





Computational Tools and Resources for the Life Sciences

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INESC-ID | BioData.pt | ELIXIR Portugal

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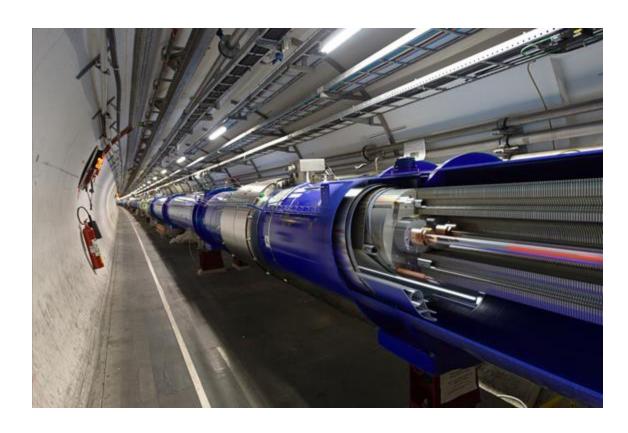
Learning outcomes

- Understand the role of ELIXIR and BioData.pt in the European bioinformatics landscape
- Identify ELIXIR and BioData.pt services and projects like FEGA,
 Beacon and TeSS
- Perform basic genetic and phenoclinic queries using Beacon and the Beacon Network
- Create a bioinformatics analysis pipeline using Galaxy workflows
- Use ELIXIR TeSS to discover new training courses and materials





What is a research infrastructure?



Large Hadron Collider - CERN, Switzerland



ELIXIR Nodes - ELIXIR, Europe

Image: © 2024 ELIXIR



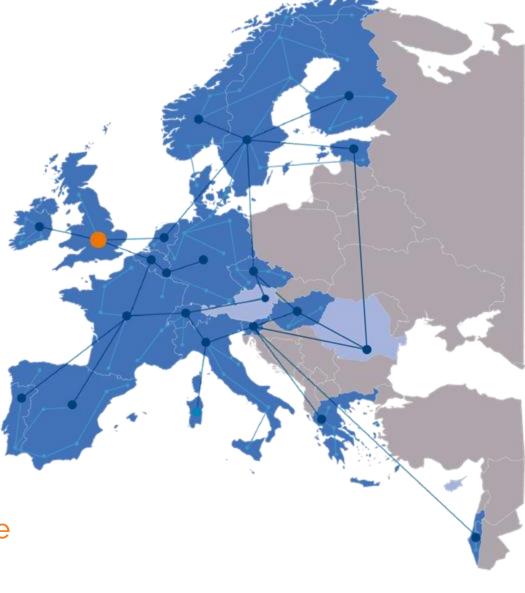


ELIXIR Europe

ELIXIR is an intergovernmental organisation that brings together life science resources such as

- databases
- software tools
- training resources
- interoperability resources
- compute resources
- data management support

The goal of ELIXIR is to coordinate bioinformatics resources from across Europe so they form a single infrastructure.









Meet BioData.pt





- Portuguese distributed infrastructure for life & health data, and home of ELIXIR Portugal
- We offer training, tools, and repositories to the life sciences community and connect them with an international network





BioData.pt Services









Training

Bioinformatics analysis

Computing

Mentorship

Bioinformatics and RDM

RNA-Seq, DE, multiomics

servers, tool hosting

1-on-1 sessions





Our associates

































If you're affiliated with one of our associates, you can benefit from our services





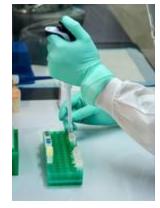




How does a patient DNA sample get into a computer?















Collection

DNA isolation & library prep

Sequencing

Assembly





Example FASTQ file



- 1. @ sample ID
- 2. Nucleotide seq.
- 3. +
- 4. Quality score

Val	Char								
33	1	53	5	73	I	93	1	113	q
34	*	54	6	74	J	94	٨	114	R
35	#	55	7	75	K	95	2	115	S
36	\$	56	8	76	L	96		116	T
37	8	57	9	77	M	97	a	117	U
38	6	58	:	78	N	98	b	118	v
39		59	7	79	0	99	C	119	W
40	(60	<	80	P	100	d	120	x
41)	61	=	81	Q	101	e	121	Y
42	*	62	>	82	R	102	f	122	Z
43	+	63	?	83	S	103	g	123	- (
44	,	64	9	84	T	104	h	124	- 1
45	-	65	A	85	U	105	i	125	1
46		66	В	86	v	106	j	126	~
47	1	67	С	87	W	107	k		
48	0	68	D	88	х	108	1		
49	1	69	E	89	Y	109	m		
50	2	70	F	90	Z	110	n		
51	3	71	G	91	1	111	0		
52	4	72	н	92	1	112	p		





1st Challenge: Getting the data

What we know:

- First recorded symptoms in Bergen, Norway
- Some carriers are asymptomatic, genetic factors may have influence
- University of Bergen has patients' sequencing data
- We are researchers at ITQB NOVA

How can we help from here?







Federated EGA, a resource for discovery and access of human data across national borders https://www.youtube.com/watch?v=bRFHyl6hnNk



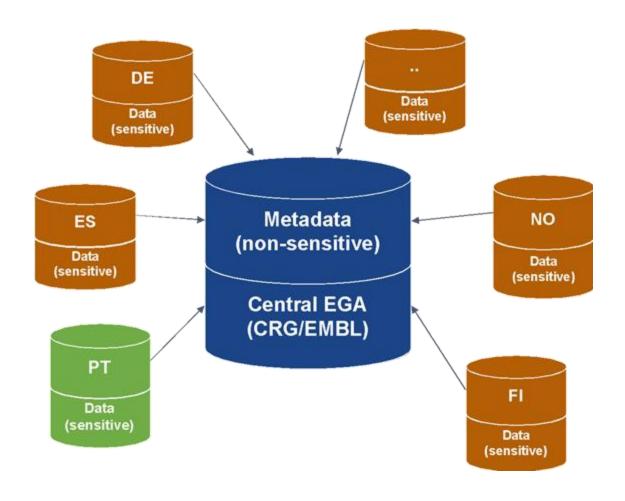




fegaportugal.biodata.pt

User journey

- User registration in EGA
- 2. User approval as **Submitter**
- Creation of Data Access Committee (DAC) and associated Data Access Policies.
- 4. Upload of a real genome file into the local server.
- 5. Submission of **metadata** by user.
- Request to access to the genome, DAC approval and rejection
- 7. Genome **download** and decryption.









A Beacon allows an anonymous queries on genomic datasets.

e.g. Check if a genome contains a genome with a given base at a particular coordinate

beacon-project.io

beacon.biodata.pt



Query all ELIXIR's beacons beacon-network.elixir-europe.org





Challenge 1

- 1. How many people in the Portuguese Beacon have an adenine instead of guanine at position 69848 of chromosome 1?
- 2. How many people have asthma?
- 3. How many of them are women?
- 4. How many of the female asthma patients are of African ethnicity?
- 5. Which country's beacon has a patient with a mitochondrial mutation at the 10th nucleotide which switches a thymine to a cytosine





Step 2: Analysing the data

Here's what a sample pipeline looks like:

Tools:

1. Trim adapters and low quality reads

e.g. Trimmomatic, seqtk_trimq

2. Perform quality control on the data

e.g. FastQC

3. Map reads against reference genome

e.g. STAR, HISAT2, Bowtie2, TopHat2

4. Analyse according to biological question

e.g. variant calling - use variant detector to compare

against reference genome

e.g. FreeBayes





- Trimmomatic
- FASTQC
- STAR
- HISAT2
- Bowtie2
- TopHat2
- FreeBays
- That cool tool you've just discovered on WoS

Minimum requirements:

- 1. A powerful enough computer...
 - Basic Unix command line knowledge
 - Introductory programming skills*
 - Familiarity with Python/R*
 - Knowledge of Pandas/matplotlib/...*
 *additionally, depending on the tool

or

A bioinformatician

or







Galaxy Project



Galaxy is a free, open-source system for analyzing data, authoring workflows, training and education, publishing tools, managing infrastructure, and more.

galaxyproject.org





Galaxy & the Pulsar Network

Self-hosted



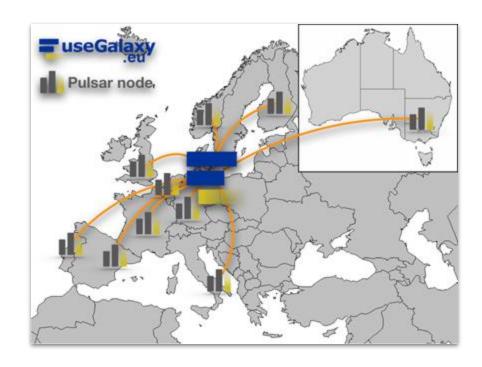


Your institute's server



Galaxy software

Pulsar Network

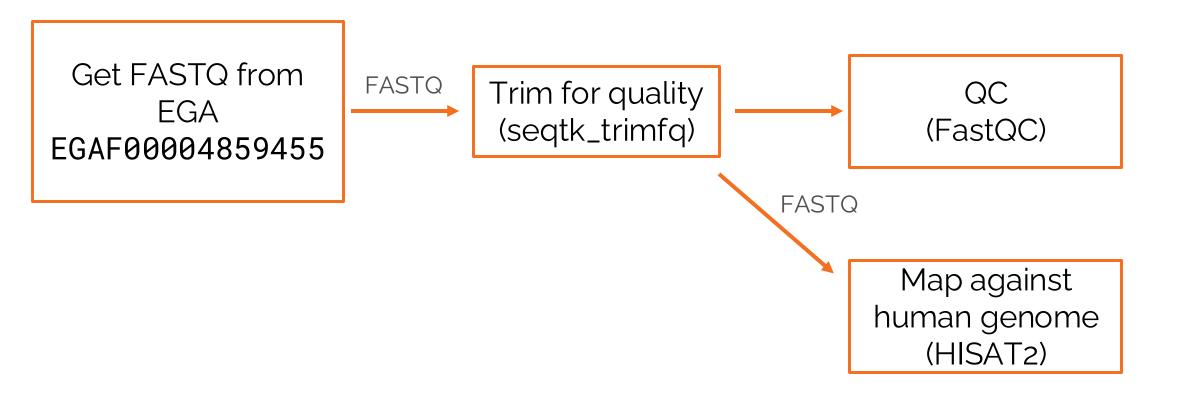


usegalaxy.eu





Challenge 2: build a workflow in Galaxy

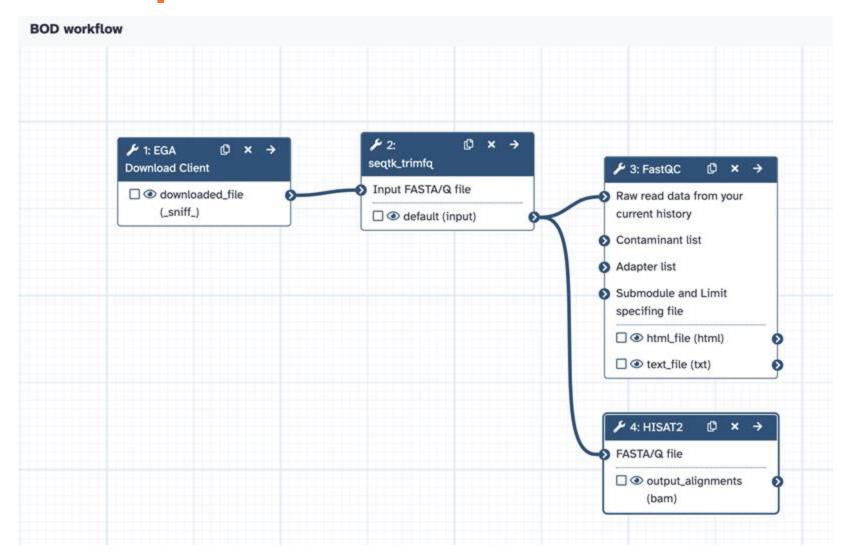






Compare with mine

https://usegalaxy.eu/u/gilpo/w/bod-workflow









Step 3: Learning more



Find training courses and materials from ELIXIR Nodes and institutes

tess.elixir-europe.org





Challenge 3: Diving into TeSS

Think about some bioinformatics/data science skill or tool that you've been meaning to learn

Bash Nextflow multiomics

disease modelling

RNA-Seq

Docker

Git

PCA

R

differential expression

metagenomics

phylogenomics

Python

data visualisation

metabolic modelling

Data Management Plans

machine learning

protein structure

FAIR principles

Linux

protein function prediction





Challenge 3: Diving into TeSS

Try to answer the following questions about your chosen topic using TeSS

- 1. How many training events are scheduled on that topic?
- 2. How many training events, in total are registered on that topic?
- 3. How many materials could you find on that topic?
- 4. How many materials, on all topics, are from the Portugal node?
- 5. How many materials, on all topics, are targeted at PhD Students?





There's many more...

bio.tools



bio.tools helps you find and select bionformatics software and connect it in workflows.

BioContainers



Search a repository of containerised software that you can build into workflows.

WorkflowHub



A registry for sharing and publishing scientific computational workflows.

FAIRsharing.org



FAIRsharing.org allows you to search for databases and data policies by aspects such as domain, species and country.

TeSS



Search for training courses, webinars, training materials and workflows in TeSS, ELIXIR's training portal.

Overview of good data management practices



The Research Data
Management Kit (RDMkit)
guides you through the whole
data management life cycle and
includes advice specific to your
domain, your role and your
country.

Step-by-step instructions

FAIR cookbook

The FAIR Cookbook contains step-by-step recipes to accomplish specific data management tasks and to make your data FAIR (Findable, Accessible, Interoperable, Reusable).

Data management plan wizard



The Data Stewardship Wizard (DSW) is an online tool that guides researchers and data stewards through their data management planning.

LS Login



The Life Science Login enables researchers to use their home organisation credentials or community or other identities o sign in and access data and services they need.

Bioconda

BIOCONDA

Bioconda lets you install thousands of software packages related to biomedical research using the conda package manager.





Take home messages

- ELIXIR is the European life sciences data research infrastructure
- BioData.pt is the national life and health data research infrastructure, and hosts the Portuguese ELIXIR node
- Both provide tools and services to support life sciences researchers, e.g. FEGA, Beacon, Galaxy, TeSS
- You can count on us to help you navigate through the complexities of biological data:)





Thanks!

This presentation will be available at github.com/BioData-PT/computational-tools-resources

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