Applying Association Rule Mining to the Analysis of Multidrug Resistance Patterns Using Phenotypic and Genotypic Indicators

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Agricultural antimicrobial use may lead to the emergence of multidrug resistant microbes in food animal populations and at subsequent levels of the food chain. Multidrug resistance (MDR) poses a unique threat by limiting or eliminating treatment options for animal and human illness. We applied association rule mining to the analysis of MDR patterns of *E. coli* sourced from retail meat products produced from cattle. Data were retrieved from the National Antimicrobial Resistance Monitoring System to include 4586 isolates tested against 12 to14 antimicrobials, spanning 17 years from 2002 to 2019. Association rule mining requires several methodological decisions to be made by the modeler including which quality measures are used to evaluate rules, how many rules are necessary to describe the sample, and the selection of quality measure thresholds. We explored a set of data-driven approaches to making these decisions. Quality measures were selected based on a combination of a principal component analysis and a consideration of the mathematical properties afforded by the candidate measures. The minimum number of rules required to represent the sample was determined by a procedure inspired by rarefaction analysis, and quality measure distributions were examined to select thresholds. Results are discussed in terms of how MDR patterns vary across years, sources, and how associations based on phenotypic indicators compare with those based on genotypic indicators.