

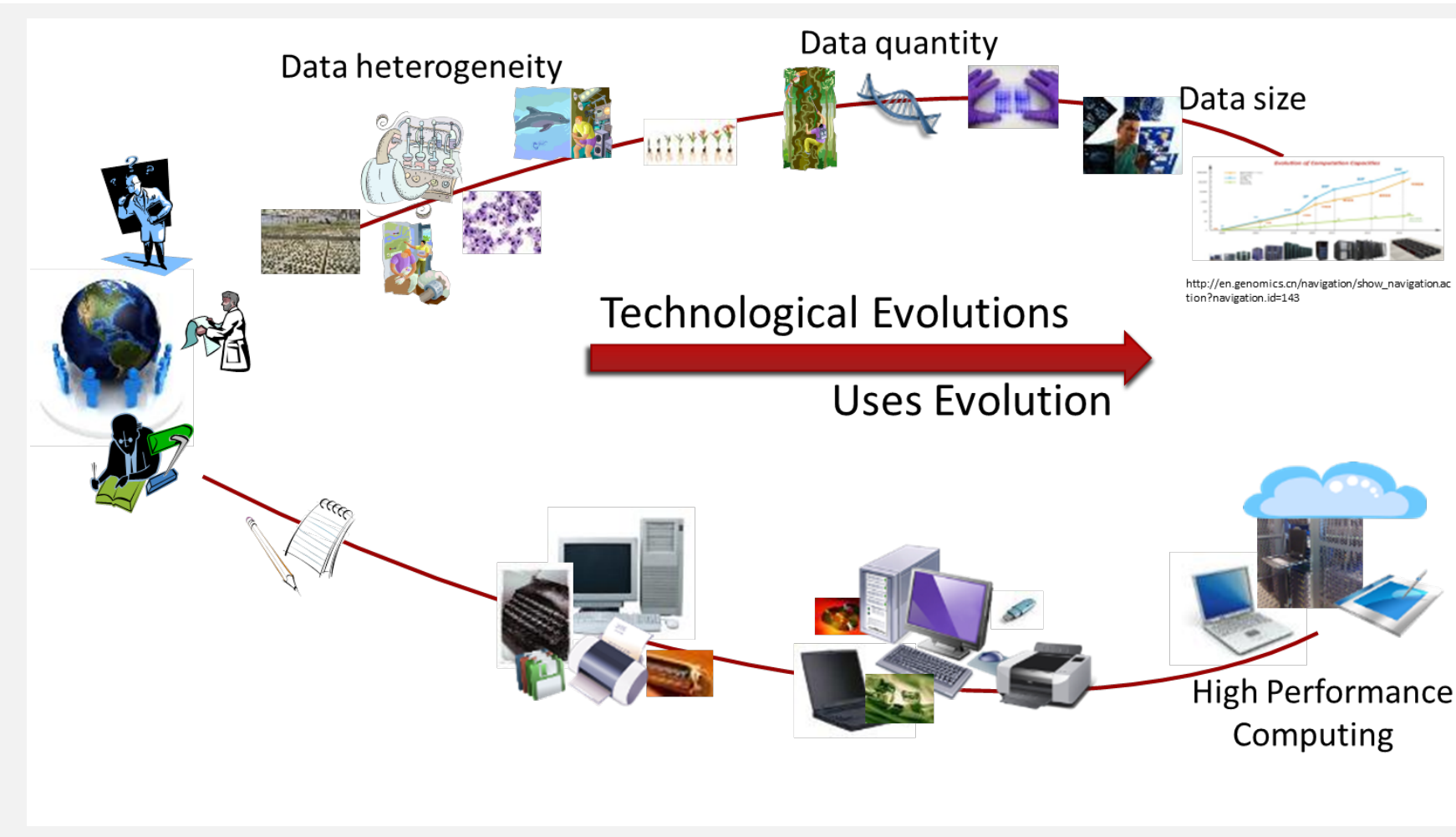
# e-Science in France, a Life science Western story

Yvan Le Bras<sup>1</sup>, Aurélien Roult<sup>1</sup>, Cyril Monjeaud<sup>1</sup>, Mathieu Bahin<sup>2</sup>, Olivier Quenez<sup>3,4</sup>, Claudia Heriveau<sup>1</sup>, Olivier Sallou<sup>1</sup>, Anthony Bretaudeau<sup>1,5</sup>, Olivier Collin<sup>1</sup>



This work is supported by Biogenouest and funded by Région Bretagne & Région Pays de la Loire

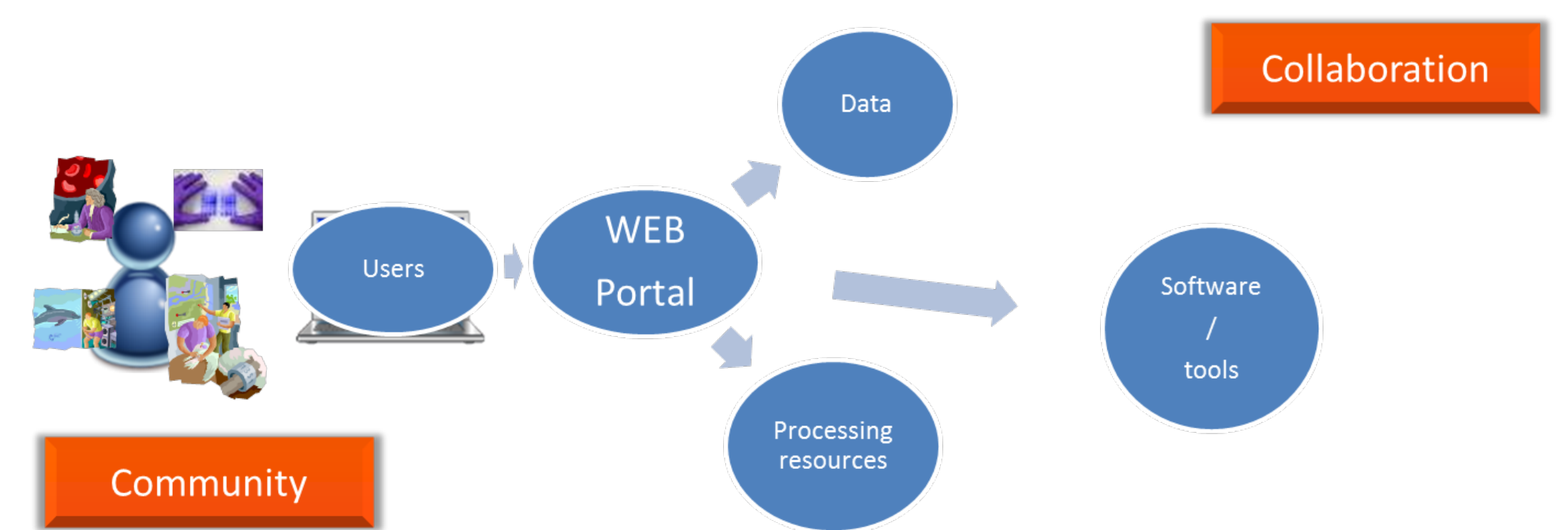
<sup>1</sup> GenOuest Core Facility, UMR6074 IRISA CNRS/INRIA/Université de Rennes1, Campus de Beaulieu, 35042, Rennes Cedex, France  
<sup>2</sup> IGDR, UMR 6290-CNRS Université de Rennes1, 2 avenue Professeur Léon Bernard, Campus de Villejean, 35065, Rennes Cedex, France  
<sup>3</sup> Inserm U1079, Institut de Recherche et d'Innovation Biomédicale (IRIB), Université de Rouen, France  
<sup>4</sup> Centre National de Référence pour les Malades Alzheimer Jeune, CHU de Rouen, Lille et Paris-Salpêtrière, Rouen, France  
<sup>5</sup> INRA IGEPP, UMR1349 Agrocampus-Ouest INRA Université Rennes1, domaine de la motte, 35653, Le Rheu, Cedex 35327, France



## [(Life) sciences data are digital

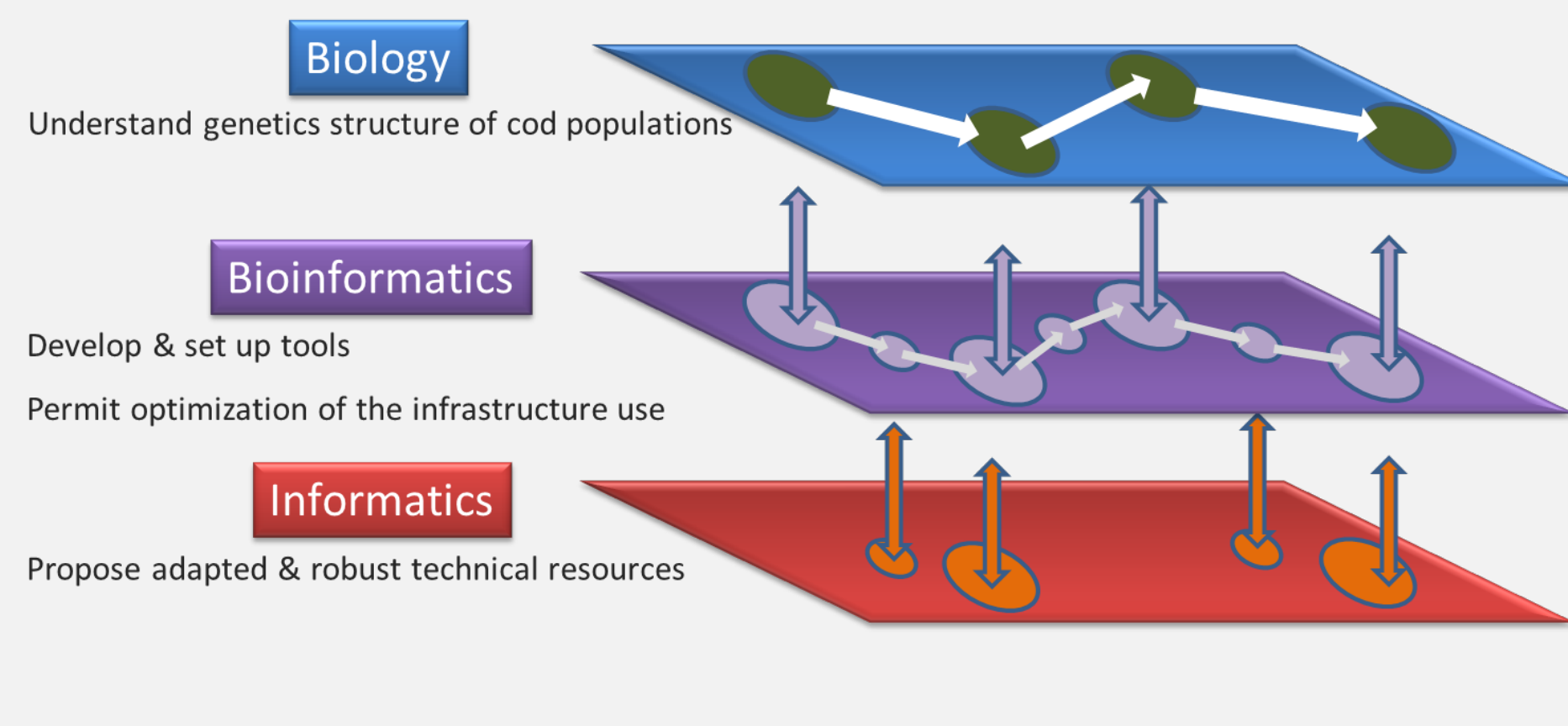
Sequencer, mass spectrometer, mri, GPS, camera, microscope... Many sensors used by scientists are providing data in digital format. This common characteristic for these heterogeneous data represents one interesting way to integrate information.

## VRE : A first step towards eScience



## A 3-layers organization

To coordinate a research project in Life Science, biologists are more and more forced to switch between different thematic layers. It first need to use Bioinformatics services and software to manage and analyse data. These tasks, in turn, need a pure computer layer.



Considering eScience as "enhancing" Science through ICT, the Virtual Research Environment (VRE) represents the eScience application "tool". Gathering Scientists with data, software and processing resources through the web, a VRE aimed to facilitate collaboration tasks and answer communities needs.

## eBiogenouest : a Western story

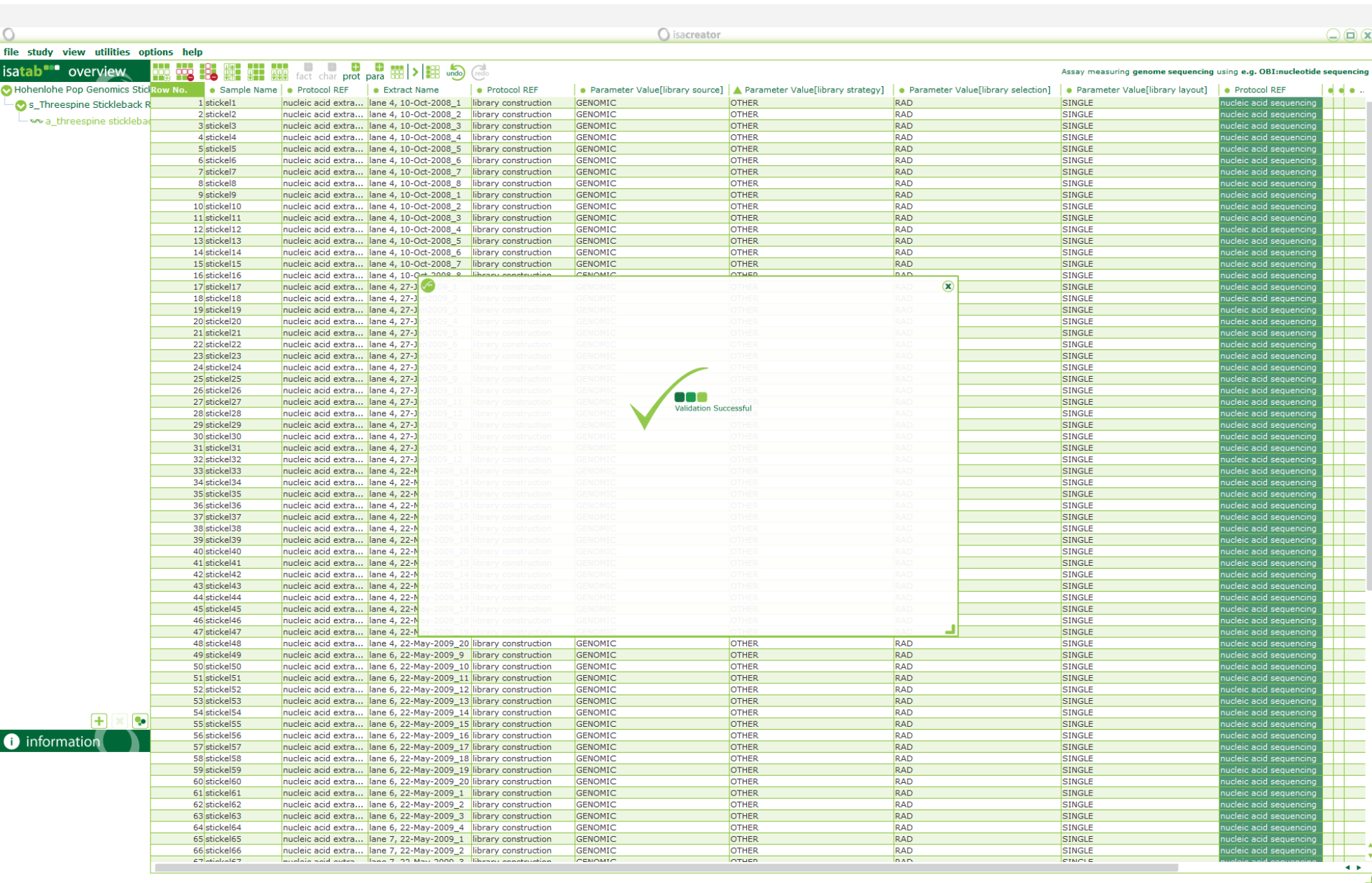
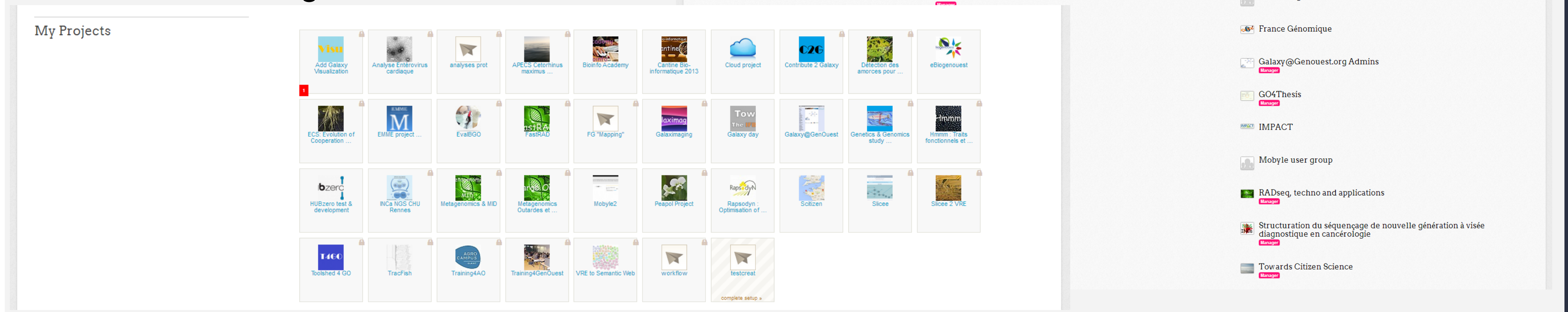
### Galaxy by GenOuest statistics

26325 jobs run to date  
 825 jobs run this month  
 27 jobs run today

At the request of scientists, we have provided a Galaxy server in late of 2012 and created the Galaxy User Group Grand Ouest (GUGGO).

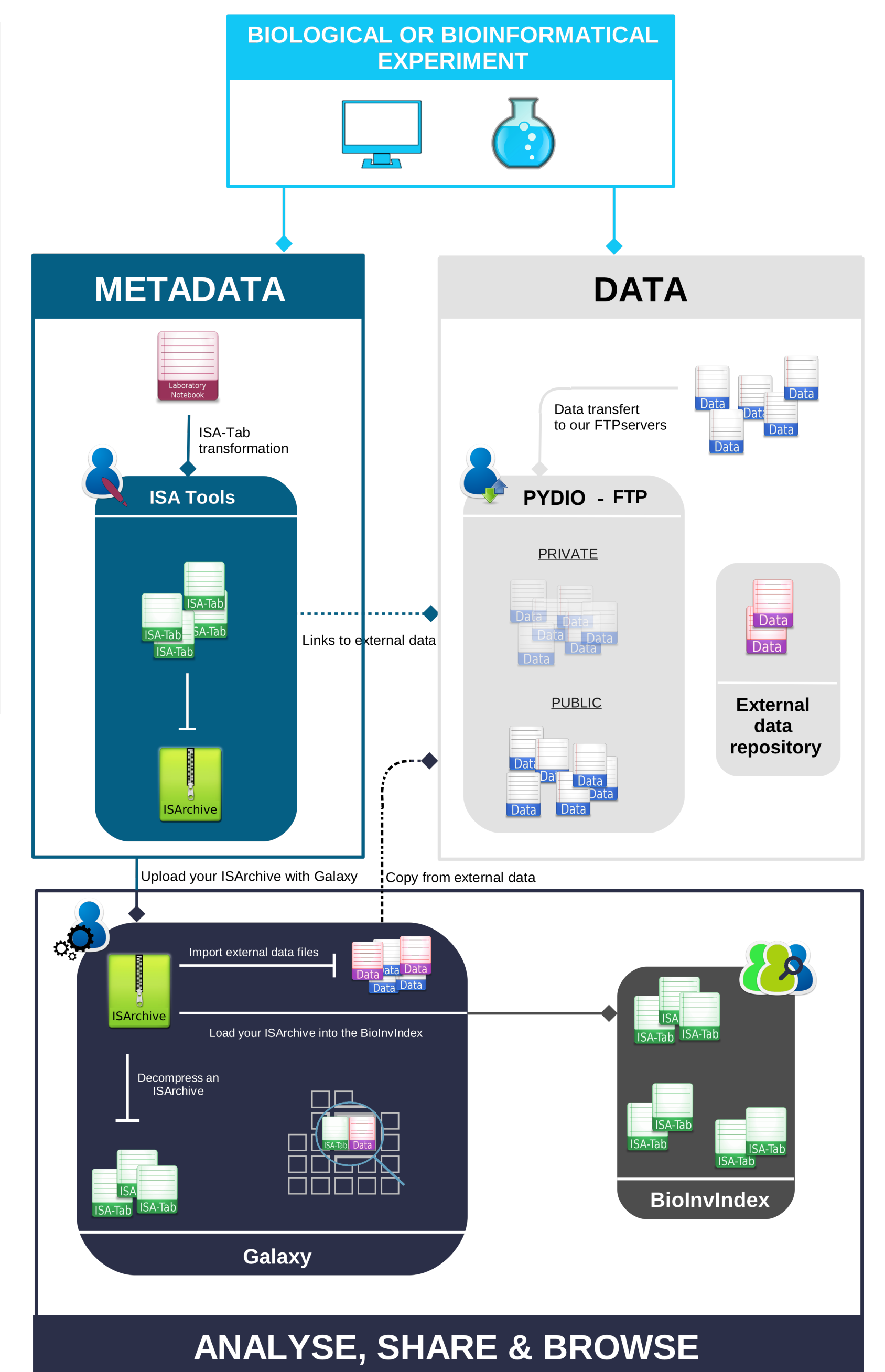
## HUBzero<sup>TM</sup>: our VRE's gate

This collaborative space is intended to help users establish new collaborations. With the Galaxy analysis platform and our metadata management environment, they can pursue their work in an integrated environment.



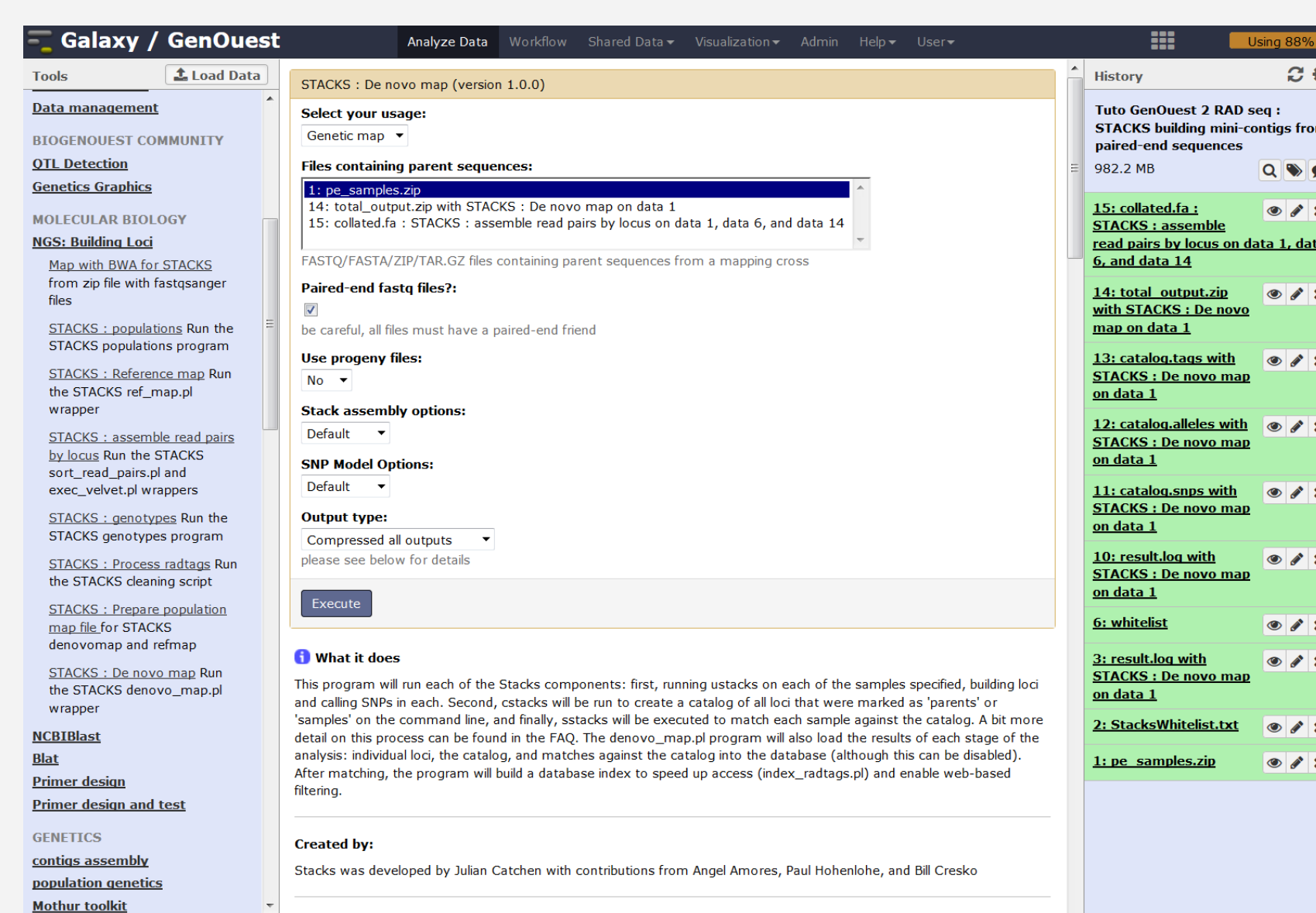
## EMME : Experimental Metadata Management Environment using ISAtools<sup>[2]</sup>

ISA for Investigation / Study / Assay. Allowing scientists to use ontologies and Excel compliant data ;) ISAtools is an interesting software suite to manage experimental metadata. We modify it to allow web execution and interact with Galaxy's API through BioBlend Python library. Endly, we create our own configuration with new protocols as for Bioinformatics treatment using EDAM ontology.

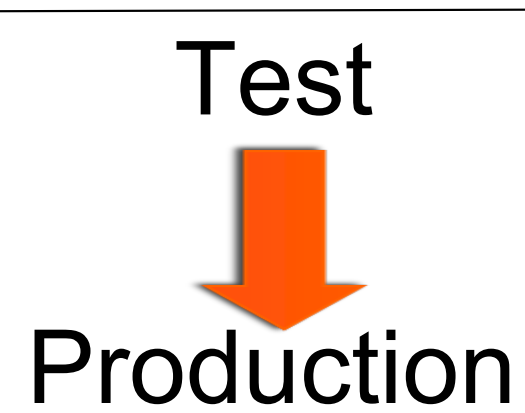


## Galaxy<sup>[3,4,5]</sup> by GenOuest

After 1,5 years, we can propose more than 800 tools to help life scientists analyse Transcriptomics, Population Genetics, Quantitative Genetics, Metagenomics, Proteomics data, and others. The Galaxy platform allows scientists without programming skills to stay in touch with the data analysis process. Although there are limitations due to infrastructure, it will facilitate re-analysis and repeatability of knowledge creation in Life Sciences.



## Prospect



Identity federation



[1] M. McLennan, R. Kennell, HUBzero: A Platform for Dissemination and Collaboration in Computational Science and Engineering. *Comput Sci Eng*, 12:48-53, 2010.  
 [2] P. Rocca-Serra, M. Brandizi, E. Maguire, N. Sklyar, C. Taylor, K. Begley, D. Field, S. Harris, W. Hide, O. Hofmann, et al. ISA software suite: supporting standards -compliant experimental annotation and enabling curation at the community level. *Bioinformatics* 26:2354-2356, 2010.  
 [3] J. Goecks, A. Nekrutenko, J. Taylor, and The Galaxy Team, Galaxy: a comprehensive approach for supporting accessible, reproducible, and transparent computational research in the life sciences. *Genome Biol*, 25:11(8):R86, 2010.  
 [4] D. Blankenberg, G. Von Kuster, N. Coraor, G. Ananda, R. Lazarus, M. Mangan, A. Nekrutenko, J. Taylor. Galaxy: a web-based genome analysis tool for experimentalists. *Current Protocols in Molecular Biology*, Chapter 19:Unit 19.10.1-21, 2007.  
 [5] B. Giardine, C. Riemer, R. Hardison, R. Burhans, L. Elmski, P. Shah, Y. Zhang, D. Blankenberg, I. Albert, J. Taylor, W. Miller, W. Kent, A. Nekrutenko, Galaxy: a platform for interactive large-scale genome analysis. *Genome Research*, 15(10):1451-5, 2005.

www.e-biogenouest.org

emme.genouest.org

