INTO THE GUT MICROVERSE
Gut microbiome and metabolome in human health and diseases

Project Proposal by Nissy Milcia William and Shourya

MOTIVATION:

Microbiome is the collection of microbes occupying a habitat and metabolome is the collection of metabolites in a biological space. Changes in the gut microbiome and the metabolome have been associated with human health and diseases. Characterisation of the human faecal microbiome and the associated metabolome could provide the opportunity to develop diagnostic approaches and personalized medicine for human diseases such as IBD, CRC, etc.

IDEA:

We intend to study the gut **microbiome** and **metabolome** composition across various "healthy" and "disease inflicted" samples and find any patterns regarding the variation, diversity and abundance of the bacteria and their metabolites. This correlation could be used to predict if an individual is at risk for specific diseases.

DATASET:

Github Repository of Borenstein Lab, Tel Aviv University, https://github.com/borenstein-lab/microbiome-metabolome-curated-data.git. Other articles if the need arises.

BASELINES TO BE IMPLEMENTED:

- Data Preparation: Collect and weight features
- Data Exploration: Study and divide data, consider K-Fold validation if needed.

Machine Learning Models: Apply the dimensionality reduction if needed, implement neural networks and K-Nearest Neighbors (KNN), further analyze the data and then choose the best suited algorithms

WORK TO BE DONE BY MIDWAY:

- Selection of appropriate model/s
- Explore QIIME for microbiome data, learn R programming.
- Stay updated on libraries, plugins, and methodologies in bioinformatics and machine learning.

TEAMMATE WITH WORK DIVISION:

Nissy will look after data management and coding part of the project, whereas Shourya will gather the domain knowledge, both will do the data analysis and look for better Machine learning models.

EXPECTED RESULTS:

Classification of disease afflicted samples based on signature microbiomic as well as metabolic data and correlation with the host metadata is expected to give more robust and accurate results.

RELATED PAPERS:

Multi-omics of the gut microbial ecosystem in inflammatory bowel diseases, https://doi.org/10.1038/s41586-019-1237-9 (2019). Gut microbiome structure and metabolic activity in inflammatory bowel disease, https://doi.org/10.1038/s41564-018-0306-4 (2018). Fecal Metabolomic Signatures in Colorectal Adenoma Patients Are Associated with Gut Microbiota and Early Events of Colorectal Cancer Pathogenesis, https://doi.org/10.1128/mbio.03186-19 (2020). Fecal Microbiota, Fecal Metabolome, and Colorectal Cancer Interrelations, https://doi.org/10.1371/journal.pone.0152126 (2016). Metagenomic and metabolomic analyses reveal distinct stage-specific phenotypes of the gut microbiota in colorectal cancer, https://doi.org/10.1038/s41591-019-0458-7 (2019). Identification of biomarkers to diagnose diseases and find adverse drug reactions by metabolomics, https://doi.org/10.1016/j.dmpk.2020.11.008 (2020). Faecal microbiome-based machine learning for multi-class disease diagnosis, https://doi.org/10.1038/s41467-022-34405-3 (2022). Learning representations of microbe-metabolite interactions, https://doi.org/10.1038/s41592-019-0616-3 (2019).