Agricultural Bioinformatics Research Unit's Educational Program

Application Guidelines FY2021

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 17 years, more than 6,800 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 by June 18 using the application form on our website. 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 (for University of Tokyo students)

Monday, April 5, 5:15 p.m. - 6:30 p.m., via Zoom.

The Zoom Meeting ID and Password will be printed in our guidelines distributed at the graduate school's guidance event on April 2.

*A video of the course guidance event will be distributed to those external students who have passed the selection process.

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

Generally, classes offered in this program have three categories.

Fundamentals:

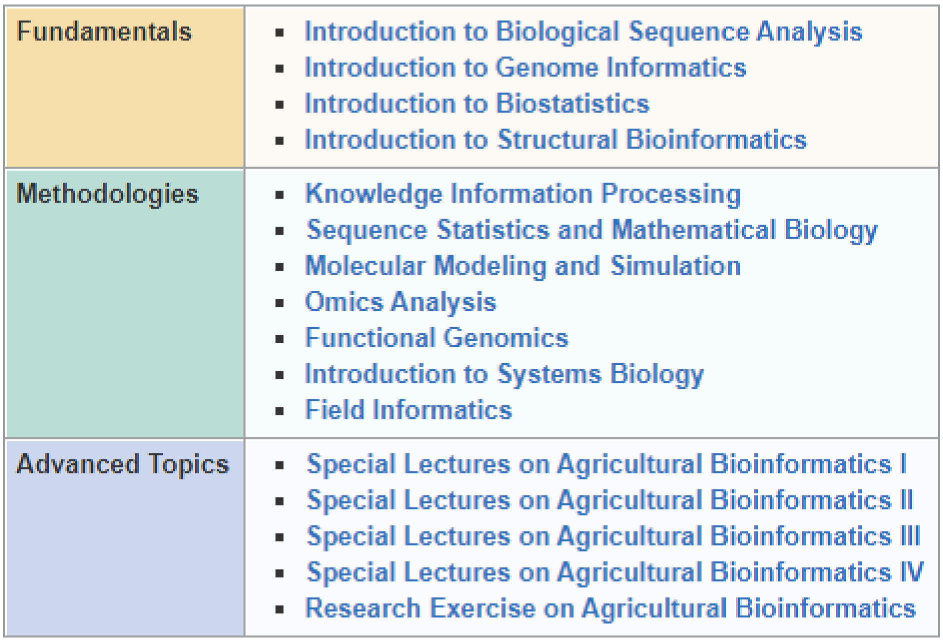
Introduction to Biological Sequence Analysis, Introduction to Genome Informatics, Introduction to Biostatistics, and Introduction to Structural Bioinformatics are mainly for those who have no research experience using bioinformatics. You will learn how to use various life science databases and bioinformatics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

Methodologies:

The Methodologies classes (Knowledge Information Processing, Sequence Statistics and Mathematical Biology, Molecular Modeling and Simulation, Omics Analysis, Functional Genomics, Introduction to Systems Biology, Field Informatics) are based on the Fundamentals classes and provide instruction on various experimental methods (transcriptome analysis, mass spectrometry, etc.) and computer applications (pattern recognition, machine learning, statistical model and model selection, molecular modelling).

Advanced Topics:

In the Special Lectures on Agricultural Bioinformatics, researchers from companies and universities will give lectures and provide practical training on their cutting-edge research topics. Our aim is to provide feedback in this way on the practical applications of bioinformatics. In Research Exercise on Agricultural Bioinformatics, you will receive research guidance from our program faculty members.



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 ▪ Research Exercise on Agricultural Bioinformatics

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	A1・1
3912105	Sequence Statistics and Mathematical Biology	—
3912106	Molecular Modeling and Simulation	S1・1
3912138	Omics Analysis	—
3912108	Functional Genomics	S1・1
3912109	Introduction to Systems Biology	S1・1
3912157	Field Informatics	SP・1
3912111	Special Lectures on Agricultural Bioinformatics I	SP・1
3912112	Special Lectures on Agricultural Bioinformatics II	—
3912140	Special Lectures on Agricultural Bioinformatics III	S1・1
3912141	Special Lectures on Agricultural Bioinformatics IV	A1・1
3912142	Research Exercise on Agricultural Bioinformatics	W・1

* 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
48101123	Computational biophysics	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

- As in the previous year, all course lectures will be conducted online (Zoom) this year.
- 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 in a course schedule will be announced on UTAS or ITC-LMS as soon as possible.
- Please make sure to prepare for online classes.
- 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.
- If you are interested in taking the course “Research Exercise on Agricultural Bioinformatics,” please contact the program office first.

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. Applications submitted outside this period will not be accepted.
- For those who are not students at the University of Tokyo, only those who have passed the selection process will be allowed to attend. Successful applicants will be notified by email by June 30 (Wed).
- Students who pass the selection process will be required to watch lectures that will be distributed on demand for a limited time. 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.
- 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

- **If your attendance is less than half of the total number of lectures, you will not receive a grade.**
- **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:3912135060700130)
Instructors	Kentaro Shimizu, Kenro Oshima
Lecture dates	4/7 (Wed), 4/14 (Wed), 4/21 (Wed), 4/28 (Wed) *University of Tokyo students only
Outside students	On-demand distribution available (distribution date scheduled for July)

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, 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.

Grade Evaluation

Students are evaluated based on attendance and completion of homework assignments.

Reference Books

The following books are helpful:

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

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

Notes on taking the course

Students should be able to use a Windows PC or Mac.

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	4/6 (Tue), 4/13 (Tue), 4/20 (Tue), 4/27 (Tue) *University of Tokyo students only
Outside students	On-demand distribution available (distribution date scheduled for July)

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 (4/6: Kadota)
2) Public databases in life sciences in general (4/13: Kodama)
3) Basics and Applications of Metagenomic Analysis (4/20, 4/27: Mori)

Teaching Methods

This course is conducted using Zoom.

Grade Evaluation

Students are evaluated based on attendance and completion of homework assignments.

Reference Books

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

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

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

Supervised by H. Bono and H. Ono, *Life Science Databases and Web Tools*, MEDSi, 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 our website (for outside students).

Course	Introduction to Biostatistics (Course code:3912103/060700150)
Instructor	Hiroyoshi Iwata
Lecture dates	4/9 (Fri), 4/16 (Fri), 4/23 (Fri), 4/30 (Fri) *University of Tokyo students only
Outside students	On-demand distribution available (distribution date scheduled for July)

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.

Grade Evaluation

Students are evaluated based on attendance and completion of homework assignments.

Reference Books

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

Notes on taking the course

Students should be able to use a Windows PC or Mac.

Other

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

Course	Introduction to Structural Bioinformatics (Course code：3912139/060700160)
Instructors	Tohru Terada, Koji Nagata, Kentaro Shimizu
Lecture dates	4/8 (Thu), 4/15 (Thu), 4/22 (Thu), 5/6 (Thu) *University of Tokyo students only
Outside students	On-demand distribution available (distribution date scheduled for July)

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) Informatics of 3D structure determination by X-ray crystallography
3) Information extraction from 3D structure database
4) 3D structure modeling

Teaching Methods

This course is conducted using Zoom.

Grade Evaluation

Students are evaluated based on attendance and completion of homework assignments.

Reference Books

None in particular

Notes on taking the course

Students should be able to use a Windows PC or Mac.

Course	Knowledge Information Processing (Course code:3912137)
Instructor	Minoru Asogawa
Lecture dates	10/8 (Fri), 10/15 (Fri), 10/22 (Fri), 10/29 (Fri), 11/5 (Fri), 11/12 (Fri),11/19 (Fri) *University of Tokyo students only *Lecture time is 17:15-18:45, unlike other lectures.
Outside students	On-demand distribution available (distribution date scheduled for end of November)

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.

Grade Evaluation

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

Notes on taking the course

Students should be able to use R system.

Other

・R is mainly used. A PC is loaned to each student at the beginning of each class. If you wish to use your own PC, please install R and the various R packages mentioned in
http://www.iu.a.u-tokyo.ac.jp/~kadota/r_seq.html#about_install
For installing R and different packages, please refer to
~kadota/r_seq.html#about_install.

Course	Molecular Modeling and Simulation (Course code:3912106)
Instructor	Tohru Terada
Lecture dates	5/13 (Thu), 5/20 (Thu), 5/27 (Thu), 6/3 (Thu) *University of Tokyo students only
Outside students	On-demand distribution available (distribution date scheduled for August to September)

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.

Grade Evaluation

Students are evaluated based on attendance and completion of homework assignments.

Reference Books

The following book is helpful:

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

Notes on taking the course

Students should be able to use a Windows PC or Mac.

Course	Functional Genomics (Course code:3912108)
Instructors	Koji Kadota, Yasuhiro Tanizawa
Lecture dates	5/11 (Tue), 5/18 (Tue), 5/25 (Tue), 6/1 (Tue) *University of Tokyo students only
Outside students	On-demand distribution available (distribution date scheduled for August to September)

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: *de novo* assembly and its surroundings (including k-mer analysis) (5/11: Tanizawa)
2) Genome Analysis: Annotation (5/11: Tanizawa)
3) Genome Analysis: k-mer analysis with R (5/18: Kadota)
4) Transcriptome Analysis: Count Data and Models (5/25: Kadota)
5) Transcriptome Analysis: Various Data Analysis (6/1: Kadota)

Teaching Methods

This course is conducted using Zoom.

Grade Evaluation

Students are evaluated based on attendance and completion of homework assignments.

Reference Books

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

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

H. Bono, *Life Science Data Analysis*, MEDSi, 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 our website (for outside students).

・It is assumed that you have already mastered the basic usage of RStudio. Please refer to "Basic usage" in http://www.iu.a.u-tokyo.ac.jp/~kadota/r_seq.html#users_guide

Course	Introduction to Systems Biology (Course code:3912109）
Instructor	Masanori Arita, Ph.D.
Lecture dates	6/11 (Fri), 6/18 (Fri), 6/25 (Fri) *University of Tokyo students only *Lecture time is 13:00-17:00 which differs from other courses.
Outside students	On-demand distribution available (distribution date scheduled for August to September)

Course objectives / Overview

This course introduces the basics for understanding omics information statistically using graph theory and other tools.

Schedule

Overview lectures on network biology, quantitative biology, and synthetic biology using PowerPoint slides. Presentation will be omnibus-style rather than theoretical due to the nature of the field. There will be 7 lectures given over 3 days.

Teaching Methods

This course is conducted using Zoom.

Grade Evaluation

Students are evaluated based on attendance and completion of homework assignments.

Reference Books

Bernhard O. Palsson, *Systems Biology: Simulation of Dynamic Network States*, Cambridge University Press, 2011

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

Notes on taking the course

Students should be able to use a Windows PC or Mac.

Other

We use CellDesigner and the standard R package. 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	6/9 (Wed), 6/16 (Wed), 6/23 (Wed), 6/30 (Wed) *University of Tokyo students only
Outside students	On-demand distribution available (distribution date scheduled for August to September)

Course objectives / Overview

The quantity and quality of plant production in fields such as arable land and agricultural facilities are not determined solely by the genomic information of crops but are determined as a result of interactions with environmental conditions, soil conditions, and microorganisms that change spatially and temporally. Currently, various observation devices including drones and field environment sensors have been developed, and big data is being generated and collected from the entire field. At the same time, the sophistication of analytical instruments has led to the accumulation of a vast amount of omics information, including genomes, transcriptomes, metabolomes, ionomes, and microbiomes for field-grown plants. In this lecture, we will explain the theory and technology of field informatics, which is necessary to realize efficient and optimized breeding and production by making the best use of this information.

Schedule

We will explain various research methods using images, genome, transcriptome, and ionome information obtained from the field.

Teaching Methods

This course is conducted using Zoom.

Grade Evaluation

Students are evaluated based on attendance and completion of homework assignments.

Reference Books

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

Notes on taking the course

Students should be able to use a Windows PC or Mac.

Course	Special Lectures on Agricultural Bioinformatics I (Course code:3912111)
Instructor	Jianqiang Sun
Lecture dates	6/8 (Tue), 6/15 (Tue), 6/22 (Tue), 6/29 (Tue) *University of Tokyo students only
Outside students	On-demand distribution available (distribution date scheduled for August to September)

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) Basic data type, basic syntax (if, for, while)
2) Text and file processing
3) Data analysis (NumPy and Pandas)
4) Data visualization (matplotlib)

Teaching Methods

This course is conducted using Zoom.

Grade Evaluation

Students are evaluated based on attendance and completion of homework assignments.

Reference Web Sites

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

Notes on taking the course

Students are expected to be able to operate one of the following systems: Windows, macOS, or Linux. Anaconda 2020.10 (Python 3.8) must be installed on the system in advance.

Course	Special Lectures on Agricultural Bioinformatics III (Course code:3912140)
Instructors	Noboru Koshizuka, Shinsuke Kobayashi, Yoshihiro Ohmori
Lecture dates	5/21 (Fri), 5/28 (Fri), 6/4 (Fri) *University of Tokyo students only *Lecture time is 13:00-17:00 which differs from other courses.
Outside students	On-demand distribution available (distribution date scheduled for August to September)

Course objectives / Overview

With the development of ICT/IoT technology and measurement devices, various data on plant growth can now be obtained in the agricultural field. In particular, monitoring the cultivation environment using environmental sensors has become an indispensable technology for analyzing the environmental response of plants and improving the efficiency and labor-saving aspects of plant cultivation. 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.

Grade Evaluation

Students are evaluated based on attendance and completion of homework assignments.

Notes on taking the course

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.

Course	Special Lectures on Agricultural Bioinformatics IV (Course code:3912141)
Instructors	Hideaki Nojiri, Haruo Suzuki, Koji Yahara, Masami Shintani, Naohiro Noda
Lecture dates	10/18 (Mon), 10/25 (Mon), 11/8 (Mon), 11/15 (Mon) *University of Tokyo students only *Lecture time is 13:15-16:30 which differs from other courses.
Outside students	On-demand distribution available (distribution date scheduled for the end of November)

Course objectives / Overview

Novel functions of microorganisms have been utilized in agriculture, fermentation, wastewater treatment, and bioremediation. Furthermore, microorganisms play a key role in the global cycles of various elements such as carbon, nitrogen, phosphorus, and iron. It is well known that some microorganisms are pathogenic and tolerant to antibiotics, resulting in serious health concerns. Since microorganisms are invisible and live as a population (consortium) consisting of many species, methods used in information science are often indispensable in their analyses. In this course, we will learn how informatics is used in microbiology and how interesting findings have been obtained.

Schedule

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.

Teaching Methods

This course is conducted using Zoom.

Grade Evaluation

Students are evaluated based on attendance and 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.

Notes on taking the course

Students should be able to use a Windows PC or Mac.

Course	Research Exercise on Agricultural Bioinformatics (Course code:3912142)
Instructors	Program faculty
Lecture dates	To be announced by the instructors

Course objectives / Overview

This is a special seminar in which program faculty members provide research guidance assistance.

Schedule

Based on an agreement with the supervisor of the laboratory to which the student belongs, a faculty member of this program will provide research guidance assistance on bioinformatics.

Teaching Methods

This is an exercise with research guidance.

Grade Evaluation

Students are required to present their research at a review meeting usually held in February of each year. If, as a result of the oral examination, it is recognized that the student has effectively applied bioinformatics to research in agriculture and life sciences or has contributed to the development of the field of bioinformatics, credit and a certificate will be given.

Other

Students who wish to take this course must contact the program office.

7.Program faculty

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

Unit Representative		
Dean, Graduate School of Agricultural and Life Sciences	**Nobuhiro Tsutsumi**	
Unit Faculty		
Assoc. Prof.	Koji Kadota	kadota@g.ecc.u-tokyo.ac.jp
Assoc. Prof.	Yoshihiro Ohmori	ayohmori@g.ecc.u-tokyo.ac.jp
Adjunct faculty (in charge of administration and lectures)		
Assoc. Prof.	Tohru Terada	Department of Biotechnology
Professor	Kentaro Shimizu	Department of Biotechnology
Professor	Hideaki Nojiri	Department of Biotechnology
Professor	Koji Nagata	Department of Biological Chemistry
Assoc. Prof.	Hiroyoshi Iwata	Department of Agricultural and Environmental Biology
Cooperating lecturers		
Professor	Kenro Oshima	Hosei University
Professor	Masaki Arita	National Institute of Genetics
Researcher	Minoru Asogawa	NEC Corporation
Program office staff		
Academic specialist	Aya Miura	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: http://www.iu.a.u-tokyo.ac.jp

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