**A 3-layers organization**

To coordinate a research project in Life Sciences, 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.

**eBiogenouest : a Western story**

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

**EMME : Experimental Metadata Management Environment using ISAtools**

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. Finally, we create our own configuration with new protocols as for Bioinformatics treatment using EDAM ontology.

**Galaxy**

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**

**HUBzero**

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.

**VRE : A first step towards eScience**

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 VRE, aimed to facilitate collaboration tasks and answer communities needs.