

SUBJECT OUTLINE DETAILS

1. Subject: Bioinformatics

- Code: BT303C
- Credits: 3 credits
- Hours: 15 theory hours, 60 practice hours, and 60 self-study hours.

2. Management Unit:

- Department: Molecular Biotechnology
- Faculty/School/Institute/Center/Department: Biotechnology Research and Development Institute

3. Prerequisites: BT302

4. Subject objectives:

4.1. Knowledge:

4.1.1. Introduce students to the current bioinformatics algorithms/concepts and their implementations.

4.1.2. Introduction of bioinformatics databases and how to access.

4.1.3. Instruction on how to use the softwares commonly used to solve and analyze problems often encountered in studying of DNA sequences, RNA and amino acid sequences, including mapping of restriction enzymes, pairwise alignment, multiple alignment, genetic diversity analysis.

4.1.4. Guideline primer and probe design

4.1.5. Introduction on database of 3D structure of protein, using software to view and analyze protein structure.

4.2. Skill:

4.2.1. Ability to design primers, probes and technical applications in molecular biology as well as constructing restriction enzyme maps.

4.2.2. Knowing how to analyze and compare DNA sequences, RNA and proteins, read the results after analysis.

4.2.3. Enhanced teamwork skills, data analysis skills, internet search skills, install and use the software.

4.2.4. English improvement.

4.3. Attitude:

4.3.1 Being hard-working student.

4.3.2 Honesty in presenting analysis results.

5. Brief description of subject content:

The course is designed to introduce the most important and basic concepts, methods, and tools used in Bioinformatics. Topics include (but not limited to) bioinformatics databases, sequence and structure alignment, protein structure prediction, and molecular dynamics. Emphasis will be put on the understanding and utilization of these concepts and algorithms. The objective is to help the students to reach rapidly the frontier of bioinformatics and be able to use the bioinformatics tools to solve the problems on their own research. The softwares include Clustal X, DNA club, FastPCR, Mega 4, PyMol, SeqVerter, TreeView, Biodiversity Pro, NTSYSpc2.1 Bioedit, PAUP 4.

6. Subject content structure:

6.1. Theory

	Content	Hours	Ojectives
Chapter 1.	General Introduction to bioinformatics and molecular biology	2	4.1.1;4.2.4
Chapter 2.	Bioinformatics database	2	4.1.2;4.2.4
Chapter 3.	Designing restriction map	2	4.1.3;4.2.4
Chapter 4.	Designing primers and probes	2	4.1.4;4.2.4
Chapter 5.	Clustal analysis based on DNA fragments polymorphism	2	4.1.3;4.2.4
Chapter 6.	Building phylogenetic trees based on DNA sequences	2	4.1.3;4.2.4
Chapter 7.	Microarray technique	2	4.1.1;4.2.4
Chapter 8.	Analysis 3D structure of protein	1	4.1.5;4.2.4

6.2. Practice

	Content	Hours	Ojectives
Unit 1.	Translating sequences	6	4.1.1; 4.2.4
Unit 2.	Searching genes in bioinformatics database	10	4.1.2; 4.2.2; 4.2.4
Unit 3.	Designing restriction maps	10	4.1.3; 4.2.1; 4.2.4
Unit 4.	Designing primers and probes	10	4.1.4; 4.2.1; 4.2.4
Unit 5.	Constructing dendrogram based on DNA fragments polymorphism	10	4.1.3; 4.2.2; 4.2.4; 4.3
Unit 6.	Building phylogenetic trees based on DNA sequences	10	4.1.3; 4.2.2; 4.2.4; 4.3
Unit 7.	Observing 3D structure of protein	4	4.1.5; 4.2.4

7. Teaching method:

- Theory
- Practice on the computer through exercises
- Group discussion
- Presentation
- Homeworks

8. Duties of student:

Students must perform the following tasks

- Attend at least 80% of the theoretical lessons.
- Join 100% full hours of practical class and report results.
- Perform a full range of group exercise and performance evaluation.
- Participate all mid-term test throughout the semester.
- Join the final exam.
- Self-study.

9. Assessment of student learning outcomes:**9.1. Assessment**

No.	Point components	Rules and Requirement	Weights	Objectives
1	Attendance	Class participation	10%	4.3
2	Exercise	Completed exercises	20%	4.1, 4.2, 4.3
3	Group assignment	- Presentation - To be confirmed the participation by group leader	10%	4.1, 4.2, 4.3
4	Final exam	- Multiple choice questions (60 phút) - Must attend 80% theoretical classes and 100% practical classes - Sitting the final exam is mandatory	60%	4.1, 4.2, 4.3

9.2. Grading

- Grading components and final test scores will be marked on a scale of 10 (0 to 10), rounded to one decimal place.
- Subject score is the sum of all the components of the evaluation multiplied by the corresponding weight. The subject score is marked on a scale of 10 and rounded to one decimal place, then is converted to A-B-C-D score and score on a scale of 4 under the academic provisions of the University.

10. Materials:

Materials information**Code number**

- [1] Course book: Bioinformatics/Tran Nhan Dung and Nguyen Vu Linh – Can Tho. Can Tho University Publisher. 154 pages. 24cm. - 572.80285/ D513
 NN.015643
 NN.015642
 SP.020384
- [2] Bioinformatics : A practical approach / Shui Qing Ye.- Boca Raton: Chapman & Hall/CRC, 2008.- xxvi, 618 p. ; ill., 25 cm (Chapman & Hall/CRC mathematical and computational biology series), 1584888105.- 570.285/ Y37
 MON.030015
- [3] Understanding bioinformatics / Marketa Zvelebil, Jeremy O. Baum.- New York: Garland Science/Taylor & Francis Group, 2008.- xxiii, 772 p. ; ill., 28 cm, 0815340249.- 572.80285/ Z.10
 MON.030047

11. Self-study Guide:

Week	Content	Theory (hours)	Practice (hours)	Students' duties
1	Chapter 1: General Introduction to bioinformatics and molecular biology	1	4	-Read: +Material [1]: read Chapter 1
2	Chapter 2: Bioinformatics database	1	4	-Read: +Material [1]: read Chapter 2 + Practise exercises 1 to 2 in Chapter 1 + Read the content of biological database in the materials [2] and [3]
3	Chapter 2: Bioinformatics database (cont)	0	5	-Read: +Material [1]: read Chapter 2 + Practise exercises 1 to 3 in Chapter 2 + Read the content of biological database in the materials [2] and [3]
4	Chapter 3: Designing restriction map	1	4	-Read: +Material [1]: read Chapter 3 + Practise exercises 1 to 2 in Chapter 3 + Read the content of restriction enzymes in the materials [2] and [3]
5	Chapter 4: Designing primers and probes	1	4	-Read: +Material [1]: read Chapter 4 + Practise exercises 1 to 2 in Chapter 4 + Read the content of oligonucleotides in the materials [2] and [3]
6	Chapter 4: Designing primers and probes (cont)	0	5	-Read: +Material [1]: read Chapter 4

				+ Practise exercises 1 to 2 in Chapter 4 + Read the content of oligonucleotides in the materials [2] and [3]
7	Chapter 5: Clustal analysis based on DNA fragments polymorphism	1	4	-Read: +Material [1]: read Chapter 5 + Practise exercises 1 to 2 in Chapter 5 + Read the content of DNA diversity in the materials [2] and [3]
8	Chapter 5: Clustal analysis based on DNA fragments polymorphism (cont)	0	5	-Read: +Material [1]: read Chapter 5 + Practise exercises 1 to 2 in Chapter 5 + Read the content of DNA diversity in the materials [2] and [3]
9	Chapter 6: Building phylogenetic trees based on DNA sequences	1	4	-Read: +Material [1]: read Chapter 6 + Practise exercises 1 to 2 in Chapter 6 + Read the content of phylogeny in the materials [2] and [3]
10	Chapter 7: Microarray technique	1	0	-Read: +Material [1]: read Chapter 7 + Read the content of microarray in the materials [2] and [3]
11	Chapter 8: Analysis 3D structure of protein	1	4	-Read: +Material [1]: read Chapter 8 + Practise using PyMol software + Read the content of protein structure in the materials [2] and [3]
12	Chapter 9: Mega 5.0	0	5	-Read: +Material [1]: read Mega 5.0 Manual + Practise using Mega 5.0 software + Read the content of sequence alignment in the materials [2] and [3]
13	Review	0	4	

Can Tho, 27/05/2014

**ON BEHALF OF RECTOR
DEAN/ DIRECTOR**

HEAD OF DEPARTMENT