Navigating Anti-Microbial Resistance (AMR) using multi-modal data analysis

Prof. Jacob Moran-Gilad, Department of Health System Management, Faculty of Business & Management
Prof. Lior Rokach, Department of software and Information Systems Engineering, Faculty of Engineering Sciences, Ben-Gurion University of the Negev, Beer-Sheva, Israel

Technology

Prof. Rokach and Prof. Moran-Gilad are working together on a multi-model AI-based solution for prediction of antimicrobial resistance and precision microbiology. Antimicrobial resistance (AMR) is a key challenge to medicine worldwide. Currently, AMT detection is based on phenotypic determination of minimum inhibitory concentrations (MIC) of antimicrobials. This is time-dependent laboratory assays. The MIC values are interpreted according to international guidance that considers *in vitro* and clinical data on treatment success/failure and pharmacological data (PK/PD). The clinical decision-making is based on the lab results and other considerations such as the site of infection, clinical severity, and patient characteristics. Moreover, whole-genome sequencing (WGS) of bacteria is becoming the new gold standard for bacterial characterization (including resistance analysis). However, genotype-to-phenotype inference of resistance is very limited and there are only a few methods for predicting MICs from sequences. Moreover, while outcome prediction based on clinical data analysis is a rapidly developing field, no research integrates microbial genomics, clinical and pharmacological data. A multi-modal approach as being developed in the current project that combines genomics, clinical and pharmacological data is the key for paving the way for precision microbiology, tailoring treatment according to genomic based prediction. Their AI-driven solution combines clinical microbiology, bioinformatics, and machine learning approaches to improve the detection and management of antimicrobial-resistant infections: (1) Novel ML-based methods for prediction of MIC and susceptibility from genomic sequences using large genomic datasets; (2) Methods for incorporating epidemiological data to focus bioinformatics and predictive analytics work; (3) A recommender system that takes into consideration both pharmacological and clinical data to improve treatment selection and safety.

Application

G_2P_2S is a genotype-to-phenotype-to-service that can be implanted in the clinic laboratories. This is a data science driven solution that combines clinical microbiology, bioinformatics and machine learning to improve the detection and management of AMR infections.

Advantages

- Rapid analysis and decision-support for management of difficult-to-treat cases
- Exploring new drug treatment combinations and individualized tailoring of treatment
- Generate institutional /regional /national treatment guidance and policy
- Lay the foundation for culture independent diagnostic solutions by further development into metagenomics platforms

Patent

A patent covering the invention was filed by BGN technology