Guest Lecture & Workshop: Metagenomics and Bioinformatics in Microbial Ecology

Students of the Graduate Program in Microbiology and other Study Programs attended a guest lecture event held in Reading Room, Department of Biology (2/8). The lecture was started after opening speech by Prof. Dr. Anja Meryandini MS.. "We are welcoming Dirk Berkelmann, a doctoral student from the Department of Genomic and Applied Microbiology, Goettingen University, Germany, who will deliver essential material in the field of metagenomics and bioinformatics in microbial ecology", she said. "I am also inviting Dr. Rika Indri Astuti S.Si. M.Si. as the moderator today", she added.

Dr. Rika explained that this particular lecture substantially met the student needs in advanced microbiological data processing. "We do hope that the lecture will enrich the student knowledge in analyzing microbial community by using the metagenomic approach as well as improving the skill in computer literacy for bioinformatics analysis," she said. At first, Dirk Berkelmann explained the culture-dependent and independent approach to analyze microbial diversity in soil. "The culture-dependent approach needs living microbes to be analyzed later. In this case, we need to purify the microbes before conducting further analysis such as identification, investigation of unique metabolic properties in order to understand the role of the microbes in the environment ", he explained. On the other hand, the independent one only needs a pool of genomic DNA from an environmental sample for microbial community analysis, rather than the living microbes. "The two approaches have pros and cons, yet, we do need a comprehensive and reliable bioinformatics analysis mainly to dig and compare the microbial community data to the publicly available gene/genomic database".

The lecture session continued to a workshop "Metagenomic Sequence Data Analysis using R", on the following day. Participants were taught to use various computer program tools to analyze metagenomic data. Not only metagenomic data for phylogenetic and microbial community analysis, the participants were also learned to conduct functional microbial analysis based on transcriptomic data through various bioinformatic tools.