

Introduction

With the development of medical science, hospitals found that during the use of antimicrobials, some microorganisms gradually develop resistance, making the antimicrobials ineffective. This greatly reduce the effectiveness of the treatment. What's worse, the resistant microorganism can also be passed from patient to patient. According to the World Health Organization, nearly half a million new MDR-TB cases are detected each year, and about 34.1% of them die. Therefore, it is of great significance to collect and analyse antimicrobial susceptibility test records.

This project mainly computes and processes the antimicrobial susceptibility test records downloaded from NHS using widely recognized Single Antimicrobial Resistance Index(SARI) and Antimicrobial Spectrum of Activity Index(ASAI). Different time-series processing methods are used for visualization, and a series of figures and data are obtained. Finally, an interactive web page is designed so that doctors could easily find key information such as SARI, ASAI, time series, number of samples, etc.

Data processing

Data collection and cleaning

The metadata includes information such as date, sample type, patient number, microorganism name, antimicrobial name, and sensitivity test results. The data is cleaned, and a series of information such as microorganisms and antimicrobials are processed and extracted respectively.

Among the classification methods widely accepted by hospitals, the classification is generally carried out according to the sample type first, such as the wound sample, blood sample and urine sample. They are further grouped into pairs, each pair containing a microorganism and an antimicrobial. This grouping allows for a clear analysis of the relationship between the sensitivity of a specific microorganism and a specific antimicrobial.

Data definition and processing

This project mainly uses two commonly used AMR indexes, SARI and ASAI. SARI is the resistance index of an organism to an antimicrobial. It is calculated as the number of all samples showing resistant and intermediate divided by the number of all samples showing resistant, intermediate and sensitive.

$$SARI = \frac{R+I}{R+I+S}$$

Where *R* stands for resistant, *I* for intermediate, and *S* for sensitive.

ASAI shows different antimicrobials are effective on which range of microorganisms. The antimicrobial spectrum is generally divided into broad, intermediate and narrow spectrum. Narrow-spectrum antimicrobials have a very limited effect, generally acting on very few microbes. Broad-spectrum antibiotics are effective against both Gram-negative and Gram-positive bacteria. The antibacterial spectrum helps doctors clearly find the characteristics of each antimicrobial.

Dynamic AMR index and time-series have great significance in clinical treatment. A common approach is Independent Time Intervals(ITI). This is a way to compute data in periods that do not overlap each other, such as monthly computes. The improved method is Overlapping Time Intervals(OTI). Start with a frequency of testing, like a month. Second, specify a compute period larger than the test frequency period, such as 3 months. It is equivalent to calculating the common susceptibility data of the current month and the previous two months once a month.

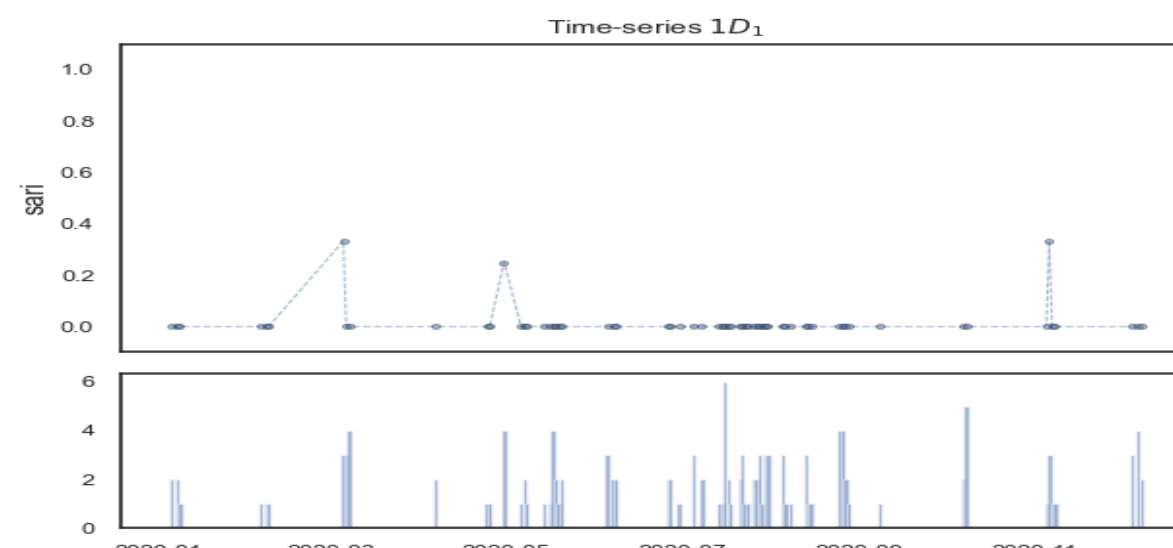


Fig1. The resistance time series for a pair (ITI)

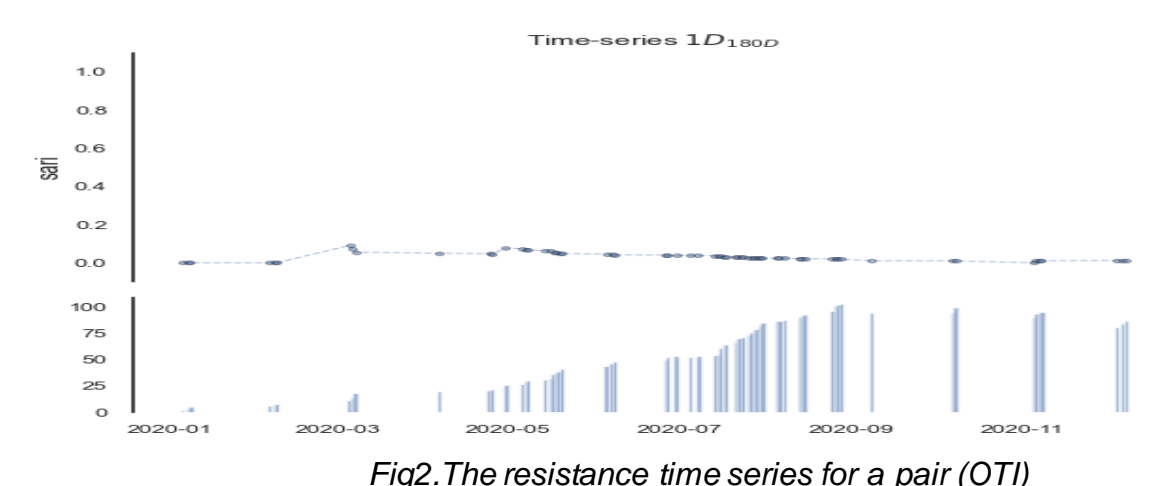


Fig2. The resistance time series for a pair (OTI)

Data visualization

This project analyzes AMR from three different dimensions to help medical staff make better and faster decisions.

Pair level(microorganism, antimicrobial)

Select the sample type first, and then select different pairs. This project will visualize the following information:
 Number of Total records per interval for a pair.
 Number of sensitive/resistant/intermediate for a pair.
 The resistance time series for a pair.
 The resistance time series will be compared and visualized under ITI and OTI methods respectively.

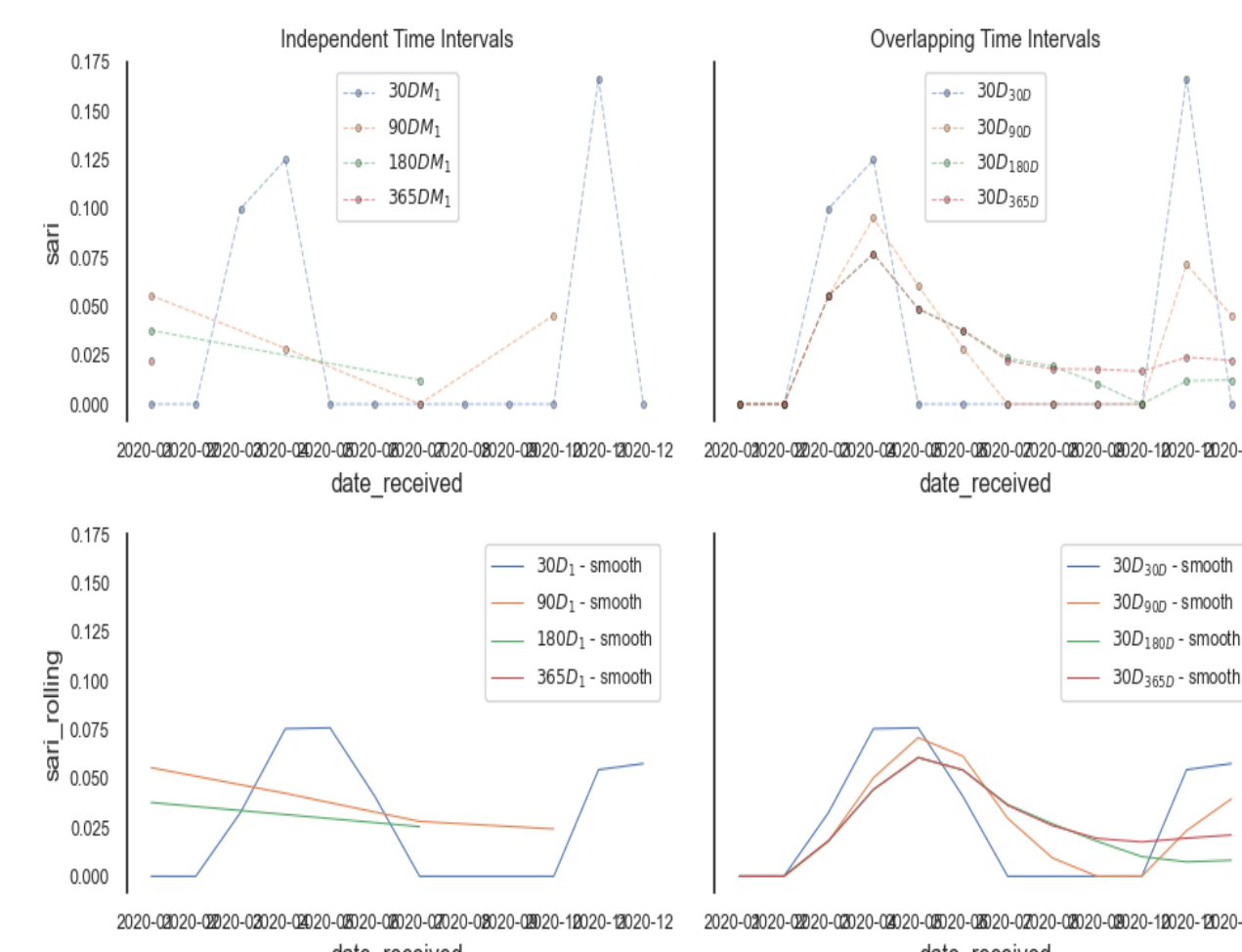


Fig3. The resistance time series for a pair

Antibiotic level

In this dimension, this project will analyze and visualize ASAI of different antibiotics on Gram-positive bacteria and Gram-negative bacteria.

Overall level

Overall Level means that key information such as microorganism name, antimicrobial name, number of samples and SARI can be found in the same figure.

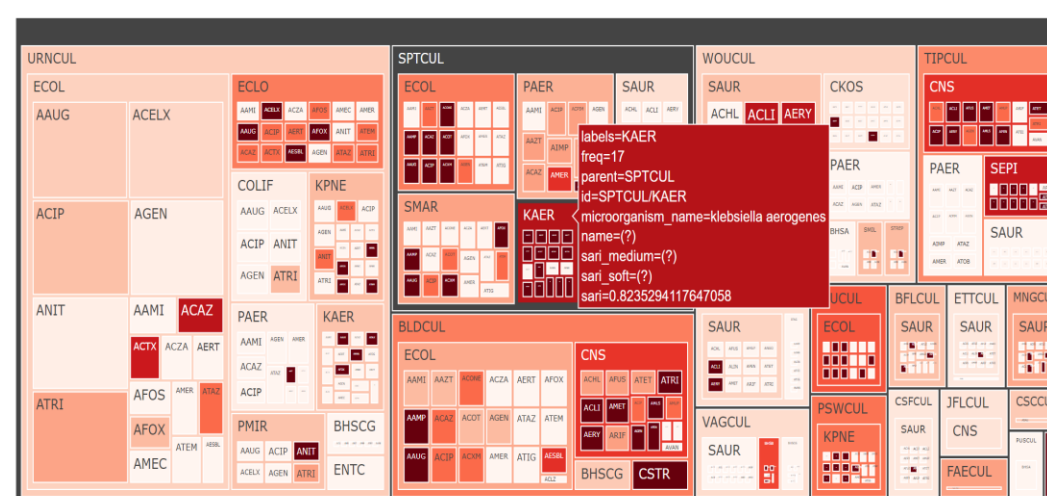


Fig4. Treemap of pairs

System design and implementation

The data system is mainly divided into the following layers:

Database layer

It stores metadata and cleaned service data

API layer

It reads the database layer based on the user's request params and returns service data

Visualization interaction layer

The visualization layer interacts with the user and provides an interactive user interface so that the user can select different specimen types and pairs from different dimensions to obtain different visualization data.

Based on this, on the basis of AdminLTE front-end framework, this paper completed the construction of the system by HTML + JS + CSS + Echarts + Node Server + Python (for data processing). The result is as follows:

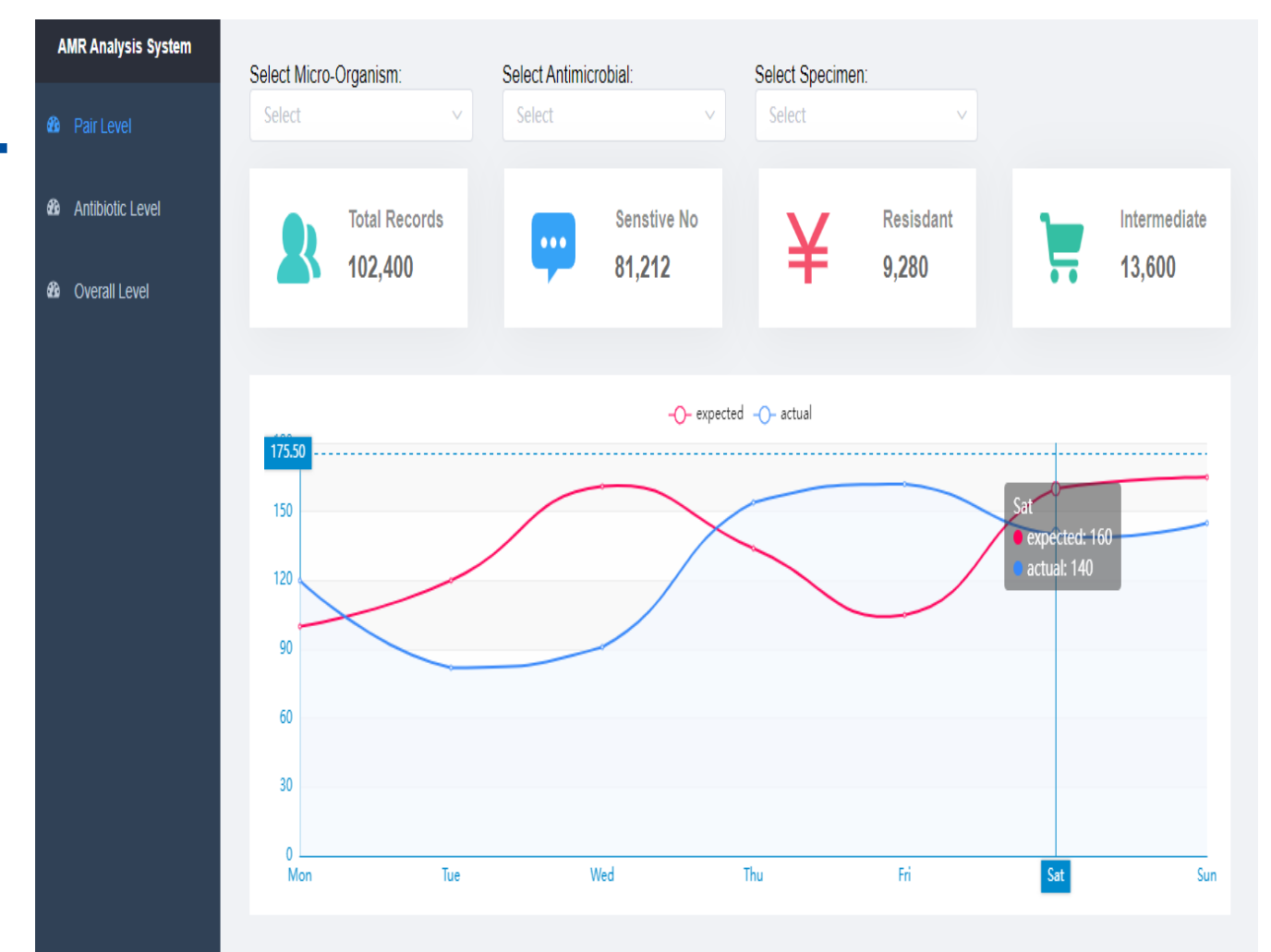


Fig5. pair level analysis

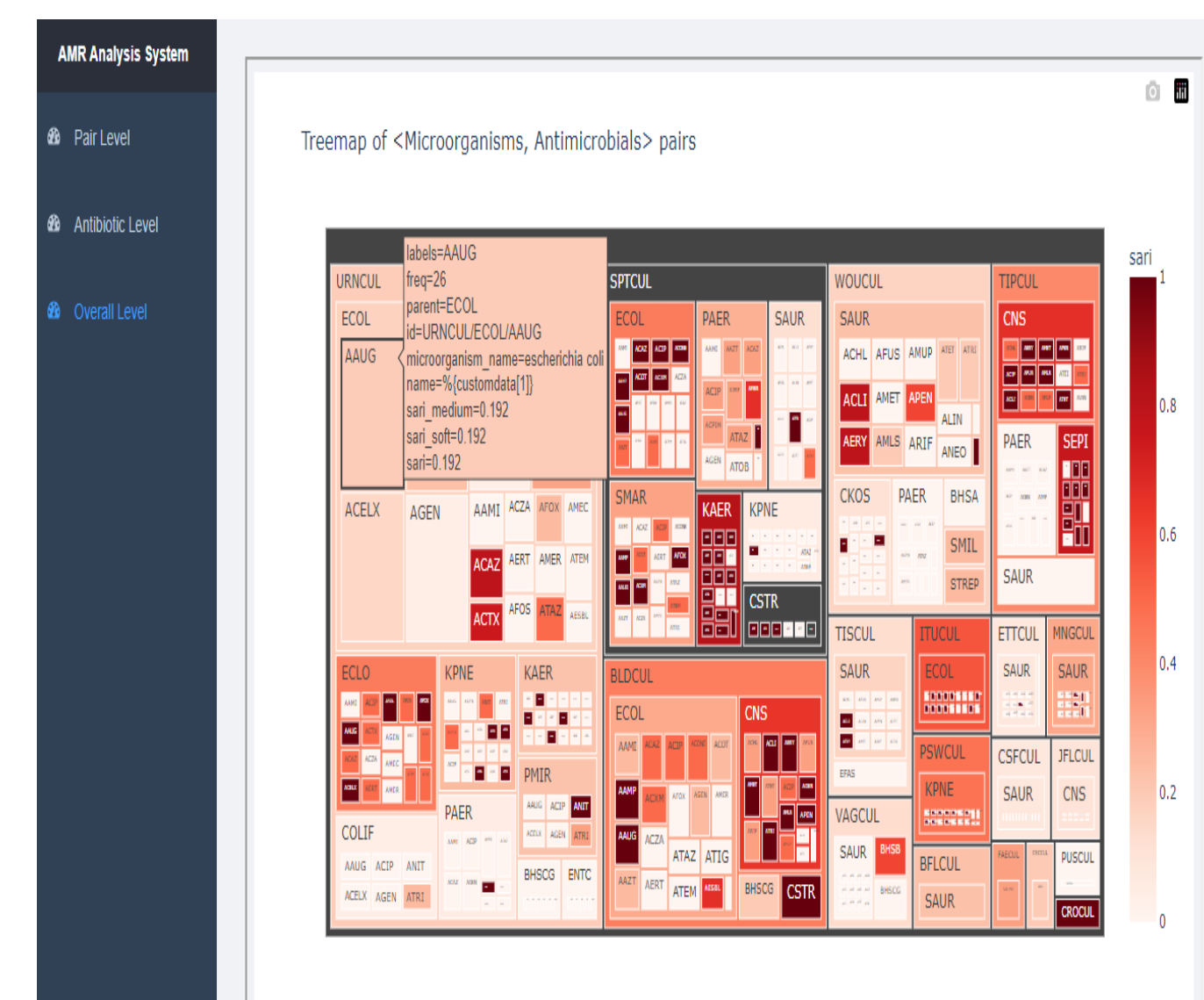


Fig6. overall level analysis

The system consists of the menu sidebar on the left and the visual function area on the right, providing users with three dimensions of the user interface, such as pair level, antibiotic level, and overall level.

Thus, the problems mentioned in the background research are solved.