

Course: PLPTH813 - Bioinformatics Applications, Spring 2017
Instructor: Sanzhen Liu, Plant Pathology, Kansas State University
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Location: 4031 Throckmorton Plant Sciences Center
Time: Tuesday & Thursday 10:30-11:20am (lecture)
Thursday 12:30-3:00pm (lab)
Office: 4022B Throckmorton Plant Sciences Center
Office hours: Wednesday 3:00-4:00pm

Goal 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 and R programming, in data analysis at the beginning of the semester, and then will apply these skills throughout the course. This course will be focused on the application of bioinformatics in next-generation sequencing (NGS) data analysis, including genome assembly, variant discovery, genotyping, RNA-Seq, and so on. The ultimate goal of this course is to help students to be prepared for the next-generation biological research that often generates large data and requires researchers to have the capability in data management and data mining.

Grading

Class participation 10%, Homework 30%, Midterm Exam 20%, Paper presentation[#] 5%, Project^{*} 10%, Final Exam 25%

[#] *During the semester, each student will present a paper in class (20 min)*

^{*} *Students either work on their own data or use publically available data for projects. Projects need to be related to biological questions. The results will be **orally presented** before the final week (15-20 min).*

Intended course content**

PART 1. Useful Unix tools and R programming

- Unix/Linux system and useful tools
- R introduction and useful R packages

PART 2. NGS technology and related important tools

- Introduction of NGS technologies
- Data formats, QC, trimming
- Tools for NGS data process and visualization

PART 3. Application of NGS in Genomics

- Genomic variant discovery, genotyping, Phylogeny
- Construction of a genetic map
- Genetic mapping (QTL and association)
- RNA-Seq (technology and assembly)
- RNA-Seq (experimental design and differential expression)
- Genome assembly (*de novo* assembly and annotation)

PART 4. Class presentations

Latest published papers related to our topics will be selected. Each student will present a paper.

PART 5. Project presentations

^{**} *The course content might be adjusted according to the field advance and the interests of audience.*

Other notes

We will use the software R throughout the course. Students in the class are required to have the Beocat account that allows you to access the Beocat server and use R-studio through Beocat.

Academic Honesty and Integrity Statement

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Students with disabilities who need classroom accommodations, access to technology, or information about emergency building/campus evacuation processes should contact the Student Access Center and/or their instructor. Services are available to students with a wide range of disabilities including, but not limited to, physical disabilities, medical conditions, learning disabilities, attention deficit disorder, depression, and anxiety. 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, 785-532-6441; for Salina campus, contact the Academic and Career Advising Center at 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.

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