

# Bioinformatics Applications - PLPTH813

**Course:** PLPTH813 - Bioinformatics Applications, Spring 2025

**Instructor:** Sanzhen Liu, Plant Pathology, Kansas State University

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**Location:** 4031 Throckmorton Plant Sciences Center

**Time:** Tuesday, Thursday 10:30am-11:20pm (lectures); Thursday 12:30-2:00pm (lab)

**Office:** 4729 Throckmorton Plant Sciences Center

**Office hours:** Tuesday 11:30-12:30pm

## Goals of the course

PLPTH813 will cover the basic principle of regular bioinformatics applications and emphasize the practice of bioinformatics in biological research. The course will introduce some useful computation skills, such as Unix commands, R, and Python, and then will apply these computational skills throughout the course. This course will be focused on the application of bioinformatics in next-generation sequencing (NGS) data analysis, including variant discovery, genotyping, RNA-seq, genome assembly, comparative genomics and so on. The ultimate goal of this course is to help students to be prepared for using powerful computational resources and effectively handling biological data, particularly large genomic data.

## Grading

Participation 5%, Homework 30%, Midterm Exam 20%, Project 15%, final Exam 30%

## Time and location of exams

Midterm: March 13th, 10:30-12:20 Th4031

Final: May 15th, 9:40-11:30am Th4031

## Intended course content

### **PART 1.** Useful Unix tools and R programming

1. Unix/Linux system and useful tools
2. R introduction and useful R packages
3. Basic Python

### **PART 2.** Useful Bioinformatics tools

1. DNA sequence alignment
2. Bedtools
3. Genbank tools

### **PART 3.** NGS technology and related important tools

1. Introduction of NGS technologies
2. Tools for NGS data process and visualization

#### **PART 4. Application of NGS in Genomics**

1. Genomic variant discovery
2. Phylogeny
3. Genetic mapping (QTL and association)
4. Genome assembly
5. Comparative genomics
6. RNA-seq (technology, experimental design, differential expression, and scRNA-seq)
7. Protein structure prediction
8. Genomic applications of LLM

These topics are not presented in the listed order. The course content will be adjusted according to the advance of computational tools and the interests of course audience.

#### **Other notes**

We will use command lines for data analysis throughout the course labs. Students are required to have the Beocat account that allows you to access the Beocat server. You can apply for an account from [the Beocat website](#).

#### **Academic Honesty and Integrity Statement**

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If you are a student enrolled in campus/online courses through the Manhattan or Olathe campuses, contact the Student Access Center at [accesscenter@k-state.edu](mailto:accesscenter@k-state.edu), 785-532-6441; for Salina campus, contact the Academic and Career Advising Center at [acac@k-state.edu](mailto:acac@k-state.edu) or call 785-826-2649.

## **Statement Defining Expectations for Classroom Conduct**

All student activities in the University, including this course, are governed by the Student Judicial Conduct Code as outlined in the Student Governing Association By Laws, Article VI, Section 3, number 2. Students who engage in behavior that disrupts the learning environment may be asked to leave the class.

## **Statement for Copyright Notification**

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## **AI Policy**

This course encourages and embraces the ethical use of Artificial Intelligence (AI). As a student in this course, you will sometimes be required to incorporate AI tools in your work. Our use of AI will allow us to develop our understanding of this technology and examine the complex challenges and opportunities it offers to us, both as students and future professionals. In accordance with university policies around academic integrity in the Student Code of Conduct, we will be transparent in our use of AI in the completion of any classroom tasks. Using an AI tool to generate assignment content without proper attribution would be a violation of [the K-State Honor Pledge](#).