

## Syllabus Reference

Course title	Bioinformatics		
Term	後期 2nd Half		
Credit(s)	1		
The main day		The main period	
Program/Department	47 Basic Biology		
Lecturers	Shuji Shigenobu, Ikuo Uchiyama		
成績評価区分 Grading Scale	A, B, C, Dの4段階評価 Four-grade evaluation		
レベル Level	Level 2		
力量 Competence	専門力 Academic expertise		

## Instructor

## Full name

\* SHIGENOBU SHUJI

UCHIYAMA IKUO

Outline	This intensive two-day course provides an introduction to the fundamental concepts and practical skills in bioinformatics, with a focus on biological sequence data analysis. Through a combination of lectures and hands-on computer tutorials, students will explore key methods used in genome and transcriptome analysis. The course also emphasizes the application of bioinformatics in evolutionary biology and discusses the role of genomics in the era of Big Data.
Learning objectives	By the end of this course, students will be able to:  1. Understand the fundamental principles of biological sequence analysis. 2. Develop foundational skills in genome and transcriptome data analysis using bioinformatics tools, with an emphasis on understanding the underlying theoretical concepts. 3. Interpret genomic and evolutionary data through molecular evolution analysis and related methods. 4. Gain insight into current trends in genomics and bioinformatics, and engage in discussions about the future of life sciences in the Big Data era.
Grading policy	In addition to sufficient attendance to the lecture, student must complete an assignment to get credit for the course. Activity in the lectures and tutorials: 50%; an assignment 50%.
Lecture Plan	This is the 2-day intensive course. Date: October 29-30, 2025 Venue: TBA (@NIBB)  Day 1 #1: Introduction / Biological sequence analysis 1 (pairwise alignment) #2: Biological sequence analysis 2 (multiple alignment, motifs) #3: Biological sequence analysis 3 (molecular evolution) #4: Genome analysis 1 (genome assembly and gene prediction)  Day 2 #5: Genome analysis 2 (gene annotation and ortholog analysis) #6: Transcriptome analysis 1 (RNA-seq) #7: Transcriptome analysis 2 (clustering, multivariate analysis) #8: Biological databases and current topics (big data and AI in biology)  Lecturer: Dr. Shuji Shigenobu and Dr. Ikuo Uchiyama (SOKENDAI / NIBB)
Location	NIBB (Room: TBA)
Language	English
Textbooks and references	No specific literatures are recommended. Familiarity with basic UNIX command line operations is recommended.
Notes for students of other programs	Students other than Basic Biology Program who wish to enroll in this class should contact Graduate Student Affairs Section, Okazaki Administration Center (r7139@orion.ac.jp) during the registration period.
Keyword	bioinformatics genome transcriptome evolution