

Prof Ir Dr Fatimah Ibrahim

Project no 1 Global microbial biodiversity of the human gut in Malaysia analysis (this project is in collaboration with MIT USA and UM). This project requires student has the statistical and computing knowledge.

The human body is a complex ecosystem, hosting tens of billions of bacteria, primarily in the gut^{1,2}. This community, known as the 'gut microbiome', is vital to human health, affecting functions ranging from metabolism, immunity, and development, to behavior^{3,4}. Conversely, reduced microbiome diversity and other imbalances of the gut community (dysbiosis) are associated with many diseases of the industrialized world, such as metabolic syndrome, asthma, and inflammatory bowel diseases among others^{5,6}. Microbiome-based interventions thus hold the potential to revolutionize our understanding of, and therapeutic approaches to, many aspects of human health and disease.

Despite many advances, current understanding of the human microbiome is largely limited to majority ethnic groups in industrialized nations, and does not reflect the full diversity of human commensal microbiota. In addition to the scientific ramifications of minority underrepresentation, there are significant translational and ethical implications as well: First, failing to capture the full diversity of healthy human microbiota may limit our ability to understand and generate effective therapeutics for many microbiome-associated diseases. Second, underrepresented groups are less likely to benefit from microbiome-based medical advances tailored to well-studied populations, propagating healthcare inequities.

The window of opportunity to characterize human microbiome diversity is closing rapidly. Human gut microbial diversity is diminishing around the globe, due to the spread of Westernized diets and lifestyles, which are associated with reduced microbiome biodiversity⁷⁻¹¹. As a result, human commensal microbes that have co-evolved with us for millions of years may soon go extinct. Preserving the full diversity of human commensal gut microbiota before it is lost thus represents an urgent imperative.

Objectives of the study

Database for stool samples have been collected to characterize the gut microbiomes of participants. Saliva samples will be collected to characterize the oral microbiome and the human DNA. Urine have been collected to characterize physiological metabolic markers. With stool, saliva and urine samples collected in Malaysia along with those collected worldwide, we aim to:

1. To Characterize the **global** microbial biodiversity of the human gut
2. To Determine to what extent human genetics vs. environmental sources and factors such as the oral microbiome, diet, geography, lifestyle etc. drive the composition of the human gut microbiome.

Project no 2 Analysis of novel microbial lipid biomarkers to elucidate the paleodietary (this project is in collaboration with MIT USA and UM)The Global Microbiome Conservancy) This project requires student has the statistical and computing knowledge.

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Objective of project no 2

Database for stool samples have be collected to characterize the gut microbiomes of participants. Saliva samples will be collected to characterize the oral microbiome and the human DNA. Urine have been collected to characterize physiological metabolic markers. With stool, saliva and urine samples collected in Malaysia along with those collected worldwide, we aim to:

1. To Characterize the **global** microbial biodiversity of the human gut
2. To Identify novel microbial lipid biomarkers to elucidate the paleodietary record.

Project no 3 Neural network modeling of glucose using bioimpedance technique. This project requires student has the statistical, matlab and computing knowledge.

This project presents an artificial intelligence modelling of glucose level using bioimpedance analysis technique. 821 subjects have been collected for the glucose test and bioimpedance measurement at University Malaya Medical Centre. An ongoing data need to be collected for further analysis and classification modelling. The data will be analysed using SPSS statistical software for analysing significant parameters towards high classification accuracy of glucose level with the bioimpedance parameters. The significant data will be fed into the various neural network techniques for training and testing to obtain the best classification model.