



**Philadelphia University**  
**Faculty of Science**  
**Department of Biotechnology & Genetic Engineering**  
**Second semester, 2009/2010**

**Course Syllabus**

<b>Course Title:</b> Bioinformatics	<b>Course code:</b> 0240462
<b>Course Level:</b> 4 <sup>th</sup> Year	<b>Course prerequisite (s):</b> 0240231 & 0240335
<b>Lecture Time:</b> 14:00-16:00 Sun. Tue. & Thu.	<b>Credit hours:</b> 2

**Academic Staff  
Specifics**

<b>Name</b>	<b>Rank</b>	<b>Office No.</b>	<b>Office Hours</b>	<b>E-mail Address</b>
Tawfiq Froukh	Assis.Prof.	918	10-11 Mon. & Wed. 14-15 Sun., Tue. & Thu.	tfroukh@philadelphia.edu.jo

**Course module description:**

This module introduces the fundamental principles of bioinformatics and uses this knowledge to tackle research problems. It covers major databases and software programs for genomic data analysis, with an emphasis on the theoretical basis and practical applications of these computational tools. The course is organized into six sections: biological databases, sequence alignment, genes and promoter prediction, molecular phylogenetics, structural bioinformatics, and genomics and proteomics.

**Course module objectives:**

This module aims to make the students familiar with many bioinformatics programs and databases to tackle the new challenges in the genomic era.

**Books (title , author (s), publisher, year of publication)**

-Essential Bioinformatics. Jin Xiong, Cambridge University Press, 1<sup>st</sup> edition, 2006 (TEXT BOOK)

**Teaching methods:**

Lectures and practical applications on PCs in the computer lab

**Learning outcomes:**

- Knowledge and understanding

The students will become familiar with various computational possibilities for modern molecular biological research and also become aware of the strengths and weaknesses of each of the software tools.

- Practical and subject specific skills (Transferable Skills).

The students will be able to use variable software to analyze genetic data such as DNA and protein sequences.

**Assessment instruments**

Quizzes & Home works

Final examination: 50 marks

<b>Allocation of Marks</b>	
<b>Assessment Instruments</b>	<b>Mark</b>
First examination	15%
Second examination	15%
Final examination: 50 marks	50%
Quizzes & Home works	20%
Total	100%

### Course/module academic calendar

<b>week</b>	<b>Basic and support material to be covered</b>
(1)	Introduction & Biological databases <i>Ch#1</i>
(2)	Introduction & Biological databases <i>Ch#2</i>
(3)	Sequence Alignment: Pairwise sequence alignment <i>Ch#3</i>
(4)	Sequence Alignment: Database similarity searching <i>Ch#4</i>
(5)	Sequence Alignment: Multiple sequence alignment <i>Ch#5</i>
(6) <b>1<sup>st</sup> exam</b>	Sequence Alignment: Profiles and hidden markov models <i>Ch#6</i>
(7)	Molecular Phylogenetics: Phylogenetics basics <i>Ch#10</i>
(8)	Molecular Phylogenetics: Phylogenetics basics <i>Ch#10</i>
(9)	Molecular Phylogenetics: Phylogenetic Tree Construction Methods and Programs <i>Ch#11</i>
(10)	Molecular Phylogenetics: Phylogenetic Tree Construction Methods and Programs <i>Ch#11</i>
(11) <b>2<sup>nd</sup> exam</b>	Genomics and Proteomics: Genome mapping, assembly and comparison <i>Ch#17</i>
(12)	Genomics and Proteomics: Genome mapping, assembly and comparison <i>Ch#17</i>
(13)	Genomics and Proteomics: Functional genomics <i>Ch#18</i>
(14)	Genomics and Proteomics: Functional genomics <i>Ch#18</i>
(15)	Genomics and Proteomics: Proteomics <i>Ch#19</i>
(16)	Final Exam

### **Expected workload:**

**On average students need to spend 2 hours of study and preparation for each 50-minute lecture/tutorial.**

### **Attendance policy:**

**Absence from lectures and/or tutorials shall not exceed 15%. Students who exceed the 15% limit without a medical or emergency excuse acceptable to and approved by the Dean of the relevant college/faculty shall not be allowed to take the final examination and shall receive a mark of zero for the course. If the excuse is approved by the Dean, the student shall be considered to have withdrawn from the course.**

### **Module references**

#### **Books**

- Introduction to Bioinformatics, Arthur M. Lesk, Oxford University Press, 2<sup>nd</sup> edition, 2005.
- Applied Bioinformatics, Selzer, Marhöfer, Rohwer, Springer, 2008
- Phylogenetic Trees Made Easy, Barry Hall, Sinauer, 2008
- Introduction to Computational Biology, Bernhard Haubold & Thomas Wiehe, Birkhäuser, 2006.

#### **Websites**

- [www.ncbi.nlm.nih.gov](http://www.ncbi.nlm.nih.gov)
- [www.ebi.ac.uk](http://www.ebi.ac.uk)