

Metagenomics Bioinformatics – Virtual course

European Molecular Biology Laboratory- European Bioinformatics Institute (EMBL-EBI)
02-06 November 2020

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Metagenomics Bioinformatics course was a five-day course (turned virtual because of COVID-19) offered by EMBL-EBI at Wellcome Genome Campus, Hinxton, UK. The course was mainly targeted on discussing the multiple ways of analysing the metagenomics data workflow with respect to newly developed pipelines leading to the final submission of the analysed data. The course was conducted through video lectures with more emphasis on group discussions over solving assignments. There were 30 participants from different countries all over the world, and we got to know each other from the flask talk with focus of explaining current research work.

How I/they prepared myself/me before the course: A notebook in OneNote, a Slack channel, a zoom room and a virtual machine (VM) to do practical were shared with all the participants.

Day 1: As it was the first day, I was introduced with all the course coordinators, instructors and fellow participants. Next, I attended a small networking event where participants were divided into groups and given a common problem to solve using our area of expertise. The lectures covered topics like quality control and host-decontamination (with a practice session in VM), metagenome-assembled genome (MAG) submission process to European Nucleotide Archive (ENA) and the last lecture focussed on different tools available to assemble short reads. I also introduced myself as a graduate student at NIG, and explained my research work on mice gut microbiome during flash talk session.

Day 2: This day, I attended two lectures about MGnify services. MGnify is an automated pipeline for the analysis and archiving of microbiome data to help determine the taxonomic diversity and functional & metabolic potential of environmental samples. There was also a practical session through VM on how to submit data and use MGnify. The last lecture was about how to analyse metagenomic data to strain resolution.

Day 3: This day, the lectures covered topics like metagenome assembly, binning, and MAG generation. Different pipelines and as well as programs were introduced, which we can be used to analyse metagenomic data. In the practical session, we were given a sample data and were taught how to analyse using the introduced pipelines.

Day 4: On the fourth day, different MGnify MAG resources were introduced along with hands-on experience with the usage. We also discussed protein annotation of the MAG generated by metagenomic analysis. And the last session was practical about the strain level analysis of the metagenome.

Day 5: This day, the concept of “comparative metagenome analysis” was introduced through theory as well as practical sessions with the emphasis on various tools combined with suitable statistical approaches for better analysis. The last session was dedicated for final question & answers regarding the topics introduced in this course.

Summary:

Overall, this course gave a good understating and training about the novel ways of doing metagenomics analysis. I also got good suggestions about my research work during the flash talk session. I really enjoyed the daily group activities where we can ask questions and solve the problems.