Development of a Machine-learning Model to Predict Resistance of Empiric Antibiotics using Urine Culture and Antibiotics Susceptibility Data

Chungsoo Kim¹, Rae Woong Park¹, ², *, Sandy Jeong Rhee³, *
¹Department of Biomedical Sciences, Ajou University Graduate School of Medicine, Suwon, Republic of Korea; ²Department of Biomedical Informatics, Ajou University School of Medicine, Suwon, Republic of Korea; ³College of Pharmacy, Ewha Womans University, Seoul, Republic of Korea;
*Co-corresponding authors

Introduction

Background
- Challenges for an empiric antibiotic therapy
  - It is difficult to prescribe appropriate antibiotics before culture and antibiotic susceptibility test
- Previous studies
  - Models showed low discrimination (AURDC 0.60-0.70) and lack of calibration.
- Local antibigrams
  - Useful tools for selection of appropriate empiric antibiotics, however, they are not well adapted.

Objectives
- To develop models for predicting antibiotic resistances using patients' medical history, culture results, antibiotics susceptibility test results, and local antibigram.

Methods

Study Population
- By AISUM database (2.7M, 1998-2020)
- Suspected urinary tract infection ≥18 years old
- Hospitalization (min 3 days)
- Having a urine culture result

Outcome
- Resistant (Unsusceptible) isolated events

Predictors
- Candidate predictors
  - Demographics, condition, drug, measurement, procedure, visit and local antibigram data
- Variable selection
  - Lasso shrinkage
  - 2-Model selection based on clinical guidelines

Table 1. Final covariates for the developed prediction model

Table 2. Performance of antibiotic resistance prediction models

Figure 1. Predictive modeling approach to improve the empirical antibiotic prescribing process

Figure 2. Discrimination and calibration curves of antibiotic resistance prediction models

Abbreviations
- AMC: amoxicillin-clavulanate; AMP: ampicillin; AMS: amoxicillin-sulbactam; CAZ: cefazolin; CIP: cefepime; CIP: ciprofloxacin; CRD: cotrimoxazole; FOF: fosfomycin; GEN: gentamicin; PPT: piperacillin-tazobactam; SXT: trimethoprim-sulfamethoxazole; TET: tetracycline; AURDC: area under the receiver operating characteristic curve; AUPRC: area under the precision-recall curve

Footnotes
- "NA" indicates no change

Conclusion
- We developed machine-learning models for predicting antibiotic resistance having promising discriminations and excellent calibration performances. It would contribute to the proper selection of empiric antibiotics susceptibles.

Acknowledgment
- This work was supported by the Bio Industrial Strategic Technology Development Program (20038833, 20005021) funded by the Ministry of Trade, Industry & Energy (MOTIE, Korea) and a grant from the Korea Health Technology R&D Project through the Korea Health Industry Development Institute (KHIDI), funded by the Ministry of Health & Welfare, Republic of Korea [grant number: HR18C0001]. This work was supported by the Ministry of Science and ICT (MIST) [2020012A2C1009224] and by Basic Science Research Program funded by the Ministry of Education (NRF-2020R1A6A1A03043528) through the National Research Foundation of Korea (NRF).

Conflict of Interest
- We have no conflict of interest. Contact: sandy.rhee@ajou.ac.kr; vertic@snu.ac.kr; FWPW