Galaksio – Self Service Bioinformatics

- Displays and runs workflows
- Python + Flask + AngularJS
- Connects to any Galaxy server by API
- No processing on the Galaksio side

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History selection

First, choose the history that contains the files that will be used in the workflow.

Remember that when data is uploaded from your computer or analysis is done on existing data using Galaxy, each output from those steps generates a dataset. These datasets (and the output datasets from later analysis on them) are stored by Galaxy in Histories.

If you wish to publish your results we strongly recommend that you run your workflow in a clean history before saving the workflow. That way you can make the entire file available as a supplementary material that can be evaluated during peer-review as a supplementary material and reviewed using Galaxy.

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Xcms.xcmsSet

Description

This tool is used for preprocessing analyze data from multiple LC/MS files (formats raw, mzXML and mzData). It extracts ion from each sample independently and using a statistic model, peaks are filtered and integrated. You can read a tutorial on how to perform xcms preprocessing which is available here.

Workflow position

<table>
<thead>
<tr>
<th>Upstream tools</th>
<th>Output file</th>
<th>Format</th>
<th>Parameter</th>
</tr>
</thead>
<tbody>
<tr>
<td>NA</td>
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<td>bp</td>
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<table>
<thead>
<tr>
<th>Downstream tools</th>
<th>Output file</th>
<th>Format</th>
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</thead>
<tbody>
<tr>
<td>VDA</td>
<td>load RData</td>
<td></td>
</tr>
<tr>
<td>Dataframe</td>
<td>data xcms raw</td>
<td></td>
</tr>
</tbody>
</table>

Contact support@workflow4metabolomics.org for any questions or concerns about the Galaxy implementation of this tool.
SAP Arms Reigning World Cup Champion Germany With Tools to Defend Title

Sports, Apps, Artificial Intelligence, Big Data, Mobile, Soccer, Trending, Video, World Cup  © June 15, 2018  Jen Booton
Motivation

SLU Global Bioinformatics centre

- Bioinformatics training
- Bioinformatics support
- And research of course

Erik Bongcam-Rudloff

- eBioKit
- Embnet, GOBLET, H3ABionet, EANBit DEANN and many more...

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eB3Kit

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Bibbox app store
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Bioinformatics

Computer science

Scientific Impact

Molecular biology

Applied biology & medicine

(www.xkcd.com, CC-NC 2.5)
Division of labour

Biologist/Medical specialist
Bioinformatician (severe shortage)
Programming/Sys admin
Support

Horizon 2020 research and innovation programme, grant agreement No 654404
"Let scientists focus on science"

www.enancio.fr

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Near future

• Release Galaksio V1.0
• Create tool for LIMS-integration (Baobab LIMS)
• Test it on as many Galaxy servers as possible
More tools being prepared for Galaxy servers

Greater citation rates and incentives to develop Galaxy tools

Greater opportunities for workflow development

More researchers using prepared workflows

- Connects to any Galaxy server using the API
- An easy way to make workflows accessible

Available at: https://github.com/SGBC/galaksio
Or "docker run -it -p 8081:80 tklingstrom/galaksio"
Contact: tomas.klingstrom@slu.se
You can also test it on our "Biobank in a box" website: www.ref.development.bibbox.org
Thank you!

Swedish University of Agricultural Sciences
Erik Bongcam-Rudloff
Rafael Hernandez
Oskar Karlsson
Theo Collard

The Galaxy community
(and in particular)
Björn Grüning
Berérencié Batut
Maurice van den Beek
Yvan le Bras/Enancio
Everyone on Gitter!

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