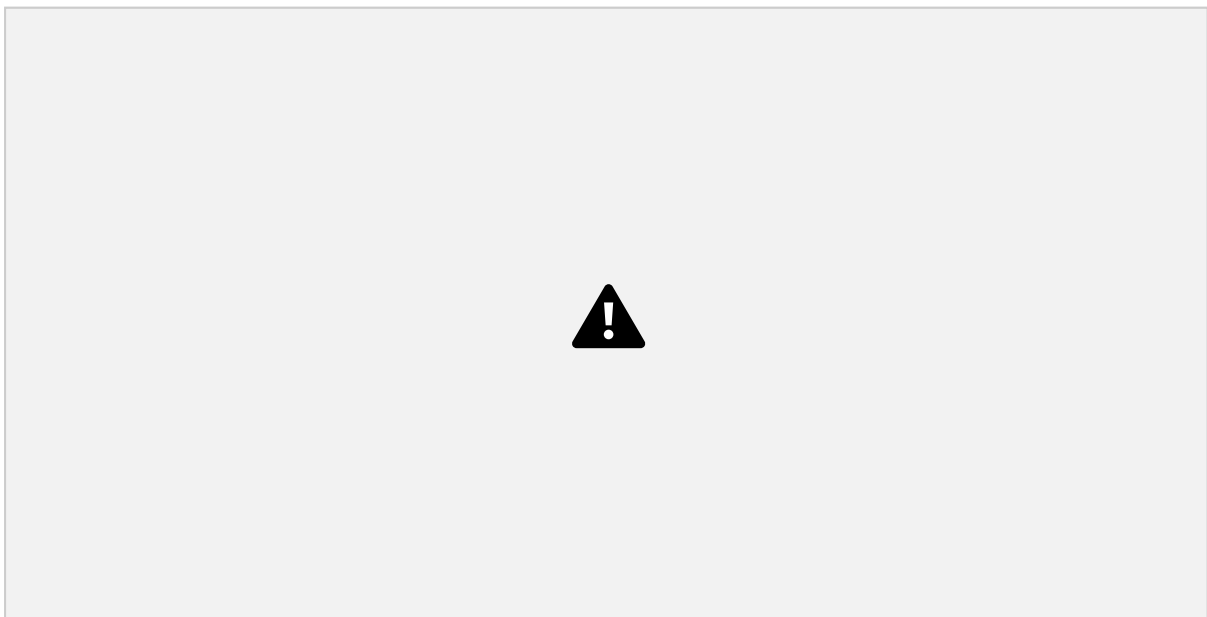


## SaxoCellOmics Galaxy Server

### What is it?

Galaxy is an open-source, web-based platform for omics data-intensive biomedical research. You can use bioinformatics (and other) tools and workflows with a graphical user interface. Galaxy enables non-tech-savvy users to run tools without coding.

At SaxoCellOmics we set up the Galaxy platform on our own servers to ensure data protection and privacy.



### Why should I use it?

- Offers reproducible workflows for Omics-data processing and analyses
- Easy to use, even for non-tech-savvy users
- Secured server inside the virtual private network of the Leipzig University
- Data and analysis on Leipzig University resources and not on commercial servers

### How do I get started?

- Please send an e-mail with the following information to:  
[gitmail+joas-galaxy-sandbox-5419-issue-@informatik.uni-leipzig.de](mailto:gitmail+joas-galaxy-sandbox-5419-issue-@informatik.uni-leipzig.de) (yes, this is a valid email address):
  - Do you have a URZ (Uni Leipzig Rechenzentrum) account?
  - Do you have the Uni Leipzig VPN installed?



- Are you interested in an onboarding call?
- After setting URZ access:
  - Now you can access the [Website](#) (when connected with VPN)
  - Now you need to register an account. Here you need to provide an email address, username, and password.
  - The Galaxy [training network](#) offers a plethora of useful tutorials.

## What's planned next?

We will test and optimize our server in Q1-Q4 as a development server. Therefore, we encourage SaxoCell partners to contact us and use the development server.

Depending on how fast we find enough test users, we will start our production server earliest in Q4 2023.

## FAQs

### **Which data sizes can the Galaxy Server handle?**

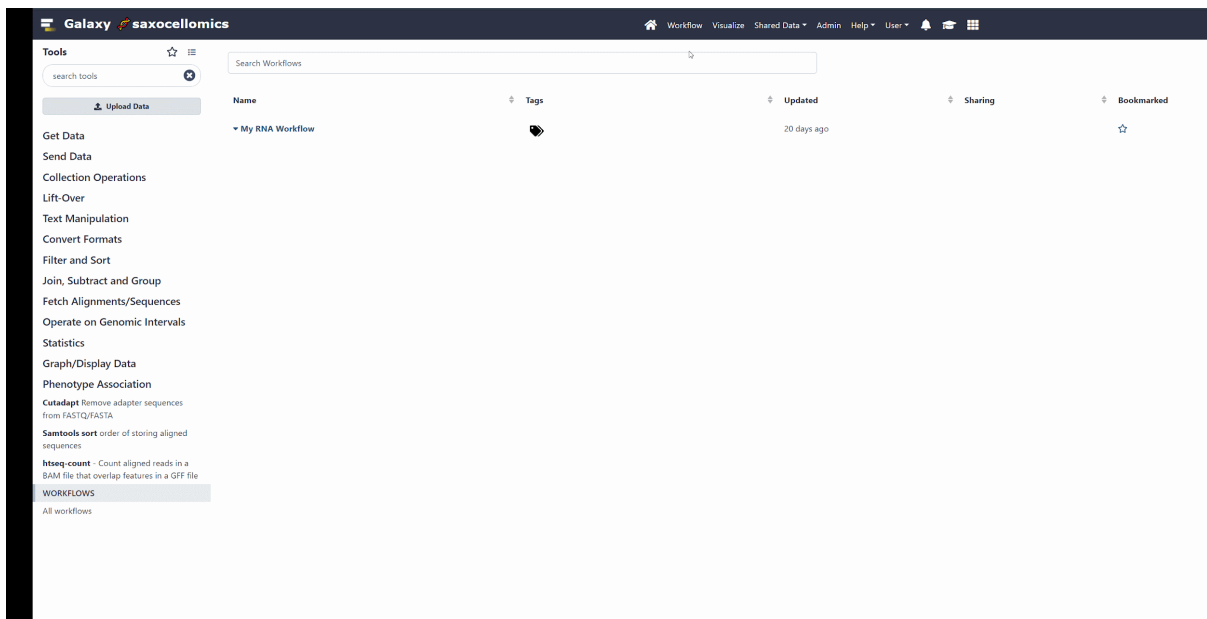
We currently have user quotas of 80GB. If you need more disk space, you can always get in touch and we try to find a solution for you.

### **Which tools can I use to process and analyze my data?**

All available tools can be found [here](#). Note: If the tool is not installed on our server, please contact us, and we will install the tool for you.

### **Can I share my data and workflows?**

Yes, you can share your workflows via link, or only with a specific user. See:



## Which workflows are already available?

All available workflows can be found [here](#). If you need custom workflows, please get in touch.

## What happens to my data?

The data is stored on the servers of the “Uni Rechenzentrum Leipzig (URZ). The server is only accessible from the Virtual Private Network (VPN) of the URZ. You can move the data yourself to a bin. In this state, only you and the server admins can recover the data. After processing and analyzing your data with Galaxy data can be permanently deleted from the servers by yourself.

## Is my data protected against third-party access?

Hosting the server inside the VPN makes it very safe against attacks from the outside world. Additionally, the data access is restricted, so that only users and admins have access rights to their own data.

## Can my data be lost?

Galaxy is by design a data processing and analysis server and you should back up raw Omics data on dedicated servers. Feel free to contact us to find backup solutions for your raw data. Your analysis results are currently not backed up but will be later in the production version of the server.

## Who can I contact for questions?

Please use this cryptic-looking email address for any support requests:

[gitmail+joas-galaxy-sandbox-5419-issue-@informatik.uni-leipzig.de](mailto:gitmail+joas-galaxy-sandbox-5419-issue-@informatik.uni-leipzig.de)

If you have problems reaching us this way, you can also contact:

- [alexander.scholz@izi.fraunhofer.de](mailto:alexander.scholz@izi.fraunhofer.de)
- [joas@informatik.uni-leipzig.de](mailto:joas@informatik.uni-leipzig.de)



### **Will there be training available?**

The first training took place on 22. September 2023. If you have data, we'll help you to analyze it. Depending on demand, we'll offer another training in the future, please get in touch!.

### **What is the difference between the development and production servers?**

The development server will **not be backed up** and can have downtime anytime. The objective here is to test our infrastructure (including workflows, tools, etc.) and adjust our offering according to user needs.

The production server will be backed up, so the risk of losing data is minimized. Furthermore, it will have more computational resources and downtimes will be communicated in advance.

### **Where to get help?**

There are multiple channels where you can get help:

- [contact us](#)
- galaxy training <https://training.galaxyproject.org>:
- galaxy community help: <https://help.galaxyproject.org>
- ask a question on <https://www.biostars.org>
- ask a question on <https://stackoverflow.com>

### **I am not allowed (legally) to upload patient data on your server, how can I still use Galaxy?**

We can set up an instance of the Galaxy server on your machines, so you can use Galaxy without ever giving any data away

Please get in touch: [gitmail+joas-galaxy-sandbox-5419-issue-@informatik.uni-leipzig.de](mailto:gitmail+joas-galaxy-sandbox-5419-issue-@informatik.uni-leipzig.de)