





# Bioinformatics with Galaxy – Hands-on Course

## Introduction to sequence analysis workflows

This short two-day course in bioinformatics is designed for absolute beginners. It is aimed at students who want to start with bioinformatics. The course provides a gentle introduction to sequencing data, shows how to work with it, and covers basics of assembling simple genomes.

-  Introduction to NGS data
-  Using Galaxy for reproducible workflows
-  Exercise with real data
-  No programming skills required



18 – 19 September 2025, 13:00 – 17:00



TUAT, Fuchu Campus  
Multi-purpose Room?



Organized by TUAT and Dr. Jörg Wennmann  
from Julius Kühn-Institut (Germany)  
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