# Bioinformatics; Code: PHC603

## A- Basic Information

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| **Programme(s) on which the course is given:** | Master degree |
| **Academic year:** | First Semester, 2023/2024 |
| **Course title and code:** | Bioinformatics, PHC603 |
| **Contact hours (credit hours):** | Lecture: 2 (2) |
| **Course Coordinator:** | Dr. Ann Ayman Elshamy |

## B- Professional Information

### 1- Overall Aims of Course

Upon successful completion of this course, the student should have a detailed background on bioinformatics and its importance in life sciences. They should understand different methods and software tools/programs needed to understand and process biological data by combining computer science, statistics, mathematics and engineering.

### 2- Intended Learning Outcomes of Course (ILOs)

#### a- Knowledge and Understanding:

The students should be able to:

a1. Enumerate and describe the different programs used for analysis of biological data including collecting and storing DNA sequences from GenBank databases.

a2. Understand different softwares used for analysis of DNA/Protein sequences in the Laboratory

a3. Identify the bases and softwares used for multiple sequence alignment, phylogenetic analysis, protein classification and structure prediction

a4. Understand the principles and bases of Quality by design

a5. Define mathematical modeling of data as well as design of experiments

#### b- Intellectual Skills

The students should be able to:

b1. Estimate and differentiate between different computerized programs involved in biological data analysis.

b2. Predict the appropriate methods and programs for interpretation and analysis of DNA/protein sequences by combining computer science, statistics, and engineering.

b3. Analyze huge data sets mathematically in order to make final conclusions and outcomes.

b4. Estimate and differentiate between relevant techniques or programs involved in gene annotation and analysis

**d. General and Transferable Skills**

The students should be able:

d1. Learn independently.

d2. Work effectively as a part of a team and as an individual.

d3. Retrieve and evaluate information from different sources to improve professional competencies

## 2. Course Contents

| Topic | No. of credit hours | Lectures |
|---|---|---|
| An introduction to bioinformatics, definition and importance; A brief introduction gene and protein expression, analysis of gene/protein expression; gene regulation | 2 | 1 |
| Identification of candidate genes and nucleotides: computational evolutionary biology, comparative genomics; Pan genomics; genetics of disease; analysis of mutations in cancer (Oncogenomics) | 2 | 1 |
| Collecting and storing of DNA sequences, homologous and heterologous primer design and verifications for Polymerase chain reaction; PCR and primer design computational programs, | 4 | 2 |
| DNA sequencing and analysis in The Laboratory: DNA sequencing; Sequence assembly; Analysis of the final assembled sequences (consensus); Open reading frame (ORF) analysis; BLAST search analysis; Submission into the GenBank database; How to submit data to GenBank? | 4 | 2 |
| Multiple sequence alignment and phylogenetic analysis:Multiple sequence alignment using ClustalW2; Clustalomega; MAFFT; MUSCLE; Pairwise sequence alignment tools; Dotplot alignment tool; and Phylogenetic analysis | 4 | 2 |

| | | |
|---|---|---|
| Protein Classification and Structure prediction: Protein structure prediction; Viewing Protein Structures; Protein Classification; Protein Structure Classification database; Alignment of protein structure | 4 | 2 |
| Structural Prediction of proteins, Evaluation the Success of structure predications; Protein Blast; Protein alignment and domain analysis | 2 | 1 |
| Phylogenetic Analysis: Molecular evolution, basics of phylogenetics, aspects of a phylogenetic tree, interpreting relatedness, construction of a phylogenetic tree, using MEGA software for phylogenetic tree construction and manipulation. | 2 | 1 |
| Understand the principles and bases of Quality by design; Define mathematical modeling of data as well as design of experiments | 6 | 3 |
| **Total** | **30** | **15** |

## 3- Teaching and Learning Methods

    1- Lectures.

    2- Discussion sessions.

    3- Presentations.

## 4- Student Assessment Methods

1. Works (assignment) to periodically asses the student knowledge and understanding

2. **Oral exam** to assess skills of analysis, scientific thinking as well as scientific discussion

3. **Final written exam** to assess the ability of student to remember and retrieve information as well we understanding of the scientific background.

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| Assessment 1 | Works Assignment | Week 10 |
| Assessment 2 | Oral exam | Week 16 |
| Assessment 3 | Final written exam | Week 16 |

**Weighing of assessments**

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|---|---|
| Works (assignment) | 10% |
| oral | 10% |
| final exam | 80% |
| **Total** | **100%** |

**5- List of references**

**1- Course notes:** handouts and assignment delivered by instructors

**2- Essential books (text books)**

David W Mount 2001: Bioinformatic: sequence and Genome analysis; Cold Spring Harbor Laboratory Press, Cold Spring Harbor,, New York

**3- Recommended books**

- Sambrook J, Russell DW (2001) *Molecular cloning*: *a laboratory manual*, 3rd Eds. Cold Spring harbor laboratory Press, Cold Spring Harbor, New York.

- Arnold K., Bordoli L., Kopp J., and Schwede T. (2006). The SWISS-MODEL Workspace: A web-based environment for protein structure homology modelling. *Bioinformatics*, 22,195-201.

- Thompson JD, Higgins DG, Gibson TJ (1994) CLUSTAL W: improving the sensitivity of progressive multiple sequence alignment through sequence weighting, position-specific gap penalties and weight matrix choice. *Nucleic Acids Res.,* 22: 4673-4680

- Bishop, O. T. ed. (2014). Bioinformatics and Data Analysis in Microbiology. Caister Academic Press.
- Singh, D. B., and Pathak, R. K. eds. (2022). Bioinformatics: Methods and Applications. Chennai, India: Elsevier doi:10.1016/C2020-0-03034-3.
- Hasija, Y. ed. (2023). All About Bioinformatics: From Beginner to Expert. Elsevier.

**4- Web sites, etc**

(Google search; www.google.com) www.ncbi.nlm.nih.gov; ; www.sciencedirect.com; www.springerlink.com;

http://www.restrictionmapper.org/http://www.ddbj.nig.ac.jp/http://www.embl.de/

**https://bioinf.comav.upv.es/courses/intro_bioinf/_downloads/staden_course.pdf**

## 6- Facilities required for teaching and learning

Lecture halls; Data show; computers and internet access, blackboard

| Course coordinator | Vice dean for post graduate affairs |
|---|---|
| **Dr. Ann Ayman Elshamy**<br><br>*Ann Elshamy* | **Prof. Dr. Khaled Aboshanab**<br><br>*Khaled Aboshanab* |

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| **Course name** | Bioinformatics |
| **Code** | PHC603 |

## Course matrix

| Course content | a1 | a2 | a3 | a4 | a5 | b1 | b2 | b3 | b4 | d1 | d2 | d3 |
|---|---|---|---|---|---|---|---|---|---|---|---|---|
| An introduction to bioinformatics | ▪ | | | | | ▪ | | | | | | |
| Identification of candidate genes and nucleotides | ▪ | | | | | ▪ | ▪ | | ▪ | | | |
| Collecting and storing of DNA sequences, homologous and heterologous primer design and verifications for Polymerase chain reaction; PCR and primer design computational programs, | | | | | | ▪ | ▪ | ▪ | | ▪ | ▪ | ▪ |
| DNA sequencing and analysis in The Laboratory | ▪ | ▪ | | | | | ▪ | | | ▪ | ▪ | ▪ |
| Multiple sequence alignment and phylogenetic analysis | | | ▪ | | | ▪ | ▪ | ▪ | | ▪ | ▪ | ▪ |
| Protein Classification and Structure prediction | | | ▪ | | | ▪ | ▪ | | | ▪ | ▪ | ▪ |
| Structural Prediction of proteins, Evaluation the Success of structure predications; Protein Blast; Protein alignment and domain analysis | | ▪ | ▪ | | | ▪ | ▪ | | | ▪ | ▪ | ▪ |
| Phylogenetic Analysis: Molecular evolution, basics of phylogenetics, aspects of a phylogenetic tree, interpreting relatedness, construction of a phylogenetic tree, using MEGA software for phylogenetic tree construction and manipulation. | | ▪ | ▪ | | | ▪ | ▪ | | | ▪ | | ▪ |
| Understand the principles and bases of Quality by design | | | | ▪ | ▪ | | ▪ | | | | | |