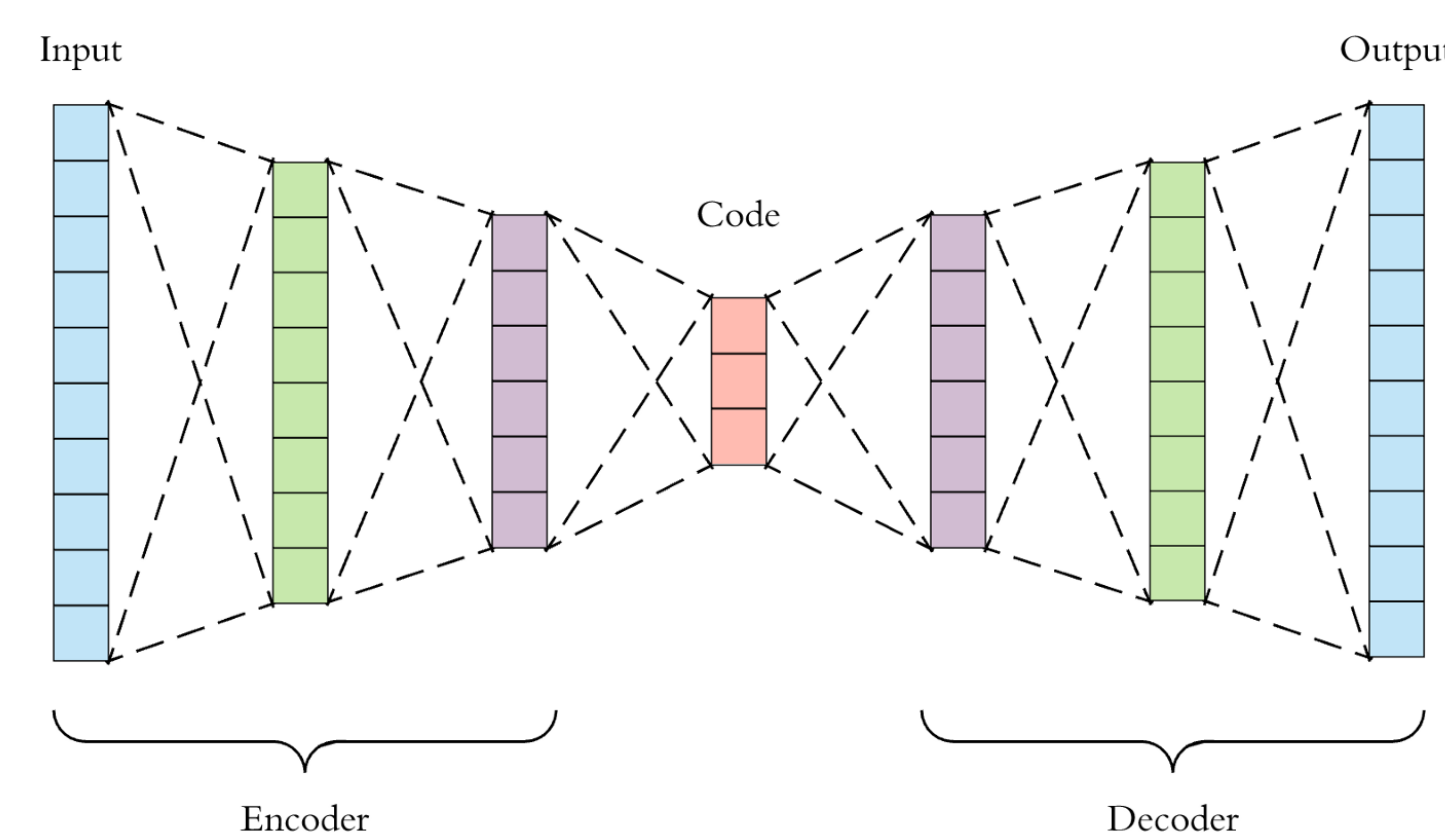


Defining the Healthy Optimal Australian Microbiome through Artificial Intelligence

Dr Xiaotao Jiang and Professor Emad El-Omar



Population level microbiome big data (Over 10,000 samples)

AI engine

Healthy Microbiome

Project Summary:

The human gut microbiome plays pivotal roles in human health and has been implicated in several diseases. Pre-emptive modification of the gut microbiome to prevent disease is certain to become the next frontier in medicine. An accurate definition of what constitutes a healthy microbiome will lay the basis for microbiome therapeutics. Current research defines a “healthy microbiome” based on samples from self-reported “healthy” participants. In our Healthy Optimal Australian Microbiome (HOAM) study, we applied a phenotypic first strategy to establish a cohort of optimally healthy Australians to define the healthy gut microbiome. Moreover, current methods mainly relied on association-based analysis to identify the health or disease-associated microbial taxa, which could be confounded by complex unknown factors. In this study, an ensemble learning method based on a collective of machine learning algorithms including traditional methods of random forest, support vector machine, logistic regression, and deep learning (autoencoder which is artificial neural network used to enable unsupervised learning) will be applied to define the optimal healthy microbiome state. Apart from the HOAM cohort, we have established a global gut microbiome catalogue that contains over 10,000 human gut microbiomes that will be used to help improve the model and selection of healthy microbiomes.

Detail research activities that are involved in this project:

- 1) Microbiome analysis with MRC bioinformatics pipeline
- 2) Several machine learning algorithms will be used to analyse the HOAM cohort and global gut catalogue.
- 3) Use autoencoder to perform feature selection and clustering
- 4) Apply the ensemble framework to generate a best performance model for the healthy microbiome
- 5) The outcome of a collection of microbial signatures that defining the healthy optimal microbiome from different perspectives.

MRC support:

MRC has established powerful high performance computing facilities and have access to Katana and NCI GPU nodes for deep learning. The global human gut microbiome catalogue has already been established from another NCI supported computing project. Hence, no further huge amounts of microbiome works will be need for this huge cohort. We also have AI support from Dr. Wei zhang from Baidu AI team.

Student role: the student will help to run different machine learning algorithms on the established HOAM and Global Human Gut Microbiome Catalogue to define the healthy microbiome. This work will generate very high impact publications.

Capabilities developing for student:

- 1) Understanding and application of various machine learning algorithms on big microbiome data
- 2) Develop bioinformatics skill and microbiome knowledge
- 3) Learn deep learning techniques and ensemble learning skills.

Importance statement:

Current research has associated gut microbiome with several dozen diseases or symptoms, even with COVID 19 infection and severity. Patients' gut microbiomes are generally in different levels of dysbiosis. However, the field still lacks a clear definition of healthy microbiome. The healthy microbiome should work as basis of a healthy status and target for directing microbiome-based therapy, which is promises to be the next generation medicine. A clear definition of the healthy microbiome will lay a solid foundation for microbiome interventions.

This research project is being conducted at St George & Sutherland Clinical school, Kogarah.

If you are interested in this project, please email:

Professor Emad El-Omar at e.el-omar@unsw.edu.au or Dr Xiaotao Jiang xiaotao.jiang@unsw.edu.au