Antibiotic interactions in treatment of chronic lung disease

Data Science | Computational Systems Biology | Human Microbiome | Complex Systems | Antibiotics | Cystic Fibrosis

Project description

Bacterial infections cause millions of deaths each year in people with chronic lung diseases, such as COPD, fibrosis, or cystic fibrosis (CF). These lungs show marked dysbiosis, pathological imbalances of the lung microbiota that cause acute pulmonary exacerbations (PEx). PEx accounts for irreversible lung function decline and high mortality in these collectives. Patients receive extensive, combined antibiotic treatments, both as maintenance therapy and to counteract acute PEx. Treatment success varies however and is apparently dependent on the present lung microbiome, the type of dysbiosis and the cocktail of antibiotic substances employed.

In the frame of an observational study on persons with CF, an extensive collection of lung microbiome dynamics (time series) has been gathered, together with clinical information on the precise therapies. To analyze the effect of therapy on individual bacterial organisms in different microbiome backgrounds, we have established a prototype Bayesian model that allows to predict treatment outcomes for individual antibiotics**. In the present MSc project**, we propose to generalize this model and **study possible positive or negative effects that are generated by interactions among therapeutic substances.** The MSc thesis is expected to **advance the understanding and prediction of real therapeutic outcomes** in clinically relevant field and could ideally **contribute to a scientific publication**.

Requirements

- Basic knowledge of data modeling and statistics (statistical testing, interest in linear mixed models, Bayesian models, time series models)
- Programming in R or Python
- Interest in microbiome research
- Context knowledge of sequence bioinformatics
- Spoken and written English

Duration

25 weeks (30h) / 30 ECTS

Supervisor & contact details

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