

Automatising 13 C-fluxomics flux calculations through a workflow hosted on the Workflow4Metabolomics Galaxy platform

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▶ To cite this version:

Loïc Le Grégam, Pierre Millard, Serguei Sokol, Yann Guitton, Gildas Le Corguillé, et al.. Automatising 13 C-fluxomics flux calculations through a workflow hosted on the Workflow4Metabolomics Galaxy platform. Analytics 2022, RFMF; AFSEP; AFSM, Sep 2022, Nantes (Cité des Congrès), France. hal-04352460

HAL Id: hal-04352460 https://hal.science/hal-04352460

Submitted on 19 Dec 2023

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An automatised ¹³C-fluxomics workflow

Automatising flux calculations through a workflow hosted on the Workflow4Metabolomics Galaxy platform



Loïc Le Grégam, Pierre Millard, Serguei Sokol, Yann Guitton, Gildas Le Corguillé, Sébastien Hutinet, Sophie Colombie, Fabien Jourdan, Floriant Bellvert, Jean-Charles Portais

MetaToul-MetaboHUB platform

Quantifying fluxes: the basics

A flux can be defined as the in vivo rates of biochemical reactions. ¹³C Carbon source Carbon fluxes Redox fluxes NADH NADPH Central Energy metabolism fluxes АТР 🌽 Precursors ĽĽ Anabolism Biomass **By-products**

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Quantifying fluxes: the basics

A flux can be defined as the in vivo rates of biochemical reactions.



Fluxes cannot be measured directly!



Data that is needed:

- Stoichiometric model
- Input-output rates (i.e extracellular fluxes)

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• Labeling distribution



Quantifying fluxes: the basics

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• Labeling distribution



Quantifying fluxes: A complex workflow



er.

Quantifying fluxes: data processing & flux calculation



Quantifying fluxes: current (manual) pipeline for flux calculation







Objective: streamline the process to increase reproducibility, robustness and throughput -> Development of an automatised ¹³C workflow

Proposed ¹³C-fluxomics workflow





Proposed ¹³C-fluxomics workflow



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Proposed ¹³C-fluxomics workflow



Galaxy – Workflow4Metabolomics (W4M)

User oriented Open source Web-based



E. Afgan et al., 2018





Genomics





Proteomics



Galaxy – Workflow4Metabolomics (W4M)







Upload to Bioconda

Step 1: Create fork of the **Bioconda-recipes** repository Step 2: Clone the repository and create recipe using *grayskull* package Step 3: Add the *meta.yml*, commit, push the changes to Bioconda-recipes and pull-request

Elaboration of the
XML wrapper

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Test and release





Upload to Bioconda

Elaboration of the XML wrapper

<tool id="isoplot" name="Isoplot: Generate plots from isocor output" profile="20.01" version="1.3.0+galaxy1"></tool>
<requirements></requirements>
<requirement type="package" version="1.3.0">isoplot</requirement>
<command/> </td></tr><tr><td>isoplot '\$datafile' 'galaxy' '\$format'value '\$value'template '\$template_file' \$SP.barplot \$SP.meaned_barplot</td></tr><tr><td><pre>\$SP.static_heatmap \$SP.static_clustermap \$IP.interactive_barplot \$IP.interactive_meanplot \$IP.interactive_heatmap</pre></td></tr><tr><td>#if \$unstack:</td></tr><tr><td></td></tr><tr><td>#end if</td></tr><tr><td>#if \$verbosity:</td></tr><tr><td></td></tr><tr><td>#end if</td></tr><tr><td>#if \$annotation:</td></tr><tr><td></td></tr><tr><td>#end if</td></tr><tr><td>-g -z '\$plots_output' > \$data_output 2> '\$log_output'</td></tr><tr><td>
<pre><inputs></inputs></pre>
<pre><pre><pre><pre><pre><pre><pre><pre></pre></pre></pre></pre></pre></pre></pre></pre>
<pre><pre><pre><pre><pre><pre><pre><pre></pre></pre></pre></pre></pre></pre></pre></pre>
param name='run_name' type='text' label='Run name' /
<pre><pre><pre>cparam name='format' type='select' label='Plot format'></pre></pre></pre>
<option value="pdf">pdf</option>
<pre><coption value="jpeg">jpeg</coption></pre>
<pre><coption value="png">png</coption></pre>
<pre><coption value="svg">svg</coption></pre>
<option value="html">html</option>
<pre><pre><pre><pre>cparam name='value' type='select' label='Data to plot' ></pre></pre></pre></pre>
<pre><option value="corrected_area">Corrected Area</option></pre>
<pre><option value="isotopologue_fraction">Isotopologue Fraction</option></pre>
<pre><coption value="mean_enrichment">Wean Enrichment</coption></pre>

The wrapper is an **XML file** that contains the configuration for the Graphical User interface that will be displayed on W4M and the logic for launching the tool (command-line interface launch)

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Test and release





This last phase is executed using the *Planemo* tool developped by the *Galaxy* team to **ease the process** of uploading tools onto the platform. Features include:



Elaboration of the
XML wrapper

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Running tool tests: \$ planemo test --galaxy_root=../galaxy randomlines.xml

Viewing in Galaxy interface: **\$** planemo serve

Test and release



Slide with W4M workflow example

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TODO





> The lack of interoperality between tools meant high expertise was needed for flux calculation

The workflow renders flux calculation more **reproductible**, **repeatable** and **increases throughput**.

Easy access and user-friendly interface through W4M

 \Rightarrow Uploading workplan is well detailed \rightarrow faster developments in the future







Extension to other ¹³C fluxomics approaches (instationary, scalable, NMR-based, etc)

Extension with preliminary computational steps (quantification by MS and/or NMR, grouping of isotopic data, etc)

Validation and application to investigate glucose & acetate co-metabolism in *E. coli* (requires large number of flux maps)



Acknowledgments





TOULOUSE

(a) MetaToul FluxoMet

Floriant Bellvert Cécilia Bergès Noémie Butin Edern Cahoreau Jean-Charles Lara Galès Hanna Kulyk Nina Lager-Lachaud Lindsay Peyriga Etienne Rifa Amandine Rocher

MetaSys team Pierre Millard

Stéphanie Heux

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