

3rd International workshop on basic fungal identification skills for Asian students

Introduction to genomic data analysis and phylogenetic tree construction

February 26–28, 2020

This three-day workshop is for students to learn how to deal with deep sequencing data and a basic introduction to systematics.

Through lectures and hands-on workshop, participants will learn about acquiring, accessing, and analyzing deep sequence data, and phylogenetic analyses using freely available software

Participants should bring their own Windows PC (some of these programs do not work on MAC).

INSTRUCRORS:

- Dr. Prof. Tom Hsiang Environmental Sciences
University of Guelph, CANADA
- Dr. Yosuke Seto Cancer Chemotherapy Center
Japanese Foundation for
Cancer Research, JAPAN

PROGRAM:

Feb 26: 1045 - 1600

- Introduces workshop
 - Introduces OMICs
- 1200 - 1300 Lunch
- Introduces some DNA analysis software
 - Basics of molecular evolution and molecular phylogeny

Feb 27: 0900 - 1600

- DNA sequence analysis (Windows tricks)
 - Retrieve sequence data from public databases
- 1200 - 1300 lunch
- DNA sequences to primitive NJ tree (90 min) - MAYBE
 - Reconstruct molecular phylogeny using MEGA software

Feb 28: 0900 - 1200

- Genome sequencing and assembly
- Interpreting molecular phylogenies

etc....

DATE: February 14 – 16, 2018

TIME: 26th 10.45 am – 17.00 pm
27th 9.00 am – 17.00 pm
28th 9.00 am – 17.00 noon

WHERE: University HALL 6
Room 201 Tamagawa University

Participation fee: 3,000 yen
Lunches in 26th - 27th are included

Workshop size limit:
10 – 15 people

This announcement (notice) applies mainly to masters and doctoral course students who are Asian.

Depending on seat availability, young scientists may patriciate.

RESISTLATION:

Send us an email with following information

1. Name, 2. affiliation,
3. Address, 4. Phone number,
5. Email address

Dead line: February 15th 2020

RSVP: [turimm@ tamagawa.ac.jp](mailto:turimm@tamagawa.ac.jp)



Tamagawa University Research Institute
Mycology & Metabolic Diversity Research Center