User feedback of a Galaxy workflow conception

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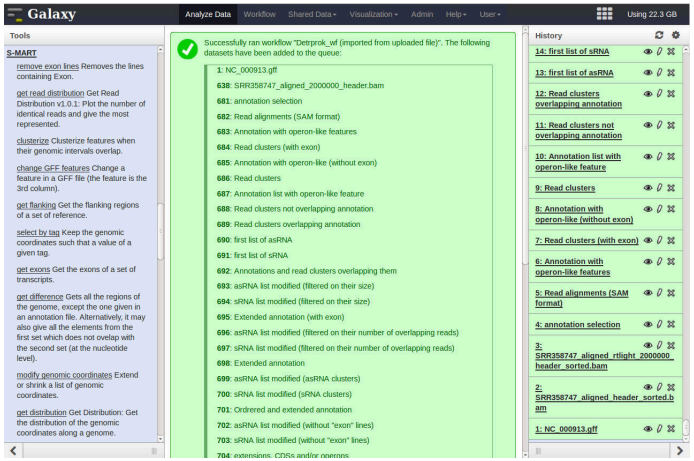
How have I built the Workflow?

step-by-step, biologist
Data = README file
s-mart tools, home-made scripts

```
### 1- select reads outside "gene" :
# select reads (-i VIBSP_chrI_smart.gff3) outside
# "annotation" (-j NC_011744_annot.gff3 -c -x), with
# keeping reads overlapping ATG (-e 10)
for i in "NC_011744" "NC_011753" ; do
        compareOverlapping.py -i ${i}_RNAseq_smart.gff3 -f gff3
-j ${i}_annot.gff -g gff3 -e -10 -x -c -o ${i}_cis_ReadsOutGene ;
done ;
### 2- clusterize reads before seed selection :
# 2 clusterization steps: strict + d < 20
for i in "NC_011744" "NC_011753" ; do
        clusterize.py -i ${i}_cis_ReadsOutGene.gff3 -f gff3 -c -o $
{i}_cis_e10_clusters ;
        clusterize.py -i ${i}_cis_e10_clusters.gff3 -f gff3 -c -d 20 -o
${i}_cis_e10_clusters20 ;
### 3- crossing cluster with seed :
for i in "NC_011744" "NC_011753" ; do
  seedGff.pl -i ${i}_annot.gff -p 25 -e 15 -o ${i}_cis_seed.gff ; #
seed creation in -15 -25 bp from ATG
  compareOverlapping.py -i ${i}_cis_e10_clusters20.gff3 -f gff3 -j $
{i}_cis_seed.gff -g gff3 -c -o ${i}_cis_e10_cluster20InSeed2515 ; #
crossing cluster with seed
done ;
#
### 4- filters: nb_reads > 10 reads + length > 50 nt
for i in "NC_011744" "NC_011753" ; do
  selectByTag.py -i ${i}_cis_e10_cluster20InSeed2515.gff3 -f gff -o
${i}_cis_e10_cluster20InSeed2515_nbEUp10 -g "nbElements" -m
10 -d 0 ; # nb_reads > 10 filter
done ;
...
```

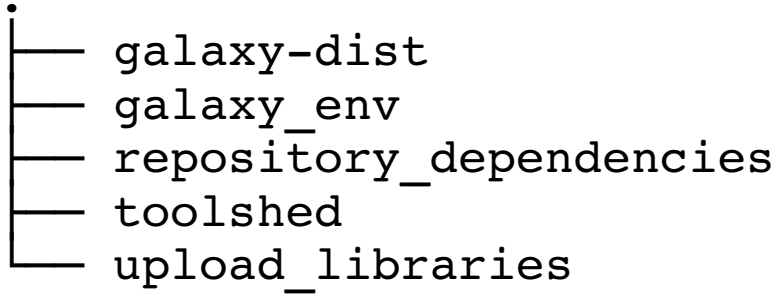
Wrap tool, share (test/toolshed)
Import on my local Galaxy instance
Manual launch, follow the readme file



Extract Workflow from History
Edit workflow: close or open parameter (« set at run time »), add comments, change name of the steps
Share Workflow (test/toolshed)

Technical issues

- Use « virtual_env »
- Dissociate « your » directories from the Galaxy distribution (configure the universe_wsgi.ini file)



- « underlying » database :

  SQLite => postgres

  allow concurential accesses, count DB in the ressources needed

- Install a Galaxy instance on a stratuslab virtual machine during revision process of the publication

stratuslab

Feedbacks

User's point of view: local instance *vs.* Galaxy server ?

User : import workflows, not the tools (admin account).

Ok in a local instance, contact the admin in a server => not so easy !

Open questions (perhaps have you the answers?):

- How expliciting the need of specific tools? **dependencies?**
- **« Global » variables?** Launching a tool many times implies to re-enter the same values for open parameters. Environment variables?
- **Meta-worflow?** Begin = bam file (user chooses the mapper). How add the mapping step? another workflow and combine the two?

DETR'PROK

Methods

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Diversity of the non-coding transcriptomes revealed by RNA-seq technologies

Detection of non-coding RNA in bacteria and archaea using the DETR'PROK Galaxy pipeline ☆

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Galaxy Tool Shed / (sandbox) Repositories Help User

2279 valid tools on Oct 24, 2013

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Available Actions
- Login to create a repository

Repositories with matching workflows

workflow name: **detrprok**
exact matches only: **False**

Repository name	Synopsis	Revision	Owner
detrprok_wf	ncRNA detection in prokaryote oriented RNAseq	f0ca0981eb86	claireth
detrprok_wf	ncRNA detection in prokaryote oriented RNAseq	8f7eb127baf3	claireth
detrprok_wf	ncRNA detection in prokaryote oriented RNAseq	bb71a378053a	claireth

For 0 selected items: Install to Galaxy

myexperiment