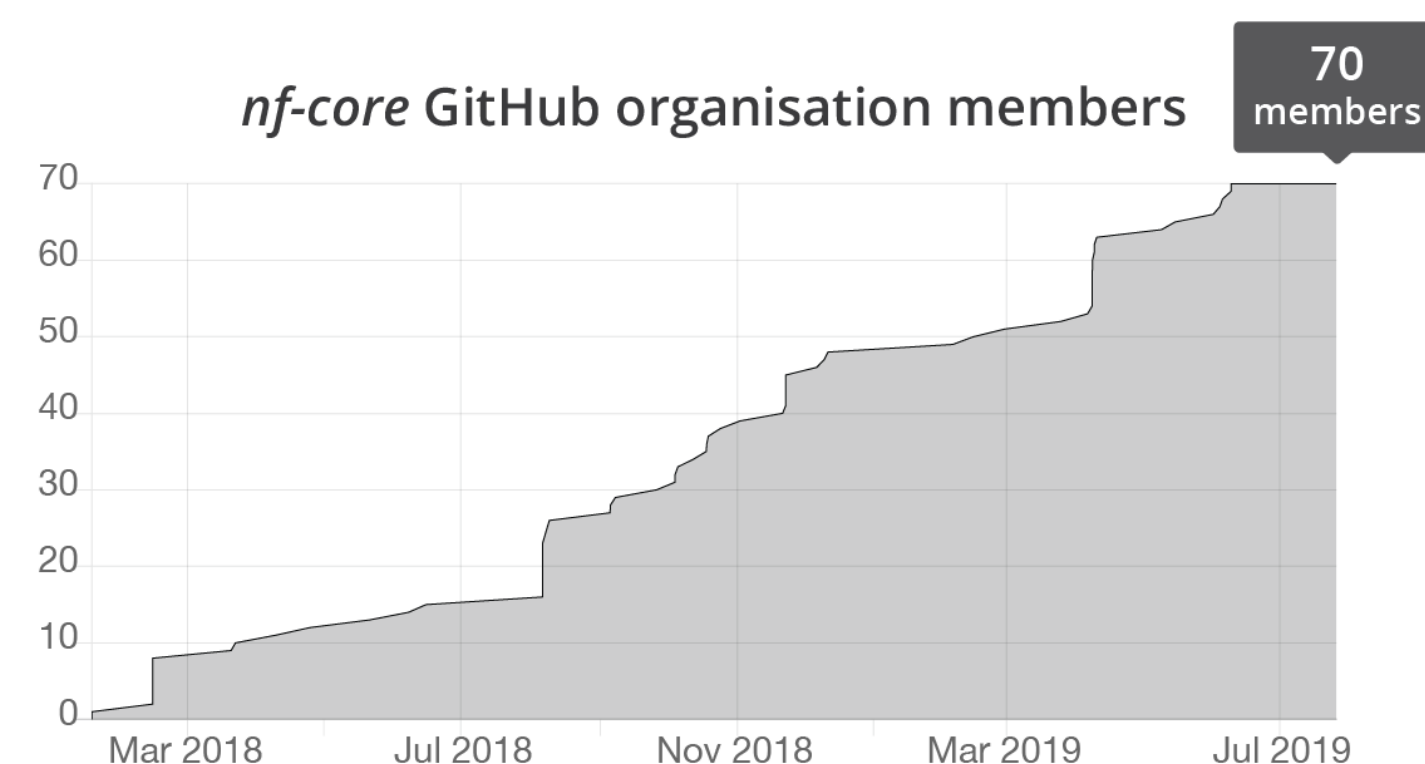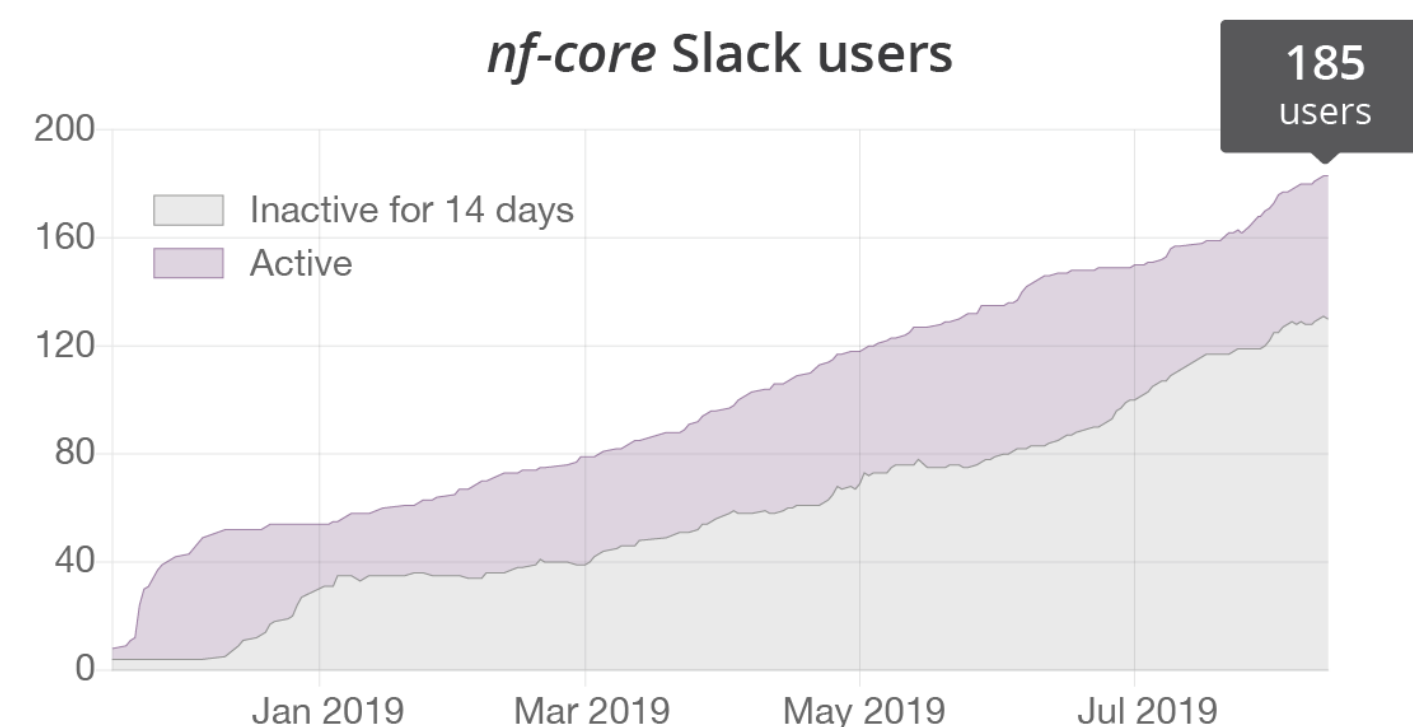
873 Slack users	**189** GitHub organisation members	**535** GitHub contributors	**1435** Twitter followers
56 Repositories	**1.37K** Pull Requests	**17.3K** Commits	**808** Issues
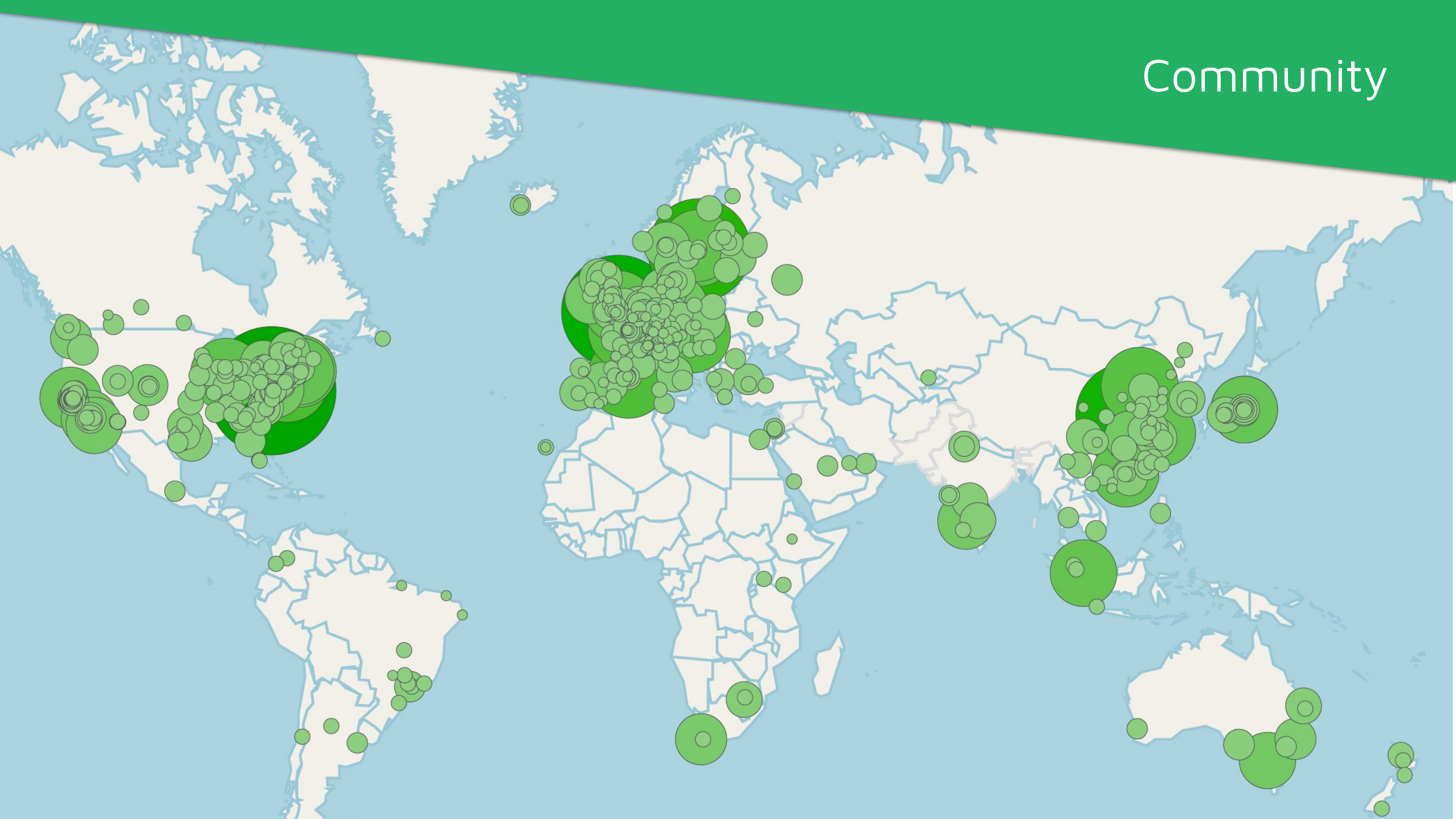
Step 1   Join the nf-core community

2

3

https://nf-co.re/join

Step 1   Join the nf-core community

2

3

#new-pipelines

1

Step 2 Create a pipeline from the template

3

nf-core create

```
    __  ___  ___  __  __  __  __  ___          ,--./,-.
   |  \ |   |   |  |  |__| |__| |__| |       /,-._.--~\
   |\ | |___ |   |  |  |  | |  | |  | |___     }  {
   |  \|                                     \`-._,-`-,
                                              `._,._,'

   nf-core/tools version 1.11.dev0




Workflow Name: demo
Description: A demo pipeline
Author: Phil Ewels
INFO      Creating new nf-core pipeline: nf-core/demo
INFO      Initialising pipeline git repository
INFO      Done. Remember to add a remote and push to GitHub:
           cd /Users/phil.ewels/GitHub/nf-core/tools/testing/nf-core-demo
           git remote add origin git@github.com:USERNAME/REPO_NAME.git
           git push --all origin
INFO      This will also push your newly created dev branch and the TEMPLATE branch for syncing.
INFO       !!!!!! IMPORTANT !!!!!!

          If you are interested in adding your pipeline to the nf-core community,
          PLEASE COME AND TALK TO US IN THE NF-CORE SLACK BEFORE WRITING ANY CODE!

          Please read: https://nf-co.re/developers/adding_pipelines#join-the-community
```

1

Step 2

3

1

Step 2

3

nf-core lint .

```
  __   __   __   __        ,--./,-.
 |  \ |  |_|  /  \ |__) |_       /,-._.--~\
 |\/| |  | |  \__/ |  \ |___     }  {
                              \`-._,-`-,
                               `._,._,'
```

nf-core/tools version 1.11.dev0

INFO   Testing pipeline: nf-core-demo/   lint.py:203

  [[!]] 32 Test Warnings

  https://nf-co.re/errors#5: GitHub Actions AWS full test should test full datasets: nf-core-demo/.github/workflows/awsfulltest…
  https://nf-co.re/errors#8: Conda package is not latest available: conda-forge::python=3.7.3, 3.8.5 available
  https://nf-co.re/errors#8: Conda package is not latest available: conda-forge::markdown=3.1.1, 3.2.2 available
  https://nf-co.re/errors#8: Conda package is not latest available: conda-forge::pymdown-extensions=6.0, 8.0 available
  https://nf-co.re/errors#8: Conda package is not latest available: conda-forge::pygments=2.5.2, 2.7.1 available
  https://nf-co.re/errors#8: Conda package is not latest available: bioconda::fastqc=0.11.8, 0.11.9 available
  https://nf-co.re/errors#8: Conda package is not latest available: bioconda::multiqc=1.7, 1.9 available
  https://nf-co.re/errors#10: TODO string found in environment.yml: Add required software dependencies here
  https://nf-co.re/errors#10: TODO string found in README.md: Update the example "typical command" below used to run the pipeli…
  https://nf-co.re/errors#10: TODO string found in README.md: Add a brief overview of what the pipeline does and how it works
  https://nf-co.re/errors#10: TODO string found in README.md: Add citation for pipeline after first release. Uncomment lines be…
  https://nf-co.re/errors#10: TODO string found in nextflow.config: Specify your pipeline's command line flags
  https://nf-co.re/errors#10: TODO string found in main.nf: Add to this help message with new command line parameters
  https://nf-co.re/errors#10: TODO string found in main.nf: Add any reference files that are needed
  https://nf-co.re/errors#10: TODO string found in main.nf: Report custom parameters here
  https://nf-co.re/errors#10: TODO string found in main.nf: Get all tools to print their version number here
  https://nf-co.re/errors#10: TODO string found in main.nf: Add in log files from your new processes for MultiQC to find!
  https://nf-co.re/errors#10: TODO string found in main.nf: Specify which MultiQC modules to use with -m for a faster run time
  https://nf-co.re/errors#10: TODO string found in main.nf: If not using MultiQC, strip out this code (including params.max_mul…
  https://nf-co.re/errors#10: TODO string found in scrape_software_versions.py: Add additional regexes for new tools in process…
  https://nf-co.re/errors#10: TODO string found in usage.md: Add documentation about anything specific to running your pipeline…
  https://nf-co.re/errors#10: TODO string found in output.md: Write this documentation describing your workflow's output

Adding a pipeline

Step 2

1

3

Adding a pipeline

✔ **nf-core**

sarek extra CI ∨
on: pull_request

1

3

✔ **Run nf-core lint**

```
1    ▶ Run nf-core lint ${GITHUB_WORKSPACE}
6
7                                      ,--./,-.
8        __   __   __   __            /,-._.--~\
9       |\ | |__  _ / ` / \ |__) |__)       } {
10      | \| |     \_, \_/ |   \ |___   \`-._,-`-,
11                                       `._,._,'
12
13   /opt/hostedtoolcache/Python/3.6.9/x64/lib/python3.6/site-packages/nf_core/lint.py:264: YAMLLoadWarning: calling yaml.load()
     without Loader=... is deprecated, as the default Loader is unsafe. Please read https://msg.pyyaml.org/load for full details.
14     self.conda_config = yaml.load(fh)
15   /opt/hostedtoolcache/Python/3.6.9/x64/lib/python3.6/site-packages/nf_core/lint.py:449: YAMLLoadWarning: calling yaml.load()
     without Loader=... is deprecated, as the default Loader is unsafe. Please read https://msg.pyyaml.org/load for full details.
16     ciconf = yaml.load(fh)
17
18   INFO: ===========
19    LINTING RESULTS
20   ================
21     88 tests passed   10 tests had warnings    0 tests failed
22
23   WARNING: Test Warnings:
24     http://nf-co.re/errors#4: Config variable not found: params.reads
25     http://nf-co.re/errors#4: Config variable not found: params.singleEnd
26     http://nf-co.re/errors#8: Conda package is not latest available: control-freec=11.4, 11.5 available
27     http://nf-co.re/errors#8: Conda package is not latest available: ensembl-vep=95.2, 97.3 available
28     http://nf-co.re/errors#8: Conda package is not latest available: freebayes=1.2.0, 1.3.1 available
29     http://nf-co.re/errors#8: Conda package is not latest available: gatk4=4.1.2.0, 4.1.3.0 available
```

✔ **Complete job**

Adding a pipeline

1

Step 2

3

Try to test GitHub comments on PR linting ✗ 6e60dfa

github-actions (bot) commented 22 days ago

`nf-core lint` **overall result: Failed** ❌

Posted for pipeline commit `6e60dfa`

```
+| ✅ 16 tests passed       |+
!| ❗  0 tests had warnings |!
-| ❌  1 tests failed       |-
```

▶ Details

ewels mentioned this pull request 22 days ago

PR auto-comment about lint warnings nf-core/tools#560

Closed

nf-core/ proteomicslfq

Proteomics label-free quantification (LFQ) analysis pipeline using OpenMS and MSstats, with feature quantification, feature summarization, quality control and group-based statistical analysis..

Julianus Pfeuffer, Lukas Heumos, Leon Bichmann, Timo Sachsenberg, Yasset Perez-Riverol.

>_ command

```
nextflow run nf-core/proteomicslf
```

↓ clones in last 11 months

2152

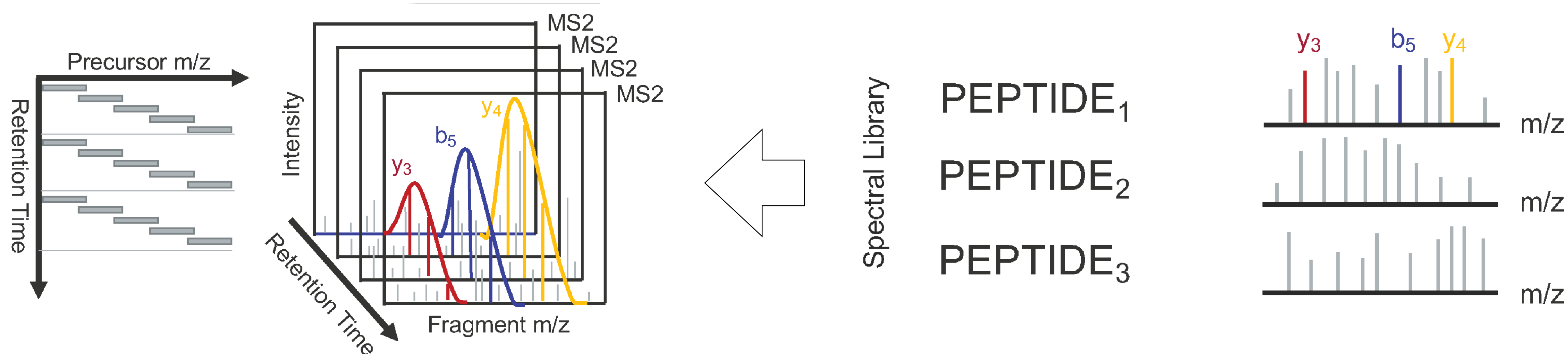| 8	12
Stars	Forks
325	6
Commits	Code contributors

https://nf-co.re/proteomicslfq/

nf-core/ diaproteomics

Automated quantitative analysis of DIA proteomics mass spectrometry measurements.

Leon Bichmann

https://nf-co.re/diaproteomics

nf-core/ mhcquant

Identify and quantify MHC eluted peptides from mass spectrometry raw data.

Pipeline for quantitative processing of data dependent (DDA) peptidomics data, specifically designed to analyse immunopeptidomics data, which deals with the analysis of affinity purified, unspecifically cleaved peptides that have recently been discussed intensively in the context of cancer vaccines.

Leon Bichmann, Lukas Heumos and Alexander Peltzer.

https://nf-co.re/mhcquant

nf-core/ ddamsproteomics

Quantitative shotgun MS proteomics.

Jorrit Boekel

https://nf-co.re/ddamsproteomics

Schema

[live demo]

nf-core/ modules

```
$ nf-core modules install fastqc
```

Copies module files in to pipeline

Metadata file tracks git hash of modules repo

CI linting checks files not edited
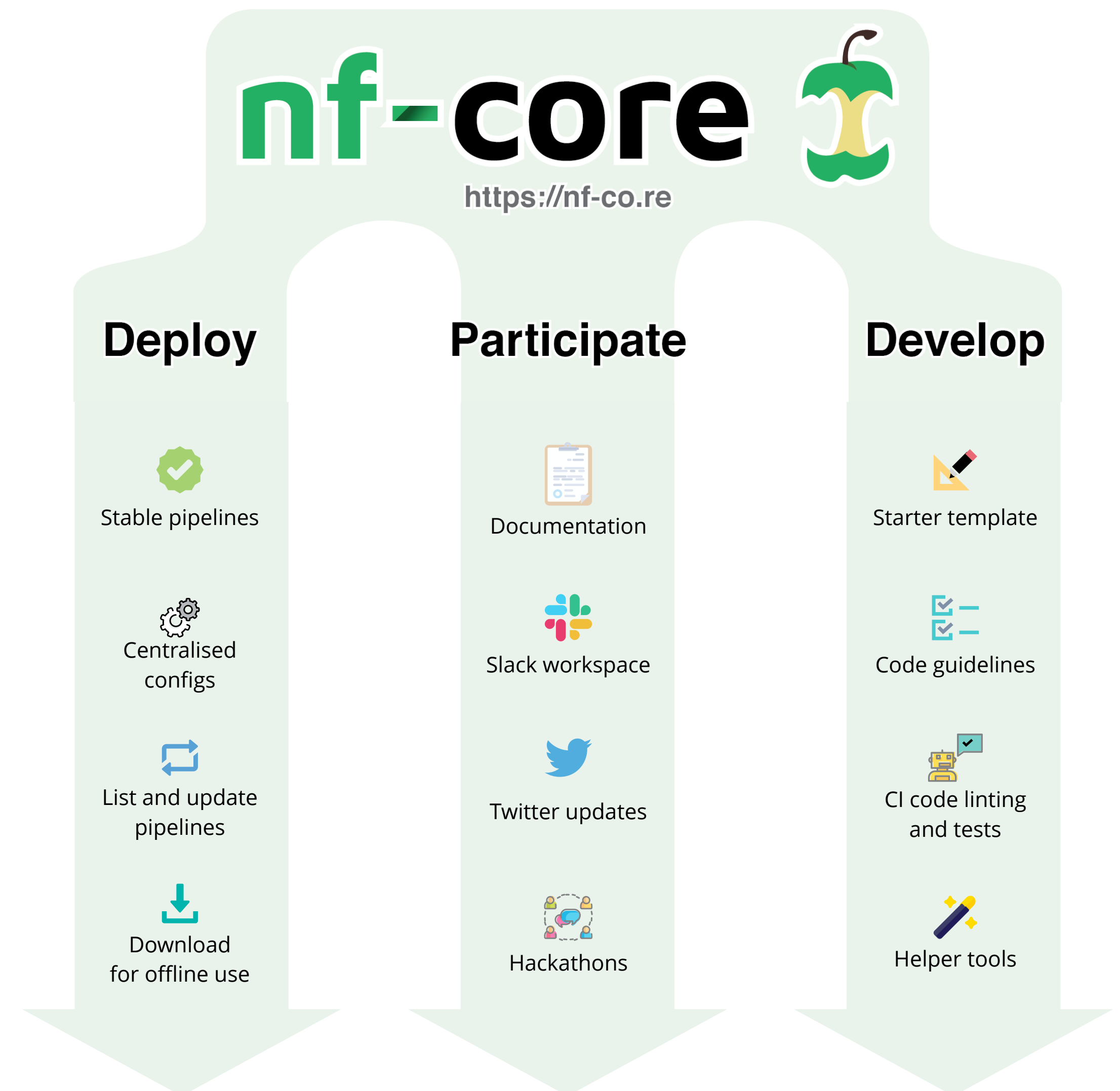
Update script pulls latest versions

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.

nf-core
https://nf-co.re

Deploy
- Stable pipelines
- Centralised configs
- List and update pipelines
- Download for offline use

Participate
- Documentation
- Slack workspace
- Twitter updates
- Hackathons

Develop
- Starter template
- Code guidelines
- CI code linting and tests
- Helper tools