

# Bioinformatics session

A two-day workshop for bioinformaticians and molecular biologists with focus on the TSO500 pipeline in InPreD

# Overview

1. Setup
2. Development & Collaboration
3. Nextflow
4. tso500\_nxf\_workflow
5. Python

# 1. Setup

# Create a GitHub account

- go to <https://github.com/> and click on `Sign up`



# Create a GitHub account

- enter your email

Welcome to GitHub!

Let's begin the adventure

**Enter your email\***

→ coder@inpred.no

Continue

## Create a GitHub account

- set a password

# **1. Setup**

**Be added to InPreD organisation at GitHub**

# 1. Resources

- [Getting started with your GitHub account](#)



## 2. Development & Collaboration

- short git introduction (basic git commands, optional)
- branching system (gitflow workflow)
- github actions (linting, testing, building)
- pull requests (best practice)
- release and semantic versioning
- licensing

## 3. Nextflow

- general (install, best practice)
- nf-core template
- stubbing

## 4. `tso500_nxf_workflow`

- status
- demonstration

## 5. Python

- general (best practice, cli)
- unit testing (pytest)

## Resources

- [Gitflow](#)
- [github actions](#)
- [nf-core](#)
- [pytest unittesting](#)
- [semantic versioning](#)