Bioinformatics session

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

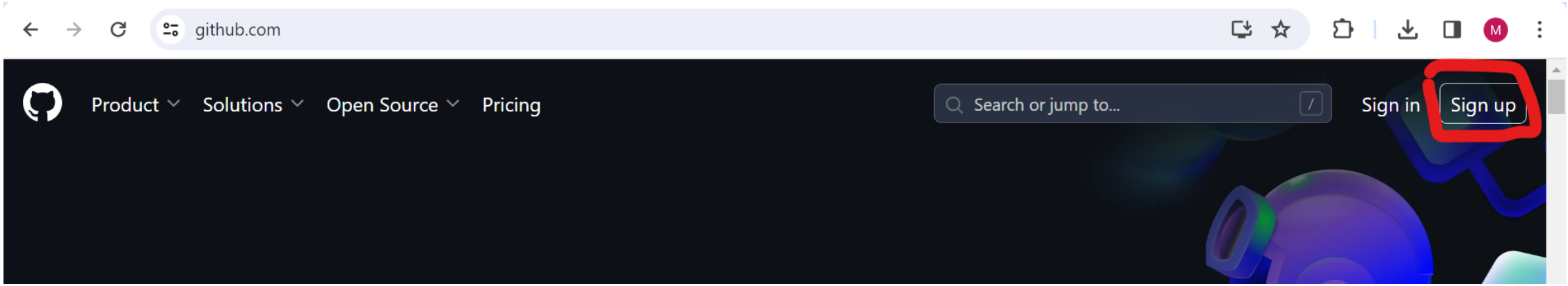
Overview

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`

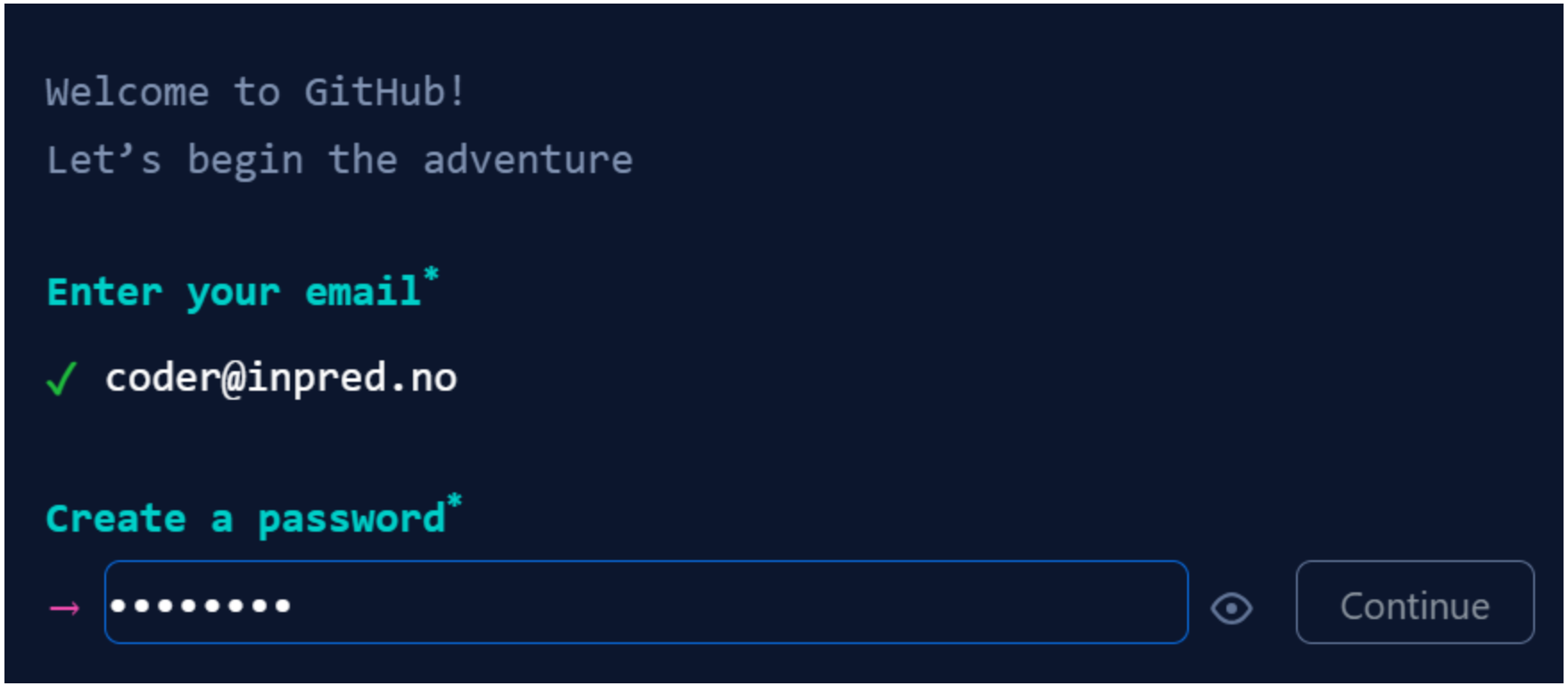


Create a GitHub account

- enter your email

Create a GitHub account

- set a password

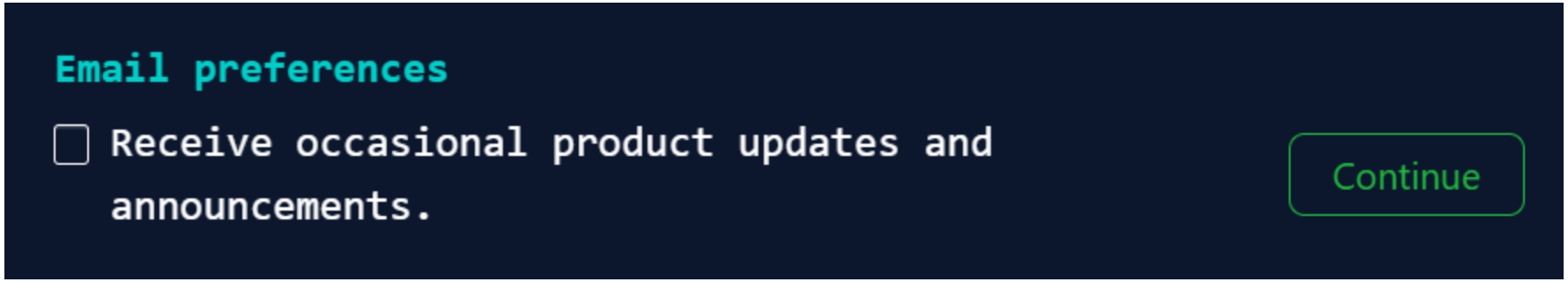


Create a GitHub account

- choose a username

Create a GitHub account

- choose email preferences



Create a GitHub account

- solve the puzzle

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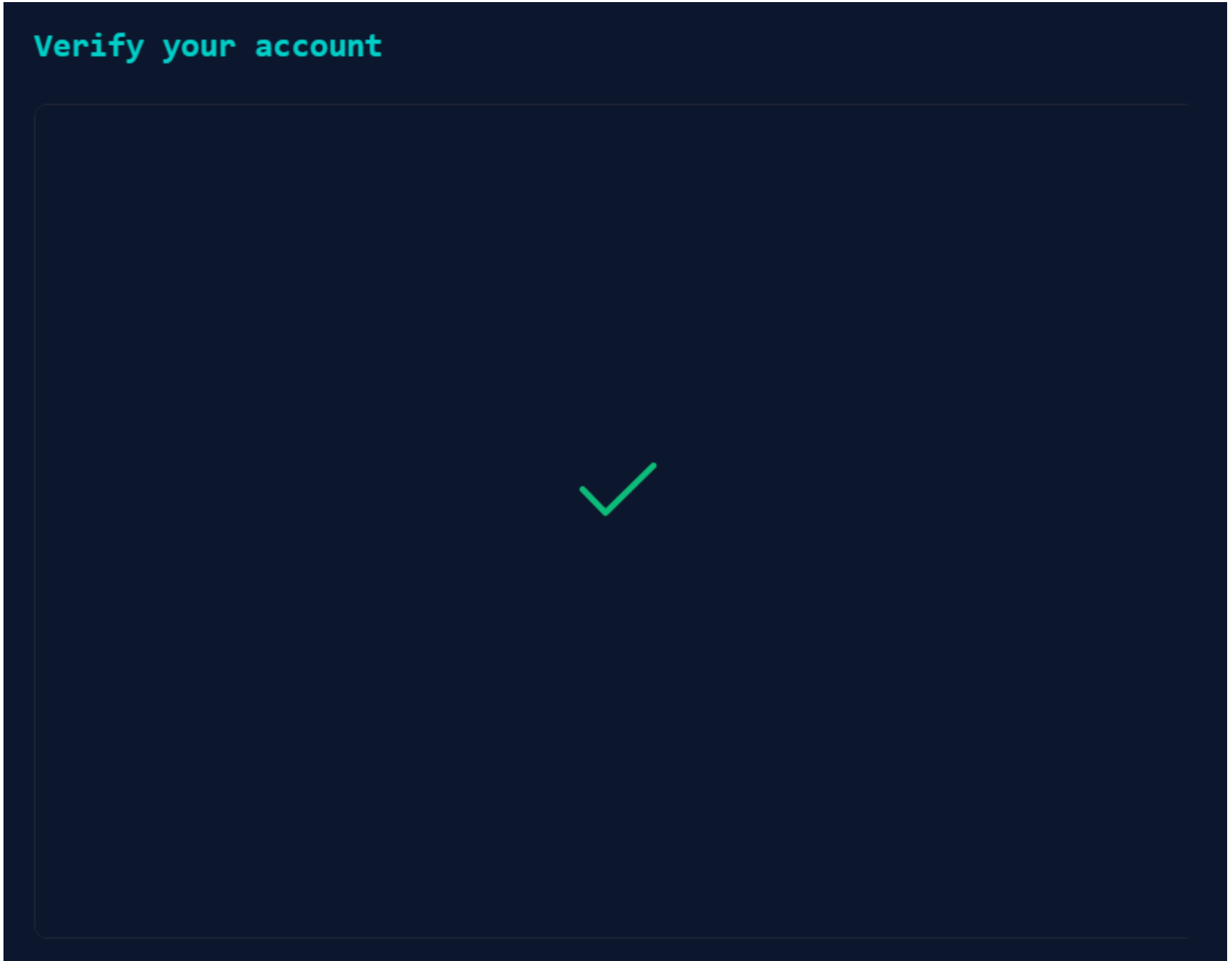
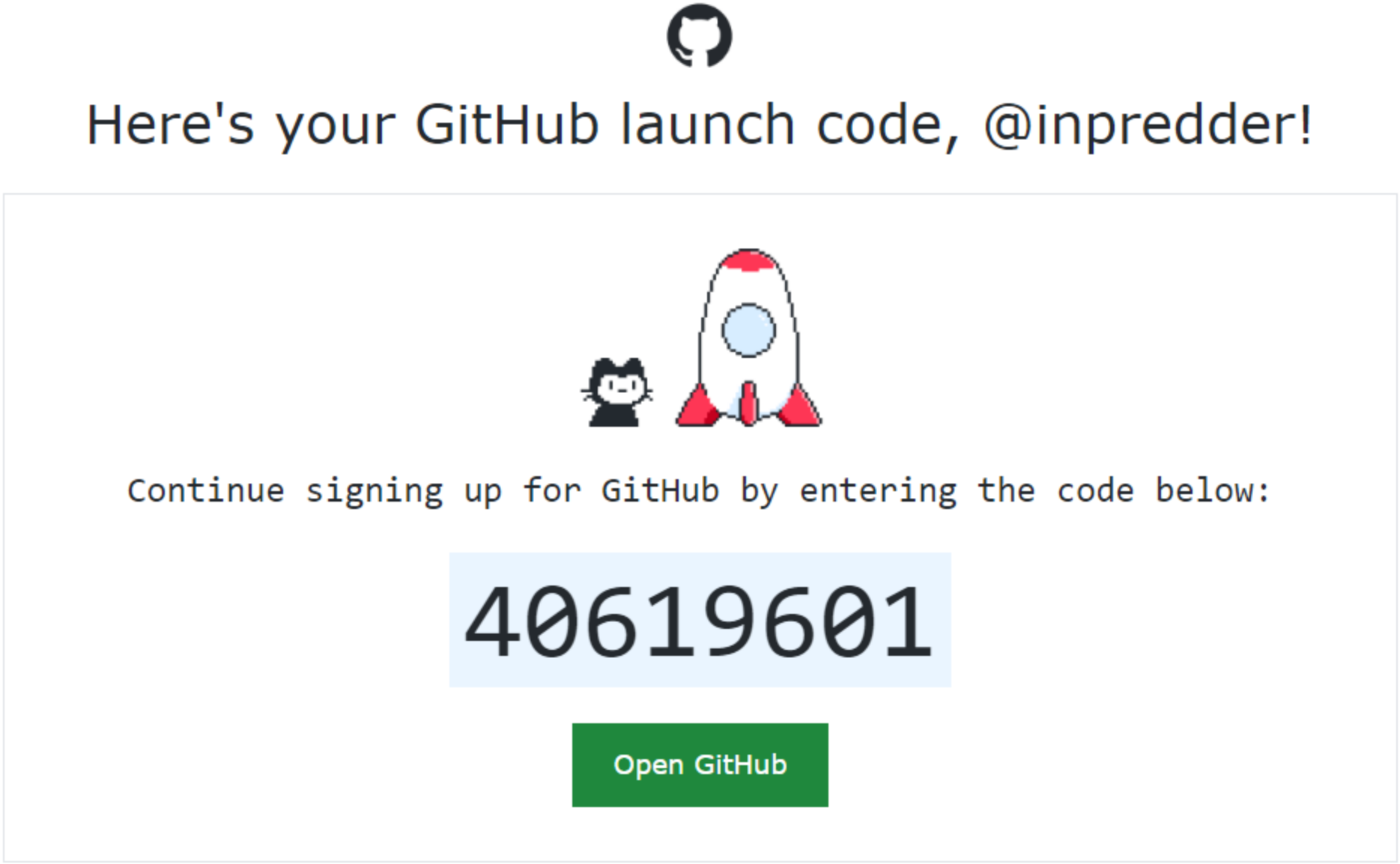
create your account



Create a GitHub account

- find the activation code in the email you received



Create a GitHub account

- select the desired options

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Free

- Unlimited public/private repositories
- 2,000 CI/CD minutes/month
  Free for public repositories
- 500MB of Packages storage
  Free for public repositories
- 120 core-hours of Codespaces compute
- 15GB of Codespaces storage
- Community support

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