

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

collaboration_docs 👥💬

how to develop tools and services in collaboration with other inpred nodes

Communication channel 🗣️

Our current channel of communication is the email list. We should try to set up a more direct channel of communication such as slack, gather, mattermost or teams. By means of the communication channel, we should share biweekly updates on projects regarding all nodes; preferably, a list with ongoing projects and a short comment or just "none" if nothing has happened. This will ensure that everyone is up to date and knows what is going on - anything that is handled through PRs can be omitted as people get notified anyways.

Project planning 📅

Prior to starting a new project, a short meeting with at least one representative of each node (option to opt out) to discuss and plan the new tool or service should be held. This meeting can be referred to as the scoping meeting

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" where 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



InPreD Norway
National infrastructure for precision diagnostics - cancer

Follow

Popular repositories

24-03_bioinfo_ws Public
presentation and resources for NorPreM bioinformatics workshop in March 2024
☆ 1 🍴 13

tso500_nxf_workflow Public
Nextflow workflow to run Illumina LocalApp and TSOPPI on TSO500 data
● Groovy 🍴 1

PRONTO Public
rePort geneRator fOr iNpred Tumor bOards
● Python 🍴 4

TSOPPI_documentation Public
Documentation for the TSOPPI images/tools.


local_app_prepper Public
creates inputs.json files to be used with the LocalApp
● Python

samplesheet_generator Public
generates samplesheet compatible with the LocalApp
● Python 🍴 1

View as: **Public**

You are viewing the README and pinned repositories as a public user.
You can [create a README file](#) visible to anyone.

People



Top languages

● Python ● Shell ● Groovy

Repositories

Type Language Sort New

25-06_bioinfo_ws Public
presentation and resources for NorPreM bioinformatics workshop in June 2025
☆ 0 🍴 0 🔄 0 📄 0 Updated 18 hours ago

PRONTO Public
rePort geneRator fOr iNpred Tumor bOards

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

Create a new repository

A repository contains all project files, including the revision history. Already have a project repository elsewhere? [Import a repository.](#)

Required fields are marked with an asterisk (*).

Repository template

No template ▾

Start your repository with a template repository's contents.

Owner *

 InPreD ▾

Repository name *

/ my_test_repo

🟢 my_test_repo is available.

Great repository names are short and memorable. Need inspiration? How about [super-guide](#) ?

Description (optional)

- ☐  Public
Anyone on the internet can see this repository. You choose who can commit.
- ☒  Private
You choose who can see and commit to this repository.

Initialize this repository with:

- ☒ Add a README file
This is where you can write a long description for your project. [Learn more about READMEs.](#)

Add .gitignore


.gitignore template: None ▾

Choose which files not to track from a list of templates. [Learn more about ignoring files.](#)

Choose a license

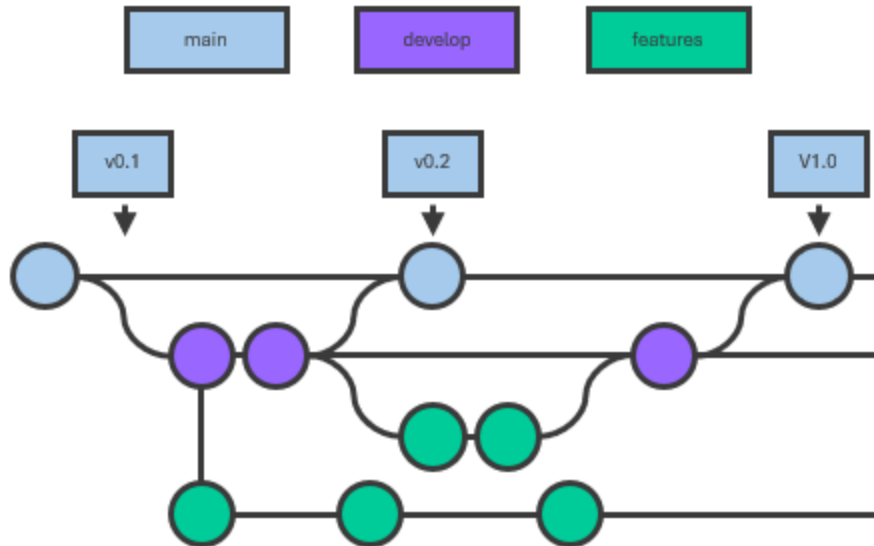
License: GNU Affero General Public License v3.0 ▾

A license tells others what they can and can't do with your code. [Learn more about licenses.](#)

This will set  main as the default branch.

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

- enable knowledge and expertise transfer between the different groups

3. Development

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

InPreD / 24-03_bioinfo_ws

Q

Type / to search

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<>

Code

Issues

Pull requests

1

Actions

Projects

Wiki

Security

Insights

Settings

← marp-to-pages

docs: add images for github actions #18

Re-run all jobs

...

Summary

Jobs

build

Run details

Usage

Workflow file

build

succeeded now in 37s

Beta

Give feedback

Search logs

↺

⚙

>

✓

Set up job

1s

>

✓

Pull marpteam/marp-cli:v3.0.2

13s

>

✓

Checkout code

0s

>

✓

Ensure build dir exists

0s

>

✓

Copy images directory (if exists)

0s

>

✓

Marp Build (README)

2s

>

✓


Marp Build (README.pdf)


3s

3. Development

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

- push them to the inpred group at docker hub




inpred
 Community User

Repositories


Starred

Displaying 1 to 4 of 4 repositories




inpred/pronto
By [inpred](#) · Updated a day ago

↓ 253 · ☆ 0




inpred/sadet
By [inpred](#) · Updated a month ago

↓ 105 · ☆ 0



inpred/local_app_prepper
By [inpred](#) · Updated 8 months ago

↓ 82 · ☆ 0



inpred/samplesheet_generator
By [inpred](#) · Updated a year ago

↓ 51 · ☆ 0

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

Takk for oppmerksomheten

