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## Assessment of antibiotic resistance from microbial genomic data

Increasing antibiotic resistance of disease-causing microbes poses a major public health problem. Resistance is caused by evolutionary changes in the microbial genome that inactivate the antibiotic's molecular mechanism of action. For diseases such as tuberculosis, single genetic variants that confer resistance are known and considered in treatment regimes. For other pathogens, relationships between variants and resistance are often not known and assessed by time-consuming lab-experimental assays. Here we focus on infection-causing *Haemophilus influenzae*. We perform regression analyses to identify genetic variants that are associated with lab-based resistance measurements. We find that single variants are not sufficient to explain resistance. Thus, we are currently identifying associated variant combinations and investigate suitable machine learning approaches for predicting resistance from the entire genome.

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### Keywords

microbial genome-wide association study  
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