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Predicting the functional potential of the gut microbiota in covid-19 severity using 16s rrna data

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Thile COVID-19 spread globally, the role of the gut microbiota in patient outcomes has remained an area of exploration especially in resource limited settings. This study compared the functional potential of the gut microbiome in Ugandan patients with severe COVID-19 disease compared to mild cases. Furthermore, machine learning (ML) models were used to assess the predictability of the gut microbiota in COVID-19 severity. 16S rRNA gene sequencing was performed on stool samples from confirmed COVID-19 patients including 34 mild cases and 47 severe cases. Data processing steps, including quality control, normalization, taxonomic classification, and other preparatory analyses, were conducted using a single QIIME 2 pipeline. Functional predictions were made using PICRUSt2 while differential abundance analysis of the pathways was done using DESeq2 package in R. To assess the predictive value on the severity of COVID-19 disease, normalized counts of three highly significant pathways were used as input in machine learning models. The dataset was divided into two (8:2), for training and testing respectively. Several models, including Random Forest, Support Vector Machine (SVM), and Gradient Boosting, were evaluated. Hyperparameter tuning and 10-fold cross-validation were used to optimize model performance. There were 52 significantly differentially abundant pathways (padj <0.05) between mild and severe cases. Among those, only three had a positive log2FoldChange above 2, implying they were significantly higher in severe cases compared to mild cases. These were the Peptidoglycan Biosynthesis V, the Superpathway of Geranylgeranyldiphosphate Biosynthesis, and the Mevalonate I Pathways (log2FoldChange = 2.68, 2.24 and 2.23 respectively). The Gradient Boosting model achieved the highest performance in predicting severity with an accuracy of 73.33% (95% CI: 44.9% to 92.21%). These findings suggest that alterations in the gut microbiome and its functional potential contribute to the severity of COVID19. The abundance of specific functional pathways can moderately predict the severity of COVID-19.

Biography

Christopher is a Data Scientist at the intersection of Bioinformatics & AI. He is passionate about Big Data, Disease Modelling, Drug Discovery and Biostatistics. He transforms complex biological and health care data into actionable insights using machine learning and cutting-edge tools.

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