

The screenshot shows the Galaxy web interface. The top navigation bar includes 'Galaxy', 'Analyze Data', 'Workflow', 'Shared Data', 'Visualization', 'Help', 'User', and 'Using 207.9 KB'. The left sidebar lists various tool categories: COMMON TOOLS (Get Data, Manipulate files, Manipulate sequence files, Manipulate BAM/SAM files), SEQUENCE PREPARATION TOOLS (Assemble paired-end sequences, Control quality, Chimera detection, dereplication, clustering... with VSEARCH, Cluster sequences, Manipulate RNA), METAGENOMIC TOOLS (Assign taxonomy on all sequence type, Analyze metabolism, Combine functional and taxonomic results), and STATISTICS AND VISUALIZATION TOOLS (Visualize data, Export to GraPhlAn, GraPhlAn to produce graphical output of an input tree, Generation, personalization and annotation of tree for GraPhlAn, Krona pie chart from taxonomic profile, Plot barplot with R, Plot grouped barplot with R, Plot generic X-Y plot with R, Histogram of a numeric column).

The central panel displays the 'GraPhlAn to produce graphical output of an input tree (Galaxy Version 0.9.7)' tool configuration. It includes fields for 'Input tree' (2: intermediary_tree.txt), 'Output format' (PNG), 'Dpi of the output image (Optional)', 'Size of the output image (in inches)' (7), and 'Distance between the most external graphical element and the border of the image (Optional)'. An 'Execute' button is at the bottom. Below the form, a 'What it does' section explains that GraPhlAn is a software tool for producing high-quality circular representations of taxonomic and phylogenetic trees.

The right sidebar shows the 'History' panel with a search bar and two entries: '3: GraPhlAn on data 2: Image' (58.4 KB, format: png, database: 2) and '2: intermediary_tree.txt' (Phyloxml data, format: phyloxml, database: 2). The second entry shows a preview of the XML data.

Figure 1 : Instantané de l'instance de Galaxy d'ASaiM ouverte sur l'outil GraPhlan
On repère sur la gauche la liste des outils disponibles, au centre l'interface de l'outil GraPhlan et sur la droite se trouve l'historique avec deux fichiers présents.

The screenshot shows the 'Galaxy Tool Shed' interface. The top navigation bar includes 'Galaxy Tool Shed', 'Repositories', 'Groups', 'Help', and 'User'. The left sidebar shows search options and valid Galaxy utilities. The main panel displays 'Repositories by Category' with a search bar and a table of repositories.

Name	Description	Repositories
Assembly	Tools for working with assemblies	74
ChIP-seq	Tools for analyzing and manipulating ChIP-seq data.	40
Combinatorial Selections	Tools for combinatorial selection	6
Computational chemistry	Tools for use in computational chemistry	21
Convert Formats	Tools for converting data formats	64
Data Managers	Utilities for Managing Galaxy's built-in data cache	32
Data Source	Tools for retrieving data from external data sources	35
Epigenetics	Tools for analyzing Epigenetic/Epigenomic datasets	3
Fasta Manipulation	Tools for manipulating fasta data	76
Fastq Manipulation	Tools for manipulating fastq data	54
Genome-Wide Association Study	Utilities to support Genome-wide association studies	20
Genomic Interval Operations	Tools for operating on genomic intervals	42
Graphics	Tools producing images	42
Imaging	Utilities to support imaging	1
Metabolomics	Tools for use in the study of Metabolomics	25

Figure 2 : Instantané du Main tool-shed de Galaxy

```

<tool id="Exemple" name="exemple" version="0.1.0">
  <requirements>
  </requirements>
  <stdio>
    <exit_code range="1:" />
  </stdio>
  <command><![CDATA[
    TODO: Fill in command template.
  ]]></command>
  <inputs>
  </inputs>
  <outputs>
  </outputs>
  <help><![CDATA[
    TODO: Fill in help.
  ]]></help>
</tool>

```

Figure 3 : Instantané du corps encore vide d'un *wrapper*

On retrouve les différentes sections : les informations sur le *wrapper*, les requirements, la section "*command*", les "*inputs*", les "*outpus*", la section "*tests*" et la section "*help*"

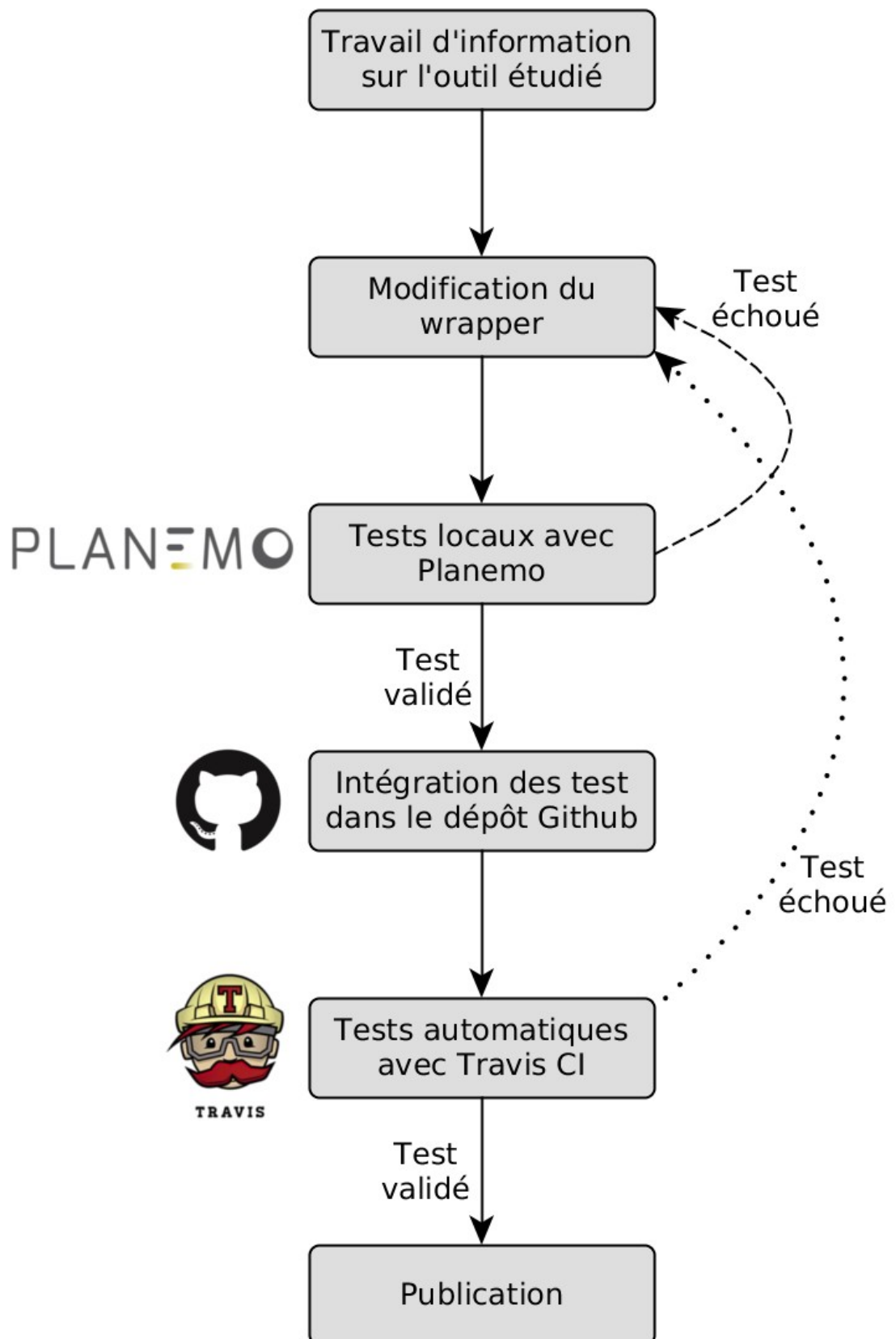


Figure 4 : Scéma représentatif des actions effectuées lors du développement de tests pour des wrappers dans Galaxy


```
<tests>  
  <test>  
  </test>  
</tests>
```



```
<tests>  
  <test>  
    <param name="input_tree" value="intermediary_tree.txt"/>  
    <param name="format" value="png"/>  
    <param name="dpi" value="100"/>  
    <param name="size" value="7"/>  
    <param name="pad" value="2"/>  
    <output name="png_output_image" file="png_image.png" />  
  </test>  
</tests>
```

Figure 6 : Evolution de la section test de l'outil GraPIAn

Addtest for `combine_methaph_lan2_human2` #16

Edit

Merged bebatut merged 6 commits into ASaiM:master from themard1:br_combine_methaphLan2_human2 on 15 Apr

Conversation 4

Commits 6

Files changed 7

+33,293 -29,435



themard1 commented on 13 Apr

+😊🔧

to resolve #1

Labels

None yet

Milestone

No milestone

Assignees

No one assigned

Notifications

🔊 Unsubscribe

You're receiving notifications because you authored the thread.

2 participants



themard1 added some commits on 12 Apr



Add missing test

b44e727



Remove some lines

✖ a5222f1



bebatut commented on an outdated diff on 14 Apr

Show 1 comment



bebatut commented on 14 Apr

+😊

I will add this test for CI



themard1 added some commits on 14 Apr



Merge branch 'master' of https://github.com/ASaiM/galaxytools into br...
br...

a34c544



Add good outputs and edit tt_blacklist

✓ e79736b



update .tt_blacklist

✓ 3f792eb



bebatut commented on 15 Apr

+😊

The test files are not good ones. I can send you some if you want



Change inputs and outputs files

✓ a34b11a



bebatut commented on 15 Apr

+😊



Figure 7 : Pool Request commentée de l'outil "combine_methalan2_humann2"

Nom de l'outil	Nombre de wrappers		Nombre de fichiers d'entrée	Nombre de paramètres	Nombre de fichiers en sortie	Nombre de tests produits
<u>extract_min_max_lines</u>	1		1	3	1	4
combine_meta phlan2_humann 2	1		2	1	1	2
plot_generic_x_ y_plot	1		1	15	1	1
normalize_datas et	1		1	2	1	3
fasta_add_barcode	1		2	0	1	1
plot_grouped_barplot	1		1	12+3*X	1	1
plot_barplot	1		1	12	1	2
compare_humann2_output	1		X	1+X	3+X	1
export2graphlan	1		1	26	2	1
format_metaphlan2_output	1		1	0	9	1
cdhit	2	est	1	5	2	1
		protein	1	6	2	1
extract_sequence_file	1		1	15 ou moins	2 ou 3	2
format_cd_hit_output	1		2	4	1	1
GraphLan	2	Graphlan	1	4	1	1
		annotate	2	0	1	1
HumanN2	6	join	X	0	1	1
		reduce	1	2	1	1
		regroup	1	3	1	2
		rename	2	2	1	1
		renorm	1	1+X	1	1
		split	1	2	X	1

Tableau 1 : Tableau résumant les caractéristiques des différents outils étudiés

# Pathway	Humann2_ Abundance	Humann2_ Coverage
HOMOSER-METSYN-PWY: L-methionine biosynthesis I	1.3149243918	0.6570127063
HSERMETANA-PWY: L-methionine biosynthesis III	1.1318619128	0.6143434179
PWY-3841: folate transformations II	1.4268868747	0.6798402001
UNINTEGRATED	435.5199558332	1.0000000000
UNMAPPED	2.6377384941	1.0000000000

Tableau 2 : Emple de données obtenues en sortie de "*humann2_join_tables*"

# Pathway	Humann2_ Abundance
UNMAPPED	2.6377384941
UNINTEGRATED	435.5199558332
PWY-3841: folate transformations II	1.4268868747
HOMOSER-METSYN-PWY: L-methionine biosynthesis I	1.3149243918
HSERMETANA-PWY: L-methionine biosynthesis III	1.1318619128

Tableau 3 : Exemple de données contenues dans un fichier d'entrée de "*humann2_join_tables*"

