

Bioinformatics

School

School of Science, Engineering and Technology (<http://www.stmarytx.edu/set>)

School Dean

Winston F. Erevelles, Ph.D. (werevelles@stmarytx.edu)

Department

Biological Science (<https://www.stmarytx.edu/academics/set/undergraduate/biological-sciences>)

Bioinformatics is an interdisciplinary and growing field in science for solving biological, biomedical and biochemical problems with the help of computer science, mathematics and information technology. Bioinformaticians are in high demand not only in research, but also in academia because few people have the education and skills to fill available positions.

The Bioinformatics program at St. Mary's University prepares students for graduate school, medical school or entry into the field. Bioinformatics is highly applicable to all branches of life sciences and also to fields like personalized medicine and pharmacogenomics — the study of how genes affect a person's response to drugs.

The Bachelor of Science in Bioinformatics offers three tracks that students can choose.

- Bachelor of Science in Bioinformatics with a minor in Biology: 128 credit hours
- Bachelor of Science in Bioinformatics with a minor in Computer Science: 125 credit hours
- Bachelor of Science in Bioinformatics with a minor in Applied Mathematics: 127 credit hours

Students will take 30 credit hours of core Bioinformatics classes, which included three credit hours of internship or research and three credit hours of a Bioinformatics Capstone course.

BS Bioinformatics Tracks

- Bachelor of Science in Bioinformatics with a minor in Biology (catalog.stmarytx.edu/undergraduate/majors-programs/science-engineering-technology/bioinformatics/bioinformatics-bl)
- Bachelor of Science in Bioinformatics with a minor in Computer Science (catalog.stmarytx.edu/undergraduate/majors-programs/science-engineering-technology/bioinformatics/bioinformatics-cs)
- Bachelor of Science in Bioinformatics with a minor in Applied Mathematics (catalog.stmarytx.edu/undergraduate/majors-programs/science-engineering-technology/bioinformatics/bioinformatics-mt)

Minor in Bioinformatics

- Bioinformatics (catalog.stmarytx.edu/undergraduate/majors-programs/science-engineering-technology/bioinformatics/bioinformatics-minor)

All courses serving as prerequisites in the School of Science, Engineering and Technology must be completed with a “C” or better in order to advance to the next sequenced course.

BIO 3311. Biostatistics for Life Sciences. 3 Semester Hours.

This course will provide the background and application of statistical tools for analyzing different types of data frequently encountered by life scientists. The emphasis will be on the applications of various statistical methodology on biological data, using R programming language. This will include contingency table analysis, linear regression and ANOVA, maximum likelihood method and application of statistical tests like t-test, chi-square test and survival analysis. Prerequisites: BL 1401, BL 1402, MT2303 and CS1310 OR permission of the instructor.

BIO 3312. Algorithms for Computational Biology with PERL. 3 Semester Hours.

The objective of this course is to teach students the basics of Linux environment and PERL scripting. Students will learn how to write PERL scripts for solving biological problems. The focus of this course will be on designing algorithms to manipulate and analyze sequence data. This will include programming strategies to store and concatenate DNA sequences. Writing scripts to generate complementary and reverse complementary sequences. Students will learn how to work with files and arrays. They will also learn to generate random numbers and simulate DNA mutations. The course will also focus on hashes and data structures.

BIO 3313. Big Data Concepts. 3 Semester Hours.

The objective of this course is to teach students the basic big data concepts. The focus of this course will be on big data analysis. Students will learn emerging techniques in proteomics and recent quantitative proteomics approaches. They will also learn the basics of the platforms and programming languages used for big data analysis. The course will also focus on the analysis of Genome-, RNA-, miRNA-, Microbiome- and ChIP-sequencing data. Students will also learn about the usage of big data in drug discovery.

BIO 3314. Internship/Research. 3 Semester Hours.

The objective of this course is to provide an opportunity for students in Bioinformatics major to participate in real-life bioinformatics internship or research. This course will be for seniors and juniors. Emphasis will be placed on commonly used genomics/transcriptomics/proteomics/metabolomics projects and the use of standard operating laboratory/industry procedures. Examples of potential collaborative organizations include medical/health centers, molecular genomics labs/companies, computational biology labs/companies, software development/labs companies and biostatistics labs/companies.

BIO 3411. Introduction to Bioinformatics. 4 Semester Hours.

The objective of the course is to teach how techniques can help with solving biological problems. Students will learn to efficiently use multiple genomics and bioinformatics tools, that are freely available, for the analysis of DNA, RNA, and protein sequences and structure. No programming skills are necessary for this course. This interdisciplinary course would be helpful for students in the department of Biology, Computer Science, Mathematics, and Chemistry who aspire to go to either graduate school or medical school, or plan to work in the Bioinformatics industry that has experienced exponential growth within the last decade.

BIO 4311. Bioinformatics Programming with R. 3 Semester Hours.

The objective of this course is to teach students bioinformatics programming techniques using R. The focus of this course will be on development of programs to perform commonly used bioinformatics techniques like pair-wise and multiple sequence alignments. Students will learn computational gene-finding and comparative genomic techniques. They will also learn to create phylogenetic trees and protein-protein interaction graphs. Students will also learn about Hidden Markov models.

BIO 4312. Bioinformatics Capstone. 3 Semester Hours.

The objective of this integrative Capstone is to provide students with an opportunity to write a thesis on their research and present it in the form of an oral presentation. This course will promote advanced scientific writing and broad perspectives of issues in current Bioinformatics research. Students will demonstrate their ability to integrate concepts to a practical situation by presenting a thesis on the research they have performed in an industrial or academic setting. The capstone must be taken during the senior year.

BIO 4411. Genes, Genomes and Genomics. 4 Semester Hours.

The objective of this course is to teach students the basics of molecular genomics. The focus of this course will be on genes, genomes and genomics. This will include strategies to clone a gene and prepare genomic and cDNA libraries. Students will learn the basics of DNA sequencing. They will also learn to analyze gene expression. The course will also focus on analysis of genomes and genetic variation. Students will also learn about transgenesis.

BIO 4412. Transcriptomics, Proteomics and Metabolomics. 4 Semester Hours.

The objective of this course is to teach students the fundamental aspects of the new instrumental and methodological developments in omics technologies, including those related to transcriptomics, epigenetics, proteomics and metabolomics. The focus of this course will be on DNA microarray analysis, next-generation sequencing technologies, genome-wide analysis of methylation and histone modifications. Students will learn emerging techniques in proteomics and recent quantitative proteomics approaches. They will also learn the basics of metabolomics and metabolome analysis. The course will also focus on statistical approaches for the analysis of microarray data, the integration of transcriptome and metabolome data and computational approaches for visualization and integration of omics data.