

DELIVERABLE 4.1 - TRAINING PORTAL, VIDEO RECORDINGS AND MATERIALS



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About this report

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Dissemination level Public

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Consortium members

Acronym	Partner
EMBL	EUROPEAN MOLECULAR BIOLOGY LABORATORY
BIOBYTE	BIOBYTE SOLUTIONS GMBH
HPCNOW	HPC NOW CONSULTING SL
UO	UNIVERSITETET I OSLO
UB	UNIVERSITAT DE BARCELONA
ZBMED	INFORMATION CENTRE FOR LIFE SCIENCE
Rlcapacity	Rlcapacity
ALU-FR	ALBERT-LUDWIGS-UNIVERSITAET FREIBURG
EPFL	ECOLE POLYTECHNIQUE FEDERALE DE LAUSANNE

Table of Contents

About this report.....	2
Consortium members.....	2
Table of Contents.....	3
Project Overview.....	4
Preface.....	4
BioNT training portal.....	4
Training curricula and materials.....	5
Basic curriculum.....	5
A Practical Introduction to Bioinformatics and RNA-seq using Galaxy.....	6
From Zero to Hero with Python:.....	6
An Introduction to High-Performance Computing (HPC):.....	6
Awareness in Data Management and Analysis for Industry and Research.....	6
Training page.....	6
Training materials.....	7
Methodological approach: "The Carpentries" model.....	7
Video recordings - Lhumos platform.....	8
BioNT space.....	8
Zenodo materials.....	10
Galaxy content.....	11
Dissemination and promotion.....	12
Conclusion and sustainability.....	14

Project Overview

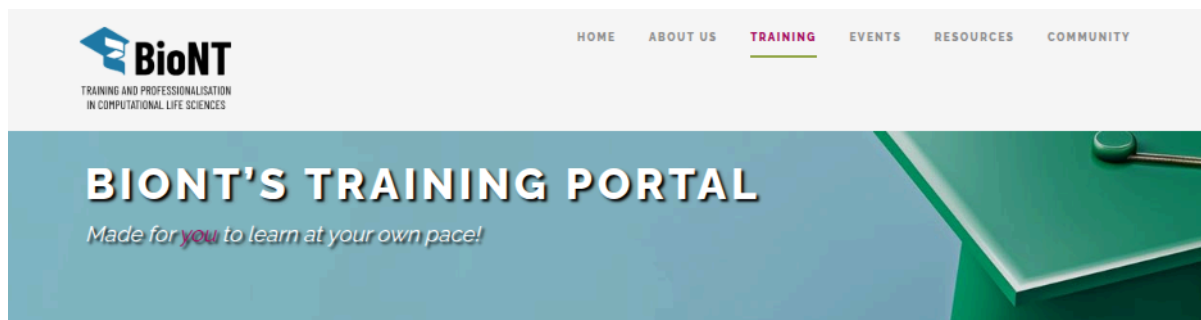
The BioNT consortium is dedicated to providing a comprehensive training program and fostering a community for digital skills relevant to the biotechnology industry and biomedical sector. With a curriculum tailored for both beginners and advanced professionals, BioNT aims to equip individuals with the necessary expertise in handling, processing, and visualising biological data, as well as utilising computational biology tools. Leveraging the consortium's strong background in digital literacy training and extensive network of collaborations, BioNT is poised to professionalise life sciences data management, processing, and analysis skills.

Preface

This report documents the establishment and publication of the BioNT project website as required under Deliverable 4.2 of Work Package 4 (Technical Infrastructure). The intended readership encompasses consortium partners, the European Commission, and the wider public, including training communities, potential adopters of BioNT materials, and professionals with an interest in digital skills development for the biotechnology and biomedical sectors.

BioNT training portal

The BioNT training portal (<https://biont-training.eu/training.html>) allocates all the educational output. It is designed to provide a seamless, self-paced learning journey for professionals in the biotechnology and biomedical sectors, ensuring that high-quality training remains accessible beyond the live sessions. This section went live during mid-March. The website template is published and maintained by ZB MED on behalf of the consortium. ZB MED commits to hosting and maintaining the website for five years beyond the end of the project funding period, ensuring continued public access to BioNT's outputs and resources.



If you missed the opportunity to join our live training workshops, do not despair!

Here you can access all our **free training materials**, which you can follow and complete at your preferred pace. For each training workshop, you will find **video recordings** of the trainers, together with the **training materials** and other supporting content to enhance your learning experience.

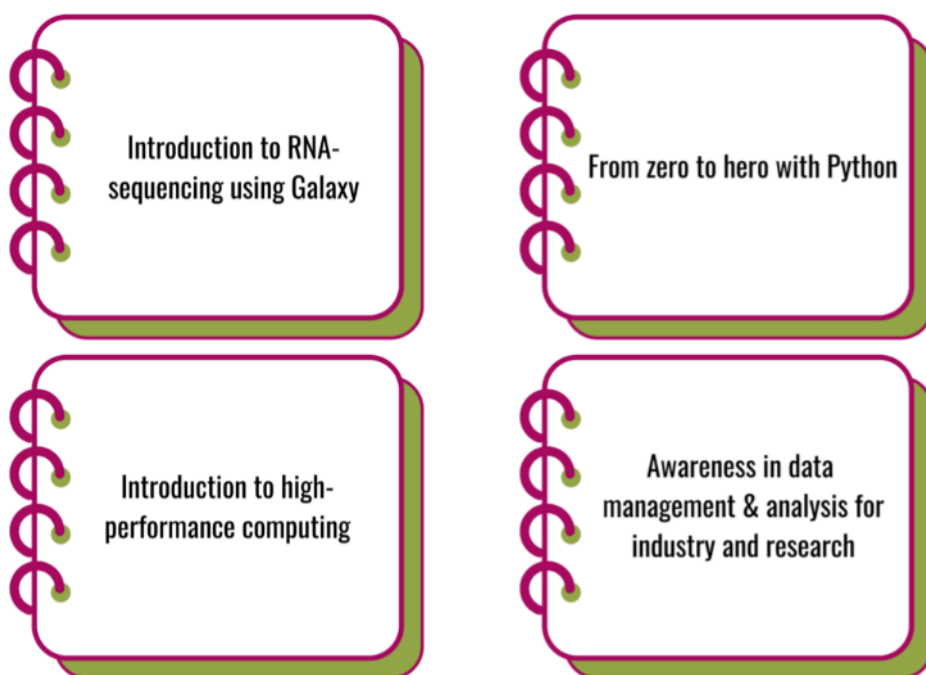


Figure 1: First view of the BioNT Training page

Training curricula and materials

The platform hosts a comprehensive suite of resources categorized into two primary tracks:

Basic curriculum

Targeted at individuals with limited prior experience in biological data processing, this curriculum focuses on foundational digital literacy. All the training of the basic curriculum has a dedicated webpage accessible by clicking on the notebook shapes with the workshop title. The following workshops are featured:

A Practical Introduction to Bioinformatics and RNA-seq using Galaxy

This course teaches how to navigate the Galaxy platform for reproducible research. Improving the skills of quality control of sequencing data, mapping, and differential expression analysis without requiring command-line expertise.

From Zero to Hero with Python:

Fundamental programming logic tailored for biological data, teaches data types, loops, conditional statements, and using libraries (e.g., Pandas) for data manipulation.

An Introduction to High-Performance Computing (HPC):

This training empowers users when moving from local computing to cluster environments by teaching how to understand schedulers (SLURM), the Unix shell, and remote file management.

Awareness in Data Management and Analysis for Industry and Research

The course explores good research practices, data management plans, and the FAIR Data Principles. Trainers learn practical strategies for organising data, using electronic lab notebooks, and making computational analyses more reproducible.

Training page

Every course from the Basic Curriculum has a dedicated webpage where information like the description, learning outcomes, target audience and requirements can be found. At the bottom, the training material is linked, alongside with the information about the trainers for that course.

Awareness in Data Management and Analysis for Industry and Research

Good data management is more than simply organising files. It helps keep research transparent, reproducible, and secure while preventing data loss and saving time and resources. Whether you work with experimental data, computational results, or shared datasets, knowing how to organise, document, and manage your data properly is an essential skill. It also supports collaboration, clarifies data ownership, and helps meet legal, ethical, and funding requirements.

This workshop introduces practical approaches to managing research data effectively. Based on training materials from FAIR4FAIR, ZB MED - Information Centre for Life Sciences, The Carpentries, and CodeRefinery, the course explores good research practices, data management plans, and the FAIR Data Principles. You will also learn practical strategies for organising data, using electronic lab notebooks, and making computational analyses more reproducible so that your research remains transparent, reusable, and well documented.

<p>Learning outcomes </p> <ul style="list-style-type: none"> Understand good data management practices in research and industry, including governance, policies, and organisational roles Plan and organise your data using Data Management Plans (DMPs) and electronic lab notebooks (ELNs) Apply FAIR principles to make your data findable, accessible, interoperable, and reusable Ensure reproducibility and transparency in analyses by using practical tools and workflows 	<p>Target audience </p> <ul style="list-style-type: none"> Interested in learning about data management Interested in learning how to manage data in a good practice in both academia and industry Anyone interested in learning about how to make your data reusable and analysis reproducible 	<p>Requirements </p> <ul style="list-style-type: none"> Just a PC/Laptop with an up-to-date browser Chrome, Safari and Firefox browsers are all supported (some older browsers, including Internet Explorer version 9, may not be) <ul style="list-style-type: none"> Ideally a two-screen setup so you can follow the workshop while trying on your own
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Training material

Video recordings

Written material

These recordings from previous workshops allow you to revisit the course content or work through it at your own pace.

Your trainers

- Justine Vandendorpe (ZB MED - Information Centre for Life Sciences)
- Birte Lindstädt (ZB MED - Information Centre for Life Sciences)
- Katja Diederichs (ZB MED - Information Centre for Life Sciences)
- Roman Riedel (ZB MED - Information Centre for Life Sciences)
- Till Sauerwein (ZB MED - Information Centre for Life Sciences)
- Silvia Di Giorgio (ZB MED - Information Centre for Life Sciences)

Here you can explore the written material and exercises which are available in several languages.

Figure 2: Look of the dedicated page for the Awareness in Data Management and Analysis for Industry and Research workshop

Training materials

The teaching materials include the video recordings taken live from the training day and edited afterwards with AI support. These videos are hosted on the [Lhumos](#) platform, hosted by EPFL. In addition, extensive written materials (handouts, tutorials, and practical exercises) are linked.

To ensure inclusivity and reach across the European landscape, these materials are available in multiple languages, catering to diverse regional needs within the SME and research sectors. The materials are available in English, Spanish, Italian and German.

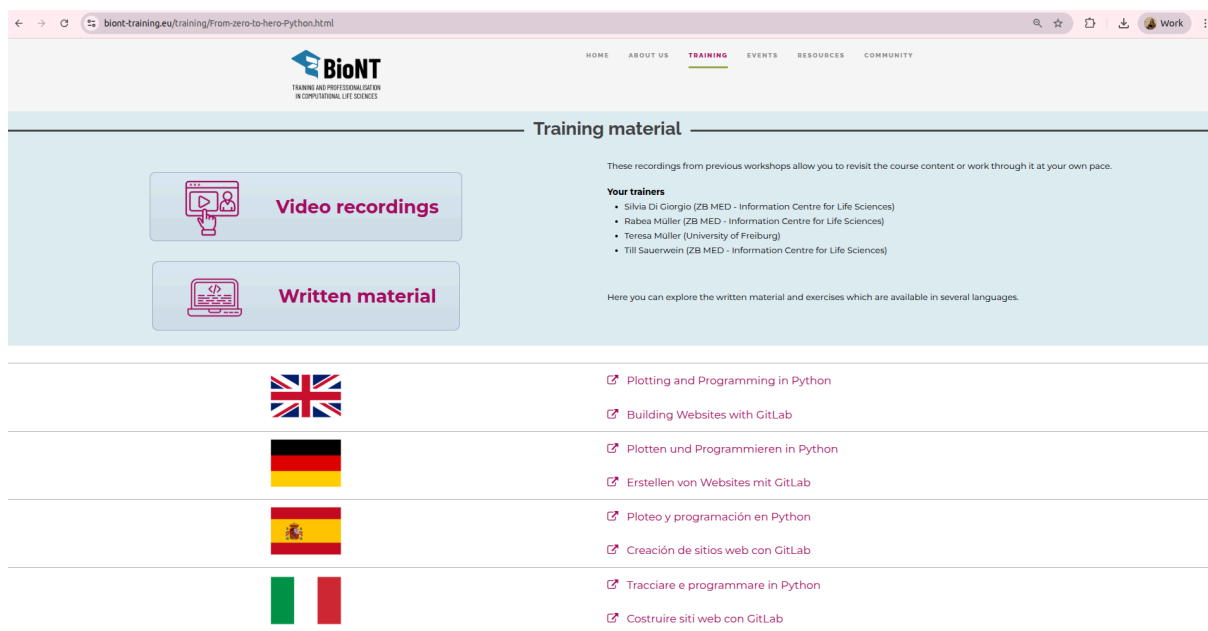


Figure 3: Look of the dedicated page of the From Zero to Hero with Python course where the written materials are translated to diverse languages within the EU

Advanced Curriculum:

The implementation is in the final stages and will be incorporated into the BioNT Training Portal in the next couples of days. Detailed materials covering advanced topics (such as Machine Learning for biological data and HPC System Administration) are scheduled for publication within the coming days. This will complete the project's training offering.

Methodological approach: "The Carpentries" model

BioNT adopts the "Carpentries" pedagogical style, characterized by:

- **Live Coding:** Instructors lead learners through real-time exercises.

- **Interactive Feedback:** Use of collaborative documents (e.g., HedgeDoc) and "sticky notes" (virtual or physical) to gauge learner progress.
- **Open Educational Resources (OER):** All materials are hosted on GitHub, Zenodo and the Galaxy Training Network (GTN), ensuring they are freely reusable under Creative Commons licenses.

Video recordings - Lhumos platform

[Lhumos](#) (Learning Hub for Modelling and Simulation) is a specialized e-learning environment co-supported by major European initiatives (CECAM, MARVEL, MaX). For the BioNT project, it functions as a Self-Paced Learning Environment, allowing learners to revisit workshop content outside of live sessions. The Lhumos space is currently in its deployment phase (Alpha). Users can track the growth of the repository as new workshops from the 2024–2026 cycle are concluded and curated.

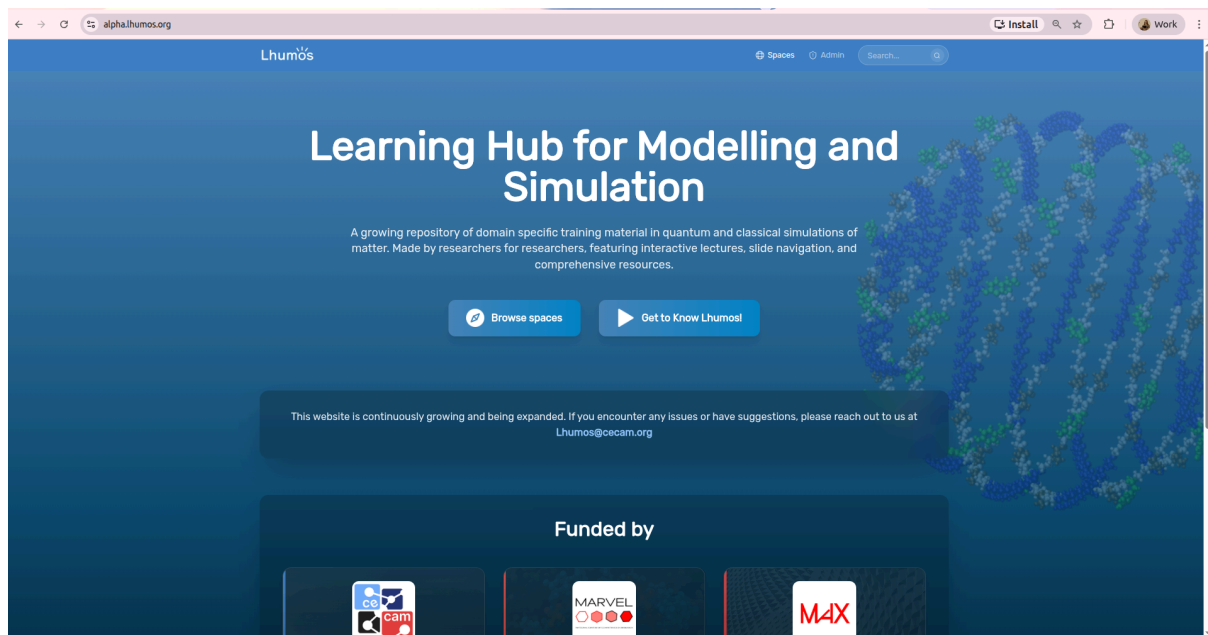


Figure 4: Screenshot of the Lhumos main page

BioNT space

BioNT has a [dedicated space](#) inside Lhumos, where all the video recordings from the training sessions are organized in collections.

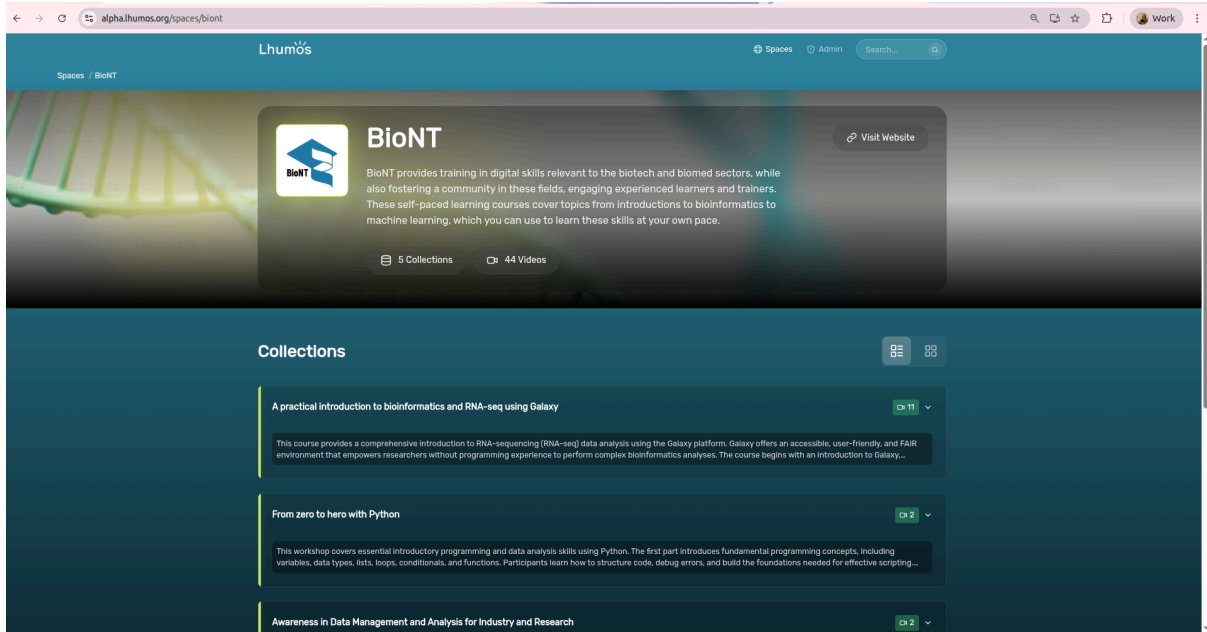


Figure 5: View of the BioNT space inside Lhumos

Every collection can be accessed to see the description of it and the corresponding video recordings. For the moment only the basic curriculum is available in the BioNT space.

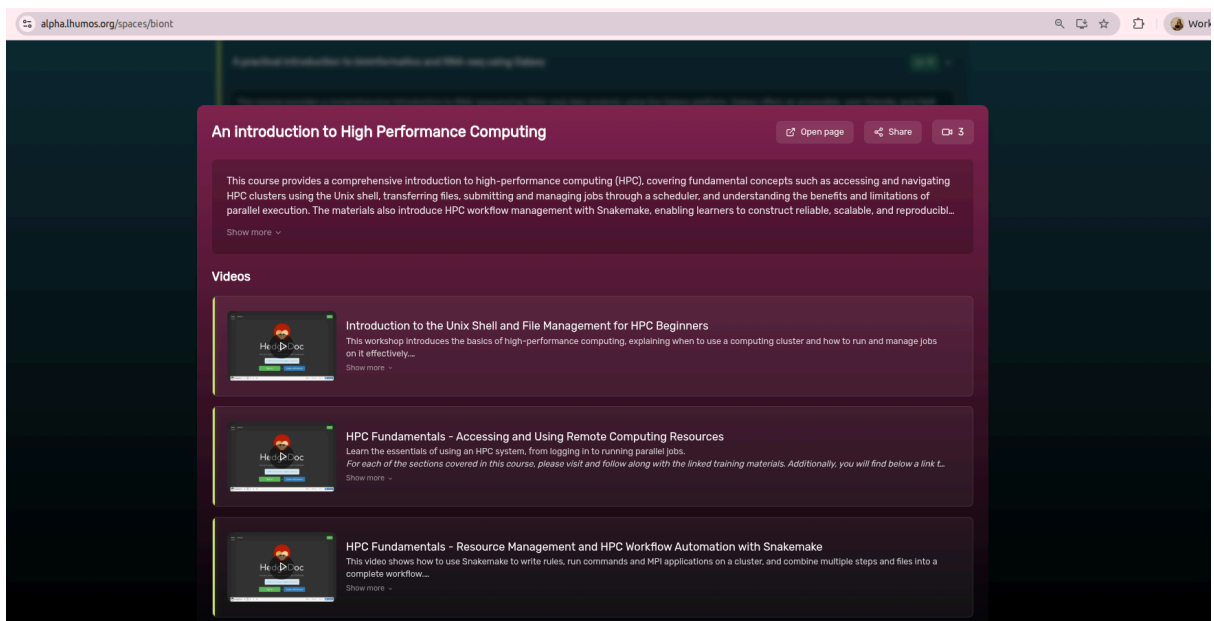


Figure 6: View of a BioNT collection inside Lhumos

Lhumos features an admin panel where the views of the videos and the collections can be consulted.

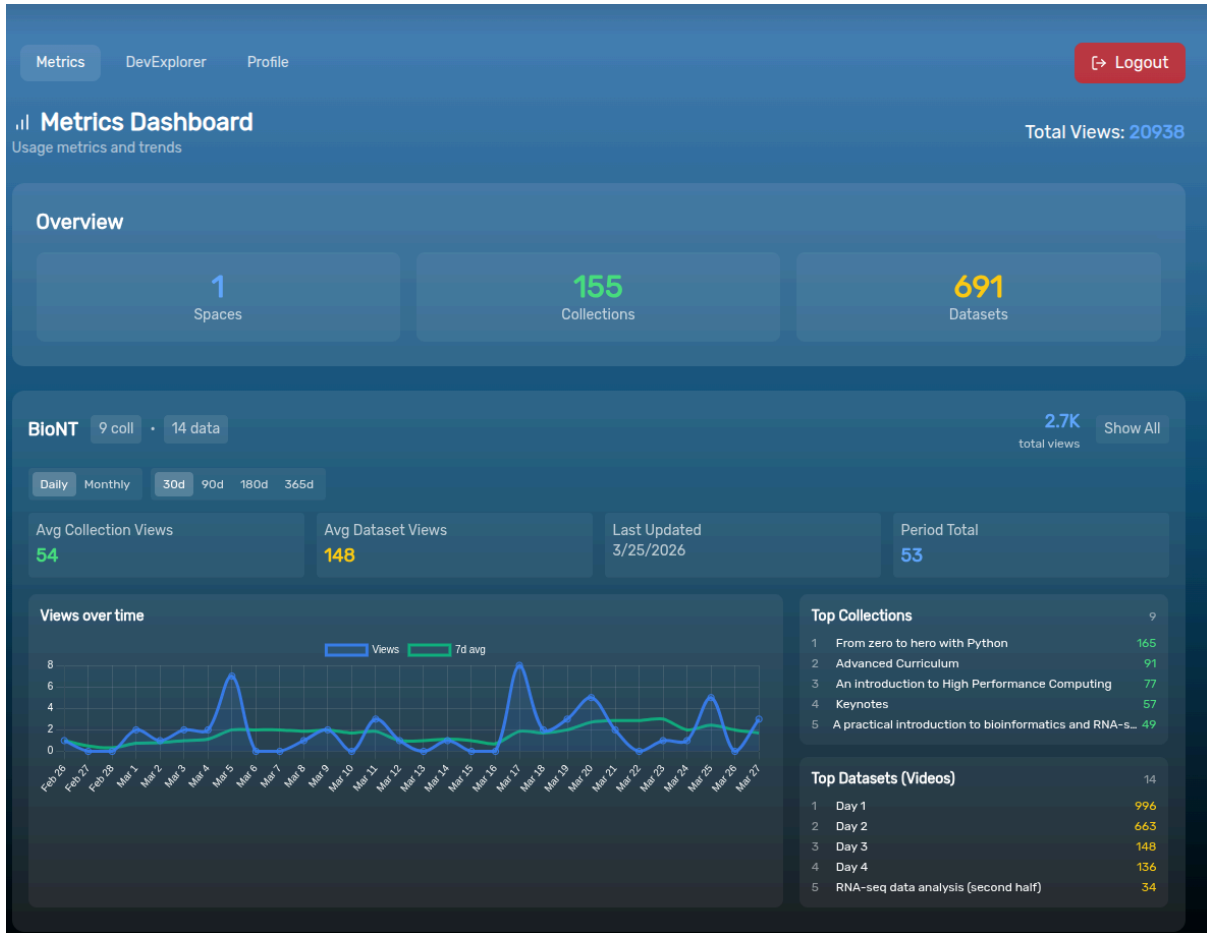


Figure 7: From Zero to Hero with Python

The top collection is From Zero to Hero with Python, and collections get a daily average of two views.

Zenodo materials

The presentations used in workshops can also be found in Zenodo under the [BioNT community](#).

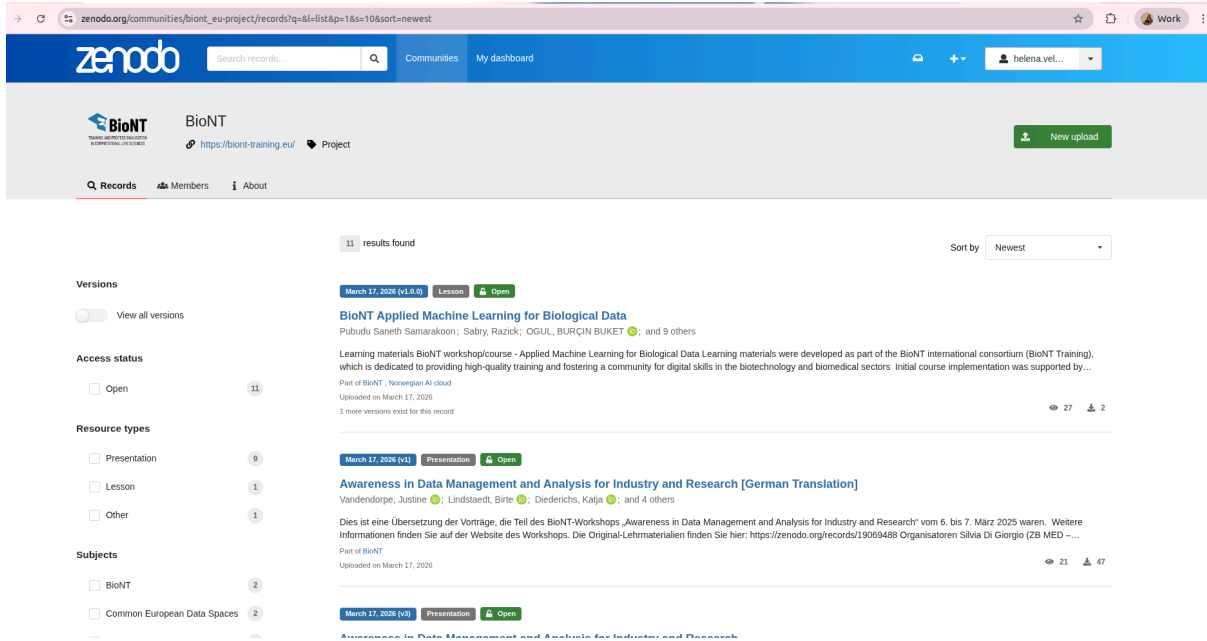


Figure 8: BioNT community in Zenodo

The materials are free to view and at the moment slides from the advanced curriculum are included too.

This use of Zenodo ensures the content is freely reusable under Creative Commons licenses, supporting the project's broader goal of digital upskilling in Europe and ensuring a broad and long-term hosting space even after the end of the project funding window.

Galaxy content

Some of the written materials are part of the Galaxy Training portal. The materials contain explanations, hands-on demonstrations and exercises with their solutions for the trainees to practice and evaluate their skills.

Reference-based RNA-Seq data analysis

Author(s)

Editor(s)

Reviewers

Overview

Questions:

- What are the steps to process RNA-Seq data?
- How to identify differentially expressed genes across multiple experimental conditions?
- What are the biological functions impacted by the differential expression of genes?

Objectives:

- Check a sequence quality report generated by Falco/MultiQC for RNA-Seq data
- Explain the principle and specificity of mapping of RNA-Seq data to a eukaryotic reference genome
- Select and run a state of the art mapping tool for RNA-Seq data
- Evaluate the quality of mapping results
- Describe the process to estimate the library strandness
- Estimate the number of reads per genes
- Explain the count normalization to perform before sample comparison
- Construct and run a differential gene expression analysis
- Analyze the DESeq2 output to identify, annotate and visualize differentially expressed genes
- Perform a gene ontology enrichment analysis
- Perform and visualize an enrichment analysis for KEGG pathways

Requirements:

- Introduction to Galaxy Analysis

Figure 9: BioNT Galaxy material introduction

to make sense of the reads, we need to first figure out where the sequences originated from in the genome, so we can then determine to which genes they belong. When a reference genome for the organism is available, this process is known as aligning or "mapping" the reads to the reference. This is equivalent to solving a jigsaw puzzle, but unfortunately, not all pieces are unique.

Mapping

Mapping
Inspection of the mapping results

Counting the number of reads per annotated gene
Analysis of the differential gene expression
Functional enrichment analysis of the DE genes
Conclusion
Frequently Asked Questions
References
Feedback
Citing this Tutorial

Comment

Do you want to learn more about the principles behind mapping? Follow our [training](#).

Question

1. What is a reference genome?
2. For each model organism, several possible reference genomes may be available (e.g. hg19 and hg38 for human). What do they correspond to?
3. Which reference genome should we use?

Solution

With eukaryotic transcriptomes most reads originate from processed mRNAs lacking introns:

Figure 9: The types of RNA-seq reads (adaption of the Figure 1a from Kim et al. 2015): reads that mapped entirely within an exon (in red), reads spanning over 2 exons (in blue), read spanning over more than 2 exons (in purple)

Therefore they cannot be simply mapped back to the genome as we normally do for DNA data. Spliced-aware mappers have been developed to efficiently map transcript-derived reads against a reference genome.

Figure 10: BioNT Galaxy material with exercises

Dissemination and promotion

The training portal was promoted via [LinkedIn](#) and received a good response from the community, with 18 times shared by today.



BioNT

994 seguidores
1 semana •



🚀🌟 WOOHOO!!! Our BioNT training portal is LIVE 🌟🚀
<https://lnkd.in/dF6j9d-i>

Free access to hands-on data science training materials for natural sciences—ready for you to explore, reuse, and share!

🔒 What's inside:

- ✓ recorded sessions
- ✓ written materials
- ✓ reusable resources for your own teaching

👉 Whether you want to learn at your own pace or build on our materials as a trainer—it's all there!

📚 Following courses are already available:

RNA-seq with Galaxy | Python for beginners | HPC basics | Data management awareness

💡 Coming very soon:

Machine Learning for biology | FAIR software practices | HPC system administration | Training strategies

🗣️ Please share with your community—we'd love to see these materials travel far and wide!

And tell us how you use them or get in touch if you need any support—we're excited to hear your feedback and see them reused in new courses 🙌

Mostrar traducción



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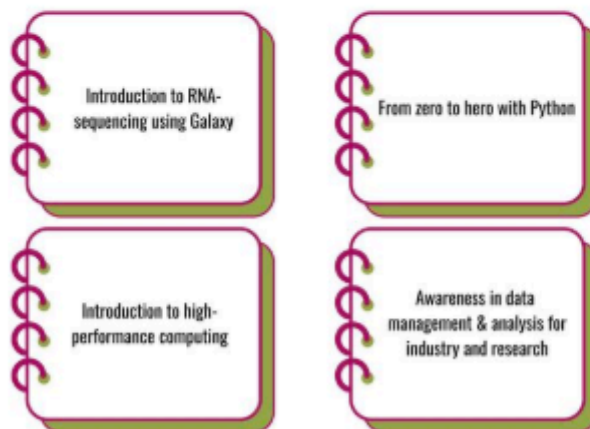


Figure 11: LinkedIn post to promote the new training website

Conclusion and sustainability

The BioNT curriculum represents a scalable model for digital upskilling in Europe. By integrating training with established networks like ELIXIR, Galaxy Project, and platforms like Zenodo, the consortium ensures that the training content remains maintained and relevant beyond the initial funding period of 2023–2026.