Netherlands Bioinformatics Centre

Opening new gateways to workflows for life scientists

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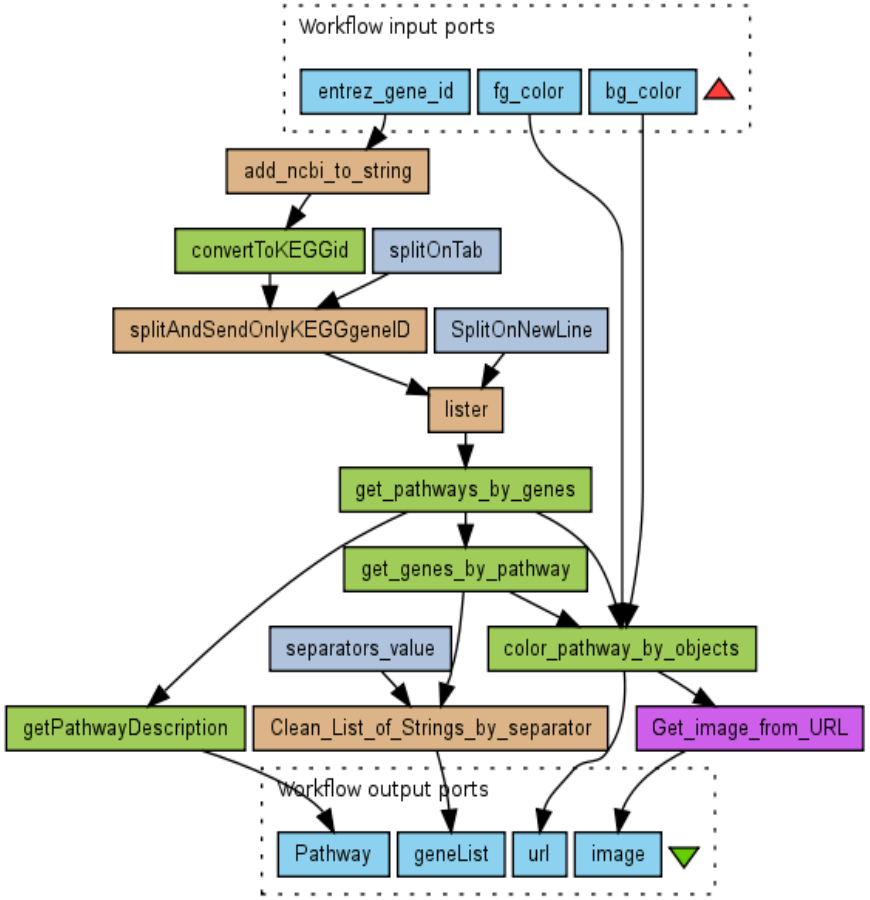
Workflow approach

- Structured approach to performing bioinformatics experiments
- Steps are exposed
- Helps evaluation by supervisors and peers
- Compares to 'Materials and Methods', but you can run them
- Easier to reuse & extend (manage complexity)



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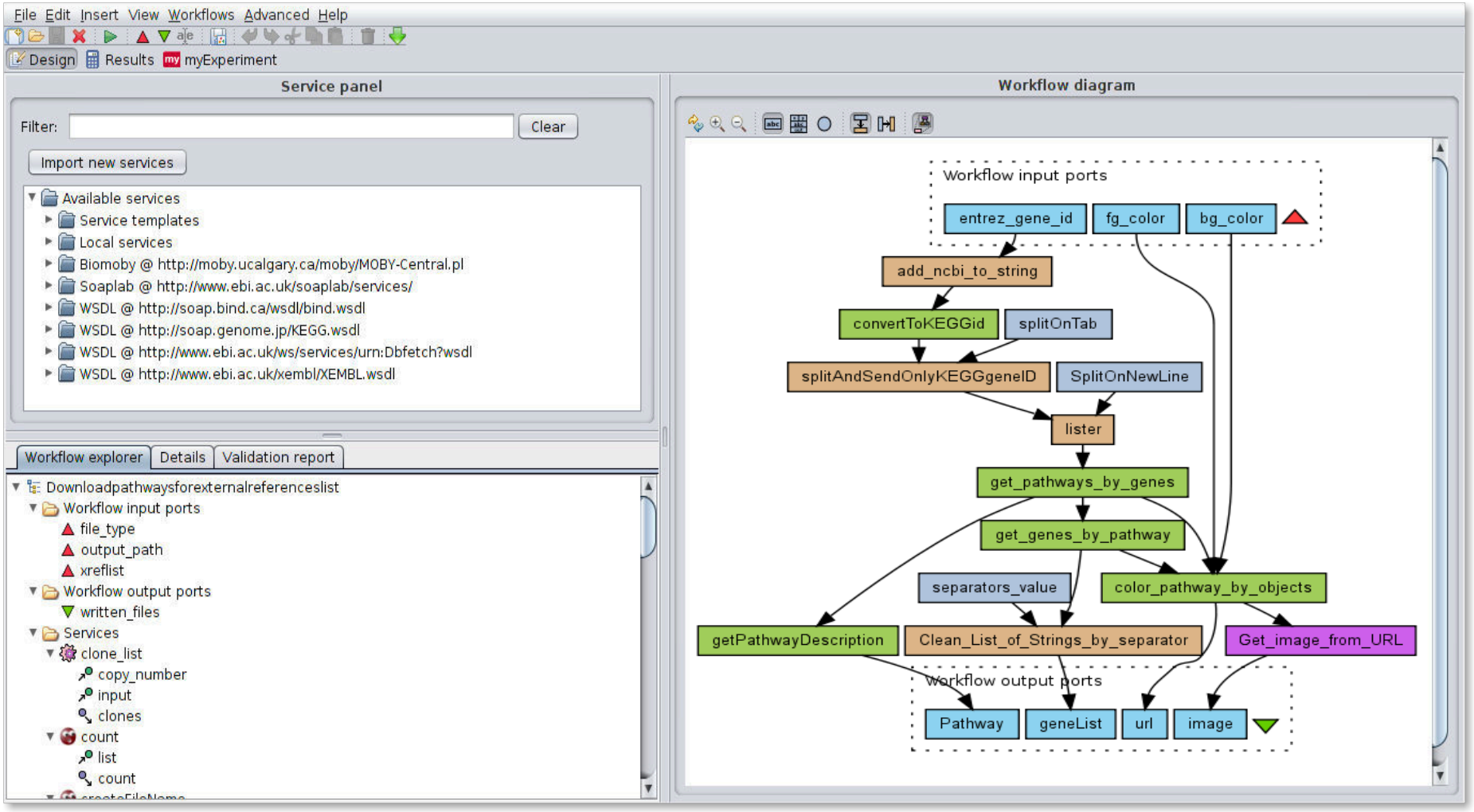
Observations

- Two widely-used systems: Galaxy & Taverna
- Typical usage scenario's
  - Galaxy:
    - 'Scripting bioinformatician' adds command line tools to local Galaxy server for their biological colleagues
    - Biologists interactively 'play with data'
      - Save interactive analysis as a workflow
    - Strength: simplicity
  - Taverna
    - Bioinformatician designs a workflow to perform complicated data analysis / data integration
    - Strength: sophisticated workflows

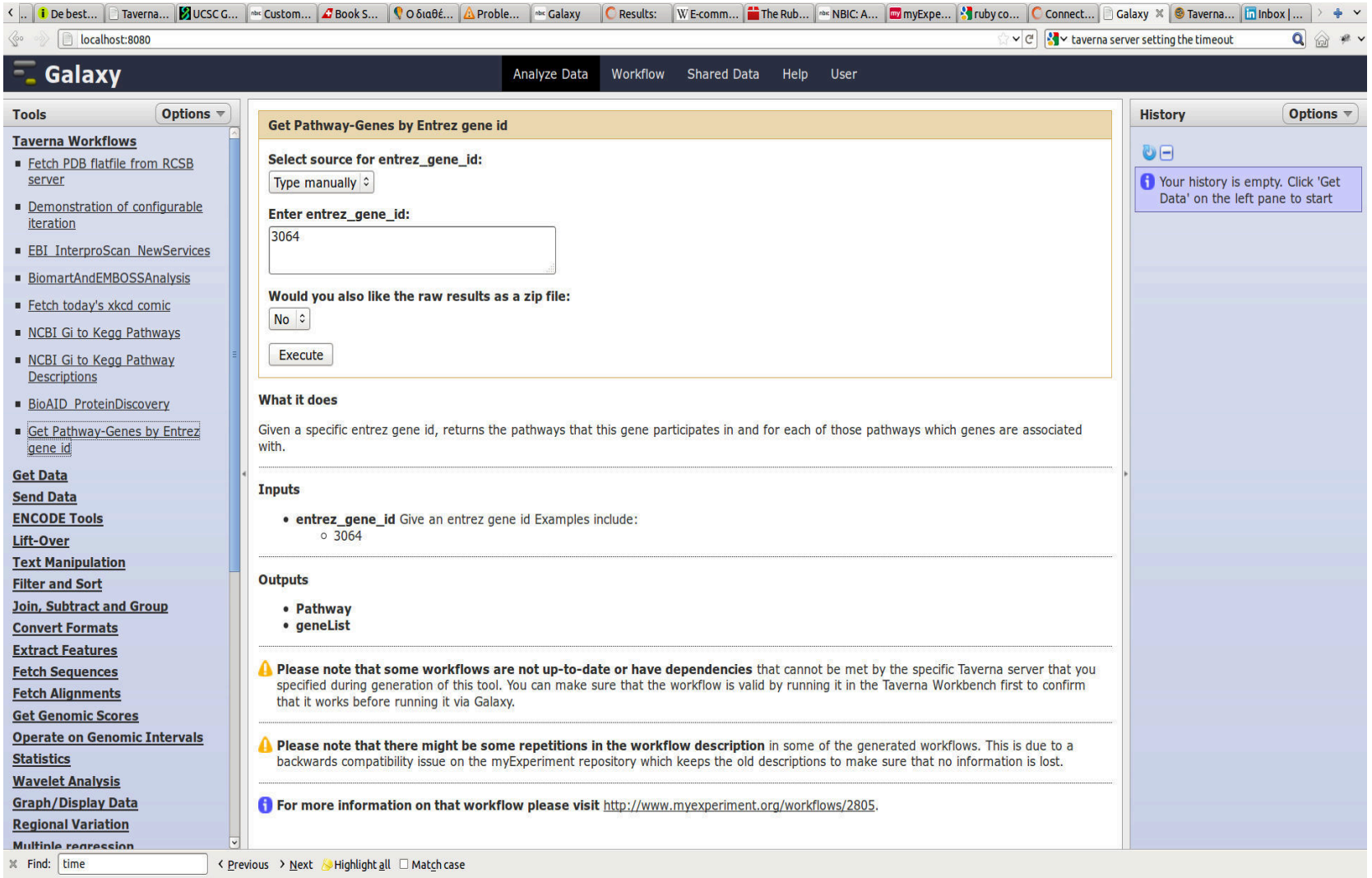
Why interoperate?

- Use each other's tools, use each other's workflows
  - Example:
    - calculate genome region overlaps in Galaxy
    - annotate genes by text mining Web Services in Taverna
- Exploit strengths
  - Galaxy: simplicity
  - Taverna: sophistication
- Allow user communities to benefit from each other's work
  - greater accessibility

Taverna Workbench



Galaxy



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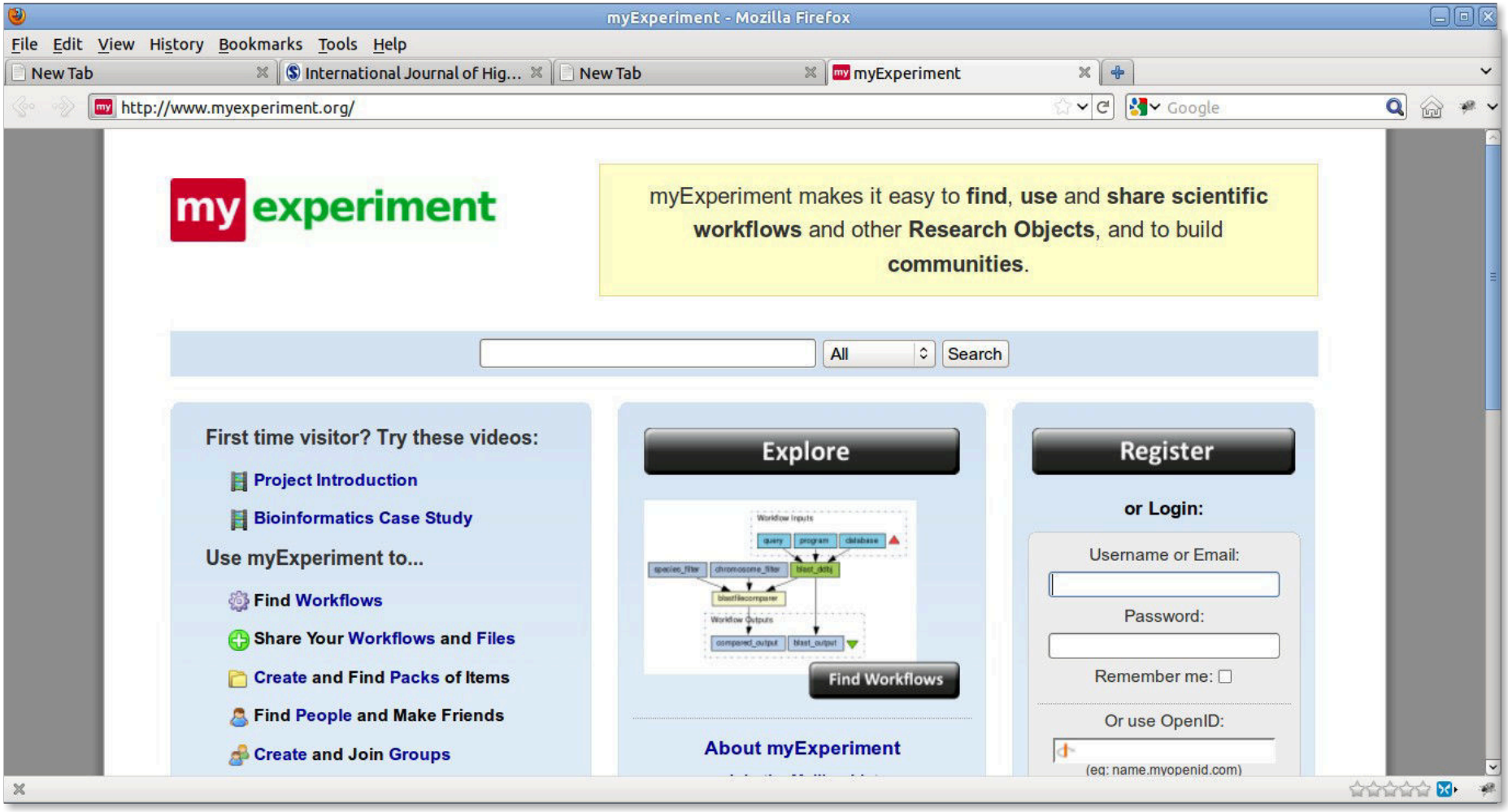
myExperiment



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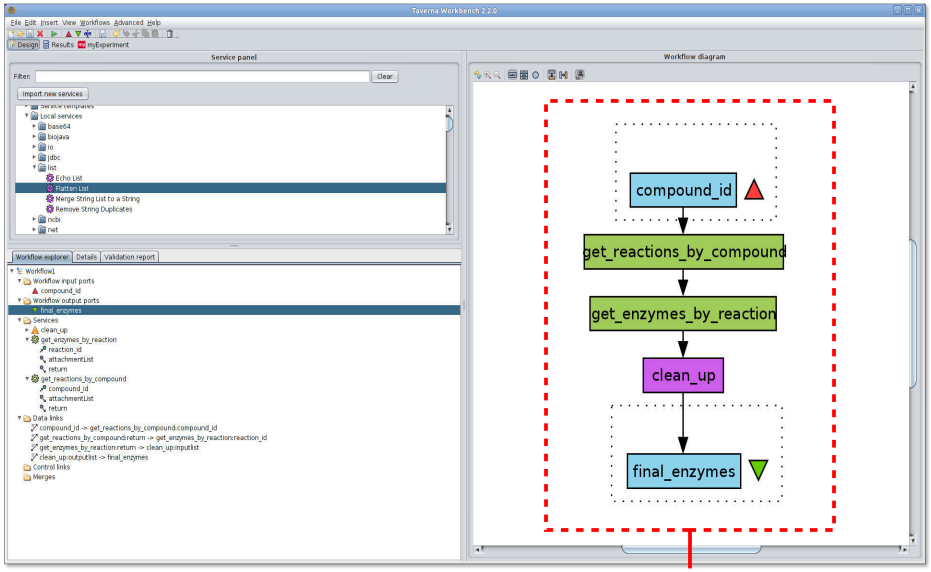
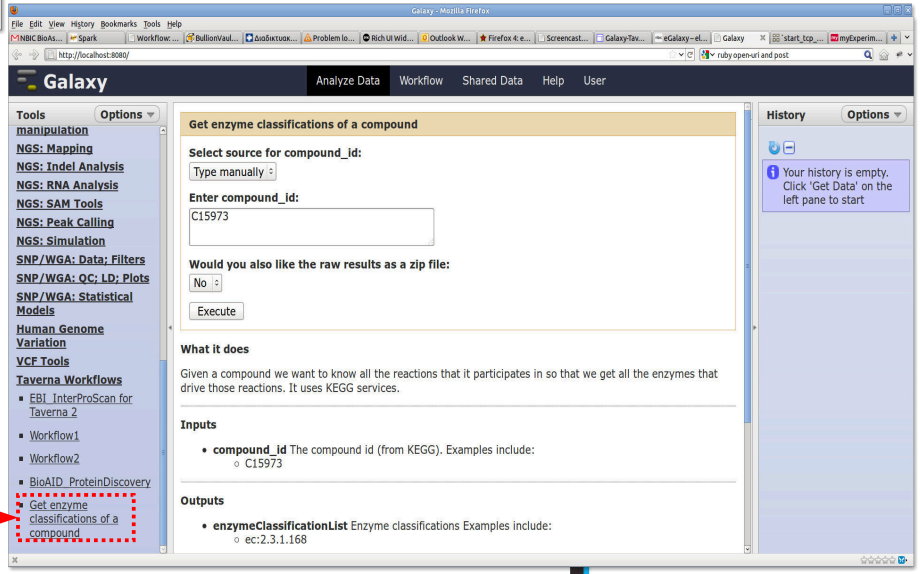
Our work

- Taverna workflows available in Galaxy
- Taverna workflows available on a web browser
- Demonstration server with Galaxy & Taverna servers, T2Web
  - Galaxy tools/workflows available in Taverna
  - Virtual Image (for production as well)

Taverna Workflows in Galaxy (1)





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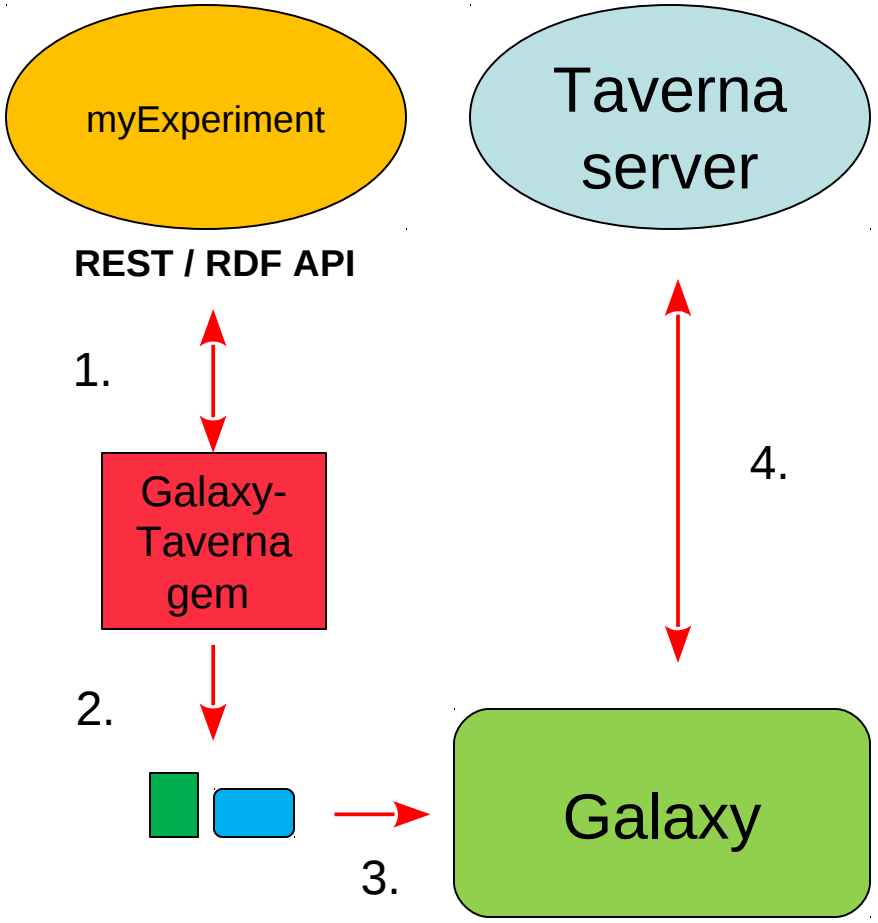
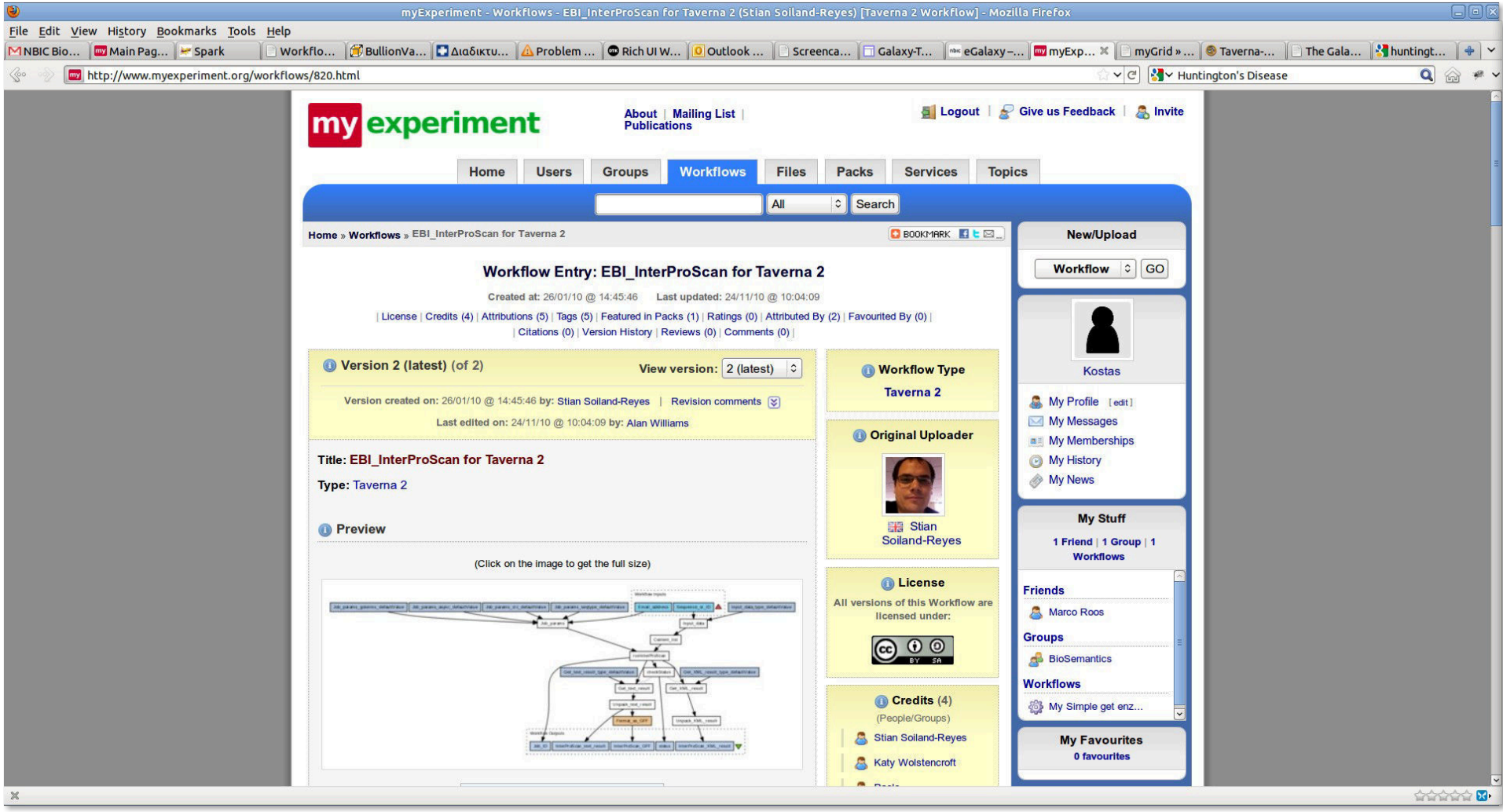
Taverna Workflows in Galaxy (2)

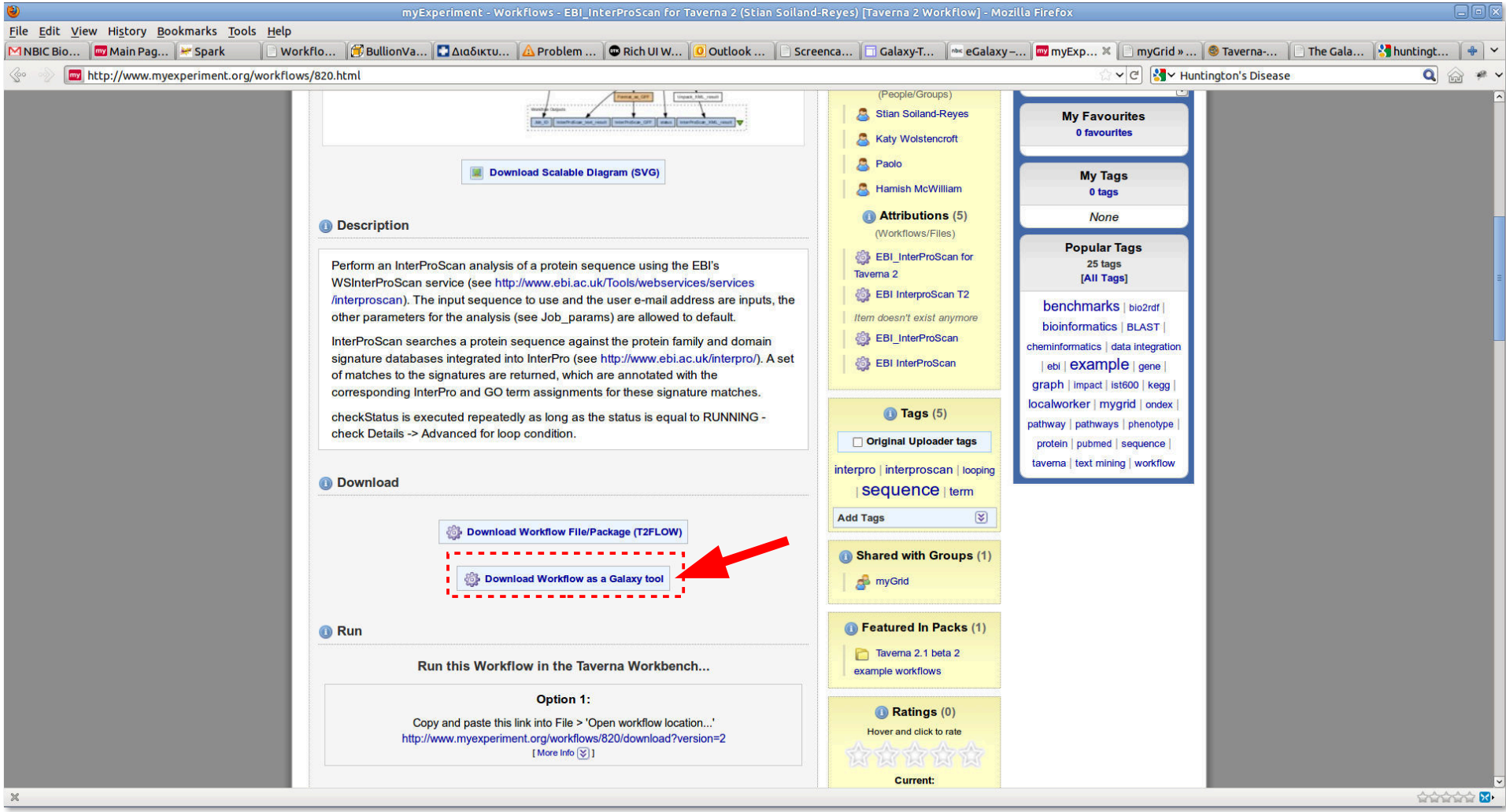
- Galaxy-Taverna component
  - ruby gem
    - behind the scenes
  - generates a Galaxy tool
  - requires a workflow description
- Workflow description
  - myExperiment
  - workflow file
- Galaxy
  - tool needs to be manually installed



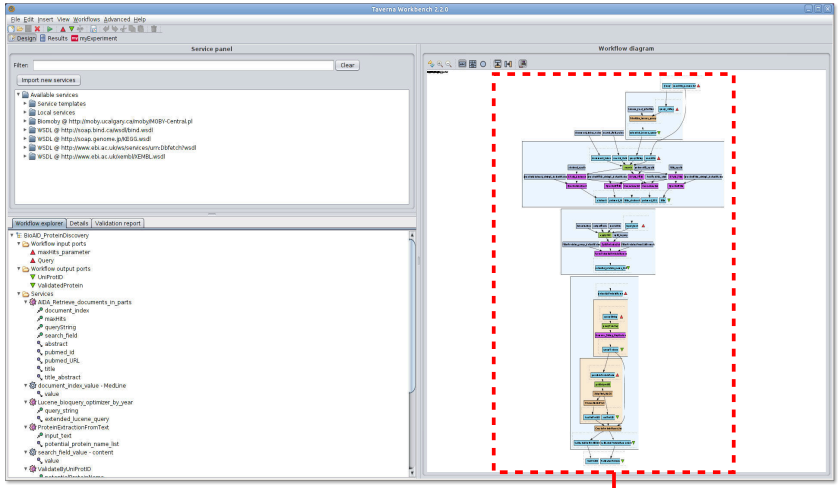
Taverna Workflows in Galaxy (3)

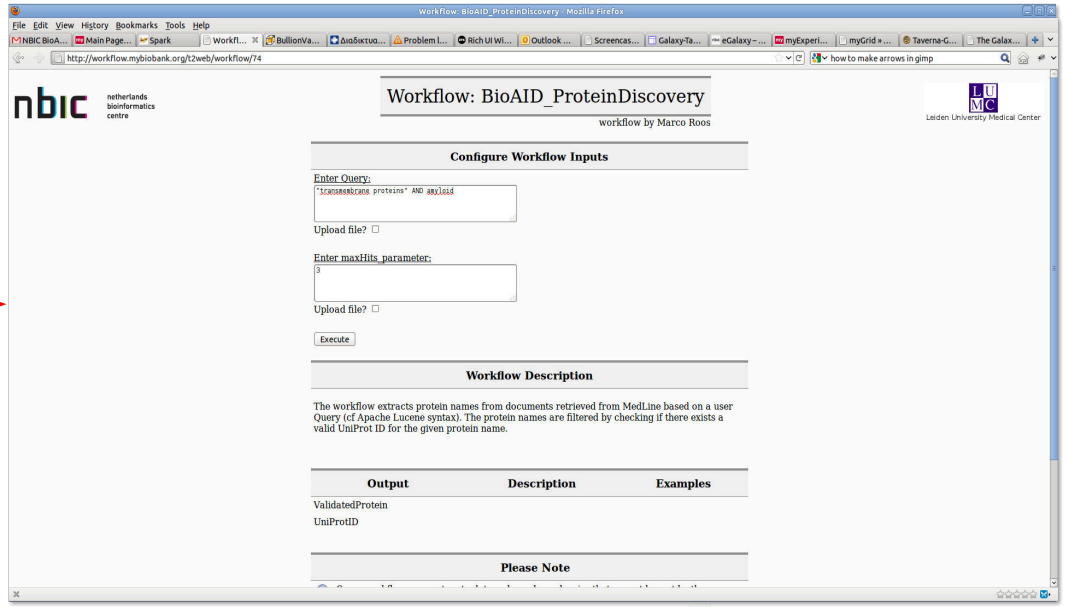


Taverna Workflows in Galaxy (4)

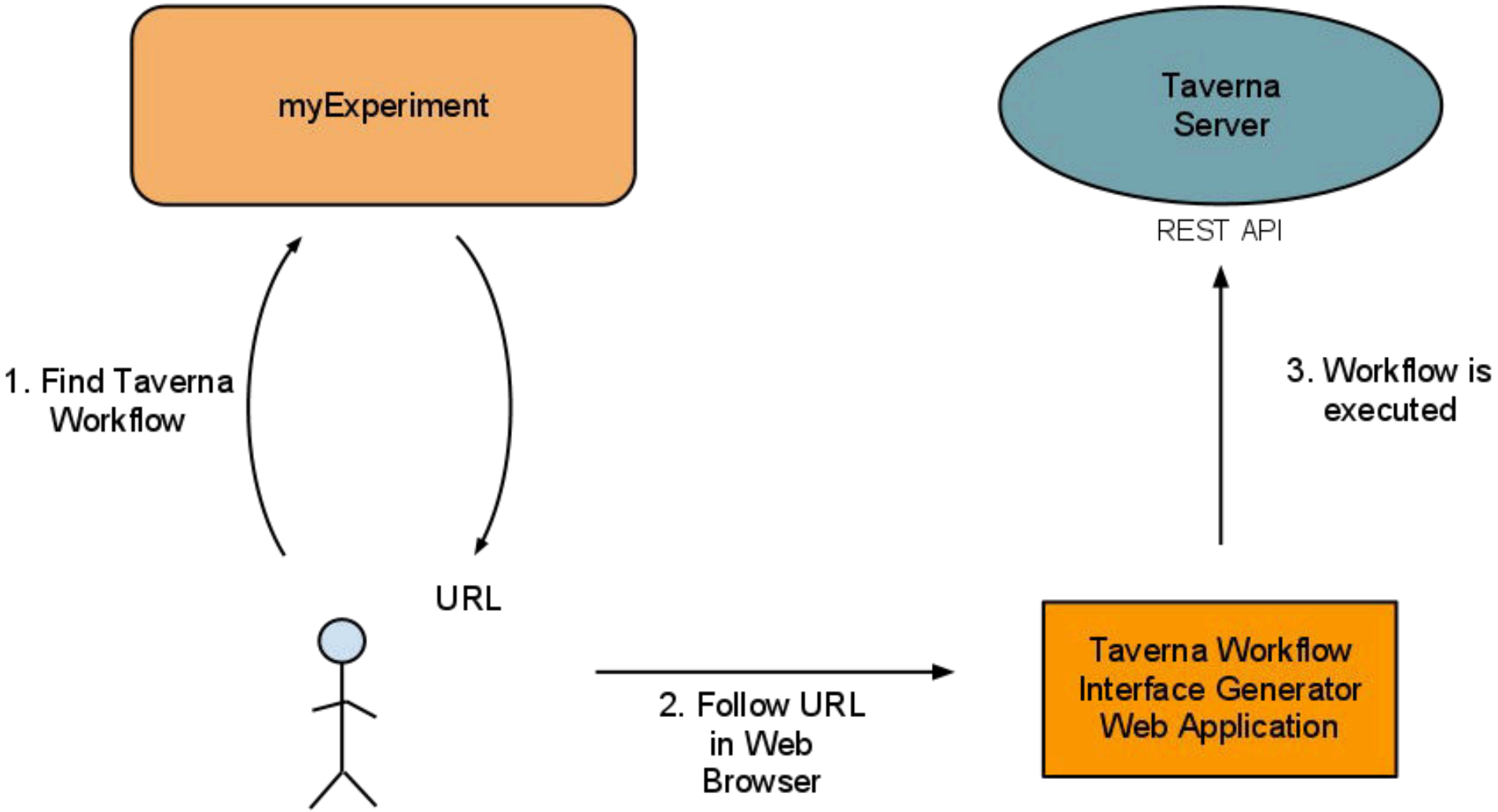


Taverna Workflows on a web browser (1)

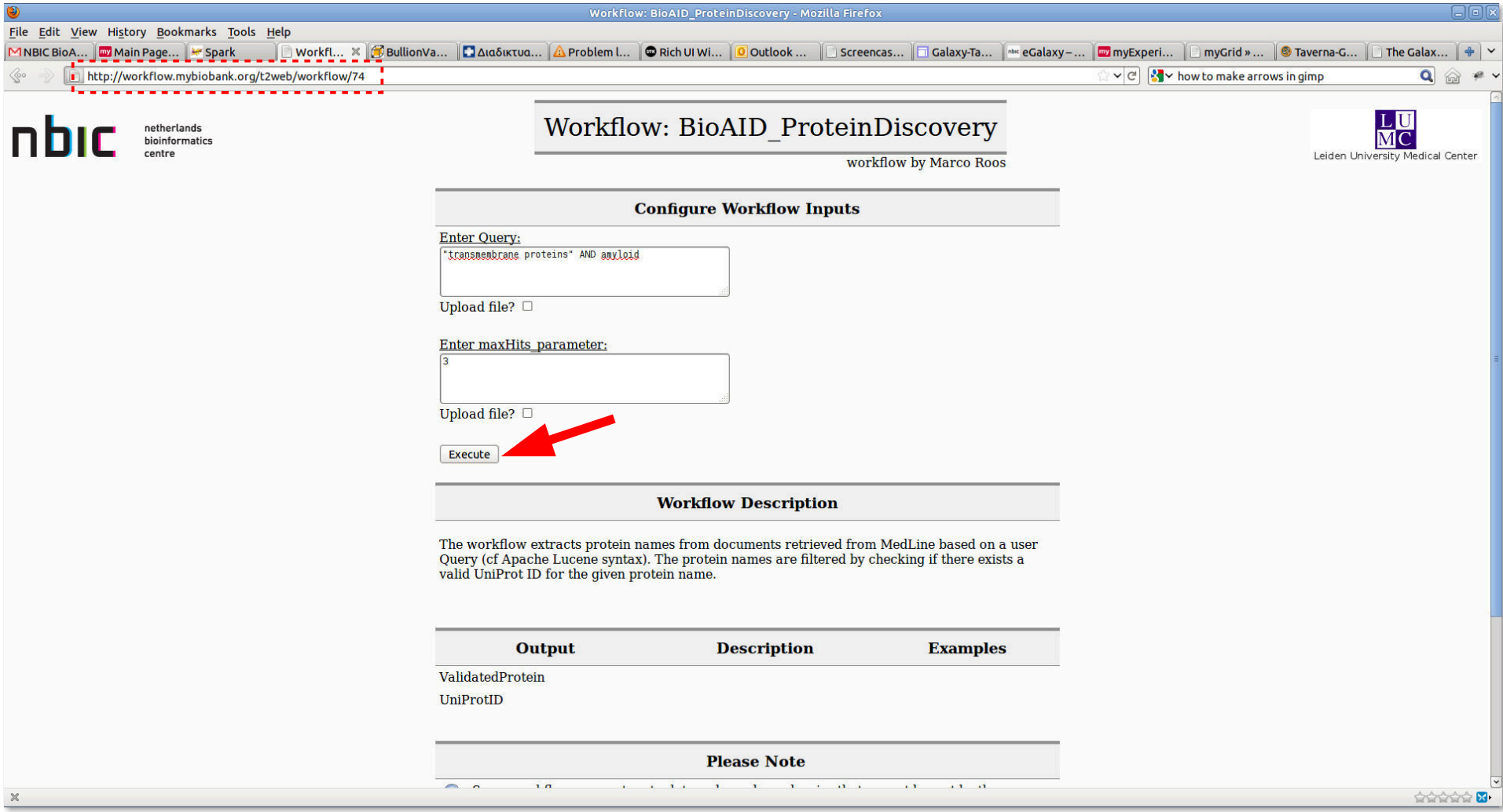




Taverna Workflows on a web browser (2)



Taverna Workflows on a web browser (3)



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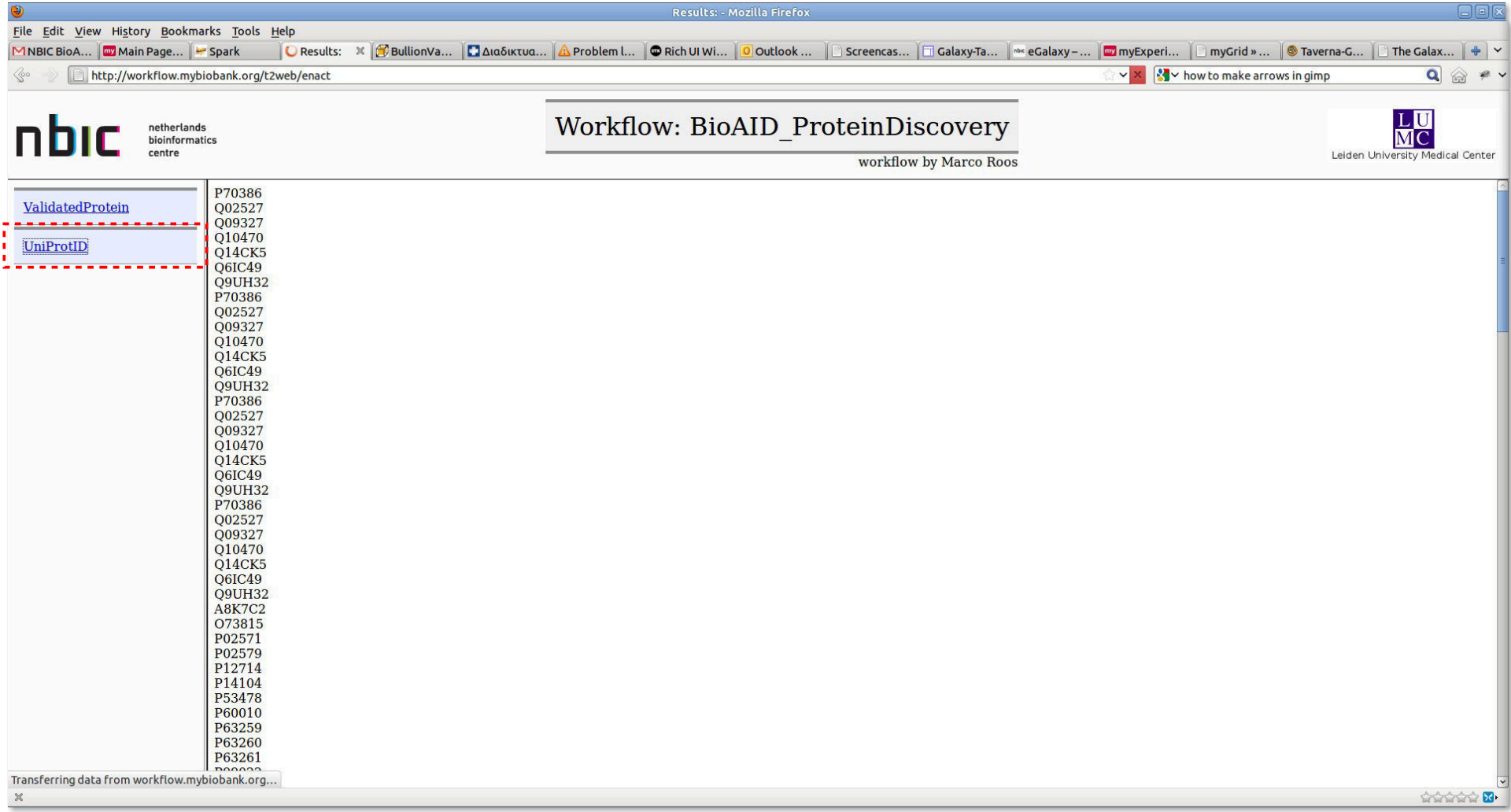
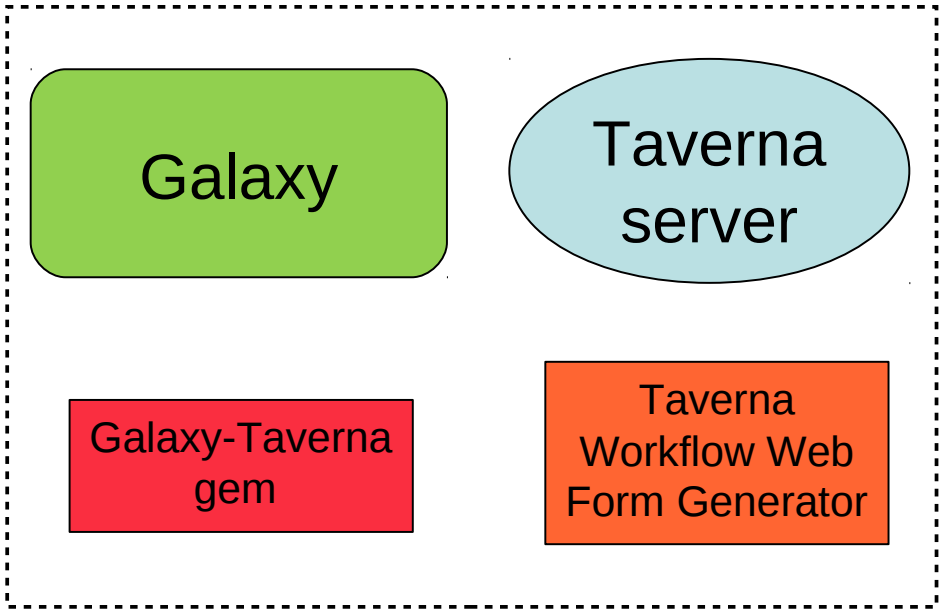


Demonstration Server (1)

- Galaxy+Taverna Server 'in one box' and more
  - demonstration
  - preconfigured
  - 'playground'
  - Taverna → Galaxy



Demonstration Server (2)

- Galaxy+Taverna Server 'in one box' and more
- Galaxy Server
  - http://galaxy.nbic.nl/galaxy
  - with some example taverna workflows
- Taverna Server
  - http://galaxy.nbic.nl/demo/taverna-server
- Taverna workflows to Galaxy tools generator
- Taverna workflows web interface generator web application
  - http://galaxy.nbic.nl/t2web/workflow/***74***

Conclusions

- More interoperable Galaxy – Taverna workflows
- Taverna workfkows can be accessed in Galaxy
  - … and thus take part in a Galaxy workflow
- Taverna workflows can be accessed via the web
  - Bioinformatician creates the workflow
  - … sends the URL to biologist
- Demonstration Server
  - Virtual machine

Acknowledgements

- NBIC BioAssist developers
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  - BioSemantics group LUMC-Leiden/EMC-Rotterdam
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Questions?

- More information
  - **Taverna-Galaxy** → https://trac.nbic.nl/elabfactory/wiki/eGalaxy
  - **Taverna-Web** → https://trac.nbic.nl/elabfactory/wiki/t2web
  - **Virtual Machine** → https://wiki.nbic.nl/index.php/Galaxy_VM
  - **Demonstration Server** → http://galaxy.nbic.nl/galaxy
  - **Galaxy** → http://galaxy.psu.edu/
  - **Taverna** → http://www.taverna.org.uk/
  - **myExperiment** → http://www.myexperiment.org/

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