Data Analysis on MIMIC-IV about Mortality Prediction

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***Abstract*—This paper presents an exploratory data analysis of the MIMIC-IV dataset, with the goal of identifying the significant factors that influence mortality rates. This study uses descriptive statistics, correlation analysis, and visualization tools to discover the links between patient characteristics, clinical factors, and mortality outcomes. The findings shed light on the complicated processes of mortality prediction, underlining the importance of additional research and specific analysis to gain a better understanding of these complex connections. This study's findings contribute to continuing attempts to improve mortality prediction approaches in healthcare settings. This study emphasizes the need for additional research and focused analysis to increase our understanding of the numerous mechanisms that influence mortality outcomes.**

***Index Terms*—MIMIC-IV, descriptive statistics; correlation analysis; data visualization; EHR; mortality prediction; exploratory data analysis; clinical factors; machine learning; random survival forrests, gradient boost models; penalized cox models.**

I. Introduction

In recent years, Electronic Health Records(EHRs) have transformed the medical industry by delivering comprehensive and detailed patient health records [1]. EHRs often cover many aspects of patients' health condition, such as demographics, diagnoses, prescriptions, procedures, vital signs, test results, medical imaging, discharge summaries, physician notes, and nursing notes in a sequence of visits [2]. They allow more accurate tracking of patient status, promoting informed decision-making through the use of data-driven solutions [1]. Despite these advances, difficulties remain in the field of EHR analysis, such as data irregularity. In response to these difficulties, some recent research [3] [4] seeks to address and overcome these barriers, notably in the context of mortality prediction. These studies investigate the use of advanced analytical approaches to fully realize the promise of EHRs in forecasting patient mortality, widening possibilities for more precise and timely treatments in healthcare settings.

One particularly popular analytical method in the field of medicine is survival analysis, which looks at the time frame just before important events like the development of a disease or a person's death. This method promotes a more comprehensive understanding of the course of illnesses in addition to providing insights into temporal trends and prognostic variables. More and more healthcare facilities are showing interest in working together to accelerate research and improve generalizability as the amount of Electronic Health Record (EHR) data available becomes more and more abundant [5]. Despite the potential, this analytical technique is primarily used on a case-by-case basis, concentrating on particular illnesses such as myeloma [6], lung cancer [7], prostate cancer [8], and heart failure [8], providing an in-depth assessment for people impacted by a single medical situation.

This paper explores EHR dataset MIMIC-IV [9], introduces a data representation suitable for a more general case using patient data from single hospital stay. Features are generated both via a data pipeline [10] and manually. For the experiments, machine learning techniques were used to compare the features and mortality prediction. Structure is as follows: After the introduction, related works are presented. Then methodology for re-structuring MIMIC-IV data is explained. It is followed by exploratory data analysis and evaluation of experiment results. Finally, concludes with a discussion of the findings and directions for future research.

II. Related Work

EHR data often contains significant patient health information, demanding meaningful reorganization to meet with specific aims, which range from improving general EHR representation to resolving more complex issues. [11] demonstrates progress in this task by creating concept-relationship-concept tuples from clinical notes and audio transcripts. In a separate study, Rasmy et. al. [12] compares the performance of raw and processed terminology representations of ICD codes in predictive models for two clinical prediction tasks, using the Cerner HealthFacts dataset [13] to forecast the risk of heart failure (DHF) in Type II diabetes mellitus (DMII) patients and the risk of pancreatic cancer. Darabi et. al. [14] uses natural language processing and a one-hot encoder to predict duration of stay, readmission, and mortality, using clinical codes and medical texts from the MIMIC-III [15]. Graph representations are also taken into account. According to a review on EHR graph representations [16], laboratory data, medications, patient information, diagnoses, anatomic data, procedures and vital signs are the mostly used features. While these techniques have demonstrated usefulness, none of them specifically focuses on survival analysis using patient data from both ICU and hospital admissions.

To represent data for MIMIC-IV [9], Rocheteau [17] extracted some of the features as graphs and used graph representation learning methods for her experiments. Majority of the papers that are published in the last four years are

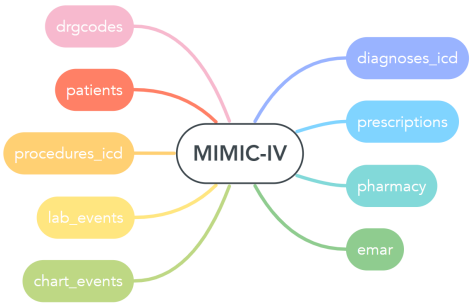

Fig. 1. Tables from MIMIC

either using hand-tailored features or they extract features with the help of some data pipelines like [18], [19], [20]. Pipelines have substantial advantages in terms of facilitating data representation easily and swiftly. Although they help to streamline data processing and representation, relying solely on these structures may limit the investigation of more complex patterns and relationships within the information.

III. Methodology

In this section, the system and methodology is explained for re-structuring the data as well as the overall arhitecture of MIMIC-IV dataset [9]. The approach of [10] is used to re-structure the dataset which creates data points that contain all the information for each stay of a single patient. [10] included MIMIC-CXR-JPG [21] and MIMIC-Note [22] but this project does not cover these two datasets.

MIMIC-IV contains 2 modules: one for hospital stays(*hosp*) and one for ICU stays(*icu*).

The hospital's administrative data, laboratory values, microbiology cultures, pharmaceutical orders, and billing methods are all stored in the *hosp* module together with the admission, discharge, and transfer records. Detailed information about all the tables in *hosp* module is introduced Table I.

Data recorded at the ICU bedside are included in the ICU module. It consists of intravenous infusions, patient outputs, recorded observations, and continuing process documentation. Detailed information about all the tables in *icu* module is introduced in Table II.

IV. Data Analysis

For the data analysis, 42,960 data points were selected. 80% of these(34,368) were random selections of living patients. Remaining 20% of them(8,592) were deceased patients. This ratio is selected to reduce computational requirements. In addition, some of the data like *poe, hcpc_events*, *pharmacy* and all information about billing is not included in the dataset. Also, precedure_events is not included as that table contains information that is not required for the documentation field, and consistency is not guaranteed [9]. The selected data tables are shown in Figure 1.

14,767 data points in total are from ICU patients, 6,452 of them are associated with deceased cases in the *icu*.

TABLE I
Description of Data Tables in Hosp Module

Data Table	Definition
omr	The Online Medical Record (OMR) table includes various EHR-sourced data.
provider	List of the deidentified provider IDs that the database uses.
admissions	Detailed information regarding hospital stays.
d_hcpcs	CPT code descriptions are given in the dimension table for hcpcsevents.
d_icd_diagnoses	Descriptions of ICD-9/10 billable diagnoses.
d_icd_procedures	Explanations of ICD-9/10 billable procedures.
d_labitems	All of the lab items are described in the dimension table for labevents.
diagnoses_icd	ICD-9 and ICD-10 diagnoses that are billed for hospital stays.
drgcodes	Hospitalizations with coded diagnostic related group (DRG) billing.
emar	Barcode scanning of pharmaceuticals at the moment of administration; the Electronic Medicine Administration Record (eMAR).
emar_detail	Additional data for electronic prescriptions that are stored in emar table.
hpcsevents.	Events that were billed while the patient was in the hospital, including CPT codes.
labevents	Measures taken in the lab from specimens obtained from patients.
microbiology_events	Microbiology cultures.
patients table	Gender, age, and date of death of the patient, if available.
pharmacy	Dosage, formulary, and further details for prescription drugs.
poe	Orders related to patient care given by clinicians..
poe_detail	Additional details regarding orders given by hospital providers.
prescriptions	Prescribed medications.
procedures_icd	Procedures that are billed to patients while they are in the hospital.
services	The hospital service or services that provided care for the patient while they were in the hospital.
transfers	Details on the transfer of patients to other units.

Remaining 2,140 deceased data points collected from *hosp* module.

At first, the information about demographics, mainly age, is investigated. It can be seen in Figure 2 that the we have at least 100 patients in every age group and no particular age group dominates over the others.

In Figure 3, the relationship between average age and most observed 20 diagnoses(diseases) is investigated. Distribution is relatively balanced and it can be said that commonly observed diseases affects mostly middle-aged to elderly people.

Lab results are investigated in such a way that considering abnormality for both deceased and living patients. Most of the results in the table have some missing information on which hospital stay(hadm_id) it belonged to. There was no distinct way to understand which hospital stay the lab results are belonged to. Because of that, each patient's all lab results

TABLE II
DESCRIPTION OF DATA TABLES IN ICU MODULE

Data Table	Definition
caregiver table	Deidentified provider identifiers used in the ICU module are listed in the caregiver database.
d_items	The itemid-describing dimension table. Explains ideas that are listed in the ICU module's events table.
chart_events	Items that are charted while a patient is in the ICU. Includes most of the data that is recorded in the intensive care unit.
datetime_events	Date-formatted information that has been documented.
ICUstays	Monitoring details on ICU stays.
Ingredient_events	Ingredients of continuous or intermittent administrations including nutritional and water content.
Input_events	Information recorded about intermittent or continuous administrations.
output_events	Details about the patient's outputs, such as their drainage and urine.
procedure_events	procedures that were recorded during the ICU stay but weren't always performed there.

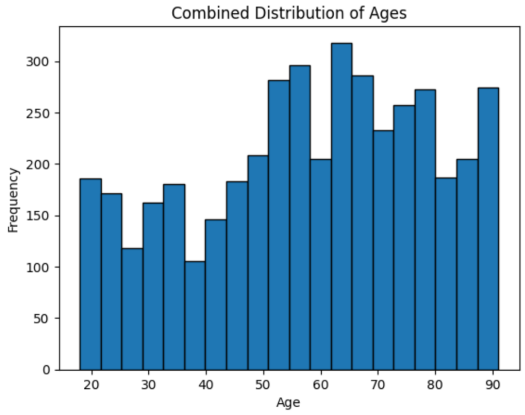

Fig. 2. Ages of Patients

are considered for the analysis. It is expected that deceased patients have more abnormal results. Figure 4, which shows the number of average abnormal results per patient, confirms this expectation.

Procedures are investigated and as expected, deceased patients had more procedures than living patients. Results can be seen in Figure 6.

Correlation analysis is made on drgcodes table as it contains similar values like drg_severity, drg_mortality which holds the patient's likelihood of dying and the severity of their condition. It can clearly seen on Figure 7 and Figure 8, there is high correlation between those 2 values so one of them should be omitted when using ML or DL methods. Drg_severity and drg_mortality values are not derived, in real life they're used to determine the billing information for the patient.

Data in the tables chart_events and datetime_events are valuable when doing mortality prediction in ICU stays with

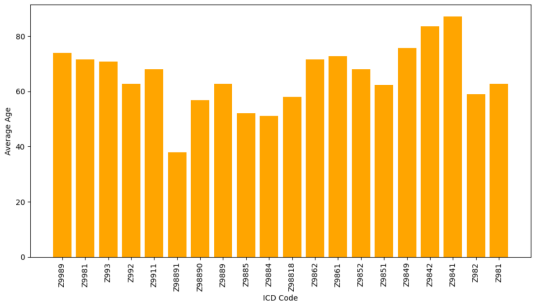

Fig. 3. Average Ages for Top 20 Diagnosis

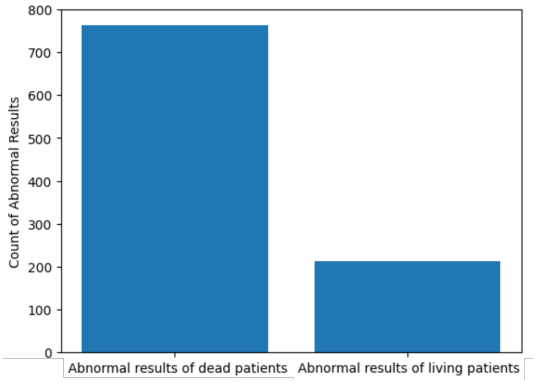

Fig. 4. Average Abnormal Lab Results

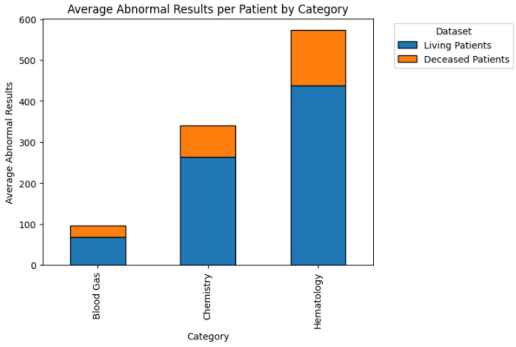

Fig. 5. Average Abnormal Lab Results by Categories

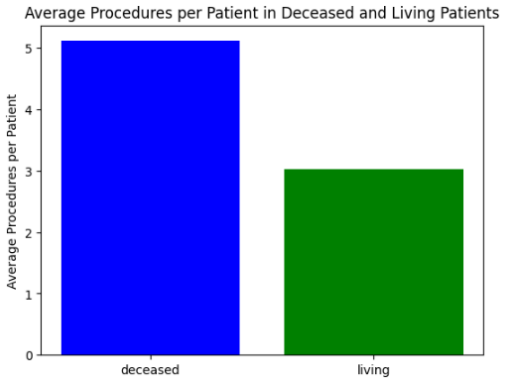

Fig. 6. Average Abnormal Lab Results

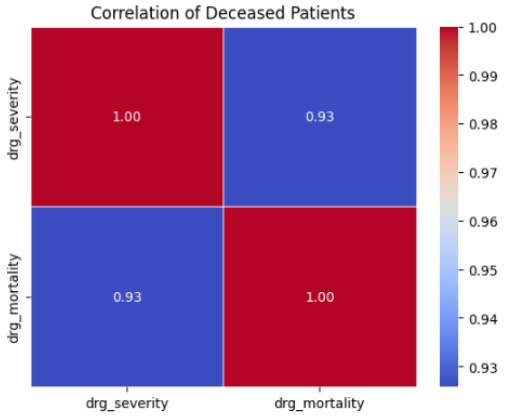

Fig. 7. Average Abnormal Lab Results

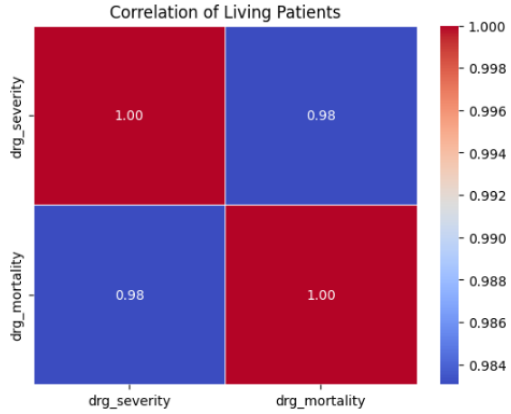

Fig. 8. Average Abnormal Lab Results

certain amount of time like [23]. After comparing the data from *hosp* and *icu* modules, it can be said that *icu* includes more details about both time of events, patient's inputs, and outputs. Therefore, data is more suitable for mortality prediction. Additionally, most of the deceased data points are from *icu* module. However, this study focuses on mortality prediction as a whole and analyses are made taking this into consideration.

V. Experiments

A dataset is created with the help of the results from data analysis. Cutoff point of deceased patient is the time of the death. For living patients, discharge time is the cutoff time. Time series data is grouped and mean value is taken.

Drg_mortality_avg is derived from the *drgcodes* table, specifically the *drg_mortality* parameter. Inspection on *Drg_codes* parameter showed that patients are likely to be associated with multiple Diagnosis Related Groups (DRG), and *drg_codes_group* holds information about how many groups the patient is associated with during their hospital stay. The severity of illness and likelihood of mortality for each associated DRG group are recorded in the *drg_severity* and *drg_mortality* parameters [9]. *Drg_mortality_avg* represents the average of the *drg_mortality* values. *Drg_severity* didn't considered because of it correlates with *drg_mortality*.

The variable *medic_count* is created using information from the *prescriptions*, *pharmacy*, and *emar* tables. The *emar* and *prescription* tables are subsets of the *pharmacy* table, containing detailed information about given doses of specific drugs, times, and contents. Number of given drugs and prescribed medicine information is scraped from these tables.

Labevents and *chartevents* tables have similar contents but *chartevents* contains only data from ICU patients. *Flag_count* variable is derived from these tables. It is the abnormal resulted lab test results a patient had.

Procedure_count is derived from *procedures_icd* table and holds the information of procedures a patient underwent.

Careunit and *gender* information are collected from patients table. *Careunit* is originally text data but each unique name is mapped to numeric values. Age value is also considered to be added to the dataset but *anchor_age* is not the real age of the patients, values are shifted and the shifting calculation is not available. So it is not included.

Remaining features(*Phosphate*, *Glucose*, *Bicarbonate*, *White Blood Cells*, *Hematocrit*, *Urea Nitrogen*, *Creatinine*, *Hemoglobin*, *pO2*, *Red Blood Cells*, *Chloride*) are derived from lab_events table. They are selected because they represent the most abnormal laboratory test results among all the deceased patients. These test findings are compared to the usual ranges for the relevant laboratory measurements. If a test result falls below the expected range, the difference between the lower interval and the measurement is calculated. When the test result falls within the usual range, a value of 0 is assigned. In contrast, if the result is excessively high, the difference between the measurement and the upper interval is calculated. Then mean of the results are calculated for the selected lab tests.

The summaries of the feature definitions can be found at Table III.

Random survival Forests, Gradient Boosted Models, and Survival Support Vector Machines from Python scikit-survival library [24] are used for the experiments. A subsample of 3000 patients from each class is collected to reduce the computational requirements. Train-test-validation sets are created with a split of 60%, 20%, and 20%.

Random Survival Forest (RSF) is utilized with the following hyperparameters using grid search: 500 decision trees (`n_estimators=500`), a minimum number of samples necessary for splitting an internal node (`min_samples_split=5`), and each leaf node contains at least 10 samples (`min_samples_leaf=10`). The model was parallelized with `n_jobs=-1`, employing all available processors. To ensure reproducibility, the random state was set to a predefined seed value of 0,2 (`random_state=0.2`).

Permutation-based feature importance matrix indicated *icd_codes_group* and *gender* is not important so they are excluded. Figure 9 shows the importance of each feature. Concordance index value of the model is 0,792. Thus, it can be said that the results are neither random nor excellent. The

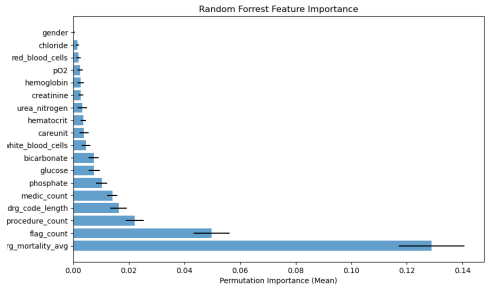

Fig. 9. Random Forrest Feature Importance

most important feature is *drg_mortality_avg*. AUC score of the model is 0,814.

Two gradient boost models are considered: one of which is component-wise least squares as base learner and the other is a regression tree base learner. Grid search is used for finding optimal hyperparameters. The least squares as base learner model uses 1000 decision trees (`n_estimators=1000`) with a learning rate of 0.1. The random state was set to a predetermined seed value of 0.2. The regression tree base learner model makes use of 1000 decision trees (`n_estimators=1000`) with a learning rate of 0.1. The random state was additionally set to a specified seed value of 0.2 (`random_state=0.2`).

The regression tree base learner model had a concordance index of 0.817 and an AUC of 0.863. In comparison, the least squares based gradient boost model did marginally worse, with a concordance index of 0.789 and an AUC score of 0.827.

Finally, tests were performed with a survival support vector machine. The alpha parameter is set to 0.0156 according to the grid search results (`alpha=0.0156`). AVL tree optimizer is used, and the maximum number of iterations is specified to 1000 (`max_iter=1000`). The tolerance parameter is set to 1e-5, and the random state is set to 20, as the model only accepts positive random variables.The results were somewhat better than random. The confidence index value is 0.691.

VI. Conclusions and Future Work

At last, this study sought to predict patient survival outcomes using multiple variables taken from a dataset generated through intensive data analysis.

Key features like *drg_mortality_avg*, *medic_count*, *flag_count*, *procedure_count*, *careunit*, and *gender* were taken into account, providing insights into patients' diagnoses, medications, abnormal lab results, medical procedures, care unit information, and gender. Additionally, a group of aberrant lab test findings was chosen for additional investigation.

Random Survival Forest, with hyperparameters adjusted for best performance, recognized *icd_codes_group* and *gender* as less relevant characteristics and excluded them. The model had a concordance index of 0.792, indicating acceptable prediction performance. The most influential feature, *drg_mortality_avg*, considerably contributed to the model's accuracy, as demonstrated by the AUC score of 0.814. The two gradient boost models, performed differently. The regression tree base model was better than the component-wise least squares model, with a concordance index of 0.817 and an AUC score of 0.863, vs 0.789 and 0.827, respectively. Finally, a Survival Support Vector Machine was used. Despite producing outcomes just slightly better than chance, the confidence index value of 0.691 indicates potential for improvement.

In conclusion, the study explored multiple survival prediction models on a handpicked dataset, offering insights into the significance of individual variables in predicting patient outcomes. Further improvement of models and feature selection may improve predicted accuracy in future iterations of this investigation.

TABLE III
Features Used for the Experiments

Data Table	**Definition**
drg_codes_group	How many DRG's patients is a member of.
drg_mortality_avg	Average of the drg_mortality parameter for each patient from the drg_codes table.
medic_count	Number of medications the patient uses.
flag_count	Average number of abnormal test results a patient had.
procedure_count	Number of procedures the patient underwent.
careunit	Care unit in which the patient stays.
gender	Gender of the patient.
phosphate	Parameter representing the average difference between the phosphate test results and the average value range.
glucose	Average difference between the glucose test results and the average value range.
bicarbonate	Average difference between the bicarbonate test results and the average value range.
white_blood_cells	Average difference between the white blood cell test results and the average value range.
hematocrit	Average difference between the hematocrit test results and the average value range.
urea_nitrogen	Average difference between the urea nitrogen test results and the average value range.
creatinine	Average difference between the creatinine test results and the average value range.
hemoglobin	Average difference between the hemoglobin test results and the average value range.
pO2	Average difference between the pO2 test results and the average value range.
red_blood_cells	Average difference between the red blood cell test results and the average value range.
chloride	Average difference between the chloride test results and the average value range.

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