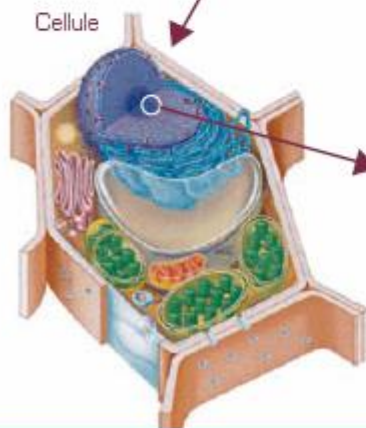
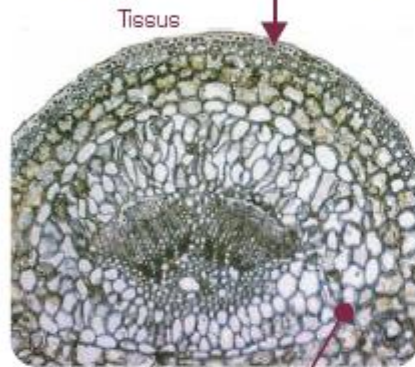
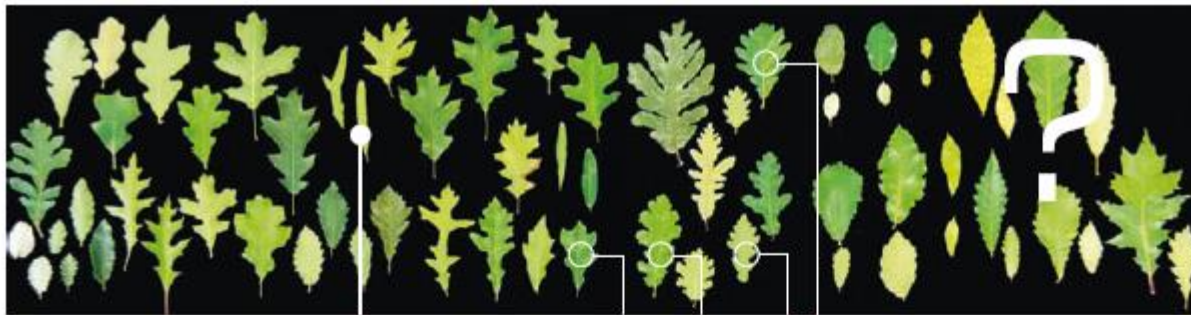


[illegible]

- [illegible]



Extraction,
Amplification,
Séquençage
ADN



ACGTGTGCTAT ▶ *Quercus petraea*
ACGCGTGCTAT ▶ *Quercus robur*
ACGT--GCTAT ▶ *Quercus pubescens*
ACGCAGTCTAT ▶ *Quercus cocinea*



Which tools are available?

ADDED TOOLS

virtual BiodiversityL@b

MAFFT alignment (basic options)

BMGE block selection

Fasta to Phylip conversion

Fasta to Nexus conversion

PHYML wrapper (maximum likelihood phylogenies)

Draw ascii tree (newick)

BEAST wrapper

DECLIC

Disseq

Distance ape

Dedlic Graph

Dedlic MDS

DIAGNO-SYST (HIDDEN TOOLS)

Diagno-Syst char format
Formats charfile

Diagno-Syst

Disseq reads to taxo

Taxonomic inventory from

Alignment (multiple)

Phylogeny

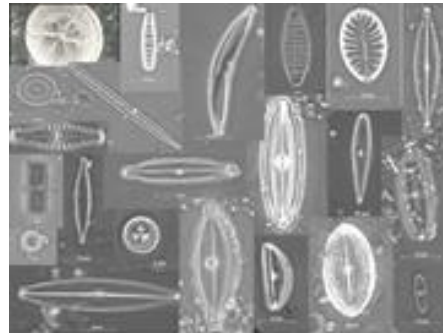
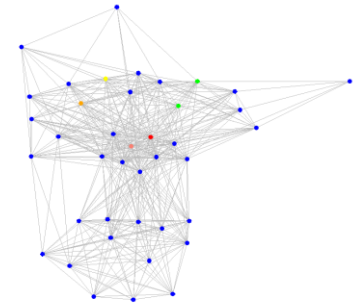
Distance based methods
Smith-Waterman (exact)
Evolution models

Graph clustering

MDS - NLM

Aggregative clustering (fast ,,,)

Diatoms_18S ; cc = 4 ; character = species ; gap = 3



Molecular based taxonomy and systematics: An open route for (new) methods

Sequences known by pairwise distances



**Distance geometry
pattern recognition
machine learning**

Clustering

Multidimensional Scaling

linear and nonlinear (e.g. Sammon, 1969)

Manifold learning

IsoMap, EigenMap, etc ...

Graph based methods

spectral clustering

Machine learning

SVM, ...

Galaxy portal

The screenshot shows a web browser window with the URL <https://galaxy-pgtp.pierroton.inra.fr/root/index>. The page features a dark blue header with the text "Galaxy / PGT Pierroton" and navigation links: "Analyze Data", "Workflow", "Shared Data", "Visualization", "Help", and "User". A status bar on the right indicates "Using 0%".

On the left, a "Tools" sidebar contains a search bar and lists of tools under "Upload Your Data" (including "virtual_BiodiversityL@b", "VBL_hidden", and "PGTP") and "STANDARD TOOLS" (including "Get Data", "Send Data", "Lift-Over", "Text Manipulation", "Filter and Sort", "Join, Subtract and Group", "Convert Formats", "Extract Features", "Fetch Sequences", "Fetch Alignments", "Get Genomic Scores", "Operate on Genomic Intervals", "Statistics", "Graph/Display Data", and "Multivariate Analysis").

The main content area displays logos for "INRA SCIENCE & IMPACT", "cgfb GÉNOME TRANSCRIPTOME", "ceba", and "xyloforest". Below the logos, a text block reads: "The Genome Transcriptome Facility of Bordeaux Pierroton is pleased to provide a Galaxy server to its users. The virtual_BiodiversityL@b has benefited from an "Investissements d'Avenir" grant managed by Agence Nationale de la Recherche (CEBA, ref. ANR-10-LABX-25-01)."

On the right, a "History" sidebar shows "Unnamed history" with "0 bytes" and a message: "This history is empty. You can [load your own data](#) or [get data from an external source](#)".

Where is it possible to compute?

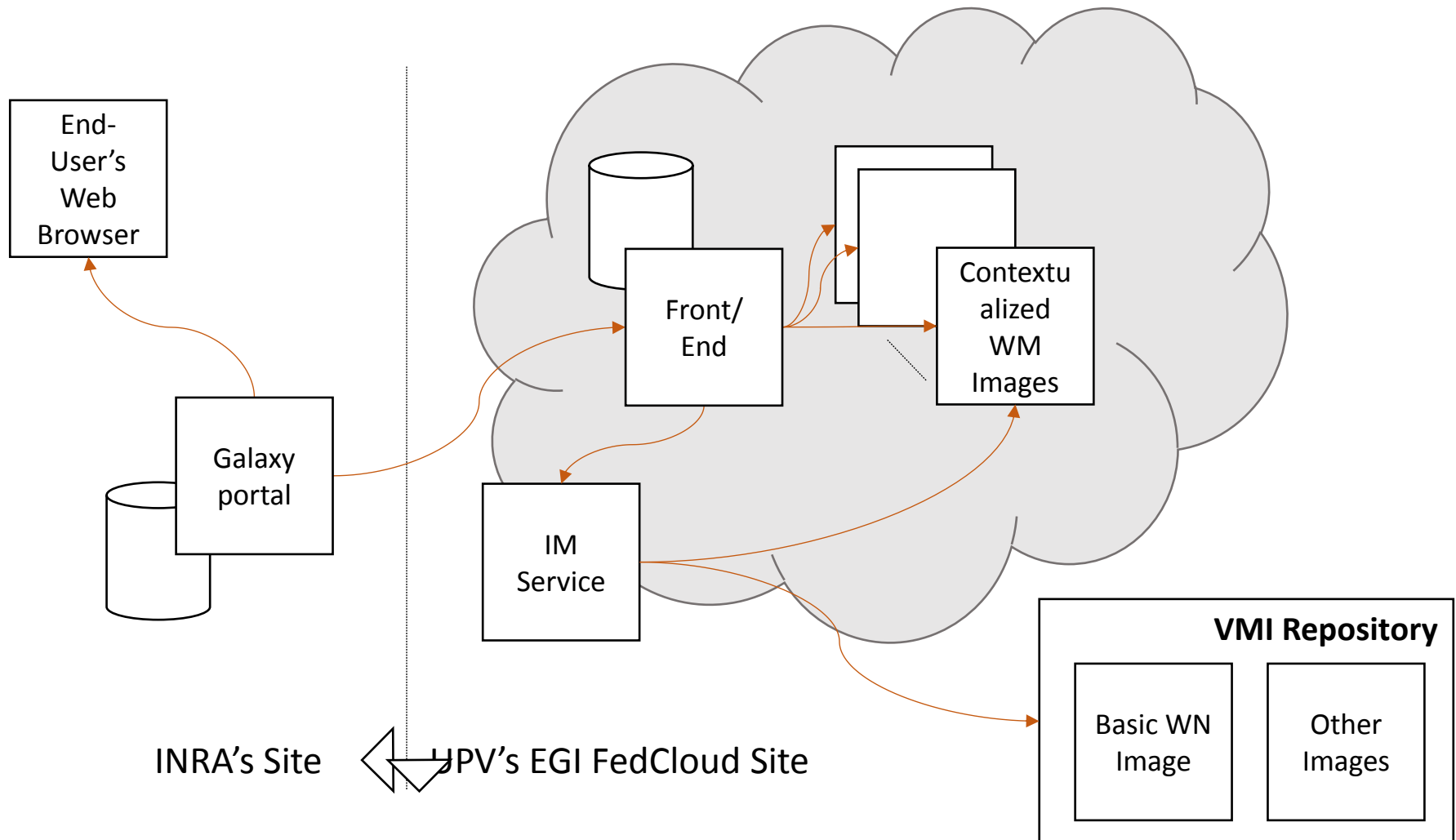
From a unique portal
the Galaxy instance

- Local Galaxy server
- Mesocentre (Tier 2)
Avakas
1000 cores
- Tier 1 (IDRIS, one pipeline, not via Galaxy)
- EGI GRID
France-Grille
- Cloud (next slides ...)

Where from?

From any computer connected to internet
Currently available from French Guiana
(IP Cayenne works with it)

Software Architecture

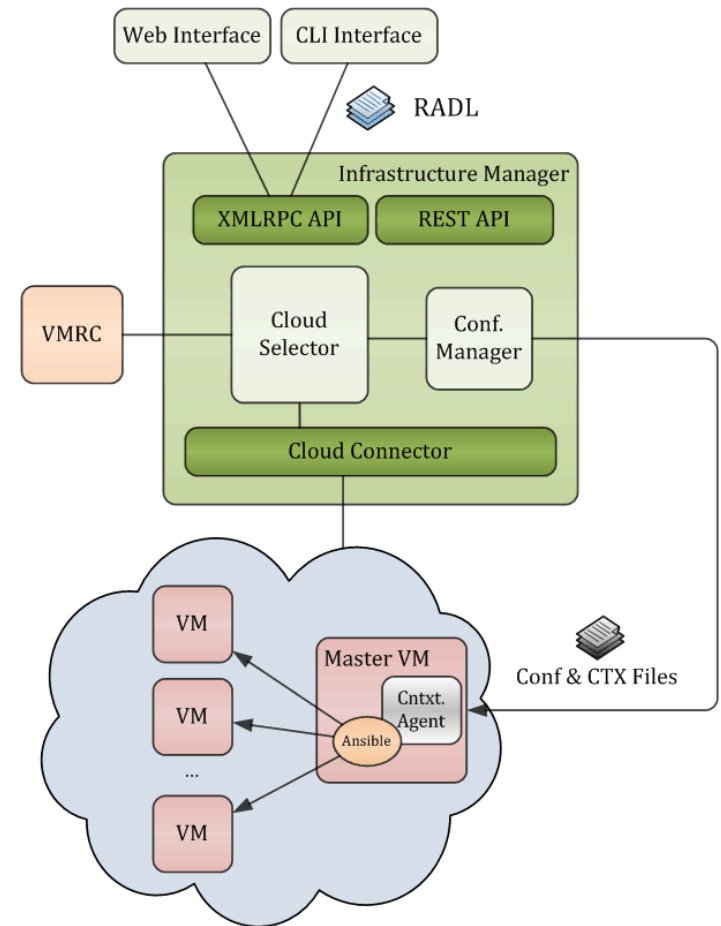


Technologies Used

- Galaxy (galaxyproject.org)
 - Bioinformatics portal that transforms operations into Jobs submitted to a back-end batch queue.
- Infrastructure Manager (IM - www.grycap.upv.es/im)
 - Platform-agnostic, dynamic configuration service that enables re-configuring a cluster.
- Elastic Compute Cloud Clusters (EC3 - www.grycap.upv.es/ec3)
 - Automatic elasticity service based on batch queue length.

(Re)-Configuration

- Infrastructure Manager configures VMs from recipes
 - It can restart a broken configuration or rearrange the changes on an active configuration.
 - It Works with a plethora of CMPs, including OCCl and EGI Federated Cloud.



Elastic Compute Cloud Cluster

- EC3 (Elastic Cloud Computing Cluster) leverages CLUES to create elastic virtual clusters in the Cloud.
- It also uses Infrastructure Manager (IM) for the reconfiguration.
- It provides
 - automatic
 - elasticity
 - based on
 - the batch
 - queue
 - workload.

