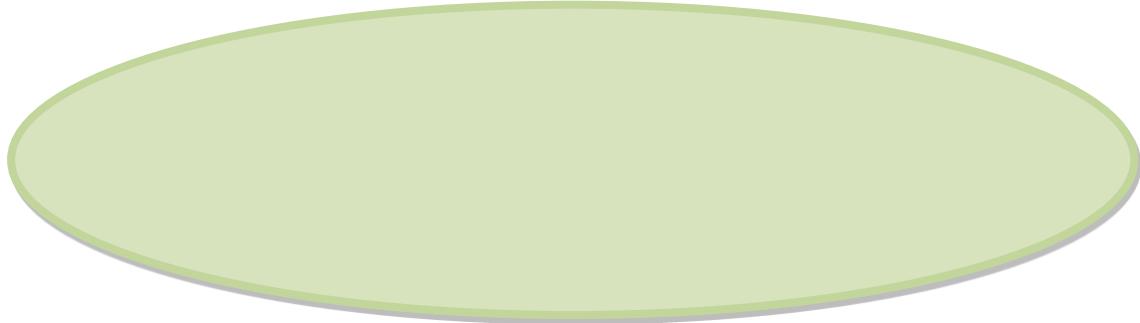


République algérienne Démocratique et Populaire
Ministère de l'Enseignement Supérieur et de la Recherche
Scientifique
Université Mohammed Seddik Ben Yahia - Jijel



Faculté des Sciences de la Nature et de la Vie
Département des Microbiologie appliquée et des sciences alimentaire
Master contrôle de qualité.

TP N°01



Responsable : **Bensalem Amel**

Par : **Benkraouche Farida**
Henanes Ibtihel

Année universitaire 2025/2026

PART I : Theoretical Study: Biopython

Introduction

Open-source software plays a central role in modern scientific research, particularly in the field of bioinformatics, where the processing of large volumes of biological data is essential. The rapid development of computational biology has led to the creation of software tools capable of automating the analysis of biological sequences. In this context, Biopython was developed as a free and flexible solution that enables the analysis and manipulation of biological data using the Python programming language.

Historical Background and Origin of Biopython (Chapman & Chang, 2000)

Biopython was first introduced by Chapman and Chang (2000) to address the growing need for programmable and accessible tools for biological data analysis. The authors emphasized the use of the Python language due to its simplicity, readability, and ability to facilitate collaborative development. The main objective of the project was to provide a collection of reusable modules that allow biologists to automate their analyses without requiring advanced programming skills.

1. General Presentation of Biopython (Cock et al., 2009)

According to Cock et al. (2009), Biopython is an open-source library developed in Python and dedicated to computational biology and bioinformatics. It enables the manipulation, analysis, and processing of biological sequences such as DNA, RNA, and proteins.

The project is supported by an international community of developers and is compatible with major operating systems (Windows, Linux, and macOS), which promotes its adoption in academic and research environments.

2. Main Functionalities of Biopython (Cock et al., 2009)

Biopython provides a wide range of functionalities, including:

- Reading and writing different biological file formats (FASTA, GenBank, EMBL)
- Manipulation of biological sequences using dedicated objects
- Performing sequence alignments
- Phylogenetic analysis
- Automated access to biological databases such as NCBI and UniProt
- Integration with external bioinformatics tools such as BLAST and ClustalW

The main functionalities of Biopython and the supported data formats are summarized in Table 1.

Table 1. Selected Bio.SeqIO or Bio.AlignIO file formats

Format	R/W	Name and reference
fasta	R+W	FASTA (Pearson and Lipman, 1988)
genbank	R+W	GenBank (Benson <i>et al.</i> , 2007)
embl	R	EMBL (Kulikova <i>et al.</i> , 2006)
swiss	R	Swiss-Prot/TrEMBL or UniProtKB (The UniProt Consortium, 2007)
clustal	R+W	Clustal W (Thompson <i>et al.</i> , 1994)
phylip	R+W	PHYLIP (Felsenstein, 1989)
stockholm	R+W	Stockholm or Pfam (Bateman <i>et al.</i> , 2004)
nexus	R+W	NEXUS (Maddison <i>et al.</i> , 1997)

Where possible, our format names (column ‘Format’) match BioPerl and EMBOSS (Rice *et al.*, 2000). Column ‘R/W’ denotes support for reading (R) and writing (W).

Table 1: Main Biopython modules and supported formats

This table highlights the diversity of modules provided by Biopython, illustrating its versatility in processing different types of biological data.

3. Technical Aspects of the Tool (Cock *et al.*, 2009)

- Type: Open-source software library
- Programming language: Python
- License: Biopython License
- Architecture: Modular and extensible
- Compatibility: Integration with other scientific Python libraries

4. Strengths of Biopython (Chapman & Chang, 2000; Cock *et al.*, 2009)

The main strengths of Biopython include:

- Free and open-source availability
- Ease of use due to the Python programming language
- Large developer community and extensive documentation
- Ability to automate biological data analysis
- Frequent use in scientific publications

5. Limitations of Biopython

Despite its many advantages, Biopython has certain limitations:

- Requires basic knowledge of Python programming
- Performance may be limited when handling very large datasets
- Lack of a complete graphical user interface, requiring the use of scripts

6. Conclusion

Biopython is a fundamental tool in modern bioinformatics. Its evolution since its creation, its rich functionality, and its use in recent scientific studies demonstrate its importance in the life sciences field. Thanks to its open-source nature and flexibility, Biopython represents a suitable solution for researchers and students in bioinformatics.

PART II – Practical Study / Scientific Platform

1. Introduction to the Zenodo Platform

Zenodo is an open-access digital repository established by CERN with the support of the European Commission, with the aim of promoting the principles of Open Science and enabling researchers to share their scientific outputs in a free, reliable, and sustainable manner. The platform provides a secure digital environment for the preservation and dissemination of research data while ensuring long-term accessibility.

2. Objectives of the Zenodo Platform

The main objectives of Zenodo are to:

- Support open access to scientific research without financial or technical barriers.
- Enable researchers to publish and preserve research data in a sustainable way.
- Provide a persistent Digital Object Identifier (DOI) for each published item, facilitating proper citation and recognition.
- Encourage data reuse, transparency, and scientific collaboration.
- Ensure long-term preservation of research outputs and prevent data loss.

3. Types of Content Hosted on Zenodo

Zenodo hosts a wide variety of scientific and academic content, including:

- Research datasets
- Scientific articles and publications
- Academic theses and dissertations
- Software and source code
- Presentations and scientific posters
- Technical reports and educational materials

This diversity makes Zenodo suitable for researchers from various disciplines, particularly in Natural and Life Sciences.

4. Importance of Zenodo in Open Science

Zenodo plays a key role in advancing Open Science by:

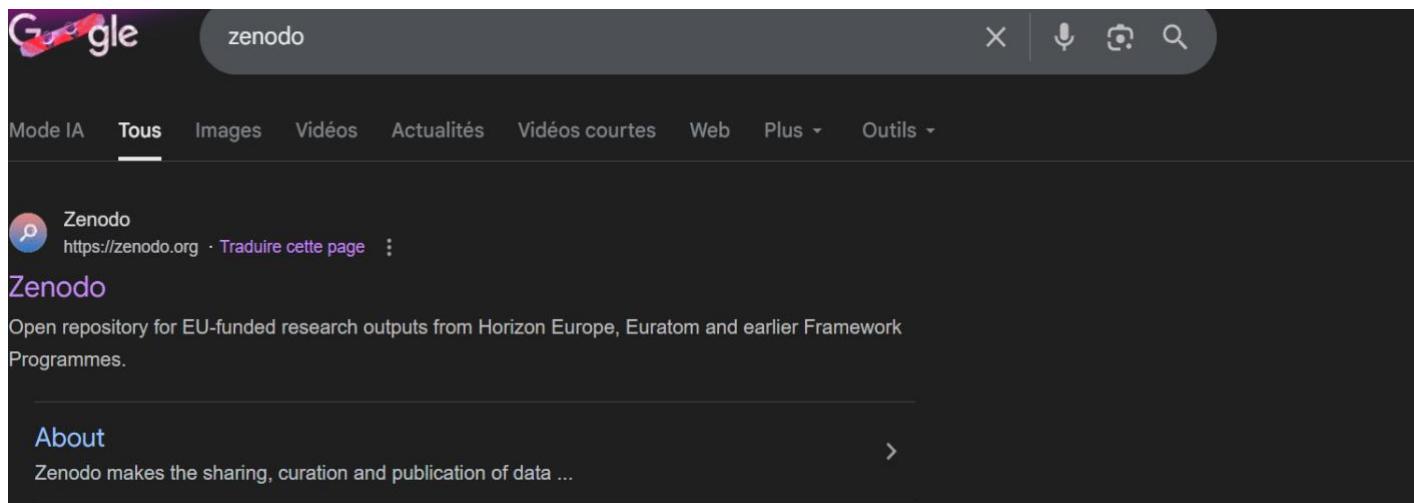
- Providing free and unrestricted access to scientific knowledge.
- Facilitating data sharing among researchers and institutions.
- Supporting reproducibility and verification of scientific research.
- Linking publications with their underlying data and software in a single platform.
- Contributing to the acceleration of scientific progress and innovation.

Steps Followed to Access and Use the Zenodo Platform

1. Accessing the Zenodo Platform

Access to the Zenodo platform was achieved through a web browser using the official link:
<https://zenodo.org>

Zenodo is an open-access digital platform dedicated to the preservation, publication, and sharing of scientific research outputs.



2. Exploring the Platform Interface

After accessing the homepage, the general interface of the platform was explored. It includes:

- A search bar
- A list of content types (Datasets, Publications, Software, etc.)
- General information about recently uploaded content

The screenshot shows the Zenodo homepage with a blue header bar. On the left is the Zenodo logo. In the center is a search bar with the placeholder "Rechercher des enregistrements". To the right of the search bar are links for "communautés", "Mon tableau de bord", "Se connecter", and "S'inscrire". Below the header, a section titled "Communautés en vedette" features the "AAS PUBLISHING" logo and a link to "Revues de l'AAS".

Téléchargements récents

Pourquoi utiliser Zenodo ?

8 février 2026 (3.0) Ensemble de données Ouvrir

i Ce site utilise des cookies. Pour en savoir plus sur notre utilisation des cookies, cliquez ici.

Accepter tous les cookies

Accepter uniquement les cookies essentiels

3. Performing a Search

The search bar was used to find relevant scientific datasets by entering keywords related to the fields of Natural and Life Sciences, such as: cell / tissue

The search button was then clicked to display the corresponding results.

The screenshot shows the Zenodo search results page for the query "cell tissue". The search bar at the top contains "cell tissue". The results summary indicates 128 542 résultats(s) trouvé(s). The results are listed in a table with columns for Versions, Access status, Resource types, and a detailed view. The first result is a dataset by TCWO/QualIFAI titled "github_zenodo", which is a Software resource linked to GitHub. The second result is a book titled "3D IMAGING NEUROSCIENCE AND SEPSIS RESEARCH: MODERN METHODS AND TECHNOLOGICAL ADVANCES" by uyanikgil, Yigit. The bottom of the page includes a cookie consent banner and a footer with the URL https://zenodo.org and the number 16,991.

4. Filtering Search Results

Once the results were displayed, they were filtered according to the content type (Dataset) in order to facilitate the selection of suitable material for the practical study.

The screenshot shows a search results page from zenodo.org. At the top, there are filters for 'Open' (121,387), 'Restricted' (6,912), and 'Embargoed' (249). Below these, under 'Resource types', there are filters for 'Publication' (93,870), 'Dataset' (16,991), 'Image' (8,530), 'Software' (5,084), 'Other' (1,532), 'Poster' (990), and 'Presentation' (690). The main content area displays two dataset entries. The first is '3D IMAGING NEUROSCIENCE AND SEPSIS RESEARCH: MODERN METHODS AND TECHNOLOGICAL ADVANCES' by uyanikgil, Yigit (published December 20, 2024, v1, Book, Open). The second is 'Neuronal cell atlas of intestinal tissue from healthy humans, healthy mice, and mice with colitis.' by Xu, Heng (published October 28, 2025, v1, Dataset, Open). Both entries include a brief description, author information, and download statistics. At the bottom, there is a cookie consent banner in French.

5. Selecting a Relevant Dataset

A relevant dataset was selected based on the following criteria: Relevance to the field of study Availability of clear and complete metadata Presence of data suitable for analysis

The screenshot shows a detailed view of a dataset page. At the top, it says 'Published February 2, 2022 | Version v1' and has buttons for 'Journal article' and 'Open'. The main title is 'Insights into the present and future of cartilage regeneration and joint repair' by Evenbratt, H.; Andreasson, L.; Bicknell, V.; Brittberg, M.; Mobini, R.; Simonsson, S. (published February 2, 2022, v1, Journal article, Open). Below the title is an abstract section. The abstract discusses knee osteoarthritis, its impact, and current research goals related to cartilage regeneration. At the bottom, there is a cookie consent banner in French.

6. Accessing the Dataset Page

After selecting the dataset, its dedicated page on the Zenodo platform was opened. This page includes:

Dataset title	Author(s)	Description	Publication date	Digital Object Identifier (DOI)	Metadata information
---------------	-----------	-------------	------------------	---------------------------------	----------------------

The screenshot shows a journal article titled "Insights into the present and future of cartilage regeneration and joint repair" by H. Evenbratt et al. The article is a REVIEW and is marked as Open Access. It includes a "Check for updates" button. The abstract discusses knee osteoarthritis, stem cell sources, and signaling molecules. Key words listed include Articular Cartilage, Osteoarthritis, Joint treatments, Stem cell therapy, Gradients, Differentiation, Chondrocyte characterization. The background section notes that OA is the most common form of chronic joint disease, associated with factors like age, obesity, and trauma. It highlights the need for mechanical load and motion to maintain healthy cartilage. The article also mentions substantial healthcare costs and indirect economic burdens. Recent reviews focus on clinical studies of cellular therapies for knee function.

Evenbratt et al. *Cell Regeneration* (2022) 11:3
https://doi.org/10.1186/s13619-021-00104-5

Cell Regeneration CSCB

REVIEW **Open Access**

Check for updates

Insights into the present and future of cartilage regeneration and joint repair

H. Evenbratt^{1*}, L. Andreasson^{1,2}, V. Bicknell¹, M. Brittberg³, R. Mobini¹ and S. Simonsson²

Abstract

Knee osteoarthritis is the most common joint disease. It causes pain and suffering for affected patients and is the source of major economic costs for healthcare systems. Despite ongoing research, there is a lack of knowledge regarding disease mechanisms, biomarkers, and possible cures. Current treatments do not fulfill patients' long-term needs, and it often requires invasive surgical procedures with subsequent long periods of rehabilitation. Researchers and companies worldwide are working to find a suitable cell source to engineer or regenerate a functional and healthy articular cartilage tissue to implant in the damaged area. Potential cell sources to accomplish this goal include embryonic stem cells, mesenchymal stem cells, or induced pluripotent stem cells. The differentiation of stem cells into different tissue types is complex, and a suitable concentration range of specific growth factors is vital. The cellular microenvironment during early embryonic development provides crucial information regarding concentrations of signaling molecules and morphogen gradients as these are essential inducers for tissue development. Thus, morphogen gradients implemented in developmental protocols aimed to engineer functional cartilage tissue can potentially generate cells comparable to those within native cartilage. In this review, we have summarized the problems with current treatments, potential cell sources for cell therapy, reviewed the progress of new treatments within the regenerative cartilage field, and highlighted the importance of cell quality, characterization assays, and chemically defined protocols.

Key Words: Articular Cartilage, Osteoarthritis, Joint treatments, Stem cell therapy, Gradients, Differentiation, Chondrocyte characterization

Background

Osteoarthritis (OA) is the most common form of chronic joint disease, affecting all joints in the body, resulting in progressive cartilage degeneration. Risk factors associated with OA include age, obesity, family history, or trauma that has caused damage to the cartilage (Haq et al., 2003). Physical inactivity has also been shown to lead to cartilage degradation as joints require mechanical load and motion to maintain healthy cartilage structure and function (Sophia Fox et al., 2009). As cartilage is an avascular tissue with sparse cell density, it has poor regenerative capacity. Due to this, OA results in pain, dysfunction, and substantial healthcare costs (Hudetz et al., 2017; Hiligsmann & Reginster, 2013). In addition to these direct effects, the disease leads to an indirect economic burden for societies due to decreased productivity and premature disability (Hiligsmann & Reginster, 2013). Since age is a substantial risk factor (Haq et al., 2003), and that the global life expectancy continues to increase, OA-related costs will also increase with time. Therefore, the potential cost savings provided by a cure, or other better alleviation methods, will also be substantial given the high prevalence of people suffering from the disease worldwide.

Recent reviews discuss cell-based treatments of OA and cartilage defects with a different focus. Both Agarwal et al. and Wiggers et al. dive deep into clinical studies of cellular therapies for improved knee function and

*Correspondence: Hanneevenbratt@clinescientific.com
1 Cline Scientific AB, SE-431 53 Mölndal, Sweden
Full list of author information is available at the end of the article.

© The Author(s) 2022. **Open Access** This article is licensed under a Creative Commons Attribution 4.0 International License, which permits use, sharing, adaptation, distribution and reproduction in any medium or format, as long as you give appropriate credit to the original author(s) and the source, provide a link to the Creative Commons license, and indicate if changes were made. The images or other third party material in this article are included in the article's Creative Commons license, unless indicated otherwise in a credit line to the material. If material is not included in the article's Creative Commons license and your intended use is not permitted by statutory regulation or exceeds the permitted use, you will need to obtain permission directly from the copyright holder. To view a copy of this license, visit <https://creativecommons.org/licenses/by/4.0/>. The Creative Commons Public Domain Dedication waiver (<http://creativecommons.org/publicdomain/zero/1.0/>) applies to the data made available in this article, unless otherwise stated in a credit line to the data.

Springer Open

7. Downloading the Dataset

The dataset files were downloaded using the Download option available on the dataset page in order to review and use them for the practical study.

8. Extracting Metadata

The metadata displayed on the dataset page were extracted and organized according to the Dublin Core standard, including:

Title

Creator

Date

Publisher

Description

Identifier (DOI)

