# Development of Data Processing and Visualization for Bacterial and Antibiotic Susceptibility Profile

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**Abstract.** Bacterial data are under-utilized in Maharaj Nakorn Chiang Mai hospital. Bacterial data contains information regarding the bacteria that are isolated from various biological samples collected in routine clinical cares. The data can be used to create bacterial profiles and antibiotics susceptibility profiles which help doctor decide on the most appropriate antibiotics agent to be given to patients with infection. The aims of this study were to develop an application which create bacterial profiles and antibiotics susceptibility profiles by utilizing the hospital bacterial data. To do this, the study was sub-divided into 4 parts 1. Development of ETL process to prepare data for utilization, 2. Data quality assessment, 3. Development of pilot application utilizing prepared data to create bacterial profiles and antibiotics susceptibility assessment, of the pilot application.

All data was extracted from Maharaj Nakorn Chiang Mai hospital database from 2017 to 2018 with an assistance from hospital information technology (IT) personnel. All extracted data was explored and compile into one table to be utilized by the pilot application. The pilot application was written in Google Collaboratory. Overall, the data quality was good. There was some missing data but should barely affect reliability and performance of the application. For feasibility assessment, the pilot application was given to 6 doctors conveniently selected from all doctors working in the hospital for test uses. Later, the doctors were interviewed and asked to provide feedbacks on the pilot application. The application received positive review overall. Improvement points were addressed focusing on data cleaning and preprocessing, minimizing any potential bias.

This study provides insight into the development processes of the pilot application that provide bacterial profiles and antibiotics susceptibility profiles to doctors. Modifications are required before such an application can be used in clinical practice.

**Keywords:** Bacterial profile, Antibiotics susceptibility profile, Antibiogram, Extract-Transform-Load, Data quality assessment.

### 1 Introduction

Health data is defined as any data related to health conditions, reproductive outcomes, causes of death, and quality of life [1] [2]. Health data ranges from individual's demographics to medical records documents during health care visits to various individual's biological samples analysis results. Health data is essential in clinical practices, health care system management, and health-related policy decision making [3] [4] [5]. Health data is also utilized in medical research [6] [7].

Microorganism isolation, identification, and profiling from biological samples are laboratory investigation routinely performed in hospitals. They help identified potential microorganisms that cause infections so that appropriate antimicrobial agent can be administered to patients. Microorganism profile and antimicrobial susceptibility profile are essential for physicians when providing care to patients with infection. Microorganism profile shows frequencies of each type of microorganism isolated from biological specimens. Antimicrobial susceptibility profile shows the percentage of a particular type of microorganism is susceptible to each type of antibiotic agent. Both microorganism profile and antimicrobial susceptibility profile can be wildly diverse in patients with different demographic, different health conditions, and different geological location to various mechanisms [8] [9].

Maharaj Nakorn Chiang Mai hospital is a medical school and medical center in Northern Thailand. Many of the health data generated here are recorded as electronic data. Microorganism isolated data is among the various health data stored electronically. However, there is no automatic process for utilizing these microorganism isolated data to create microorganism profile and antimicrobial susceptibility profile to assist physicians in clinical practice in the hospital.

The following are the main objectives of this study

1. To develop ETL for utilizing bacterial culture data from Maharaj Nakorn Chiang Mai hospital electronic medical record to analyze for bacterial profiles and antibiotic susceptibility profiles

2. To evaluate data quality of the bacterial culture data

3. To create a application that summarized data of bacterial profiles and antibiotic susceptibility profiles of Maharaj Nakorn Chiang Mai hospital that are filterable (can specified sub-group characteristics)

4. Assess feasibility of the pilot application

## 2 Literature Review

# 2.1 Bacterial profile, antibiotic susceptibility profile, and how they are utilized

Antibiotics contain substances that kill bacterial or inhibit bacterial proliferation. Therefore, antibiotic agents are usually given to patients that are infected with bacteria. The importance of selecting an appropriate antibiotic agent comes from the fact that antibiotics administration for bacterial infections is one of the driving forces that increase the prevalence of multi-drug resistance organisms (MDROs) [10] [11] [12]. MDROs are microorganisms, primarily bacteria, that develop resistance to one or more classes of antibiotic agents. MDROs are less affected by antibiotic agents that they are resistant to. This makes diseases that are caused by MDROs more resilient to antibiotic administration, making treatment more complicated. Patients with MDROs infection have longer hospital length of stay, require more health resources, and have higher mortality rates [10] [13].

The rationale for antibiotics usage nowadays is to use as much specific bacterialkilling activity as possible [10]. Selecting an antibiotic agent that targets specific bacteria rather than a broad-spectrum agent that attacks a wide range of bacteria is one component for appropriate antibiotic agents. Bacterial profile and antibiotic susceptibility profile provide crucial information that helps guide physicians to decide best optimal appropriate antibiotic agent for a given patient.

#### 2.2 Extract-Transform-Load (ETL)

ETL is a data pipeline processes used for extract data from multiple sources, combine the extracted data together, then load the combined data into a data warehouse or other target system [14]. This data pipeline processes are important to make the most uses out of available data.

Development of ETL pipeline is a challenging process. Many variables need to be considered during the development process. It starts from understand data structure of data sources, plan how data will be cleaned and transformed, all the way up to decide target data warehouse operating system. The number of variables need to be considered can escalate quickly throughout the development process. Below are 10 steps of ETL development framework presented by [15] to help guide with the development of ETL pipeline.

|   | Step                       | Brief description                                |  |
|---|----------------------------|--|--|
| 1 | Draw the high-level plan   | Design on overall processes, from data sources   |  |
|   |                            | to target table. No detail in each process needs |  |
|   |                            | to be decided/presented yet.                     |  |
| 2 | Choose an ETL tool         | Choose an available ETL tool to use for the      |  |
|   |                            | ETL pipeline. Using an ETL tool is preferred     |  |
|   |                            | over pure coding. Although, there are some       |  |
|   |                            | learning to be done when start using new tool,   |  |
|   |                            | but after some period of time, the tool would    |  |
|   |                            | become useful when things need to be added       |  |
|   |                            | or edited to the ETL pipeline later.             |  |
| 3 | Develop default strategies | Design a detailed processes of how data be ex-   |  |
|   |                            | tracted from data sources and how should the     |  |
|   |                            | data be transferred to the ETL pipeline.         |  |

Table 1: Steps of ETL development framework

| 4  | Drill down by target table  | Design a detailed processes of how the data,     |
|----|-----------------------------|--|
|    |                             | after transferred to the ETL pipeline, be pro-   |
|    |                             | cessed/manipulated to create target table.       |
| 5  | Populate dimension tables   | Further build up ETL pipeline by execute the     |
|    | with historic data          | designed processes for dimension tables using    |
|    |                             | historical data                                  |
| 6  | Perform the fact table his- | Execute the designed processes for fact table    |
|    | toric load                  | using historical data                            |
| 7  | Dimension table incremen-   | Connect the ETL pipeline to the data sources.    |
|    | tal processing              | Further build up ETL pipeline.                   |
| 8  | Fact table incremental pro- | Update fact table and set up process to periodi- |
|    | cessing                     | cally update fact table.                         |
| 9  | Aggregate table and OLAP    | Create aggregate table and OLAP loads.           |
|    | loads                       |  |
| 10 | ETL system operation and    | Implement ETL pipeline. Make the pipeline to     |
|    | automation                  | be automatic as much as possible, e.g., auto-    |
|    |                             | matic update of data, algorithm to handle un-    |
|    |                             | expected errors.                                 |

### 2.3 Data quality assessment

Health-related data are used by health professionals and health policy makers to make clinical decisions and plan health-related policy. It is important to have reliable health data – data that accurately reflect what is happening to a patient or health care system.

There are many frameworks for DQA available which are all similar. According to the reference **"DATA QUALITY ASSESSMENT HANDBOOK"** [16], DQA is divided into seven dimensions as follow:

|   | Dimension   | Definition  | Method   |
|---|-------------|---|--|
| 1 | Accuracy    | Degree in which data correctly<br>describes real-world event/ob-<br>ject.   | Compare with actual real-<br>world data would be ideal<br>(Primary research). If not<br>able to obtain real-world<br>data, a reliable surrogate<br>data would be the next ref-<br>erence choice. |
| 2 | Reliability | Degree to which the values<br>(measurement, calculation, or<br>any specification) within the<br>data are stable, consistent, and<br>repeatable over time. | Established through primary<br>research. Identify how a<br>clinical value is measured.<br>Estimate reliability of the<br>measurement method.   |

Table 2: Dimensions, definitions, and brief analysis method in DQA

| 3 | Consistency        | Information of the same feature<br>is represented stored in the<br>same format. | Explore how values in a fea-<br>ture are stored. Compare its<br>format to one other within<br>the same feature. |
|---|--------------------|---|---|
| 4 | Complete-<br>ness  | Degree in which data are com-<br>plete  | Identify all blank data that should not left blank  |
| 5 | Relevance          | Data fitness to serve its purpose<br>in a given context                         | Established through primary<br>research. Explore how much<br>information is useful to the<br>users.             |
| 6 | Accessibil-<br>ity | Data are easily accessed.   | Describe how user or IT<br>personnel are able to access<br>to the data.   |
| 7 | Timeliness         | The data are up to date as much<br>as the intended use need it to<br>be.        | Explore how fast new input data are updated within the data storage system.                                     |

# 3 Methodology

Methodology is divided into 4 components following 4 main objectives that together pieces into a bigger picture of process required to utilizing bacterial culture data from a hospital

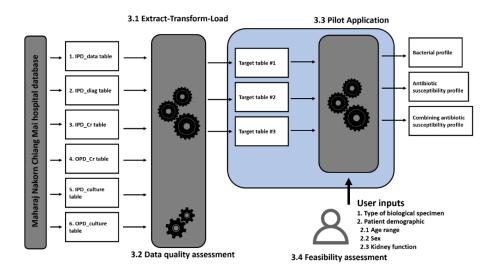


Figure 1: High-level overview methodology of the project

#### 3.1 Data extraction, transformation, and loading

Data was extracted from Maharaj Nakorn Chiang Mai hospital database using an automated software developed by Information Technology (IT) team of Maharaj Nakorn Chiang Mai hospital. All identifiable information was encrypted.

Data structure of each table will be explored. Numbers of rows and columns were counted. All features were statistically described. Numerical data, means and standard errors were calculated. Distributions of the numerical data were presented in histograms. For categorical data, frequencies of the categories were reported. For data regarding date and time, date was aggregated into months then presented as histogram, time was aggregated into hours and presented as histogram. For text data, the pattern of the data was described. Missing data was counted.

[15] was used as a guidance for the development of ETL process to transform all the extracted tables into necessary target tables.

#### 3.2 Data quality assessment

Framework presented in "DATA QUALITY ASSESSMENT HANDBOOK" was used for performing data quality assessment [16]. The 6 dimensions will be assessed including accuracy, reliability, consistency, completeness, relevance, and accessibility. Timeliness dimension was not assessable since we did not have access to the real database.

3.2.1. Accuracy

Accuracy assessment was done by comparing data from the extracted tables and actual data in the hospital information system (HIS). The data was large that was impractical to compare them all manually. Subset of data was sampled for manual comparison. five hospital numbers were randomly chosen and re-identification for manual comparison.

3.2.2. Reliability

Reliability assessment was done by unstructured interview with people responsible for entry data into the hospital database. This would include people who involved in the patient registration processes and lab technicians.

3.2.3. Consistency

All features will be explored for any inconsistency format/pattern. The finding will be described qualitatively.

3.2.4. Completeness

All features will be counted for missing data or incompleteness. The finding will be described with simple descriptive statistics.

3.2.5. Relevance

Relevance assessment will be assessed. Availability of necessary data to develop ETL process and pilot application from the extracted data will be explored. This also includes doctor interviews whether there should be any additional information provided to the end users. The interviewing process is included in feasibility assessment (3.4) of this project.

3.2.6. Accessibility

Accessibility assessment will not be systematically assessed, instead it will be described qualitatively by the principal investigator of this project.

#### 3.3 Pilot application

Pilot application was done in Google Collaboratory [17]. All target tables were uploaded to google drive that connect to the same Google Collaboratory. All target tables were used to create 3 summary tables called bacterial profile, antibiotic susceptibility profile, and combining antibiotic susceptibility profile.

3.3.1 Bacterial profile shows the prevalent distribution of isolated bacteria

3.3.2 Antibiotic susceptibility profile shows how a bacterium is susceptible to each antibiotic agent

3.3.3 Combining antibiotic susceptibility profile shows overall coverage of each antibiotic agent

All summary tables were filterable by the users – users could give specific characteristics of subpopulation they interested in, and all the summary tables would recalculate based on the characteristics given. Characteristics that could be specified included age, sex, and kidney function at admission. Type of specimen that the bacteria was isolated could also be given to the application.

#### 3.4 Feasibility assessment of the pilot application

Total of 6 physicians were conveniently sampled from all the physicians working in Maharaj Nakorn Chiang Mai hospital. All participating physicians were asked for their consent prior to the assessment, and they are free to leave the assessment process at any time. Consented physicians were given an URL link to Google Collaboratory with instructions (**Appendix 1: Instruction on how to use the pilot application**). They were free to use the application whenever they like for 2-3 weeks, then they were appointed for semi-structured interview and provide any feedback. The guide for interview questions in shown in **Appendix 2: Interview guide.** All information gathered will be combined together and described qualitatively.

#### 3.5 Ethical considerations

This study received ethical approval from Chiang Mai University ethical committee, Chiang Mai, Thailand (FAM-2565-08889).

#### 4 Results

#### 4.1 Data extraction, transformation, and loading.

Total of 6 relational tables were extracted from Maharaj Nakorn Chiang Mai hospital database as follows:

|   | Name of the table | Description  | Number of<br>rows | Number of<br>columns |
|---|-------------------|--|-------------------|----------------------|
| 1 | IPD_data table    | Contains information re-<br>garding patients who<br>were admitted in the hos-<br>pital during 2017 to 2018   | 92,436            | 25                   |
| 2 | IPD_diag table    | Contains information re-<br>garding diagnosis of pa-<br>tients who were admitted<br>in the hospital during<br>2017 to 2018   | 307,454           | 5                    |
| 3 | IPD_Cr table      | Contains information re-<br>garding the creatinine<br>level of all patients admit-<br>ted during 2017 and<br>2018. Creatinine is a bi-<br>omarker that reflects per-<br>formance of kidney func-<br>tion | 199,425           | 8                    |
| 4 | OPD_Cr table      | Contains information re-<br>garding the blood creati-<br>nine level of all patients<br>during outpatient depart-<br>ment (OPD) visit   | 348,169           | 7                    |
| 5 | IPD_culture table | Contains information re-<br>garding all the bacterial<br>culture results of all pa-<br>tients admitted to Maha-<br>raj Nakorn Chiang Mai<br>hospital between 2017<br>and 2018                            | 557,798           | 16                   |
| 6 | OPD_culture table | Contains information re-<br>garding all the bacterial<br>culture results of all pa-<br>tients admitted to Maha-<br>raj Nakorn Chiang Mai<br>hospital between 2017<br>and 2018                            | 215,257           | 15                   |

Table 3: Summary of numbers of rows and columns of all extracted tables

All descriptive information on all the extracted tables is shown in the full report of this study (**Supplement material 1**).

All extracted tables were transformed to one target table then uploaded to google drive that linked with the pilot application Google Collaboratory.

#### 4.2 Data quality assessment

4.2.1. Accuracy Table 4: Manual comparisons of the 5 sampled patients

| Table's<br>name | Number of<br>data points<br>identified in<br>the extracted<br>data | Number of<br>data points<br>identified in<br>the hospital<br>electronic med-<br>ical record | Number of<br>matched re-<br>sult | Accuracy<br>rate<br>(%) |
|-----------------|--|---|----------------------------------|-------------------------|
| IPD_data        | 132  | 120   | 120                              | 100.00                  |
| IPD_diag        | 66   | 66  | 66                               | 100.00                  |
| IPD_Cr          | 90   | 90  | 90                               | 100.00                  |
| OPD_Cr          | 12   | 12  | 12                               | 100.00                  |
| IPD_culture     | 1,204  | 1,204   | 1,204                            | 100.00                  |
| OPD_culture     | 14   | 14  | 14                               | 100.00                  |

Overall accuracy of the extracted data based-on sampling of 5 patients for manual comparison is 100.00%.

#### 4.2.2. Reliability

All patient's demographic information in Maharaj Nakorn Chiang Mai medical records is from governmental documents/information.

Bacterial culture results and Creatinine level results – According to a Maharaj Nakorn Chiang Mai hospital laboratory technician, both laboratory investigations had passed the International Organization for Standardization (ISO) 15189: Medical laboratories since 2006. ISO 15189 specifies requirements for quality and competence in medical laboratories [18].

All date and time records were electronically documented into the hospital electronic system.

#### 4.2.3. Consistency

Information stored in each feature was consistent. Date and time information was store in the same format in all the extracted tables. Creatinine level was stored with milligram/deciliter (mg/dl) as value unit. All information store in "IPD\_Cr table" were in the same pattern as "OPD\_Cr table". All information store in "IPD\_culture table" were in the same pattern as "OPD culture table".

Detail information regarding the consistency is in full report of this study (**Supplement material 1**).

#### 4.2.4. Completeness

In **"IPD\_data table"**, 18 out of 25 features had no missing value. Five features had less than 1% missing rate. Two features contain more than 30% missing rate. Features with missing data were not utilized by the pilot application

In "IPD\_diag table", there was no missing data.

In "IPD\_Cr table", there was no missing data.

In "OPD\_Cr table", there was no missing data.

In **"IPD\_culture table"**, 7 out of 16 features had no missing value. The rest feature had more than 25% missing rate. There was one feature contain more than 99% missing rate.

In **"OPD\_culture table"**, 5 out of 15 features had no missing value. There was one feature with less than 1% missing rate. The rest feature had more than 25% missing rate. There was one feature contain 100% missing rate.

Detail information regarding the completeness is in full report of this study (**Supplement material 1**).

#### 4.2.5. Relevance

All necessary information required to develop the pilot application are included in the extracted data. Information regarding admitting medical ward was included in the **"IPD\_data table"** but was not utilized, however, infectious doctors commented that this information is very important and should be included in the pilot application as bacterial profiles and antibiotics susceptibility profiles may be different from a medical ward to the others.

#### 4.2.6. Accessibility

Data in Maharaj Nakorn Chiang Mai hospital's database was not open to public access. To access the data, one of the following conditions must be met:

1. The data was requested by health personnel working in the hospital with the goal to utilize the data to improve health-related service(s) of Maharaj Nakorn Chiang Mai hospital.

2. Receive ethic approval from the Maharaj Nakorn Chiang Mai hospital ethical committee to extract the requested data from the hospital database.

All data extraction must be done through Maharaj Nakorn Chiang Mai hospital's IT personnel.

#### 4.3 Pilot application

The application was created in Google Collaboratory within the same Google drive as the target table. Sample images of the application are shown in **Appendix 3: Sample images of the pilot application.** 

#### 4.4 Feasibility assessment of the pilot application

The application was stored in the project's Google drive. Instruction on how to use the application is shown in **Appendix 1: Instruction on how to use the pilot applica-tion.** 

Total of 7 Doctors were invited to participate in feasibility assessment, only 6 agree to participate. Of all the 6 doctors, there are 2 internists with 1.5 years of clinical experience; 2 family doctors with 4 and 5 years of clinical experience; and 2 infectious doctors with 6 and 14 years of clinical experience.

| Doctor<br>No | Role              | Years of clinical<br>experience |
|--------------|-------------------|---------------------------------|
| 1            | Internist         | 1.5                             |
| 2            | Internist         | 1.5                             |
| 3            | Family doctor     | 4                               |
| 4            | Family doctor     | 5                               |
| 5            | Infectious doctor | 6                               |
| 6            | Infectious doctor | 14                              |

Table 5: Summary of doctor's role and years of clinical experience

The summary of interview results is shown below

|   | Doctor 1<br>(Internist)                                     | Doctor 2<br>(Internist)                            | Doctor 3<br>(Family doctor)                             | Doctor 4<br>(Family doctor)  |
|---|---|--|---|--|
| 1. Clinical experience (year)   | 1.5   | 1.5  | 4   | 5  |
| 2. Do the results shown in the application similar to what you experience in clinical practice? | -   | Similar to clinical experience                     | Similar to clinical experience                          | Similar to clinical experience   |
| If there is something different, could you specify?   |   |  |   |  |
| 3. Do you think the application   | The application would be use-                               | The application would be use-                      | The application would be use-                           | The application would be use-  |
| would be any useful in your   | ful.  | ful.   | ful.  | ful.   |
| clinical practice?  | It would help doctor deciding on which empirical antibiotic | It provides an organized framework to present data | It helps processing data from the laboratory department | It provides information on which empirical antibiotic  |
| Please provide reason(s)  | agent should be given to a pa-<br>tient                     |  |   | agent to use.<br>However, there is a suggestion<br>to do internal validation with<br>other source of data or do ex-<br>ternal validation with other<br>similar hospital. |

 Table 6: Summary of comments, feedbacks, and opinion from internists and family doctors

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| <ul><li>4. Do you think the application<br/>at the current state is enough<br/>to be implemented into clinical<br/>practice?</li><li>Please provide reason(s)</li></ul> | No.<br>The source of data should in-<br>clude outpatient department<br>(OPD) as well.<br>The application should be<br>easier to use – minimize num-<br>ber of steps required to run<br>the application | Not yet.   | May be.<br>However, the application<br>should be more user friendly | May be.<br>Information on the internal<br>and/or external validation may<br>require                              |
|---|--|--|---|--|
| 5. How should the application<br>be improved?   | The application<br>The application should utilize<br>data from OPD.<br>The application should be ac-<br>cessible via mobile devices<br>and may not require Gmail<br>log-in                             | Modify input panel to make it<br>easier to fill-in | Minimize the steps required to access the application               | The interface should be im-<br>proved to make it more intui-<br>tive to use without the need for<br>user manual. |
| 6. Other comments   | -  | -  | -   | -  |

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|   | Doctor 5  | Doctor 6  |
|---|---|---|
|   | (Infectious doctor)   | (Infectious doctor)   |
| 1. Clinical experience (year)                         | 6   | 14  |
| 2. Do the results shown in the application similar to | Similar to routine practice                                 | -   |
| what you experience in clinical practice?             |   |   |
| If there is something different, could you specify?   |   |   |
| 3. Do you think the application would be any useful   | It is useful in assisting with the decision-making pro-     | It is useful in assisting with the decision-making process for empir- |
| in your clinical practice?                            | cess for empirical antibiotic agents                        | ical antibiotic agents while waiting for the bacterial culture result |
| Please provide reason(s)                              |   |   |
| 4. Do you think the application at the current state  | May need to make the application more user friendly         | Must be careful when interpreting the information shown by the ap-    |
| is enough to be implemented into clinical practice?   |   | plication as some antibiotic agents are rarely used in clinical prac- |
| Please provide reason(s)                              |   | tice but are relatively frequently presented.                         |
| 5. How should the application be improved?            | 1. Medical ward in which the patient admitted should        | 1. Medical ward should be added into the input features               |
|   | be add in the input features                                | 2. Label prescription indication for each antibiotics agent so that   |
|   | 2. The result calculations should only include patient      | these information can be used to filter out irrelevant suggestions    |
|   | that actually have infection. In this case, the application | 3. Include Gram stain in the input feature might also be useful       |
|   | include all data without know whether those data is ac-     |   |
|   | tually from patient with infection.                         |   |
|   | 3. If possible, the application may suggest antibiotic      |   |
|   | agent and it dosage to the user                             |   |
| 6. Other comments                                     | -   | Suggest consulting with laboratory personnel before real-world im-    |
|   |   | plementation  |

# Table 7: Summary of comments, feedbacks, and opinion from infectious doctors

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### 5 Discussion

Data extraction was done through Maharaj Nakorn Chiang Mai hospital IT personnel consultation. The data structure of the extracted tables was derived from several discussion sessions with the IT personnel. The main reason for the data to be separated into multiple relational tables was that the hospital health information system (HIS) was primary created to support hospital health care services. As each aspect of the health services required different storing data format, thus, resulted in multiple relational tables.

Overall, the quality of the extracted data was relatively good for providing summary profiles of bacteria isolated within the hospital. However, from the assessment, there were some points of concern.

Some extracted tables contained relatively high proportion of missing data. Upon manual exploration from the accuracy domain, missing value in the extracted data was matched with empty value from the hospital's database. True missing value in the context of bacterial culture data was difficult to determine, as missing values may result from not having bacterial growth, or there was bacterial growth but laboratory technician decide not to perform antibiotic susceptibility test due to various reasons. This might indicate an improvement point in database design.

The way the HIS recorded type of specimen was text-based in the majority of the bacterial culture data, making classification of type of specimen problematic. Method for classification the type of specimen presented in this project was developed from exhaustive trial and error process, the process could only classify approximately 85% of the entire dataset. Improving data encodings for type of specimen would benefit uses of this aggregated data. Nevertheless, in the perspective of providing health care services, the quality of the data was excellent for the tasks.

All functions of the application on Google Collaboratory seemed to work as intended. The platform was stable; allow easy access and sharing. The platform was suitable for the pilot project. However, for actual implementation of the application. The platform should be carefully considered.

The "**Combining antibiotic susceptibility profile**" was discouraged by infectious doctor as the summary data shown in the table deviated clinically significantly from expected result.

Tables shown from the application were built using the previous table data. The **"antibiotic susceptibility profile"** (2<sup>nd</sup> and 3<sup>rd</sup> table) were built from **"Bacterial pro-file"** (1<sup>st</sup> table) and the **"Combining antibiotic susceptibility profile"** was the built from **"antibiotic susceptibility profile"**. At each step of data selection and aggregation hided biases within. The **"Combining antibiotic susceptibility profile"** would suffer from biases the most, to the point where infectious doctor discourage using it clinically.

Generally, the application received positive reviews. Non-infectious doctors commented that the summarized data provided by the application match with their knowledge and experience, and their feedbacks seemed to be focused on optimizing user experience. While infectious doctors really discuss down to the mechanism of data collection and generation, and pointed out many potential for biases and provided suggestions to counter these biases, which is discussed further in **Limitation**.

The application had filtering function that allowed users to specified populational characteristics of interest. All interviewed doctors agreed that the function is useful, however, which health characteristics should be used for the filter may need further discussions.

Both infectious doctors suggested adding medical ward in which patients were admitted. This feature, according to both doctors, is very important for determining which initial antibiotics to use. As each medical ward admitted patients with primarily different conditions (e.g. orthopedics ward would admitted patients with primarily musculoskeletal problem, while neurosurgery ward would admitted patients with primarily structural brain problem.) resulting in different infectious disease distribution, thus, different bacterial profiles. Medical ward in which patients were admitted can be found in table "IPD\_data table". They contain information regarding the place where patients were admitted.

There have been other organizations as well that publish bacterial profiles and antibiotics susceptibility profiles. National Antimicrobial Resistant Surveillance Center, Thailand (NARST) have been collecting samples and regularly publish these profiles in the national level for microbial surveillance and monitoring purposes, while World Health Organization (WHO) have been doing the same in global level. The organizations also published their methodology for samples collection and susceptibility testing which may be a more appropriate approach compared to the method used in this project. This issue had also been raised during the interview with the infectious doctors. However, they did not totally agree with the methods used by NARST or WHO as they thought that the methods were designed for surveillance and monitoring purposes but not for supporting frontline clinical decision making. Further discussions are needed.

#### Limitation

The application treated each biological sample record as if they were independent from one other, which is not true in real-life situation. A dozen of biological samples could be originated from the same person over the course of an admission. This caused the results to deviate toward group of people that biological samples had been collected multiple times and not representing the true information. This is a problem of repeated measures and, according to both infectious doctors, is difficult to dealt with. To minimize this problem in future work, algorithms on biological sample record selection must be created, with inputs from infectious doctor and laboratory technician.

Results in the addition table (the 4<sup>th</sup> table) was also subject to biases. One main problem was the record selection as mentioned in previously. Another problem was that for a type of biological specimen, there could be multiple different combinations of antibiotic agents that were tested against for the susceptibility test. This was evident from the result table "Antibiotic susceptibility profile, count (3<sup>rd</sup> table)" that for a bacterial name, the number of counts in the denominators were different across different antibiotic agents. This means that for a same type of biological specimen, in some specimen, there were some information hidden (not tested). This leads to an unreliable estimate of coverage percentages. One way to fix the problem is to test the same

combination of antibiotic agents in all biological specimens. Another way is to understand why laboratory technicians test different combinations of antibiotic agents in the first place, so that counter measures could be included in the application. Or, at least, inform users of this biases so that they would be caution when interpreting the result table.

This project only explored bacteria-related data store in Maharaj Nakorn Chiang Mai hospital. Any result shown here are specific to the local context. Generalizing any of the findings need to be cautioned.

#### **Considerations for future work**

For a successful project implementation, a multidisciplinary team needs to be assembled. The team should at least include one health provider and one engineer. The health provider should have experience in clinical practice and has some knowledge regarding database management. The engineer should have experience in data warehouse set up. Multiple sessions of expert consultations should be done, e.g., hospital's stakeholders consultation for resources support; hospital's IT personnel consultation for ETL pipeline set up, preferably setting up in the hospital database server so that IT personnel can help with system maintenance; infectious disease and laboratory technician consultation for ideas on how to best utilize bacterial data. All targeted users of the application should be involved in the testing phase of the implementation to optimized user experience.

#### Conclusion

This pilot project demonstrated that ETL pipeline and bacterial profile visualization application can be done. All key components and problems with potential solutions were addressed. Data quality of Maharaj Nakorn Chiang Mai hospital was in good quality. Feasibility assessment of the application from interviewing doctors showed potential for implementation in clinical practice. Filtering function of the application was said to be beneficial. Hospital's stakeholder consultation, and expert consultation are needed to ensure a successful implementation and maintenance of the pipeline and application in clinical practice.

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### Appendix **Appendix 1: Instruction on how to use the pilot application** 1. Log in to the following g-mail

- 2. Go to google drive

| My Drive 👻                             |  |        | 81 |
|--|--|--------|----|
| Suggested                              |  |        |    |
|  | co                                       |        | Ø  |
| database_final.csv<br>You opened today | CO Prototype01.ipynb<br>You edited today |        | +  |
| Files                                  |  | Name 个 |    |
|  | co                                       |        |    |
| database_final.csv                     | CO Prototype01.ipynb                     |        |    |

3. Double click on file name "Prototype01.ipynb"

| CO A Prototype01.ipynb ☆<br>File Edit View Insert Runtime Tool: | s Help <u>All changes saved</u>  | 🗖 Comment 斗 Share 💠 🖸     |
|---|--|---------------------------|
| ≔ Files   | + Code + Text  | 🗸 Connected 👻 🧪 Editing 🖍 |
| α   | Data preprocessing     [ ] L1 cell hidden     Input detail for filter  |                           |
|   | <ul> <li>Select "specimen" or "organ system" (required)</li> </ul>   | ↑↓⋴■‡₽∎:                  |
|   | Specimen: <u>spullum</u><br>Organ_system: <u>Pneumonia</u><br>Select age range in year (required)<br>Age_start: <u>20</u><br>Age_stop: <u>65</u> |                           |
| <u>،</u>  | Select age range, in years (required)  |                           |
|   |  |                           |

4. Go to Runtime -> Run all. Then wait all processes have been run. This should take approximately no more than 2 minutes. If there is any error appear, please contact me.

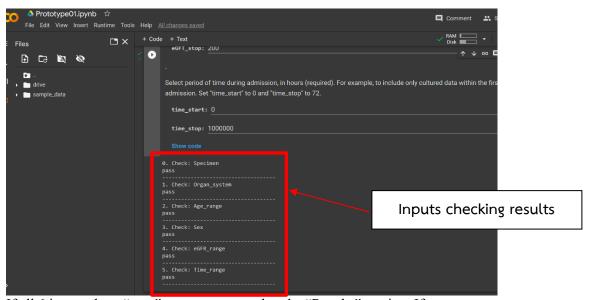
| CO Prototype01.ipyn<br>File Edit View Insert | b ☆<br>Runtime Tools Help & | All changes saved    |                             | Comment | 🚉 Share 🏟   | С   |  |  |  |
|--|-----------------------------|----------------------|-----------------------------|---------|-------------|-----|--|--|--|
| ⊟ Files                                      |                             |                      |                             |         | - 🖌 Editing |     |  |  |  |
|  | Run before                  | Ctrl+F8              |                             |         |             |     |  |  |  |
| a 🖬 🖬 🖬 🐼                                    |                             | Ctrl+Enter           |                             |         |             |     |  |  |  |
| {x}  | Run selection               | Ctrl+Shift+Enter     | ing                         |         |             |     |  |  |  |
| autipic_uatu                                 | Run after                   | Ctrl+F10             |                             |         |             |     |  |  |  |
| D  | Interrupt execution         | Ctrl+M I             |                             |         |             |     |  |  |  |
| '  | Restart runtime             | Ctrl+M.              | ilter                       |         |             |     |  |  |  |
|  |                             |                      | inter                       |         |             |     |  |  |  |
|  | Disconnect and delete ru    |                      |                             |         | ◎ ■ ✿ ₽     | • • |  |  |  |
|  | Change runtime type         |                      | * "organ system" (required) |         |             |     |  |  |  |
|  | Manage sessions             |                      |                             |         |             |     |  |  |  |
|  |                             |                      |                             |         |             |     |  |  |  |
|  |                             |                      |                             |         |             |     |  |  |  |
|  |                             |                      |                             |         |             |     |  |  |  |
|  |                             | Select age range in  | year (required)             |         |             |     |  |  |  |
|  |                             | Age_start: 20        |                             |         |             |     |  |  |  |
|  |                             | Age_stop: 65         | Age_stop: 65                |         |             |     |  |  |  |
|  |                             |                      |                             |         |             |     |  |  |  |
| <u>ه</u>                                     |                             | Select age range, in | vears (required)            |         |             |     |  |  |  |
|  |                             | Sex: both            |                             |         |             |     |  |  |  |
| Disk   |                             | Sex: both            |                             |         |             |     |  |  |  |

The file is divided into 3 parts – "Data preprocessing", "Input detail for filter", and "Results".

In "Input detail for filter" part, you can try fill in different values. The data will be filtered accordingly to your inputs. After you satisfy with your input values, click on the "play" button just below the "Input detail for filter" heading.

| CO Prototype01.ipynb ☆<br>File Edit View Insert Runtime | e Tools Help <u>All changes saved</u>          | luce sta |
|---|--|----------|
| ≔ Files C   | □ × + Code + Text                              | Inputs   |
| Q 🔁 C3 🖬 🐼  | Data preprocessing                             |          |
| sample_data   | 4 1 cell hidden                                |          |
|   | - Input detail for filter                      |          |
|   | Select "specimen" or "organ system" (required) |          |
|   | Specimen: sputum                               | <u> </u> |
|   | Organ_system: Pneumonia                        | <u> </u> |
|   | Select age range in year (required)            |          |
| ,   | Age_start: 20                                  |          |
| /   | Age_stop: 65                                   |          |
| /   |  |          |
|   | Select age range, in years (required)          |          |
| The "play" but  | ton sex: both                                  | <b>•</b> |
|   | ✓ 0s completed at 1:15 PM                      | • ×      |

After it finish running, scroll down to check whether the inputs pass all the requirements.



If all 6 inputs show "pass", you can proceed to the "Results" section. If at least one of the inputs shows "fail", please change your inputs to match constraints show on the screen then run the "play" button again.

|   | + Coo          | de + Text  | KAM<br>Disk |       |    | •     |
|---|----------------|--|-------------|-------|----|-------|
| 2 | <b>9</b><br>08 | time_start: 0  |             |       | ≁  | Θ.    |
|   |                | time_stop: 1000000   |             |       |    |       |
|   |                |  |             |       |    |       |
|   |                | 0. Check: Specimen<br>pass   |             |       |    |       |
|   |                | 1. Check: Organ_system<br>pass   |             |       |    |       |
|   |                | 2. Check: Age_range<br>pass  |             |       |    |       |
|   |                | 3. Check: Sex<br>pass  |             |       |    |       |
|   |                | 4. Check: eGFR_range<br>fall   |             |       |    |       |
|   |                | 5. Check: Time_range<br>pass   |             |       |    |       |
|   |                | For input named "eGFR_range", "eGFR_start" and "eGFR_stop" must be between 0 and 1000.   | "eGFR_s     | tart' | mı | ust a |
|   |                | <pre>ValueError Traceback (most recent call last) <i putton_input_5-9b9f063a1732=""> in <module>() 60 print(text_disp) 61&gt; 62 table01, table02, table03 = result(preprocess(df))</module></i></pre> |             |       |    |       |
|   |                | 🗘 3 frames   |             |       |    |       |

In the "Results" section, you can see the triangle mark in front of the heading, this helps contract and expand items within the "Results" section. Within the "Results" section, there are 4 tables which report bacterial profile of the inputs data (table 1), antibiogram (table 2), and the coverage of each antimicrobial agents (table 3). You must run the "play" button to update tables. You can run them individually when the section is expanded, or run them simultaneously when the section is contracted.

| Results 4 7 cells hidden Contracted | The triangle mark |  |
|-------------------------------------|-------------------|--|
| - Results                           |                   |  |
|                                     |                   |  |
| [7] table01                         |                   |  |
| Enterobacter spp.                   | 71 0.709          |  |
| Haemophilus influenzae              | 50 0.500          |  |
| Aeromonas hydrophila                | 47 0.470          |  |
| Citrobacter koseri                  | 47 0.470          |  |
| Klebsiella pneumoniae (CRE)         | 42 0.420          |  |
| Providencia rettgeri<br>Expanded    | 36 0.360          |  |

Expanded

Interpret results as you please.

You can try change any input values and see how the results change.

# Appendix 2: Interview guide แบบสอบถาม

1. ท่านเป็นแพทย์สาขาอะไร?

□ General doctor
 □ Internal medicine doctor
 □ Infectious disease doctor
 □ Other specialty โปรดระบุ

2. ท่านมีประสบการณ์ดูแลผู้ป่วยในฐานะแพทย์มาแล้วกี่ปี?

 ผลที่ได้ในส่วน Results เหมือนหรือแตกต่างจากประสบการณ์ของท่าน? หากมีกรณีที่ แตกต่าง ขอท่านโปรดยกตัวอย่างกรณีดังกล่าว?

4. ท่านคิดว่าโปรแกรมนี้จะมีประโยชน์ในเวชปฏิบัติของท่านหรือไม่? โปรดให้เหตุผลประกอบ

 ท่านคิดว่าโปรแกรมนี้ในขณะนี้น่านำไปใช้ในเวชปฏิบัติของท่านหรือไม่? โปรดให้เหตุผล ประกอบ

6. ท่านคิดว่าโปรแกรมนี้ควรพัฒนาให้ดีขึ้นกว่านี้อย่างไร?

7. ข้อเสนอแนะอื่นๆ

| la co |  |                    |                              |                          |               |                 |              |                  |                 |             |             |             |                 |            |                 |
|-------|--|--------------------|------------------------------|--------------------------|---------------|-----------------|--------------|------------------|-----------------|-------------|-------------|-------------|-----------------|------------|-----------------|
| - inp | ut detail for filter                           |                    |                              |                          |               |                 |              |                  |                 |             |             |             |                 |            |                 |
| ~     |  |                    |                              |                          |               |                 |              |                  |                 |             |             |             |                 |            |                 |
|       | Select "specimen" or "organ                    | i system (required |                              |                          |               |                 |              |                  |                 |             |             |             |                 |            |                 |
|       | Specimen: sputum                               |                    |                              |                          |               |                 |              |                  |                 |             |             |             |                 |            | •<br>•          |
|       | Organ_system: Pneumoni                         |                    |                              |                          |               |                 |              |                  |                 |             |             |             |                 |            | -               |
|       |  |                    |                              |                          |               |                 |              |                  |                 |             |             |             |                 |            |                 |
|       | Select age range in year (re                   | quired)            |                              |                          |               |                 |              |                  |                 |             |             |             |                 |            |                 |
|       | Age_start: 15                                  |                    |                              |                          |               |                 |              |                  |                 |             |             |             |                 |            |                 |
|       |  |                    |                              |                          |               |                 |              |                  |                 |             |             |             |                 |            |                 |
|       | Age_stop: 100                                  |                    |                              |                          |               |                 |              |                  |                 |             |             |             |                 |            |                 |
|       |  |                    |                              |                          |               |                 |              |                  |                 |             |             |             |                 |            |                 |
|       | Select age range, in years (                   | required)          |                              |                          |               |                 |              |                  |                 |             |             |             |                 |            |                 |
|       |  |                    |                              |                          |               |                 |              |                  |                 |             |             |             |                 |            | •               |
|       |  |                    |                              |                          |               |                 |              |                  |                 |             |             |             |                 |            |                 |
|       | Select range of eGFR at adr                    | mission (required) |                              |                          |               |                 |              |                  |                 |             |             |             |                 |            |                 |
|       | eGFT_start: 0                                  |                    |                              |                          |               |                 |              |                  |                 |             |             |             |                 |            |                 |
|       |  |                    |                              |                          |               |                 |              |                  |                 |             |             |             |                 |            |                 |
|       |  |                    |                              |                          |               |                 |              |                  |                 |             |             |             |                 |            |                 |
|       |  |                    |                              |                          |               |                 |              |                  |                 |             |             |             |                 |            |                 |
|       | Select period of time during                   | admission, in ho   | urs (required). For exa      | imple, to incl           | lude only cul | tured data with |              | nours of admiss  | ion. Set "time_ | start" to 0 | and "time_s | top" to 72. |                 |            |                 |
|       |  |                    |                              |                          |               |                 |              |                  |                 |             |             |             |                 |            |                 |
|       | time_stop: 48                                  |                    |                              |                          |               |                 |              |                  |                 |             |             |             |                 |            |                 |
| Tak   |  |                    |                              |                          |               |                 |              |                  |                 |             |             |             |                 |            |                 |
| - Tab | ble 1  |                    |                              |                          |               |                 |              |                  |                 |             |             |             |                 |            |                 |
| 0     | display_tab(table01)                           |                    |                              |                          |               |                 |              |                  |                 |             |             |             |                 |            |                 |
| C.    |  |                    | count %                      |                          |               |                 |              |                  |                 |             |             |             |                 |            | A               |
|       | Klebsiella ppeur                               | noniae             | 2984 24,790                  |                          |               |                 |              |                  |                 |             |             |             |                 |            |                 |
|       | Pseudomonas aen                                | uginosa            | 2546 21.151                  |                          |               |                 |              |                  |                 |             |             |             |                 |            | - 1             |
|       | Staphylococcus a                               |                    | 1201 9.978                   |                          |               |                 |              |                  |                 |             |             |             |                 |            |                 |
|       | Acinetobacter bau                              | ımannil            | 1020 8.474                   |                          |               |                 |              |                  |                 |             |             |             |                 |            |                 |
|       | Escherichia d                                  |                    | 638 5.300                    |                          |               |                 |              |                  |                 |             |             |             |                 |            |                 |
|       | Klebslella pneumoniae ESBL                     |                    | 538 4.470                    |                          |               |                 |              |                  |                 |             |             |             |                 |            |                 |
|       | Enterobacter cic<br>Escherichia coli ESBL pr   |                    | 492 4.087<br>314 2.609       |                          |               |                 |              |                  |                 |             |             |             |                 |            |                 |
|       | Haemonhilue Infle                              |                    | 314 2.009<br>950 9.077       |                          |               |                 |              |                  |                 |             |             |             |                 |            | -               |
|       |  |                    |                              |                          |               |                 |              |                  |                 |             |             |             |                 |            |                 |
| - Tab | ole 2  |                    |                              |                          |               |                 |              |                  |                 |             |             |             |                 |            |                 |
|       |  |                    |                              |                          |               |                 |              |                  |                 |             |             |             |                 |            |                 |
|       | display_tab(table02[0])                        |                    |                              |                          |               |                 |              |                  |                 |             |             |             |                 |            |                 |
|       |  | Amikacin Amoxic    | cillin/Clavulanic An<br>Acid | picillin C               | efotaxime C   | eftaroline Ce   | ftazidime Ci | profloxacin Cl   | Lindamicin Co   | listin D    | pripenem Er | tapenen Er  | ythromycin Etam | butol Fost | fonycin ^       |
|       | Klebsiella pneumoniae                          |                    |                              |                          |               |                 |              |                  |                 |             |             |             |                 |            | 0.0             |
|       | Pseudomonas aeruginosa                         |                    |                              |                          |               |                 | 83.544       |                  |                 |             | 77.848      |             |                 |            |                 |
|       | Staphylococcus aureus                          |                    |                              |                          |               |                 |              |                  |                 |             |             |             |                 |            |                 |
|       | Acinetobacter baumannii<br>Escherichia coli    | 57.059<br>100.0    |                              |                          |               |                 |              | 41.765<br>70.909 |                 |             |             |             |                 |            | 0.0             |
|       | Klebsiella pneumoniae<br>ESBL producing strain |                    | 30.435                       |                          |               |                 |              | 32.609           |                 |             |             |             |                 |            | 0.0             |
|       |  |                    |                              |                          |               |                 |              |                  |                 |             |             |             |                 |            |                 |
|       | Enterobacter cloacae                           | 97.674             | 0.0                          |                          | 69.767        |                 | 69.767       | 90.476           |                 |             |             | 100.0       |                 |            | <u>0.0</u><br>► |
| - Tat | -1- 0  |                    |                              |                          |               |                 |              |                  |                 |             |             |             |                 |            |                 |
| - Tac | ble 3  |                    |                              |                          |               |                 |              |                  |                 |             |             |             |                 |            |                 |
| L 1   | display_tab(table03)                           |                    |                              |                          |               |                 |              |                  |                 |             |             |             |                 |            |                 |
|       |  |                    | total_count covera           |                          |               |                 |              |                  |                 |             |             |             |                 |            |                 |
|       | Etambutol                                      | 24                 |                              | 10.000                   |               |                 |              |                  |                 |             |             |             |                 |            | - 1             |
|       | Rifampicin                                     | 24                 |                              | 0.000                    |               |                 |              |                  |                 |             |             |             |                 |            |                 |
|       | Streptomycin                                   | 24                 |                              |                          |               |                 |              |                  |                 |             |             |             |                 |            |                 |
|       | Colistin                                       | 18                 |                              | 00.000                   |               |                 |              |                  |                 |             |             |             |                 |            |                 |
|       | Ertapenem                                      | 541                |                              |                          |               |                 |              |                  |                 |             |             |             |                 |            |                 |
|       | Isoniazid                                      | 22                 |                              | 91.667                   |               |                 |              |                  |                 |             |             |             |                 |            |                 |
|       | Amikacin<br>Levofloxacin                       | 933<br>821         |                              | 90.495<br>35.789         |               |                 |              |                  |                 |             |             |             |                 |            |                 |
|       | Ovacillin                                      | 921                |                              | 55.769<br>R5 <u>aa</u> r |               |                 |              |                  |                 |             |             |             |                 |            | *               |
|       |  |                    |                              |                          |               |                 |              |                  |                 |             |             |             |                 |            |                 |

# Appendix 3: Sample images of the pilot application