

Figure 1 : Capture d'écran de l'instance de Galaxy d'ASaiM et de l'interface de l'outil GraPhlan

On retrouve 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.

Galaxy Tool Shed		
3904 valid tools on May 15, 2016		
Search <ul style="list-style-type: none"> Search for valid tools Search for workflows 		
Valid Galaxy Utilities <ul style="list-style-type: none"> Tools Custom datatypes Repository dependency definitions Tool dependency definitions 		
All Repositories <ul style="list-style-type: none"> Browse by category 		
Available Actions <ul style="list-style-type: none"> Login to create a repository 		
Repositories by Category		
search repository name, description		
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 : Capture d'écran du ToolShed principal de Galaxy


```

<tool id="Exemple" name="exemple" version="0.1.0">
  <description></description>
  <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>
  <citations>
  </citations>
</tool>

```

Figure 3 : Capture d'écran 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*"

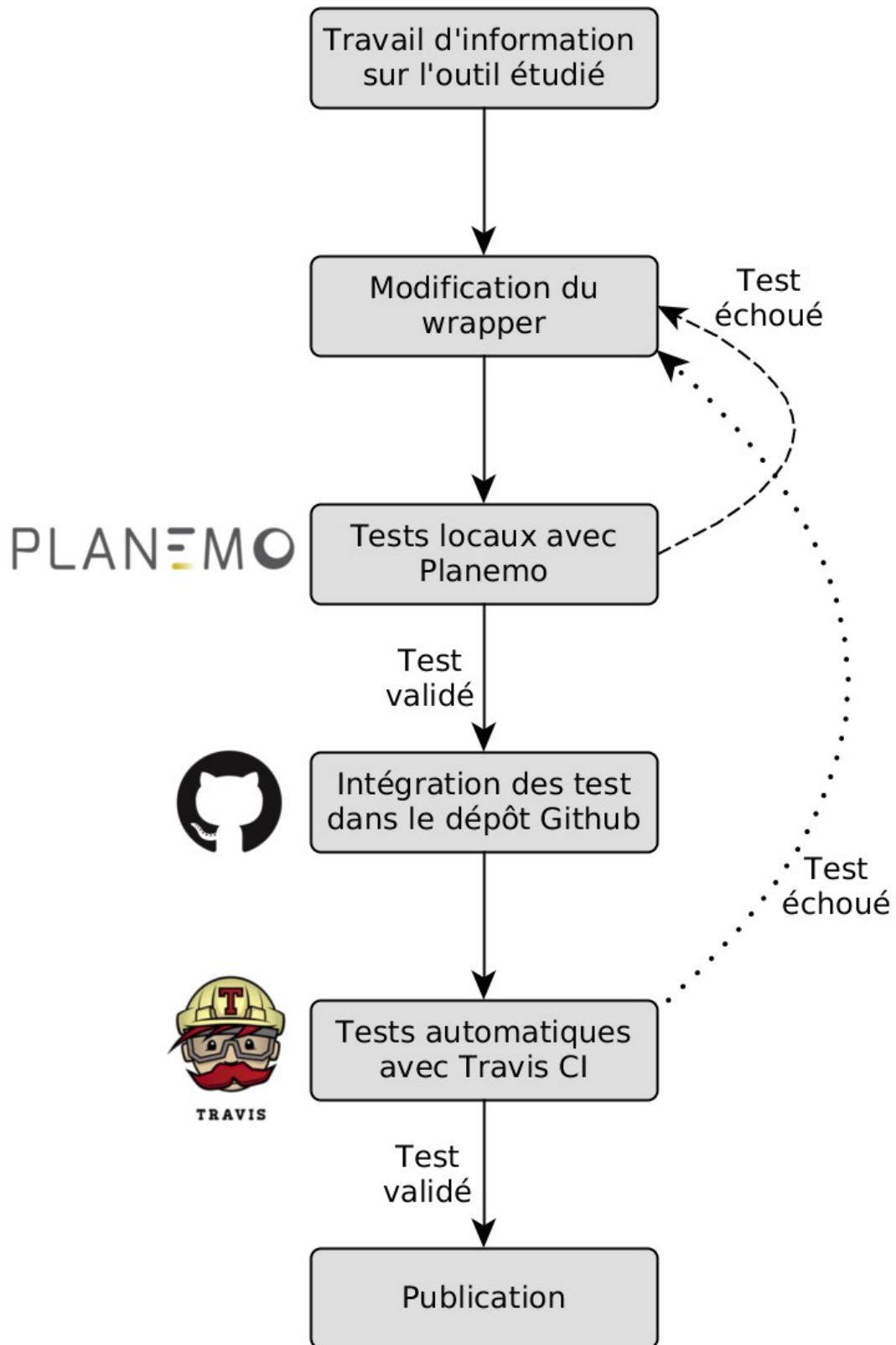


Figure 4 : Schéma pour la mise en place de tests automatiques des wrappers dans l'environnement Galaxy

Atlassian
Bitbucket

Features Pricing

Find a repository... ? English Sign up Log in

Nicola Segata / GraPhlAn

Wiki

Clone wiki

GraPhlAn / Home

View History

GraPhlAn tutorial

GraPhlAn is a software tool for producing high-quality circular representations of taxonomic and phylogenetic trees. It focuses on concise, integrative, informative, and publication-ready representations of phylogenetically- and taxonomically-driven investigation.

Contents

- Overview
- Introduction and some informations about GraPhlAn
 - Download and Installation
 - Scripts
- A step-by-step example
 - Default plot (step 0)
 - Global options (step 1)
 - Node options (step 2)
 - Label options (step 3)
 - External options (step 4)
- Other examples
 - Human Microbiome Project
 - Gut microbiome
 - PhyloPhlAn
 - IBD biogeography
- Complete list of parameters
- GraPhlAn integration with other tools
- Support

Figure 5 : Exemple de source de documentation, ici le wiki de *Bitbucket*, la plateforme où se trouve les données de GraPhlAn

```
<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 : Section test de l'outil GraPlAn après modification


Addtest for `combine_methaph_lan2_human2` #16

[Edit](#)

Merged bebatut merged 6 commits into `ASaiM:master` from `theymard1:br_combine_methaphLan2_human2` on 15 Apr


Conversation 4 Commits 6 Files changed 7

+33,293 -29,435






theymard1 commented on 13 Apr

to resolve #1




theymard1 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




theymard1 added some commits on 14 Apr

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

👍

Labels
None yet

Milestone
No milestone

Assignees
No one assigned

Notifications
[Unsubscribe](#)
You're receiving notifications because you authored the thread.



2 participants
 

Figure 7 : Pull 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_metaphlan2_humann2	1		2	1	1	2
plot_generic_xy_plot	1		1	15	1	1
normalize_data_set	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 I : Caractéristiques des outils et des tests mis en place durant le stage

# 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 II : Exemple 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 III : Exemple de données contenues dans un fichier d'entrée de *'humann2_join_tables'*

