



Omics Integration and Systems Biology Workshop

Oct 14 – 18, 2024

Rasool Saghaleyni, PhD

Bioinformatician National Bioinformatics Infrastructure Sweden (NBIS), Chalmers University

Consultations



Future compute infrastructure



Compute projects
Software and databases



Data publishing and open science
Secure sharing of sensitive data



Training



Efficient tools and workflows



Research support

- Drop-in sessions at all universities (now online) 14.00 Tuesdays
- Consultations
- Courses
- Support:
 - Long-term support (Peer reviewed)
 - Fee-for-service support, hourly fee
 - Partner projects
- Data management
- PhD advisory program

Training at NBIS



NBIS offers training and workshops within the area of bioinformatics. The training events are primarily for PhD students, postdocs, investigators and other researchers at Swedish universities, but also for industrial researchers in Sweden. There is a small fee for the participants.



We offer both introductory level training events as well as niched and advanced level training events within specialized research and/or technology areas.

Please note that NBIS training events do not provide any formal university credits. The training content is estimated to correspond to a certain number of credits; however, the estimated credits are just guidelines. If formal credits are important, you need to confer with your home department before submitting a course application to establish if the course is valid for formal credits or not.

Course Title	Dates	Deadline	Location
Introduction to Data Management Practices	2024-11-19 to 2024-11-21 (3 days)	Deadline 2024-10-13	Uppsala
Introduction to bioinformatics using NGS data	2024-11-25 to 2024-11-29 (5 days)	Deadline 2024-10-13	Linköping


► More info

Homepage  Apply 

Homepage  Apply 

See all future courses

See all previous courses

In addition, we offer PhD students a 2 year long mentoring program with a senior bioinformatician [Swedish Bioinformatics Advisory Program](#) .

NBIS is also offering Tailor-made training events – courses or workshops that are tailored to your specific needs, to the same price as fee based support.

For any questions related to the NBIS Training activities, please contact education@nbis.se for inquiries.

<http://www.nbis.se/>

OISB 2024 Teachers and TAs



Nikolay Oskolkov



Sergiu Netotea



Yuan Li



Rasool Saghaleyni

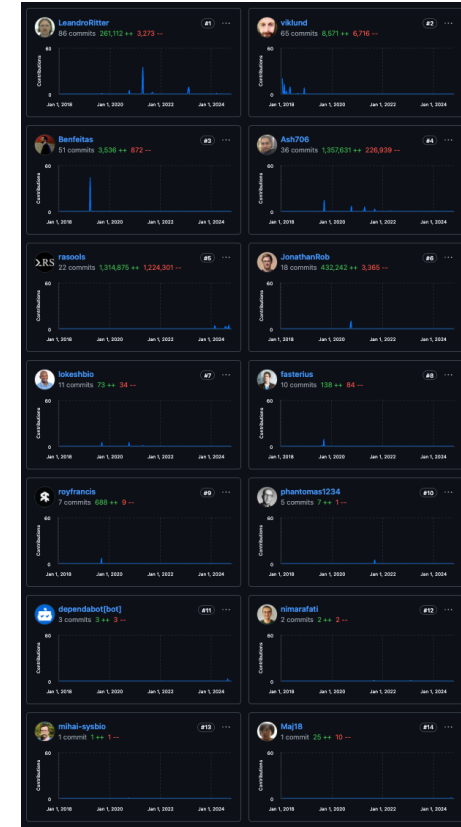


Stefan Ebmeyer



Jennifer Fransson

Contributors



For information about the course
please check the course website

Omics Integration and Systems Biology



Omics Integration and Systems Biology Workshop, 2024

[Github repository](#).

[Course canvas homepage](#).

Contact nikolay.oskolkov@scilifelab.se or rasool.saghaleyni@nbis.se for questions.

Course information can be found under the following pages:

- [Practical information](#)
- [Schedule](#)
- [Reading materials](#)
- [Pre-course preparation](#)
- [Invited speakers](#)
- [Contact](#)

https://nbisweden.github.io/workshop_omics_integration/

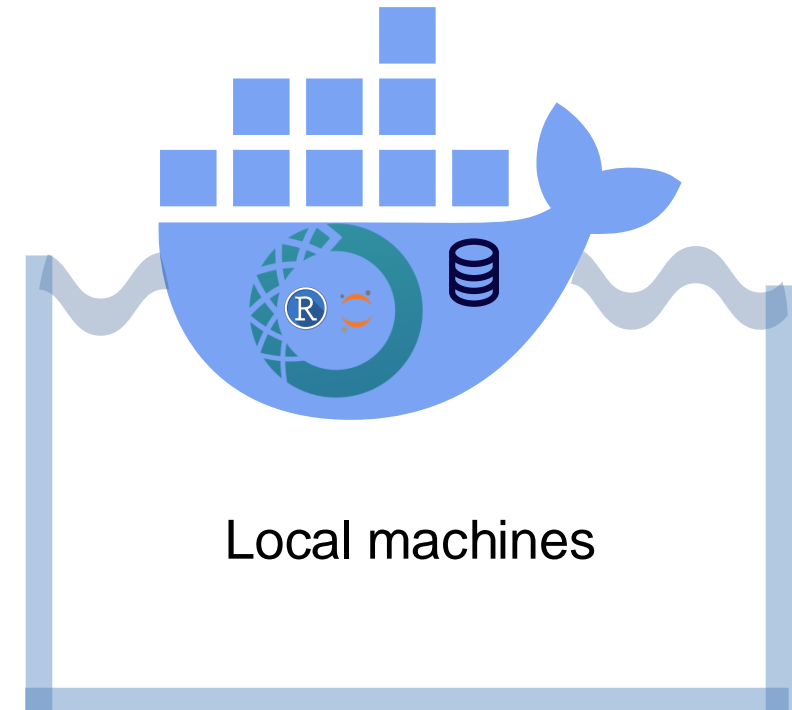
For communication during the course
please use the course slack



https://join.slack.com/t/omicsintegrat-ooou8386/shared_invite/zt-2qke3cai9-LyaWeaN8ZPB0q0cED~dmFQ



Plan B



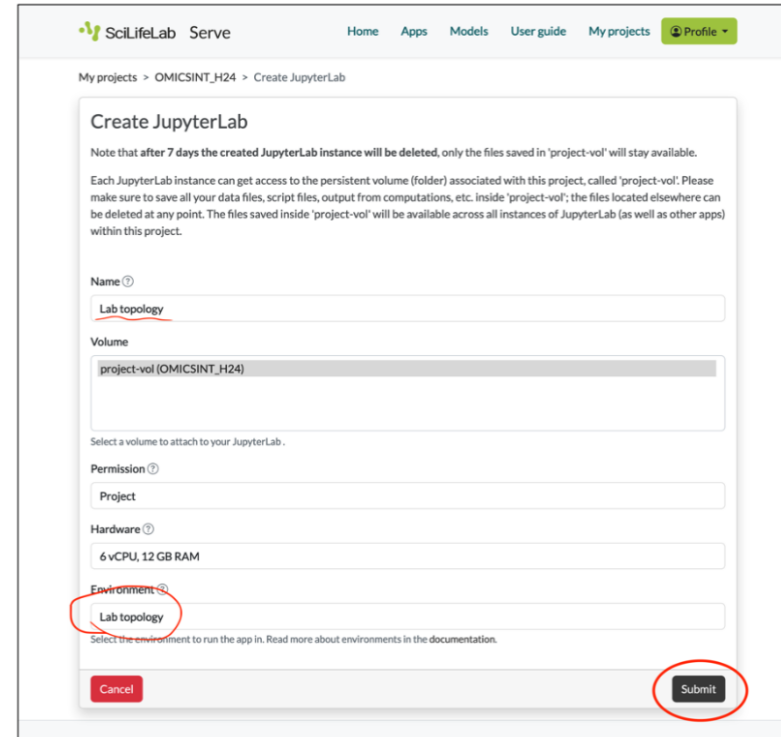
- 1- Go to <https://serve.scilifelab.se> and Log in with your account.
2. Go to *My projects* from the main menu. You should see a project called OMICSINT_H24 there. Click *Open*.



3. To launch a particular lab, you first need to know if it is a Jupyter or Rstud on the button *Create* under a corresponding lab type.



4. You will now see a form to create a lab. Under Name put the name of the lab, under Environment select the lab name. Leave the rest of the fields unchanged. Now lick Submit.



SciLifeLab Serve

Home Apps Models User guide My projects Profile

My projects > OMICSINT_H24 > Create JupyterLab

Create JupyterLab

Note that after 7 days the created JupyterLab instance will be deleted, only the files saved in 'project-vol' will stay available.

Each JupyterLab instance can get access to the persistent volume (folder) associated with this project, called 'project-vol'. Please make sure to save all your data files, script files, output from computations, etc. inside 'project-vol'; the files located elsewhere can be deleted at any point. The files saved inside 'project-vol' will be available across all instances of JupyterLab (as well as other apps) within this project.

Name ⓘ
Lab topology

Volume
project-vol (OMICSINT_H24)

Select a volume to attach to your JupyterLab.

Permission ⓘ
Project

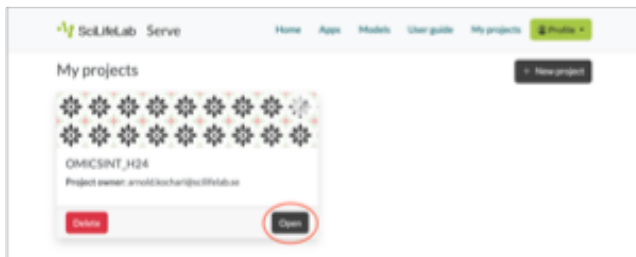
Hardware ⓘ
6 vCPU, 12 GB RAM

Environment ⓘ
Lab topology

Select the environment to run the app in. Read more about environments in the documentation.

Cancel Submit

- 1- Go to <https://serve.scilifelab.se> and Log in with your account.
2. Go to *My projects* from the main menu. You should see a project called OMICSINT_H24 there. Click *Open*.

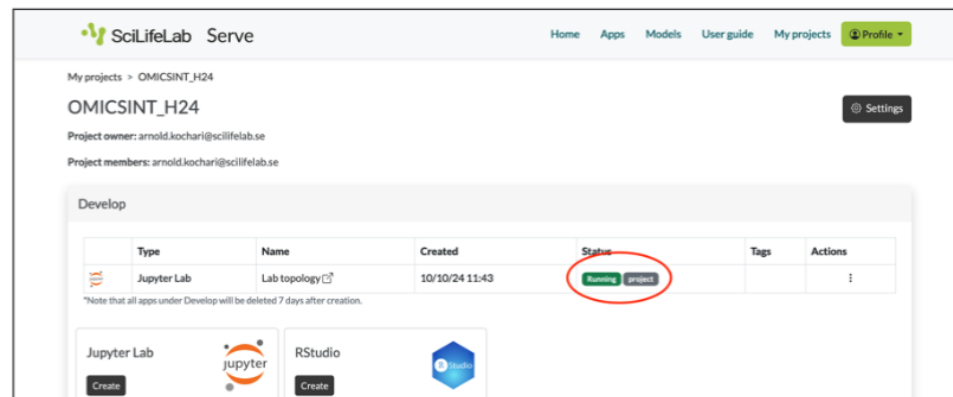


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4. You will now see a form to create a lab. Under Name put the name of the lab, under Environment select the lab name. Leave the rest of the fields unchanged. Now lick Submit.

5. The lab will now be created for you. Wait a few minutes to see the status "Running" in green. You can now click on the lab name and open the lab. If the status does not turn to "Running" within 5 minutes click on the three dots under Actions, click on "Delete". Wait a few minutes until you see the status "Deleted". Now you can refresh the page and start over.



All code for the exercises is available as R-markdown documents, or Jupyter notebooks, in the GitHub repo :

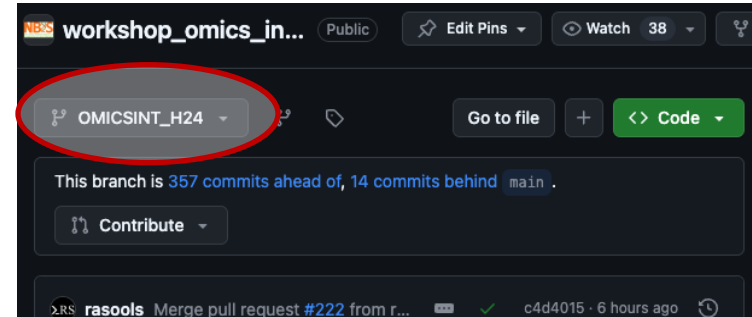
https://github.com/NBISweden/workshop_omics_integration/tree/OMICSINT_H24

Please report to us if you find any errors in the code!

- Slack channel **#exercises**

- An Issue on the GitHub repo:

https://github.com/NBISweden/workshop_omics_integration/issues



We may find bugs and update the code – in that case, update your git repo with command:

```
git pull
```

Slack channel: **#exercises**

It is important that you learn how to troubleshoot:

- Look at your error messages, perhaps the answer is there?
- If not – Google is your best friend! Forums like Seqanswers, Stackexchange, Bioconductor support forum, specific forums (or Github issues) for each package may have the answer.
- **Ask for help** from your colleague in the room
- **Be kind and help** if your colleague in need or ask for assistance
- If the question persists, ask for help in the room

Instructors are here to answer any questions and give suggestions, but we may not always have the answer.

Daniel Muthas



Head of Data Science & Bioinformatics at AstraZeneca

Talk Title: *Deriving actionable insight from omics data – an industry perspective*

Time: October 15, 10:00 – 11:15 CET onsite and online on zoom

Onsite and broadcasting

https://nbisweden.github.io/workshop_omics_integration/invited_speakers.html

Johan Gustafsson



Postdoctoral Fellow, Broad institute, USA

Talk Title: *Generation of context-specific genome-scale metabolic models using single-cell RNA-Seq data*

Time: October 17, 13:00 – 14:15 CET online on zoom

Mats Nilsson



Professor of Biochemistry at Stockholm University, Head of In Situ Sequencing unit Spatial Biology platform Scilife Lab

Talk Title: *Targeted in situ sequencing for characterization of the genetic, molecular and cellular diversity of healthy and disease tissues*

Time: October 18, 10:00 – 11:00 CET online, only for course participants

Please ask questions!

