Physiology and Biotechnology of Algae Laboratoty (PBA) – IFREMER Nantes (FRANCE)

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File : PBA-A-001	Made the : 26 november 2017	

PiRATE:
a Pipeline to Retrieve and Annotate TEs

2 December 2017

Wrote by :	**Supervised by :**
Jérémy BERTHELIER	Grégory CARRIER

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TABLE OF CONTENT

Physiology and Biotechnology of Algae Laboratoty (PBA) – IFREMER Nantes (FRANCE)

https://wwz.ifremer.fr/pba_eng/

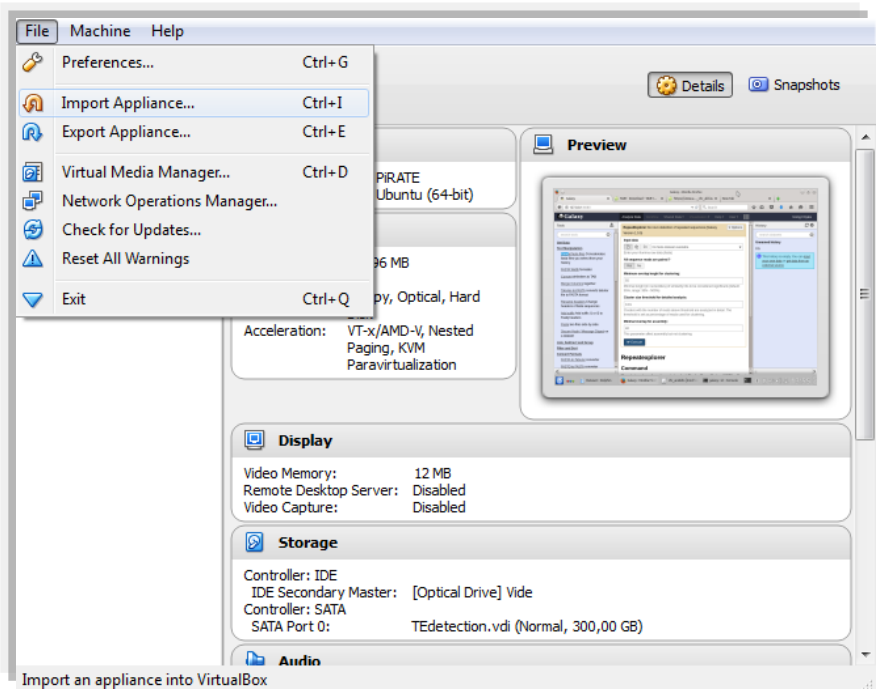
File : PBA-A-001	Made the : 26 november 2017	

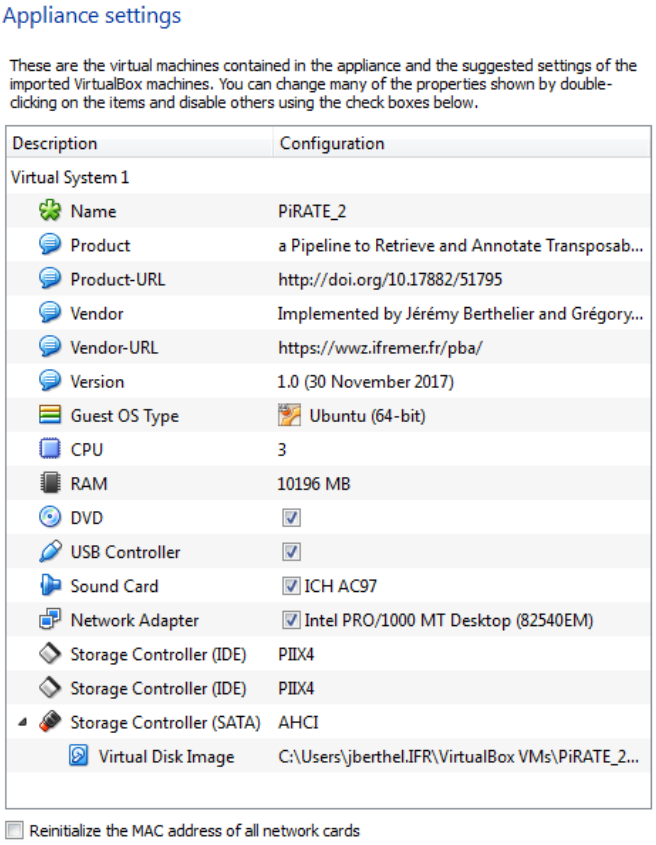
Requirement

- The PiRATE-Galaxy is installed on a virtual machine name PiRATE-VM.
  The PiRATE Virtual Machine (PiRATE-VM) can be download at the following URL
  http://doi.org/10.17882/51795
- To use the PiRATE-VM a virtual machine monitor need to be installed, for example VirtualBox

  https://www.virtualbox.org/.

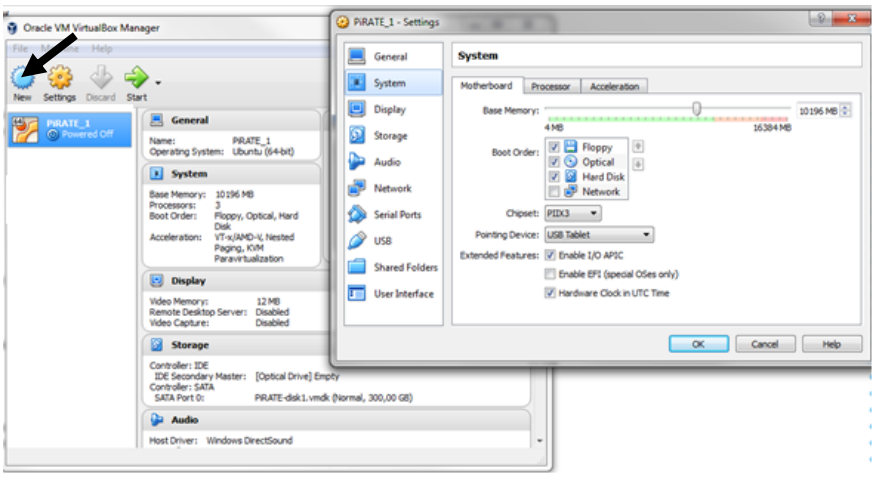
- Once your virtual machine monitor is installed, you need to import the PiRATE-VM.





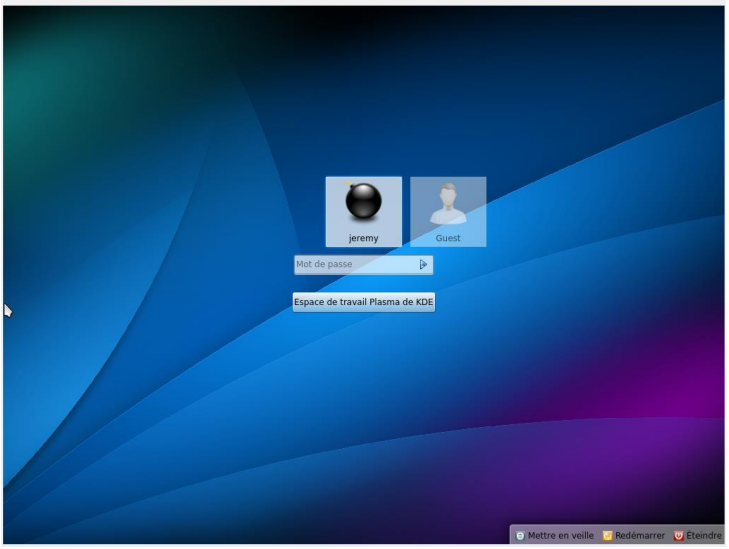
- Made changes according to your computer setting.

Your network setting have to be correctly configured to use the PiRATE-Galaxy.



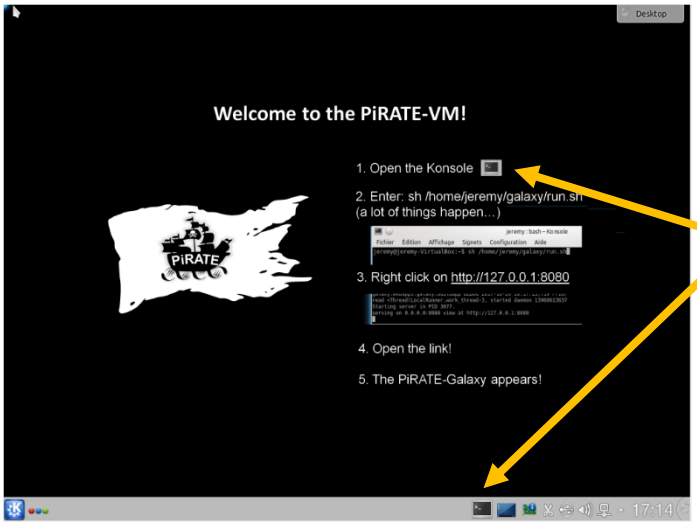
- Open the PiRATE-VM and the “Jeremy” account, the password is: jeremy07

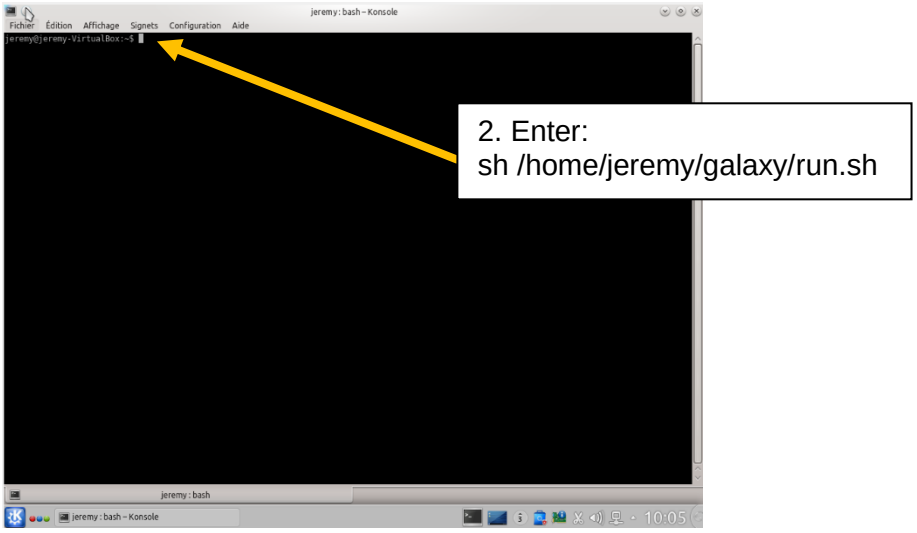
File : PBA-A-001	Made the : 26 november 2017	

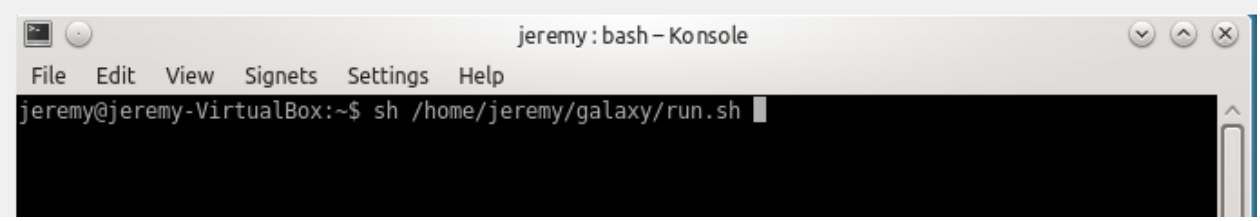


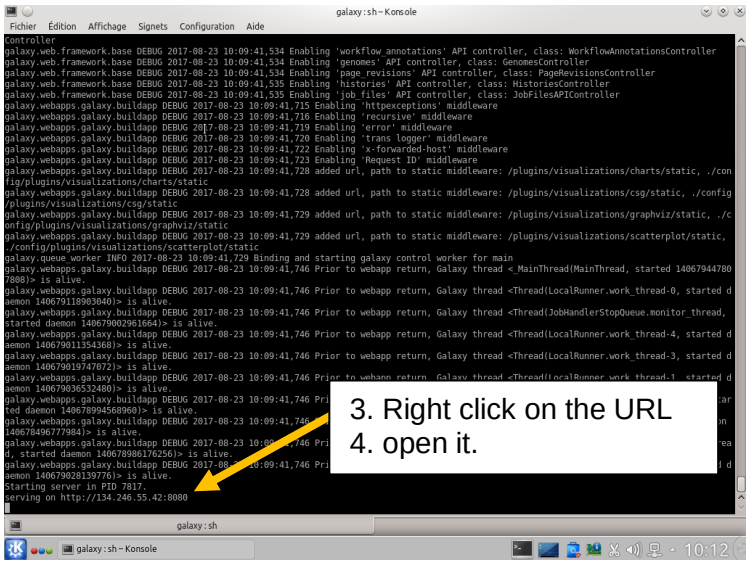
2. How to run your PiRATE-Galaxy

Now the PiRATE-Galaxy can be launched.









The PiRATE-Galaxy is alive!

If not… Check that the network setting of your VM is correctly configured.

Physiology and Biotechnology of Algae Laboratoty (PBA) – IFREMER Nantes (FRANCE)

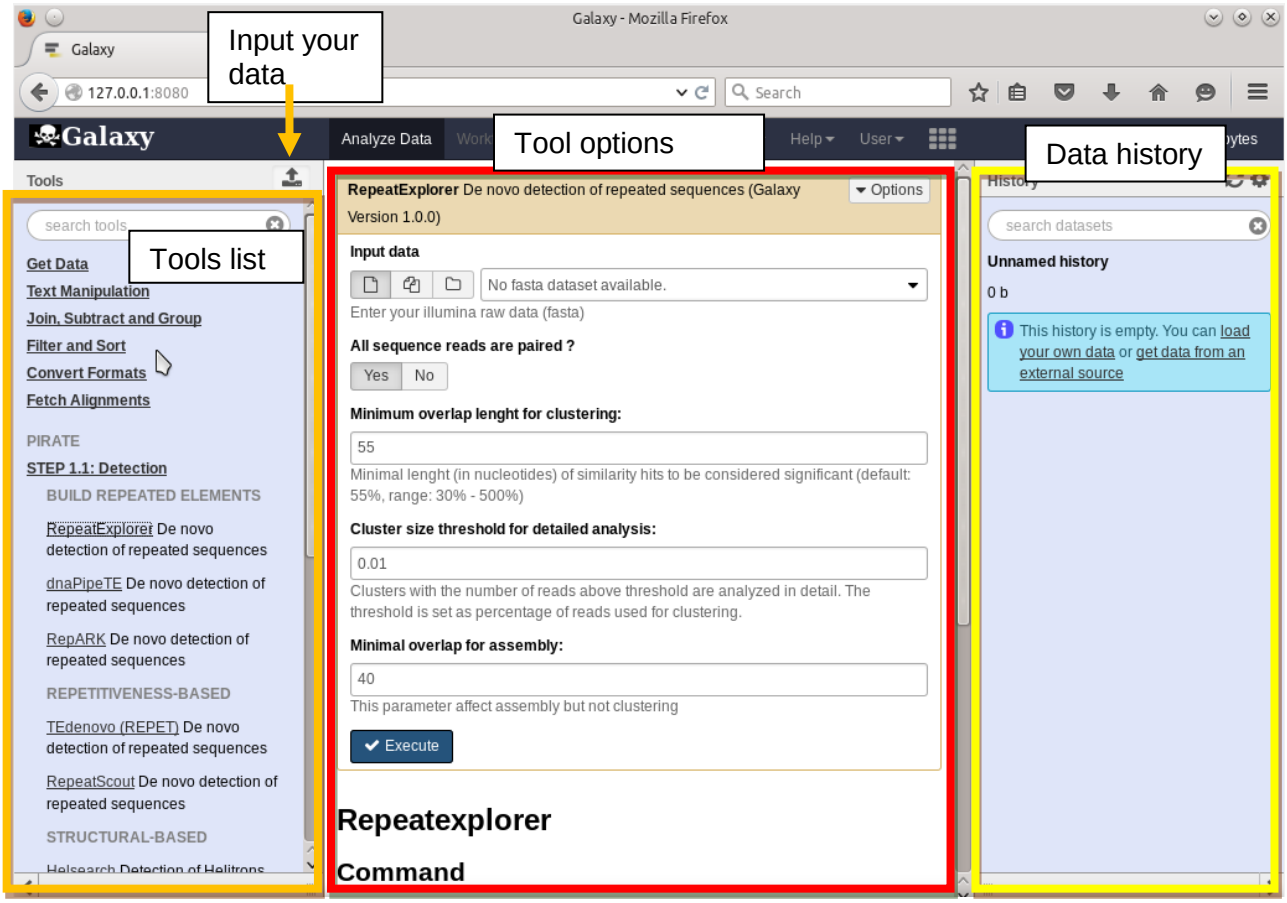
https://wwz.ifremer.fr/pba_eng/

File : PBA-A-001	Made the : 26 november 2017	

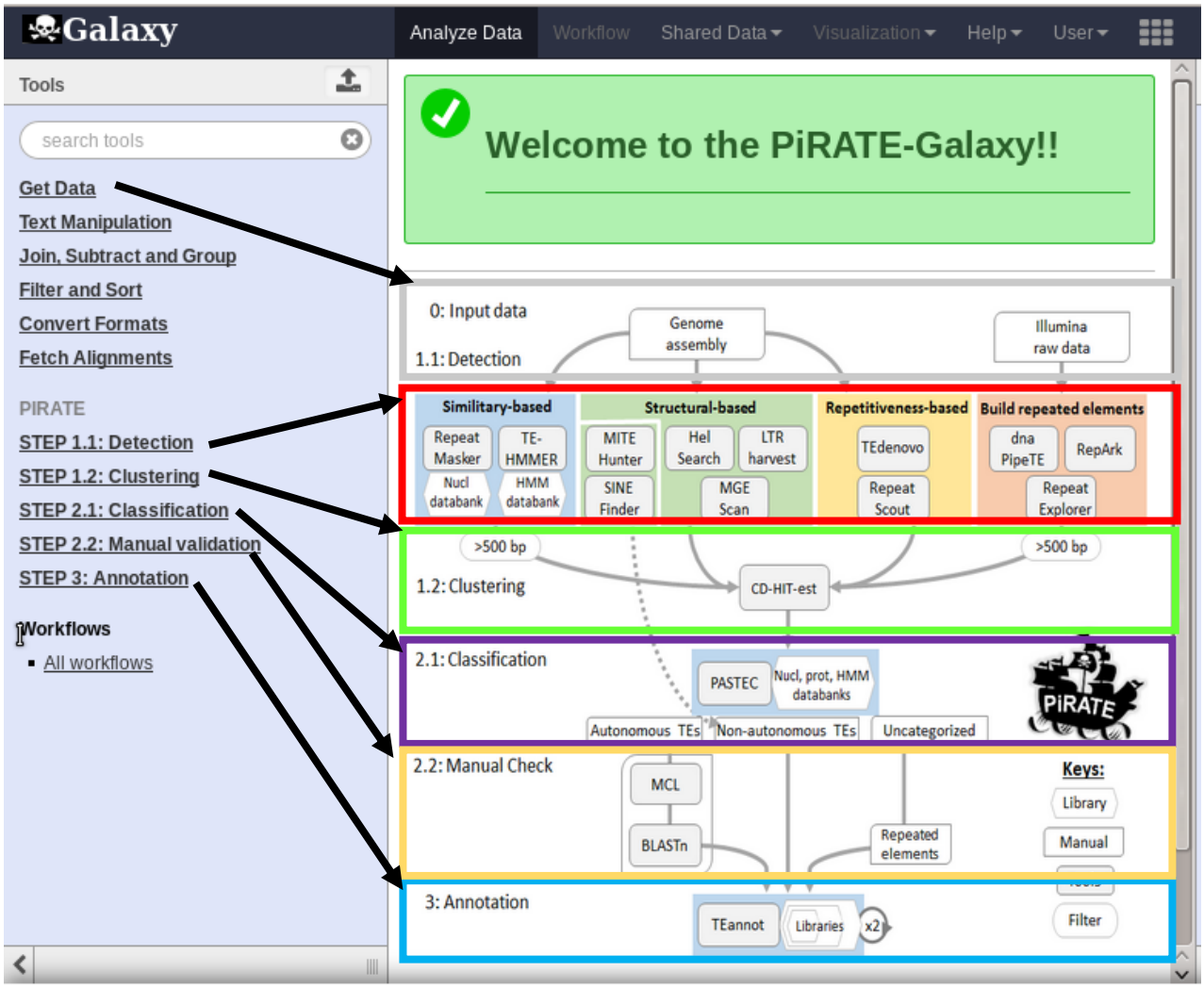
1. Started with your PiRATE-Galaxy

"*Galaxy is an open source, web-based platform for data intensive biomedical research. If you are new to Galaxy start here or consult our help resources. You can install your own Galaxy by following the tutorial and choose from thousands of tools from the Tool Shed.*"

(Giardine et al., 2005) https://usegalaxy.org/



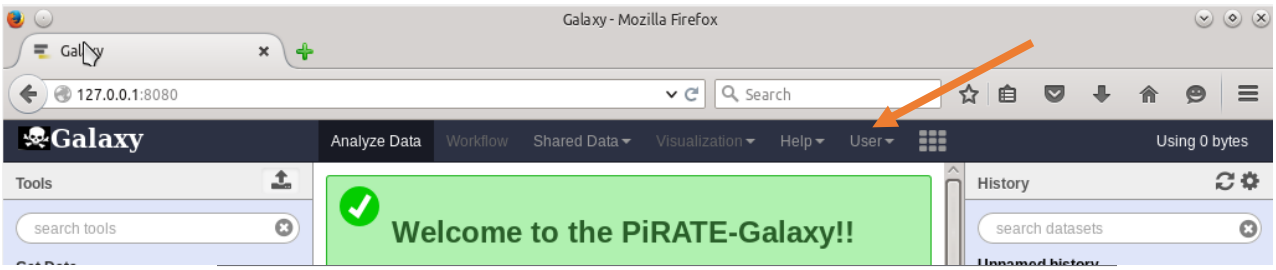
4. Started with the PiRATE pipeline

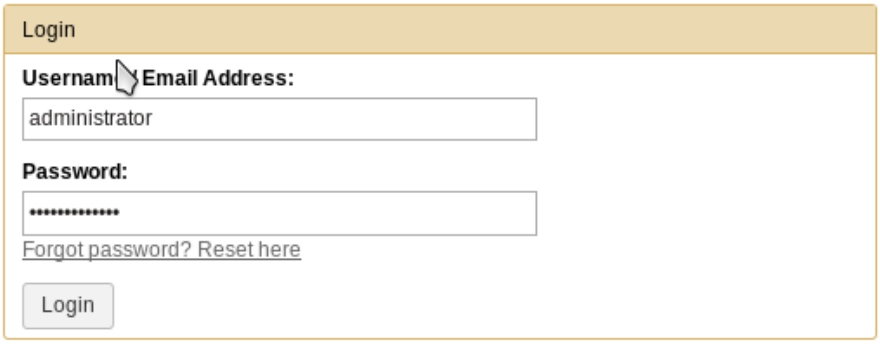


File : PBA-A-001	Made the : 26 november 2017	

STEP 0: Load and prepare your dataset

- Connect you as administrator to the PiRATE-Galaxy





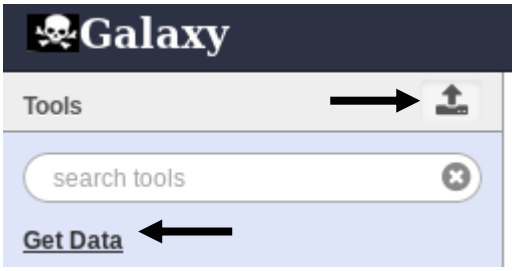
Username: administrator

Password: administrator

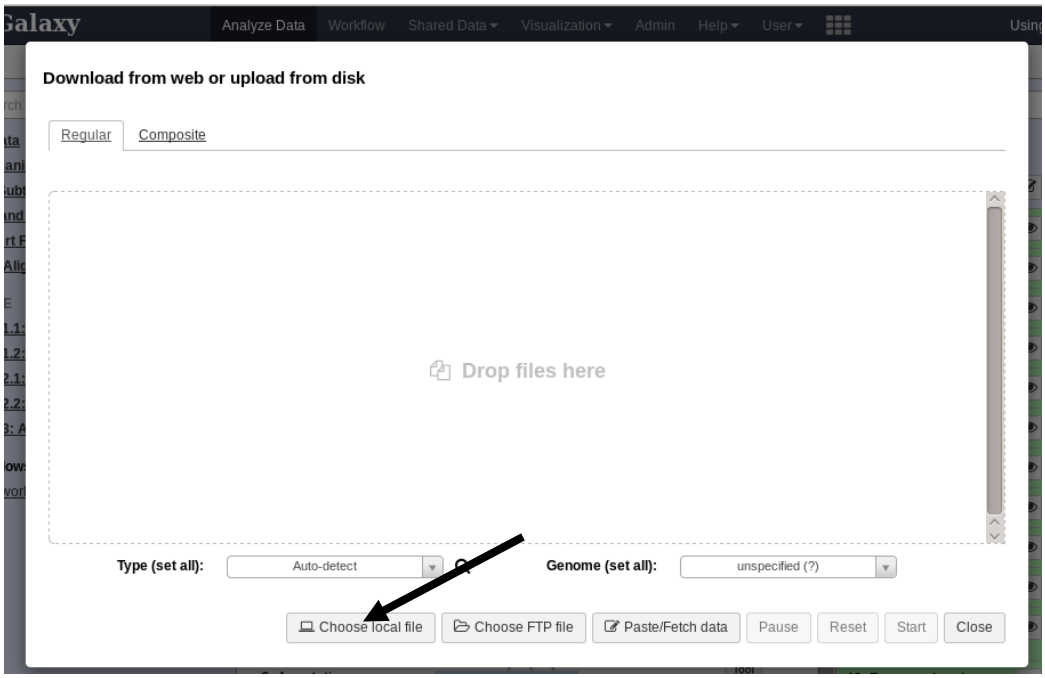
- Three types of data is needed to perform the complete PiRATE pipeline:

  1) A genome assembly (FASTA)
  2) Illumina raw data (FASTQ)
  3) Illumina raw data (FASTA)

- How to load your data?



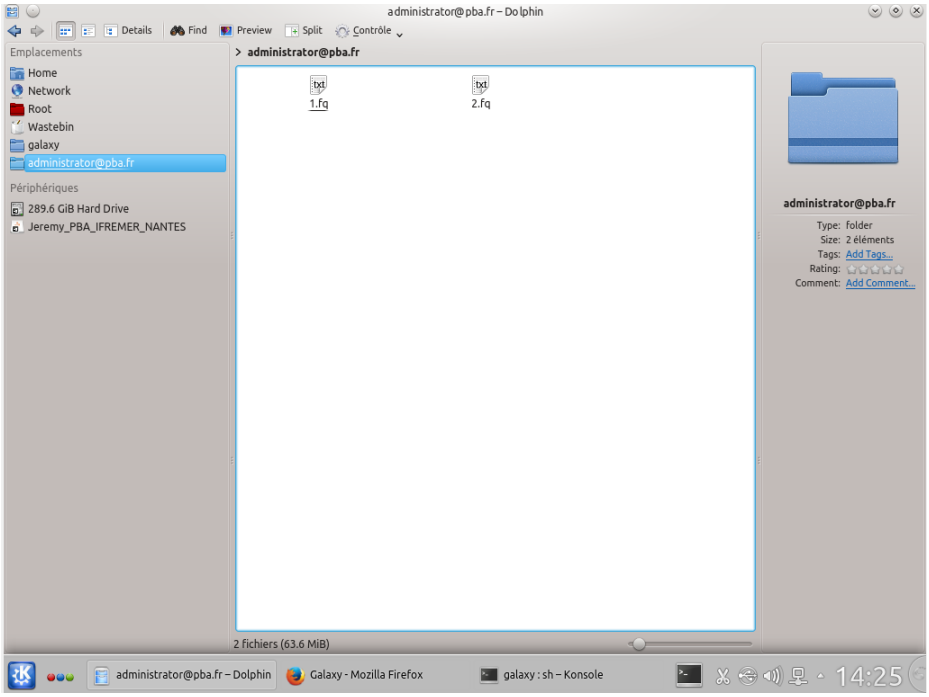
Your genome assembly should have a weight below 1 Go and can be directly download from your computer to the Galaxy environment with the “choose local file” button and launch “Start”.



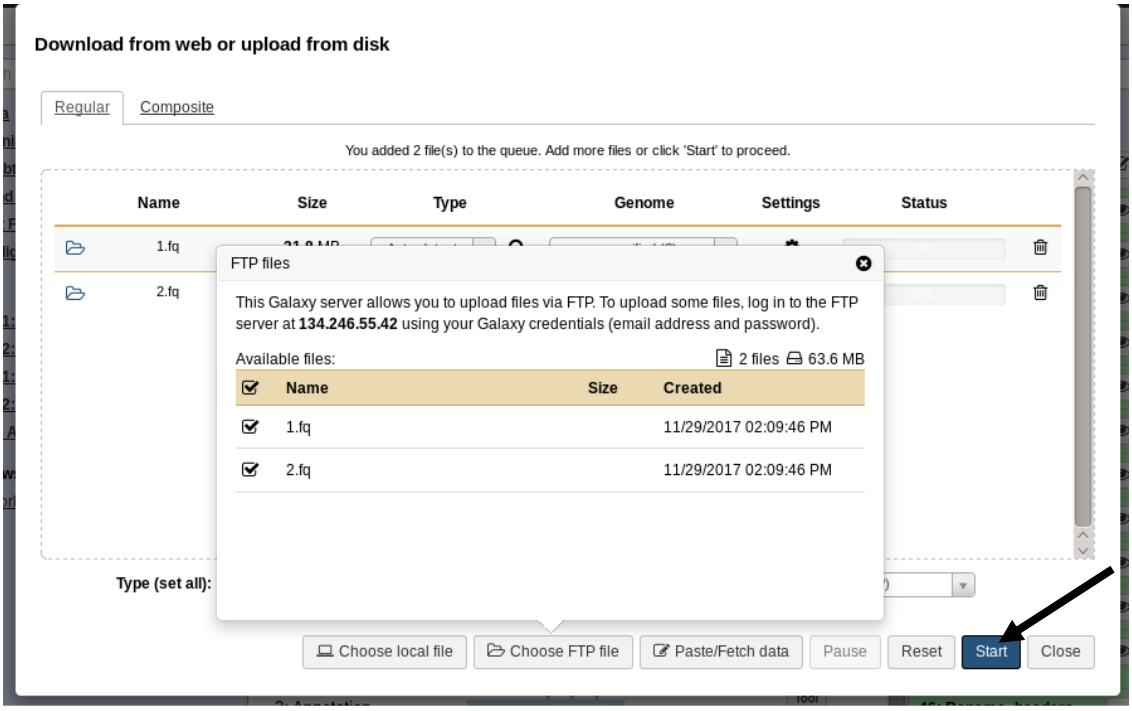
However, your Illumina raw data should have a weight of more than 1 Go. Thus it will be necessary to import it with FTP:

1) You need to copy-past your files in the directory “administrator@pba.fr” of the PiRATE-VM /home/Jeremy/Documents/administrator@pba.fr

File : PBA-A-001	Made the : 26 november 2017	



2) You can now load them into the PiRATE-Galaxy



1) The genome assembly (FASTA)

To avoid any problems with the tools, your FASTA file containing the genome assembly needs to be formatted with short and simple header names (example: Chromosome1)

```
>Chromomose1
AAATTTTAAAATTTGGGCCCAAAACCCCAAACCCAAACCCCAAACCCAACCCCAATTTTTAA
…
>Chromosome2
AAATTTTAAAATTTGGGCCCAAAACCCCAAACCCAAACCCCAAACCCAACCCCAATTTTTAA
….
```

You can rename the headers of your FASTA file with the tool “Rename headers” in the ‘’Text Manipulation’’ section.

- Your FASTA sequences must be formatted with 60 pb per line.

You can do this task with the tool “FASTA within” in the ‘’Text Manipulation’’ section.

Your genome assembly is ready!

2) The Illumina raw data (FASTA and FASTQ)

You should probably have your data in the FASTQ format, it’s ok for the tools dnaPipeTE and RepARK.

However, RepeatExplorer uses FASTA file:

a) Use a single data file for RepeatExplorer

You can convert your single FASTQ file into FASTA with the tool ‘’FASTQ to FASTA converter’’ in the ‘’Convert Formats’’ section.

b) Use paired data (advised) for RepeatExplorer

File : PBA-A-001	Made the : 26 november 2017	

To use the tool RepeatExplorer with the paired data option, the headers of your FASTQ files need to finish by the indication “/1” (forward) or “/2” (reverse).

Exemple:

```
>readname/1
AAATTTTAAAATTTGGGCCCAAAACCCCAAACCCAAACCCCAAACCCAACCCCAATTTTTAA

>readname/2
AAATTTTAAAATTTGGGCCCAAAACCCCAAACCCAAACCCCAAACCCAACCCCAATTTTTAA
```

If not, you can add them by using the tool “Add suffix” in the “Text Manipulation” section.
Do this manipulation for each of your file (forward and reverse). This can be time consuming.

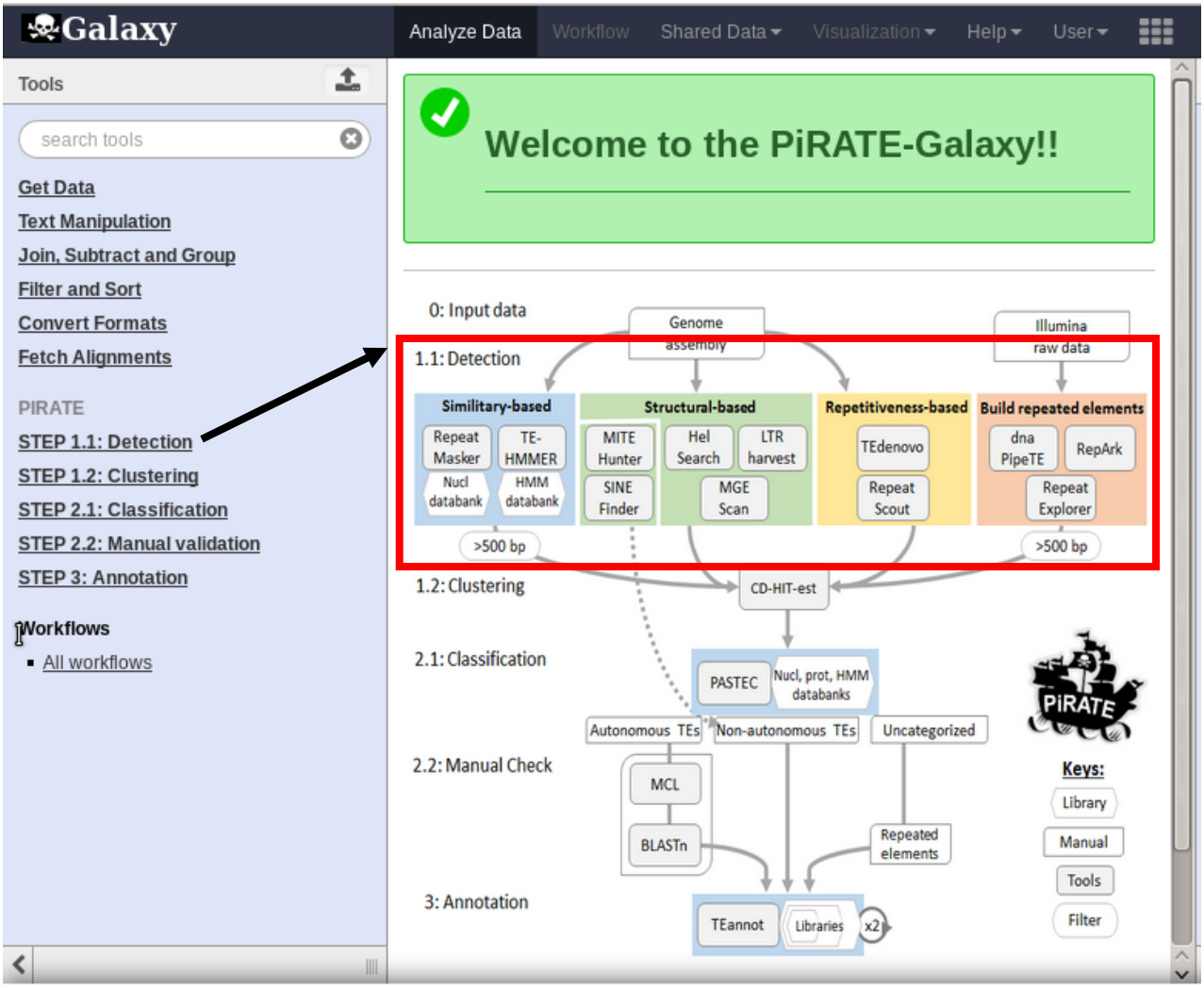
Then, you need to join your forward and reverse file in once with the tool ‘’FASTQ interlacer’’ in the section “Join, Substract and Group”.

Then, you can convert your FASTQ file containing the forward and reverse into one FASTA file by using the tool ‘’FASTQ to FASTA converter’’ in the ‘’Convert Formats’’ section.

Your Illumina raw data in FASTQ and FASTA are ready!

File : PBA-A-001	Made the : 26 november 2017	

STEP1: Detection of putative TEs



The detection step of PiRATE is flexible, you can use every tools one after one or only select your favorite ones.

Here is the list of the available tools with their authors and the URL:

***Approach 1**: Similarity-based detection*

- **RepeatMasker** (Smit, A. F., Hubley, R., & Green, P. (1996).) www.repeatmasker.org/

This tool detects putative TE sequences from the comparison of the genome assembly and a nucleotide databank of known TEs. It is possible to use the default databank of PiRATE or yours.

- **TE-HMMER is a** made-self-tool using HMMER (Eddy and others, 1995) and BLAST (Altschul et al., 1990)

This tool detects putative TE sequences from the comparison of the genome assembly of your studied organism and a databank composed of profile HMM of known TEs. It is possible to use the default databank of PiRATE or yours.

***Approche 2**: Structural-base detection*

- **LTRharvest** (Ellinghaus et al., 2008) http://www.zbh.uni-hamburg.de/?id=206

This tool detects LTR from a genome assembly.

- **MGEScan non-LTR** (Rho and Tang, 2009) http://mgescan.readthedocs.io/en/latest/nonltr.html

This tool detects LINE from a genome assembly.

- **Helsearch** (Yang and Bennetzen, 2009) http://omictools.com/helsearch-tool

This tool detects Helitron from a genome assembly.

- **MITE-Hunter** (Han and Wessler, 2010) http://target.iplantcollaborative.org/mite_hunter.html

This tool detects MITE from a genome assembly.

- **SINEfinder** (Wenke et al., 2011) http://www.plantcell.org/content/23/9/3117

This tool detects SINE from a genome assembly.

***Approche 3**: Repetitiveness-base detection*

- **TEdenovo** (Flutre et al., 2011) https://urgi.versailles.inra.fr/Tools/REPET

This tool belongs to the REPET pakage, it allow to detect repeated sequences with RECON, GROUPER and PILER, group them into cluster and create consensus sequences for each cluster.

- **RepeatScout** (Price et al., 2005) https://bix.ucsd.edu/repeatscout/

This tool detects repeated sequences by using k-mer method, group them into cluster and create consensus sequences for each cluster.

***Approche 4**: Build repeated sequences*

- **RepeatExplorer** (Novak et al., 2013) http://repeatexplorer.umbr.cas.cz/

This tool samples reads and compare them with BLAST. Overlapping read are connected with a graph-based algorithm and grouped into cluster. Read belonging to each cluster are assembled with CAP3.

- **dnaPipeTE** (Goubert et al., 2015) https://lbbe.univ-lyon1.fr/-dnaPipeTE-.html

This tool samples reads and assemble repeated elements with Trinity.

- **RepARK** (Koch et al., 2014) https://github.com/PhKoch/RepARK

This tool uses a graph-based method to detect abundant k-mers from illumina reads. Abundant k-mers were isolated and assembled using, resulting in a *de novo* repeat libraries.

File : PBA-A-001	Made the : 26 november 2017	

Important:

I advised you to change the format of output files obtained from each detection tools.

- Change the headers name by the tool name to know where they come from.

Example:

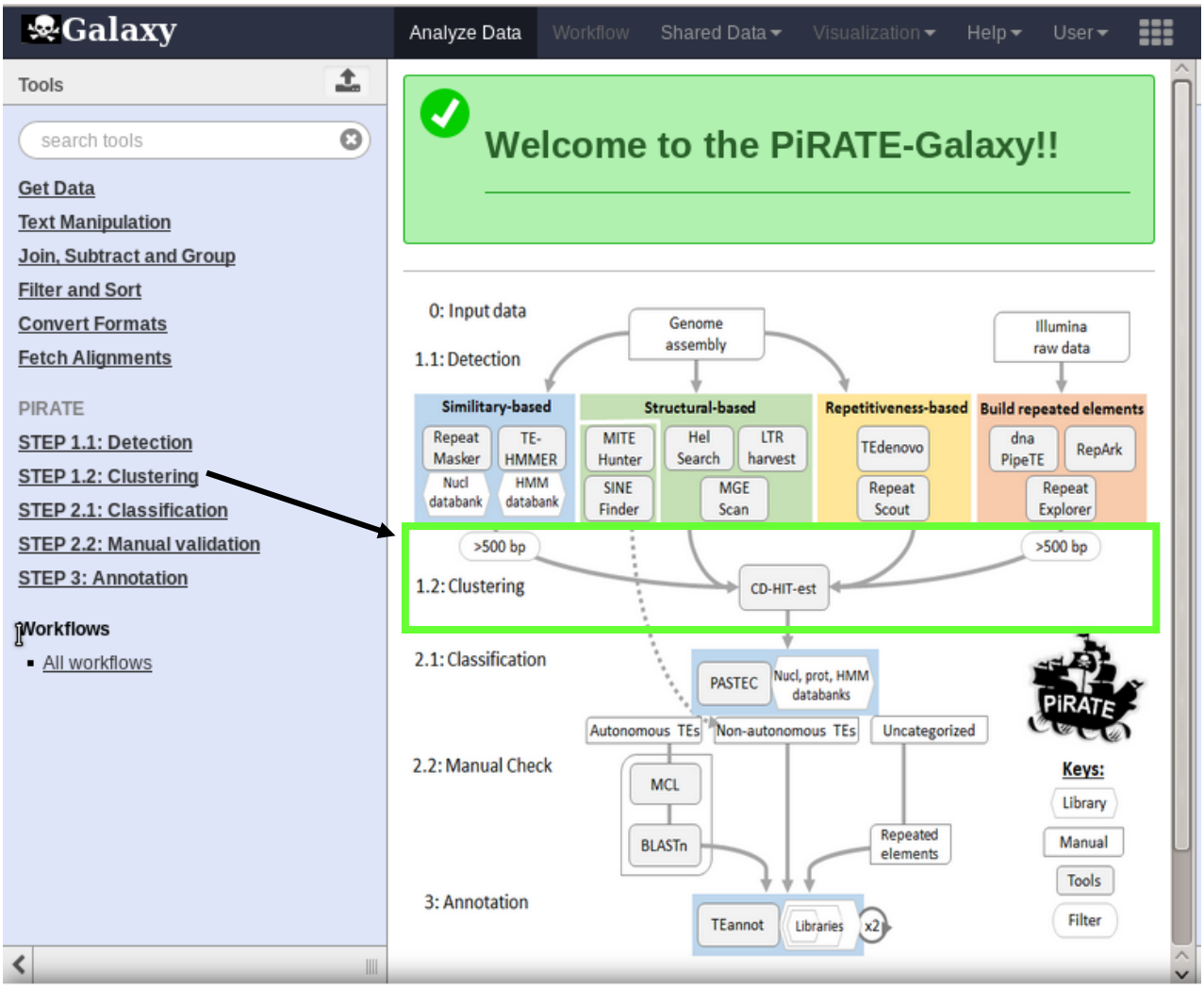
>LTRharvest_1
>LTRharvest_2
….

You can rename the header of your output file with the tool “Rename headers” in the ‘’Text Manipulation’’ section.

- Your FASTA sequences must be formatted with 60 pb per line.

You can do this task with the tool “FASTA within” in the ‘’Text Manipulation’’ section.

STEP 2: Sort your detected sequences



- ***Remove short sequences:***

It is possible that the approach 1 and the approach 2 give a high number of short sequences. In order to be more efficient in time and decreased the high number of repeated sequences, you can choose to remove the sequences below a length of 500 pb. The tool “remove short sequences” realizes this task.

- ***Concatenated outputs sequences:***

Sequences detected from the step 1 (without those obtained with MITE-hunter and SINEfinder) can be concatenated for the “Clustering step”. You can use the tool “concat FASTA files” in the ‘’Text Manipulation’’ section.

- ***Clustering to remove redundant sequences:***

In order to decrease the redundancy, PiRATE uses the tool CD-HIT-est (Li and Godzik, 2006) http://weizhongli-lab.org/cd-hit/. We use it to cluster sequences that are 100% identical to a part of a larger sequence. This allows to remove the redundant shorter sequences which are already detected with a longest length in another sequence. If necessary, it is possible to decrease the percentage of identity.

We used as setting: aS= Sa/S=1 and c=%identity=1

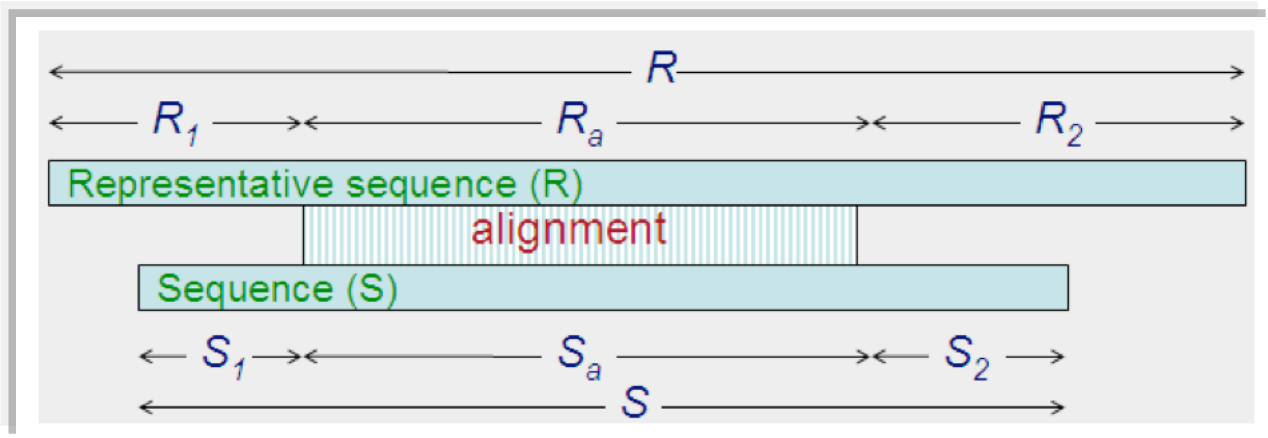
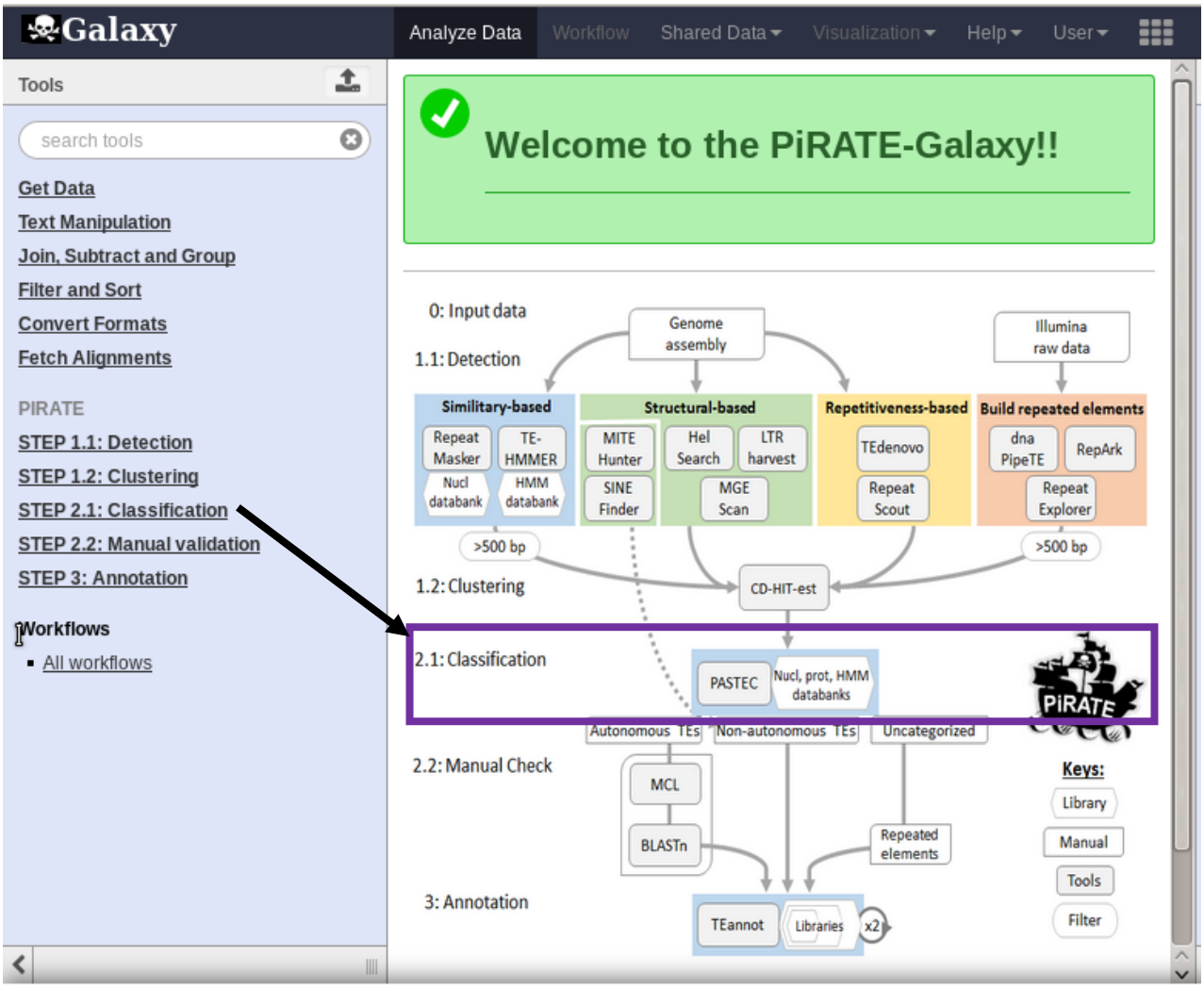


Figure from https://github.com/weizhongli/cdhit/wiki/3.-User's-Guide#CDHITEST

STEP 3: Classification

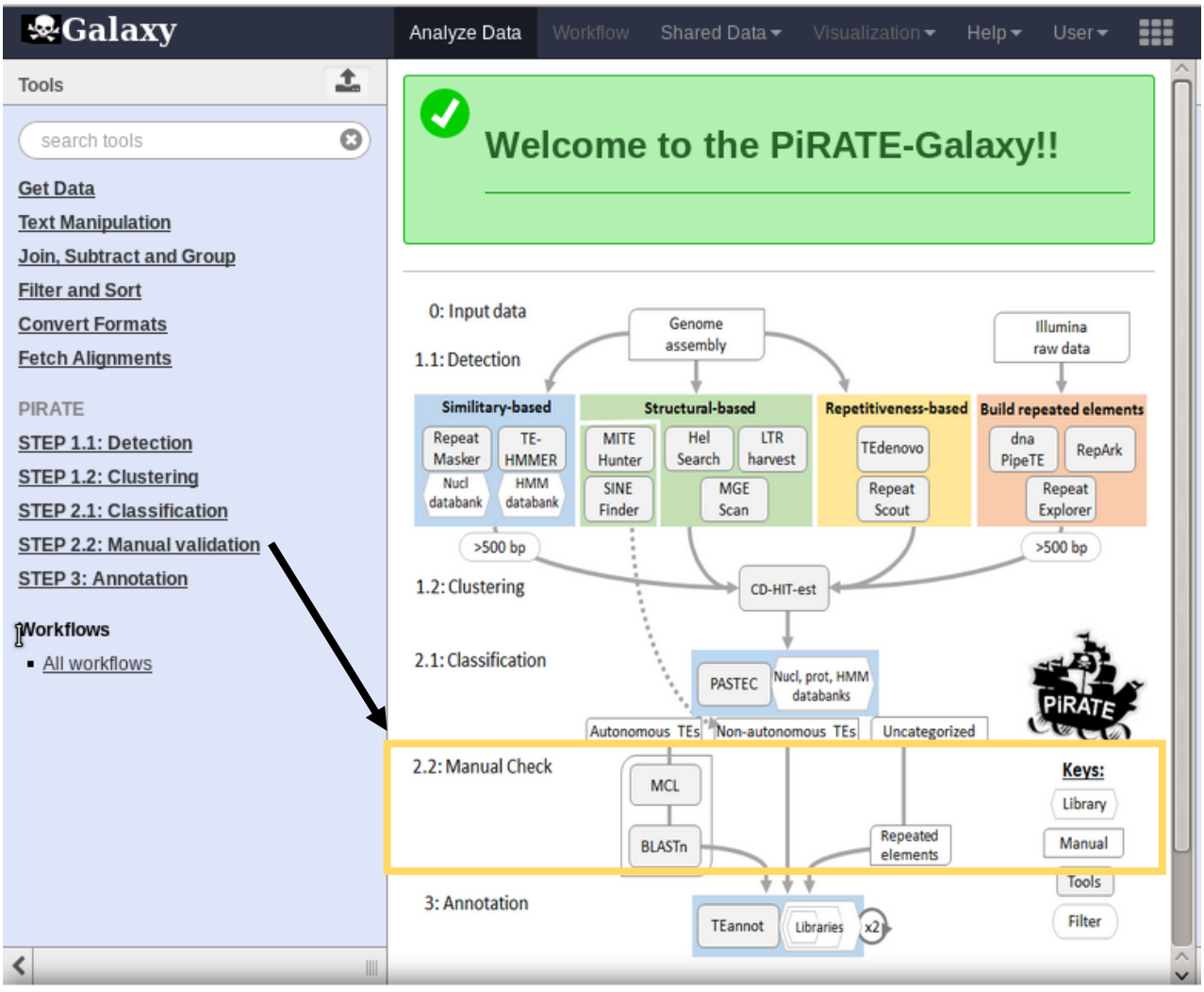


Once your putative TE sequences have been clustered with CD-HIT-est to reduce the redundancy, it generate an output file that you will submitted to classification.

To realize the classification of your putative TEs, PiRATE uses PASTEC (Hoede et al., 2014)
https://urgi.versailles.inra.fr/Tools/PASTEClassifier
This tool works with as input data a FASTA file with simple headers and with a width of 60 pb for every nucleotide line.

Currently, it is only possible to use PASTEC with the PiRATE databanks (nucleotide, protein and profil HMMs). The use of your own custom databank is still in progress and will be possible in the upgrade version of PiRATE.

STEP 4: Manual Check



The manual check step is advised. Here is the method that we used for the annotation of the *T. lutea* genome:

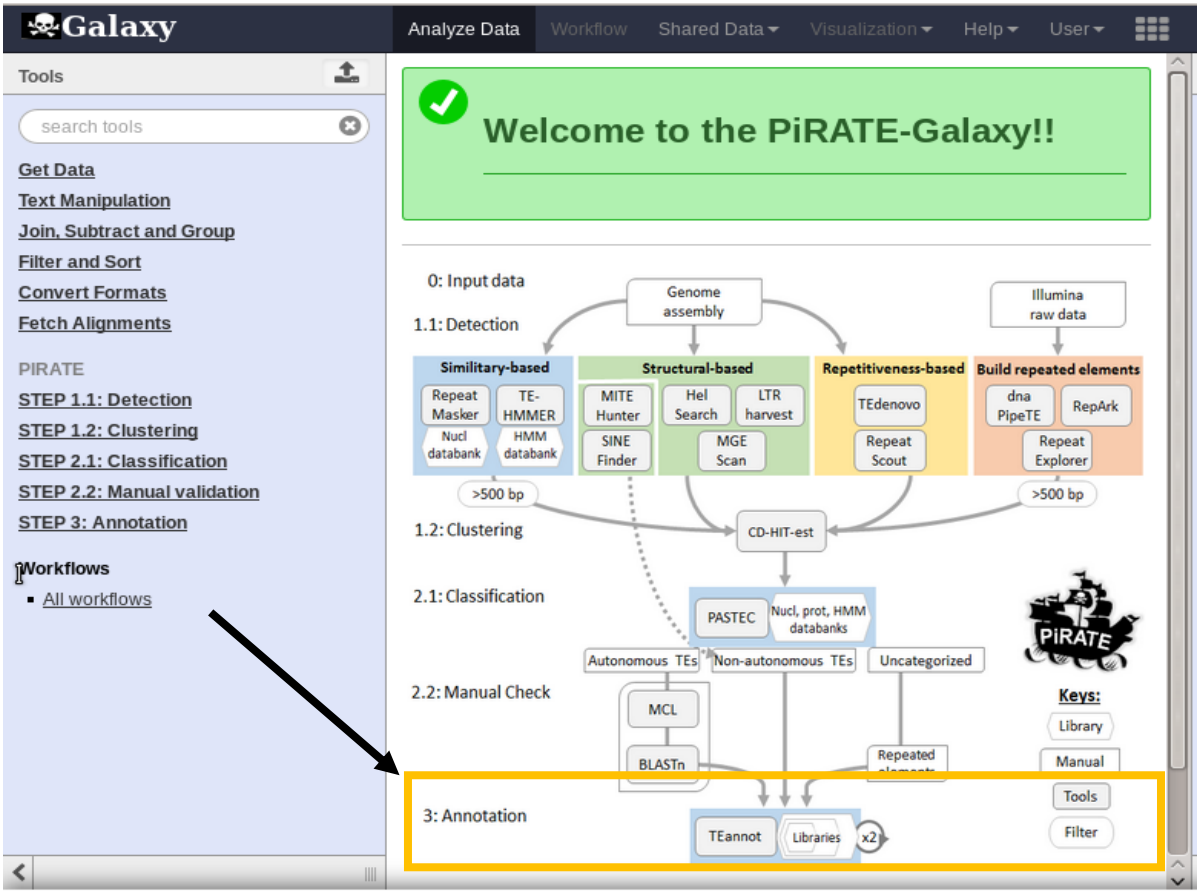
- Three libraries were manually constructed with a “Russian doll” strategy in order to perform separated annotations, a “potentially autonomous TEs library”, a “total TEs library” containing the potentially autonomous TEs and the non-autonomous TEs and a “repeated elements library” containing in addition the uncategorized repeated sequences. Sequences classified as LTR, LINE and TIR were manually sorted in superfamily (according to the evidence section produced by PASTEC).

- To facilitate their manual check, sequences belonging to the same putative superfamily were grouped into families with MCL. The percentage of identity between sequences belonging to the same family were checked with Blastn (-identity: 80%). We followed the 80-80-80 Wicker rules to form families.

- Finally, larger sequences from each TE family were checked and selected for the “potentially autonomous TEs library” according to the presence of TE domains or similarities with Pfam (http://pfam.xfam.org/), NCBI-BLASTx and Censor (http://www.girinst.org/censor/). We define as potentially autonomous LTR, sequences bearing at least a reverse transcriptase and an integrase domain and having similarity with LTR sequences in databanks. We define as potentially autonomous LINE, sequences bearing at least a reverse transcriptase domain and sharing similarity to LINE sequences in databanks. We define as potentially autonomous TIR, sequences having an evidence of a transposase domain or similarity to TIR sequences in databanks.

No manual check were performed for sequences classified as non-autonomous TEs. Sequences classified as SINE, MITE and TRIM were directly selected for the “total TEs library”. Only sequences classified as LARD, which were obtained with the repetitiveness-based approach of TE detections (TEdenovo or Repeatscout) were selected. Sequences detected by SINE-Finder and MITE-Hunter were also directly selected for the “total TEs library”. Finally, the sequences classified as noCat (uncategorized) and obtained with the repetitiveness-based approach of TE detections were selected for the “repeated elements library”.

STEP 5: Annotation



The annotation can be performed by TEannot (Flutre et al., 2011)

https://urgi.versailles.inra.fr/Tools/REPET

Here is the method that we used for the annotation of the *T. lutea* genome:

Three libraries were built a “potentially autonomous TEs library” 2) an “total TEs library” and 3) a “repeated elements library”. A first run of TEannot was performed for each library to known sequences matching with a full-length size on the genome (FLC sequences) and remove potential chimeric data. A second run of TEannot was performed with these FLC sequences for each of the final library and three annotations were obtained.

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Price, A.L., Jones, N.C., and Pevzner, P.A. (2005). De novo identification of repeat families in large genomes. Bioinformatics *21*, i351–i358.

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Smit, A. F., Hubley, R., & Green, P. (1996). RepeatMasker.

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