

# Yet another Galaxy Genome Viewer

Thomas Darde<sup>1,2</sup>, François Moreews<sup>2</sup>, Yvan le Bras<sup>3</sup>, Cyril Monjeaud<sup>3</sup>, Frédéric Chalmel<sup>1</sup>

1 INSERM U1085, IRSET, Université de Rennes1, Rennes, France  
2 Genscale team, IRISA, Rennes, France  
3 GenOuest core facility, UMR6074 IRISA CNRS/INRIA/Université de Rennes1, Rennes, France



## Genome Browser

Galaxy owns its own genome viewer<sup>1</sup>. Another alternate popular genome viewer is JBrowse. We developed a server application that acts as a gateway between Galaxy and the JBrowse viewer.

Unlike Trackster, which benefits of a strong GALAXY integration, we used a loosely coupled service architecture. Our gateway application exposes services than can retrieve the configuration of a genome view or update it, using JSON data produced by a set of scripts wrapped as GALAXY tools.

These dedicated Galaxy Tools perform the pre-processing of BAM, SAM, BED, GTF or GFF files to produce the JSON configuration files used by JBrowse to display new tracks.

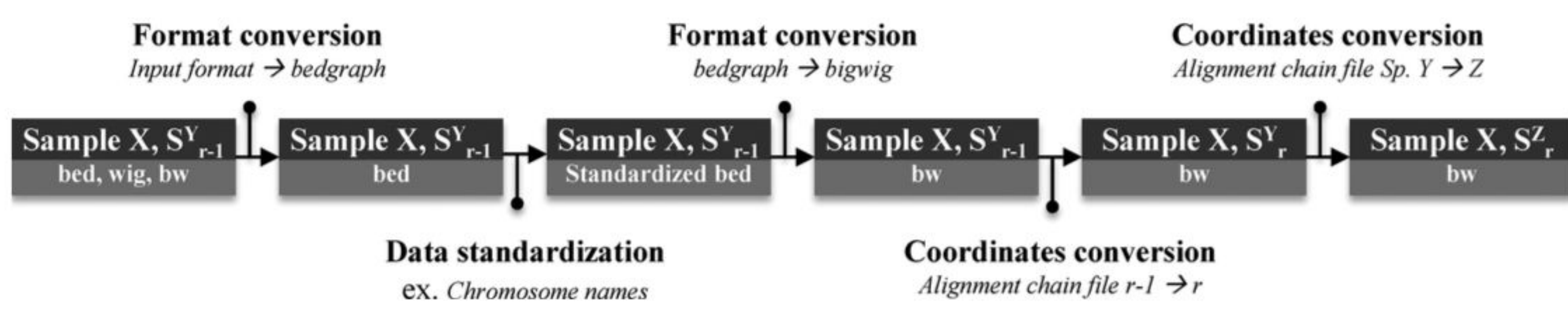
Our application includes a session mechanism allowing one user to restore, display or update the configuration of an already existing JBrowse genome view.

## JBrowse

The client-server architecture of Jbrowse<sup>2</sup> offers several advantages over other genome browser solutions, such as Gbrowse :

- Jbrowse is fully compatible with a wide spectrum of data types : fasta, gff, bam, bedGraph, wig, bigWig
- Rapid even when multiple users are processing data simultaneously
- User-friendly and highly flexible graphical interface

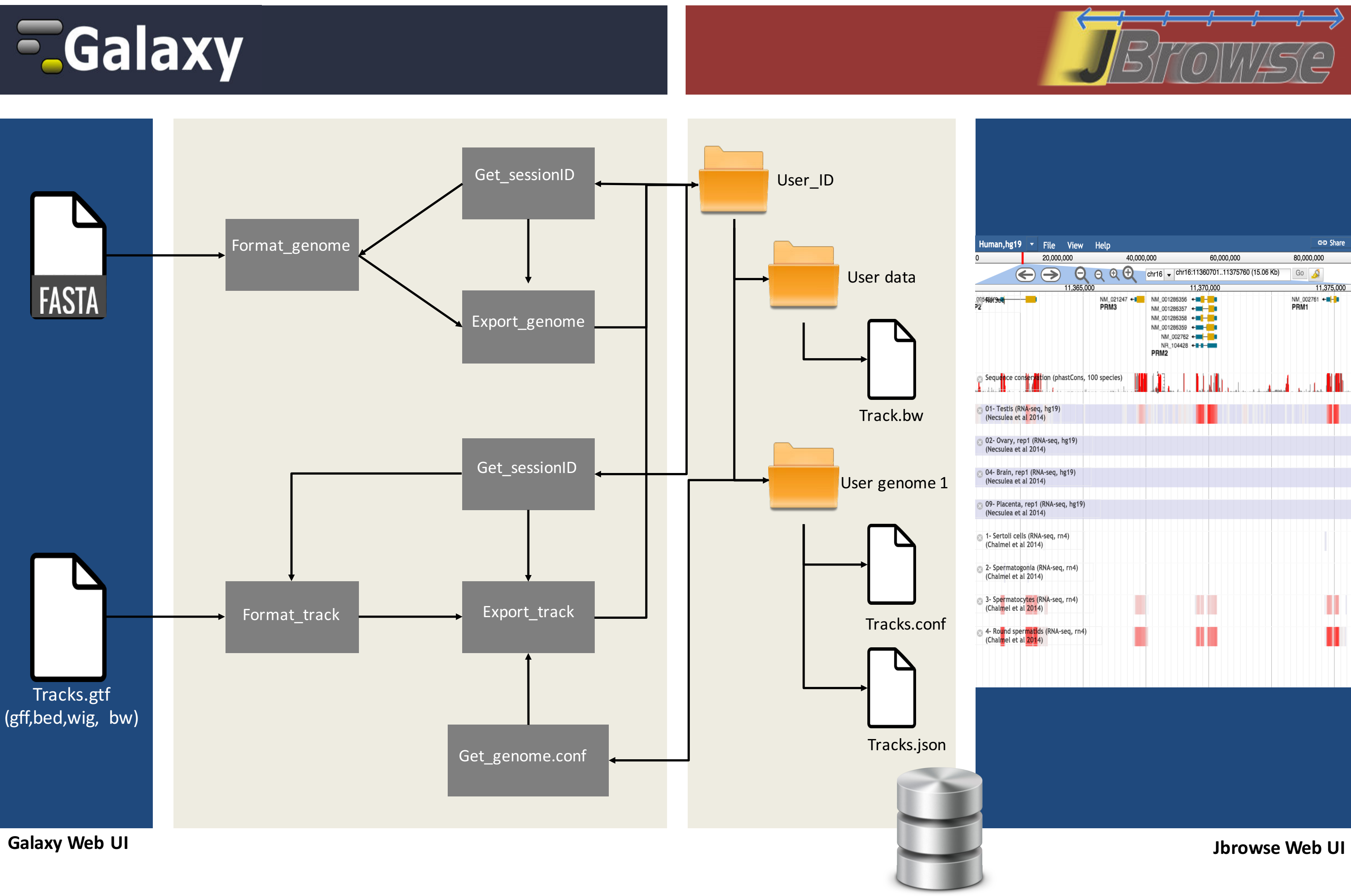
## A Cross species solution



The ‘data processing’ workflow described in the RGV publication<sup>3</sup> was conveniently implemented as a Galaxy module. This pipeline is based on the implementation of three tool suites: UCSC tools<sup>4</sup>, bedtools<sup>5</sup> and CrossMap<sup>6</sup>.

The former is used for all data file format conversions in either bedGraph or bigWig formats. The second is employed for the data standardization step. Finally, the latter is used in both cross-assembly and cross-species conversions of genome coordinates and makes use of pair-wise alignment files (chain format) provided by UCSC. The entire process takes roughly 30 min for an input file (bam format) of 200 Mb.

## Link Galaxy and JBrowse



## Perspectives

A first proof of concept has been done. But to entirely link Galaxy and Jbrowse some upgrades need to be achieved :

- Create a dynamical tool descriptor
- Display Jbrowse directly in Galaxy
- Link Jbrowse database with Galaxy database
- Improve the conversion pipeline

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