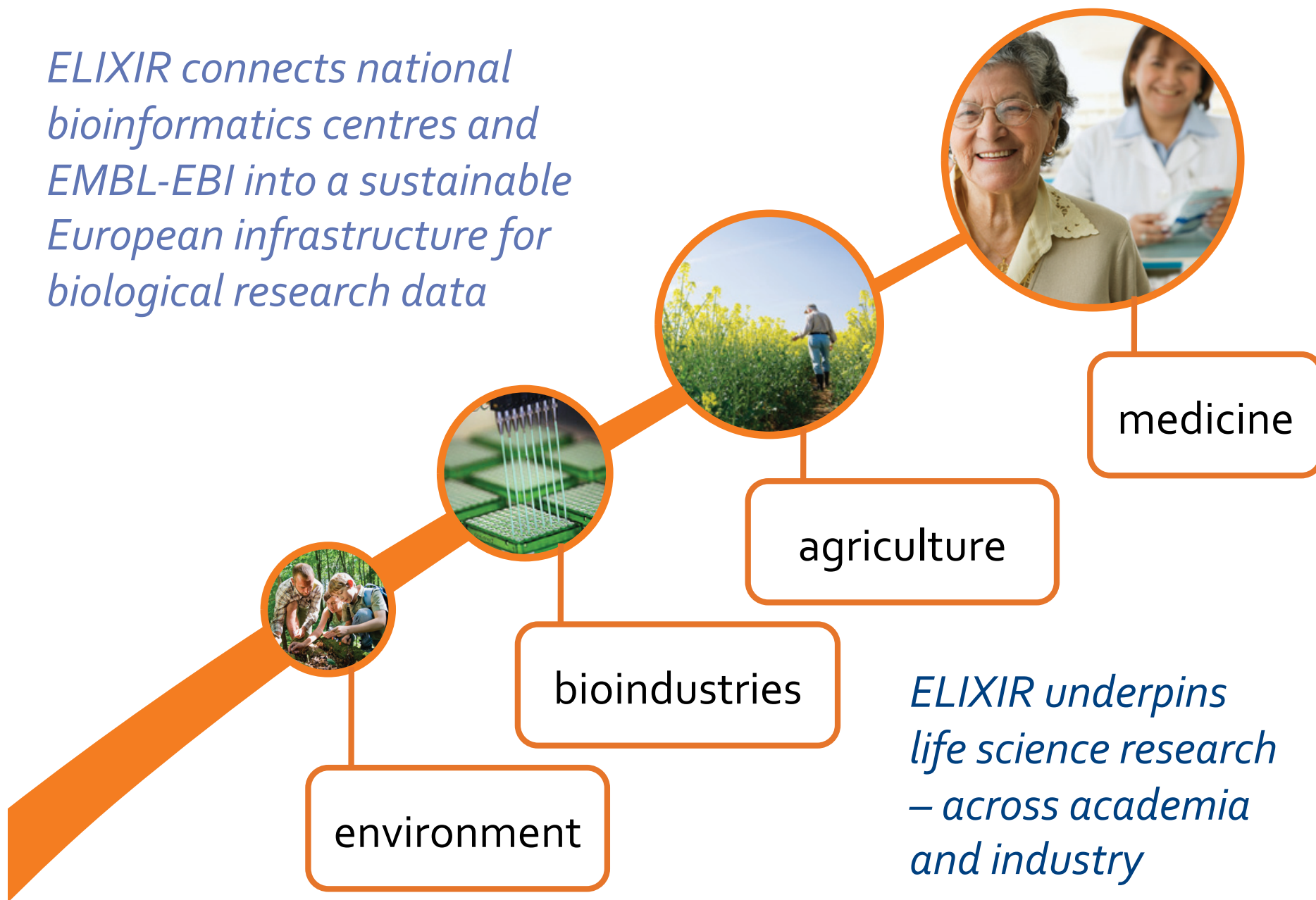


Enabling a federated environment to support biomedical research

Gianmauro Cuccuru – CRS4

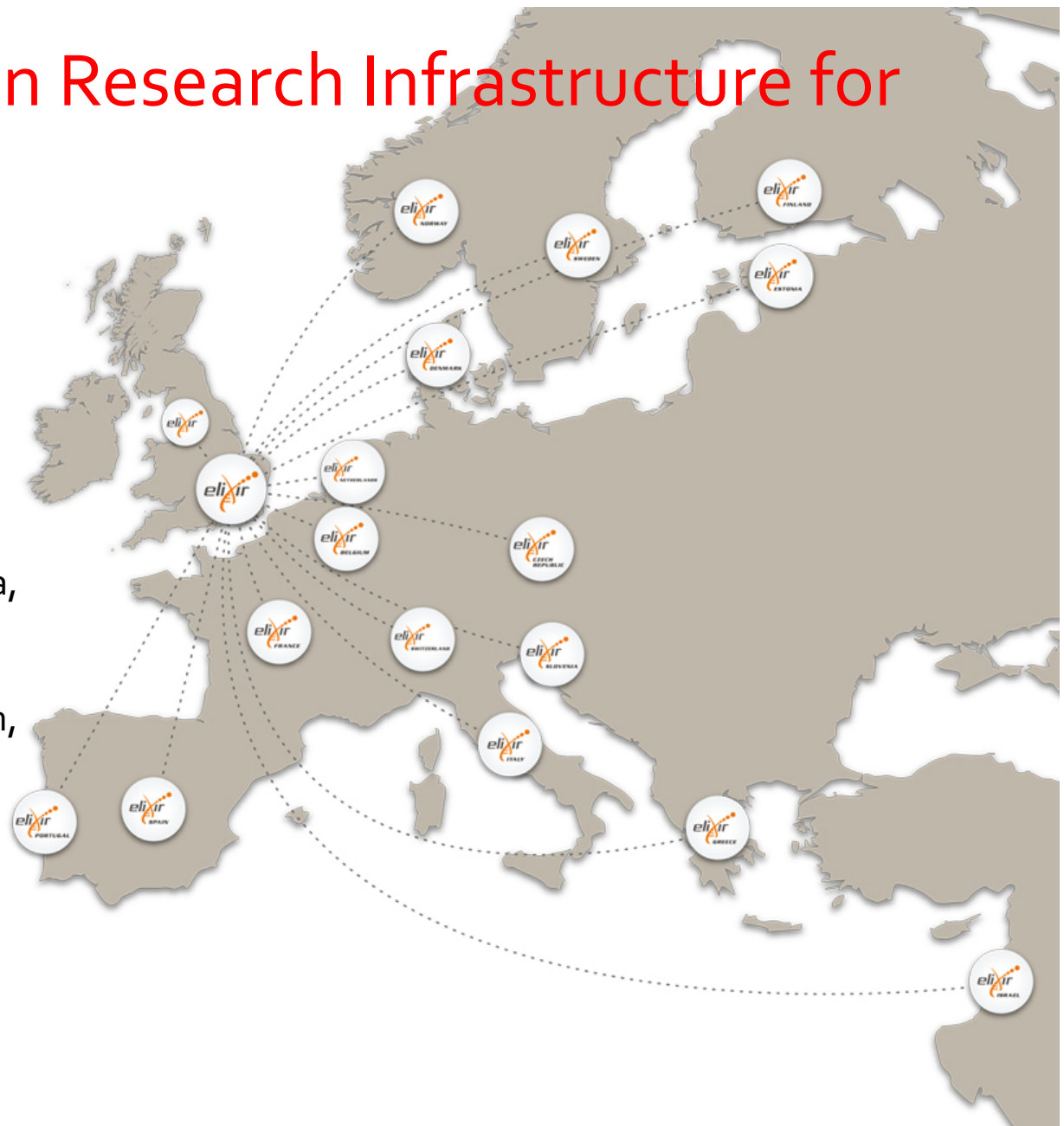


*ELIXIR connects national
bioinformatics centres and
EMBL-EBI into a sustainable
European infrastructure for
biological research data*



ELIXIR: the European Research Infrastructure for biological data

- ELIXIR connects national infrastructures and EMBL-EBI
- 16 Member states + EMBL
 - Belgium, Czech Republic, Estonia, Denmark, Finland, France, Israel, Italy, Netherlands, Norway, Portugal, Slovenia, Spain, Sweden, Switzerland, UK
- 2 countries working towards membership
 - Greece, Ireland



Green light for Italy

Thursday, January 7, 2016

Italy is the latest country to sign the ELIXIR Consortium Agreement and join ELIXIR as Member, following the ELIXIR Board's approval of Italy's application.

The ELIXIR Node in Italy is organised as a Joint Research Unit, coordinated by the National Research Council (CNR). It brings together 13 partners, including seven Italian universities and four High Performance Computing (HPC) centres.

The Italian bioinformatics community has a strong track record in human, animal and plant genomics and has been involved in several genome projects (for example the Sardinians genome project, the domestic horse and the grape and peach genomes). Other areas of focus for the Node include metagenomics, epigenomics, proteomics and bioinformatics training. ELIXIR will in turn also benefit from the experience and expertise of Italy's four High Performance Computing centres in managing HPC services in various scientific fields.

Prof. Graziano Pesole from the University of Bari and the ELIXIR Italy Head of Node said: "Our goal is to drive the development of bioinformatics resources in Italy and integrate them with our European partners across ELIXIR. We are looking forward to sharing our expertise and resources with ELIXIR partners and bringing them closer to the European research community."

Italy is the 16th ELIXIR Member, and most recent country to join following France, Spain, and Belgium.

Read more about ELIXIR Italy: <https://www.elixir-europe.org/about/elixir-italy>



Structure scales with the

ELIXIR-ITA: supporting the growth of bioinformatics in Italy with research, infrastructures and training.

Our main ambition is to stimulate and assist the development, rationalization and integration of bioinformatics research in Italy, and to transfer the benefits of all these activities to our European partners and in particular to other ELIXIR Nodes, towards the achievement of a pan-European bioinformatics infrastructure able to cope with the present and future challenges posed by life sciences.

ELIXIR-ITA members -

H2020 projects

Call: H2020-INFRADEV-1-2014
Proposal: ELIXIR-EXCELERATE - accelerate the implementation of Europe's life-science data infrastructure over the next four years (approved, grant preparation)
Call: H2020-INFRADEV-1-2014
Proposal: EMBRIC - European Marine Biological Research Infrastructure Cluster to promote the BlueBioeconomy (approved, grant preparation)
Call: H2020-INFRA-2014
Proposal: INIGO - Integrating Distributed data Infrastructures for Global Exploitation (approved, project started in April 2015)

Facilities, Resources & Research support

- Computing and sequencing resources
 - Large Scale computing and storage facilities at CSCs, BPR and CHECA.
 - HSC facility at CSCs.
- Public and project bound Galaxy resources
 - OMEGA@CSCs: Galaxy for metabolomics, variant analysis and transcriptomics.
 - GALAXY@CSCs: Galaxy for the ENIGMA flagship project.
 - GALAXY@CSCs: metagenomics and viral data.
- Enabling network infrastructure provided by GARR
 - State-of-the-art, user-driven, fully integrated with high speed pan-European backbone GARR and with worldwide research networks.

Training

Participation in grant proposals

- FIT@UG - Reproducible data analysis of Exelixis
- ELIXIR Practical Course: Spring School for HSC variant analysis

Selected courses 2015:

- <http://www.bioinformatics.cit.roma1.it>
- HSC met-bio and exome data analysis [6 hours]
- GALAXY@CSCs: Development of a Galaxy workflow for metagenomic analysis of metagenomic data [10 hours]
- <http://www.bicomp.uniba.it/bicomp/>
- International master in Bioinformatics (two years)

excelerate

Collaborating in ...

- WIPs: "Bring Your Own Data" (BYOD) Capacity Building Workshops
- WIPs: Exelixis met-bio metagenomic data analysis and Gold standard for metagenomics analysis
- WIPs: Gold standard for metagenomics analysis
- WIPs: Handling of metagenomic data and tools
- WIPs: Creation of reference database adequate for the

- # ELIXIR-ITA: supporting the growth of bioinformatics in Italy with research, infrastructures and training.

elixir
ITALY
@BITS20

Our main ambition is to stimulate and assist the development, rationalization and integration of bioinformatics research in Italy, and to transfer the benefits of all these activities to our European partners and in particular to other ELIXIR nodes, towards the achievement of a pan-European bioinformatics infrastructure able to cope with the present and future challenges posed by life scientists.

- ELIXIR-ITA members -

H2020 projects

 - Call: H2020-INFRADE-1-2014**
 - Proposal: **ELIOR-EXCELERATE**: accelerating the implementation of Europe's life-science data infrastructure over the next four years (approved, grant preparation)
 - Call: H2020-INFRADE-1-2014**
 - Proposal: **EHBIRC** - European Marine Biological Research Infrastructure Cluster to promote the Blue Bioeconomy (approved, grant preparation)
 - Call: H2020-INFRA-1-2014**
 - Proposal: **INDIGO** - Integrating Distributed Data Infrastructures for Global Environmental Research (approved, project started in April 2015)

Service registry: 333 services run by ELIXIR-ITA

Facilities, Resources & Research support

 - Computing and sequencing resources**
 - Large Scale computing and storage facilities at CINECA, INFN and CIECR.
 - High capacity of CPUs.
 - Public and private biological resources**
 - GMO/GEACs: Gateway for microbiology, variant analysis and transcriptomics.
 - GenomeGrid: Gateway for the ENIGMA flag ship project.
 - GlobalGEMs: metagenomes, selected variant.
 - Bioinformatic infrastructure provided by GARR**
 - State-of-the-art, worldwide, fully integrated with high speed pan-european backbone GEANT and with worldwide research network.

Training

 - Participation in grant proposals**
 - ETBIOseq - PopBioInfo (Genomics) of Exelixis
 - EUROPE Clinical Genome Shave Siblings HGS-related analysis
 - Selected courses 2015:**
 - [http://www.bioinformatics.csi.it/training](#)
 - HSC and real world case studies (all hours)
 - GALAXY/EDR/EDM: Development of a Galaxy tooland management workflow (no fee hours)
 - [http://www.bioinform.unibo.it/bits15/](#)
 - International network in Bioinformatics (free years)

ORIONE
datacenter/wireless

Expanding the node.

The first ITA JGU is open to new institutions to member willing to join us, after the University of Bari has been the first member to join the JGU after its creation, allowing currently three more ongoing preliminary contracts, with other important research institutions

ICGAs for pilot projects & future resources

 - Reasoning on a national NGIS data repository
 - Cloud-based Galaxy-on-demand platform (HDIOG use case)
 - Disease Biobank: integrating IMAcData with GenCAREx and Signor
 - Classification of HGS-workflows and integration of HPGCC-infrastructures
 - The Virus-Human Host Project: integration of Virus-related Bioinformatics resources
 - Workshop to compile an agreed list of requisites for "ELIXIR-branded" training courses
 - Integrating ELIXIR reference datasets within the Europe-wide Grid Infrastructure collaboration with EGI

Contacts

Giuseppe Pirovano g.pirovano@unibo.it
Francesca Zambelli f.zambelli@unibo.it, Stefano Zambelli s.zambelli@unibo.it
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ELIXIR Infrastructure

- **Data**

Sustain core data resources

- **Tools**

Services & connectors to drive access and exploitation

- **Compute**

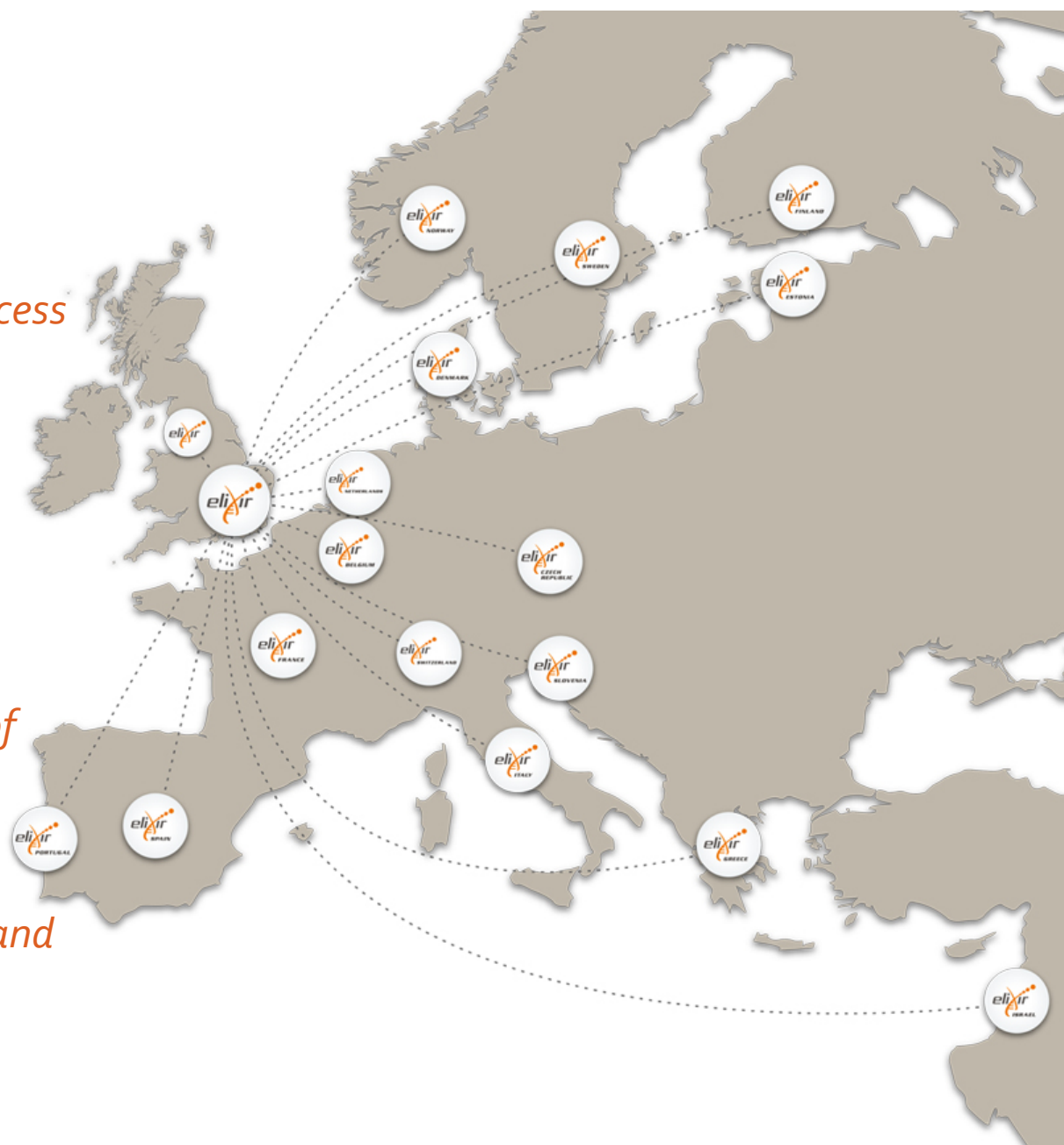
Access, Exchange & Compute on sensitive data

- **Standards**

Integration and interoperability of data and services.

- **Training**

Professional skills for managing and exploiting data



ELIXIR-ITA




Cerca ...




[HOME](#)
[STRUTTURA](#)
[SERVIZI](#)
[NEWS](#)
[EVENTI](#)
[TRAINING](#)
[PROGETTI](#)
[CONTATTI](#)
[LOGIN](#)



IIB

ELIXIR è l'infrastruttura di ricerca europea (www.elixir-europe.org) per i dati biologici che ha come obiettivo primario quello di supportare la ricerca nel campo delle "scienze della vita" e le attività traslazionali per la medicina, l'ambiente, le industrie biotecnologiche e la società.

ELIXIR è costituita come una infrastruttura distribuita su diversi Nodi, uno per Stato membro, ospitati da centri di eccellenza localizzati in tutta Europa (i "Nodi ELIXIR"). I Nodi sono collegati ad un hub centrale ("ELIXIR-Hub") che è localizzato ad Hinxton (Regno Unito) presso il "Wellcome Genome Campus" dove è anche ospitato l'European Bioinformatics Institute dell'EMBL (EMBL-EBI). Il nodo italiano di ELIXIR è coordinato dal CNR e attualmente comprende 17 partner che includono istituti di ricerca, università e istituzioni tecnologiche.

Il Nodo italiano di ELIXIR, che ha l'ambizione di costituire un Istituto Italiano di Bioinformatica (IIB) distribuito su più centri, si propone di aggregare tutti i ricercatori italiani che operano nel campo della Bioinformatica, favorendo lo scambio e lo sviluppo di competenze, di mettere a sistema le varie risorse bioinformatiche già riconosciute in ambito internazionale e pubblicamente disponibili, e di contribuire alla loro integrazione in seno all'infrastruttura europea.

Un altro obiettivo primario di ELIXIR-ITA è quello di organizzare attività di training, sia di base che avanzato, nei diversi settori applicativi della Bioinformatica al fine di favorire la formazione di giovani bioinformatici, la cui domanda è in fortissima crescita in ambito nazionale ed internazionale.

<

Giugno 2016

>

LUN	MAR	MER	GIO	VEN	SAB	DOM
30	31	1	2	3	4	5
6	7	8	9	10	11	12
13	14					
20	21					
27	28					




MARTEDÌ

training IIB 09:00-12:00

RNA-seq data analysis



Martedì 30 marzo alle ore 14.00 prof. Torsten Schwede dell'Università di Basilea&Swiss Institute of Bioinformatics terrà un seminario dal titolo: "Using evolutionary information for

[leggi >](#)

EVENTI

BITS2016

15/06/2016 - 17/06/2016 Giorno Intero

13° Meeting Annuale della Società di Bioinformatica Italiana 15-17 Giugno 2016, Università di Salerno, Italia La Società di Bioinformatica Italiana, insieme all'Università degli Studi di

[leggi >](#)

TRAINING

Workshops

14/06/2016 09:00

[leggi >](#)

The IIB/ELIXIR-ITA Training Programme

[Courses](#) [Events&Collaborations](#) [Trainers](#) [Contacts](#)

2016

1. High Performance Molecular Dynamics

CINECA, via dei Tizi 6, Rome - 5-7 April 2016

This course is designed for those users who wish run classical molecular dynamics programs such as GROMACS and NAMD on modern supercomputers. By understanding better the HPC infrastructures and the algorithms used to exploit them, the aim is to give researchers the tools to run simulations in the most efficient way possible on current and future supercomputers. At least half the course will be devoted to practical sessions where students will be able to prepare and run GROMACS or NAMD examples on the supercomputers of Cineca.

2. NGS for evolutionary biologists: from basic scripting to variant calling

Biblioteca, Consiglio Nazionale delle Ricerche, via P. Castellino 111, 80131 Naples - May 2-6, 2016

This course will provide an introduction to next generation sequencing platforms, data analysis and tools for data quality control, including alignment to a reference sequence, data handling and visualisation, and variant calling and filtering (single nucleotide polymorphisms and structural variants). The course will be delivered using a mixture of lectures and computer based hands-on practical sessions, including group projects to be completed by the participants using the knowledge gained at the course. Projects will cover the general topics of population structure and admixture, demographic changes and natural selection.

3. RNA-seq data analysis workshop

University of Naples Federico II, Naples - June 6-10, 2016

This course will provide an introduction on the application of the RNA-seq technology to the study of non-model organism transcriptomes and it will be centered on the Trinity software suite for the de novo transcriptome assembly and analysis. The course will be delivered by the lead developer of the Trinity

ELIXIR AAI history – where we are now

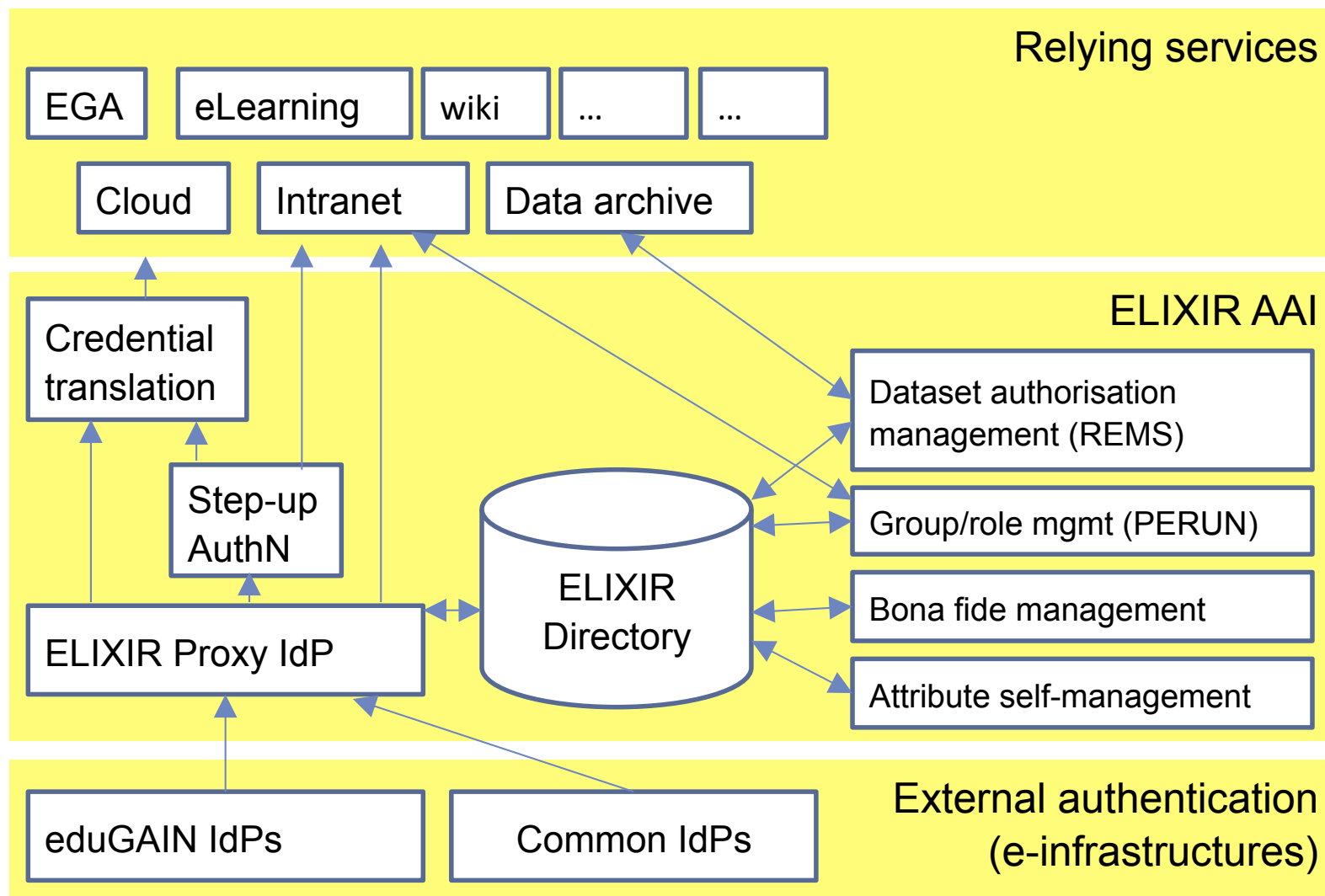
- Use case gathering -- Autumn 2014
 - <https://www.elixir-europe.org/documents/elixir-aai-use-cases>
- Requirements and design – Spring 2015
 - <https://www.elixir-europe.org/documents/aai-requirements-and-design>
- Deployment starts – Autumn 2015 – EXCELERATE WP4.3.1
 - Part of ELIXIR Compute platform
- First release -- August 2016
 - Until that ELIXIR AAI in pilot status
 - Key components up and running already

Mikael Linden, Michal Prochazka

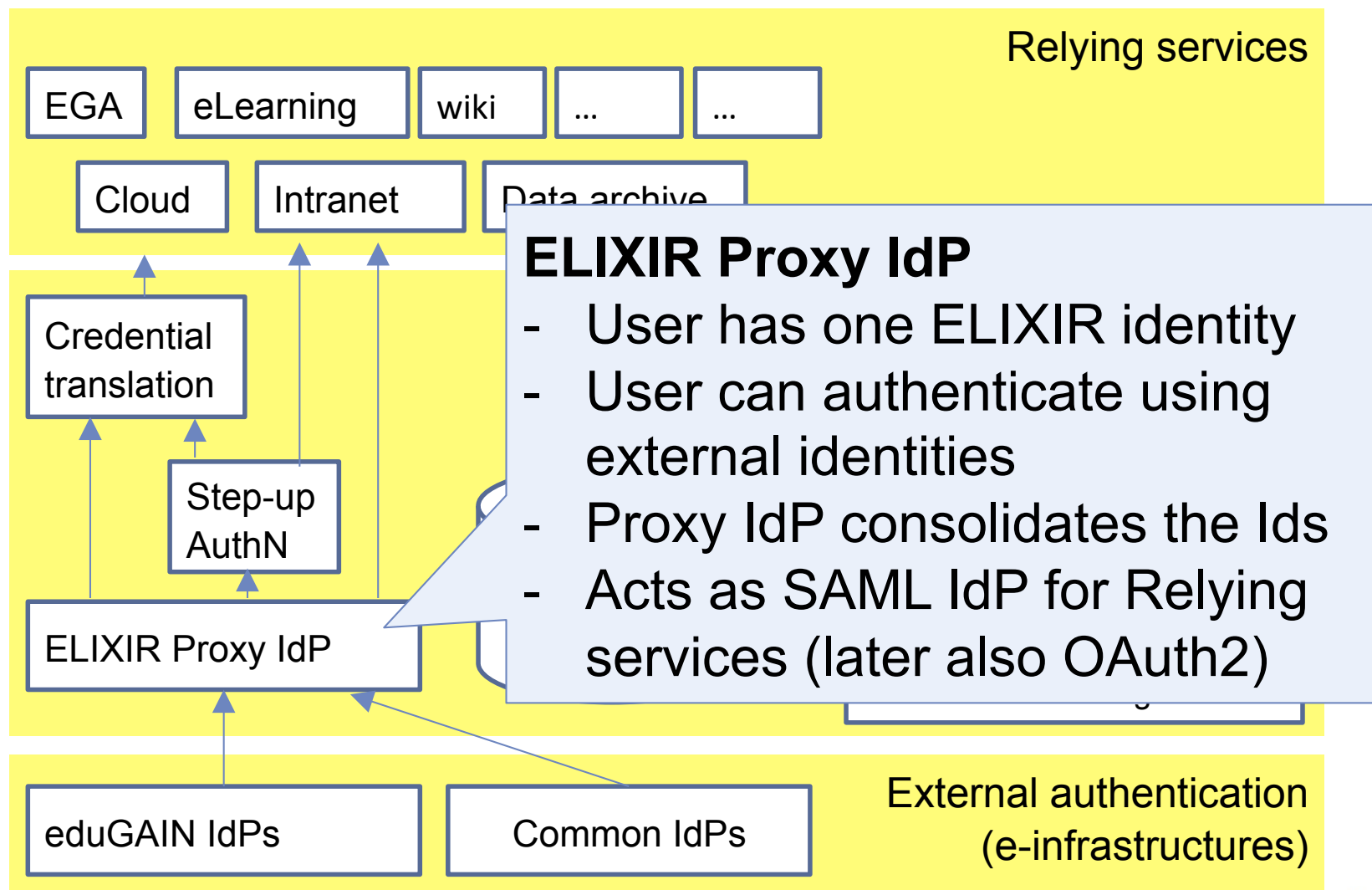
AAI workshop 15-16 March 2016 Manchester



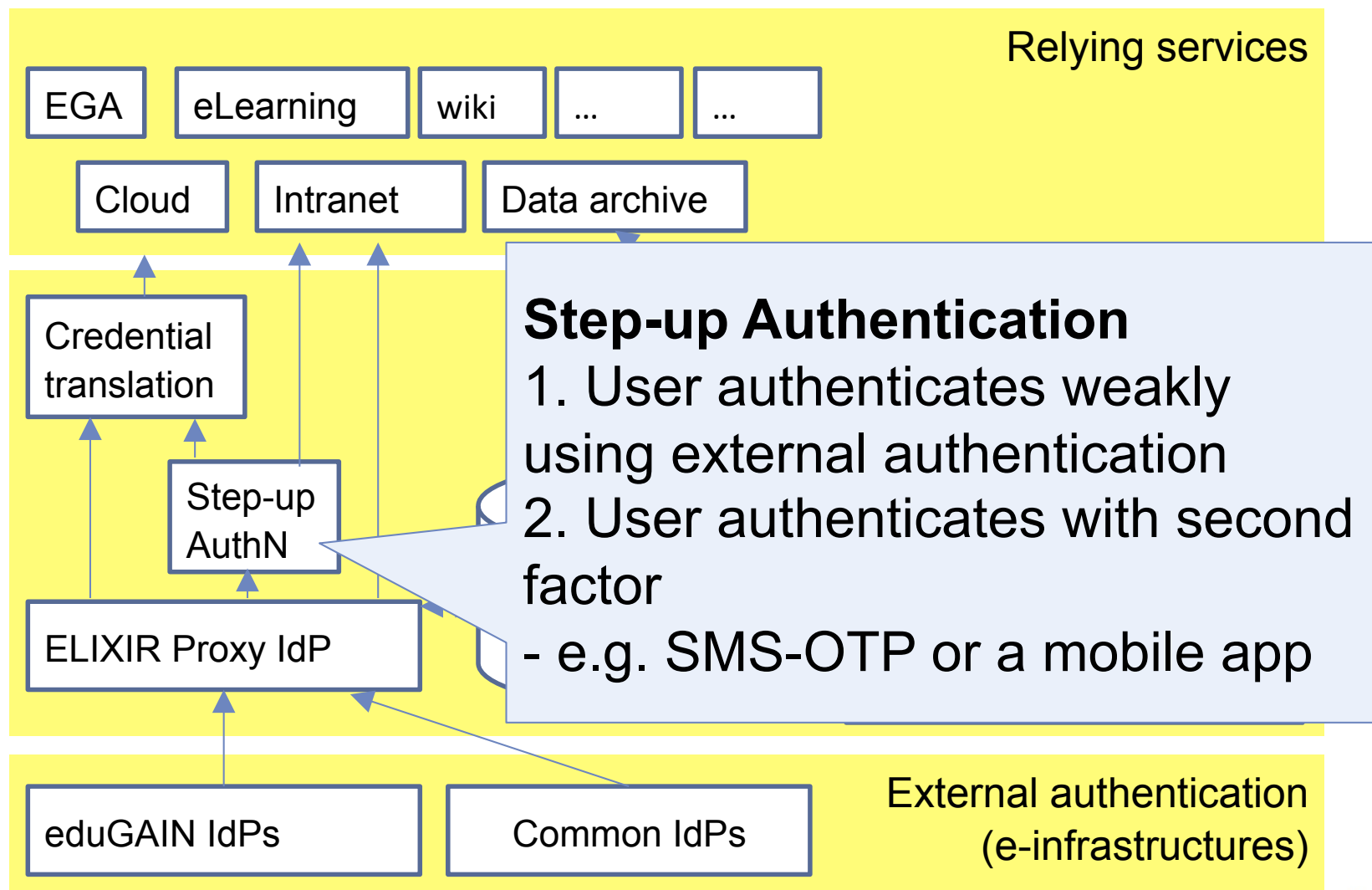
ELIXIR AAI design



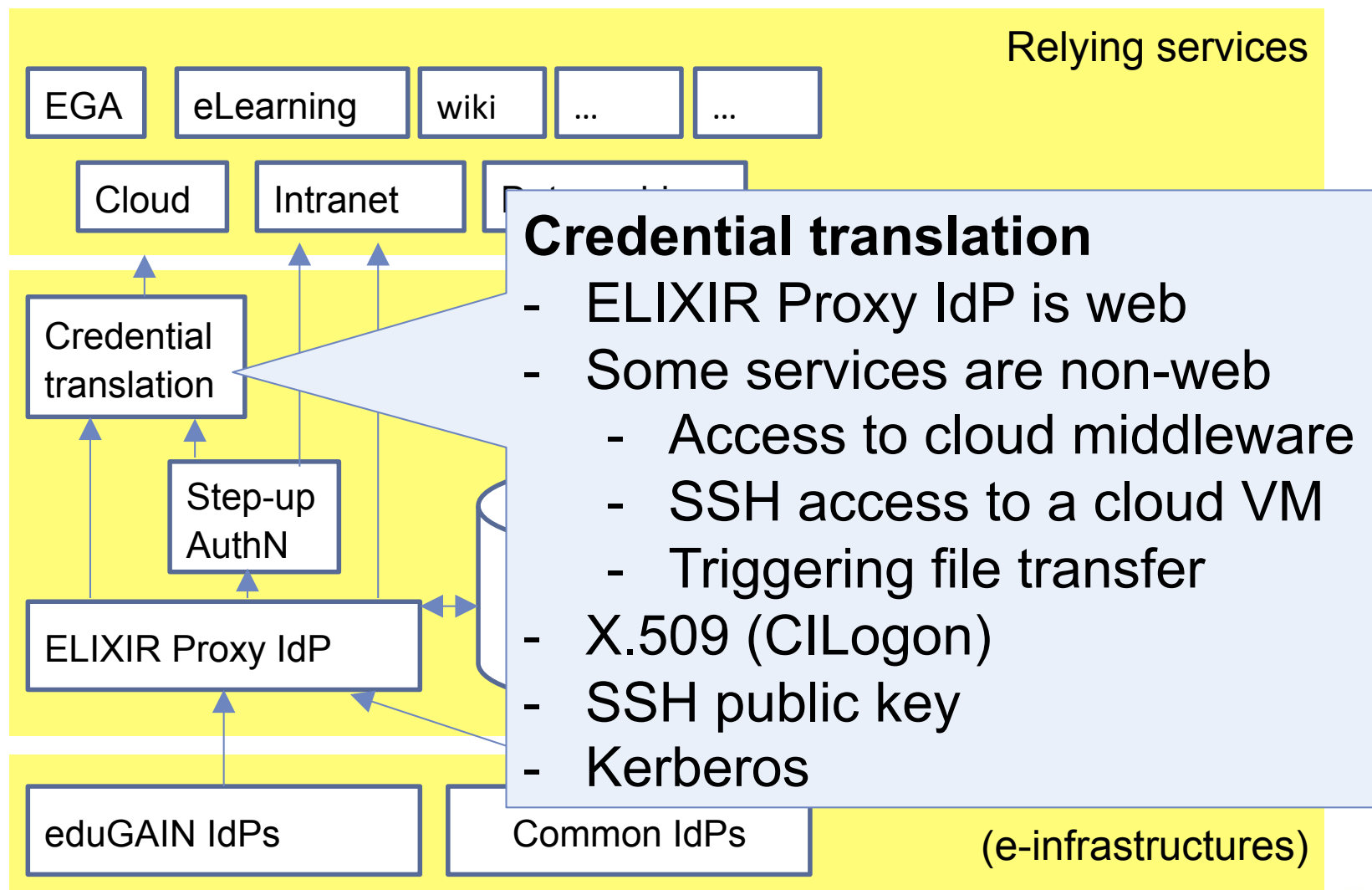
ELIXIR AAI design



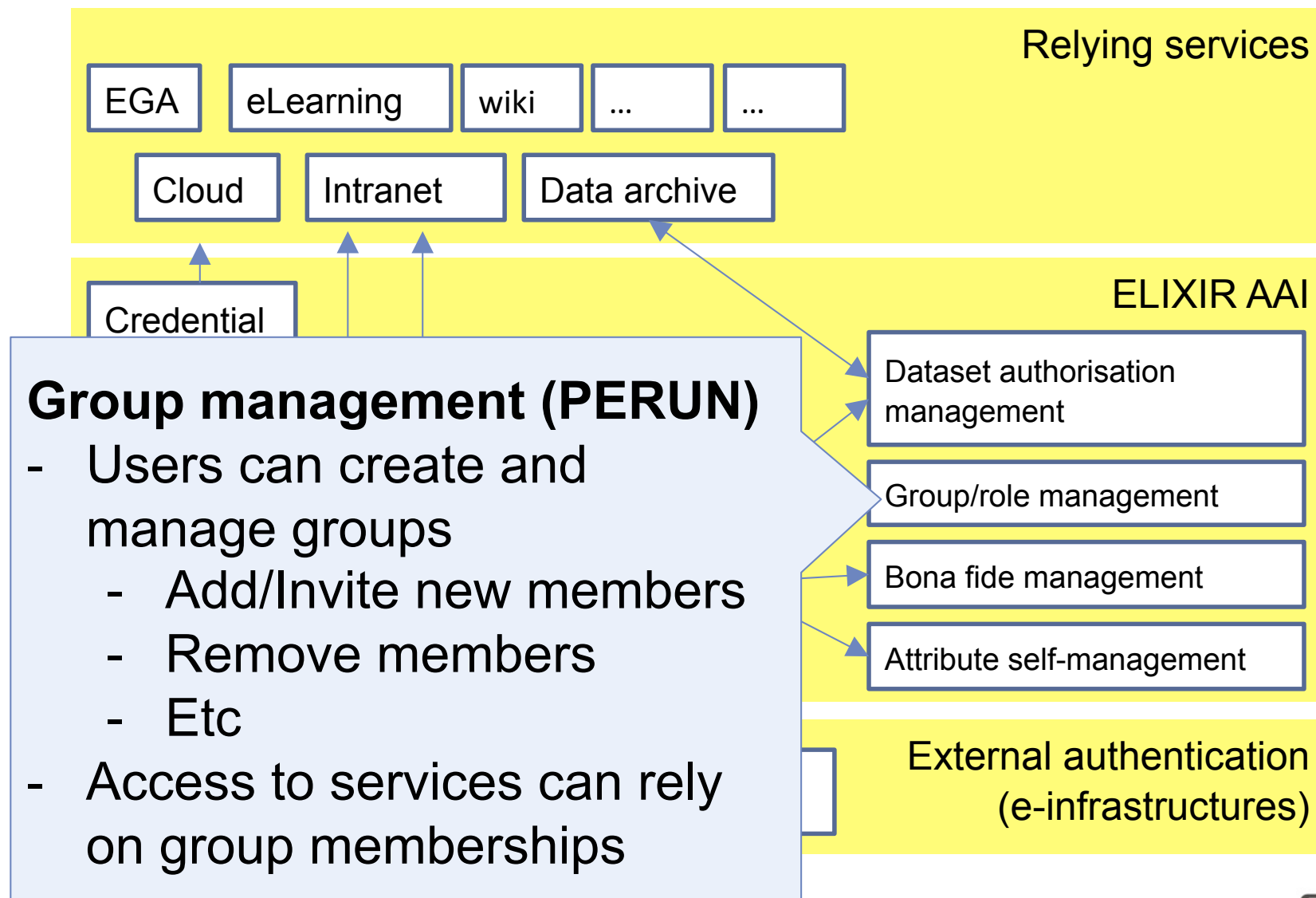
ELIXIR AAI design



ELIXIR AAI design

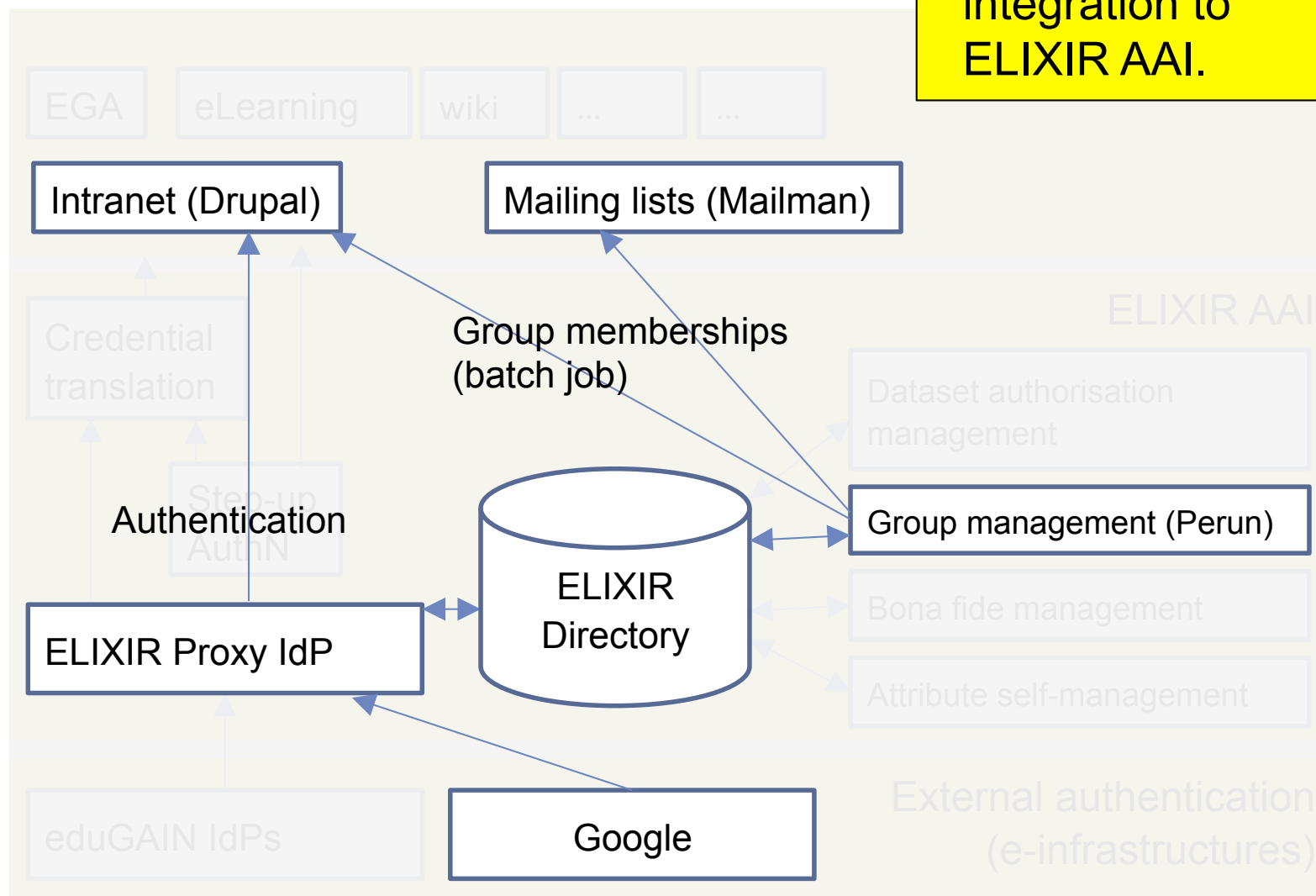


ELIXIR AAI design



Intranet and mailing lists

Current operational
integration to
ELIXIR AAI.



Galaxy

Galaxy is an open, web-based platform for accessible, reproducible, and transparent computational biomedical research.

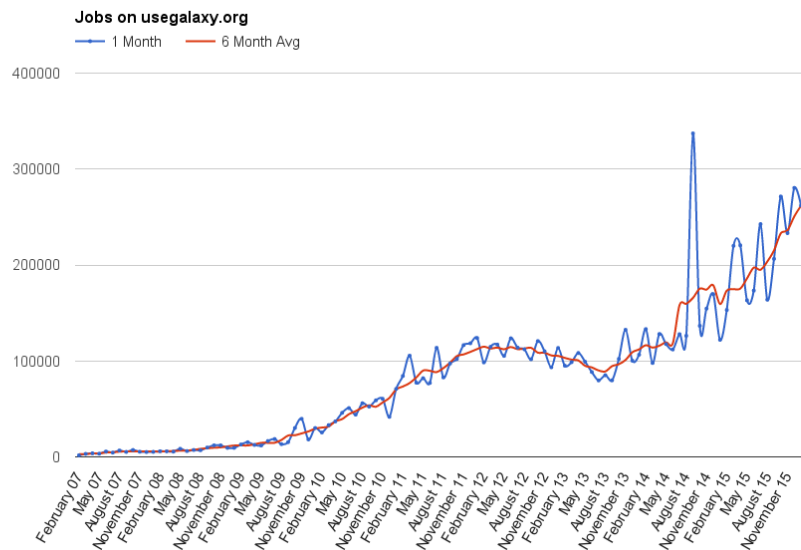
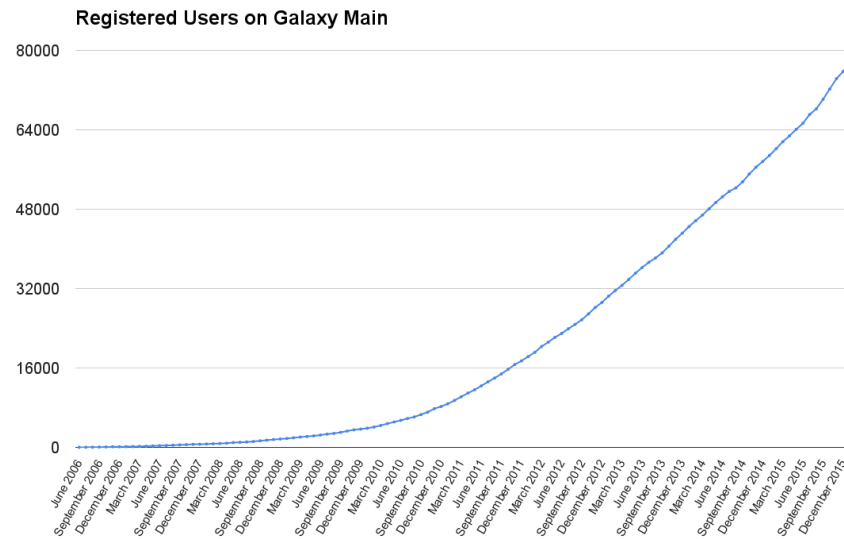
Accessible: Users without programming experience can easily specify parameters and run tools and workflows. Galaxy integrates a multitude of different tools by giving them the same “look and feel”

Reproducible: Galaxy captures information so that any user can repeat and understand a complete computational analysis.

Transparent: Users share and publish analyses via the web and create Pages, interactive, web-based documents that describe a complete analysis.



Galaxy main usage



Publicly accessible server

Date	# Servers
2011/07	15
2012/01	21
2012/07	20
2013/01	25
2013/02	27
2013/07	35
2014/01	54
2014/07	60
2015/01	70
2015/07	73
2016/01	84


<https://wiki.galaxyproject.org/GalaxyProject/Statistics>



Galaxy

The screenshot shows the Galaxy web interface. At the top is a navigation bar with links: **Analyze Data**, **Workflow**, **Data Libraries**, **Help**, and **User**. On the left is a sidebar with a **Tools** section containing links like [Get Data](#), [Send Data](#), [ENCODE Tools](#), [Lift-Over](#), [Text Manipulation](#), [Convert Formats](#), [File manipulation](#), and [Sort](#). Below this is a section for **Metagenomic analyses** with links like [EMBOSS](#), **NGS TOOLBOX BETA**, [NGS: QC and manipulation](#), [NGS: Mapping](#), and [NGS: SAM Tools](#). The main center column displays a document titled "Galaxy in 2010..." with a large heading "Mapping Pipeline for Illumina, 454, and SOLiD" dated "March 2010". Below the document is a scrollable area showing text about the Galaxy team and funding. On the right is a **History** panel with an **Options** dropdown, a "refresh | collapse all" link, and a section for "Unnamed history" which contains a message: "Your history is empty. Click 'Get Data' on the left pane to start." Three blue callout boxes provide context: one on the left sidebar says "contains links to the downloading, preparation and analysis tools.", one in the center says "The center column is where the forms and data will appear", and one on the right says "show you the history of your analysis steps, allow you view data and results, and more." The bottom right corner features a logo with the letters "IR" and a stylized orange graphic.

Galaxy


 Atlassian
Features Pricing

owner/repository

English

Sign up

Log in

 galaxy-dist
galaxy Fork of galaxy-dist-staging

Clone Fork Compare

Overview Source Commits Branches Pull requests 2 Downloads

Bitbucket is a code hosting site with unlimited public and private repositories. We're also free for small teams!

Sign up for free

GALAXY
=====

<http://galaxyproject.org/>

The latest information about Galaxy is always available via the Galaxy website above.

HOW TO START
=====

Galaxy requires Python 2.6 or 2.7. To check your python version, run:

```
% python -V
Python 2.7.3

Start Galaxy:

% sh run.sh
```

HTTPS <https://bitbucket.org/galaxy/>

2 Branches

8 Tags


41 Forks

75 Watchers

Owner	galaxy
Access level	Public
Type	Mercurial
Last updated	2013-12-19
Created	2009-08-28
Size	151.8 MB (download)



Galaxy - Pages

 Galaxy / CRS4 IRGB

Analyze Data Workflow **Shared Data** Visualization Admin Help User

Using 52.1 Mb

Published Pages | [gmauro](#) | Pre-check merge individuals

About this Page

How to verify your list of individuals to be merged

The workflow described here, will check merging individuals info using informations from a csv file like this:

```
source,target
V08E18411BC66F4987BCA43EFC6F636224,V0AE5660BF4A7149589BE90B3308B50327
```

source will be substituted from target

This workflow moves all informations related to an individual (source) to another (target).
Moved informations are:

- children (Individual objects)
- ActionOnIndividual
- Enrollments
- EHR records

Only the first time:
click on this link [Workflow 'pre-check data before merge individuals'](#) and then click on the button "import workflow" on the right top corner


1. upload your csv file with the list of individuals to be merged into the history
2. if you haven't done yet, rename the history in a more valuable way
3. from the "Workflow" tab, click on "imported: pre-check data before merge individuals" workflow and the "Run" from the pop-up menu
4. In Step1, verify that "in Query" field point to your uploaded csv file.
5. Run workflow

At the end of the workflow, in your history will be two more green boxes, labelled:

- individuals 2 be merged
- VLT.check_merge_individuals.logfile

if you don't see any error messages into the logfile, the pre-check is finished and the first box can be used with the "merge individuals" workflow.
Otherwise, check the error messages, correct your csv file, upload it again and re-run the workflow

Author

gmauro

Related Pages

[All published pages](#)
[Published pages by gmauro](#)


Rating

Community (0 ratings, 0.0 average) ★★★★★

Yours ★★★★★

Tags

Community: none

Yours:




Galaxy - Histories

Galaxy / CRS4

Analyze Data Workflow Shared Data Visualization Admin Help User

Using 39%

Tools

search tools

COMMON TOOLS

Get Data

NGS: Quality control

FastQC: Read QC reports using FastQC

NGS: manipulation

NGS: Mapping

NCBI BLAST+

TOOLS BY TOPIC

MICROBIOLOGY

NGS: de novo assembly

Aligning and Phylogeny

Gene annotation

VARIANT CALLING

NGS: SNP Effects

NGS: SAM Tools

NGS: GATK2

VCF Tools

BED Tools

FreeBayes

Copy number variation

METAGENOMICS

MetaPhlAn

Other metagenomics tools

NGS: RNA ANALYSIS

RNA-seq

CHIP-SEQ

NGS: Peak Calling

Motif Tools

OTHER TOOLS

Unknown Tool

Name:

Map with BWA for Illumina on data 14: mapped reads

Created:

Fri Jul 31 13:48:36 2015 (UTC)

Filesize:

21.6 GB

Dbkey:

hg19

Format:

sam

Galaxy Tool ID:

bwa_wrapper

Galaxy Tool Version:

1.2.3

Tool Version:

0.7.9a-r786

Tool Standard Output:

stdout

Tool Standard Error:

stderr

Tool Exit Code:

0

API ID:

824843df326fb7d1

History ID:

0072e017d28ba2de

UUID:

e9754268-f9d4-4e48-a620-a954b42e62ea

Full Path:

/home/igmauro/orione/database/files/000/278/dataset_278399.dat

Job Command-Line:

python /u/galaxy/orione-tools/toolshed/repos/devteam/bwa_wrappers/ffa8aaa14f7c/bwa_wrappers/bwa_wrapper.py --threads="\${GALAXY_SLOTS:-4}" --fileSource="indexed" --ref="/SHARE/USERFS/els7/users/biobank/genome/hg19/bwa_index/hg19full/hg19full.fa" --input1="/SHARE/USERFS/els7/users/galaxy/orione/user_library_import_dir/andrea.pinna@crs4.it/120702_SN526_0205_AC0BVMACXX/rare_000063_R2_L5.fastq" --input2="/SHARE/USERFS/els7/users/galaxy/orione/user_library_import_dir/andrea.pinna@crs4.it/120702_SN526_0205_AC0BVMACXX/rare_000063_R2_L5.fastq" --output="/SHARE/USERFS/els7/users/biobank/galaxy/central/files/000/278/dataset_278399.dat" --genAlignType="paired" --params="full" --maxEditDist="0" --fracMissingAligns="0.04" --maxGapOpens="1" --maxGapExtends="1" --disallowLongDel="16" --disallowIndel="5" --seed="-1" --maxEditDistSeed="2" --mismatchPenalty="3" --gapOpenPenalty="11" --gapExtendsPenalty="4" --suboptAlign="" --noIterSearch="false" --outputTopN="3" --outputTopNDisc="10" --maxInsertSize="500" --maxOccurPairing="100000" --rgid="120702_SN526_0205_AC0BVMACXX.L5.10" --rgcn="CRS4" --rgds="" --rgdt="" --rgfo="" --rgks="" --rglb="ex12" --rgpg="" --rgpi="" --rgpl="ILLUMINA" --rgpu="None" --rgsm="rare_063" --suppressHeader="false"

SGE_STDIN_PATH (runtime environment variable)

/dev/null

SGE_JOB_SPOOL_DIR (runtime environment variable)

/var/ge2011_11/execd_spool/entu212/active_jobs/8688189.1

UPSTART_EVENTS (runtime environment variable)

runlevel

ENVIRONMENT (runtime

History

search datasets

Sex check

19 shown, 14 deleted

71.2 GB

33:

VLT.all_enrollments.logfile

32:

VLT.all_enrollments.csv

31: Map with BWA for Illumina on data 14: mapped reads

~58,000,000 lines, 95 comments

format: sam, database: hg19

BWA Version: 0.7.9a-r786

BWA run on paired-end data

View details

AG 3. RNAME 4. POS 5. MAPQ

ESQ

SN:chrM LN:16571

ESQ

SN:chr1 LN:249250621

ESQ

SN:chr2 LN:243199373

ESQ

SN:chr3 LN:198022430

ESQ

SN:chr4 LN:191154276

ESQ

SN:chr5 LN:180915260

29:

VLT.all_enrollments.logfile

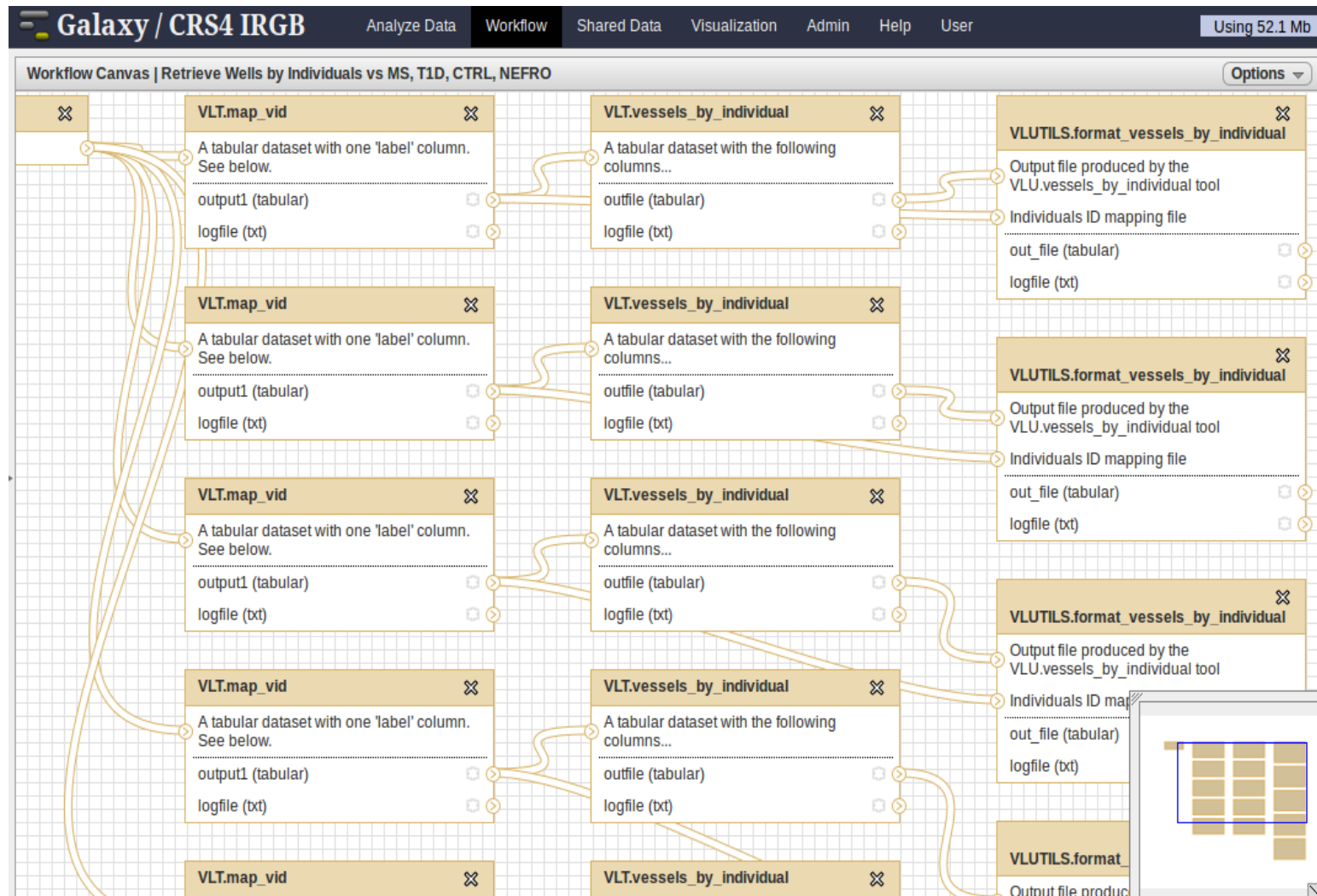
28:

VLT.all_enrollments.csv


27: Compute XY ratio.logfile

26: Compute XY ratio.csv

Galaxy - Workflows



Galaxy - Libraries


 Galaxy

Analyze Data Workflow Shared Data Visualization Cloud Help User

Using 0%

Data Libraries


search dataset name, info, message, dbkey



[Advanced Search](#)

<u>Data library name</u>	<u>Data library description</u>
1000 Genomes	Data from the 1000 Genomes Project FTP site
AC-exome	
Bushman	Data for Nature Letter "Complete Khoisan and Bantu genomes from southern Africa"
ChIP-Seq Mouse Example	Data used in examples that demonstrate analysis of ChIP-Seq data
Chobi	
Codon Usage Frequencies	
Coleman	IonPGM
Erythroid Epigenetic Landscape	Dynamics of the epigenetic landscape during erythroid differentiation after GATA1 restoration
Evolutionary Trajectories in a Phage	Experimental evolution (Illumina)
GATK	
GCAT	Consortium
Genome Diversity	Nucleotide polymorphisms for several threatened species
guru_1000GP	
He-2010	
Heteroplasmy	Data for Genome Biology 2011 manuscript
iGenomes	Selected files from Illumina iGenomes collection
Illumina BodyMap 2.0	RNA-seq data for the Illumina BodyMap 2.0 project
Illumina iDEA Datasets	

Galaxy – Tool Shed


Galaxy Tool Shed

[Repositories](#)
[Groups](#)
[Help](#)
[User](#)

3904 valid tools on May 15, 2016

Search

- [Search for valid tools](#)
- [Search for workflows](#)

Valid Galaxy Utilities

- [Tools](#)
- [Custom datatypes](#)
- [Repository dependency definitions](#)
- [Tool dependency definitions](#)

All Repositories

- [Browse by category](#)

Available Actions

- [Login to create a repository](#)

Repositories by Category

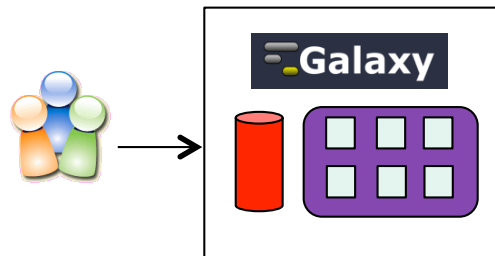
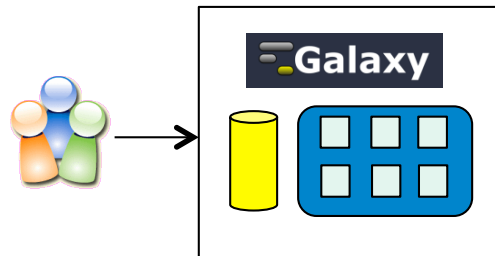
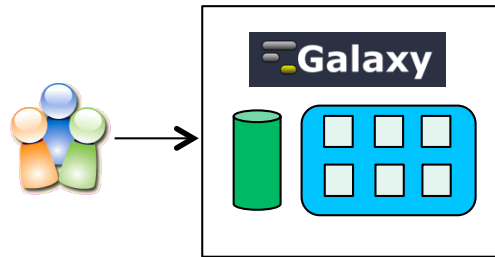
Name	Description	Repositories
Assembly	Tools for working with assemblies	75
ChIP-seq	Tools for analyzing and manipulating ChIP-seq data.	40
Combinatorial Selections	Tools for combinatorial selection	6
Computational chemistry	Tools for use in computational chemistry	24
Convert Formats	Tools for converting data formats	64
Data Managers	Utilities for Managing Galaxy's built-in data cache	32
Data Source	Tools for retrieving data from external data sources	35
Epigenetics	Tools for analyzing Epigenetic/Epigenomic datasets	3
Fasta Manipulation	Tools for manipulating fasta data	77
Fastq Manipulation	Tools for manipulating fastq data	56
Genome-Wide Association Study	Utilities to support Genome-wide association studies	20
Genomic Interval Operations	Tools for operating on genomic intervals	42
Graphics	Tools producing images	42
Imaging	Utilities to support imaging	1
Metabolomics	Tools for use in the study of Metabolomics	25
Metagenomics	Tools enabling the study of metagenomes	58
Micro-array Analysis	Tools for performing micro-array analysis	8
Next Gen Mappers	Tools for the analysis and handling of Next Gen sequencing data	105
Ontology Manipulation	Tools for manipulating ontologies	10



GALAXY@ELIXIR-ITA

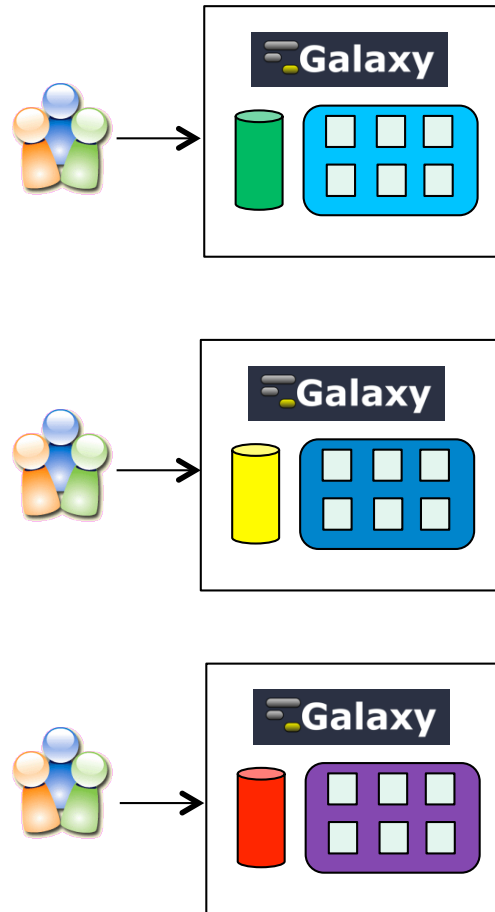
- ORIONE@CRS4: microbiology, variant analysis and transcriptomics.
- Galaxy@EPIGEN: EPIGEN flagship project.
- Galaxy@INFN: metagenomics oriented
- ...

NGalaxy?

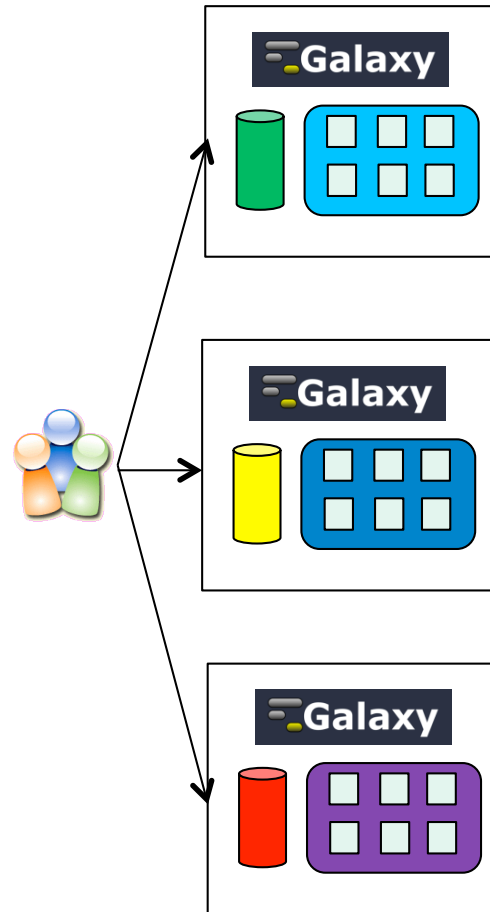


Local

NGalaxy?

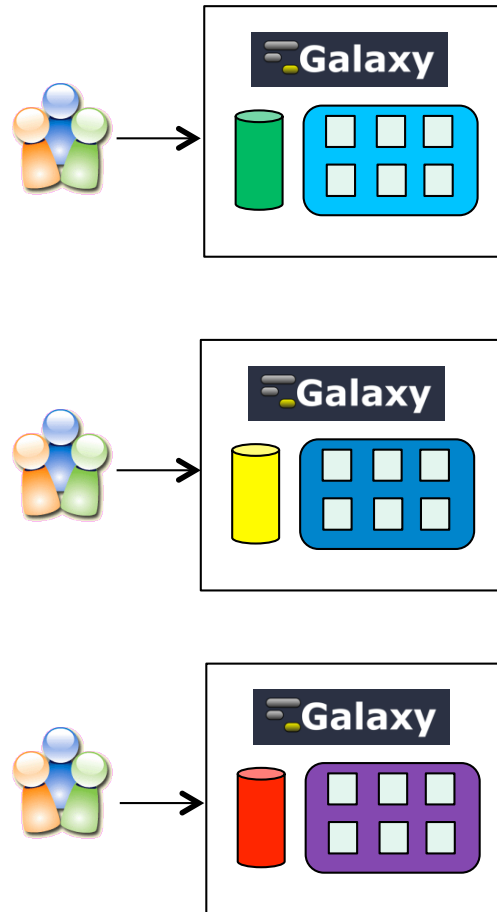


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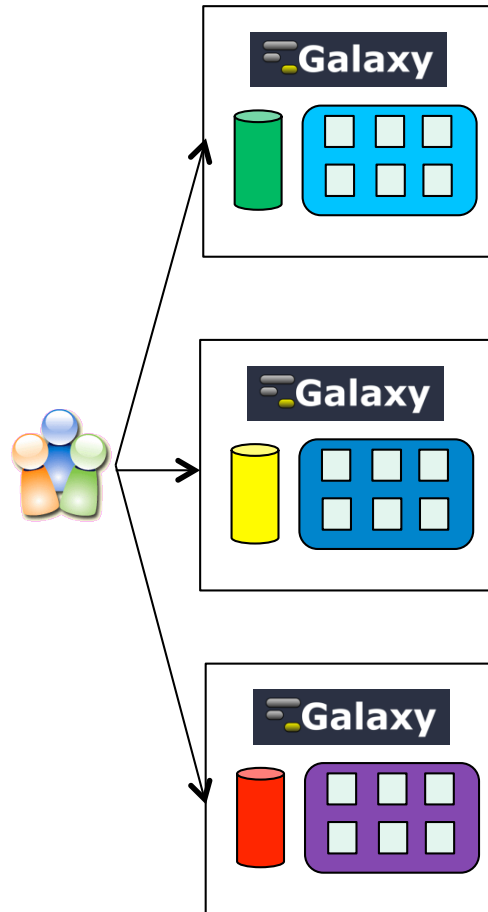


Federated

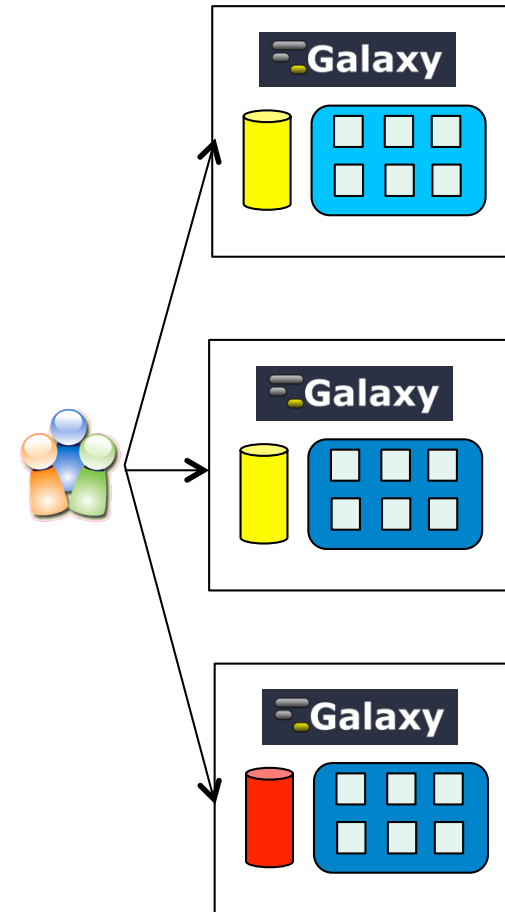
NGalaxy?



Local



Federated



Federated+

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← ⓘ 🔒 https://galaxy-uit.bioinfo.no/simplesaml/module.php/saml/disco.p | 🔍 Search ☆ 📖 ✓ 🟢 ⬇️ 🏠 😊 📺 ⓘ 🗑️ ☰

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