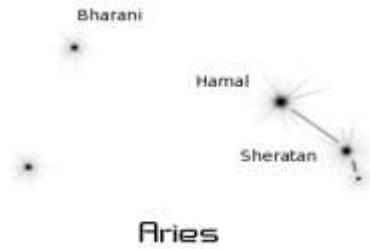


NGS solutions in Microbiology

(in 30 min)





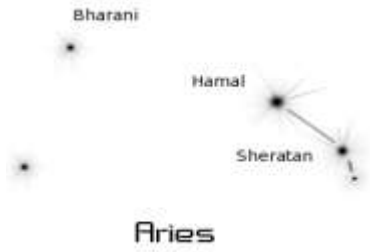
Before Starting

What I've to do with sequences?

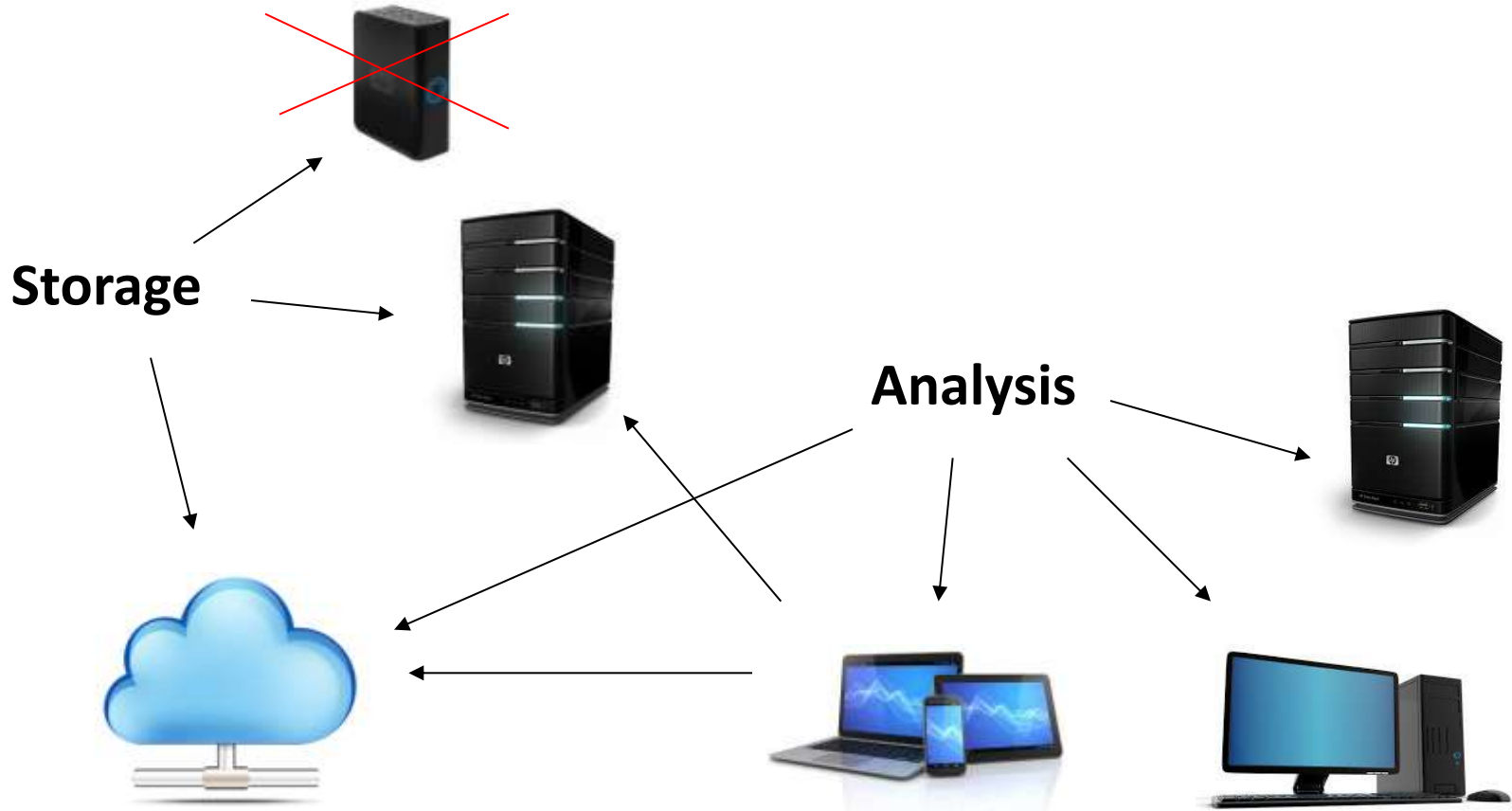
What kind of results do I expect?

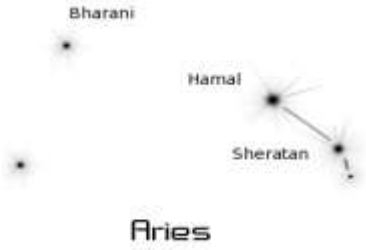
What are my applications?

What do my collaborators expect? Can I satisfy them?

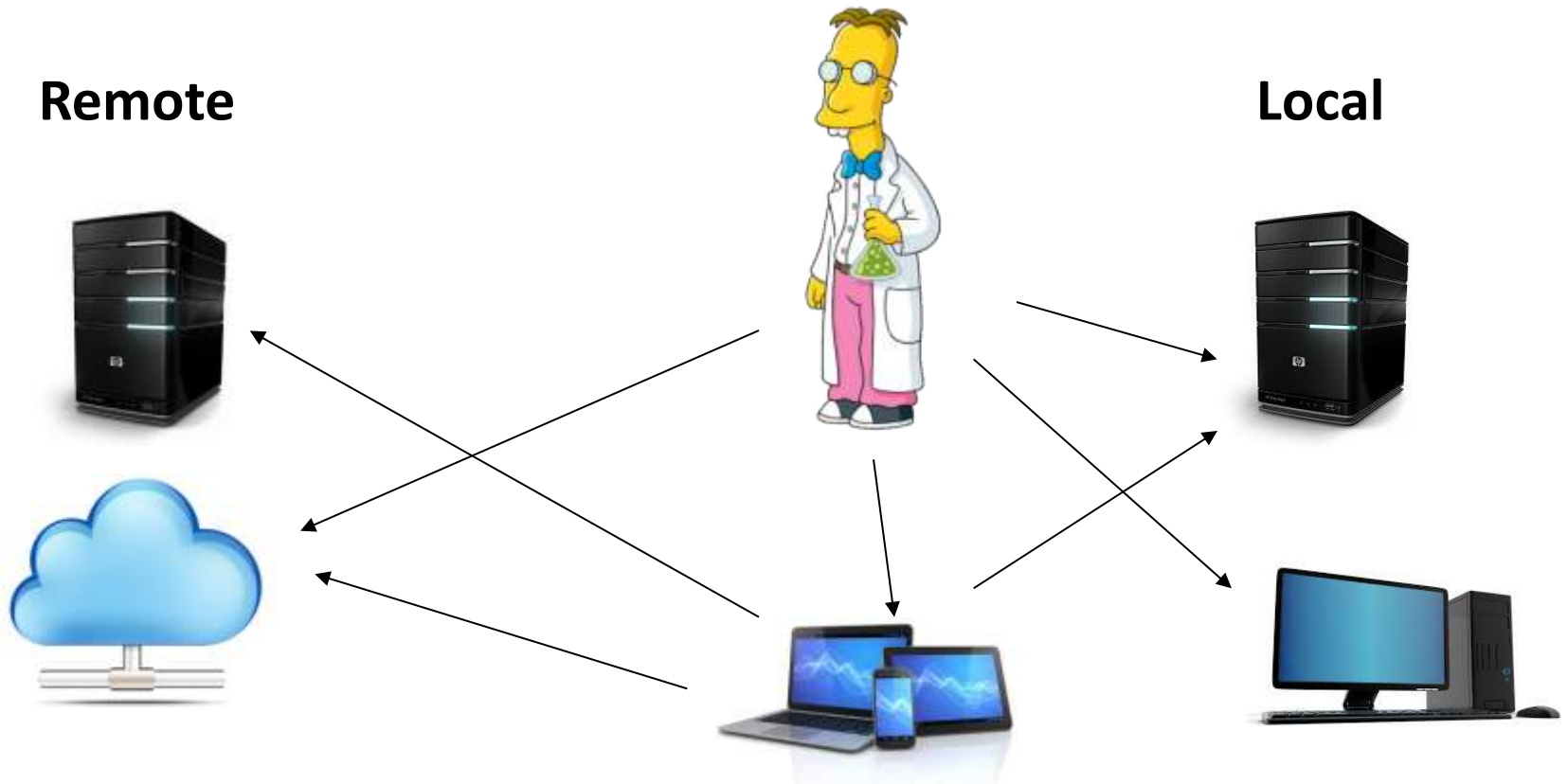


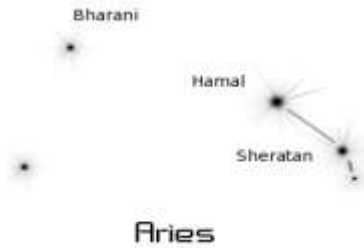
My brand-new sequencer has just produced 200GB of data...
What can I do with them?





Let's focus on Analysis



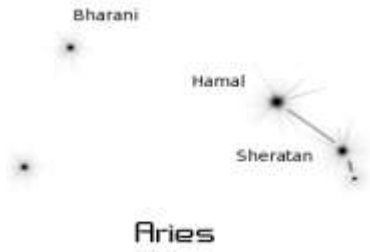


Remote Servers

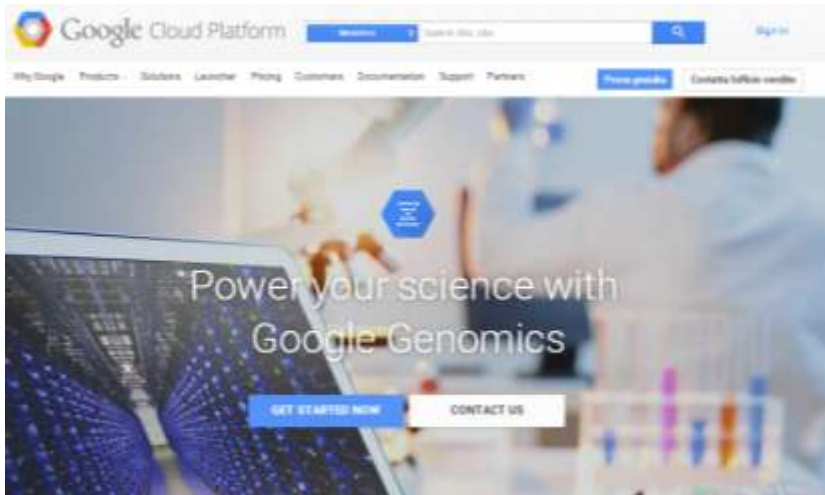


```
root@ip-10-10-10-10:~# ssh root@10.10.10.10
root@10-10-10-10:~# cat /etc/passwd
root:x:0:0:root:/root:/bin/bash
daemon:x:1:1:daemon:/usr/sbin:/usr/sbin/nologin
bin:x:2:2:bin:/bin:/usr/sbin/nologin
sys:x:3:3:sys:/dev:/usr/sbin/nologin
cron:x:4:4:cron:/var/spool/cron/root:/usr/sbin/nologin
mail:x:8:8:mail:/var/mail:/usr/sbin/nologin
nobody:x:65534:65534:nobody:/nonexistent:/usr/sbin/nologin
mysql:x:123:123:MySQL Server:/usr/bin:/usr/sbin/nologin
root@10-10-10-10:~#
```

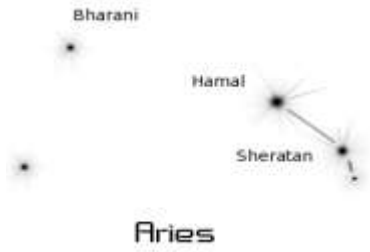
**Are you familiar with ssh?
Command line?
Modules environment?
Sftp?
Pay what you use...**



Cloud Solutions



Are you familiar with API?
Low flexibility
High powerful resources
Do you trust in data security?
Reachable anywhere



Local Solutions

Workstation

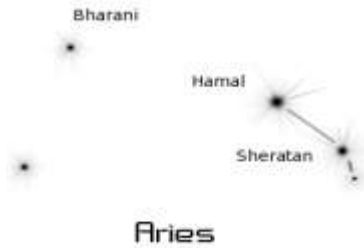


Small scale projects
Affordable costs
Low management efforts

Local Server



Higher costs, scalability
Storage
medium scale requests
People to manage it !!



And Software???

Open or Commercial?

Burrows-Wheeler Aligner

Home

Introduction

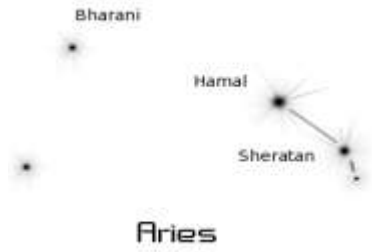
Burrows-Wheeler Aligner (BWA) is an efficient program that aligns relatively short nucleotide sequences against a long reference sequence such as the human genome. It implements two algorithms, `bwa-short` and `BWA-SW`. The former works for query sequences shorter than 200bp and the latter for longer sequences up to around 100kbp. Both algorithms do gapped alignment. They are usually more accurate and faster on queries with low error rates. Please see the [BWA manual page](#) for more information.

BWA:

- [SF project page](#)
- [SF download page](#)
- [Mailing list](#)
- [BWA manual page](#)
- [Repository](#)

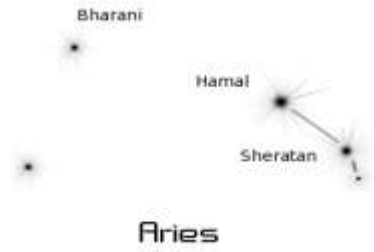
...





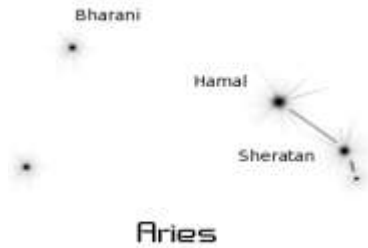
And People???





Did you think about these aspects?

Would you tell us your experience...?



Where is Galaxy framework in this scenario?

Data intensive biology *for everyone.*

Galaxy is an open, web-based platform for data intensive biomedical research. Whether on the free public server or your own instance, you can perform, reproduce, and share complete analyses.

Use Galaxy



Use project's free server or other public servers

Get Galaxy



Install locally or in the cloud or get Galaxy on SlipStream

Learn Galaxy

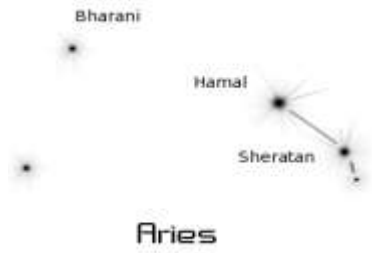


Screencasts, Galaxy 101, ...

Get Involved



Mailing lists, Tool Shed, wiki



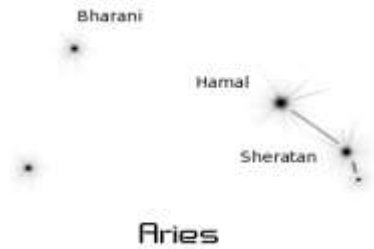
What is Galaxy?

an open **web based** platform

- **Accessible**, reproducible, and transparent community standard
- **Personalized** data access and specialized tools for data analysis
- Use “Big Data” technologies to help **scale** computation

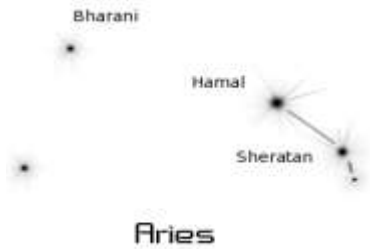


Layer between you and hardware resources



Galaxy Main Features

- Galaxy integrates a multitude of different tools by giving them the same “**look and feel**”
- **Histories** Every step of your analyses is recorded in Galaxy's history system...
- **Share your analyses** share histories between users
- **Results are reproducible** replace “the data were analyzed using a collection of in-house scripts” with an url pointing to Galaxy's history



Galaxy Specialized Instances

Galaxy Wiki Accedi | Cerca: Titoli Testa

PublicGalaxyServers Locked History Actions

060+

Public Galaxy Servers
and *still* counting

Publicly Accessible Galaxy Servers

The Galaxy Project's public server (UseGalaxy.org, *Main*) can meet many needs, but it is not suitable for everything (see Choices for why) and cannot possibly scale to meet the entire world's needs.

Fortunately the Galaxy Community is helping out by installing Galaxy at

Indice

1. General Purpose Servers
 1. Andromeda
 2. Biomina
 3. CIBR Galaxy

GCC 2015
Norwich, UK
<http://gcc2015.tsl.ac.edu>
4-8 July
[Register Now](#)

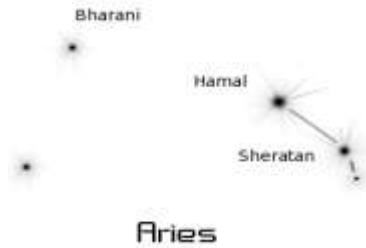
Use Galaxy

[Servers](#) • [Learn](#)
[Main](#) • [Choices](#)
[Share](#) • [Search](#)

Communicate

[Support](#) • [Biostar](#)
[Events](#) • [Mailing Lists](#)

<https://wiki.galaxyproject.org/PublicGalaxyServers>



How does ARIES look like?

Galaxy / ISS

search tools

--- COMMON TOOLS ---

- Get Data
- View Data
- URL-Over
- Text Manipulation
- Filter and Join
- Join, Subsets and Group
- Convert Formats
- Genome Browser
- FASTQ Submitters

--- OTHER TOOLS ---

- Fetch Annotations
- Get Contents, Issues
- Download Genomes, Genesets
- Statistics
- Graph/Cluster Data
- Reference Annotation
- Statistics
- SNP Tools
- FASTA manipulation
- FASTQ QC and manipulation
- NGS Mapping
- NGS Simulations
- SNP pipelines

--- VISUAL TOOLS ---

- HeatMap
- Phylogenetic Association
- Gene Annotation
- Network
- Assembly
- Blat
- Manipulation

--- METAGENOMICS ---

- Metaphlan
- Metacatena

Workflows

- MULT. Tool. Workflow
- Assembly, E. coli. Taxonomy
- E. coli. Reference Profile
- Taxonomic Index
- All workflows

Galaxy Instance n. 70

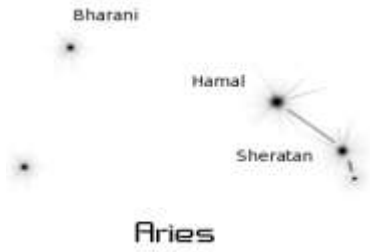
ISTITUTO SUPERIORE DI SANITÀ

Galaxy is an open, web-based platform for data intensive biomedical research. The Galaxy team is a part of IS at Pisa, Italy, and the Biology and Mathematics and Computer Science departments at Utrecht University. The Galaxy Project is supported in part by: INdG, MIUR, The Dutch Ministry of Health, Science and Education, The Italian Ministry of Health, the Italian Ministry of Education, University of Pisa, and the University of Utrecht.

Jobs

| | | |
|------|--------------------|---|
| 1410 | SPMMS_Subsystems | ✓ |
| 1411 | SPMMS_Subsystems | ✓ |
| 1412 | MULT. jobs | ✓ |
| 1413 | Check bacterial co | ✓ |
| 1414 | Check bacterial co | ✓ |
| 1415 | SPMMS job | ✓ |
| 1416 | SPMMS jobs | ✓ |
| 1417 | SPMMS jobs | ✓ |
| 1418 | SPMMS jobs | ✓ |
| 1419 | SPMMS jobs | ✓ |
| 1420 | SPMMS jobs | ✓ |
| 1421 | SPMMS jobs | ✓ |
| 1422 | SPMMS jobs | ✓ |
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| 1444 | SPMMS jobs | ✓ |
| 1445 | SPMMS jobs | ✓ |
| 1446 | SPMMS jobs | ✓ |
| 1447 | SPMMS jobs | ✓ |
| 1448 | SPMMS jobs | ✓ |
| 1449 | SPMMS jobs | ✓ |
| 1450 | SPMMS jobs | ✓ |

<https://aries.iss.it>



Aries' three main sections

tools

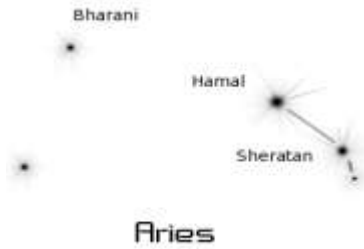


The screenshot shows the Galaxy/ISS web interface. On the left, a sidebar contains a 'Tools' menu with categories like 'FASTA TOOLS', 'FASTA TOOLS', 'FASTA TOOLS', and 'FASTA TOOLS'. The central main section features a large logo for 'ISTITUTO SUPERIORE DI SANITA' and a green header with the text 'Galaxy/ISS'. On the right, a 'History' table lists various jobs with columns for job ID, name, and status. An arrow labeled 'tools' points to the left sidebar, and an arrow labeled 'History' points to the right sidebar.

History



Main Section
Input/Results



Are you ready?

Get Data

Upload File from your computer

UCSC Main table browser

UCSC Archaea table browser

EBI SRA ENA SRA

Get FASTA from taxid (NCBI taxonomy ID)

GO!
...load data in your histories...

