

### The multiple-genomes browser of the IFB cloud

Marie-Laure Franchinard, Frederic Sapet, Sandra S. Derozier, Franck F. Samson, Valentin Loux, Jean-François Gibrat

#### ▶ To cite this version:

Marie-Laure Franchinard, Frederic Sapet, Sandra S. Derozier, Franck F. Samson, Valentin Loux, et al.. The multiple-genomes browser of the IFB cloud. Journées SUCCES 2015, Nov 2015, Paris, France. , pp.1, 2015. hal-02795851

### HAL Id: hal-02795851 https://hal.inrae.fr/hal-02795851v1

Submitted on 5 Jun 2020

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.



# The multiple-genomes browser of the IFB cloud



Marie-Laure Franchinard<sup>1</sup>, Frédéric Sapet<sup>2</sup>, Sandra Derozier<sup>1</sup>, Franck Samson<sup>1</sup>, Valentin Loux<sup>1</sup>, Jean-François Gibrat<sup>1</sup> 1 INRA, UR1404 Mathématiques et Informatique Appliquées du Génome à l'Environnement, F-78352 Jouy-en-Josas, France 2 BIOGEMMA - Upstream Genomics Group, Centre de Recherche de Chappes, CS 90126, 63720 Chappes, France

Auteur à contacter: marie-laure.franchinard@jouy.inra.fr



## **Motivation**

IGV (Integrative Genomics Viewer) [1] is a very efficient genome browser written in Java, allowing users to visualize and explore a large variety of genomic data types, but limited to a single genome. However, to perform comparative genomic studies, it is very useful to be able to observe different types of data simultaneously on several genotypes.

As part of the BioDataCloud project, which received funding from the call for proposals "Cloud computing 3 - Big data" of Investments for the Future Initiative program, a collaboration between the INRA Migale platform and the Biogemma company was established to tackle this issue.

[1] Helga Thorvaldsdóttir, James T. Robinson, Jill P. Mesirov. Integrative Genomics Viewer (IGV): high-performance genomics data visualization and exploration. Briefings in Bioinformatics 14, 178-192 (2013).

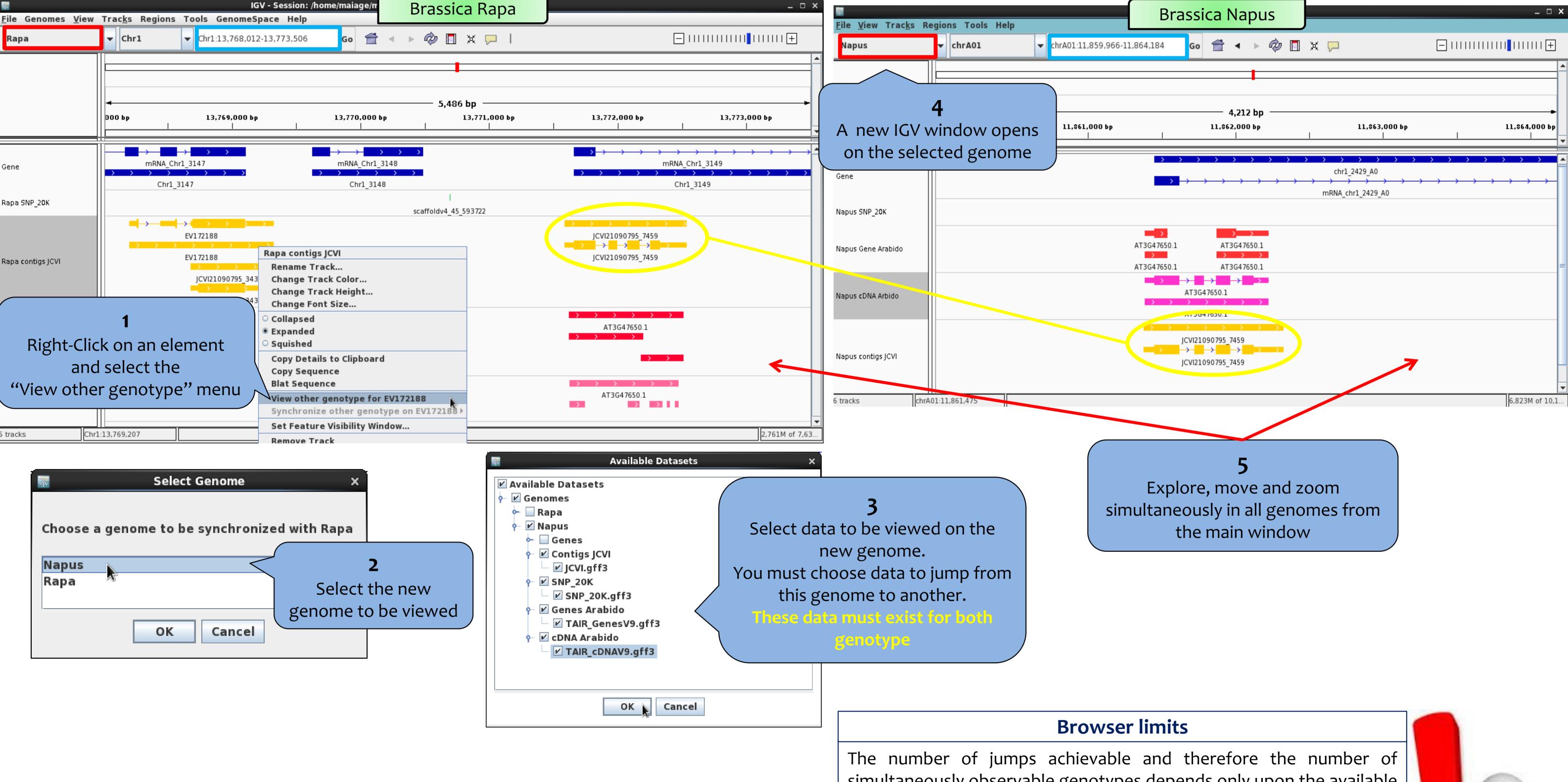
## Development

According to the technical specifications set by Biogemma, a new feature has been added to IGV that allows users to jump to a new genotype from different types of data (genes, regions in genomic sequence, genetic markers) selected by the user on the reference genome.

This jump results in the opening of a new IGV window on these data, if they are available for the new genotype. This window retains all IGV features and synchronizes simultaneously with the main window.

All jumps can be saved in an IGV session file allowing users to quickly restore already used genotypes and data or to share them with other. With this new feature, the user can now compare different genotypes with the reference genome and navigate between them synchronously while keeping the IGV performance.





## Deployment on the IFB cloud

The deployment of this new version of IGV in the "BioDataCloud-IGV" virtual machine (appliance) allows users to benefit from:

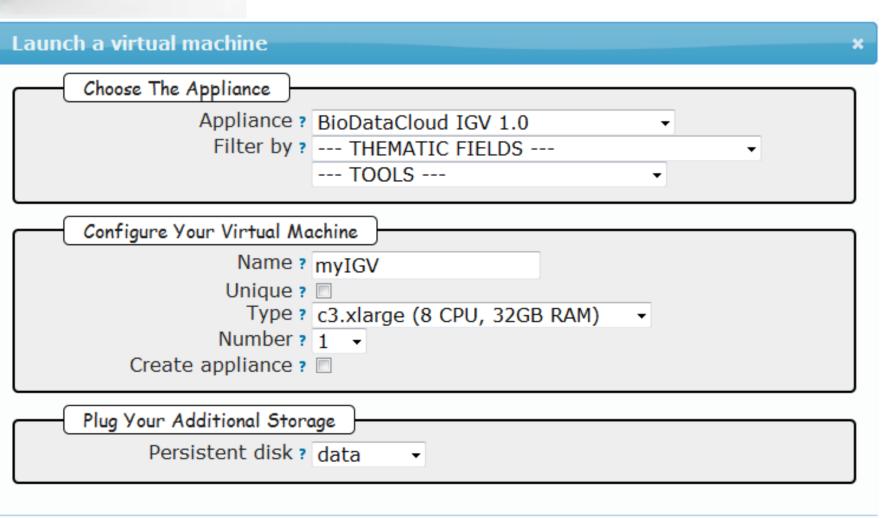
- ✓ Large material resources in terms of CPU, RAM, storage, network
- ✓ User-friendly environment for users as well as developers
- ✓ On-demand and flexible self service

The software is thus readily available to the whole life sciences community

simultaneously observable genotypes depends only upon the available hardware capabilities and the availability of the corresponding resources:

>IGV is by default RAM guzzling and this new feature requires around 4NGo where N is the number of genomes to be compared

>Large storage capacities and efficient network are required to explore large genomic data



]	IFB BIOINFORMATICS CLOUD											News   D	News   Dashboard   Monitor   Settings   Help   Sign out				
INSTITUT FRANÇAIS DE BIOINFORMATIQUE					DASHBOARD							Hoste					
	Shutdown → Go Get IPs Rename					New Instance New vDisk						Show Inst	ances	Show vDisks	now vDisks Show Appliances		
1	Showing	1 to 1 of 1	entries												Search:		
		≎ ID	≎ Name	<b>\$</b>	<b>\$</b>	Appliance		<b>\$</b>	CPU%	0	CPU	<b>\$</b>	Mem.	<b>\$</b>	#Storage	Access	•
_		5558	mylGV		Bi	oDataCloud IGV 1.0	C	1%			8		0		1	ssh	•







Run Cancel









YOU ARE SIGNED IN AS MLFRANCHINARD



