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To cite this version:

Dagmara Robakowska Hyzorek, Marie Mirouze, Pierre Larmande. Integration and Visualization of Epigenome and Mobilome Data in Crops. JOBIM: Journées Ouvertes Biologie Informatique Mathématiques, Jun 2016, Lyon, France. , 2016. hal-01411668

HAL Id: hal-01411668

https://hal.science/hal-01411668v1

Submitted on 9 Dec 2016

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Integration and Visualization of Epigenome and Mobilome Data in Crops

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Introduction:

In the coming years, the study of the interaction between the epigenome and the mobilome is likely to give insights on the role of TEs on genome stability and evolution.

In the present project we have created tools to collect epigenetic datasets from different laboratories and databases and translate them to a standard format to be integrated, analyzed and finally visualized.

Visualization:

For data visualization we used Circos, a powerful standalone tool. The circular layout representations greatly enhance the visualization of scientific results.

Data Integration:

We aim to integrate our data in online epigenome and mobilome database for the rice and arabidopsis data.

- GBrowse graphical interface: 1 : pop up menu 2 : part of detailed report, both available for each feature.
- Quick search: search through all databases and display search results as tables.

Conclusion:

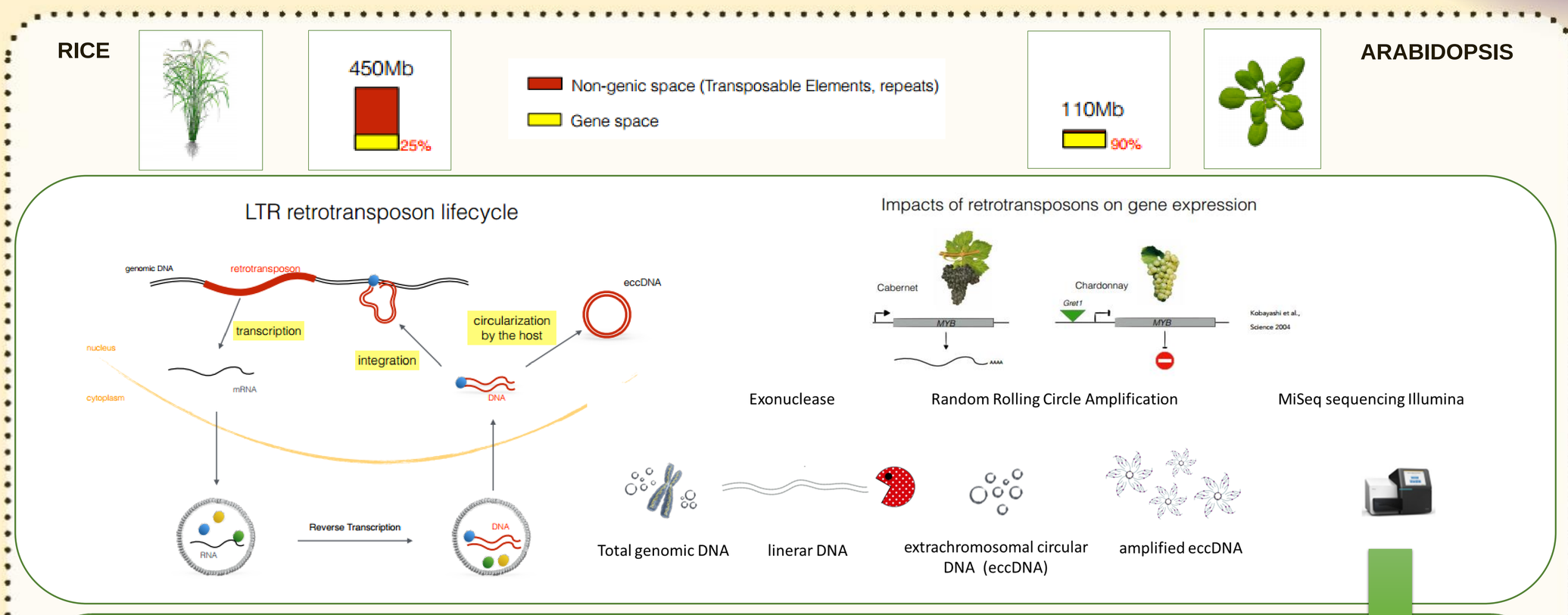
Playing on different filter parameters and tools, this versatile workflow will be useful in the detection of active transposable elements. It has already been run on different data sets, from *Arabidopsis thaliana* and *Oryza sativa.*

Perspectives:

This tool will be adapted to other crops (maize, potato etc..)

Participation financée par le Labex NUMEV
http://www.lirmm.fr/numev/

Transposable elements (TEs) in plant genomes



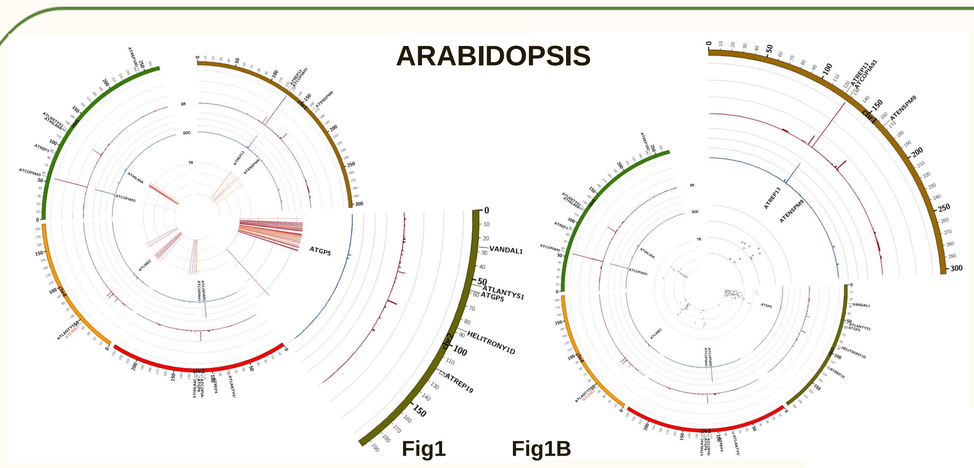
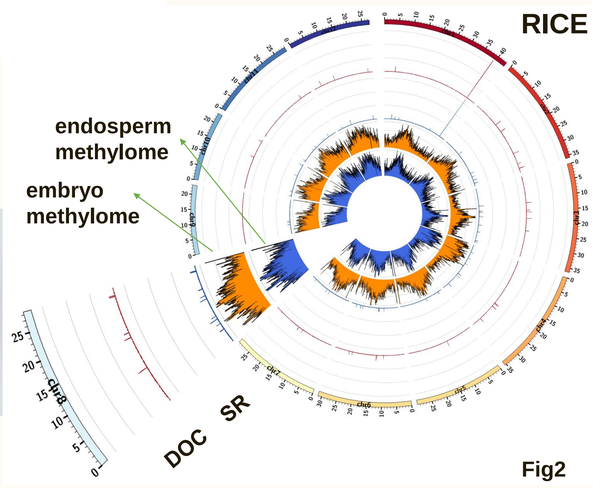


Fig1, Fig1B - Circos plots of Mobilome-seq from Arabidpsis mutants, track red and blue represents TEs coverage per million reads per 100bp) in two experiments (SR, DOC) as histograms. Track TR – transcriptome coverage, represents as heatmap and scatter plot respectively.



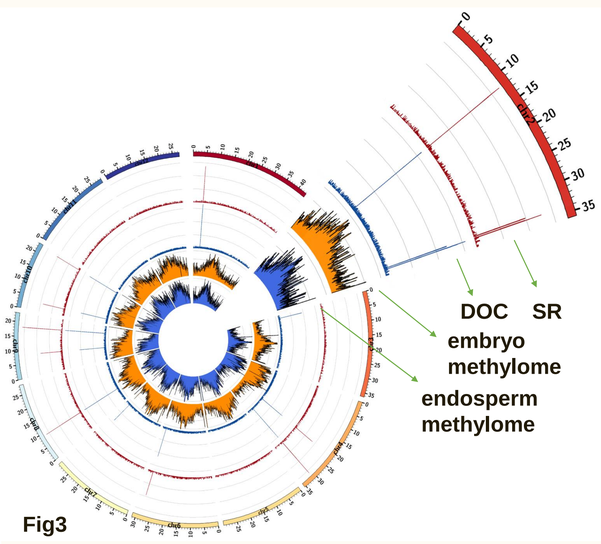
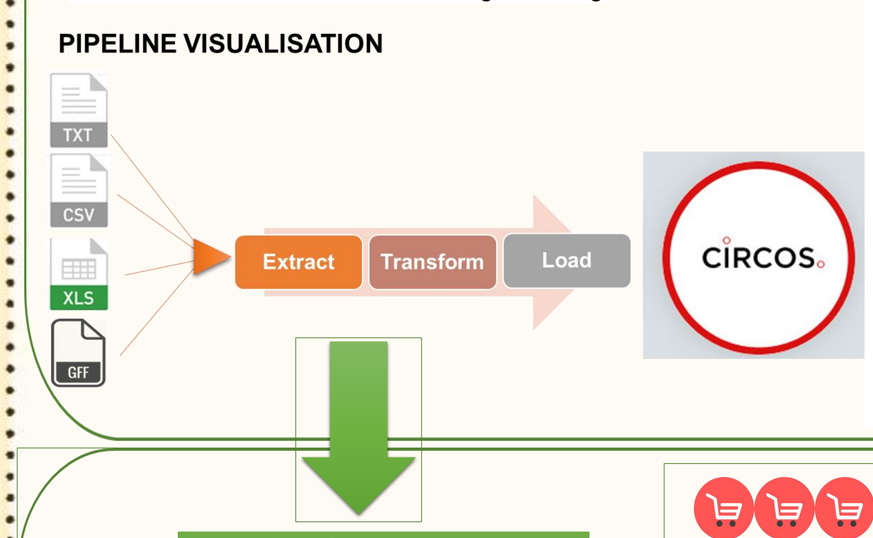


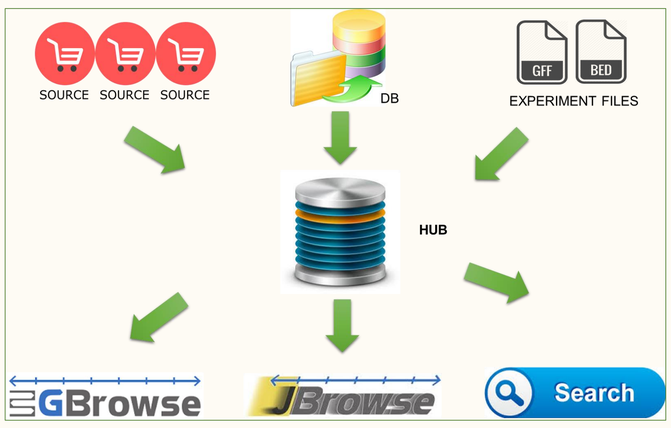
Fig2, Fig3 - Circos plots of Mobilome-seq from Rice seeds, track red and track blue represents TEs coverage per million reads per 100bp) in two experiments (SR, DOC). Track yellow and blue coverage of endosperm and embryo methylome respectively. All tracks are histograms .

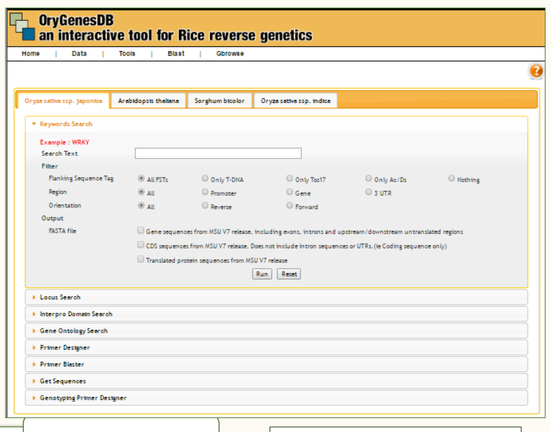


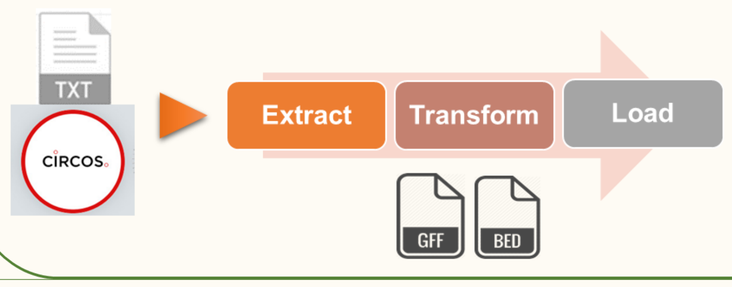
List of source types
Transcriptome
Methylome
Gene annotations
TE annotations
Protein annotations

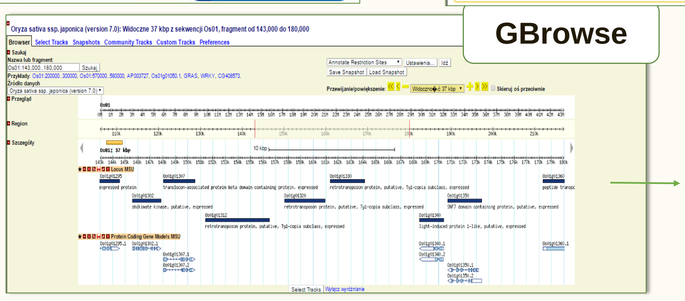
ETL

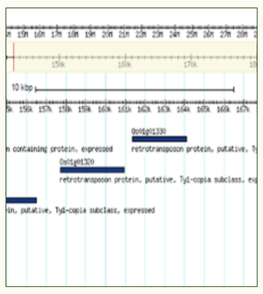
PIPELINE











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