

Catalog Copy for Courses listed on the 3-02-07 Consent Calendar

CS011707

ESTABLISH A PROFESSIONAL MASTER'S DEGREE IN BIOINFORMATICS (PSM)

BIOINFORMATICS

Bioinformatics Program

Cameron Applied Research Center, Room 206

704-687-8541

<http://www.bioinformatics.uncc.edu/>

Degrees

Professional Science Masters in Bioinformatics

Ph.D. in Information Technology (Bioinformatics Track)

Program Director

Dr. Lawrence Mays

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Cynthia Gibas, Associate Professor

Dennis Livesay, Associate Professor

Lawrence Mays, Professor

Zhengchang Su, Assistant Professor

PROFESSIONAL SCIENCE MASTERS IN BIOINFORMATICS

Additional Admission Requirements

In addition to the general requirements for admission to the Graduate School, the following are required for study toward the Professional Science Masters (PSM) in Bioinformatics:

Under most circumstances, students admitted to the program will have:

1. A baccalaureate degree from an accredited college or university in Biology, Biochemistry, Chemistry, Physics, Mathematics, Statistics, Computer Science, or another related field that provides a sound background in life sciences, computing, or both.
2. A minimum undergraduate GPA of 3.0 (4.0 scale) and 3.0 in the major.
3. A minimum combined score of 1000 on the verbal and quantitative portions of the GRE, and acceptable scores on the analytical and discipline-specific sections of the GRE.
4. A combined TOEFL score of 220 (computer-based) or 557 (paper-based) is required if the previous degree was from a country where English is not the common language.
5. Positive letters of recommendation.

Degree Requirements

The Professional Science Masters (PSM) in Bioinformatics degree requires a minimum of 37 graduate credit hours, and a minimum of 33 credit hours of formal course work. A minimum of 24 credit hours presented toward a PSM in Bioinformatics must be numbered 6000 or higher. A maximum of 6 hours of graduate credit may be transferred from other institutions.

1. Total hours required.

The program requires 37 post-baccalaureate credit hours. Because of the interdisciplinary nature

of this program, which is designed to provide students with a common graduate experience during their professional preparation for the PSM in Bioinformatics degree, all students will be required to take a general curriculum that includes a two-year sequence of courses as described below:

2. Core Requirements.

a. Fundamentals Courses

The **Fundamentals** course sequences are intensive graduate-level courses designed to provide accelerated training in a second discipline that complements the student's undergraduate training. Students entering the program are expected to have achieved proficiency in either Biological Sciences or Computing, and to require at most two of the **Fundamentals** courses.

Fundamental Biology track: This course sequence is designed for students entering with a degree in Computer Science or another quantitative science discipline. The Fundamental Biology course sequence provides accelerated training in Genetics, Cell and Molecular Biology, and Biochemistry for students entering Bioinformatics from computer science or quantitative science. BINF 6100, 6101.

Fundamental Computing track: The Fundamental Computing track is designed for students entering with a degree in a life science discipline. The Fundamental Computing course sequence provides accelerated training in programming and data structures for students entering Bioinformatics from life sciences. BINF 6111, 6112.

b. Core Bioinformatics Courses

Fundamentals courses prepare students for the required **Core Bioinformatics** courses. Students must take BINF 6200, Statistics for Bioinformatics, and 9 additional credit hours of **Core Bioinformatics** courses, which include four core methods courses, BINF 6201, Molecular Sequence Analysis, BINF 6202, Computational Structural Biology, BINF 6203, Genomics, Transcriptomics & Proteomics, and BINF 6204, Mathematical Systems Biology, as well as two core computational skills courses, BINF 6210, Numerical Methods for Bioinformatics, and BINF 6211, Design and Implementation of Bioinformatics Databases.

c. Professional Preparation Requirement

Students are required to take at least 3 credit hours of an elective designed to prepare them to function effectively and ethically in a professional environment. Some recommended electives in this category include PHIL 6050/8050, Research Ethics, and ITIS 6362, Information Technology Ethics, Policy, and Security. Additional elective choices that may fulfill this requirement can be identified by the student and the student's Advisory Committee.

d. The remaining credit hours of formal course work can be completed in additional **Core Bioinformatics** courses and/or other recommended program electives. The student's Advisory Committee will review the student's plan of study each semester.

Bioinformatics Electives: Any courses with BINF numbers, with the exception of **Fundamentals** courses that share common subject matter with the student's undergraduate degree, are open to PSM students seeking to complete their coursework requirements.

Recommended Electives offered by other units: A wide range of courses in Biology, Chemistry, Computer Science, Software and Information Systems, and other departments may be appropriate electives for PSM in Bioinformatics students. As course offerings change frequently, the Bioinformatics Program maintains a list of current recommended electives, which can be found on the Professional Science Masters in Bioinformatics home page at <http://www.bioinformatics.uncc.edu/psm/>.

e. Other requirements

In addition to 30 hours formal coursework, students are required to enroll in the Bioinformatics Program seminar (BINF 6600) for at least one semester (1 credit hour) and to enroll in either an approved internal or external internship (BINF 6400) or a faculty-supervised original research project leading to a thesis (BINF 6900).

2. Grades required.

An accumulation of three C grades will result in suspension of the student's enrollment in the graduate program. If a student makes a grade of U in any course, enrollment in the program will be suspended.

3. Amount of transfer credit accepted.

A maximum of 6 credit hours of coursework from other institutions will count toward the PSM in Bioinformatics degree requirements. Only courses with grades of A or B from accredited institutions are eligible for transfer credit.

Ph.D. in INFORMATION TECHNOLOGY (BIOINFORMATICS TRACK)

The Bioinformatics Program admits students seeking the Ph.D. degree under the Ph.D. in Information Technology (Bioinformatics Track). All requirements for the Ph.D. in Information Technology are described (on page ### of this catalog). The Bioinformatics Track follows all of the common requirements of the Information Technology Ph.D. program with the exception stated below.

Bioinformatics Track Requirements

Students will be required to demonstrate competence, by coursework, examinations, or projects, in the areas of biochemistry, cellular and molecular biology, genetics, statistics, and computer science related to core concepts in bioinformatics. The student's advisor and at least one other dissertation committee member must be faculty in the Bioinformatics Program. Students in this track must also take at least 6 hours of Pre-dissertation Research (ITSC 8990) under the direction of Bioinformatics track faculty members. A major goal of this course will be to prepare the student for the Qualifying Examination.

Core Requirements

Plans of Study for Bioinformatics Ph.D. students are developed on an individual basis, by the student and his or her advisory committee. However, Bioinformatics Ph.D. students and their advisors may wish to consult the Professional Science Masters Core Requirements, above, for guidance in selecting the initial Plan of Study to complement the student's undergraduate background. 8000-numbered versions of course offerings are open to Ph.D. students.

COURSES IN BIOINFORMATICS

BINF 6100. Biological Basis of Bioinformatics. (3)

Prerequisites: Admission to graduate standing in Bioinformatics and undergraduate training in Computer Science or other non-biological discipline. Provides a foundation in molecular genetics and cell biology focusing on foundation topics for graduate training in bioinformatics and genomics. (Fall)

BINF 6101. Energy and Information in Biological Modeling. (3)

Prerequisites: Admission to graduate standing in Bioinformatics. This course covers: the major organic and inorganic chemical features of biological macromolecules, the physical forces that shape biological molecules, assemblies and cells, the chemical driving forces that govern living systems, the molecular roles of biological macromolecules and common metabolites, and the pathways of energy generation and storage. Each section of the course builds upon the relevant

biology and chemistry to explain the most common mathematical and physical abstractions used in modeling in the relevant context. (Spring)

BINF 6111. Bioinformatics Programming I. (3)

Prerequisites: Admission to graduate standing in Bioinformatics. Students in this course will learn how to use object-oriented programming to solve common problems in bioinformatics. Topics covered will include creation and manipulation of relational databases and interfacing with standard bioinformatics programs such as CLUSTAL, BLAST and HMMer. Emphasis will be placed on the creation of memory and time efficient algorithms to handle the large data sets of post-genomic biology. (Fall)

BINF 6112. Bioinformatics Programming II. (3)

Prerequisite: BINF 6111. This is a continuation of Bioinformatics Programming I (BINF 6111). While the previous course emphasized fundamentals of Bioinformatics programming, this course emphasizes efficiency in speed, data structures and file size. Students will learn how to optimize code and databases so that the demanding analyses of modern biology can be performed in acceptable amounts of time while minimizing hardware requirements. Topics covered will include algorithm optimization, optimization of database queries and parallel processing to allow bioinformatics calculations to be performed on clusters. (Spring)

BINF 6200. Statistics for Bioinformatics. (3)

Prerequisite: BINF 6100 and 6111 or equivalents. The aim of this 3-credit course is to introduce students to statistical methods used in further more technical courses. Basic relevant concepts from probability, stochastic processes, information theory, statistics and experimental design will be introduced and illustrated by examples from molecular biology, genomics and population genetics with an outline of algorithms and software. R is introduced as the programming language for homework. (Fall)

BINF 6201. Molecular Sequence Analysis. (3)

Prerequisite: BINF 6100 or equivalent. Introduction to bioinformatics methods that apply to molecular sequence. Intro to biological databases online. Sequence databases, molecular sequence data formats, sequence data preparation and database submission. Local and global sequence alignment, multiple alignment, alignment scoring and alignment algorithms for protein and nucleic acids, genefinding and feature finding in sequence, models of molecular evolution, phylogenetic analysis, comparative modeling. (Fall)

BINF 6202. Computational Structural Biology. (3)

Prerequisite: BINF 6101, 6201 or equivalents. This course will cover: **(a)** the fundamental concepts of structural biology (chemical building blocks, structure, superstructure, folding, etc.); **(b)** software for visualization, visualization styles, publication quality images; **(c)** the hierarchical nature of biomacromolecular structure classification; **(d)** computational methods to evaluate and compare biomacromolecular structure; **(e)** inferring structure/function relationships from structure; and **(f)** computational prediction of protein and nucleic acid structure from sequence. (Fall)

BINF 6203. Genomics, Transcriptomics & Proteomics. (3)

Prerequisite: BINF 6100 or equivalent, and BINF 6201. This course surveys the application and interpretation of high-throughput molecular biology and analytical biochemistry methods used to produce the kinds of high-volume biological data most commonly encountered by bioinformaticians. The relationship between significant biological questions, modern biotechnology methods, and the bioinformatics solutions that enable interpretation of complex data is emphasized. Topics include: Genome sequencing and assembly, genome annotation, genome comparison. Genome evolution. Function prediction and gene ontologies. Microarray assay design, data acquisition, data analysis. Proteomics and methods and data analysis. Methods for identification of molecular interactions. Metabolic databases, pathways and models. (Spring)

BINF 6204. Mathematical Systems Biology. (3)

Prerequisites: BINF 6200 and 6210 or equivalents. Introduction to concepts and common methods in systems biology. The class emphasizes molecular networks, models and applications, and covers the following topics: complexity and robustness of cellular systems; hierarchy and modularity of molecular interaction networks; biological data acquisition for system level modeling; introduction to systems biology markup language (SBML); Bayesian inference of biological systems; stoichiometric and constraint-based modeling; modeling molecular interaction networks with nonlinear ordinary differential equations; quantitative approaches to the analysis of genetic regulatory networks; stochastic modeling of intracellular kinetics; multilevel modeling. (Spring)

BINF 6210. Numerical Methods in Bioinformatics. (3)

Prerequisites: Ability to program in a high-level language (Perl, Java, C#, Python, Ruby, C/C++). Calculus. This course will focus on mathematically complex problems and show students how to implement efficient numerical methods to solve those problems. The focus on the class will depend on instructor expertise but may include: applying linear models and principal component analysis to analysis of microarrays, application of ordinary and partial differential equations to modeling cellular pathways, applying Markov Chains to gene finding and gene predictions algorithms and application of stochastic models and Monte Carlo simulations to molecular dynamics and protein folding. (Fall)

BINF 6211. Design and Implementation of Bioinformatics Databases. (3)

Prerequisite: BINF 6111 and 6112 or equivalent. Students will acquire skills needed to exploit public biological databases and establish and maintain personal databases that support their own research; such skills include learning underlying data models and the basics of DBMS, and SQL. Particular topics will include formats and schemas in important bioinformatics databases (Genbank, EMBL, PDB), XML schema and XML exchange methods, using CGI for the query interface, using generic database tools to browse and manage databases (Tomcat and Pgadmin), relevant database applications of SOAP and CORBA, the types of models used in designing databases, and how ontologies (such as GO) affect database design and queries. (Spring)

BINF 6310. Analysis of Microarray Data. (3)

This course focuses on recent literature concerning algorithms for analysis of microarray data. The course will start with a review of normal statistics (t-test, ANOVA, etc.) and their non-parametric, robust equivalents. We then turn to primary literature for a survey of the techniques of analyzing microarray data: background subtraction, normalization across samples, assignment of p-values, evaluation of algorithms on control data sets, clustering algorithms, self organizing maps, bootstrap estimations of significance and over-representation of gene ontology terms. Special attention will be given to the problem of appropriate correction of significance for multiple measurements. Students should have fluency in a high-level programming language (PERL, Java, C# or equivalent) and will be expected in assignments to manipulate and analyze large public data sets. The course will utilize the R statistical package with the bioconductor extension. (On demand)

BINF 6311. Biophysical Modeling. (3)

This course will cover: **(a)** overview of mechanical force fields; **(b)** energy minimization; **(c)** dynamics simulations (molecular and coarse-grained); **(d)** Monte-Carlo methods; **(e)** systematic conformational analysis (grid searches); **(f)** classical representations of electrostatics (Poisson-Boltzmann, Generalized Born and Colombic); **(g)** free energy decomposition schemes; and **(h)** hybrid quantum/classical (QM/MM) methods. (On demand)

BINF 6312. Computational Comparative Genomics. (3)

Prerequisite: BINF 6210 or equivalent. Computational methods for comparative genomics analysis. The course covers the following topics: the architecture of prokaryotic and eukaryotic

genomes; the evolutionary concept in genomics. databases and resources for comparative genomics; principles and methods for sequence analysis; evolution of genomes; comparative gene function annotation; evolution of the central metabolic pathways and regulatory networks; genomes and the protein universe; cis-regulatory binding site prediction; operon and regulon predictions in prokaryotes; regulatory network mapping and prediction. (*On demand*)

BINF 6313. Structure, Function, and Modeling of Nucleic Acids. (3)

Prerequisite: BINF 6100-6101 or equivalent. The course covers the following topics: atomic structure, macromolecular structure-forming tendencies and dynamics of nucleic acids; identification of genes which code for functional nucleic acid molecules, cellular roles and metabolism of nucleic acids; 2D and 3D abstractions of nucleic acid macromolecules and methods for structural modeling and prediction; modeling of hybridization kinetics and equilibria; hybridization-based molecular biology protocols, detection methods and molecular genetic methods, and the role of modeling in designing these experiments and predicting their outcome. (*On demand*)

BINF 6400. Internship Project. (1-3)

Prerequisites: Admission to graduate standing in Bioinformatics. Project chosen and completed under the guidance of an industry partner, which results in an acceptable technical report. (*Fall, Spring*)

BINF 6600. Seminar. (1)

Prerequisites: Admission to graduate standing in Bioinformatics. Departmental seminar. Weekly seminars will be given by bioinformatics researchers from within UNCC and across the world. (*Fall, Spring*)

BINF 6601. Journal Club. (1)

Prerequisites: Admission to graduate standing in Bioinformatics. Each week, a student in the class is assigned to choose and present a paper from the primary bioinformatics literature. (*Fall, Spring*)

BINF 6900. Masters' Thesis. (1-3)

Prerequisites: Twelve graduate credits and permission of instructor. Project chosen and completed under the guidance of a graduate faculty member, which results in an acceptable master's thesis and oral defense. (*On demand*)

ITSC 8100. Biological Basis of Bioinformatics. (3)

Prerequisites: Admission to graduate standing in Bioinformatics and undergraduate training in Computer Science or other non-biological discipline. Provides a foundation in molecular genetics and cell biology focusing on foundation topics for graduate training in bioinformatics and genomics. (*Fall*)

ITSC 8101. Energy and Information in Biological Modeling. (3)

Prerequisites: Admission to graduate standing in Bioinformatics. This course covers: the major organic and inorganic chemical features of biological macromolecules, the physical forces that shape biological molecules, assemblies and cells, the chemical driving forces that govern living systems, the molecular roles of biological macromolecules and common metabolites, and the pathways of energy generation and storage. Each section of the course builds upon the relevant biology and chemistry to explain the most common mathematical and physical abstractions used in modeling in the relevant context. (*Spring*)

ITSC 8111. Bioinformatics Programming I. (3)

Prerequisites: Admission to graduate standing in Bioinformatics. Students in this course will learn how to use object-oriented programming to solve common problems in bioinformatics. Topics covered will include creation and manipulation of relational databases and interfacing with

standard bioinformatics programs such as CLUSTAL, BLAST and HMMer. Emphasis will be placed on the creation of memory and time efficient algorithms to handle the large data sets of post-genomic biology. (Fall)

ITSC 8112. Bioinformatics Programming II. (3)

Prerequisite: ITSC 8111. This is a continuation of Bioinformatics Programming I (ITSC 8111). While the previous course emphasized fundamentals of Bioinformatics programming, this course emphasizes efficiency in speed, data structures and file size. Students will learn how to optimize code and databases so that the demanding analyses of modern biology can be performed in acceptable amounts of time while minimizing hardware requirements. Topics covered will include algorithm optimization, optimization of database queries and parallel processing to allow bioinformatics calculations to be performed on clusters. (Spring)

ITSC 8200. Statistics for Bioinformatics. (3)

Prerequisite: ITSC 8100 and 8111 or equivalents. The aim of this 3-credit course is to introduce students to statistical methods used in further more technical courses. Basic relevant concepts from probability, stochastic processes, information theory, statistics and experimental design will be introduced and illustrated by examples from molecular biology, genomics and population genetics with an outline of algorithms and software. R is introduced as the programming language for homework. (Fall)

ITSC 8201. Molecular Sequence Analysis. (3)

Prerequisite: ITSC 8100 or equivalent. Introduction to bioinformatics methods that apply to molecular sequence. Intro to biological databases online. Sequence databases, molecular sequence data formats, sequence data preparation and database submission. Local and global sequence alignment, multiple alignment, alignment scoring and alignment algorithms for protein and nucleic acids, genefinding and feature finding in sequence, models of molecular evolution, phylogenetic analysis, comparative modeling. (Fall)

ITSC 8202. Computational Structural Biology. (3)

Prerequisite: ITSC 8101, 8201 or equivalents. This course will cover: **(a)** the fundamental concepts of structural biology (chemical building blocks, structure, superstructure, folding, etc.); **(b)** software for visualization, visualization styles, publication quality images; **(c)** the hierarchical nature of biomacromolecular structure classification; **(d)** computational methods to evaluate and compare biomacromolecular structure; **(e)** inferring structure/function relationships from structure; and **(f)** computational prediction of protein and nucleic acid structure from sequence. (Fall)

ITSC 8203. Genomics, Transcriptomics & Proteomics. (3)

Prerequisite: ITSC 8100 or equivalent, and ITSC 8201. This course surveys the application and interpretation of high-throughput molecular biology and analytical biochemistry methods used to produce the kinds of high-volume biological data most commonly encountered by bioinformaticians. The relationship between significant biological questions, modern biotechnology methods, and the bioinformatics solutions that enable interpretation of complex data is emphasized. Topics include: Genome sequencing and assembly, genome annotation, genome comparison. Genome evolution. Function prediction and gene ontologies. Microarray assay design, data acquisition, data analysis. Proteomics and methods and data analysis. Methods for identification of molecular interactions. Metabolic databases, pathways and models. (Spring)

ITSC 8204. Mathematical Systems Biology. (3)

Prerequisites: ITSC 8200 and 8210 or equivalents. Introduction to concepts and common methods in systems biology. The class emphasizes molecular networks, models and applications, and covers the following topics: complexity and robustness of cellular systems; hierarchy and modularity of molecular interaction networks; biologically data acquisition for system level modeling; introduction to systems biology markup language (SBML); Bayesian inference of

biological systems; stoichiometric and constraint-based modeling; modeling molecular interaction networks with nonlinear ordinary differential equations; quantitative approaches to the analysis of genetic regulatory networks; stochastic modeling of intracellular kinetics; multilevel modeling. (Spring)

ITSC 8210. Numerical Methods in Bioinformatics. (3)

Prerequisites: Ability to program in a high-level language (Perl, Java, C#, Python, Ruby, C/C++). Calculus. This course will focus on mathematically complex problems and show students how to implement efficient numerical methods to solve those problems. The focus on the class will depend on instructor expertise but may include: applying linear models and principal component analysis to analysis of microarrays, application of ordinary and partial differential equations to modeling cellular pathways, applying Markov Chains to gene finding and gene predictions algorithms and application of stochastic models and Monte Carlo simulations to molecular dynamics and protein folding. (Fall)

ITSC 8211. Design and Implementation of Bioinformatics Databases. (3)

Prerequisite: ITSC 8111 and 8112 or equivalent. Students will acquire skills needed to exploit public biological databases and establish and maintain personal databases that support their own research; such skills include learning underlying data models and the basics of DBMS, and SQL. Particular topics will include formats and schemas in important bioinformatics databases (Genbank, EMBL, PDB), XML schema and XML exchange methods, using CGI for the query interface, using generic database tools to browse and manage databases (Tomcat and Padmin), relevant database applications of SOAP and CORBA, the types of models used in designing databases, and how ontologies (such as GO) affect database design and queries. (Spring)

ITSC 8310. Analysis of Microarray Data. (3)

This course focuses on recent literature concerning algorithms for analysis of microarray data. The course will start with a review of normal statistics (t-test, ANOVA, etc.) and their non-parametric, robust equivalents. We then turn to primary literature for a survey of the techniques of analyzing microarray data: background subtraction, normalization across samples, assignment of p-values, evaluation of algorithms on control data sets, clustering algorithms, self organizing maps, bootstrap estimations of significance and over-representation of gene ontology terms. Special attention will be given to the problem of appropriate correction of significance for multiple measurements. Students should have fluency in a high-level programming language (PERL, Java, C# or equivalent) and will be expected in assignments to manipulate and analyze large public data sets. The course will utilize the R statistical package with the bioconductor extension. (On demand)

ITSC 8311. Biophysical Modeling. (3)

This course will cover: **(a)** overview of mechanical force fields; **(b)** energy minimization; **(c)** dynamics simulations (molecular and coarse-grained); **(d)** Monte-Carlo methods; **(e)** systematic conformational analysis (grid searches); **(f)** classical representations of electrostatics (Poisson-Boltzmann, Generalized Born and Colombic); **(g)** free energy decomposition schemes; and **(h)** hybrid quantum/classical (QM/MM) methods. (On demand)

ITSC 8312. Computational Comparative Genomics. (3)

Prerequisite: ITSC 8210 or equivalent. Computational methods for comparative genomics analysis. The course covers the following topics: the architecture of prokaryotic and eukaryotic genomes; the evolutionary concept in genomics. databases and resources for comparative genomics; principles and methods for sequence analysis; evolution of genomes; comparative gene function annotation; evolution of the central metabolic pathways and regulatory networks; genomes and the protein universe; cis-regulatory binding site prediction; operon and regulon predictions in prokaryotes; regulatory network mapping and prediction. (On demand)

ITSC 8313. Structure, Function, and Modeling of Nucleic Acids. (3)

Prerequisite: ITSC 8100-8101 or equivalent. The course covers the following topics: atomic structure, macromolecular structure-forming tendencies and dynamics of nucleic acids; identification of genes which code for functional nucleic acid molecules, cellular roles and metabolism of nucleic acids; 2D and 3D abstractions of nucleic acid macromolecules and methods for structural modeling and prediction; modeling of hybridization kinetics and equilibria; hybridization-based molecular biology protocols, detection methods and molecular genetic methods, and the role of modeling in designing these experiments and predicting their outcome. *(On demand)*

ITSC 8600. Seminar. (1)

Prerequisites: Admission to graduate standing in Bioinformatics. Departmental seminar. Weekly seminars will be given by bioinformatics researchers from within UNCC and across the world. *(Fall, Spring)*

ITSC 8601. Journal Club. (1)

Prerequisites: Admission to graduate standing in Bioinformatics. Each week, a student in the class is assigned to choose and present a paper from the primary bioinformatics literature. *(Fall, Spring)*

A&S 2703

(DANC 11-7-02a)

CROSS LIST EXISTING UNDERGRADUATE COURSES AS GRADUATE COURSES: DANC 5227, DANC 5227L, DANC 5257, DANC 5257L, & DANC 5400

DANC 4227 CROSS LISTED AS:

DANC 5227. Dance Education Methods I. (3)

Prerequisites: Acceptance into the fast track licensure, MAT in Dance program or consent of instructor. Co-requisite: DANC 5227L. Creative movement theories; techniques and skills for teaching the elementary school child. *(Fall)*

DANC 4227L CROSS LISTED AS:

DANC 5227L. Elementary Clinical Experience. (1)

Co-requisite: DANC 5227. Observation and teaching in an elementary school setting. Application of methodologies introduced in DANC 5227. (2 contact hours) *(Fall)*

DANC 4257 CROSS LISTED AS:

DANC 5257. Dance Education Methods II. (3)

Prerequisite: Acceptance into the fast track licensure, MAT in Dance program or consent of instructor. Co-requisite: DANC 5257L. Experiences in techniques for teaching dance in elementary schools. *(Spring)*

DANC 4257L CROSS LISTED AS:

DANC 5257L. Secondary Clinical Experience. (1)

Co-requisite: DANC 5257. Observation and teaching in a secondary school setting. Application of methodologies introduced in DANC 5257. (2 contact hours) *(Spring)*

DANC 4400 CROSS LISTED AS:

DANC 5400. Internship in Dance. (3-6)

Prerequisite: GPA of at least 2.5, junior status, and permission of Department Chair. Research and/or in-service training for dance majors and minors in cooperating organizations. Specific content is based upon a contract between the student's department and professional organization. Graded on a Pass/Fail basis. (*Fall, Spring, Summer*)