

# 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](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](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**

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You can [create a README file](#) visible to anyone.

People



Top languages

🍴 Python

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🍴 Groovy

Repositories

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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 ▾

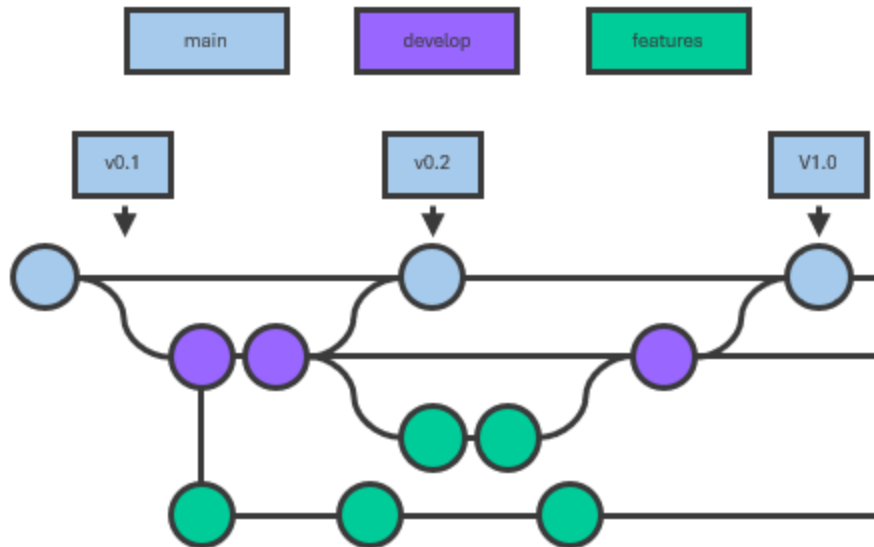
A license tells others what they can and can't do with your code. [Learn more about licenses.](#)

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

>\_

+ ▾

🕒

🔗

✉

<> 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

Beta Give feedback

Q Search logs

🔄

⚙

succeeded now in 37s

> ✅ 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




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By [inpred](#) · Updated a day ago

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↓ 105 · ☆ 0



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↓ 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

