Diabetes Mellitus Forecasting Using Population Health Data in Ontario, Canada

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Abstract
Leveraging health administrative data (HAD) datasets for predicting the risk of chronic diseases including diabetes has gained a lot of attention in the machine learning community recently. In this paper, we use the largest health records datasets of patients in Ontario, Canada. Provided by the Institute of Clinical Evaluative Sciences (ICES), this database is age, gender and ethnicity-diverse. The datasets include demographics, lab measurements, drug benefits, healthcare system interactions, ambulatory and hospitalizations records. We perform one of the first large-scale machine learning studies with this data to study the task of predicting diabetes in a range of 1 – 10 years ahead, which requires no additional screening of individuals.

In the best setup, we reach a test AUC of 80.3 with a single-model trained on an observation window of 5 years with a one-year buffer using all datasets. A subset of top 15 features alone (out of a total of 963) could provide a test AUC of 79.1. In this paper, we provide extensive machine learning model performance and feature contribution analysis, which enables us to narrow down to the most important features useful for diabetes forecasting. Examples include chronic conditions such as asthma and hypertension, lab results, diagnostic codes in insurance claims, age and geographical information.

1. Introduction
Preventable chronic conditions such as heart diseases, stroke, cancer and type 2 diabetes mellitus (T2DM) are the main causes of morbidity and mortality as of 2019 (Ding et al., 2018; Wu et al., 2018; Bhardwaj et al., 2018). In 2014, in the United States, 7 out of 10 top causes of mortality were chronic diseases. Chronic diseases formed 86% of the US health care expenditures in 2010 and costed $345 billion for diabetes and pre-diabetes alone in 2012 (Bhardwaj et al., 2018).

As a long-lasting chronic disease, diabetes occurs due to pancreas failure in producing insulin, which controls the blood sugar level; or when the body is inefficient in using the existing insulin (Samer El Jerjawi and Abu-Naser, 2018). Late diagnosis of diabetes could result in increased macro-vascular and capillaries difficulties risk, kidney failure, etc that might increase the healthcare cost (Rosella et al., 2016) and/or even threaten the life of the patient (Choi et al., 2019). Hence, early prediction of diabetes is of utmost value.
Diabetes Forecasting

The availability of clinical big data opens up a lot of opportunities to revolutionize healthcare with the use of machine learning techniques (Osmani et al., 2018). Machine learning experts can help clinicians understand how, when and what data is desired to solve their problems (Joyce Lee, 2018). It has been demonstrated in several literature works that machine learning techniques applied to large health administrative datasets can benefit the areas of risk prediction, hospital readmission reduction, treatment guidance, cost reduction, etc. (Bhardwaj et al., 2018; Mikalsen, 2019; Thesmar et al., 2019; Garske, 2018; Miotto et al., 2016). Moreover, they have been proved useful in management of chronic diseases such as diabetes mellitus and could help mitigate the disease burden (Bhardwaj et al., 2018).

Machine learning techniques can be used in two different setups for chronic diseases prediction. In the first setup (Alhassan et al., 2018; Zou et al., 2018), individuals are classified as currently being with or without diabetes. In the second setup, the task is forward prediction: predicting whether patients will get diabetes or not in the future (Choi et al., 2019; Razavian et al., 2015b). In this work, we tackle this latter task.

A number of demographic (fixed) features are useful in predicting diabetes. For example, age and gender have been utilized in a lot of literature works (Samer El Jerjawi and Abu-Naser, 2018; Razavian et al., 2015b). In this work, we use (among others) country of origin (Rosella et al., 2012) and geographical information such as latitude and longitude.

As demonstrated in a number of literature works (Razavian et al., 2015a; Nagata et al., 2018), health insurance claims with diagnostic codes in an International Classification of Diseases (ICD) format could contain a significant signal for anticipating diabetes. Despite the sparsity associated with such data, we found these claims to strongly help diabetes prediction, especially when linked with other immune diseases or hypertension.

Lab test data obtained from health checkups or tests conducted at hospitals also play a significant role in our diabetes prediction (Nagata et al., 2018). For instance, HbA1c (or A1c for short) is proven to be useful in predicting type 2 in different common scenarios and in diagnosing individuals with elevated T2D risk in both the short and long term (Leong et al., 2018). We will showcase its contribution to the task of diabetes prediction further.

The single-payer healthcare system in Canada, similarly to UK and a few other countries provides a unified collection of HAD records for all residents and that makes the Institute for Clinical Evaluative Sciences (ICES) collection of datasets extremely valuable for related healthcare studies. Moreover, ICES is quite diverse in terms of gender (53-47 male-female ratio in our cohort), age (year of birth from the 1890s to 2010s) and country of birth (more than 100).

In this work, we perform diabetes mellitus (type I and II combined) onset prediction using raw features from a total of 20 datasets obtained from ICES recorded in Ontario, Canada for 146,371 individuals. Among them, 78,021 individuals have been diagnosed with diabetes between 2008 and 2018. Each dataset corresponds to a different source of data, including: lab results (OLIS), insurance claims (OHIP), drug benefits (ODB), hospitalizations (DAD), ambulatory usage (NACRS) and emergency claims (ERCLAIM).

We use these features as inputs to five different machine learning models (i.e. XGBoost (Chen and Guestrin, 2016), Highway networks (Srivastava et al., 2015), regularized logistic regression (LR) (Razavian et al., 2015b), CNN-LSTM (Tonekaboni et al., 2018) and LSTM sequence to sequence (LSTM-Seq2Seq) (Sutskever et al., 2014)) to predict diabetes onset using a variable length window of temporal data.
**Technical Significance**  To the best of our knowledge, we propose the first comprehensive large-scale machine learning study on relevant datasets from ICES collection in Ontario to solve the diabetes prediction problem. In fact, we provide: a data pipeline that efficiently aggregates sparse temporal data from multiple tables with different sizes into a unique sparse representation vector, a fair comparison of five models of different natures, multiple metrics for performance evaluation, and finally an exhaustive feature selection/contribution analysis, that investigates features' contribution to the prediction of diabetes. The latter is often of lesser interest in performance-focused studies; versus in this paper, we aim to interpret all the top features in depth.

**Clinical Relevance**  Our model predictions can be used as a risk score for evaluating future onset of diabetes. We believe that our prediction model could be deployed to better understand the distribution of diabetes (and its main contributing features) in the population. Our method does not require additional screening cost as it simply looks at all the historical health data available.

By adopting an extensive set of input features and investigating their contribution, we attempt to reverse engineer feature selection and give a machine learning model point of view on which features should be used in priority. This feature contribution-based method can be used in recommending policies in health planning and strategies to prevent the onset of diabetes among those at high risks. Our feature contribution analysis suggests that other chronic diseases such as asthma are linked with future diabetes. It also demonstrates the importance of lab testing results in diabetes prediction. Finally, by varying the buffer size (see study design), we show how far in advance we can forecast diabetes with a reasonable accuracy.

### 1.1. Related work

Generally, we found two categories of works based on the machine learning problems they define for prediction of diabetes: current time (diagnosis, classification) (Zou et al., 2018; Wu et al., 2018; Alhassan et al., 2018) and forward prediction (Choi et al., 2019; Nagata et al., 2018; Razavian et al., 2015b; Krishnan et al., 2013). As we are interested in predicting the diabetes incidence in advance (latter problem), we review the relevant forward prediction work here.

Considering the diabetes-related features used in literature works, we observed two main approaches. In the first approach, a few important features are selected or engineered manually/systematically and are used for diabetes prediction or diagnosis (Samer El Jerjawi and Abu-Naser, 2018; Alhassan et al., 2018). In the second category, all available features are inputted to a machine (or deep) learning model (Razavian et al., 2015b; Krishnan et al., 2013) and it is the model’s responsibility to realize the important features (Razavian et al., 2015b). In this paper, we adopt the second approach.

One of the most relevant literature works is presented in Razavian et al. (2015b). The authors propose a data-driven model for predicting type 2 diabetes in advance (as well as current time diagnosis). They consider claims, pharmacy records, healthcare utilization and laboratory results of 4.1 million people recorded between 2005 and 2009. The novel risk factors emerging from their model is studied for different age groups at different stages before the onset. They achieve an AUC (area under curve) measure of 78 with about 900
features for prediction of diabetes one year in advance (i.e. with a buffer of one year). They adopted logistic regression as the machine learning model of choice. Similarly, in an earlier work (Krishnan et al., 2013) studied the same problem with the same method. For 22 selected features and a complete list of 1054 features, AUCs of 75.2 and 75.6 were achieved, respectively, also for one year in advance prediction.

A recent study on machine learning-based diabetes prediction is presented in Choi et al. (2019). A group of 8454 individuals (with no diabetes history) were studied over a period of 5-year followup. 28 variables were extracted from individual’s electronic medical records to train a number of models for predicting the occurrence of diabetes within the followup period (a different problem setup compared to ours). Authors confirmed that the regularized logistic regression performed the best among their models and results in an AUC of 78.0. Finally, they performed feature selection based on information gain attribute evaluation. In fact, their work is one of the few ones that studies features contributions. Similarly to our findings (using our top model, XGBoost), HbA1c shows up as the most important feature among theirs. Both their study and ours also give strong importance to glucose values, while we found age to be of a lesser importance than them.

The study in Nagata et al. (2018) confirms the usefulness of lab test data and health claim text data including ICD10 codes and pharmacy information. They used three models for diabetes prediction: L1-regularized logistic regression, XGBoost and a family of LSTM-based models. Among them, XGBoost provides the best performance with an AUC of 87.0 when using ICD10 and medical text data for predicting diabetes, one year ahead. Note that we did not use any medical text data in this work due to the very small coverage on our population with diabetes.

2. Data Cohort

In this section, we describe how our cohort was selected among numerous datasets within ICES, where some might not be relevant to diabetes prediction.

2.1. Cohort Selection

2.1.1. Diabetes Cohort

The Ontario Diabetes Dataset (ODD) is used to identify individuals with diabetes. The dataset contains all individuals in the Registered Persons Database (RPDB), who have been flagged as ones with diabetes based on the algorithm originally introduced by E Hux et al. (2002). This algorithm flags Physician Service Claims (PSCs) and fee codes and hospitalizations associated with diabetes based on Hospital Discharge Abstracts (HDAs).

1. ODD would also include the diagnosis date of individuals, which is determined based on the described algorithm. Details are listed in the supplementary materials. We randomly selected 10% of people appearing at least once in the ODD.

1. This part was not present in E Hux et al. (2002). In fact, we used the 2016 version of ODD, where the algorithm is updated to what we described here. The algorithm applies to all individuals in RPDB (even before 2016)
2.1.2. Control Cohort

Since our task is a binary prediction, we need to build a negative class of individuals without diabetes. The control cohort are individuals also selected from the RPDB. It has a similar number of individuals, who are alive at the time of study and not flagged in ODD. Besides, the control cohort has the same age and gender distribution as the diabetes cohort.

2.1.3. Exclusion Criteria

The ODD algorithm imposes certain properties for an individual (see supplementary materials) in how the diagnosis date is determined. It is not surprising that not all individuals in the ODD would satisfy these properties, as healthcare labels are not perfect. Luckily, this contributes to a small portion (4.1%) of our diabetes cohort and thus we excluded these individuals. We also removed the individuals in the control cohort that violate these properties.

We also scoped down to individuals diagnosed between 2008 to 2017 (both included). As our task is to forecast diabetes onset, it would be more relevant to focus on more recent data which are cleaner and contain lab values (OLIS, see Table 1). Lastly, we dropped the individuals who are younger than 20, mostly corresponding to type I diabetes (Atkinson et al., 2014; Harjutsalo et al., 2008). Note that our final, adult-only cohort still contains type I cases, and we predict future incidence of type I and type II combined, The resulting cohort consists of a total of 146,371 individuals, in which 78,021(53.3%) individuals have diabetes and 68,350(46.7%) do not.

2.2. Dataset Selection

After constructing the cohort, we first extracted data about each individual from several sources (eight datasets). These data have no timestamps - we call them fixed features. Then we selected datasets that are both relevant and useful to our study.

The derived chronic diseases (Asthma, CHF, COPD, HYPER, OCCC, ORAD) consist of the incidence and prevalence of the chronic disease in each year for each individual. We kept all the six validated chronic diseases as they are all clinically related to diabetes.

The observations datasets contain more detailed information associated with timestamps, and are typically very sparse. Based on the coverage of the diabetes and the control cohort appearing in the dataset, we selected six observations datasets (OLIS², DAD, NACRS, ODB, OHIP and ERCLAIM) in our final data processing setup. They cover lab values, hospitalizations, ambulance services, and drugs, health and emergency claims. These datasets and their descriptions are outlined in Table 1 and the coverage of all the datasets are outlined in the supplementary materials.

2.3. Feature Selection

We manually selected relevant features from each dataset, as required by the data owner. We dropped features that are 1) missing from the data most of the time; 2) overlapping with other features; or 3) without a timestamp in the observations dataset 4) occurring

². OLIS is a relatively new dataset and is being organized and cleaned continuously. Right now, we just have access to part of OLIS data, most of which are diabetes-related.
Table 1: Dataset Descriptions

| Dataset         | Full Name                                | #Obs.      | Available Time | Description               |
|-----------------|------------------------------------------|------------|----------------|---------------------------|
| OLIS            | Ontario Laboratories Information System  | 76,009,197 | 2006–          | Lab Values                |
| DAD             | Discharge Abstract Database               | 23,699,596 | 1989–          | Hospitalization Records   |
| NACRS           | National Ambulatory Care Reporting System | 44,811,484 | 1999–          | Ambulatory Records        |
| ODB             | Ontario Drug Benefit Claims               | 1,412,758,247 | 1990–      | Drugs Claims              |
| OHIP            | Ontario Health Insurance Plan Claims Database | 1,855,101,924 | 1990–    | Insurance Claims          |
| ERCLAIM         | OHIP’s Emergency Claims Database          | 37,692,110 | 1991–          | Emergency Claims          |

after the prediction date. We then performed feature engineering based on each feature’s type. Details are in the supplementary materials.

Our model input is built based on a $w$-year observation window (see Section 3.1). As multiple observations can occur per year, we aggregated each observation feature within each year. By default, we averaged observations within each year. We found it useful to also include the maximum values of observations within each year. We also included in all cases the number of observations per year per dataset for each individual.

Chronic diseases are recorded yearly hence they do not require aggregation. The date of each chronic disease in a specific year is set to be January 1st of that year. We concatenated the aggregated observations and the chronic diseases as temporal vectors. Thus, for each individual, the feature vector contains a fixed vector portion, and $w$ temporal vectors corresponding to each year. We then experimented with concatenating these $w$ yearly vectors, averaging them, or inputting them in a sequential (temporal) fashion for our LSTMs. See Figure 1 for illustration. The number of raw features and input features for each dataset is described in Table 2.

Figure 1: Feature vector for an individual observation window

![Feature vector for an individual observation window](image)

year 0       year 1       year 2       year 3       year 4       year 5
agg          agg          agg          agg          agg          agg

| temporal     | temporal     | temporal     | temporal     | temporal     | temporal     |
|--------------|--------------|--------------|--------------|--------------|--------------|

+ fixed features

| concat       | average      |
|--------------|--------------|
| or           |              |
Table 2: Statistics of the selected datasets. Number of observations refers to the 10-year window under study (2008-2017) for the final cohort. Raw features correspond to the number of columns in the used raw database. Input features corresponds to the features for each year from the dataset fed into the model. The last column corresponds to the average number of non zero values among yearly feature vectors.

| Dataset                  | #Obs | #Raw Features | #Input Features | Avg # non-zero |
|--------------------------|------|---------------|-----------------|----------------|
| Fixed Features (RPDB)    | -    | 36            | 240             | 18.76          |
| Chronic Diseases         | -    | 12            | 12              | 0.54           |
| OLIS                     | 512,593 | 6            | 34              | 0.65           |
| DAD                      | 446,890 | 16           | 305             | 1.77           |
| NACRS                    | 852,374 | 12           | 63              | 1.19           |
| ODB                      | 13,857,648 | 4           | 41              | 1.08           |
| OHIP                     | 37,701,635 | 4           | 153             | 18.27          |
| ERCLAIM                  | 857,249 | 6            | 115             | 1.85           |
| Total                    | -    | 96            | 963             | 44.11          |

3. Methods

3.1. Study design

We designed our study to predict the possibility for an individual to have diabetes in the future. We built the feature vectors from data described above by considering \( w \) years before the current date. We then predicted whether the individuals were to have an onset of diabetes in \( b \) years in the future. To formulate the diabetes prediction problem for the training data, we set the “current date” to be \( b \) years before the prediction date. For the diabetes cohort, the prediction date is the diagnosis date. For the control cohort, the prediction date is sampled to match the distribution of the diagnosis dates of the diabetes cohort (from 2008 to 2017). The design of the prediction task at an individual level is illustrated in Figure 2. In our study, \( b = 1, \ldots, 10 \) and \( w = 1, 3, 5, 10 \). If the individual does not have enough history in the observation window, we pad with zeros.

3.2. Split

As our main focus is on the clinical application, we used out-of-time test split. As such, all the individuals with prediction date in 2016 or 2017 were set as test data, while the ones between 2008 and 2015 (all inclusive) formed the training data. The goal of deploying our model in production for future diabetes risk screening naturally led to this setup. The train-test distribution is outlined in Table 3.
3.3. Models

As depicted in Figure 1, we have two kinds of final input vectors, *avg* and *concat*. While *concat* carries temporal information that may be helpful, it also increases the size of the feature vector *w*-fold (*w* is the observation window size). We experimented both types of input vectors for our study below, except for LSTMs as they are designed to capture the temporal aspect. Details of these models are described in the supplementary materials.

**Logistic Regression** We use an L1-regularized logistic regression (LR) model as our baseline.

**XGBoost** We use XGBoost, introduced by Chen and Guestrin (2016), as our main model due to its popularity, high performance and ability to handle missing values well.

**Highway Network** We also use a relatively simple deep neural network without temporal aspect called the Highway network (Srivastava et al., 2015). It combines the linear and non-linear outputs providing greater modeling flexibility for the network compared to the vanilla multi-layer perceptron (MLP). We found that this network is better than vanilla MLPs in our application. This neural network has 14,944,001 parameters in the case of *avg* input vectors.

**CNN-LSTM** This model is inspired by the architecture in Tonekaboni et al. (2018) with a number of changes as follow: We removed the max pooling layers as we found them damaging the performance. No feature dimensionality reduction was performed in our setup. We added batch normalization (Ioffe and Szegedy, 2015) after each CNN layer, which increased the performance and convergence speed simultaneously. Dropout in the reference architecture was kept in the same place, i.e. after CNN layers. Two layers of LSTM were used. Finally, we applied a three layer perceptron followed by sigmoid to perform binary prediction. This model has a total of 22,744,136 parameters.

**LSTM-Seq2Seq** We borrowed the LSTM-based sequence to sequence architecture from Sutskever et al. (2014). We used it to reconstruct the concatenation of all (fixed + temporal) features over time and applied a three layer perceptron on the encoder last hidden layer to perform the prediction. Hence, this model is data-regularized due to the reconstruction cost and that makes it different from the CNN-LSTM model. We applied dropout after each LSTM layer as advised by Zaremba et al. (2014). Teacher forcing (Williams and Zipser, 1989) was also applied to remove the reconstruction drift (bias) and increase the convergence speed. This model has a total of 32,027,456 parameters.

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### Table 3: Train-Test Split Statistics

| Data   | #Positives | #Negatives | #Total   |
|--------|------------|------------|----------|
| Train  | 67,499 (53.3%) | 59,048 (46.7%) | 126,547 (86.5%) |
| Test   | 10,522 (53.1%) | 9,302 (46.9%) | 19,824 (13.5%) |
| Total  | 78,021 (53.3%) | 68,350 (46.7%) | **146,371** |
4. Results

4.1. Evaluation Approach

We use the area under receive-operation curve (AUC) as our primary metric for model evaluation. It is a standard metric for binary classification among related literature Choi et al. (2019); Leong et al. (2018); Razavian et al. (2015b). We also output the usual accuracy, sensitivity, specificity and positive predictive values for reference. In these cases, we just use the standard threshold of 0.5.

4.2. Model Performance

Table 4 shows the performance of all models. Note that we experimented with different values of window size \( w \) and buffer size \( b \) as well as the corresponding hyperparameters for training. Detailed results are listed in the supplementary materials.

| Model            | AUC  | Accuracy | Sensitivity | Specificity | PPV  |
|------------------|------|----------|-------------|-------------|------|
| LR - avg         | 77.7 | 70.8     | 67.2        | 74.8        | 75.1 |
| LR - concat      | 78.0 | 71.1     | 68.9        | 73.4        | 74.6 |
| XGBoost - avg    | 79.9 | 71.9     | 72.2        | 71.5        | 74.1 |
| XGBoost - concat | 80.3 | 72.3     | 70.5        | 74.4        | 75.7 |
| Highway - avg    | 78.6 | 71.7     | 70.3        | 73.2        | 74.8 |
| Highway - concat | 77.2 | 69.9     | 66.8        | 73.4        | 74.0 |
| CNN-LSTM         | 78.4 | 71.3     | 72.3        | 72.2        | 73.5 |
| LSTM-Seq2Seq     | 78.4 | 71.3     | 72.3        | 70.1        | 73.2 |
| weighted average | 81.1 | 72.8     | 72.2        | 73.5        | 75.5 |

As seen, XGBoost has the best performance among all single models. Moreover, averaging the observations over all years seems to have a similar effect as concatenating them. This means that the temporal effect is not as useful in the XGBoost model. It is interesting to notice the disappointing performance of LSTM-based models, comparable to non-temporal model LR-avg and Highway-avg in this case.

We also show the corresponding AUCs in Figure 3 with different observation window sizes \( w \) for various models and different buffer sizes \( b \) for our XGBoost model. Here, we used both concatenation and averaging aggregation over all years for different window sizes. It is evident that the larger the observation window, the more accurate the model would be. But, we observe that for \( w = 10 \) in both the XGBoost and Highway models, the model performs slightly worse than \( w = 5 \). This is an indicator that the observation data in the far past does not contribute much to the prediction performance, possibly due to adding more noise or mismatching data distributions.

We can also see that the larger the buffer size, the lower the performance of the XGBoost model, as the task becomes more challenging. It is interesting that even for a buffer of 10 years, the model performance is still better than the models with only fixed features (See Section 4.5). We see that AUC is maintained above 70 for up to six years ahead prediction.
4.3. Feature Contribution

For all models, we can compute how much each feature contributes to the results. We use the additive feature contribution framework. Given a model \( y = \sigma(f(X)) \), and an input sample \( x \in \mathbb{R}^m \), where \( \sigma \) is the logistic function and \( X \) is the input, the framework will output the feature contribution \( \phi_j \) for feature \( x_j \), which satisfies efficiency,

\[
\sum_j \phi_j = f(x) - E_X(f(X)).
\]

As \( f(x) \) is in the logit space, the feature contribution \( \phi_j \) can be interpreted as the log odds ratio between toggling the feature on and off.

Note that as the framework requires an input sample, we aggregate it using the sum of absolute values to get the feature contribution of each feature across all samples in the test set. Absolute values are used so that positive and negative effects do not cancel each other across different samples.\(^3\)

For LR and XGBoost, we used the Shapley value (Shapley, 1953; Lundberg et al., 2018) as our feature contributions. For feed-forward neural network models, we used integrated gradients (Sundararajan et al., 2017) as our feature contributions method, which is an approximation of the Shapley value (Sundararajan et al., 2017).

**Results** We listed the top 10 features for logistic regression in Table 5(a). As seen, the fasting glucose and glucose in serum or plasma are contributing a lot, with an aggregated Shapley value of about 0.65. We also observe that the geographical region contributes a lot to our prediction using logistic regression. It’s interesting to note the appearance of landing

\(^3\) Note that the aggregated feature contribution values do not tell the correlation between the feature values with respect to the outcome.
date here, which takes non-null values only for immigrants as it’s their date of arrival in Canada.

Table 5: Feature Contributions on test set. Here \( w = 5 \) and \( b = 1 \).

| Feature                        | Contribution | XGBoost | Contribution |
|--------------------------------|--------------|---------|--------------|
| Fasting Glucose               | 0.665        |         |              |
| Glucose                       | 0.632        |         |              |
| Max Blood HbA1c               | 0.321        |         |              |
| LHIN Central                  | 0.302        |         |              |
| Landing date                  | 0.277        |         |              |
| LHIN Central East             | 0.258        |         |              |
| LHIN Champlain                | 0.239        |         |              |
| LHIN Hamilton Niagara         | 0.23         |         |              |
| LHIN Mississauga Halton       | 0.214        |         |              |
| Max A1c Mass Fraction         | 0.209        |         |              |

The top 10 features for XGBoost are in Table 5(b). As seen, A1c contributes the most (i.e. an aggregated Shapley value of 0.908), followed by lab values. Prevalence of asthma in the top 10 corroborates studies stating that the use of steroids in the treatment of asthma can result in an increase in blood sugar level (Suissa et al., 2010). There is also correlation between individuals with diabetes having increased risk of getting asthma and other chronic diseases (Ehrlich et al., 2010). We also see that an OHIP (insurance) claim for hypertension and immunity appear among the top features, suggesting that they may be relevant to diabetes onset.

Table 5(c) shows the top 10 features for the Highway model. It is mainly lab values but it includes a geographical feature (longitude). Note that in the Highway model, age seems to be more important than the other two models. We can see that the contribution values are much higher than those of the logistic regression and XGBoost, but this can be shown in the distribution of the model predictions. (See supplementary materials)

In conclusion, it seems that the glucose and A1c are very important lab results as they appear in all three models. Geographical feature (LHIN, longitude among others) in logistic regression and Highway network indicate that the location does affect the probability of having diabetes based on the data we have (Booth et al., 2012).

4.4. Evaluation on Different Demographics

As our models are trained on the whole training set, we are interested in discovering how they would perform on each demographic. We thus report performance and feature contributions for different demographics. When not specified, the model is XGBoost-avg with \( w = 5 \) and \( b = 1 \) as it is our best model with avg and second-best overall. It is only slightly worse than concat all the years which takes a much longer time and much more resources.

**Age, Gender and Country of Origin** Table 6 shows the model performances for the demographic groups gender, age and country of origin. As we can see, our results scale to
most subcategories, especially when the sample size is high. It is worth noting the decrease in AUC for people younger than 40.

The feature contributions for each demographic is detailed in the supplementary materials. It is worth noticing that the prevalence of asthma is relatively more important for individuals younger than 50. As for country of origin, landing date is an important feature for people from China. This is in line with Alangh et al. (2013).

Table 6: XGBoost-avg performance on different demographics for \( w = 5 \) and \( b = 1 \)

| Age  | #Test Individuals | AUC |
|------|------------------|-----|
| 20-29| 662              | 73.9|
| 30-39| 1808             | 75.8|
| 40-49| 3251             | 81.6|
| 50-59| 5426             | 81.6|
| 60-69| 4673             | 79.6|
| 70-79| 2735             | 79.1|
| 80-89| 1016             | 76.4|
| 90+  | 248              | 76.8|

| Gender | #Test Individuals | AUC |
|--------|------------------|-----|
| Male   | 10565            | 80  |
| Female | 9259             | 79.7|

| Country of Origin | #Test Individuals | AUC |
|-------------------|------------------|-----|
| Canada            | 18144            | 79.6|
| India             | 519              | 81.9|
| China             | 374              | 84.9|
| Philippines       | 353              | 75.4|
| Pakistan          | 233              | 75  |
| Sri Lanka         | 201              | 67.5|

4.5. Ablation Study

Datasets  We investigated the effect of each dataset in the performance of our model framework. Table 7 outlines the results. It is clear that OHIP and OLIS contain a lot of effective features that frequently show up among the top features. It is also worth noting that combining all datasets still gives much better performance. We outline the most important features for each dataset in the corresponding table in the supplementary material.

Table 7: Model performance when we only train on the mentioned datasets. We use XGBoost-avg here with \( w = 5 \) and \( b = 1 \)

| Dataset(s) | All | Fixed | Chronic | DAD | ERCLAIM | NACRS | ODB | OHIP | OLIS |
|------------|-----|-------|---------|-----|---------|-------|-----|------|------|
| AUC        | 79.9| 62.6  | 63.1    | 56.7| 57.9    | 58.6  | 59.4| 69.8 | 72.6 |

Top Features  Similarly, we perform pruning at the feature level by training the model only on the top \( k \) features. Table 8 summarizes the results. As seen, our top feature A1c only achieves an AUC of 68.8. On the other hand, using the top 15 features is approximately as good as using all features, suggesting the possibility of having a decent model by only using a small subset of features. Our study points out relevant features for further studies hand-picking input features.
Table 8: Model performance when we only train on the top $k$ features. We use XGBoost-avg here with $w = 5$ and $b = 1$

| Number of top features used | 1    | 5    | 10   | 15   | 963 (All) |
|-----------------------------|------|------|------|------|-----------|
| AUC                         | 68.8 | 70.9 | 76.4 | 79.1 | 79.9      |

5. Discussion

5.1. Technical Significance - Revisited

The examined models, i.e. XGBoost, regularized logistic regression, (Highway) multi layer perceptron, CNN-LSTM and LSTM Seq2Seq are among the most frequently used models in the recent literature. XGBoost performs the best among the examined models for diabetes prediction using an observation window of five years and a buffer of one year (i.e. predicting one year ahead). This is consistent with other studies using ICD codes (Nagata et al., 2018).

One of the challenges entangled with our cohort is the sparsity of features. For the raw data, only 44 features out of 963 are non-zero, when averaged over years and patients (see Table 2). XGBoost has been shown to perform extremely well on tabular and sparse data (Chen and Guestrin, 2016), particularly compared to deep-learning alternatives as demonstrated in (Nagata et al., 2018) and our work.

LSTM-Seq2Seq with teaching forcing was found to outperform CNN-LSTM (Tonekaboni et al., 2018). This is expected as sequence to sequence models benefit from data-based regularization (Ghasedi Dizaji et al., 2017). However, both our temporal LSTMs do not improve on the Highway network. This is counter-intuitive as temporal models should aggregate important information over the input sequence, enriching the pre-classification states. But recurrent networks are hard to train (Pascaru et al., 2013), and in our case, it is possible that the aggregation within each year constrained the learning capability of recurrent neural networks.

5.2. Clinical Relevance - Revisited

As observed, A1c and fasting glucose contribute the most to the prediction of diabetes. It confirms the common practice that A1c is used in diabetes tests to categorize individuals into having no diabetes, being pre-diabetic or living with diabetes (NIDDK, 2018).

Our study also finds that the prevalence of asthma will affect the diabetes onset (Suissa et al., 2010) in Ontario. This could lead to taking further steps for individuals with asthma on their prescribed steroids as it increases blood sugar, that might eventually result in weight gain and diabetes diagnosis (Suissa et al., 2010).

Our findings regarding hypertension contribution confirms the corresponding literature studies (Schutta, 2007; Berraho et al., 2012; Hashemizadeh et al., 2013). Besides, geographical information plays a role too, recommending targeted interventions in higher risk areas.

As noted in Alangh et al. (2013), there is an increase in Chinese-Canadian diabetes incidence between 1996–2005. Landing date is one of the important features we study in predicting onset of diabetes for Chinese immigrants (or permanent residents). Hence, it is
worth further research on to figure out the reason behind this fact. We also found that it is a harder task to predict diabetes on people under 40 years old. It was found that approximately 80 – 92% of patients with early onset of diabetes are obese compared to only 56% of older ones Wilmot and Idris (2014). We do not have obesity nor BMI as input features, which probably makes it harder for our model to capture the specifics of early diabetes onset.

Our diabetes prediction method can be run without requiring additional data sources, as it relies on routine health data. It is modular, can be applied to any individual and generalizes well across all subcategories of gender, age and country of origin. If low computational resources are imposed, using 15 features would still get a strong AUC.

5.3. Limits
The data that we use has numerous limitations. BMI has been shown to be a key component of diabetes pre-screening (Edelstein et al. (1997)) but is missing in our datasets. Our study lacks other important lab values such as cholesterol and glutamate decarboxylase antibodies. Finally, we only have country of origin as a proxy for ethnicity. All of this affects our model's prediction capacity.

5.4. Future Work

Predicting diabetes from self-reported results A similar (yet distinct) task compared to ours is predicting whether an individual will get diabetes in a range of 5 – 10 years based on yearly survey data (Rosella et al., 2011). Surveys typically include some more personal level information such as dietary practice, physical activity, stress level and BMI, which are absent from the datasets used in this study. It is also possible to propose a model to make personalized recommendations for individuals at higher risk of diabetes.

Diabetes clustering Diabetes can be roughly classified into 3 different types (Type I, Type II and gestational diabetes). It is believed that type II is very heterogeneous, and recent work by Ahlvist et al. (2018) applied a clustering method using six important features to cluster a diabetes cohort into five types. We plan to explore different clustering methods (including the deep learning ones) on our diabetes cohort. A potential clinical application is that different types can be treated differently, i.e. a major step towards personalized treatment.

6. Conclusion
In this study, we demonstrated the effectiveness of machine learning algorithms to predict future onset of diabetes considering an individual's medical history over the last few years. Using a single XGBoost model, we reached a test-AUC of 80.3, predicting diabetes one year ahead, which outperforms any other model we examined. The provided features' contribution show that lab results (led by A1c) are essential for the task, which advocates for A1c screening. Other chronic diseases' flags (such as asthma, hypertension, etc) as well as diagnosis codes in insurance claims are among the top feature contributors, containing signals on future diabetes incidence more than five years ahead.
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