**Doctor AI: Predicting Clinical Events via Recurrent Neural Networks**

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**Abstract**

Large amount of Electronic Health Record (EHR) data have been collected over millions of patients over multiple years. The rich longitudinal EHR data documented the collective experiences of physicians including diagnosis, medication prescription and procedures. We argue it is possible now to leverage the EHR data to model how physicians behave, and we call our model Doctor AI. Towards this direction of modeling clinical behavior of physicians, we develop a successful application of Recurrent Neural Networks (RNN) to jointly forecast the future disease diagnosis and medication prescription along with their timing. Unlike a traditional classification model where a single target is of interest, our model can assess entire history of patients and make continuous and multilabel prediction based on patients’ historical data. We evaluate the performance of the proposed method on a large real-world EHR data over 250K patients over 8 years. We observe Doctor AI achieves up to 79% recall@30, significantly higher than several baselines.

**1 Introduction**

The introduction of Electronic Health Records (EHR) in health care has made available a massive amount of high-quality data. This has created an opportunity to perform sophisticated clinical analysis that was too complex to efficiently perform before. Forecasting future clinical events for patients is an especially challenging, yet important task that attempts to predict occurrence of various diseases over time for individual patients and what type of actions will be taken by the physicians. Successful forecasting will be, in a sense, equivalent to modeling the behavior of human doctors, which will not only facilitate patient-specific care and timely intervention, but also reduce the healthcare costs.

Although parts of this problem such as disease progression modeling has been studied by many researchers over several decades, e.g. (Heckerman, 1990; Chapman et al., 2001; Lange et al., 2015), most works do not achieve the required accuracy and scalability, lack generality, or need excessive expert domain knowledge. With our work, the Doctor AI will be able to diagnose multiple problems and prescribe appropriate medications for anyone who can provide his/her medical history. Furthermore, the Doctor AI is able to predict when the patient will make the next visit, a service doctors are not known to often provide. The Doctor AI has huge potential to help both service providers (e.g. insurance companies, hospitals) and service consumers (e.g. individual patients). Additionally, the fact that it does not need any domain knowledge such as medical ontologies makes it easier to learn from the EHR of various sources.

The problem in its full generality can be described as a multilabel marked point process modeling task. The task is different from common sequential learning tasks such as those in natural language processing as it requires prediction of multiple categories over the continuous time axis. The key challenge in this task is to find a flexible model that is capable of jointly performing multiple types of prediction for patients.
The two main class of techniques, continuous-time Markov chain based models (Nodelman et al., 2002; Lange et al., 2015; Johnson & Willsky, 2013), and intensity based point process modelling techniques such as Hawkes processes (Liniger, 2009; Zhu, 2013; Choi et al., 2015) are expensive to generalize to nonlinear and multilabel settings. Furthermore, they often make strong assumptions about the data generation process which make them not only inaccurate, but also not scalable to large scale datasets.

The key idea of this paper is to solve these challenges via learning an effective representation of the patient status over time. Once we concisely summarize the status of patients in a numerical vector, we would be able to jointly predict different future quantities about the patients such as their future diagnoses and medications and the time until their next visit. To learn such patient representations we propose to use recurrent neural networks, considering the fact that patients have different length of medical records and that recurrent neural networks have been shown to be particularly successful for representation learning in sequential data, e.g. (Graves, 2013; Graves & Jaitly, 2014; Sutskever et al., 2014; Kiros et al., 2014; Zaremba & Sutskever, 2014).

In particular, we make the following main contributions in this paper:

- We demonstrate a successful application of recurrent neural networks in representing the status of patients, predicting the future medical events and the timing of the events on the patient record. The trained RNN is able to achieve above 64% recall in its top 10 predicted diagnosis codes, proving that it can serve as an effective differential diagnosis machine.
- We propose an efficient initialization scheme for RNNs using Skip-gram embedding (Mikolov et al., 2013) and show that it improves the performance of the RNN in our problem.

2 Methodology

This section describes the main proposed neural network model. After mathematically describing the problem as a multilabel point process modeling, we outline our approach for addressing the challenges. The proceeding sections are devoted to details of the model and the technical details of the learning procedure.

Problem setting. For each patient, we are given a sample of size $n$ from a univariate multilabel marked point process in the form of $(t_i, x_i)$ for $i = 1, \ldots, n$. Each pair represents an event, such as a hospital visit, during which multiple medical codes such as ICD-9 diagnosis codes, procedure codes, or medication codes are assigned to a patient. The multi-hot label vector $x_i \in \{0, 1\}^p$ represents the medical codes assigned at time $t_i$, where $p$ denotes the number of unique medical codes. At each time stamp, we may extract higher-level codes for prediction purposes and denote it by $y_i$, see the details in Section 4.1. The number of events for each patient may differ.

Description of neural network architecture. Our goal is to learn an effective vector representation for the status of patients at each time stamp $t_i$. Using the representation for the status of patients, we would be
able to jointly predict different future quantities about this patient such as future diagnoses and medications \(y_{i+1}\) and the time duration until next event \(d_{i+1} = t_{i+1} - t_i\). Finally, we would like to perform all these steps jointly in a single supervised learning scheme. As we discussed in the introduction, we use recurrent neural networks to learn such patient representations. We treat the state vector of RNNs as the latent representation for the patient status and use it for predicting multiple forms of outputs.

The proposed architecture is shown in Figure 2. The input at each timestamp \(t_i\) is the concatenation of the multi-hot coding \(x_i\) of the multilabel categories and the duration \(d_i\) since the last event. In our datasets, this input have as large as 40,000 dimensions. Thus, the next layer maps into a lower dimensional space. Then, we pass the lower dimensional vector through units of an RNN. The RNN units can be simple RNN units (Le et al., 2015) or more complex recurrent units such as Long Short-Term Memory (LSTM) (Hochreiter & Schmidhuber, 1997; Graves et al., 2009) or Gated Recurrent Units (GRU) (Chung et al., 2014). We also can stack multiple units of RNN on top of each other to increase the representative power of the network. Finally, we use a softmax layer to predict the future codes and a rectified linear unit to predict the time duration until next event.

Details of the RNN. Specifically, we implemented our RNN with GRU. Although LSTM has drawn much attention from many researchers, GRU has recently shown to have similar performance as LSTM, while employing a simpler architecture (Chung et al., 2014). In order to precisely describe the network used in this work, we reiterate the mathematical formulation of GRU as follows:

\[
\begin{align*}
    z_i &= \sigma(W_z x_i + U_z h_{i-1} + b_z) \\
    r_i &= \sigma(W_r x_i + U_r h_{i-1} + b_r) \\
    \tilde{h}_i &= \tanh(W_h x_i + r_i \circ U_h h_{i-1} + b_h) \\
    h_i &= z_i \circ h_{i-1} + (1 - z_i) \circ \tilde{h}_i
\end{align*}
\]

where \(z_i\) and \(r_i\) respectively represent the update gate and the reset gate, \(\tilde{h}_i\) the intermediate memory unit, \(h_i\) the hidden layer, all at time stamp \(t_i\). For predicting the diagnosis codes and the medication codes at each time stamp \(t_i\), a Softmax layer is stacked on top of the GRU, using the hidden layer \(h_i\) as the input: \(\hat{y}_{i+1} = \text{softmax}(W_{\text{code}} \cdot h_i + b_{\text{code}})\). For predicting the time duration until the next visit, a rectified linear unit (ReLU) is placed on top of the GRU, again using the hidden layer \(h_i\) as the input: \(\hat{d}_{i+1} = \max(w_{\text{time}} \cdot h_i + b_{\text{time}}, 0)\). The objective of training our model is to learn the weights \(W_{\{z,r,h,\text{code}\}}\), \(U_{\{z,r,h\}}\), \(b_{\{z,r,h,\text{code}\}}\), \(w_{\text{time}}\) and \(b_{\text{time}}\). The values of all \(W\)’s and \(U\)’s were initialized to orthonormal matrices using singular value decomposition of matrices generated from the normal distribution (Saxe et al., 2013). The initial value of \(w_{\text{time}}\) was chosen from the uniform distribution between \(-0.1\) and \(0.1\). All \(b\)’s and \(b_{\text{time}}\) were initialized to zeros. The joint loss function consists of the cross entropy for the code prediction and the squared loss for the time duration prediction, as described below for a single patient:
As mentioned above, the multi-hot vectors $x_i$ of almost 40,000 dimensions are first projected to a lower dimensional space, then put into the GRU. We employed two different approaches for this: (1) We put an extra layer of a certain size between the multi-hot input $x_i$ and the GRU, and call it the embedding layer. We denote the weight matrix between the multi-hot input vector and the embedding layer as $W_{emb}$. Then we learn the weight $W_{emb}$ as we train the entire model. (2) We initialize the weight $W_{emb}$ with a matrix generated by Skip-gram algorithm (Mikolov et al., 2013), then refine the weight $W_{emb}$ as we train the entire model. This can be seen as using the pre-trained Skip-gram vectors as the input to the RNN and fine-tuning them with the joint prediction task. The brief description of learning the Skip-gram vectors from the EHR is provided in Appendix A. The first and second approach can be formulated as follows:

$$h^{(1)}_i = [\tanh(x_i^T W_{emb} + b_{emb}), d_i] \quad (1)$$

$$h^{(1)}_i = [x_i^T W_{emb}, d_i] \quad (2)$$

where $[\cdot, \cdot]$ is the concatenation operation used for appending the time duration to the multi-hot vector $h^{(1)}_i$ to make it an input vector to the GRU.

3 RELATED WORK

In this section, we briefly overview the common approaches to modeling multilabel event data with special focus on the models that have been applied to medical data.

**Discretization vs Continuous-time modeling.** There are two main approaches to modeling point process data: with or without discretization (binning) of time. When the time axis is discretized, the point process data can be converted to binary time series (or time series of count data if binning is coarse) and analyzed via time series analysis techniques (Truccolo et al., 2005; Bahadori et al., 2013; Ranganath et al., 2015). However, this approach is inefficient as it produces long time series whose elements are mostly zero. Furthermore, discretization of time introduces noise in the time stamps of visits. Finally, these models are often not able to model the duration until next event. Thus, it is advantageous not to discretize the data both in terms of modeling and computation.

**Continuous-time models.** Among the continuous-time models, there are two main techniques: continuous-time Markov chain based models (Nodelman et al., 2002; Foucher et al., 2007; Johnson & Willsky, 2013; Lange, 2014) and intensity function modeling techniques such as Cox and Hawkes processes (Liniger, 2009; Zhou et al., 2013; Linderman & Adams, 2014; Choi et al., 2015). The latter has been shown to have computational advantages over the former. Moreover, modeling multilabel marked point processes with continuous-time Markov chains expands their state-space and make them even more expensive.

However, Hawkes processes only depend linearly on the past observation times; while there are limited classes of non-linear Hawkes process (Zhu, 2013), the temporal dynamics can be more complex. Moreover, there is no scalable multi-label extension for Hawkes processes. Finally, Hawkes processes are known to have a flat loss function near optimal value of the parameters which renders the gradient-based learning algorithms inefficient (Veen & Schoenberg, 2008). In this paper we address these challenges by designing a recurrent neural network which has been shown to be successful in learning complex sequential patterns.

4 EXPERIMENTS

In this section, we describe the details of our experiments, the datasets that we have used and the baselines. Throughout this section, we demonstrate the success of the proposed approach in forecasting the future events of the patients.
Table 1: Basic statistics of the Sutter Health clinical records dataset.

|                        |      |                        |      |
|------------------------|------|------------------------|------|
| # of patients          | 263,706 | Total # of codes      | 38,594 |
| Avg. # of visits       | 54.61 | Total # of 3-digit Dx codes | 1,183 |
| Avg. # of codes per visit | 3.22  | # of top level Rx codes | 595   |
| Max # of codes per visit | 62    | Avg. duration between visits | 76.12 days |

4.1 Dataset description

We use a health records dataset provided by Sutter Health; its basic statistics are summarized in Table 1.

**Population and source of data** The source population for this study was primary care patients from Sutter Palo Alto Medical Foundation (PAMF) Clinics, a multispecialty group practice with large primary care practices that has used EHR for more than 8 years. The dataset was extracted from a case-control study for heart failure nested within Sutter-PAMF. The dataset consists of encounter orders, medication orders, problem list records and procedure orders.

**Data processing** For input, we used diagnosis codes, medication codes, and procedure codes. Diagnosis codes, which are presented in the ICD-9 format, could be found in the encounter orders, medication orders, problem list records and procedure orders. Medication and procedure codes could be found in medication orders and procedure orders respectively. We extracted all diagnosis, medication and procedure codes from the dataset for each patient, and laid them out in a temporal order. If a patient received multiple codes in a single visit, those codes were assigned the same timestamp. By excluding patients that made less than two visits, we were left with 263,706 patients who made on average 54.61 visits per person.

**Medical code grouping** The number of ICD-9 diagnosis codes are approximately 11,000. The number is approximately 18,000 for medication codes. Many codes in this set are very granular; for example, pulmonary tuberculosis (ICD-9 code 011) is divided into 70 subcategories (ICD-9 code 011.01, 011.02, ..., 011.95, 011.96). In a practical perspective, however, simply knowing that a patient is likely to have pulmonary tuberculosis is enough to increase the doctor’s awareness of the severity of the clinical situation. Therefore, in order to predict future diagnosis codes and medication codes, we group the codes into a higher-order codes to decrease the granularity among the codes that we predict. For the diagnosis codes, we use the 3-digit ICD-9 code system, where the the number of unique codes are 1,183 in our dataset. For the medication codes, we use the Sutter in-house medication grouper, which groups the medication codes into 595 unique codes. Therefore, the future code prediction problem reduces from approximately a 29,000 class classification to a 1,778 class classification. The $y_i$ in Figure 2 is the 1,778-dimensional vector representing the grouped diagnosis codes and medication codes.

**Training specifics.** For training all models including the baselines, we used 85% of the patients as the training set and 15% as the test set. We did not use a validation set as we fixed the hyperparameters to reasonable values as described in the following paragraphs. We used dropout between the GRU layer and the prediction layer (i.e. code prediction and time duration prediction). Dropout was also used between GRU layers if we were using a multi-layer GRU. We also apply norm-2 regularization on both $W_{code}$ and $w_{time}$. The both regularization parameters were set to 0.001.

The size of the hidden layer $h_i$ of the GRU was set to 2000. After sets of preliminary experiments where we tried the size from 100 to 2000, we noticed that the code prediction performance saturated around 1600~1800. Therefore we chose 2000 to guarantee the best performance. The model was implemented with Theano (Bastien et al., 2012) and trained on a machine equipped with two Nvidia Tesla K80 GPUs.

4.2 Evaluation metrics

We use the following metrics for evaluating the performance of the algorithms in predicting the codes and the time duration until next visit.
Top-k recall. In order to evaluate the performance of algorithms for forecasting next events, we use the top-k recall measure defined as follows:

\[
\text{top-k recall} = \frac{\text{# of true positives in the top } k \text{ predictions}}{\text{# of true positives}}
\]

This metric is consistent with the differential diagnosis framework where the machine suggests \(k\) possible codes and we measure the fraction of true codes that are correctly retrieved. We choose \(k = 10, 20, 30\) because as shown in Table 1 on average every visit includes more than three codes. Thus, selecting small \(k\) may result in inaccurate evaluation.

Coefficient of determination or \(R^2\) is a metric for evaluation of predictive performance of regression and forecasting algorithms. It compares the accuracy of prediction with respect to simple prediction by mean of the target variable.

\[
R^2 = 1 - \frac{\sum_i (y_i - \hat{y}_i)^2}{\sum_i (y_i - \bar{y})^2}
\]

Given the fact that the time duration varies significantly over time and the interest in accurately predicting the durations decreases as the patients visit after a long period of time, we measure the \(R^2\) performance of the algorithms in predicting \(\log(d_i)\) to lower the impact of anomalous long durations in the performance metric. In the same spirit, we train all models to predict the logarithm of the time duration between visits.

4.3 Baselines

We compare our model against several baselines as described below. Some of the existing techniques based on CTMC and latent space models were not scalable enough to be trained in the entire dataset in a reasonable amount of time; thus comparison could not be fair.

Intuitive baselines. We compare our algorithms against simple baselines that are based on experts’ intuition about the dynamics of events in clinical settings. The first baseline is to use a patient’s medical codes in his last visit as the prediction for his current visit. This baseline is competitive when the status of a patient with a chronic condition stabilizes over time. We can make this baseline stronger, by using the top-k most frequent labels observed in visits prior to the current visits. In the experiments we observe that the second baseline is quite competitive.

Logistic and Neural Network time series models. A common way to perform prediction task is to use \((x_{i-1}, d_{i-1})\) to predict the codes in the next event \(x_i\). We can use logistic regression or multilayer perceptron (MLP). To make this baseline stronger, we can use the data from \(L\) time lags before and concatenate the \((x_{i-\ell}, d_{i-\ell})\) for \(\ell = 1, \ldots, L\) to create the features for prediction of \(x_i\). Similarly, we can have a model that predicts the time until next event using rectified linear units as the output activation. While increasing the number of lags allows the model to capture longer history, it results in two disadvantages compared to RNNs: it increases the number of parameters of the model and also prevents the model to be used for prediction of the first \(L\) visits of the patients. Because of this limitation, we do not choose \(L\) to be bigger than 5 because the model loses its practicality for patients with short visit history. Due to lack of space, we describe the details of MLP design in Appendix B.

4.4 Results

Table 2 compares the results of different algorithms with RNN based Doctor AI. We report the results in three settings: when we are interested in (1) only predicting disease codes (Dx), (2) only medication codes (Rx), and (3) jointly predicting Dx, Rx, and time to next visit. The results confirm that the proposed approach is able to outperform the baseline algorithms by a large margin. Note that the recall values for the joint task are lower than those for single Dx or Rx prediction because the hypothesis space is larger for the joint prediction.
Table 2: Accuracy of algorithms in forecasting the future medical activities.

| Algorithms      | Dx Only Recall @k=10 | Rx Only Recall @k=20 | Dx,Rx,Time Recall @k=30 | R²      |
|-----------------|----------------------|----------------------|-------------------------|---------|
|                 | k=10 | k=20 | k=30 | k=10 | k=20 | k=30 | k=10 | k=20 | k=30 |       |
| Last visit      | 29.17 | 13.81 | 26.25 | 48.11 | 60.23 | 66.00 | —     |
| Most freq.      | 56.63 | 67.39 | 71.68 | 62.99 | 69.02 | 70.07 | 17.66 | 26.12 | 31.23 | 0.0013 |
| Logistic (L=1)  | 22.97 | 32.20 | 36.58 | 28.01 | 39.75 | 43.79 | 19.49 | 30.80 | 38.13 | 0.0017 |
| MLP (L=1)       | 26.09 | 39.19 | 48.04 | 32.27 | 51.12 | 61.50 | 18.79 | 29.13 | 35.63 | 0.0013 |
| Logistic (L=5)  | 26.04 | 39.17 | 48.19 | 32.39 | 51.06 | 61.03 | 19.32 | 30.77 | 38.08 | 0.0002 |
| MLP (L=5)       | 26.14 | 39.41 | 48.28 | 32.39 | 51.18 | 61.66 | 19.32 | 30.77 | 38.08 | 0.0002 |
| RNN-1           | 63.12 | 73.11 | 78.49 | 67.99 | 79.55 | 85.53 | 53.86 | 65.10 | 71.24 | 0.2519 |
| RNN-2           | 63.32 | 73.32 | 78.71 | 67.87 | 79.47 | 85.43 | 53.61 | 64.93 | 71.14 | 0.2528 |
| RNN-1-IR        | 63.24 | 73.33 | 78.73 | 68.31 | 79.77 | 85.52 | 54.37 | 65.68 | 71.85 | 0.2492 |
| RNN-2-IR        | 64.30 | 74.31 | 79.58 | 68.16 | 79.74 | 85.48 | 54.96 | 66.31 | 72.48 | 0.2534 |

The results also suggest that increasing the number of lags in the logistic and MLP approaches may not significantly improve the performance. Given the size of the dataset, this can be due to overparameterization of the model that may push the models to the boundary of high-dimensionality. While we use $L_1$ regularization in both cases, the result indicates that it cannot fully prevent noise accumulation due to noisy input dimensions.

Table 2 confirms that learning patient representation with RNN is easier with the input vectors that are already efficient representations of the medical codes. The RNN trained with the Skip-gram vectors (denoted by RNN-IR) consistently outperforms the RNN that learns the weight matrix $W_{emb}$ directly from the data, with only one exception, the medication prediction Recall@30, although the differences are insignificant. The results also confirm that having multiple layers when using RNN improves its ability to learn more efficient representations. The results also indicate that a single layer RNN might have enough representative power to capture the dynamics of medications, and adding more layers may not improve the performance.

The results also indicate that our approach significantly improves the accuracy of predicting the time duration until the next visit compared to the baselines. However, the absolute value of $R^2$ metric shows that accurate prediction of time intervals remains as a challenge. We believe achieving significantly better time prediction without extra features should be difficult because the timing of a clinical visit can be affected by many personal factors such as financial status, location of residence, means of transportation, and life style, to name a few. Thus, without such sensitive personal information, which is rarely included in the EHR, accurate prediction of time intervals should be unlikely.

In order to study the applicability of our model in a real-world setting where patients have varying length of medical records, we conducted an additional experiment to study the relationship between the length of the patient medical history and the prediction performance. To this end, we selected 5,800 patients from the test set who had more than 100 visits. We used the best trained model to predict the diagnosis codes at visits at different times and found the mean and standard error of recall across the selected patients. Figure 3 shows the result of the experiment. We believe that the increase in performance can be due to two reasons: (1) RNN is able to learn a better estimate of the patient status as it sees longer patient records and (2) the patient’s status stabilizes over time and the prediction task becomes easier.

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Figure 3: Prediction performance of Doctor AI as it sees a longer history of the patients. The increase in performance can be due to two reasons: (1) RNN is able to learn a better estimate of the patient status as it sees longer patient records and (2) the patient’s status stabilizes over time and the prediction task becomes easier.

Another interesting experiment was conducted to evaluate how the performance of Doctor AI changes as the duration since the last visit of the patient increases. To find this relationship, we create pairs of \((d_i, r_i)\) where \(d_i = t_i - t_{i-1}\) and \(r_i\) denote the duration before and the recall for estimation of \(i^{th}\) visit in a patient. We find the non-linear correlation between \(d_i\) and \(r_i\) using Spearman’s \(\rho\) coefficient. The corresponding correlation coefficients are \(-0.1066\), \(-0.1119\), and \(-0.1081\) for top 10, 20, and 30 recalls. The negative sign confirms our hypothesis that the longer it has been since a patient last visited a hospital, the more difficult it becomes to predict the outcome of his/her next visit.

In order to take a closer look at the performance of Doctor AI, in Table 3 (in Appendix C) we list the predicted, true, and historical diagnosis codes for five visits of different patients. The blue items represent the correct predictions. The results are promising and show that, given the history of the patient, the Doctor AI can predict the true diagnostic codes. The results highly mimic the way a human doctor will interpret the disease predictions from the history. For all five of the cases shown in Table 3, the set of predicted diseases contain most, if not all of the true diseases. For example, in the first case, the top 3 predicted diseases match the true diseases. A human doctor would likely predict similar diseases to the ones predicted with Doctor AI, since old myocardial infarction and chronic ischemic heart disease can be associated with infections and diabetes (Stevens et al., 1978). In the fourth case, visual disturbances can be associated with migraines and essential hypertension (Keith et al., 1939). Further, essential hypertension may be linked to cognitive function (Kuusisto et al., 1993), which plays a role in anxiety disorders and dissociative and somatoform disorders. Regarding codes that are guessed incorrectly with the fourth case, they can still be plausible given the history. For example, cataracts, and disorders of refraction and accommodation could have been guessed based on a history of visual disturbances, as well as strabismus and disorders of binocular eyemovements. Allergic rhinitis could have been guessed, because there was a history of allergic rhinitis. In summary, Doctor AI is able to very accurately predict the true diagnoses in the sample patients. The results are promising and should motivate future studies involving the application of Doctor AI on different datasets exhibiting other populations of patients.

5 Conclusion

In this work, we proposed Doctor AI, which is able to analyze patient records and predict the future outcomes for patients. We demonstrated that using a system based on recurrent neural networks, we can achieve 64.30% recall@10. This is a significant improvement compared to the baselines and indicates that the computational algorithms are on the path to be an assistant in improving the quality of health care. The qualitative analysis by a medical expert confirms that Doctor AI not only mimics the predictive power of human doctors, it also provides diagnostic results that are clinically meaningful in that all the predicted codes
were within the boundary of medical possibility, indicating its potential to be used as a differential diagnosis machine.

The success of Doctor AI opens up new avenues for further improvement of computational health algorithms. Application of Doctor AI in diverse clinical settings should follow to discover the extent of its power. Furthermore, since many hospitals provide clinical data in various forms such as lab measures and clinical note, successfully incorporating such information into Doctor AI would take it to a new level of intelligent medical assistance.

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A Learning the Skip-gram vectors from the EHR

Learning efficient representations of medical codes (e.g., diagnosis codes, medication codes, and procedure codes) may lead to improved performance of many clinical applications. We specifically used Skip-gram (Mikolov et al., 2013) to learn real-valued multidimensional vectors to capture the latent representation of medical codes from the EHR.

We processed the Sutter PAMF dataset so that diagnosis codes, medication codes, procedure codes are laid out in a temporal order. If there are multiple codes at a single visit, they were laid out in a random order. Then using the context window size of 5 to the left and 5 to the right, and applying Skip-gram, we were able to project diagnosis codes, medication codes and procedure codes into the same lower dimensional space, where similar or related codes are embedded close to one another. For example, hypertension, obesity, hyperlipidemia all share similar values compared to pneumonia or bronchitis. The trained Skip-gram vectors are then plugged into RNN so that a multi-hot vector can be converted to vector representations of medical codes.

B Details of the baselines

We use a multilayer perceptron with a hidden layer of width 2,000. We use dropout with $p = 0.3$ and apply $L_1$ regularization to all of the weight matrices. The activation functions in the first and output layers are selected to be sigmoid and softmax functions, respectively. For prediction of time intervals, we used rectified linear units. The regularization parameter has been increased with the number of lags to keep the performance of the model in high-dimensional regimes.

C Detailed inspection of results
| ICD9 | Description | True | Predicted |
|------|-------------|------|-----------|
| 414 | Other forms of chronic ischemic heart disease | 752 | 722 |
| 414 | Other forms of chronic ischemic heart disease | 719 | 719 |
| 414 | Other forms of chronic ischemic heart disease | 790 | 790 |
| 414 | Other forms of chronic ischemic heart disease | 715 | 715 |
| 414 | Other forms of chronic ischemic heart disease | 712 | 712 |
| 414 | Other forms of chronic ischemic heart disease | 740 | 740 |
| 414 | Other forms of chronic ischemic heart disease | 721 | 721 |
| 414 | Other forms of chronic ischemic heart disease | 751 | 751 |
| 414 | Other forms of chronic ischemic heart disease | 731 | 731 |
| 414 | Other forms of chronic ischemic heart disease | 731 | 731 |
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