# Team 40: Predicting Mortality in ICU Setting (Project Draft).

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#### Abstract

Medical data capturing and electronic health records are now improving to the point where we are rapidly improving the amount and quality of data we get about a patient. Socioeconomic data is often captured such as race, marital status, and even insurance type (e.g. Medicaid or Medicare). Electronic Health Record (EHR) systems often track key clinical values like certain labs, prescription history, and acute diagnoses. We also have access to real-time vital signs that becomes available in intensive care unit (ICU) settings. However, the challenge comes in modeling this data due to the high density and heterogeneous data types. Furthermore, because any modeling will ultimately support human decision making (doctors and other clinical staff), interpretability comes at a premium. Because of this, using natural language processing tools to decompose free-text clinical notes into meaningful features is very attractive and valuable since it offers a potentially richer set of meaningful features that are hard to capture in structured form. In this project, we fit three models: a baseline model composing purely of static and demographic features, a model with structured clinical data, and a model that does Natural Language Processing over free-text clinical notes. The baseline model achieves an AUROC of about 70%. [PLACEHOLDER FOR PERFORMANCE OF MORE ADVANCED MODELS

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## 1 Introduction

Accurate knowledge of patient's clinical state is critical in a clinical setting. Patients in an intensive care unit are particularly in a critical state. Thus, if we can have better accurate mortality prediction within an ICU, we can use this to better understand which patients should be prioritized for clinical care and how we can better allocate resources. Within an ICU, there are many measurements being made from from various devices, but we know that there are both problems in terms of false positives and false negatives. While false negatives might seem to be more problematic, being too sensitive and introducing a lot of false positives also has problems as well. Too many false positives results in information fatigue and providers lose trust in signal as it's hard to separate from noise. By improving mortality prediction using data from EMRs and other clinically-relevant data, we can provide better predictions to improve efficiency and quality of care.

# 2 Background and Literature Review

Siontis et. al (2011) [7] provide an empirical review of methodologies around mortality models. In this paper, the authors use Medline to identify studies published in 2009 that assessed AUC of predicting all cause mortality. What they find is that most studies at the time predicted mortality with modest accuracy, with large variability across populations, which makes sense since for since very high risk populations it may be easier to predict mortality, but for lower risk general populations, the class imbalance is very high with relatively few patients actually dying. A full list of the studies that the authors review and the approaches they use are documented in the paper (linked above). However, we also copy a portion of that table in Table 1 as an illustrative example.

Taking a step back, we note that there have been many attempts to predict mortality, with some models being quite complicated. However, there have also been more technically simple models that attempt to predict mortality. For example, in DeSalvo et. al (2005) [2], the authors attempt to predict mortality using a single question: "In general, would you say your health is ... Excellent, Very Good, Good, Fair, or Poor". Similarly, we will provide a baseline model that only uses demographics and static variables (see Table 2 for the specific variables used) as features to predict mortality. While we know that we can do better using a richer feature set, doing a simple model with demographics and static variables provides us with a baseline to benchmark against.

Table 1: Literature Review

Disease Clinical Condition	Predictive Model	Variables Used
Cardiovascular Disease	Acute Kidney Injury Network (AKIN)	serum creatinine criteria or urine output criteria
Critical Illness	Acute Myocardial Infarction in Switzerland (AMIS) model	age, Killip class, systolic blood pressure, heart rate, prehospital cardiopulmonary resuscitation, history of heart failure, history of cardiovascular disease
Critical illness Gastroenterology-related	Acute Physiology And Chronic Health Evaluation (APACHE) II	temperature, mean arterial pressure, heart rate, respiratory rate, oxygenation or PaO2 , arterial pH, serum sodium, serum potassium, serum creatinine, hematocrit, white blood cell (WBC) count, Clasgow Coma Score

Next, there are a few papers that actually use the MIMIC III data for mortality prediction using ICU data. In Unfolding Physiological State: Mortality Model in Intensive Care Units, Ghassemi et. al (2014)[3], the authors use Latent Variables Models to decompose free-text hospital notes into meaningful features to predict patient mortality. For the actual prediction, they use linear SVM in various setting (e.g. patient first arrives at hospital, In hospital mortality, 30 day mortality, etc.) and they largely find that using hospital notes improved AUCs.

# 3 Methodology

What we will do in this project is to try to reproduce and improve models motivated by Unfolding Physiological State: Mortality Model in Intensive Care Units (Ghassemi et. al). In particular, what we find interesting is the use of free-text hospital notes to better predict mortality. This is because in many cases, there are already many mortality models, built both on Business Rules, and machine learning to predict mortality. Perhaps the biggest methodology to improve on existing mortality models is to use unstructured data, to see if there is any additional signal from notes and other text that we don't already get from structured data using EHRs.

To be more specific, we will use the same dataset as indicated in the Project guidelines, MIMIC III. This data set has 46,520 patients, 58,976 Hospital Admissions, about 200,000 Clinical notes, and about 6,000 mortality events. We will then divide into 70% training and validation, 30% test set. Similar to what is presented in the paper, we will first extract clinical baseline features, including age, sex, and SAPS-II score, from the database for ev-

ery patient. We will then perform topic modeling, perhaps LDA, to do natural language processing on the notes to extract meaningful features. In terms of evaluating our model, we will predict on multiple iterations of the outcome variable, just as the paper does. For example, to evaluate 24 hour mortality predictions, in the training set, we will create a 24 hour prediction window and using the data that is transformed into features, we will measure AUC of mortality where outcome variable is mortality within 24 hours. We will then test on held-out test data set to report final test AUC.

## 3.1 Data Exploration

The dataset contains 58,976 distinct hospital admissions with 46,520 distinct patients. Thus, most people in this dataset were admitted once, which makes sense, but there is also a long tail of readmissions.

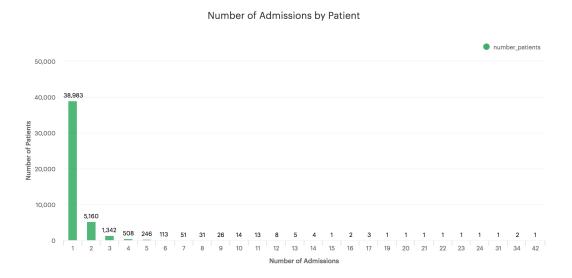


Figure 1: Admissions Distribution

About 39,000 patients were admitted once, with 5,160 admitted twice. However, there s a long tail of about 2,000 remaining patients who have been admitted more than twice in this time period, with the maximum being 42 admissions over this time period.

Furthermore, we note that admission lengths on average are about 10 days, but the median length of stay is closer to 6.5 days. This makes sense as again, the distribution is likely right skewed. There are patients with very long outlier lengths of stays dragging mean up, but the median, which is less sensitive to outliers is lower.

Figure 2: Admissions Lengths (In Days)

Note that there are a few patients with negative lengths of stays. This is likely bad data. The longest a patient was in the hospital is about 290 days which is almost 10 months.

Next, we look at the breakdown of admissions by patients' insurance. This is interesting because the type of insurance a patient has is likely to be very correlated with patient characteristics. For example, Medicare patients will likely be older and have more acute risk. Medicaid is likely correlated with meaningful socioeconomic characteristics. As expected, many of the patients are Medicare patients, at about 48% of the total population. This makes sense as Medicare patients are older and higher risk, so will comprise more of the admissions.

Figure 3: Admissions by Patients' Insurance

	insurance	number_patients	percentage_patients
1	Government	1783	0.03
2	Medicaid	5785	0.098
3	Medicare	28215	0.478
4	Private	22582	0.383
5	Self Pay	611	0.01

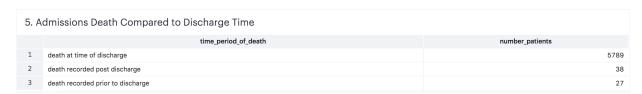
In addition, we note that about 5,800 patients are recorded as having died at some point after the admission.

Figure 4: Admissions Deaths



In fact, if we look at the distribution of times to death, we see that the vast majority of deaths are recorded at the same time as the discharge time.

Figure 5: Admissions Deaths Time Period



Given this, it very likely means that mortalities recorded before the discharge time are due to clerical error. It's also possible that mortalities recorded after the discharge time are also a result of clerical error; although it is possible that the study followed up with the patient post-discharge.

#### 3.2 Feature Extraction

Now that we have done some data exploration, this next section will discuss feature extraction and what features we actually used in our model to predict mortality.

Table 2: Features

	(1)	(2)
Categories	Features	Extracted
Demographic and Static Features	Age, Gender, Ethnicity, Admission Type, Insurance Type	
Vital Signs	Heart Rate	Min, Max

#### 3.3 Model Architecture

#### 3.3.1 Baseline Model

We first provide a baseline model that is a Random Forest model that only uses the Demographic and Static Features as described in Table 2. The purpose of this is to provide a simple model that can serve as a baseline. We then split the data into 70% Training and 30% Test, so the Training dataset had 41,283 rows and the Test data set contained 17,693 rows. We then use Stratified K-Fold Validation with  $n_splits = 6$ . For features, we one-hot encoded  $admission_type$ , insurance, language,  $marital_status$ , and ethnicity. In the end, this yielded a total of 137 features, one for each value, including when the value is null.

### 3.3.2 Improved Model: With Structured Clinical Data

#### 3.3.3 Best Model: Using LDA

# 4 Experimental Results

#### 4.0.1 Baseline Model

We first show results of the baseline Random Forest model that only uses the Demographic and Static Features as described in Table 2.

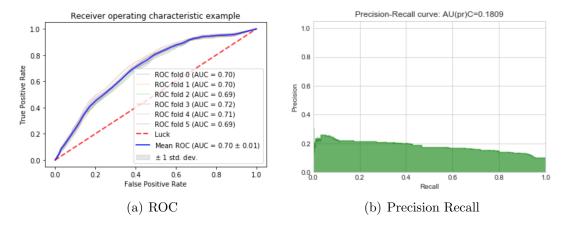


Figure 6: Baseline Model Performance

As Figure 6 shows, even with just basic Demographic and Static Features, the model does OK. Average AUROC is about 0.70, and precision recall curve is about 0.1809 (with baseline mortality rate of about 9% as we saw in Section 3.1.

- 4.0.2 Improved Model: With Structured Clinical Data
- 4.0.3 Best Model: Using LDA
- 5 Discussion

## 6 Conclusion

Filler

## References

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