

## **Syllabus:** **Development of New Applications for Next Generation Sequencing**

### **Bulletin Description:**

Development of New Applications for Next Generation Sequencing.

Prerequisites: Biol 201 & 202

This class is designed to shed new light on wide variety of tools available for developing new ideas for NGS applications.

### **General Course Info:**

Term: Fall 2021  
Department: Genetics  
Course number: GNET747  
Number of Students: between 3 and 10

### **Instructor Info:**

Name: P.A. Mieczkowski, PhD  
Office: 4256 Genome Sciences Building  
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Phone #: 919 6196832  
Web:  
Office hours: Tuesday at 11:30am

### **Textbooks and Resources:**

**Textbook:** There is no required textbook for this class. Students will be provided with the list of reading assignments, which will include scientific, peer-reviewed publications.

**Website:** We use the Sakai course website, for access to handouts, papers, and presentations. You will need an Onyen to log into Sakai. / My website is open source, available without need to login.

**Supplemental videos/materials:** These will be provided as needed during the semester.

**Disabilities:** If you have a physical or learning disability, please let us know about your special requirements. Also, please see:  
<http://disabilityservices.unc.edu>

**Prerequisites:** Biol 201 & 202

**Course Objectives:** In this class you will learn:

- Learn about current NGS applications
- Learn about chemistry behind NGS applications
- Design NGS application: design and problem solving

**Course Requirements:** This class is meant to be explorative in nature, which has several implications:

**Reading:** Students will be required to read preparatory literature before most of classes to enable their participation in discussion following lecture part of the class. There will be approximately 1-3 papers per class assigned. Supplemental reading will be also suggested.

**Seeking help:** Information in this class is linked. If you do not understand one element, you may trouble in understanding implications later. Do not hesitate to ask questions during the class, email your instructor, take advantage of office hours.

**Key Dates:** See Master Course Schedule for details.

**Basic Structure:**

- Class consists of lecture and discussion/student presentation and discussion;
- Midterm: successful DNA library prep
- Practical part - library preparation
- Final: successful RNAseq library prep and Oral Exam

**Grading Criteria:** Your course grade is based on your cumulative performance on participation, presentation, midterm, and final.

Discussion/preparation/quizzes	25%
Library preparation	35%
Midterm	15%
Final	25%

**Exams** (Midterm 15%, Final 35%): There will be one midterm and one final exam. The dates for exams will be posted on Sakai/website. Each student will have a separate time slot for his/her oral exam. If the campus is closed for any reason during a scheduled exam, then the exam will be rescheduled to first available, mutually agreeable date.

**Course Policies:**

**Attendance:** Attendance is recommended in order to stay on top of the material. Lectures will start promptly at the beginning of each class. If you must be absent for an extended period of time, please contact the instructor

to make arrangements to receive in-class handouts and directions. It is your responsibility to read assigned literature.

## **Honor Code:**

**Academic Honesty:** Refer to UNC's honor code at <http://instrument.unc.edu/> for discussion on academic honesty. If you are in doubt about any of the honor code, please ask me.

**Plagiarism:** If you consult any outside sources when doing your work, you are expected to fully document those sources. Give credit where credit is due. Plagiarism will not be tolerated.

**Cheating:** Cheating in any form on assignments or exams will not be tolerated.

**Civility:** UNC places a priority on student learning. We value the inherent worth and dignity of every individual. We expect all to be civil to each other by:

**Etiquette:** With the exception of laptops used to take notes or to run MATLAB, please keep all other electronic devices (i.e. cell phones) turned off or silenced in class.

**Respecting Others:** Respect faculty, staff, students, guests, other peoples' private property, university property, policies, rules and regulations.

**Being Responsible:** Take responsibility for your choices and actions. Accept consequences for your inappropriate choices and actions.

**Being Professional:** Communicate in a professional and courteous manner in all forms, and at all times, whether verbal, non-verbal or written.

**Course Schedule:** A preliminary course schedule is posted on Sakai/website. While we will make every attempt to follow this schedule, we reserve the right to adjust the schedule as the course progresses; however, you will be given advance notification of any changes.

## **Master Course Schedule:** (DRAFT)

Class 1: **Introduction. How to choose Sequencing System right for your project?**

Course overview and structure  
Overview of current and upcoming DNA Sequencing systems  
Types of available chemistry for Illumina Sequencing Systems  
Students select topics of their presentations

Class 2: **Illumina Sequencing Systems**

Class 3: **NovaSeq platform and v1.5 chemistry**

Class 4: **DNA library preparation**

Whole Genome DNA sequencing: Strategies  
Types of repetitive elements in the genomes: Student presentation (10 mins)  
Short reads sequencing strategies  
Long reads sequencing strategies

Class 5: **Advanced methods for DNA library preparation part 1**

Workflows for clinical Whole Genome Sequencing.  
Student presentation.

Class 6: **Advanced methods for DNA library preparation part 2**

Ancient DNA  
Whole Genome Bisulfate libraries.

Class 7: **Advanced methods for DNA library preparation part 3**

Modifications of bisulfate methodologies  
Library QC

Class 8: **Amplicon and Metagenomics 16S/ITS studies**

Detection of low frequency DNA variants: Student presentation (10 mins)  
Development of the amplicon system for Illumina systems  
Examples of high throughput amplicon studies on PacBio

Class 9: **Amplicons on PacBio, Duplex adapters and epicPCR**

Examples Amplicon strategies.

Class 10: Catch up

Class 11: **Target Enrichment systems**

Student presentation (10 mins)  
DNA target capture for NGS  
MIPS technology  
Modifications of DNA capture strategies (NuGen and Archer)  
Customization of chemistry for low frequency DNA variants detection

Week of Class 12: **DNA preps**

Class 12: **RNA-seq methodologies part 1**

Class 13: **RNA-seq methodologies part 2**

Class 14: **RNA-seq methodologies part 3**

Week of Class 14-15: Total RNAseq library preparation – practice

Class 15: **“low input” RNA-seq methodologies part 4**

Class 16: **Advanced RNA-seq methodologies part 5**

Class 17: **Epigenetics**

Buffers content: Student presentation (10 mins)  
Practical information about protein/protein modification  
mapping – ChIPseq, Cut and Run  
ATACseq  
Mapping 3D structure of the genome Hi-C, Micro-C

Class 18: **Single cell applications**

Student presentation (10 mins)  
Single cell transcription analysis technologies  
Whole genome sequencing from single cell

Class 19: **Spatial Transcriptomic (Multi-omic)**

Class 20: Makeup day  
Catch -up

### **Reading Assignments:**

#### **Sakai:**

<https://sakai.unc.edu/portal/site/gnet747>