Galaxy in MetaCentrum
(introduction)

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Galaxy, our instance

- open source scientific work-flow system
- web server based front-end for bioinformaticians (you can run computations through web browser)
- lightweight, modularly written in python
- many tools for bio data manipulations, managed by wrappers and allow pipe-lining (workflows)
- running analyses in the background
- primarily designed for single user and run in VM

MetaCentrum instance

- sends jobs to the grid under real user’s accounts
- **login:** [https://galaxy.metacentrum.cz](https://galaxy.metacentrum.cz)
HTTPS authentication; use std. MetaCentrum login/password for https://galaxy.metacentrum.cz

Use login page to renew user’s tickets (allow access to the infrastructure) **every day!**
Galaxy instance is running! After day of not using...
...login address, log in by
https://galaxy.metacentrum.cz/login to renew
tickets for the access of MetaCentrum and for details
see
You can still use old address
https://galaxy.meta.zcu.cz/login, but there is not valid ssl
certificate.

WWFSMD?
grow noodly appendages...

(tools menu) (body) (history)
**Hello World example:** Click on HelloMetaCentrum tool in the tools menu and then to Execute.
Hello MetaCentrum!

In the history: you can view, tag, download and edit attributes of the result(s), you can re-run the analysis too.
Uploading files:

- directly in the tools menu: Get Data - Upload File
- large files are often uploaded by SFTP and later you see these files in the tools menu: Get Data - Upload File
  - connect to galaxy.metacentrum.cz machine by std. sftp protocol, eg. WinSCP program
  - use std. MetaCentrum user/password
  - copy your files to some directory and send the name of the directory, you will use for galaxy uploads, to the meta@cesnet.cz

Later you will see uploaded files in the history.

Example data: download and unzip for upload
http://nihlibrary.ors.nih.gov/bioinfo/ngs/sourcedata1.zip
Uploading files SFTP
Uploading files SFTP

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Files were successfully uploaded in the history.
Click in the tools menu: NGS: QC and manipulation - FASTQ Groomer, choose fasq file and click on Execute.

If you need a tool, not in menu, send request to meta@cesnet.cz.
Analysis finished: download results, re-run analysis or use outputs for other analyses.
You can easily join several analyses together (output of one as input of other)

▶ click on Workflow (upper menu) - Create new workflow and fill some name, click on Create
▶ click on your new workflow and choose Edit
▶ add two Input Datasets, FASTQ Gromer (NGS: QC and manipulation) and Map with BWA for Illumina (NGS: Mapping) and connect them as it is on the following slide
▶ click on wheel and choose Save
▶ click on Workflow, choose your one and click Run
▶ choose input Datasets and click Run workflow

You can change inputs and re-run workflow or share/publish it.
Final notes

- read
  https://wiki.metacentrum.cz/wiki/Galaxy_application
- always (every day) login through
  https://galaxy.metacentrum.cz
- clean (delete) history items if you will not use them anymore
- ask for help or report problem at the meta@cesnet.cz

Questions/comments?

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