Objective

To predict the MIC values for four -lactam agents for *E. coli* and *K. pneumoniae* isolates using MIC and genomic data from the SENTRY Antimicrobial Surveillance Program using the Random Forrest machine learning algorithm.

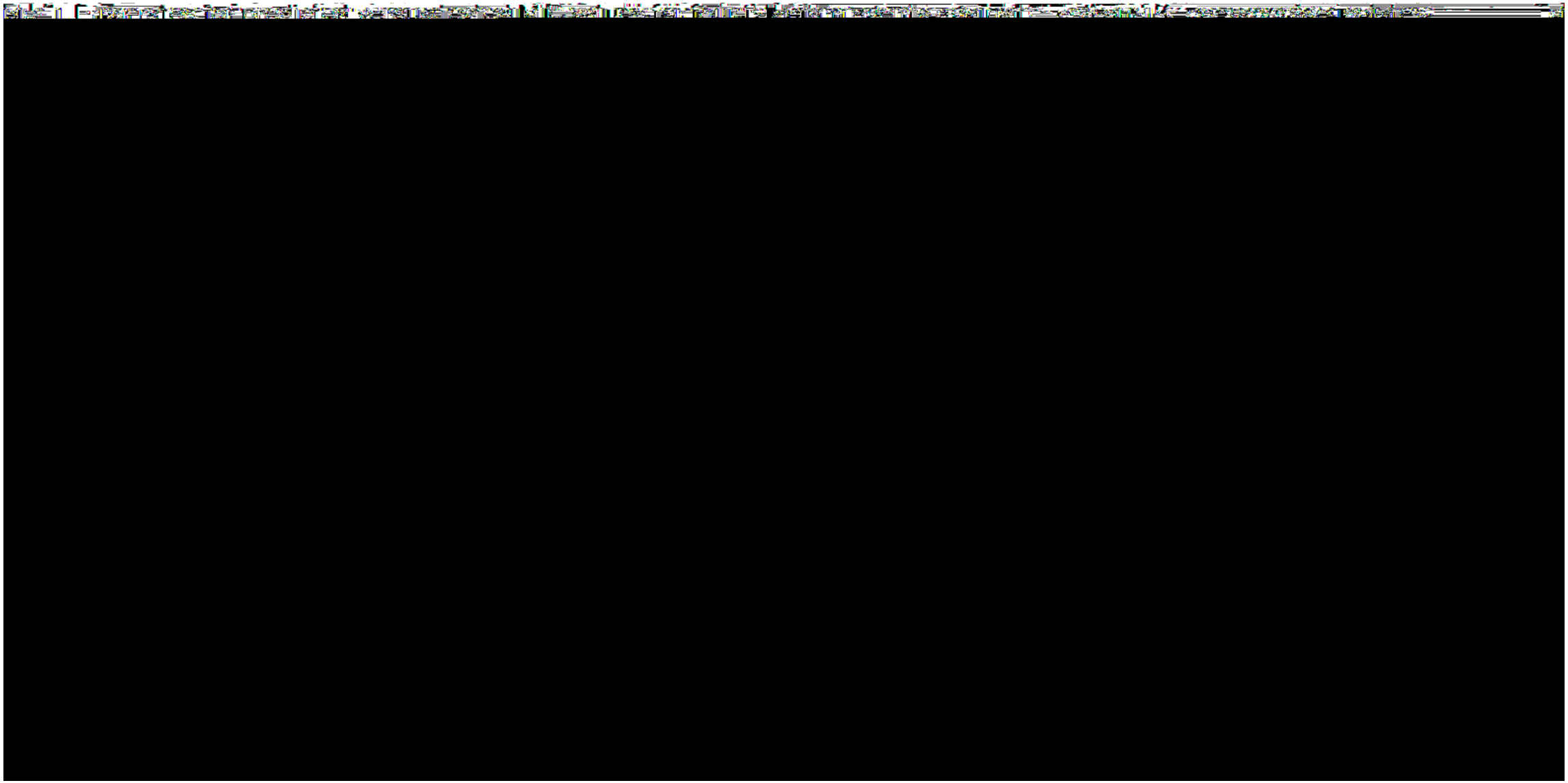
Methods

A total of 3054 *E. coli* and 2940 KPN isolates from 2016 and 2017 were susceptibility tested using the CLSI reference broth microdilution method.

Isolates displaying -lactam and/or aminoglycoside resistance were submitted to whole genome sequencing for the identification of genes encoding -lactamases.

MIC and genetic results from 2016 and 2017 were used to train the Random Forrest machine learning algorithm.

Results



Conclusions

Among machine learning prediction methods, the Random Forrest algorithm is capable of learning complex data representations to make accurate predictions that generate random decision trees.

The Random Forrest machine learning algorithm was able to predict MICs for ceftriaxone for *K. pneumoniae* with acceptable error rates.

For other cephalosporins, ECVs generated acceptable error rates, but not clinical breakpoints.

Meropenem MIC predictions had high error rates, potentially due to the small sample of carbapenem-resistant isolates in the studied population.

Machine learning algorithms should be further explored to predict MIC results, but the use of breakpoints that are established from clinical outcomes and PK/PD outcome studies might not be ideal to interpret these predictions.

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