Development of an Automated Process for Antibiogram Generation

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Abstract

Background: CLSI recommends the use of antibiograms to track the incidence of antimicrobial resistance. Antibiograms are arduous to develop and require a significant time commitment. The purpose of this study was to develop a quick and reliable process to generate institutional antibiograms.

Methods: Antimicrobial susceptibility testing data from 1/1/14 through 12/31/14 were obtained from the clinical microbiology laboratory for antibiogram creation. An algorithm was created to handle susceptibility data using open-source programs (RSstudio v0.98 and R v3.1.2). Original raw data contain observations for multiple facilities, surveillance cultures, and multiple observations for individual isolates. Data were initially cleaned by selecting the locations of interest, eliminating surveillance cultures (i.e., axilla, groin, nares/perirectal swabs), and eliminating exact duplicate observations. Data were then transposed from “narrow” format into “wide” format with only one row for each observation. This “semi-clean” data still contains multiple observations per isolate, duplicate isolates, and many “missing” values generated by the transposition process. The final clean dataset is generated by combining multiple observations into one primary observation. This is accomplished by combining testing methods (E-test® and MIC), selecting the first isolate of the year, and removing duplicated isolates by selecting the more resistant biotype. CLSI breakpoints are applied to the current data and percent susceptible is calculated for each drug and organism to generate the antibiogram, which may undergo post-processing for optimal visual interpretation of antibiogram results.

Results: Antibiogram generation was significantly faster after development of the algorithm. Prior to algorithm development, the antibiogram was developed manually using Microsoft Excel®, taking approximately one month. The algorithm produces a completed antibiogram with CLSI interpretations of the MIC data in less than 60 minutes from raw data.

Conclusion: Antibiogram development can be significantly streamlined through the use of open-source data science technology. Automated antibiogram generation functionally significantly reduces the time and resource commitment of previous antibiogram creation processes.

Objective

Develop a quick and reliable process to generate institutional antibiograms while minimizing time required by the practitioner

Methods

• Antimicrobial susceptibility data from 1/1/14 through 12/31/14 were obtained from the clinical microbiology laboratory (Sunquest®)
• CLSI breakpoints (M100-S24) and antibiogram guidance (M39-A4) were utilized in the creation of all antibiograms
• A conventional antibiogram was created using Microsoft Excel® to compare results to the automatic algorithm
• All automated antibiogram processes were conducted using RStudio v0.98 (RSstudio: Integrated Development for R. RStudio, Inc., Boston, MA) and R v3.1.2 (R Foundation for Statistical Computing, Vienna, Austria)
• All susceptibility testing was performed via BD Phoenix 2® E-test®

Methods (continued)

Figure 1: Raw microbiology data
• Multiple facilities represented in data
• Surveillance cultures present
• Many observations per isolate

Table 1: Organism, drug, MIC, and breakpoints

<table>
<thead>
<tr>
<th>Organism</th>
<th>Drug</th>
<th>MIC (μg/mL)</th>
<th>Breakpoints</th>
</tr>
</thead>
<tbody>
<tr>
<td>KLEBSIELLA PNEUMONIAE</td>
<td>AM</td>
<td>16</td>
<td>≤4</td>
</tr>
<tr>
<td></td>
<td>CAZ</td>
<td>4</td>
<td>≤6</td>
</tr>
<tr>
<td></td>
<td>SS</td>
<td>16</td>
<td>≤4</td>
</tr>
<tr>
<td></td>
<td>TMP/SMX</td>
<td>16</td>
<td>≤8</td>
</tr>
<tr>
<td></td>
<td>R</td>
<td>16</td>
<td>≤4</td>
</tr>
</tbody>
</table>

Results

Figure 2: Semi-clean data
• Multiple observations for each isolate (different testing methods)
• Multiple isolates per patient
• Character values in numeric columns
• Many “missing” values for each isolate

Figure 3: Clean isolated data
• One observation per isolate/patient with useful MIC values
• CLSI breakpoints applied to raw data

Figure 4: Completed antibiogram

Antibiogram generation:
• Percent susceptible, intermediate, and resistant calculated for each drug-organism combination
• Compiled into antibiogram format
• Post-processing for visual interpretation
• Exported as an Excel document for sharing