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Analyse evolutionary conserved CDS, orthologs, syntenies, pan-genome, fusion, etc., for your bacteria of interest

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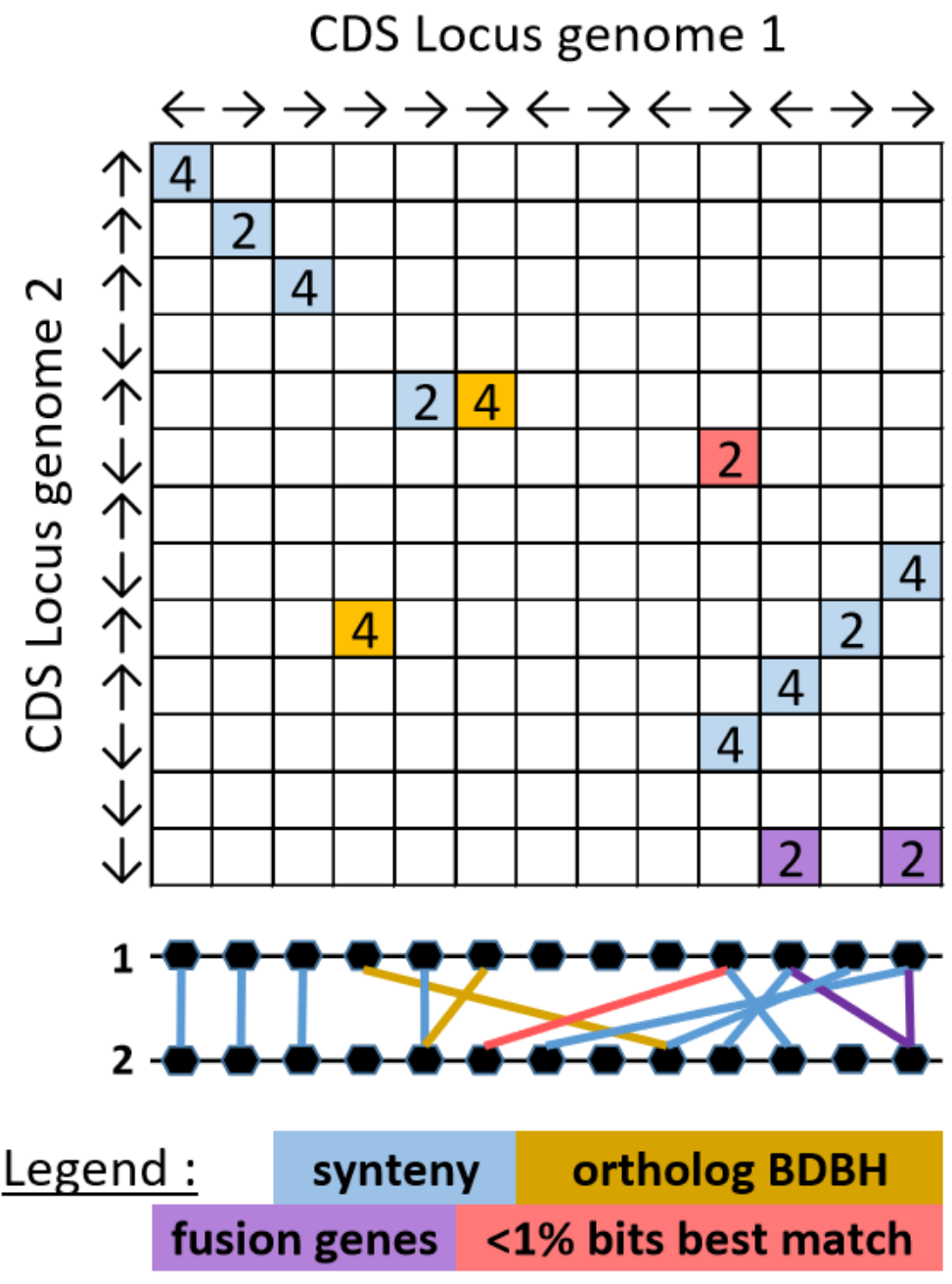
Why ? How ?

Do you wish to quickly grasp the extent of strongly evolutionary conserved CDS among your bacterial organisms ?

Insyght (<http://genome.jouy.inra.fr/Insyght/>) helps you to quickly generate the relevant data and navigate among abundant orthologs, syntenies and gene fusions. The navigation among the various pieces of information (annotations, localization) and comparisons (presence / absence, gene set, compared organisms, etc...) is practical and extensive, even within large datasets.

It detects strongly evolutionary conserved CDS by comparing proteomes (bi-directional best hit) and by leveraging information on syntenies (using dynamic programming) and gene fusions. The presence of strongly evolutionary conserved CDS is a compelling evidence in analysis such as inference of functions, core genome, or phylogenomic relatedness. A functionality highlights overrepresented orthologs among group of genomes, which is useful to investigate niche-specific CDS for a particular phenotype of interest.

A graphical way to analyze data



Orthologs table view

A spreadsheet adapted to browse orthologs :

- Familiar layout: gene = col, organism = row
- Info on annotations, alignments, location, etc. at your fingertip
- Genes in adjacent columns with similar background color = synteny
- Multiple "off shoots" homologs stacked in 1 cell
- Build your own gene set
- More: sort the table, quickly navigate CDS, etc.

Annotations comparator

For a given CDS and its orthologs, what are the functional annotations that are shared or not ? The annotations are classified into 3 categories (Shared, Missing, and Unique) :

- Browse those 3 categories and subcategories: functional annotation, homologous genes, sequence alignment, etc.
- Restrict the set of organisms considered, filter homologs, etc.

Genomic context view

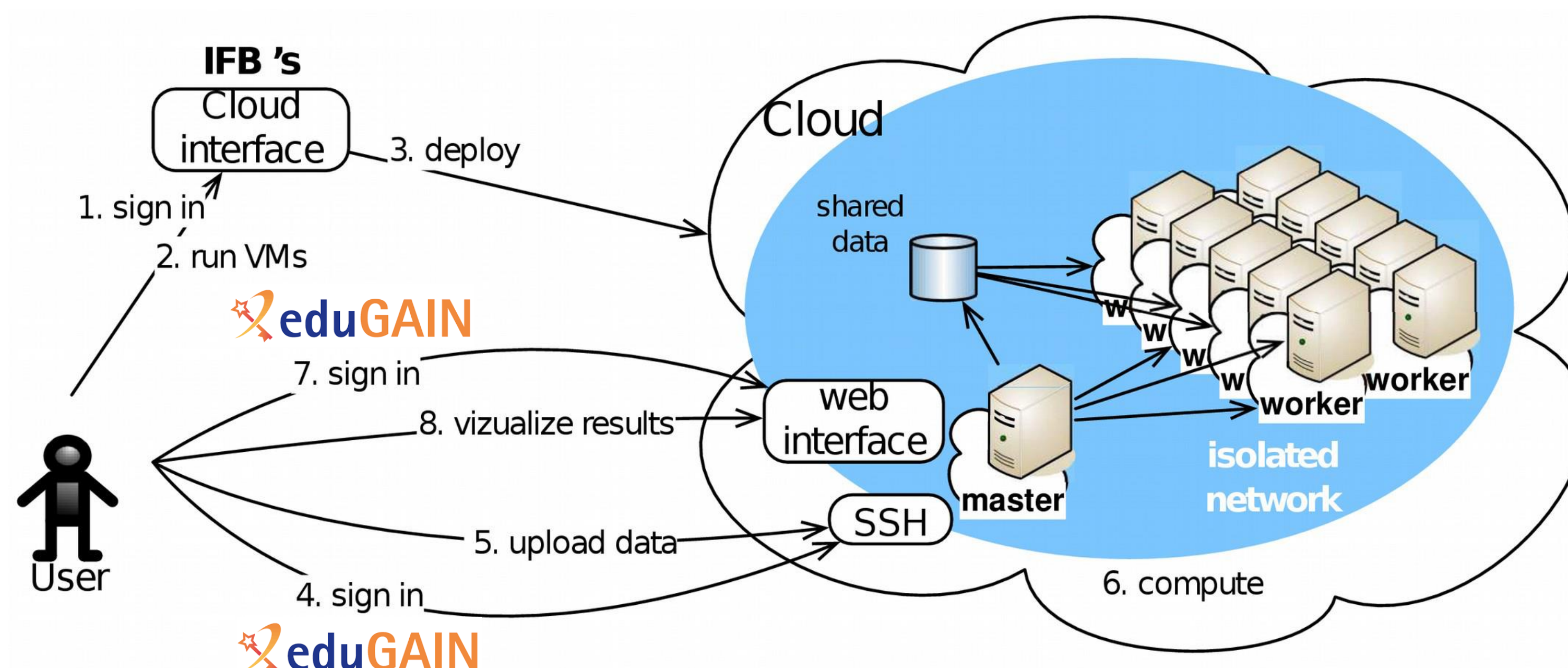
A new way to visualize genomic rearrangements :

- Browse syntenies, insertions, etc. using symbols along the genomes and visualize rearrangements
- Synchronize among multiple compared genomes
- More: expands genes within syntenies, find CDS

Analyze your data with a VM, either locally or in the IFB cloud

The Insyght virtual machine (VM) is ready to use, you can customize the genomes to compare and various parameters. You can generate and analyze private data "in the cloud" as well by using the French Institute of Bioinformatics (IFB) cloud infrastructure : <https://biosphere.france-bioinformatique.fr/catalogue/>. The IFB appliances features:

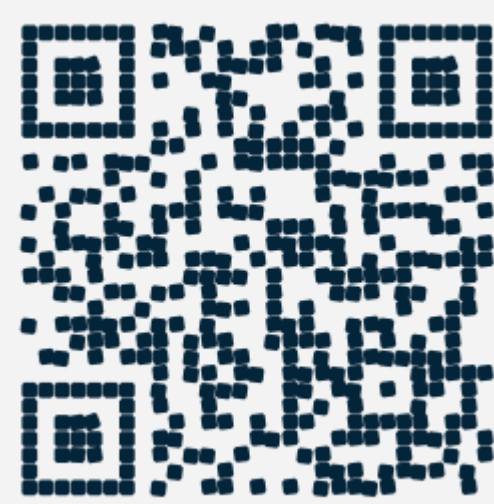
- Authentication using academics federation for SSH (command line) and web access
- Access to a cluster to leverage parallel computing and speed up data generation
- automatic installation
- recipes (slipstream)
- multicloud deployment support (ifb-core-cloud, prabi-girofle, genouest-genostack, etc.).



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Insyght: navigating amongst abundant homologues, syntenies and gene functional annotations in bacteria, it's that symbol!

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Try the tool, check out our public datasets :

- 2692 complete bacteria from Ensembl Bacteria
- 210 reference archaea genomes from Uniprot
- coming soon : ~5000 complete reference bacteria from Uniprot