

# Towards reliable prediction of significant changes in microbial communities based on time series data

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Changes in the microbiome can be an indicator of the onset of an infectious disease such as sepsis. The ability to distinguish these significant changes from naturally occurring fluctuations in the microbiome could aid in the early detection of potentially harmful diseases. We aim to take a step toward this prediction of microbial abundance trends based on analysis of 16S rRNA data. To this end, we apply Long Short-Term Memory (LSTM) models to publicly available long-term microbial time series data from two healthy subjects. To increase the explanatory power of the model, Shapley Additive Explanations (SHAP) is used for feature significance analysis. So far, the model has shown good performance in predicting the overall abundance of bacterial genera in the samples from the healthy subjects. We plan to test different model architectures and extend the model to other data types such as environmental data. Our overall goal is to optimize early therapeutic approaches and provide a treatment advantage to physicians and patients on the one hand, and to create an environmental monitoring system on the other.

## Keywords

Machine learning

## Registration-ID code

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## Professional Status of the Speaker

PhD Student

## Junior Scientist Status

Yes, I am a Junior Scientist.

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