



BiTmaP

bioinformatics
training certificate
program



CURRICULUM OVERVIEW

BiTmaP's curriculum provides hands-on training with programs and protocols used widely throughout industry and academia. Classes provide trained programmers and data systems engineers exposure to life-science applications in bioinformatics. Through BiTmaP, students immediately develop marketable skills and experience. Courses are offered by the University of Illinois at Chicago (UIC), host of the only accredited M.S. and Ph.D. bioinformatics programs in the state of Illinois. The UIC faculty provides instruction and support for all four of BiTmaP's online courses. Students must complete one required course (Introduction to Bioinformatics) and two electives to earn their certificate. In addition, university and industry seminars are offered to BiTmaP students. Students are also encouraged to complete an industrial internship arranged through the BiTmaP program.

Course I: Introduction to Bioinformatics

All BiTmaP students are required to take this general introductory bioinformatics course. This course focuses on the fundamental techniques related to sequence analysis and includes applications for gene identification, genome sequencing, sequence comparison, database searching, and phylogenetic tree analysis. Core concepts in molecular biology are introduced, including the central dogma of molecular biology, principles of nucleic acid, and protein sequences. Students are introduced to biological concepts necessary to apply the application of bioinformatics algorithms and software taught in this course.

Algorithms and software taught in this course include:

- **Sequence-comparison algorithms and the software program FASTA**
- **Sequence database searching with BLAST**
- **PSI-BLAST**
- **HMMER**
- **Functional database searches with GO**
- **Using PFAM for gene identification and functional assignment**
- **Biological database design using SQL/mysql**
- **Programming with Perl for bioinformatics tasks**
- **Using the BioPerl database to search for available programs**
- **Phylogenetic analysis with PHYLIP**

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Course II: Biostatistics

This course provides practical biostatistics experience and introduces the theory of statistical analysis within the framework of bioinformatics. Programming knowledge of Java (preferred), Perl or C++ is required. Students address biostatistics problems with biologically relevant data sets using industry standard statistics software, such as R and S++. Students are introduced to basic algorithms and the theory behind statistical analysis and are provided examples and small practical projects to gain experience with R and Java in problem solving with bioinformatics.

Topics covered also include:

- **Sample analysis**
- **Interval-censored survival data analysis**
- **Longitudinal data analysis**
- **Multivariate analysis**
- **Theory of distributions in statistics**
- **Experimental design and analysis**

Course III: Computational Genomics

This course focuses on the study and implementation of methods of data mining and machine learning that are useful in the analysis of gene expression data from genome comparison, microarray experiments, and protein function prediction. Students gain practical skills, especially in the area of microarray data analysis, in addition to the theoretical knowledge behind the methods. Students employ multiple tools used extensively by industry for gene expression analysis; R and Bioconductor packages are used for microarray data analysis and MATLAB for other tasks.

Topics covered in this course include:

- **Microarray technology**
- **Microarray experiments**
- **Preprocessing of microarray data**
- **Statistical methods (e.g., hypothesis testing, resampling, bootstrap, multiple testing)**
- **Distances and expression measures**
- **Feature selection**
- **Cluster and classification analysis for microarray data inferring genetic networks.**

R and Bioconductor packages are used for microarray data analysis. MATLAB is used for other implementation tasks. All three tools are used extensively by industry for gene expression analysis.

Course IV: Molecular Modeling in Bioinformatics

In this course, students learn how to elucidate the structure of a biopolymer using related modeling tools and algorithms in bioinformatics. The targeted areas are in protein structure modeling, structure-based drug design, drug screening, cheminformatics, and binding prediction. Students learn the principles and applications of each of the following algorithms and programs used in structure modeling: DOCK and AUTODOCK for protein-ligand (drug) binding; SYBYL, QUANTA, and INSIGHT II, which are general packages aimed at structure modeling; CHARMM and AMBER for molecular dynamics simulations.