



GÖTEBORGS UNIVERSITET

New AI-based methods for studying antibiotic-resistant bacteria

Juan Salvador Inda Díaz

Institutionen för matematiska vetenskaper
Naturvetenskapliga fakulteten

Akademisk avhandling för filosofie doktorsexamen i Matematik, inriktning tillämpningar, som med tillstånd från Naturvetenskapliga fakulteten kommer att offentligt försvaras fredag den 24 november, 2023 kl. 09.00 i Euler, Institutionen för matematiska vetenskaper, Chalmers tvärgata 3, Göteborg.

ISBN: 978-91-8069-503-9 (PRINT)

ISBN: 978-91-8069-504-6 (PDF)



GÖTEBORGS UNIVERSITET

Abstract

Antibiotic resistance is a growing challenge for human health, causing millions of deaths worldwide annually. Antibiotic resistance genes (ARGs), acquired through mutations in existing genes or horizontal gene transfer, are the primary cause of bacterial resistance. In clinical settings, the increased prevalence of multidrug-resistant bacteria has severely compromised the effectiveness of antibiotic treatments. The rapid development of artificial intelligence (AI) has facilitated the analysis and interpretation of complex data and provided new possibilities to face this problem.

This is demonstrated in this thesis, where new AI methods for the surveillance and diagnostics of antibiotic-resistant bacteria are presented in the form of three scientific papers.

Paper I presents a comprehensive characterization of the resistome in various microbial communities, covering both well-studied *established* ARGs and *latent* ARGs not currently found in existing repositories. A widespread presence of latent ARGs was observed in all examined environments, signifying a potential reservoir for recruitment to pathogens. Moreover, some latent ARGs exhibited high mobile potential and were located in human pathogens. Hence, they could constitute emerging threats to human health.

Paper II introduces a new AI-based method for identifying novel ARGs from metagenomic data. This method demonstrated high performance in identifying short fragments associated with 20 distinct ARG classes with an average accuracy of 96%. The method, based on transformers, significantly surpassed established alignment-based techniques.

Paper III presents a novel AI-based method to predict complete antibiotic susceptibility profiles using patient data and incomplete diagnostic information. The method incorporates conformal prediction and accurately predicts, while controlling the error rates, susceptibility profiles for the 16 included antibiotics even when diagnostic information was limited.

The results presented in this thesis conclude that recent AI methodologies have the potential to improve the diagnostics and surveillance of antibiotic-resistant bacteria.

Keywords: Transformers, Antibiotic Resistance, Infectious Diseases, Metagenomics, Data-driven Diagnostics