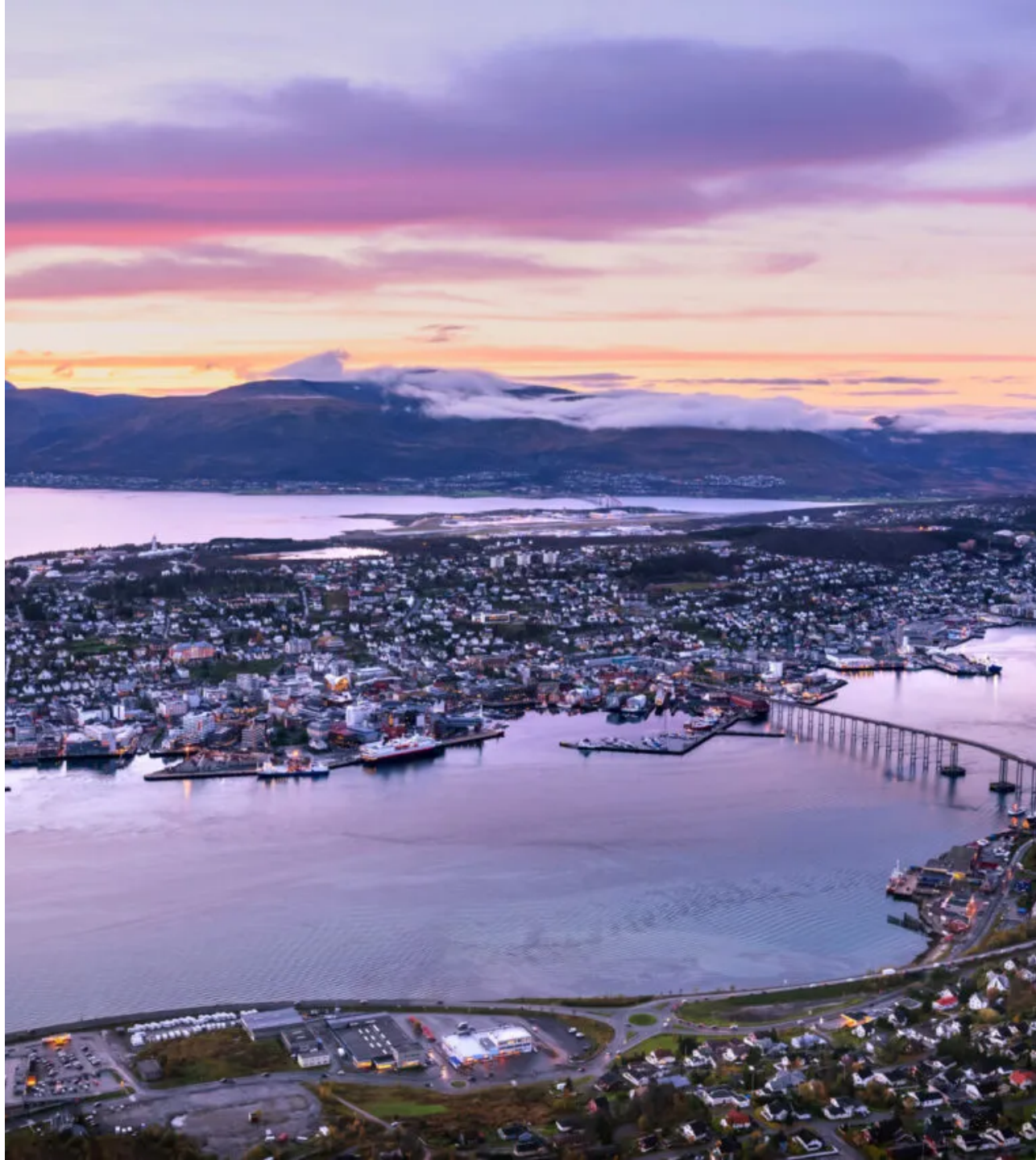
In-house development and collaboration in InPreD-Norge

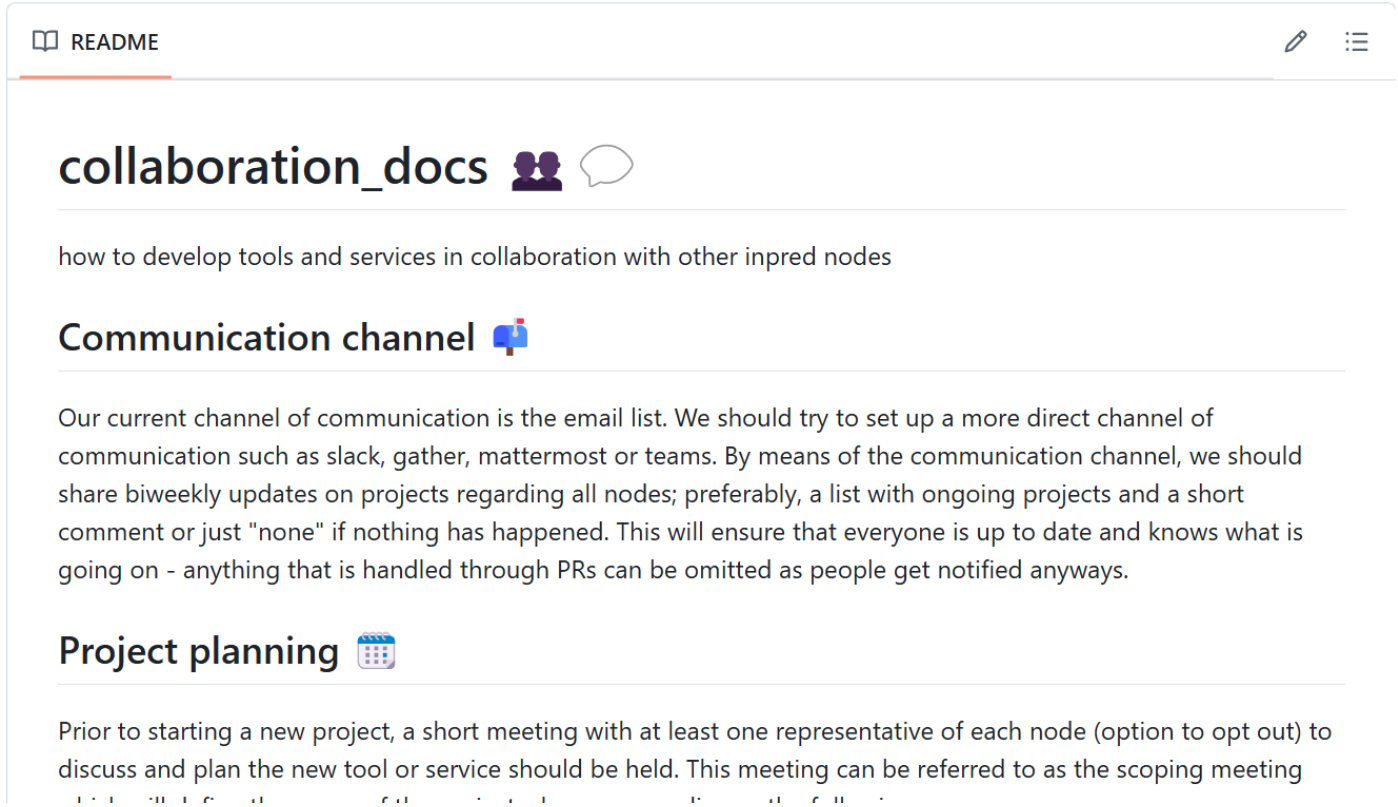
3rd Annual workshop on bioinformatics and variant interpretation in InPreD

https://inpred.github.io/25-06_bioinfo_ws/develop_and_collab



Overview

1. Communication channel
2. Project planning
3. Development
4. Issue and bug handling
5. New features



This is a **private repo** at https://github.com/InPreD/collaboration_docs

1. Communication channel

Current situation

- as of today we communicate mainly via email
- some communication via Teams (most of us are "external" lacking some important features features)
- discussions on GitHub via PRs
- we have monthly meetings for updates and discussions

1. Communication channel

Future plans

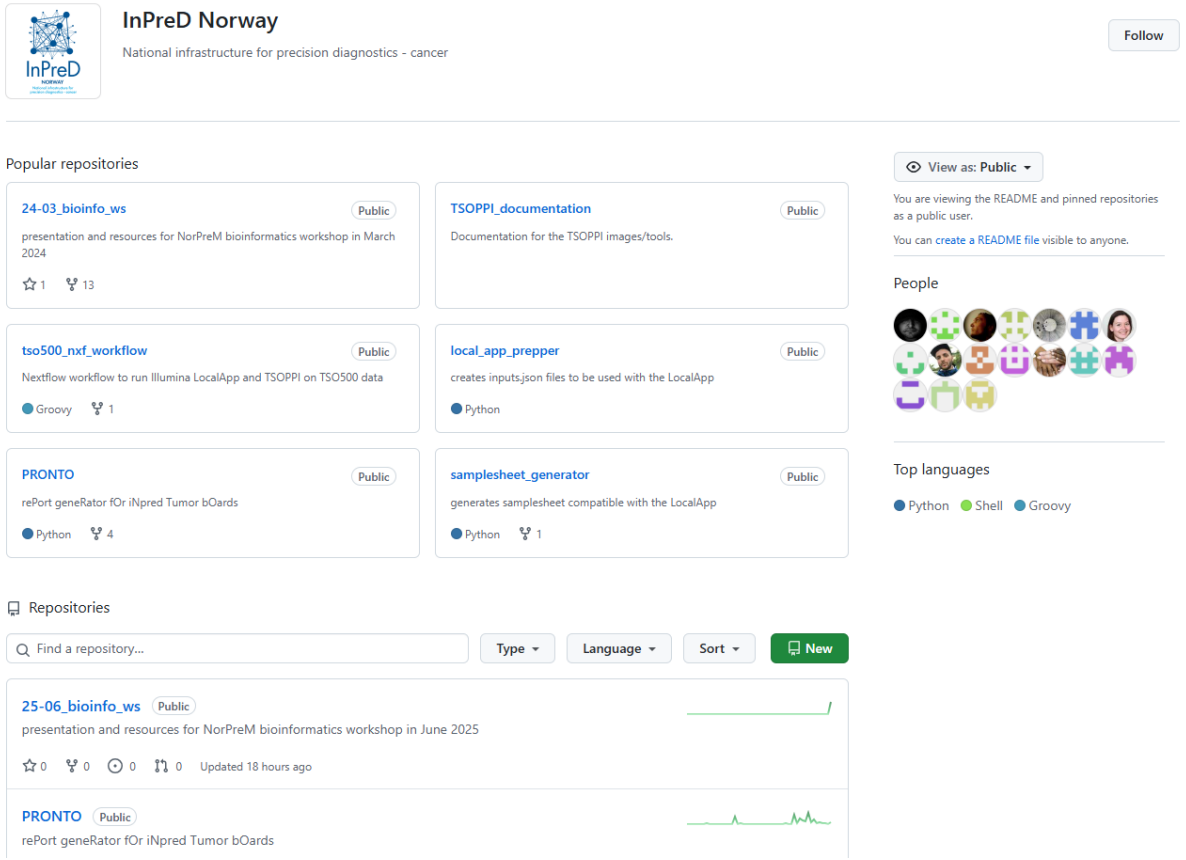
- requirements for platform/service for communication between nodes:
  - open source
  - easy and safe data sharing between nodes
  - free
  - self-hosted
- include bioinformaticians from clinical genetics departments (some of us are involved in CG already)
- currently, we are testing Zulip and Rocket.Chat
- biweekly updates from all nodes

2. Project Planning

- new projects should be started with a "scoping meeting" were at least one representative of each node
- the following should be discussed and agreed upon:
  - purpose
  - language (default: python)
  - interface (e.g. command line interface, web server)
  - data flow and storage (input and output location, database/filesystem)
  - involved collaborators (which nodes have resources to contribute)
  - deployment options (e.g. baremetal, docker/apptainer)
  - integration with existing projects
  - license (default: GNU AFFERO GENERAL PUBLIC LICENSE - Version 3)
  - intended timeline

3. Development

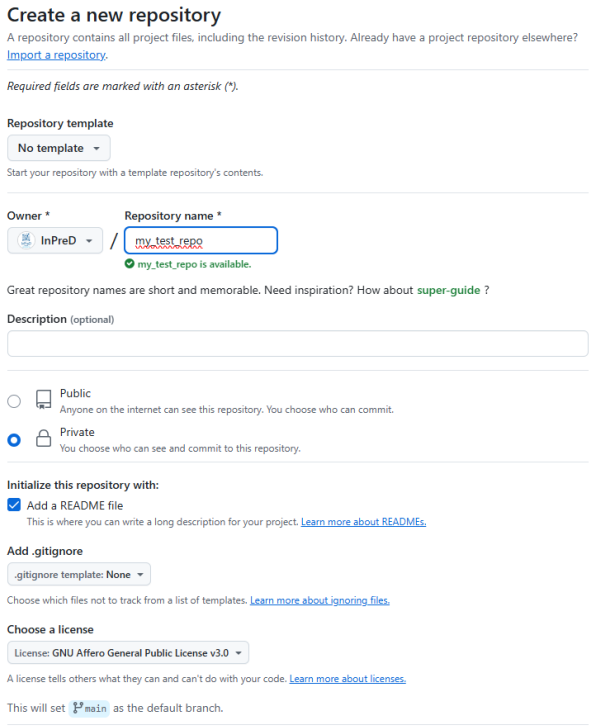
1. Code should be made available through InPreD group on GitHub



3. Development

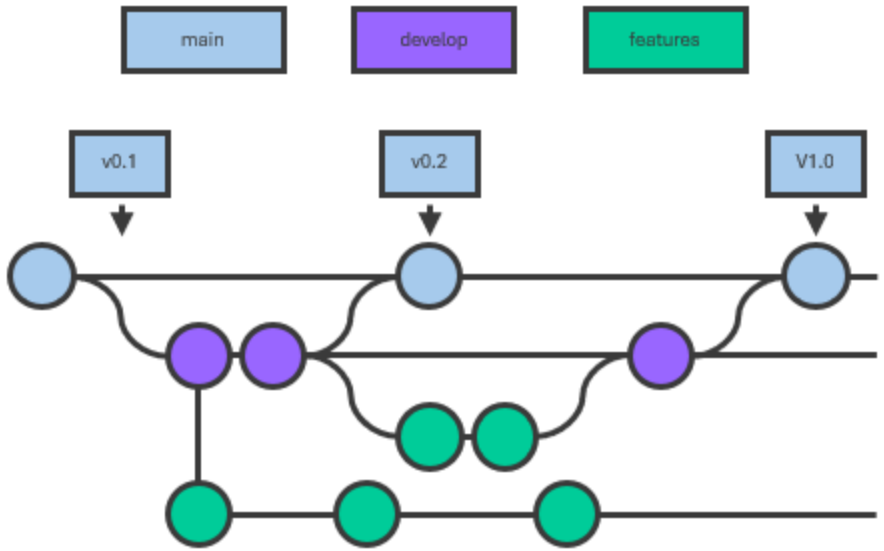
2. Start off by creating a repository with an empty README.md and LICENSE file

- clone it to your local environment and then start developing



3. Development

3. Use the agreed branching strategy (suggested: simplified Gitflow workflow)



3. Development

4. Commit and push changes early and often to allow others to follow along

```
marrip@hp06 ~/c/g/i/25-06_bioinfo_ws (main)> git add develop_and_collab/README.md
marrip@hp06 ~/c/g/i/25-06_bioinfo_ws (main)> git commit -m "docs: add slides to presentation"
[main 062d23d] docs: add slides to presentation
 1 file changed, 92 insertions(+), 4 deletions(-)
marrip@hp06 ~/c/g/i/25-06_bioinfo_ws (main)> git push
Enumerating objects: 11, done.
Counting objects: 100% (11/11), done.
Delta compression using up to 24 threads
Compressing objects: 100% (6/6), done.
Writing objects: 100% (7/7), 2.41 KiB | 2.41 MiB/s, done.
Total 7 (delta 1), reused 0 (delta 0), pack-reused 0
remote: Resolving deltas: 100% (1/1), done.
To https://github.com/InPreD/25-06_bioinfo_ws.git
   75f4de3..062d23d  main -> main
```

3. Development

5. Follow best practices for the selected programming language

- unit testing (cover test cases from different nodes)
- keeping functions short
- avoid hard-coding
- sensible use of packages and libraries

3. Development

6. Use git commit message conventions

- `feat`, `fix`, `ci`, `test`, `chore`, `docs`, `style`, `perf`, `build`, `refactor`

3. Development

7. Keep the features and PRs small (ideally one PR per feature) to have a tight feedback loop

- focus on one small problem for one feature
- include at least one representative from each node (option to opt out) and set a deadline (e.g. two weeks)

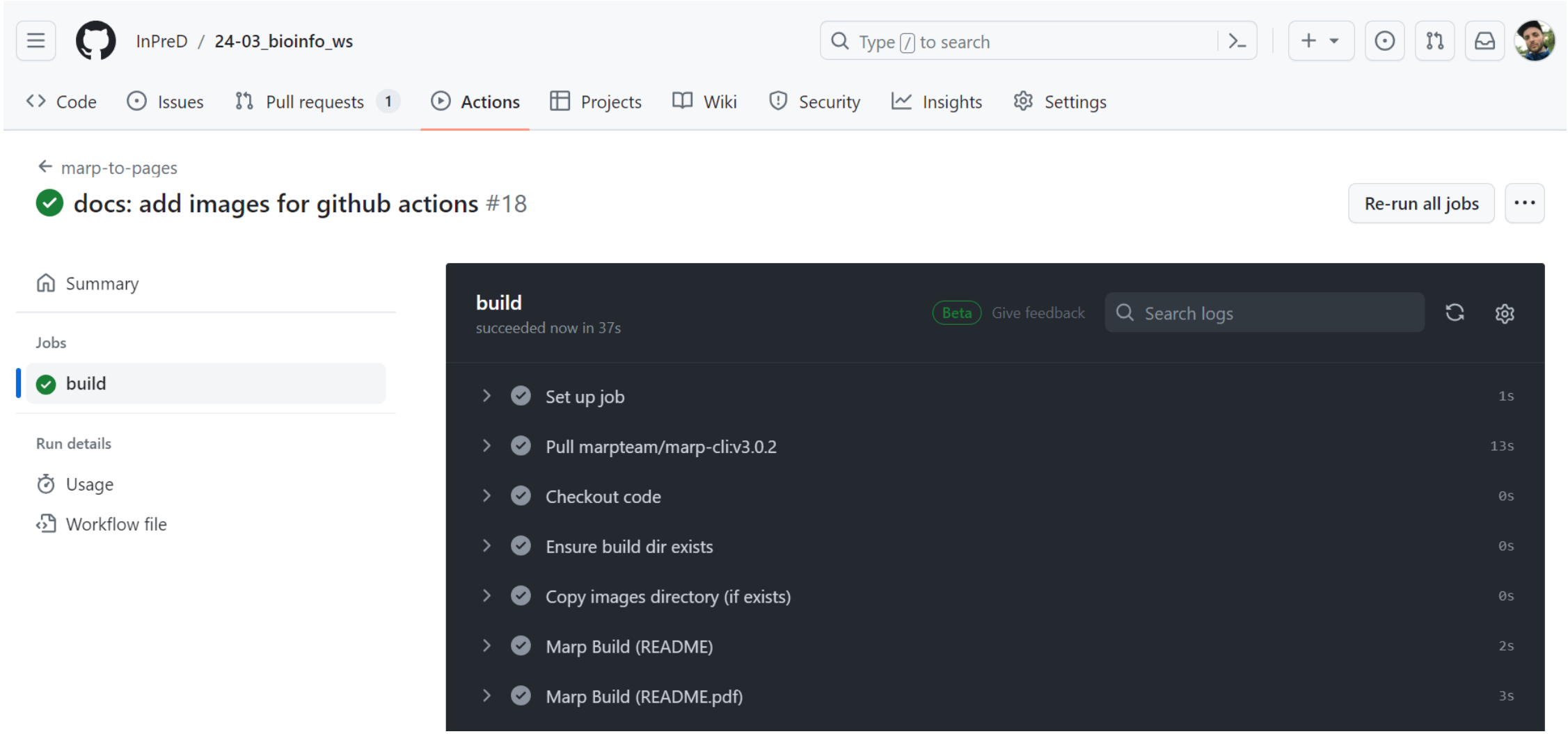
3. Development

8. Pair-programming should be used where it makes sense

- **pair-programming:** two programmers work together at one workstation; *driver* writes code while *observer/navigator* reviews each line of code as it is typed
- enable knowledge and expertise transfer between the different groups

3. Development

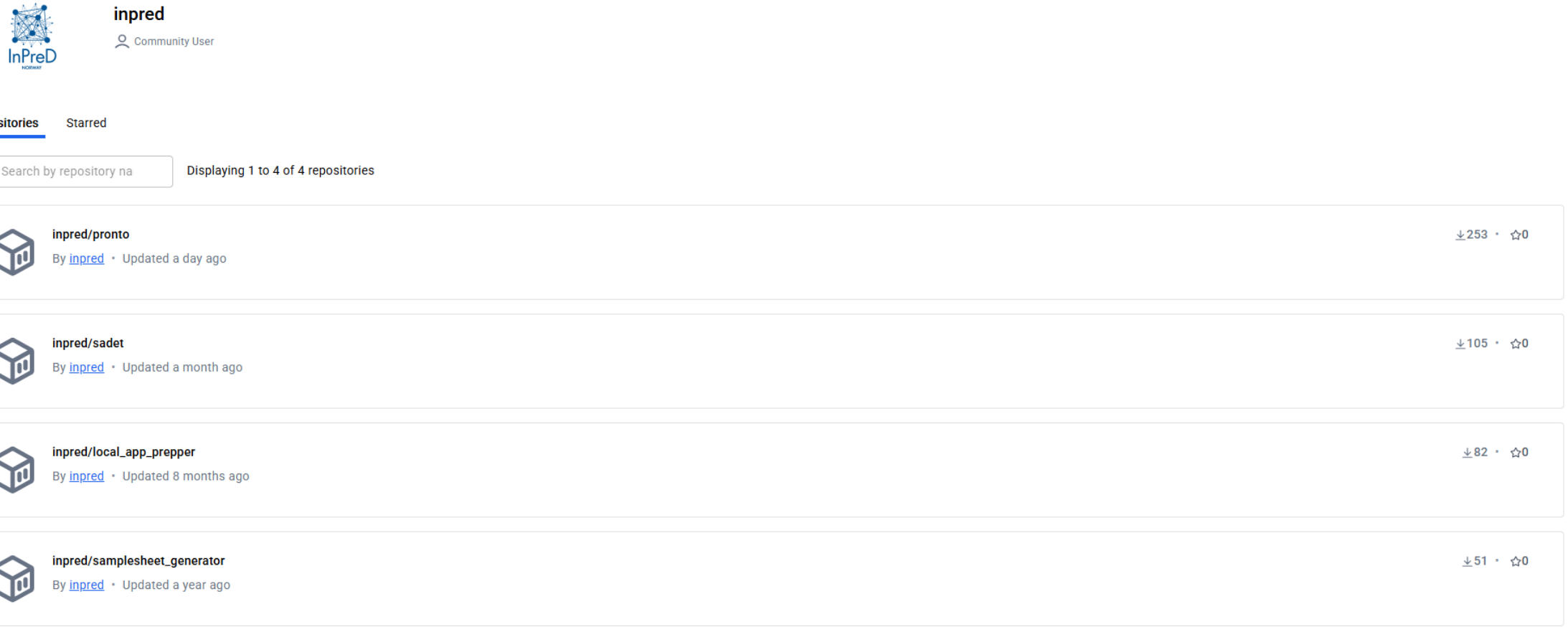
9. Use GitHub actions to test, lint and publish or build your project



3. Development

10. Provide at least a docker image (can be converted to apptainer)

- push them to the inpred group at docker hub



3. Development

11. Write documentation and check with others that it is understandable

3. Development

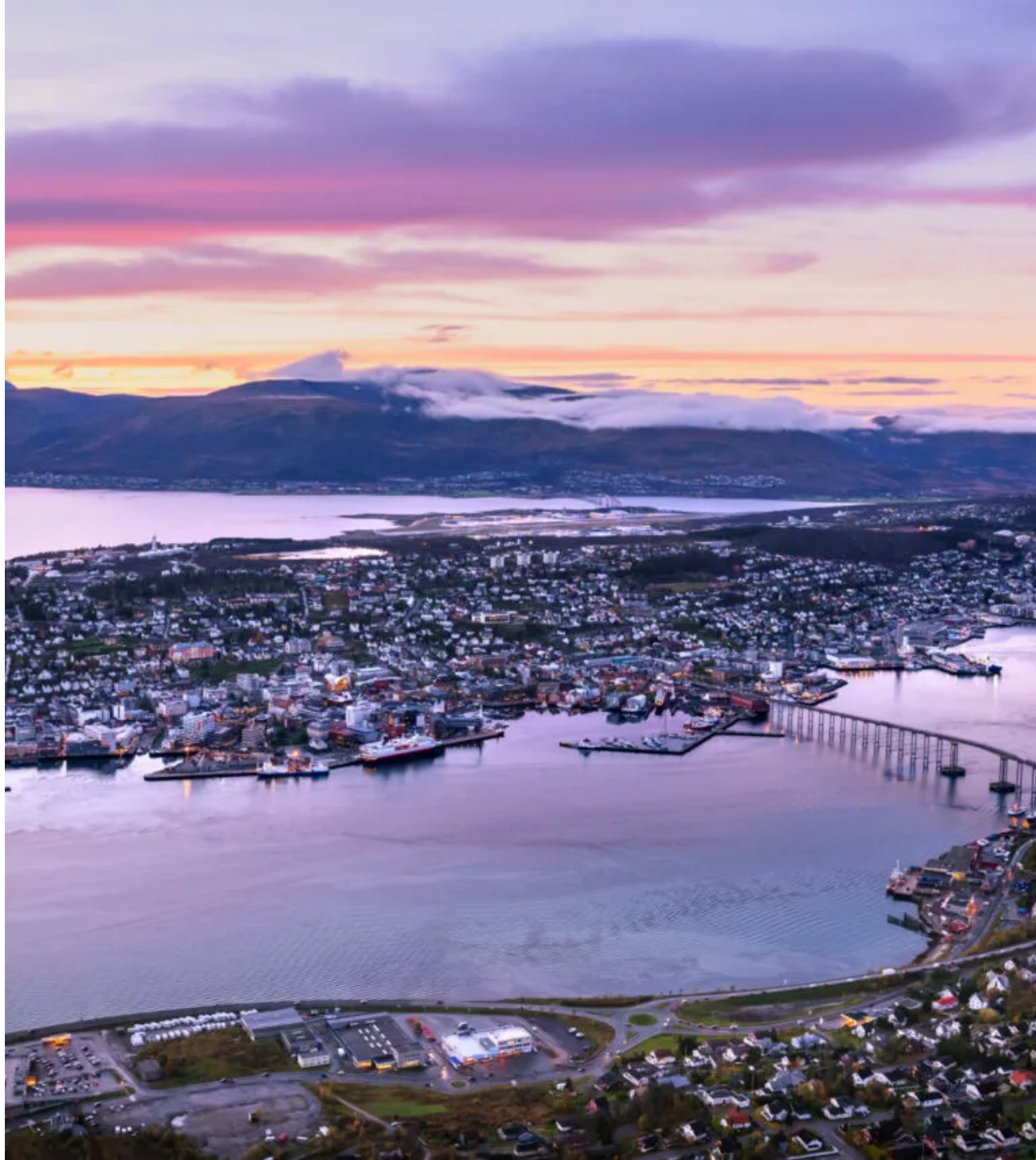
12. Tag and release code that is ready for production using semantic versioning

- `MAJOR`.`MINOR`.`PATCH`

4. Issue and bug handling

- report on GitHub and then handled there - discussion and code fixing tightly linked
- easier to find previous problems, share knowledge and track the development process

5. New features

- add as issues to the corresponding project
- discuss in the bioinformatics meetings or a small focus group meeting
- create a pull request from the issues and allow all nodes to give feedback on the implemented changes

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