Mortality Prediction via Physicians’ Notes

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## Abstract

Sepsis is the leading cause of death in the hospitals. The disease also adds a severe financial burden on the healthcare system being the leading contributor to the medical expenses. In this paper, we explore the possibility of mortality prediction using free text notes available for each patient.

## Introduction

Sepsis is the most expensive condition to treat in the US hospitals with an expense of $23.7 billion in the year 2013. Of the 1.6 million+ per year cases of sepsis, 40% with severe sepsis do not survive. Additionally, there has been an increase in hospitalization in the last 10 years for adult patients.

Consequently, it will be immensely beneficial to have an early detection of Sepsis. In fact, an early detection carries a cost of $3000/case as opposed to $32,000/case after admission into a hospital.

On admission into the hospital, there are several attributes already present for each patient; additionally more attributes are generated constantly due to various tests being conducted for the patient. In this paper, we focus primarily on the notes written by various physicians. The aim of a machine learning based analysis of patient data is eventually to replicate the intuition and decision making of a physician. As such, what better place to start at than the free text notes generated by various physicians for a given patient.

Although “Sepsis” has been described for over 2000 years, there is no “gold standard” to define it conclusively. Many conditions or infections if left untreated can eventually lead to festering which can cause organ failure and septic shock. Now, intuitively, there is a close relationship between an “icu” admission and infection leading to “Sepsis”. And in 2016, Sepsis and Septic Shock have been defined as, “*A life-threatening organ dysfunction due to a dysregulated host response to infection*”. We can exploit this implicit relationship by looking at the mortality data in the ICU to arrive at Sepsis diagnosis.

We plan to use the MIMIC-III openly available dataset developed by the MIT lab for Computational Physiology. This database contains health data for approximately 40,000 critical care patients from the Beth Israel Deaconess Medical Center collected over a period of 10 years.

We demonstrate the use of free text notes as features for each patient. These features can then be leveraged in further machine learning analyses for prediction.

## Previous Research

There is a well-established and prevalent system used in the hospitals, called “qSOFA” or quick Sequential Organ Failure Assessment. A qSOFA score of 2 or greater indicates “Sepsis”. However, this test takes into account just three indicators – Respiratory rate, systolic blood pressure and altered Mentation or mental activity. qSOFA considers low blood pressure (SBP≤100 mmHg), high respiratory rate (≥22 breaths per min), or altered mentation (Glasgow coma scale<15).

Ghassemi et al focused on the free text notes for the same analysis. They devised a range of three prediction regimes, in which the free text notes are used to buttress the baseline indicators for analysis. Additionally, the authors considered prediction under two separate timelines – 30 day and 1 year post discharge. The authors normalized each note to a 50-dimension vector and the notes were then aggregated on a 12-hour scale.

Other related works focused on clinical notes used to enhance the structured physiological data.

DeSautels et al applied a machine learning system called “Insight” focused on easily obtained patient data such as the vitals. They were able to achieve a better classification score than qSOFA. The authors considered a window of 48 hours before admission to 24 hours after the admission. The study demonstrates the potential of vital signs in predicting sepsis and mortality if applied with intelligent modifications.

## Approach

**Big Data Technology Stack and Rationale**

The analysis relies upon big data technologies, specifically yarn and Spark. The data extraction and preparation shall be performed using Postgres relational database. The advanced machine learning analyses will be performed using the machine learning library ML-lib on Spark.

The rationale for using the big data technology is simply the desire to process ever growing amount of data. Although the current analysis is based on the freely available MIMIC-III database, our objective is that this type of analysis is generic enough to be abstracted into a pattern and as such can be applied to similar information privately available as well.

Apache Spark leverages the power of a distributed cluster by fanning out the data storage and computation across hundreds or thousands of computers and cores. The most basic unit of data in Spark is called a Resilient Distributed Dataset or *RDD*. It is assumed that a dataset is so large that it cannot fit on a single node. Consequently, it’s broken up into chunks and distributed across the entire cluster of machines. A “*Partition*” is the most atomic chunk of data that can fit on a single node. An RDD is a collection of multiple partitions. Spark then schedules these partitions for computation or processing across the nodes of the cluster. Spark will be used for data transformation as well since it can utilize the power of a Hadoop cluster.

The attraction of ML-lib is that it is designed for Spark and as such works on RDD. The algorithms have been designed for distributed processing on Spark. The first step of the analysis will revolve around “topic modeling” out of the free text notes.

**Latent** **Dirichlet** **Allocation**

LDA is a very effective method for topic generation out of a corpus of document. LDA aims to generate a collection of topics, where each topic is a collection of words and an assignment of topics for each document based on probability. These probability distributions have an interesting property called, “*sparsity*”, which penalizes the assignment of a word to a topic and a topic to a document. The belief is that a topic has only a very few words that truly representative of it. Similarly, a document truly has a very small number of topics, mostly a single one, which it manifests based on the words. A document has a propensity towards a small number of topics and a topic has a propensity towards a small number of words and these two goals are in conflict with each other. LDA aims to strike a balance between the two.

**Clustering by K-Means**

Clustering aims to group objects in such a way that objects in the same group are more similar to each other than objects from other groups. K-means is a centroid-based clustering algorithm, which aims to decrease the distance between each point represented by a feature vector and the centroid. Each point is thus assigned to a centroid with the smallest distance among all the centroids. Spark ML-lib provides a parallelized K-means implementation which we plan to use for our analysis.

We chose K-means over Gaussian mixture model because of its simplicity, ability to produce accurate results and the “certainty” desired of a point belonging to one of the clusters. K-means has a better running time and works well with larger number of dimensions. In case we choose to increase the number of topics, K-means will scale well. The results are easier to interpret being part of spherical clusters. Additionally, the number of clusters is small; especially in case of mortality, we plan to use two clusters – dead and alive.

**Flow**

Each patient may have multiple entries in the database with unique notes. Each of these notes, represents a story at the given moment in time. The objective of our analysis is to cobble together a representative “*narrative*” based on the individual stories which can present a singular picture vis-à-vis Sepsis and Mortality.

We extract the “*NOTEEVENTS*” table from the MIMIC-III database, focusing on two fields – subject and the notes.

This data is loaded into HDFS, the distributed file system employed in the Hadoop or Yarn cluster. HDFS enables us to process data without worrying about the size. If the available data is truly large in size, our approach will still work without modification as it simply piggy-backs on the power of the yarn cluster which can be scaled horizontally by increasing the number of nodes in the cluster. On loading into HDFS, the data is automatically broken up into chunks called “blocks” based on the block size configured on the cluster. The block size usually ranges from 128 MB to even 1GB. Since the size of the “*NOTEEVENTS*” table is relatively small, we chose a block size of *128 MB*. With the cluster size available, this enabled us to extract optimal level of parallelism from the nodes.

Next, we run the LDA analysis on the input data stored in HDFS. This generates three output files – topic information, map of documents to topics and map of topics to document. The topic output can be used for general understanding, while the document to topics map is used for the next phase of analysis.

The “*topTopicsPerDocument*” file is used for the next stage in the pipeline, which is the K-means analysis. The output of the K-means is a mapping of cluster to the identifier. The identifier for each document in this case is the “subject\_id” or the patient.

The final stage in the pipeline is the performance measurement. We employed the “*purity*” measure to evaluate the performance of the clustering step. [Purity is an external evaluation criterion of cluster quality](http://nlp.stanford.edu/IR-book/html/htmledition/evaluation-of-clustering-1.html#fig:clustfg3) and is expressed by,

Where

N = number of data points,

K = number of clusters,

ci = a cluster

tj = classification with the max count for cluster c**i**

## Method

**Preparation**:

We leverage the MIMIC-III database for our analysis. This database contains 26 tables distributed as zipped “CSV” files. Each table has a “*subject\_id*” which refers to the patient under consideration and can be used to link with other tables. These files once downloaded and extracted are loaded into Postgres database. Postgres is chosen for it stability and flexibility in addition to being an open source and freely available product. It can be installed on multiple operating systems and has a mature ecosystem of client tools. Special care needs to be taken while importing the “*free text notes*”, primarily because the notes are enclosed in quotations and contain carriage return characters as well as can be quite long. Postgres makes this task easier by interpreting all these cases while importing the data.

It is important to review the AMIA Call for Participation (CFP) where types of submissions considered and general requirements for each submission type are listed. All submissions must conform to the format and presentation requirements described in the CFP and at the submission site.

Another Major Heading and References

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More text of an additional paragraph, with a figure reference (Figure 1) and a figure inside a Word text box below. Figures need to be placed as close to the corresponding text as possible and not extend beyond one page.



**Figure 1.** Total allergy alerts, overridden alerts, or drug order cancelled.

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**Table 1.** Submission type, abstract length, and page length maximum for AMIA submissions.

|  |  |  |
| --- | --- | --- |
| **Submission Type** | **Abstract Length** | **Page Length Maximum – *If your submission is longer than what is specified below, it will be rejected without review*** |
| Paper  Stu | 125-150 words | Ten  TenTen tenTen ttem  Ten |
| Student Paper | 125-150 words | Ten  tem |
| Poster | 50-75 words\* | One |
| Podium Abstract | 50-75 words\* | Two |
| Panel | 150-200 words | Three |
| System Demonstrations | 150-200 words | One |

**\*** All podium abstract and poster submissions must have a brief (50-75 words) abstract. The abstract does NOT have to be part of the document, but must be entered on the submission website in the Abstract box in Step 2.

This is another paragraph.

Conclusion

Your conclusion goes at the end, followed by References, which must follow the Vancouver Style (see: www.icmje.org/index.html). References begin below with a header that is centered. Only the first word of an article title is capitalized in the References.

References

1. Pryor TA, Gardner RM, Clayton RD, Warner HR. The HELP system. J Med Sys. 1983;7:87-101.
2. Gardner RM, Golubjatnikov OK, Laub RM, Jacobson JT, Evans RS. Computer-critiqued blood ordering using the HELP system. Comput Biomed Res 1990;23:514-28.

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2. <https://nlp.stanford.edu/IR-book/html/htmledition/evaluation-of-clustering-1.html#fig:clustfg3>