

Antibiogram Resistance Pattern Detection And Tracking

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Background

- The antibiogram test results provide the drug resistance status of the patient. It can be represented as a vector with the following resistance states:
 - NULL—the resistance is unknown
 - Sensitive (S)—the patient is not resistant to the drug
 - Intermediate (I)—the patient is in the intermediate state, but generally not resistant to the drug
 - Resistant (R)—the patient is resistant to the drug
- Figure 1 shows a sample antibiogram test result.

Drug	Amoxicillin	Clindamycin	Erythromycin	...	Vancomycin
State	NULL	I	R	...	S

Figure #1

- To effectively track the spread of the pathogen it is critical to identify significant spatio-temporal patterns in antibiogram resistance.

Results

- Significant rules found so far include:

Ampicillin/sulbactam -> Oxacillin	Ciprofloxacin & Penicillin -> Oxacillin
Levofloxacin -> Ciprofloxacin	Ciprofloxacin & Penicillin -> Cefazolin
Ampicillin -> Penicillin	Clindamycin -> Erythromycin
Cefazolin -> Oxacillin	Erythromycin & Penicillin -> Oxacillin
Ceftriaxone -> Amoxicillin/clavulanate	Clindamycin -> Levofloxacin

- Example: spatial distribution of rule based on HSA city (figure 5).

2003 Erythromycin & Penicillin -> Oxacillin

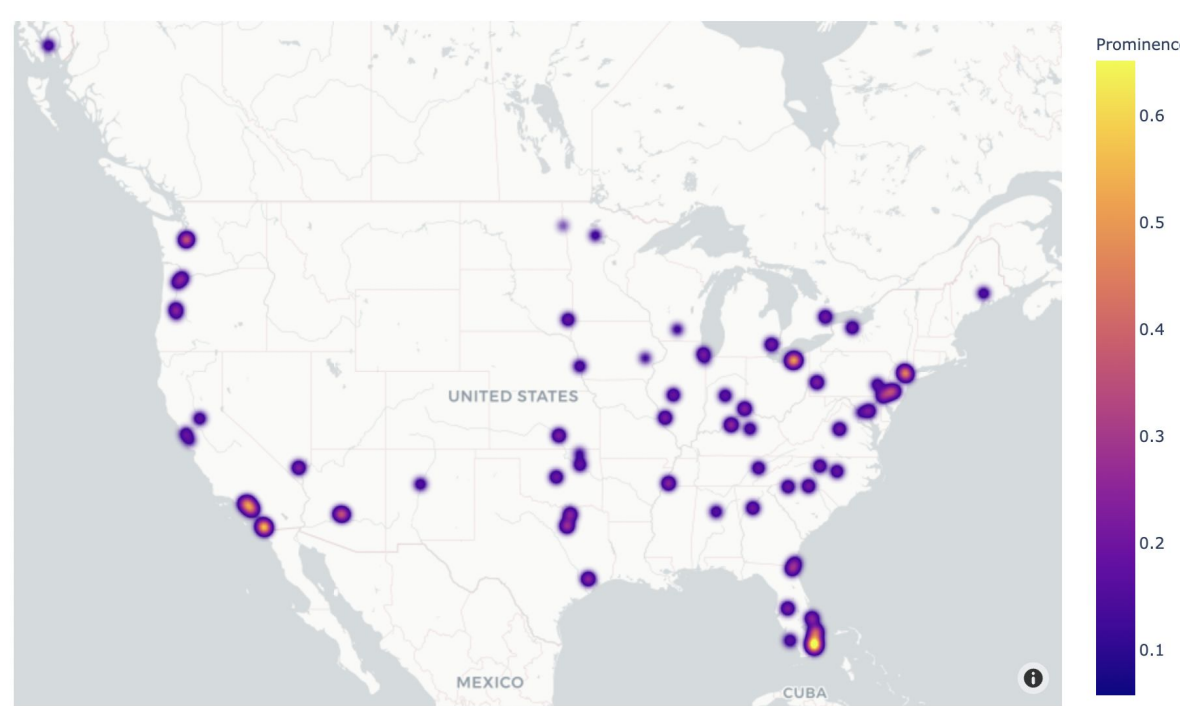


Figure #5

- Studied temporal distribution of mined rules (figure 6).

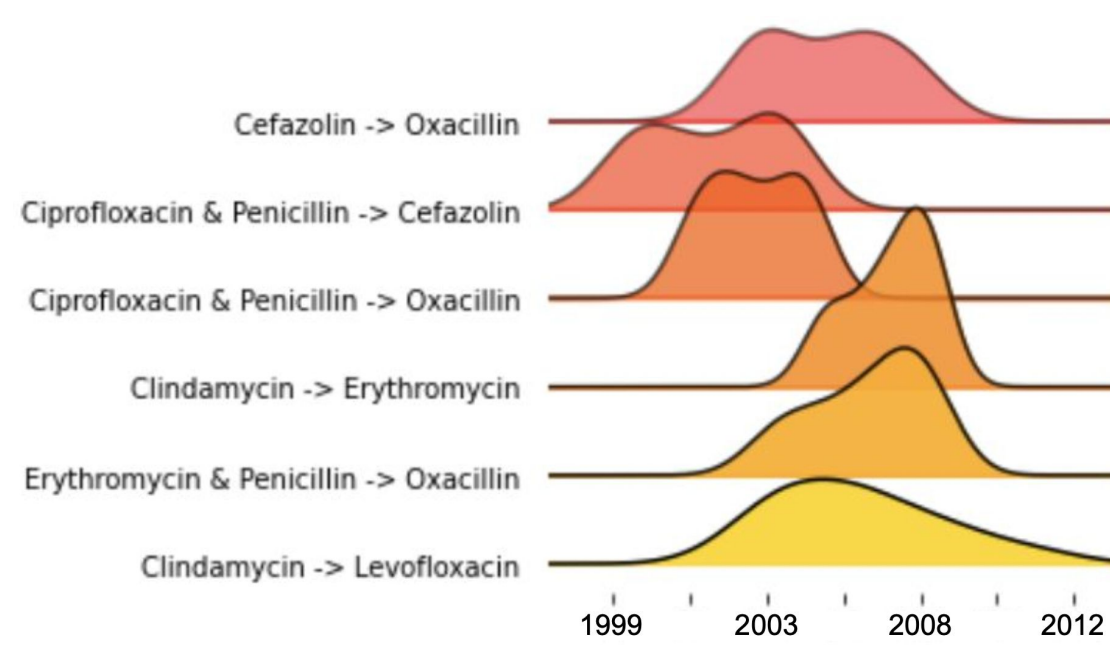


Figure #6

- Using the haversine formula, the shortest distances between HSA cities were found based on the geocoded data.
- A spatial network of HSA cities was constructed (figure 7), treating each HSA city as a node and an edge exists between two cities that are geologically adjacent.
- Studied significant pattern flow on the spatial network.

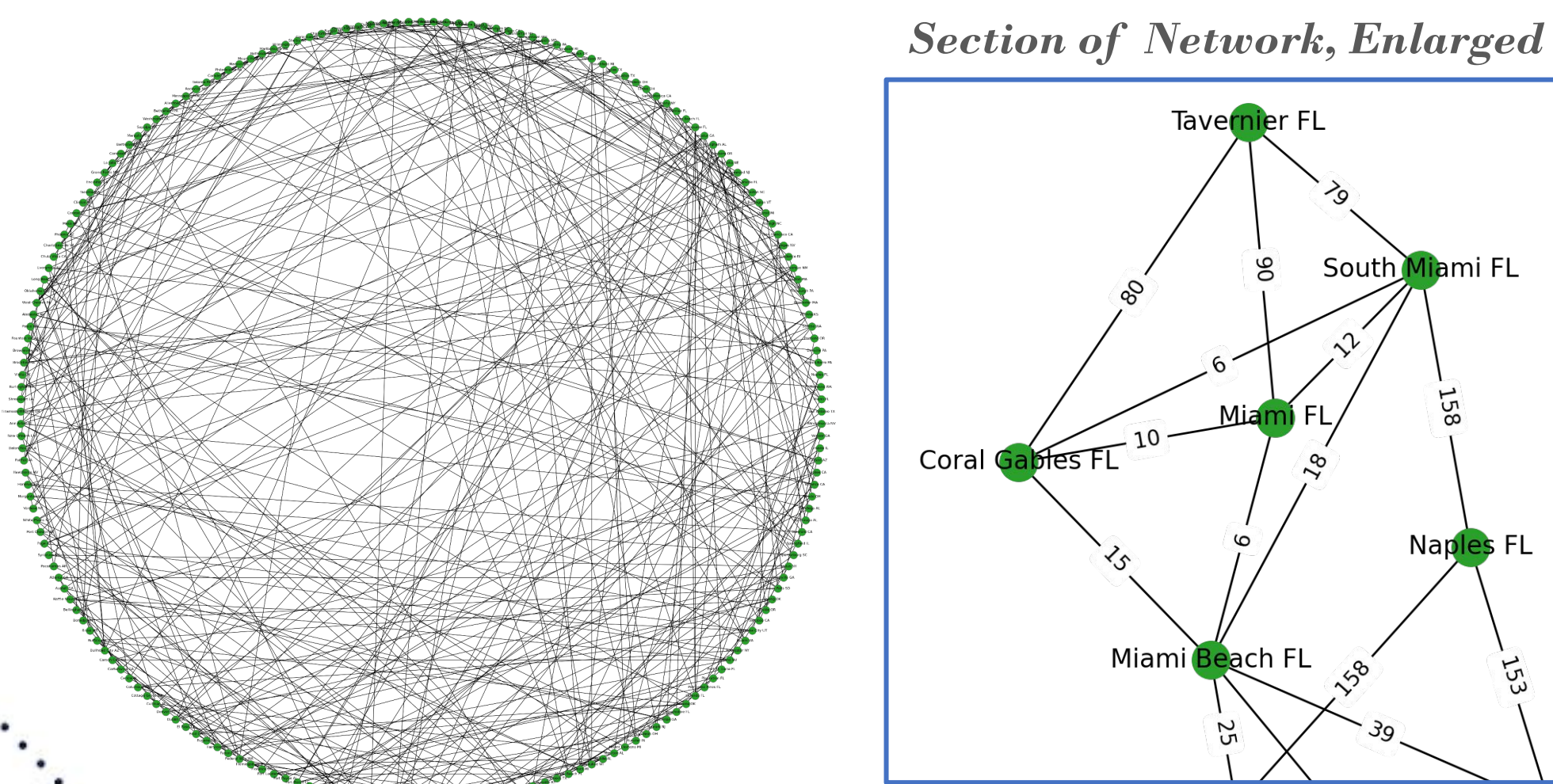


Figure #7

Project Goals

- Run association data mining tools on the data to find dependencies between antibiotic drugs.
- Track the spread of these dependencies over time and space.
- Use these results to find methods of predicting the spread of antibiotic resistance in the future.

Current Work

- Dataset contains 2.5 million antibiogram test results across 14 years (1999-2012) for 22 drugs tested on Staph Aureus.
- Spatially partitioned raw data into HSA cities based on Dartmouth Atlas Data using zip codes.
- Some cities are missing data for certain years and each year has some cities with < 100 records (figure 2).

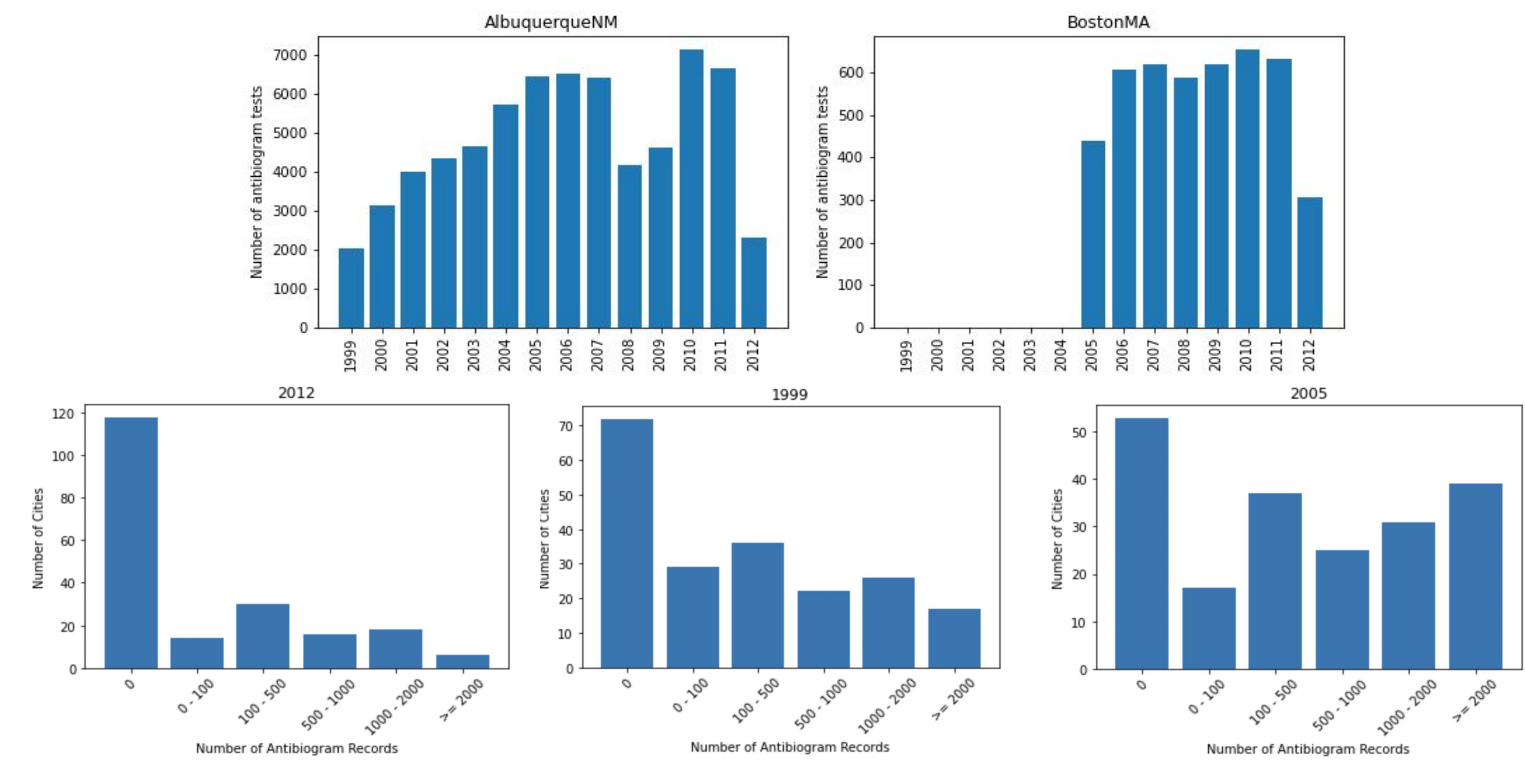


Figure #2

- Association Rule Mining aims to observe frequently occurring patterns, correlations, or associations from datasets.
- Describes dependency of one data item on another data item: A -> B. The dependency can be thought of as an antecedent (If) and a consequence (Then) statement.
- Mapped each drug to a number for association rule mining. If a particular test result showed up as "R" it was included as true in the input vector, false otherwise.
- Performed yearly association rule mining for each HSA city. Sample association rules are displayed in figure 4.
- Used a geocoding API (Nominatim) to find OSM data for each city. Regions are unevenly spread but represent the population density (figure 3).
- Studied spatial and temporal patterns in the mined rules and converted significant rules back to drugs using the mapping. Explored clinical significance of the observed patterns.

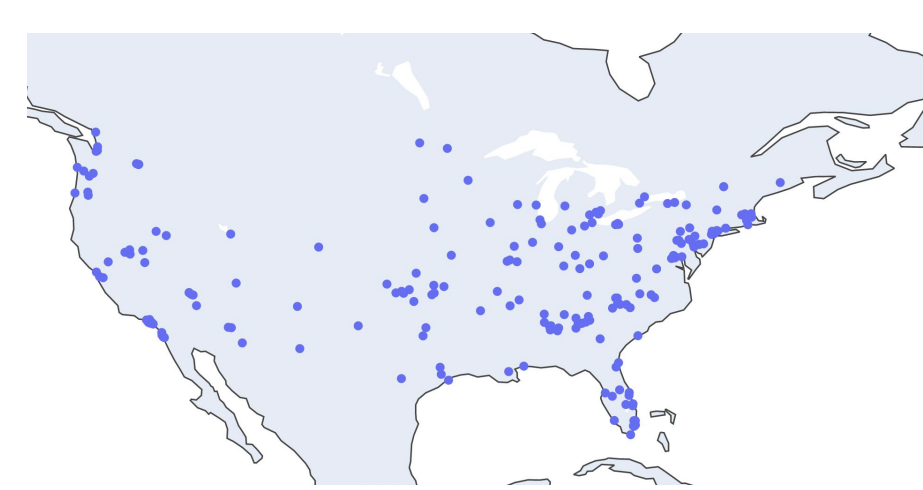


Figure #3

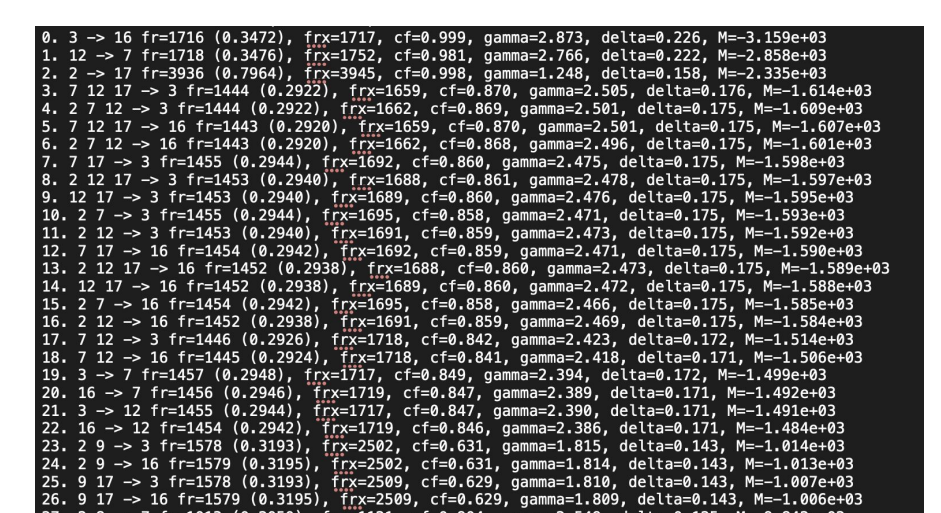


Figure #4

Future Work

- Split data into groups depending on Oxacillin resistance in order to determine how antibiogram patterns differ with MRSA / MSSA strains (hospital/community).
- Find significant antibiogram patterns and identify specific patterns for future use in prediction models.
- Write a research paper of findings alongside Eili Klein, clinician at Johns Hopkins.

References

- Wilhelmiina H'am'al'ainen. Kingfisher: an efficient algorithm for searching for both positive and negative dependency rules with statistical significance measures. Knowledge and information systems, 32(2):383–414, 2012.
- Dartmouth Atlas Project. Dartmouth atlas data. <https://data.dartmouthatlas.org/supplemental/#crosswalks>.
- Wilhelmiina H'am'al'ainen. Kingfisher - a tool for searching statistical dependencies/association rules. <https://sites.google.com/site/whsivut/home?authuser=0>.