

# Agricultural Bioinformatics Research Unit's Educational Program Application Guidelines FY2024

**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. Serving as a vital methodology, bioinformatics plays an indispensable role in addressing today's critical social issues of food, the environment, and life. Moreover, it serves as a means of integrating diverse disciplines. Hence, there is a pressing need for education encompassing both the fundamental and applied aspects of this discipline. Our program provides hands-on education in bioinformatics and conducts cutting-edge research in agricultural and life sciences related to bioinformatics. Over the past 20 years, more than 8,300 individuals have participated in courses and earned credits through our program. Through our educational and research endeavors, we strive to establish a platform for social collaboration and international cooperation in agricultural bioinformatics.

## **2. Application Procedures**

This program offers graduate-level classes based on an undergraduate-level knowledge of life sciences. Additionally, as many classes require computer usage, students are expected to possess some proficiency in basic computer operations. Therefore, we anticipate that our courses will be attended by graduate students in the natural sciences as well as by working professionals engaged in research and development in agricultural and life sciences, including medical and pharmaceutical sciences.

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 using the application form available on the website from May 7 to June 18. Only applicants who have successfully passed the selection process will be eligible to participate in the program. Successful applicants will be notified via email by June 28.

### **Program guidance**

We will post the guidance materials on our website starting Wednesday, April 3.

### 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.

<b>Fundamentals</b>	<ul style="list-style-type: none"><li>▪ <b>Introduction to Biological Sequence Analysis</b></li><li>▪ <b>Introduction to Genome Informatics</b></li><li>▪ <b>Introduction to Biostatistics</b></li><li>▪ <b>Introduction to Structural Bioinformatics</b></li></ul>
<b>Methodologies</b>	<ul style="list-style-type: none"><li>▪ <b>Knowledge Information Processing</b></li><li>▪ <b>Sequence Statistics and Mathematical Biology</b></li><li>▪ <b>Molecular Modeling and Simulation</b></li><li>▪ <b>Omics Analysis</b></li><li>▪ <b>Functional Genomics</b></li><li>▪ <b>Introduction to Systems Biology</b></li><li>▪ <b>Field Informatics</b></li></ul>
<b>Advanced Topics</b>	<ul style="list-style-type: none"><li>▪ <b>Special Lectures on Agricultural Bioinformatics I</b></li><li>▪ <b>Special Lectures on Agricultural Bioinformatics II</b></li><li>▪ <b>Special Lectures on Agricultural Bioinformatics III</b></li><li>▪ <b>Special Lectures on Agricultural Bioinformatics IV</b></li></ul>

#### 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	—
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.
- **All lectures will be conducted in Japanese.** Please refer to the current year's Graduate School Handbook for the availability of materials in English.
- 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, UTOL, or X (Formerly Twitter) as soon as possible.
- Reflection from UTAS to UTOL takes one day. Even if you register for the course just before the lecture, you cannot view the UTOL, 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 UTOL.
- 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.
- Please install the necessary software for each lecture beforehand.

### 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 7 to June 18. 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 28.
- 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.
- Please install the necessary software for each lecture beforehand.
- Even after registration is accepted, on-demand distribution may be canceled due to circumstances.

#### **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	4/10 (Wed), 4/17 (Wed), 4/24 (Wed), 5/1 (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

### Notes on taking the course

We use BLAST, MEGA, and Python. Please install them before attending the class.

### 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, Hiroshi Mori
Lecture dates	4/9(Tue), 4/16 (Tue), 4/23 (Tue), 4/30 (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)
<p><u>Course objectives / Overview</u></p> <p>In this course, we will discuss the basics of the fields of genome information analysis and metagenomic analysis. Included are lectures on k-mer analysis frequently used in the bioinformatics field.</p> <p><u>Schedule</u></p> <ol style="list-style-type: none"> <li>1) General introduction to genome information analysis system and RStudio (4/9: Kadota)</li> <li>2) Basics of Metagenomic Analysis (4/16: Mori)</li> <li>3) Applications of Metagenomic Analysis (4/23: Mori)</li> <li>4) Basics and applications of k-mer Analysis (4/30: Kadota)</li> </ol> <p><u>Teaching Methods</u></p> <p>This course is conducted using Zoom, and students can watch recorded lectures.</p> <p><u>Grade Evaluation</u></p> <p>Students are evaluated based on the completion of homework assignments.</p> <p><u>Reference Books</u></p> <p>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</p> <p>H. Bono, <i>Life Science Data Analysis</i>, 2nd Edition, MEDSi, 2021</p> <p>Nagata, N., <i>Introduction to Bioinformatics Reading by Evolution</i>, Morikita Publishing, 2019.</p> <p>Hiroyuki Toh (ed.), <i>Understanding Bioinformatics</i>, Kodansha, 2018.</p> <p><u>Notes on taking the course</u></p> <p>We use RStudio. Please install R and RStudio. Please install various R packages by referring to UTOL (for University of Tokyo students) or slack (for outside students).</p>	



Course	Introduction to Biostatistics (Course code:3912103/060700150)
Instructor	Hiroyoshi Iwata
Lecture dates	4/12 (Fri), 4/19 (Fri), 4/26 (Fri), 5/10 (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)
<p><u>Course objectives / Overview</u></p> <p>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.</p> <p><u>Schedule</u></p> <ol style="list-style-type: none"> <li>1) Visualizing data in R</li> <li>2) Regression analysis, analysis of variance</li> <li>3) Principal component analysis, multidimensional scaling</li> <li>4) Hierarchical cluster analysis, non-hierarchical cluster analysis</li> </ol> <p><u>Teaching Methods</u></p> <p>This course is conducted using Zoom, and students can watch recorded lectures.</p> <p><u>Grade Evaluation</u></p> <p>Students are evaluated based on the completion of homework assignments.</p> <p><u>Reference Books</u></p> <p>Reference books for further study will be introduced during the course.</p> <p><u>Notes on taking the course</u></p> <p>We use RStudio. Please install R and RStudio. Please install them before attending the class.</p>	

Course	Introduction to Structural Bioinformatics (Course code : 3912139/060700160)
Instructors	Tohru Terada, Koji Nagata, Takeshi Kawabata
Lecture dates	4/11 (Thu), 4/18 (Thu), 4/25 (Thu), 5/2 (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)
<p><u>Course objectives / Overview</u> 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.</p> <p><u>Schedule</u> 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</p> <p><u>Teaching Methods</u> This course is conducted using Zoom, and students can watch recorded lectures.</p> <p><u>Grade Evaluation</u> Students are evaluated based on the completion of homework assignments.</p> <p><u>Notes on taking the course</u> We use UCSF Chimera, Modeller, and CCP4 Software Suite. Please install them before attending the class.</p>	

Course	Knowledge Information Processing (Course code:3912137)
Instructor	Minoru Asogawa
Lecture dates	9/20(Fri), 9/27 (Fri), 10/4 (Fri), 10/11 (Fri), 10/18(Fri), 10/25 (Fri), 11/1 (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 10/31 to 1/23, Assignment submission until 12/26)
<p><u>Course objectives / Overview</u> This course provides an introduction to pattern recognition and machine learning using bioinformatics data.</p> <p><u>Schedule</u> 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.</p> <p><u>Teaching Methods</u> This course is conducted using Zoom, and students can watch recorded lectures.</p> <p><u>Grade Evaluation</u> In the previous year, the course grade was determined on the basis of five report assignments. This evaluation method may be altered depending on the student's proficiency level.</p> <p><u>Notes on taking the course</u> We use R. Please install R and RStudio. It's assumed that you have already mastered the primary usage of R (or RStudio). Please refer to <a href="https://www.iu.a.u-tokyo.ac.jp/textbook/appendix.html">https://www.iu.a.u-tokyo.ac.jp/textbook/appendix.html</a> and understand the basics.</p>	

Course	Molecular Modeling and Simulation (Course code:3912106)
Instructor	Tohru Terada
Lecture dates	5/9 (Thu), 5/16 (Thu), 5/23 (Thu), 6/6 (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)
<p><u>Course objectives / Overview</u> 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.</p> <p><u>Schedule</u> 1) Molecular orbital method 2) Molecular mechanics method 3) Molecular dynamics method 4) Monte Carlo method 5) Complex modeling method</p> <p><u>Teaching Methods</u> This course is conducted using Zoom, and students can watch recorded lectures.</p> <p><u>Grade Evaluation</u> Students are evaluated based on the completion of homework assignments.</p> <p><u>Reference Books</u> Andrew R. Leach, <i>Molecular Modeling: Principles and Applications</i>, Prentice Hall, 2001.</p> <p><u>Notes on taking the course</u> We use UCSF Chimera, NAMD, and Python. Please install them before attending the class.</p>	

Course	Omics Analysis (Course code:3912138)
Instructors	Koji Kadota
Lecture dates	10/2 (Wed), 10/9 (Wed), 10/16 (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)
<p><u>Course objectives / Overview</u> 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.</p> <p><u>Schedule</u></p> <ol style="list-style-type: none"> <li>1) Basics of epigenome analysis and CGI region prediction (section 2.4 in the textbook)</li> <li>2) PSO algorithm (first half of section 2.6 in the textbook)</li> <li>3) Elongation of the CGI domain using reinforcement learning (second half of section 2.6 in the textbook)</li> </ol> <p><u>Teaching Methods</u> This course is conducted using Zoom, and students can watch recorded lectures.</p> <p><u>Grade Evaluation</u> Students are evaluated based on the completion of homework assignments.</p> <p><u>Textbook</u> 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</p> <p><u>Notes on taking the course</u> We use RStudio. Please install R and RStudio before attending the class.</p>	

Course	Functional Genomics (Course code:3912108)
Instructors	Koji Kadota, Yasuhiro Tanizawa, Koichi Higashi
Lecture dates	5/14 (Tue), 5/21 (Tue), 5/28 (Tue), 6/4 (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)
<p><u>Course objectives / Overview</u></p> <p>This lecture focuses on methods used in the fields of genome analysis and transcriptome analysis.</p> <p>We will cover <i>de novo</i> assembly and annotation of bacterial genomes, Linux basics, comparative genomic analysis, chromosome structure analysis, and single cell analysis.</p> <p><u>Schedule</u></p> <ol style="list-style-type: none"> <li>1) Genome analysis: Bacterial genome analysis and its surroundings (5/14: Tanizawa)</li> <li>2) Linux basics: Comparative genomic analysis on Linux (5/21: Kadota)</li> <li>3) Genome Analysis: Chromosome structure analysis centered on Hi-C data (5/28: Higashi)</li> <li>4) Transcriptome Analysis: (6/4: Higashi)</li> </ol> <p><u>Teaching Methods</u></p> <p>This course is conducted using Zoom, and students can watch recorded lectures.</p> <p><u>Grade Evaluation</u></p> <p>Students are evaluated based on the completion of homework assignments.</p> <p><u>Reference Books</u></p> <p>H. Bono (ed.), <i>RNA-Seq Data Analysis Iron Plate Recipes for Wet Labs</i>, Yodosha, 2019.</p> <p>Hiroyuki Toh (ed.), <i>Understanding Bioinformatics</i>, Kodansha, 2018.</p> <p>H. Bono, <i>Life Science Data Analysis</i>, MEDSi, 2021</p> <p>Platform for Advanced Genome Science (ed.), <i>Self-study Python Bioinformatics Analysis</i>, Yodosha, 2021</p> <p><u>Notes on taking the course</u></p> <p>We use RStudio. Please install R and RStudio before attending the class. (side students).</p>	

Course	Introduction to Systems Biology (Course code:3912109)
Instructor	Masanori Arita
Lecture dates	7/5(Fri), 7/12 (Fri), 7/19 (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	6/5 (Wed), 6/12 (Wed), 6/19 (Wed), 6/26 (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)
<p><u>Course objectives / Overview</u></p> <p>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.</p> <p><u>Schedule</u> (This course provides omnibus lectures covering topics below)</p> <p>6/5: Image analysis in agriculture  6/12: Genome Wide Association Study and Genomic Prediction  6/19: Field-transcriptome analysis  6/26: Measurement of plant traits from image (The first half)  Machine learning using ionome -classification- (The second half)</p> <p><u>Teaching Methods</u></p> <p>This course is conducted online using Zoom, and students can watch recorded lectures. We will use R and RStudio for the hands-on practice.</p> <p><u>Grade Evaluation</u></p> <p>Evaluation is based on the submission of report on any topic of interest treated in the course.</p> <p><u>Textbook</u></p> <p>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</p> <p><u>Notes on taking the course</u></p> <p>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.</p>	



Course	Special Lectures on Agricultural Bioinformatics I (Course code:3912111)
Instructor	Jianqiang Sun
Lecture dates	10/8 (Tue), 10/15 (Tue), 10/22 (Tue), 10/29 (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 10/31 to 1/23, Assignment submission until 12/26)
<p><u>Course objectives / Overview</u></p> <p>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.</p> <p><u>Schedule</u></p> <ol style="list-style-type: none"> <li>1) Python basics (variable, data type, control flow)</li> <li>2) Text data processing</li> <li>3) Data analysis (CSV file processing, data visualization)</li> <li>4) Machine learning in agriculture (deep learning, Web API, etc)</li> </ol> <p><u>Teaching Methods</u></p> <p>This course is conducted using Zoom, and students can watch recorded lectures.</p> <p><u>Grade Evaluation</u></p> <p>Students are evaluated based on the completion of homework assignments.</p> <p><u>Reference Web Sites</u></p> <p><a href="http://diveintopython3-ja.rdy.jp/">http://diveintopython3-ja.rdy.jp/</a>  <a href="https://utokyo-ipp.github.io/">https://utokyo-ipp.github.io/</a></p> <p><u>Notes on taking the course</u></p> <p>Miniconda3 (<a href="https://docs.conda.io/">https://docs.conda.io/</a>) will be used for the lecture, but students may also use Google Colab (<a href="https://colab.research.google.com/">https://colab.research.google.com/</a>).</p>	

Course	Special Lectures on Agricultural Bioinformatics II (Course code:3912112)
Instructor	Gen Sakurai, Yoshihiro Ohmori
Lecture dates	6/7 (Fri), 6/14 (Fri), 6/21 (Fri), 6/28 (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 mathematical model in each crop cultivation system, we will learn the method of mathematically modeling and simulating the growth of plants, the relationship between plants and micro-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. In this lecture, we will learn the basic knowledge of them using R, so even those without experience with R can take this course.

#### Schedule

1. Modelling of plant light reception and transpiration
2. Modelling of photosynthesis and plant growth
3. Basics of water potential, diffusion equation, and the dynamics of water in soil
4. 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 it before attending the class.

Course	Special Lectures on Agricultural Bioinformatics III (Course code:3912140)
Instructors	Noboru Koshizuka, Shinsuke Kobayashi, Yoshihiro Ohmori
Lecture dates	5/15 (Fri), 5/22 (Fri), 5/29 (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)
<p><u>Course objectives / Overview</u></p> <p>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.</p> <p><u>Schedule</u></p> <p>Lecture / Practice</p> <p>Day 1: Overview of IoT Environment / Basic programming using Python</p> <p>Day 2: Fundamentals of IoT Technology1 / Data processing programming</p> <p>Day 3: Fundamentals of IoT Technology2 / Presentation of assignments</p> <p><u>Teaching Methods</u></p> <p>This course is conducted using Zoom, and students can watch recorded lectures.</p> <p><u>Grade Evaluation</u></p> <p>Students are evaluated based on the completion of homework assignments.</p> <p><u>Notes on taking the course</u></p> <p>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.</p> <p>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.</p>	

## 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.

<b>Unit Representative</b>		
<b>Dean, Graduate School of Agricultural and Life Sciences</b>		<b>Yasuhiro Nakashima</b>
<b>Unit Faculty</b>		
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
<b>Adjunct faculty (in charge of administration and lectures)</b>		
Professor	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
<b>Cooperating lecturers</b>		
Professor	Kenro Oshima	Hosei University
Visiting Lecturer	Minoru Asogawa	Tokai University School of Medicine
Senior Researcher	Jianqiang Sun	National Agriculture and Food Research Organization
<b>Program office staff</b>		
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.

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

