Overseas Practice on（Field Epidemiology・Collaborative Research）
report form（For Student）

30/11/2019 (Year/Month/Day)

Name	Wessam Mohamed Ahmed
Laboratory	Division of Bioinformatics
Year (Grade)	D4
Place of practice	Foundation of Edmund Mack, Italy
Period of practice	19/11/2019 - 29/11/2019
Purpose	To conduct an academic network with researchers in Italy To learn new technique that help me to improve my research.

Summary of activities（about 800 words, provide photos, tables and figures that clearly show the activities during the period）

Edmund Mack Foundation is a well-known research organization in the world, where Research and innovation center is a part. I conducted my overseas practice at the division of Computational biology under super vision of Professor Claudio Donate the head of this Division. His work group coordinated and performed several research projects integrating veterinary medicine with other disciplines, especially biology, ecology, epidemiology, spatial and mathematical modelling. This division have experts in spatio-temporal and Microbiome data analysis. Which can help me to improve my ongoing research and through my further career path.

I Introduce my research study to the lab members and discuss with them to hear their ideas. I discussed in detail with Dr Claudio about estimating the epidemiological parameters of H5N1 which can help me to improve my research.

I learnt a new technique for the microbiome data analysis and visualizations. In the division of computational biology, they have their own pipeline for microbiome data analysis. They devolved a software called micca (MICrobial Community Analysis), which is a software pipeline for the processing of amplicon sequencing data, from raw sequences to OTU tables, taxonomy classification and phylogenetic tree inference. The pipeline can be applied to a range of highly conserved genes/spacers, such as 16S rRNA gene. It characterizes the enormous biodiversity of the microbiome communities and understand the profound influence that they have on the ecosystem.

Also, I learnt how to visualize the microbiome abundance and the influence of different ecological factors on the microbiome abundance using R packages called Phyloseq. This package is very efficient R package, where we can calculate the relative abundance and/or the maximum abundance. Moreover, I learnt how to visualize the data through heatmap function.

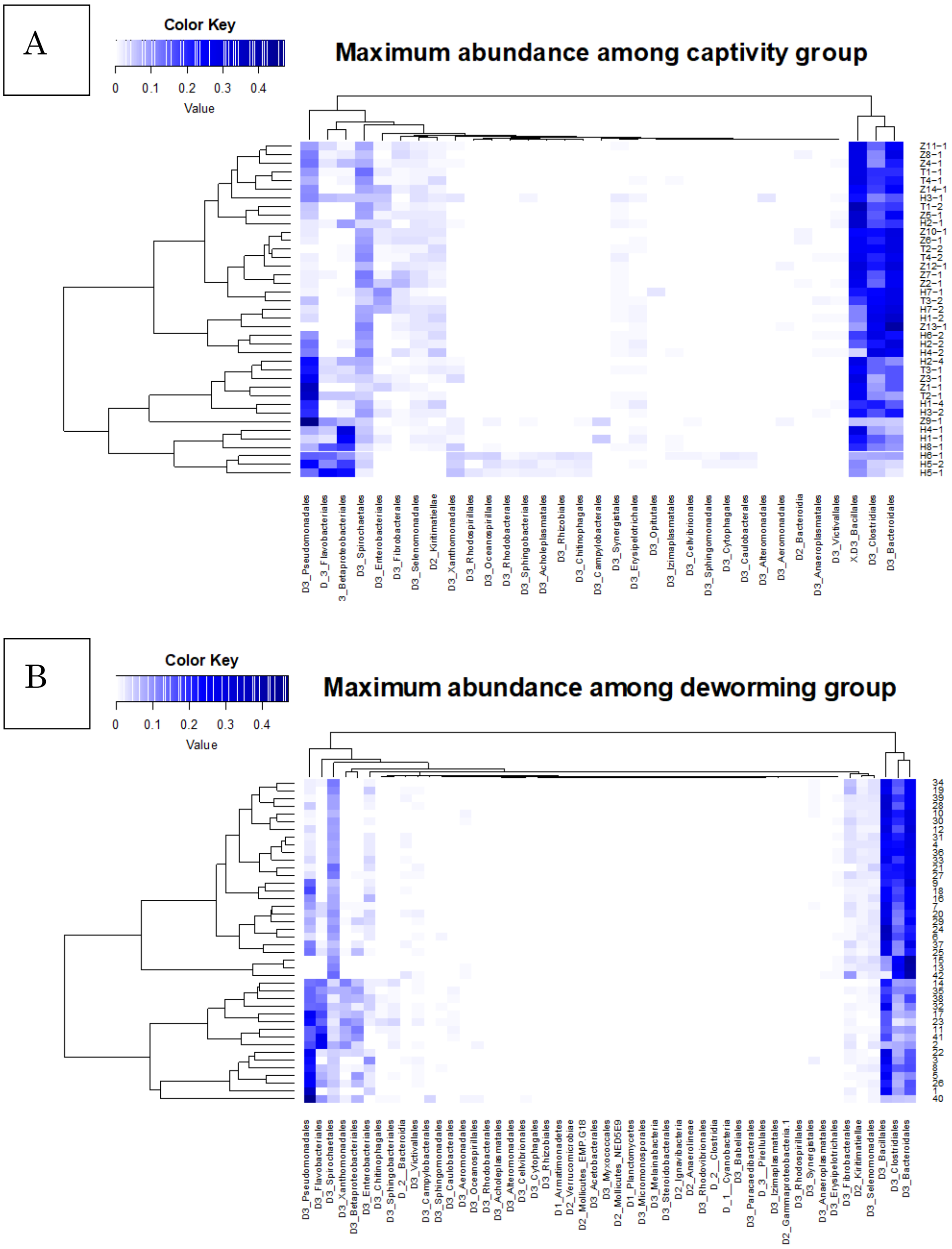

Figure 1. Heatmap of microbiome data. A) maximum abundance of the microbiome in samples of animals in captivity. B) maximum abundance of the microbiome in samples of animals after deworming.

（Field Epidemiology・Collaborative Research） Evaluation by supervisor

Institution・Official title・Name	Kimihito Ito	印

Describe overall evaluation on the applicant’s activity in overseas practice.

Ms. Wessam Mohamed have learned how to use the software called micca, which is developed by Professor Claudio Donate’s group. The experience will be useful for her future career development.

※1 The Steering Committee of the Leading Program will first confirm the content of this report and the report will be forwarded to the Educational Affairs Committee for credits evaluation.

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