



HAL
open science

Integration and Visualization of Epigenome and Mobilome Data in Crops

Dagmara Robakowska Hyzorek, Marie Mirouze, Pierre Larmande

► **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-01411668>

Submitted on 9 Dec 2016

HAL is a multi-disciplinary open access archive for the deposit and dissemination of scientific research documents, whether they are published or not. The documents may come from teaching and research institutions in France or abroad, or from public or private research centers.

L'archive ouverte pluridisciplinaire **HAL**, est destinée au dépôt et à la diffusion de documents scientifiques de niveau recherche, publiés ou non, émanant des établissements d'enseignement et de recherche français ou étrangers, des laboratoires publics ou privés.

Integration and Visualization of Epigenome and Mobilome Data in Crops

Dagmara Robakowska Hyzorek¹, Marie Mirouze², Pierre Larmande^{2,3,4}

¹ d.robakowska@yahoo.fr

² Parcours « Bioinformatique, Connaissances, Données » du Master Sciences & Numérique pour la Santé de l'Université de Montpellier

³ Institut de Recherche pour le Développement (IRD), UMR232 DIADE, Laboratoire Génome et Développement des Plantes, Perpignan

⁴ Institut de Biologie Computationnelle (IBC), Montpellier, ⁵ Equipe Zenith, INRIA et LIRMM, Montpellier

Transposable elements (TEs) in plant genomes

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.

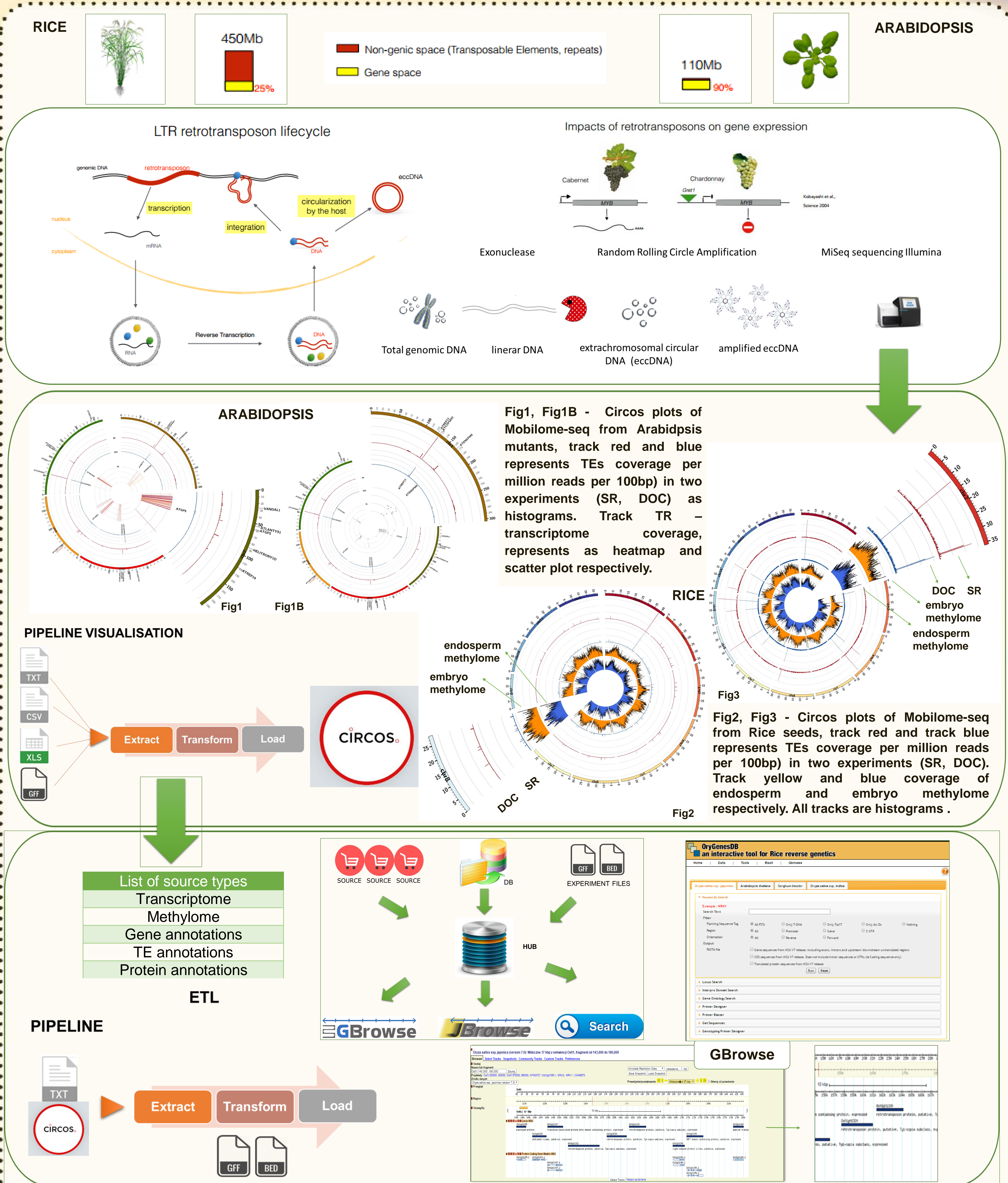
- Quick search: search through all databases and display search results as tables.

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..)



References: * Lanciano et al., *submitted*. (contact marie.mirouze@ird.fr for further details)
 Aguiar-Pulido V., et al. (2015). "Computational Methods in Epigenetics, In Personalized Epigenetics" Editor: T. Tollefsbol, Springer, Book Chapter 6:153-180.
 Buels R., et al. (2016). "JBrowse: a dynamic web platform for genome visualization and analysis." *Genome Biol.* 17(1):66.
 Krzywinski M., et al. (2009). "Circos: An information aesthetic for comparative genomics." *Genome Research* 19(9): 1639-1645.
 Springer N.M. (2013). "Epigenetics and crop improvement." *Trends Genet.* 29(4):241-7.

