Agricultural Bioinformatics Research Unit's Educational Program

Application Guidelines FY2023

Notice! All lectures will be conducted in Japanese.

1. Introduction

The importance of bioinformatics in the fields of agricultural and life sciences has significantly increased. As a concrete methodology, bioinformatics has become indispensable in addressing today's critical social issues of food, the environment, and life, and as a means of integrating fragmented disciplines, and because of this education in both the fundamental and applied aspects of the discipline is called for. Our program provides hands-on education in bioinformatics and conducts cutting-edge research in agricultural and life sciences related to bioinformatics. Over the past 19 years, more than 7,800 people have taken courses and earned credits in this program. Through our educational and research activities, we aim to form a social collaboration and international base for agricultural bioinformatics.

2. Application Procedures

This program provides graduate-level classes premised on an undergraduate-level knowledge of life sciences. Also, since many classes use computers, students are expected to already have some knowledge of basic computer operations. For these reasons, we envision graduate students majoring in the natural sciences and working adults involved in research and development related to agriculture and life sciences (including medicine and pharmacology).

If you are a student at the University of Tokyo, please register through UTAS. If you are not a student at the University of Tokyo, please apply from the application form on the website from May 9 to June 20. Only those who have passed the selection process may participate in the program. Successful applicants will be notified by email by June 30.

Program guidance

From Monday, April 3, A video of the course guidance will be distributed.
The video address will be announced on our website.

3. Classes (see page 6 and after for details)

Generally, classes offered in this program have three categories.

Fundamentals:

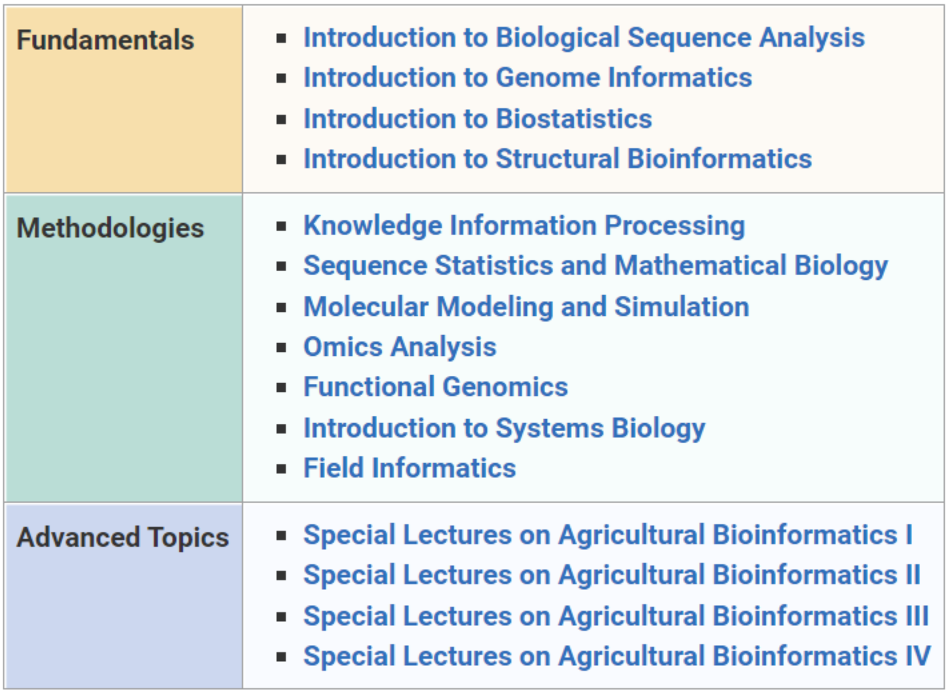
Introduction to Biological Sequence Analysis, Introduction to Genome Informatics, Introduction to Biostatistics, and Introduction to Structural Bioinformatics are mainly for those who have no research experience using bioinformatics. You will learn how to use various life science databases and bioinformatics tools and will also be taught the basic elements of statistics.

Methodologies:

Based on the Fundamentals classes. These lectures focus on various Big data generation methods, observation devices, and computer methods for analyzing them (pattern recognition, machine learning, statistical model and model selection, molecular modeling).

Advanced Topics:

You can learn about programming, which is becoming increasingly important as a means of utilizing IoT, analyzing large amounts of diverse experimental and observational data, and improving the efficiency and development of research. We aim to provide feedback on individual research issues by touching on actual use cases of bioinformatics.



Fundamentals	▪ Introduction to Biological Sequence Analysis ▪ Introduction to Genome Informatics ▪ Introduction to Biostatistics ▪ Introduction to Structural Bioinformatics
Methodologies	▪ Knowledge Information Processing ▪ Sequence Statistics and Mathematical Biology ▪ Molecular Modeling and Simulation ▪ Omics Analysis ▪ Functional Genomics ▪ Introduction to Systems Biology ▪ Field Informatics
Advanced Topics	▪ Special Lectures on Agricultural Bioinformatics I ▪ Special Lectures on Agricultural Bioinformatics II ▪ Special Lectures on Agricultural Bioinformatics III ▪ Special Lectures on Agricultural Bioinformatics IV

4. List of lecture courses

Course Code	Course Name	semester*/credit
3912135	Introduction to Biological Sequence Analysis	S1・1
3912136	Introduction to Genome Informatics	S1・1
3912103	Introduction to Biostatistics	S1・1
3912139	Introduction to Structural Bioinformatics	S1・1
3912137	Knowledge Information Processing	SP・1
3912105	Sequence Statistics and Mathematical Biology	—
3912106	Molecular Modeling and Simulation	S1・1
3912138	Omics Analysis	A1・1
3912108	Functional Genomics	S1・1
3912109	Introduction to Systems Biology	S1・1
3912157	Field Informatics	S1・1
3912111	Special Lectures on Agricultural Bioinformatics I	A1・1
3912112	Special Lectures on Agricultural Bioinformatics II	S1・1
3912140	Special Lectures on Agricultural Bioinformatics III	S1・1
3912141	Special Lectures on Agricultural Bioinformatics IV	S1・1
3912142	Research Exercise on Agricultural Bioinformatics	—

[*] Semester for registering courses using UTAS

The four fundamental subjects are Intermediate Subjects. University of Tokyo undergraduate students can add these to their course credits.

060700130	Introduction to Biological Sequence Analysis
060700140	Introduction to Genome Informatics
060700150	Introduction to Biostatistics
060700160	Introduction to Structural Bioinformatics

University of Tokyo graduate students who complete and pass the following courses may count them toward the credits required for completion of this program.

3901159	Biometrics	S1・2
3908101	Biotechnology informatics	S1・1
4917490	Advanced Lectures in Applied Computer Science XVII	S1・1
4917491	Advanced Lectures in Applied Computer Science XVIII	S1・1
4917891	Advanced Lectures in Applied Computer Science 13A	S1・1

5. Notes

For University of Tokyo students

- Most lectures are online (Zoom) only. However, special Lectures on Agricultural Bioinformatics IV is a hybrid of face-to-face and online.
- All lectures will be conducted in Japanese.
- Lectures for University of Tokyo students (students who can register through UTAS) will generally take place 17:15-18:45 and 19:00-20:30. Changes to the course schedule will be announced on UTAS, ITC-LMS, or Twitter as soon as possible.
- Reflection from UTAS to ITC-LMS takes one day. Even if you register for the course just before the lecture, you cannot view the ITC-LMS, get the lecture materials, or register for attendance. Please complete the course registration through UTAS at least two days before the class starts.
- Please prepare online classes, referencing utelecon (Online Class and Web Conference Portal Site).
- The Zoom URL and information about the lectures will be posted on UTAS or ITC-LMS.
- If you receive an error message when you register at UTAS even though the lecture schedules do not overlap, please register one of the courses at UTAS and submit an additional registration form to the Educational Section of the graduate school to which you belong.
- In the Graduate School of Agricultural and Life Sciences of the University of Tokyo, and in many other graduate schools of the University of Tokyo, credits for some courses taken in this program can be added to the credits required to complete a master's degree. For details, please refer to the current year's Graduate School Handbook.

For students outside of the University of Tokyo

- If you are not a student at the University of Tokyo, please apply during the application period from May 9 to June 20. Applications submitted outside this period will not be accepted.
- Only those who have passed the selection process will be allowed to attend. Successful applicants will be notified by email by June 30.
- Students who pass the selection process will be required to watch lectures that will be distributed on-demand from July 4.
- Outside students will not be able to attend course lectures on the same

days and times as University of Tokyo students. Please refer to the course details for the lectures that will be delivered on-demand.

- The information about the lectures will be posted on dedicated slack.
- Before attending a lecture, please install the necessary software on your PC by referring to the software installation page on our website.
- Details of the on-demand streaming will be sent to you via email. You can watch a lecture as many times as you like during the on-demand streaming period, and you may also ask questions to the teacher.
- Credits earned by taking this program cannot be used to complete a master's degree at another university or to apply for a degree from the National Institution for NIAD-QE Evaluation.

For all students

- **Those who have acquired at least 8 credits will be recognized as having completed the specialized education course and will be awarded a "Certificate of Completion."**

6. Course details

Course	Introduction to Biological Sequence Analysis (Course code:3912135/060700130)
Instructors	Kentaro Shimizu, Kenro Oshima, Koji Kadota
Lecture dates	4/19 (Wed), 4/26 (Wed), 5/10 (Wed), 5/17 (Wed) *University of Tokyo students only
Outside students	On-demand distribution available (Distribution period from 7/4 to 10/31, Assignment submission until 8/31)

Course objectives / Overview

This course focuses on the use of databases and basic analysis methods for life sciences. The use of sequence and functional databases will be introduced, and basic methods such as homology search, motif analysis, Python programming, and phylogenetic analysis will be explained in a hands-on format.

Schedule

1) Sequence database and homology search
2) Genome Database and Programming
3) Various methods for predicting functions from sequences
4) Molecular evolution and phylogenetic tree construction

Teaching Methods

This course is conducted using Zoom, and students can watch recorded lectures.

Grade Evaluation

Students are evaluated based on the completion of homework assignments.

Reference Books

門田幸二、清水謙多郎、岸野洋久、寺田透　共編著、Web連携テキスト　バイオインフォマティクス　基礎から応用、培風館、2022

Hiroyuki Toh (ed.), *Understanding Bioinformatics*, Kodansha, 2018.

H. Bono, *Life Science Data Analysis*, MEDSi、2021

Other

If you have never accessed various databases related to bioinformatics, please take this course.

Course	Introduction to Genome Informatics (Course code:3912136/060700140)
Instructors	Koji Kadota, Yuichi Kodama, Hiroshi Mori
Lecture dates	4/11(Tue), 4/18 (Tue), 4/25 (Tue), 5/2 (Tue) *University of Tokyo students only
Outside students	On-demand distribution available (Distribution period from 7/4 to 10/31, Assignment submission until 8/31)

Course objectives / Overview

In this course, we will discuss the general trends in the fields of genome information analysis, public sequence databases, and metagenomic analysis. Included are lectures on general trends in the field of genome information analysis, public nucleotide sequence databases in general, and practical training on metagenomic analysis.

Schedule

1) General introduction to genome information analysis system (4/11: Kadota)
2) Public databases in life sciences in general (4/18: Kodama)
3) Basics and Applications of Metagenomic Analysis (4/25, 5/2: Mori)

Teaching Methods

This course is conducted using Zoom, and students can watch recorded lectures.

Grade Evaluation

Students are evaluated based on the completion of homework assignments.

Reference Books

門田幸二、清水謙多郎、岸野洋久、寺田透　共編著、Web連携テキスト　バイオインフォマティクス　基礎から応用、培風館、2022

H. Bono, *Life Science Data Analysis*, 2nd Edition, MEDSi, 2021

Nagata, N., *Introduction to Bioinformatics Reading by Evolution*, Morikita Publishing, 2019.

Hiroyuki Toh (ed.), *Understanding Bioinformatics*, Kodansha, 2018.

Notes on taking the course

We use RStudio. Please install R and RStudio. Please install various R packages by referring to ITC-LMS (for University of Tokyo students) or slack (for outside students).

Course	Introduction to Biostatistics (Course code:3912103/060700150)
Instructor	Hiroyoshi Iwata
Lecture dates	4/7 (Fri), 4/14 (Fri), 4/21 (Fri), 4/28 (Fri) *University of Tokyo students only
Outside students	On-demand distribution available (Distribution period from 7/4 to 10/31, Assignment submission until 8/31)

Course objectives / Overview

This course teaches introductory biostatistics using the statistical analysis software R. This course is designed for students who are using R for the first time and will focus on practical training using laptop computers.

Schedule

1) Visualizing data in R
2) Regression analysis, analysis of variance
3) Principal component analysis, multidimensional scaling
4) Hierarchical cluster analysis, non-hierarchical cluster analysis

Teaching Methods

This course is conducted using Zoom, and students can watch recorded lectures.

Grade Evaluation

Students are evaluated based on the completion of homework assignments.

Reference Books

Reference books for further study will be introduced during the course.

Notes on taking the course

We use RStudio. Please install R and RStudio. Please install various R packages by referring to ITC-LMS (for University of Tokyo students) or slack (for outside students).

Course	Introduction to Structural Bioinformatics (Course code : 3912139/060700160)
Instructors	Tohru Terada, Koji Nagata, Takeshi Kawabata
Lecture dates	4/6 (Thu), 4/13 (Thu), 4/20 (Thu), 4/27 (Thu) *University of Tokyo students only
Outside students	On-demand distribution available (Distribution period from 7/4 to 10/31, Assignment submission until 8/31)

Course objectives / Overview

This course instructs students on how to use a protein 3D structure database and illustrates its applications. This course also explains information processing methods used in 3D structure determination.

Schedule

1) Use of 3D structure database and visualization of 3D structure data
2) Information extraction from 3D structure database
3) Informatics of 3D structure determination by X-ray crystallography
4) Informatics of 3D structure determination by cryo-electron microscopy

Teaching Methods

This course is conducted using Zoom, and students can watch recorded lectures.

Grade Evaluation

Students are evaluated based on the completion of homework assignments.

Notes on taking the course

We use UCSF Chimera, Modeller, and CCP4 Software Suite. Please install them before attending the class.

Course	Knowledge Information Processing (Course code:3912137)
Instructor	Minoru Asogawa
Lecture dates	9/8(Fri), 9/15 (Fri), 9/22 (Fri), 9/29 (Fri), 10/6(Fri), 10/13 (Fri), 10/20 (Fri) *University of Tokyo students only *Lecture time is 17:15-19:00, unlike other lectures.
Outside students	On-demand distribution available (Distribution period from 11/2 to 1/23, Assignment submission until 12/26)

Course objectives / Overview

This course provides an introduction to pattern recognition and machine learning using bioinformatics data.

Schedule

1) Neural network basic, 2) Discrimination analysis and application examples, 3) Analysis method for trained neural network, deep learning and correlation analysis, 4) Clustering analysis and principal component analysis, 5) Kernel based learning (SVM), 6) Decision tree, and 7) Hidden Markov model.

Teaching Methods

This course is conducted using Zoom, and students can watch recorded lectures.

Grade Evaluation

In the previous year, the course grade was determined on the basis of four report assignments. This evaluation method may be altered depending on the student's proficiency level.

Notes on taking the course

We use R. Please install R and RStudio. Please install various R packages by referring to ITC-LMS (for University of Tokyo students) or slack (for outside students). It's assumed that you have already mastered the primary usage of R (or RStudio). Please refer to https://www.iu.a.u-tokyo.ac.jp/kadota/r_seq.html#users_guide and understand the basics.

Course	Molecular Modeling and Simulation (Course code:3912106)
Instructor	Tohru Terada
Lecture dates	5/11 (Thu), 5/18 (Thu), 5/25 (Thu), 6/8 (Thu) *University of Tokyo students only
Outside students	On-demand distribution available (Distribution period from 8/1 to 12/26, Assignment submission until 10/31)

Course objectives / Overview

This course teaches students about the molecular orbital, molecular mechanics, molecular dynamics, Monte Carlo, and complex modeling methods. This course also provides training in each of these methods.

Schedule

1) Molecular orbital method
2) Molecular mechanics method
3) Molecular dynamics method
4) Monte Carlo method
5) Complex modeling method

Teaching Methods

This course is conducted using Zoom, and students can watch recorded lectures.

Grade Evaluation

Students are evaluated based on the completion of homework assignments.

Reference Books

Andrew R. Leach, *Molecular Modeling: Principles and Applications*, Prentice Hall, 2001.

Notes on taking the course

We use UCSF Chimera, NAMD, and Perl.

Please install them before attending the class.

Course	Omics Analysis　(Course code:3912138)
Instructors	Koji Kadota
Lecture dates	10/4 (Wed), 10/11 (Wed), 10/18 (Wed) *University of Tokyo students only *Lecture time is 13:00-17:00, unlike other lectures.
Outside students	On-demand distribution available (Distribution period from 11/2 to 1/23, Assignment submission until 12/26)

Course objectives / Overview

Many students struggle with mathematical formulas and algorithms. This course focuses on the problem of identifying regions with specific characteristics in the genome sequence and carefully explains the thought process of algorithm development researchers, including basic concepts and performance evaluation metrics.

Schedule

1) Basics of epigenome analysis and CGI region prediction (section 2.4 in the textbook)
2) PSO algorithm (first half of section 2.6 in the textbook)
3) Elongation of the CGI domain using reinforcement learning (second half of section 2.6 in the textbook)

Teaching Methods

This course is conducted using Zoom, and students can watch recorded lectures.

Grade Evaluation

Students are evaluated based on the completion of homework assignments. The lecture itself includes some R programming, but the main focus is on understanding formulas and algorithms, so reports may be submitted in Python.

Textbook

門田幸二、清水謙多郎、岸野洋久、寺田透　共編著、Web 連携テキスト　バイオインフォマティクス　基礎から応用、培風館、2022

Notes on taking the course

We use RStudio. Please install R and RStudio before attending the class.

Course	Functional Genomics (Course code:3912108)
Instructors	Koji Kadota, Yasuhiro Tanizawa, Koichi Higashi
Lecture dates	5/23 (Tue), 5/30 (Tue), 6/6 (Tue), 6/13 (Tue) *University of Tokyo students only
Outside students	On-demand distribution available (Distribution period from 8/1 to 12/26, Assignment submission until 10/31)

Course objectives / Overview

This lecture focuses on methods used in the fields of genome analysis and transcriptome analysis, including basic concepts of k-mer analysis and its use (*de novo* assembly and genome size estimation), genome annotation, and RNA-seq data analysis.

Schedule

1) Genome analysis: Bacterial genome analysis and its surroundings (5/23: Tanizawa)
2) Genome Analysis: Basics and applications of K-mer analysis (5/30: Kadota)
3) Genome Analysis: Chromosome structure analysis centered on Hi-C data (6/6: Higashi)
4) Transcriptome Analysis: (6/13: Higashi)

Teaching Methods

This course is conducted using Zoom, and students can watch recorded lectures.

Grade Evaluation

Students are evaluated based on the completion of homework assignments.

Reference Books

H. Bono (ed.), *RNA-Seq Data Analysis Iron Plate Recipes for Wet Labs*, Yodosha, 2019.

Hiroyuki Toh (ed.), *Understanding Bioinformatics*, Kodansha, 2018.

H. Bono, *Life Science Data Analysis*, MEDSi, 2021

Platform for Advanced Genome Science (ed.), *Self-study Python Bioinformatics Analysis*, Yodosha, 2021

Notes on taking the course

We use RStudio. Please install R and RStudio. Please install various R packages by referring to ITC-LMS (for University of Tokyo students) or slack (for outside students).

Course	Introduction to Systems Biology　(Course code:3912109）
Instructor	Masanori Arita
Lecture dates	7/7(Fri), 7/14 (Fri), 7/21 (Fri) *University of Tokyo students only *Lecture time is 13:00-17:00, unlike other lectures.
Outside students	On-demand distribution available (Distribution period from 8/1 to 12/26, Assignment submission until 10/31)

Course objectives / Overview

Introduction of statistical and graph-theoretic analyses for omics information to understand life as a system.

Schedule

Seven lectures in 3 days. The course explains the underlying ideas and methods of dimensional reduction and sparse modeling in big- and omics data, and network analysis. This course also covers recent research trends with concrete examples.

Teaching Methods

This course is conducted using Zoom, and students can watch recorded lectures.

Grade Evaluation

Students are evaluated based on the completion of homework assignments.

Reference Books

門田幸二、清水謙多郎、岸野洋久、寺田透　共編著、Web 連携テキスト　バイオインフォマティクス　基礎から応用、培風館、2022

Uri Alon, *An Introduction to Systems Biology: Design Principles of Biological Circuits*, Chapman & Hall/CRC, 2019

Notes on taking the course

CellDesigner and R software programs are necessary. Please install before attending the class.

Course	Field Informatics (Course code:3912157）
Instructors	Yoshihiro Ohmori, Takeshi Izawa, Hiroyoshi Iwata, Wei Guo, Naoyuki Sotta
Lecture dates	6/7 (Wed), 6/14 (Wed), 6/21 (Wed), 6/28 (Wed) *University of Tokyo students only
Outside students	On-demand distribution available (Distribution period from 8/1 to 12/26, Assignment submission until 10/31)

Course objectives / Overview

The quantity and quality of crop production are not determined solely by genomic information but are determined as a result of interactions with environmental conditions of field, such as weather, soil, nutrient, and microorganisms, etc. that change spatially and temporally. In this lecture, we will introduce various research methods using images, genome, transcriptome, and ionome information obtained from the field.

Schedule (This course provides omnibus lectures covering topics below)

6/7: Image analysis in agriculture
6/14: Genome Wide Association Study and Genomic Prediction
6/21: Field-transcriptome analysis
6/28: Measurement of plant traits from image (The first half)
Machine learning using ionome -classification- (The second half)

Teaching Methods

This course is conducted online using Zoom, and students can watch recorded lectures. We will use R and RStudio for the hands-on practice.

Grade Evaluation

Evaluation is based on the submission of report on any topic of interest treated in the course.

Textbook

門田幸二、清水謙多郎、岸野洋久、寺田透　共編著、Web連携テキスト　バイオインフォマティクス　基礎から応用、培風館、2022

Notes on taking the course

We use Rstudio. Please install R and RStudio before attending the class. Field informatics relates to lectures, Introduction to Biostatistics, Special Lectures on Agricultural Bioinformatics II and III.

Course	Special Lectures on Agricultural Bioinformatics I (Course code:3912111)
Instructor	Jianqiang Sun
Lecture dates	10/3 (Tue), 10/10 (Tue), 10/17 (Tue), 10/24 (Tue) *University of Tokyo students only *Lecture time is 13:15-16:30, unlike other lectures.
Outside students	On-demand distribution available (Distribution period from 11/2 to 1/23, Assignment submission until 12/26)

Course objectives / Overview

Smart agriculture enables high quality and large crop production by utilizing advanced technologies such as ICT and IoT, which are currently being promoted worldwide. One of the technologies that supports the foundation of smart agriculture is programming languages. Python is one of the easiest programming languages to learn and has a wide range of applications. In this course, we will cover the basics of Python and introduce examples of the latest practical applications of Python in agriculture as well as in molecular biology fields.

Schedule

1) Python basics (variable, data type, control flow)
2) Text data processing
3) Data analysis (CSV file processing, data visualization)
4) Machine learning in agriculture (deep learning, Web API, etc)

Teaching Methods

This course is conducted using Zoom, and students can watch recorded lectures.

Grade Evaluation

Students are evaluated based on the completion of homework assignments.

Reference Web Sites

http://diveintopython3-ja.rdy.jp/
https://utokyo-ipp.github.io/

Notes on taking the course

Miniconda3 (https://docs.conda.io/) will be used for the lecture, but students may also use Google Colab (https://colab.research.google.com/).

Course	Special Lectures on Agricultural Bioinformatics II (Course code:3912112)
Instructor	Gen Sakurai, Yoshihiro Ohmori
Lecture dates	6/9 (Fri), 6/16 (Fri), 6/23 (Fri), 6/30 (Fri) *University of Tokyo students only
Outside students	On-demand distribution available (Distribution period from 8/1 to 12/26, Assignment submission until 10/31)

Course objectives / Overview

In this lecture, to learn the basics of building a simulation model in each crop cultivation system, we will learn the method of mathematically modeling and stimulating the growth of plants, the relationship between plants and meteorology, and plant-physiological phenomena. We aim to use this lecture as a starting point for constructing mathematical models of biological phenomena such as plant growth and the dynamics of minerals in plants. Lectures will include instruction on important mathematical models relating to agrometeorology, plant growth, and the dynamics of minerals and coding exercises on the formulas.

Schedule

1. Formulation of plant light reception and transpiration
2. Formulation of photosynthesis and plant growth
3. Basics of water potential, diffusion equation, and the dynamics of water in soil
4. Mathematical modeling of water flow in plants

Teaching Methods

This course is conducted using Zoom, and students can watch recorded lectures.

Grade Evaluation

Students are evaluated based on the completion of homework assignments.

Reference Books

Reference books for further study will be introduced during the course.

Notes on taking the course

We use RStudio. Please install before attending the class.

Course	Special Lectures on Agricultural Bioinformatics III (Course code:3912140)
Instructors	Noboru Koshizuka, Shinsuke Kobayashi, Yoshihiro Ohmori
Lecture dates	5/12 (Fri), 5/19 (Fri), 6/2 (Fri) *University of Tokyo students only *Lecture time is 13:00-17:00, unlike other lectures.
Outside students	On-demand distribution available (Distribution period from 8/1 to 12/26, Assignment submission until 10/31)

Course objectives / Overview

In this course, students will learn to write a simple data processing program for environmental monitoring using data from environmental sensors installed in the greenhouse of the Institute for Sustainable Agro-ecosystem Services (UTokyo ISAS). The goal is to be able to write data processing programs in Python, handle data in JSON and CSV formats, and perform statistical processing and graphing.

Schedule

Day 1 (4 hours): Learn to write Python with Jupyter Notebook.
Day 2 (4 hours): Learn to process JSON and CSV data.
Presentation of exercise tasks (e.g., Visualize, etc.)
Day 3 (4 hours): Presentation of assignments from Day 2.
Supplementary lecture

Teaching Methods

This course is conducted using Zoom, and students can watch recorded lectures.

Grade Evaluation

Students are evaluated based on the completion of homework assignments.

Notes on taking the course

Use Google Colaboratory (Colab: Python execution environment in the cloud). In this lecture, the content will be understandable even for students who are new to programming, but it is desirable to have some programming experience regardless of language.

This course is related to the Methodology "Field Informatics" and the Advanced Topics "Special Lectures on Agricultural Bioinformatics II." Therefore, we recommend that you also take them.

Course	Special Lectures on Agricultural Bioinformatics IV (Course code:3912141)
Instructors	Hideaki Nojiri, Haruo Suzuki, Yoshiyuki Ohtsubo, Masami Shintani, Naohiro Noda, Motomu Matsui
Lecture dates	6/5 (Mon), 6/26 (Mon), 7/3 (Mon), 7/10 (Mon), 7/24 (Mon) *University of Tokyo students only *Lecture time is 13:15-16:30, unlike other lectures.
Outside students	On-demand distribution is not available

Course objectives / Overview

In this course, we will learn how informatics is used in microbiology and how interesting findings have been obtained. The course will cover informatics to explore diverse microbial phenomena and their functional mechanisms, including the analysis to understand the contents of populations and various analyses to understand the expression patterns of genomic functions.

Schedule

1. How to analyze microbial genomic data
2. How to utilize bioinformatics in environmental microbial research
3. Reproducible bioinformatics using R language
4. From microbial flora analysis to standardization of biometric technology
5. Understand the behavior of plasmids that promote the evolution and adaptation of microorganisms using bioinformatics

Teaching Methods

Except for July 10, we will conduct a hybrid lecture method. The lecture room is Lecture Room 3 on the 1st floor of Building No. 2, Faculty of Agriculture. Students are encouraged to participate in face-to-face classes as much as possible. But, of course, you can also watch recorded lectures.

Grade Evaluation

Students are evaluated based on the completion of homework assignments.

Reference Books

No special preparation is required. In some cases, literature for further study in the field will be introduced during the course.

7.Program faculty

Program faculty includes full-time faculty members of the Agricultural Bioinformatics Research Unit, which is the main organizer of the program, as well as adjunct faculty and lecturers belonging to other universities and research institutes.

Unit Representative		
Dean, Graduate School of Agricultural and Life Sciences		**Yasuhiro Nakashima**
Unit Faculty		
Assoc. Prof.	Koji Kadota	koji.kadota@gmail.com
Assoc. Prof.	Yoshihiro Ohmori	ayohmori@g.ecc.u-tokyo.ac.jp
Proj.Prof.	Kentaro Shimizu	shimizu@bi.a.u-tokyo.ac.jp
Adjunct faculty (in charge of administration and lectures)		
Assoc. Prof.	Tohru Terada	Department of Biotechnology
Professor	Masanori Arita	National Institute of Genetics
Professor	Hiroyoshi Iwata	Department of Agricultural and Environmental Biology
Professor	Hideaki Nojiri	Department of Biotechnology
Professor	Koji Nagata	Department of Biological Chemistry
Cooperating lecturers		
Professor	Kenro Oshima	Hosei University
Visiting Lecturer	Minoru Asogawa	Tokai University School of Medicine
Senior Researcher	Jianqiang Sun	National Agriculture and Food Research Organization
Program office staff		
Academic Support Staff		Aya Miura
Project Academic Specialist		Tomoko Terada

8. Contact information, program secretariat

In addition to questions about courses, we also accept inquiries about how to use bioinformatics in your own research. Please feel free to contact us by e-mail.

Graduate School of Agricultural and Life Sciences, Agricultural Bioinformatics Research Unit, The University of Tokyo
1-1-1 Yayoi, Bunkyo-ku, Tokyo 113-8657, Japan
Secretariat contact: Aya Miura
Email: info@iu.a.u-tokyo.ac.jp
URL: https://www.iu.a.u-tokyo.ac.jp
Twitter: @Agribio_utokyo

Yayoi Campus Map: The program office is located on the first basement floor of the Faculty of Agriculture Building 2 (Room 14-2).