An evaluation of randomized machine learning methods for redundant data: Predicting short and medium-term suicide risk from administrative records and risk assessments

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Abstract

Accurate prediction of suicide risk in mental health patients remains an open problem. Existing methods including clinician judgments have acceptable sensitivity, but yield many false positives. Exploiting administrative data has a great potential, but the data has high dimensionality and redundancies in the recording processes. We investigate the efficacy of three most effective randomized machine learning techniques – random forests, gradient boosting machines, and deep neural nets with dropout – in predicting suicide risk. Using a cohort of mental health patients from a regional Australian hospital, we compare the predictive performance with popular traditional approaches – clinician judgments based on a checklist, sparse logistic regression and decision trees. The randomized methods demonstrated robustness against data redundancies and superior predictive performance on AUC and F-measure.

Keywords: Suicide risk, Electronic medical record, Predictive models, Randomized machine learning, Deep learning

1. Introduction

Every year, about 2000 Australians die by suicide causing huge trauma to families, friends, workplaces and communities\(^1\). This death rate exceeds transport related mortality

\(^1\)Work done when Thuong was with Deakin.
Worldwide, suicide remains one of the three leading causes of death among age groups of 15 to 34 years [3]. Studies on the immediate precursors to suicide – suicidal ideation, and attempts – reveal shocking statistics. The number of medically serious attempts amount to more than 10 times the total number of suicide deaths [5, 6]. For every attempt, two to three people seriously consider suicide without attempting it [7]. This suggests that given patient data, timely intervention between suicide ideation and attempts can save lives.

People frequently make contact with health services in the months leading up to their suicide attempt [8, 9, 10]. A recent study revealed about 85% of suicidal patients contacted primary care providers months before their suicide attempt [11]. In such scenarios, the crucial problem is to identify people at risk [12, 13], and prescribe intervention strategies for preventing suicide deaths [14]. Current care practices involve assessing prescribed suicide risk factors [15, 16, 17, 18, 19] and estimating a risk score [20, 21, 22]. However, the reliability and validation of suicide risk assessments is not well understood in terms of predictive power, and remains a controversial issue in risk management [23, 24]. One of the reasons could be that many of the patient visits before suicide attempts are not directly related to mental health problems or self-harm [25]. Also, a high prevalence of coexistent physical illnesses was found in such patients [26]. Hence, for a better understanding of suicide risk, the suicide risk factors need to be analyzed along with the patient clinical information [27, 8].

In our previous work, we advocate a statistical risk stratification model based on patient data from electronic medical records (EMR), which outperformed clinical risk assessment practices [8, 28, 29]. Besides known risk factors for suicide, EMR patient data contains demographic and clinical information, including patient history, disease progression, medications. Two major issues are high dimensionality and redundancy. Our previous work resorts to sparsity-inducing techniques based on lasso [30]. However, lasso is linear and has a tendency to discard useful information. More severely, it is highly unstable under redundancy, leading to conflicting subsets of explanatory risk factors under
small data variations [29, 31].

Given the poor predictive power of risk assessment, we conjecture that the link between historical risk factors and future suicide risk may be nonlinear. Thus a good predictive method should be nonlinear and insensitive to high dimensionality and redundancy. To this end, we investigate three most effective randomized machine learning techniques – random forests, gradient boosting machines, and deep neural nets with dropout – in predicting suicide risk. These methods perform multiple random subspace sampling, and thus efficiently manage high dimensionality and redundancy. All information is retained, there is no discarding of potentially useful information. This property is highly desirable since there are no well-defined risk factors that are conclusive for predicting suicide [32, 33].

Our experiments are conducted on a real world hospital data set containing 7,399 mental health patients undergoing 16,858 suicide risk assessments. Prediction horizons (how far ahead the model predicts) are 15, 30, 60, 90, 180, 360 days.

We compare our proposed randomized methods with existing traditional approaches to predicting suicide risk: sparse logistic regression and decision trees. We also compare the performance of our methods with clinicians who rely on an 18 point checklist of predefined risk factors. In our experiments, the randomized methods demonstrate better predictive accuracy than clinicians and traditional methods in identifying patients at risk on measures of AUC (area under the ROC curve) and F1-score.

2. Data extraction

We use a retrospective cohort from Barwon Mental Health, Drugs and Alcohol Services, a regional provider in Victoria, Australia. Ethics approval was obtained from the Hospital and Research Ethics Committee at Barwon Health (approval number 12/83). It is the only tertiary hospital in a catchment area with over 350,000 residents. The hospital data warehouse recorded approximately 25K suicide risk assessments on 10K patients in the period of 2009-2012.

We focus our study on those patients who had at least one hospital visit and a mental
### Feature Statistics

| Feature                        | Statistics                                      |
|--------------------------------|-------------------------------------------------|
| **Demographics**               |                                                 |
| Patients                       | 7,399                                           |
| Gender                         | Male: 49.3%, Female: 50.7%                      |
| Age                            | $< 21$: 16.4%, $21 - 35$: 28%                   |
| Marital Status                 | Married: 20%, Divorced/Separated: 11%, Single: 54.4% |
| Occupation                     | Unemployed/home duties: 16.7%, Pensioner/Retired: 19.2% |
| Post code changes              | in 12 months: 33.5%, in 12-24 months: 16.2%, 24-48 months: 24.4% |
| Suicide risk assessment score   | based 18 item checklist developed in Barwon health |

Table 1: Characteristics of suicide patient cohort.

condition recorded prior to a risk assessment. This resulted in a dataset of 7,399 patients and 16,858 assessments. Among patients considered, 49.3% are male and 48.7% are under 35 of age at the time of assessment. The main characteristics of our study cohort are summarized in Table 1.

#### 2.1. Ground-truth of suicide risk

Each risk assessment is considered as an evaluation point from which we predict the future suicidal risk. We aim to predict multiple outcomes for different time windows from the evaluation point – 15, 30, 60, 90, 180 and 360 days. Future risk is determined based on a lookup table of ICD-10 codes that are deemed risky by a senior psychiatrist, as previously reported in [8]. Examples of risky diagnostic codes are S51 (open wound of forearm) and S11 (open wound of neck). These risk events are considered as a proxy measure for suicide attempts, which are rare events. Further class distributions are summarized in Table 2.

#### 2.2. Feature extraction

Historical data prior to each assessment are used to extract features (or risk factors), following the methodology in [29]. There are two types of features: static and temporal.
| Horizon (day) | 30     | 60     | 90     | 180    |
|--------------|--------|--------|--------|--------|
| Risk (%)     | 1,243 (7.1) | 1,816 (10.3) | 2,294 (13.1) | 3,275 (18.6) |
| Suicide (%)  | 24 (0.14) | 32 (0.18)  | 41 (0.23)  | 63 (0.36) |

Table 2: Outcome class distribution following risk assessments.

Static features include **demographic information** such as age, gender, spoken language, country of birth, religion, occupation, marital status and indigenous status. Patient age is categorized into intervals. Temporal features are those recorded as events or changing over time. A history of 48 months was used and split into non-overlapping intervals: [0-3], [3-6], [6-12], [12-24], [24-48]. For each interval, events of the same type are counted and normalized. Interval-specific features are then stacked into a long feature vector. The following event groups are used:

- **Life events**: Postcode changes are considered as events based on the hypothetical basis that a frequent change could signify social-economic problems.

- **ICD-10 codes**: The EMR records contain ICD-10[^1] diagnostic codes. We map diagnoses into 30-element **Exlixhauser comorbidities**[^34], as they are known to be predictive of mortality/readmission risk. We also derive Mental Health Diagnosis Groups (MHDGs) from ICD-10 codes using the mapping table in [^35]. The MHDGs provide another perspective to the mental health code groups in ICD-10 hierarchy.

- **Suicide risk assessment**: At Barwon Health, protocol mandates suicide risk assessments for mental health patients. Every patient is required to be assessed at 3 intervals: at admission time, 91 days later, and at time of discharge. This process is performed by clinicians using ordinal assessments for 18 items covering all mental aspects such as suicidal ideation, stressors, substance abuse, family support and psychiatric service history. In our data, 62% patients had one assessment while 17% of patients had two assessments. About 3% of patients had more than 10 assessments.

[^1]: International Statistical Classification of Diseases and Related Health Problems 10th Revision, available at: [http://apps.who.int/classifications/icd10/browse/2010/en](http://apps.who.int/classifications/icd10/browse/2010/en)
assessments. For each assessment, we collect statistics on risk factors and record the maximum values. An extreme value in a risk factor, either at present or in past 3 months, is a definite indicator for potential suicide. Thus we create an extra subset of features with the maximum values: (i) Max of (overall ratings) over time (ii) Sum of (max ratings over time) over 18 items (iii) Sum of (mean ratings over time) over 18 items (iv) Mean of (sum ratings over 18 items) over time (v) Max of (sum ratings over 18 items)

The feature vector is then fed into the classifier to predict future suicide risk. The most challenge in dealing with the aforementioned data is redundancy. A piece of information might be presented in multiple feature groups, e.g. ICD-10 codes, MHDG codes or assessments. In this study, we investigate the suitability of randomized classifiers against this redundancy.

3. Randomized machine learning

We now describe the randomized methods employed in this paper: Random Forests (RF) [36], Gradient Boosting Machine (GBM) [37] and Deep Neural Networks with Dropout (DNND) [38]. At present, these three methods are considered as best performing techniques in data sciences practice. The prediction is binary – risk versus non-risk over multiple periods of time.

3.1. Random Forests

A RF is a collection of decision trees. A decision tree makes a class decision based on a series of tests on values of features. At each test, a feature is selected from all features, and the splitting value is chosen within the value range. At the terminal nodes, class decision will be made. The result of this process is a highly interpretable decision tree. However, decision trees are not very robust – a slight change in training data will lead to a vastly different tree. The prediction variance, as a result, is high. Random forests aim at reducing such variance by using many trees [36]. Each tree is trained on a bootstrap
resample of data. At each splitting decision, only a small random subset of features is considered. The final outcome is voted among trees.

A nice property of RF is that it handles high dimensionality well – at each decision step, only one feature is selected if it offers the best improvement in predictive performance. Hence, important features are repeatedly selected but unimportant features are ignored. Another property is that redundancy is also taken care of – at each step, only a small subset of features is considered, thus the chance of having redundancy is small.

3.2. Gradient Boosting Machine

Suppose the goal is to estimate a predictive function \( F(x) \) which has an additive form:

\[
F(x) = \sum_{t=1}^{T} \lambda_t h_t(x)
\]

where \( h_t(x) \), known as “weak learner”, and \( \lambda_t > 0 \) is a small step size. In binary classification, the decision can be made by checking if \( F(x) \geq 0 \). We choose the following loss function:

\[
L = \log(1 + \exp(-yF(x)))
\]  

(1)

for binary output \( y \in \{\pm 1\} \), which is essentially the loss for logistic regression coupled with the nonlinear \( F(x) \).

GBM is a sequential method for minimizing the loss \( L \) by estimating a pair \( \{\lambda_t, h_t(x)\} \) at a time. At each step, the function is updated as \( F_{t+1}(x) \leftarrow F_t(x) + \lambda_t h_t(x) \). The weak learner \( h_t(x) \) is estimated by approximating the functional gradient of the loss function:

\[
\nabla L = -y [1 + \exp(yF(x))]^{-1}
\]

Typically, \( h_t(x) \) is learnt by regression trees, but other regression methods such as neural networks are applicable. We implemented a randomized variant of GBM [37] in that each weak learner is estimated on a portion \( \rho \in (0, 1) \) of training data. Further, only a subset of features is used in building the weak learner.

In this paper we use regression trees for weak learner. Following RF, each tree node split involves only a small sub-subset of features. Thus this retains the capacity of handling
high dimensional and redundant data of the RF while offering more flexibility in controlling overfitting through learning rate \( \lambda_t \).

3.3. Deep Neural Networks with Dropout and Multitask Learning

Deep Neural Networks (DNNs) are multilayer perceptrons with more than one hidden layer. We aim at estimating the predictive function \( F(x) \) of the following recursive form:

\[
F(x) = b + w^\top \sigma (b_L + W_L \sigma (...) ) \tag{2}
\]

where \( \sigma \) is a nonlinear transformation, also known as activation function. In the past, typically \( \sigma \) is a sigmoid or tanh function, but more recently, a rectified linear \( (\sigma(x) = \max(0, x)) \) is used due to the ease of passing gradient in back-propagation. Here we use the same loss as in Eq. (1).

With sufficient non-linear hidden layers, DNNs are able to learn any complex function \( F(x) \) [39]. This flexibility, however, makes them susceptible to overfitting [40]. Traditionally, parameter shrinkage methods, also known as weight decay, are used to prevent overfitting. However, these methods do not create an ensemble, which has been proven to be highly successful in the case of RFs and GBMs. Second, they are not designed for high dimensionality and redundancy.

**Dropout.** We use a recently introduced elegant solution – “dropout” [38] – with these desirable properties. At each training step, some hidden units and features are randomly removed. In effect, exponentially many networks are trained in parallel sharing the same set of weights. At test time, all the networks are averaged by weight, and thus creating a single consensus network of the original size. The result is that dropout achieves model averaging similar to RF but without storing multiple networks. The use of random feature subsets also helps combat against high dimensionality and redundancy, similar to RF and GBM. Due to its effectiveness, dropout is considered as one of the best advances in neural networks in the past decade. A more detailed account of dropout is presented in Appendix A.1.
Figure 1: Short and medium-terms suicide risk prediction using multitask deep neural networks.

*Multitask learning.* Since we are predicting risk for multiple future periods, the problem can be considered in the multitask learning framework. Neural networks are natural candidate as multiple outcomes can be predicted as the same time. Eq. (2) can be extended as follows:

$$F_m(x) = b_m + w_m^s (b_L + W_L \sigma(...))$$

where $m$ denotes the $m$-th outcome. That is, all the layers except for the top remain the same. The loss function is now a composite function: $L = \sum_m \log (1 + \exp(-y_m F_m(x)))$.

Learning using back-propagation and dropout is carried out as usual. See Fig. 1 for an illustration.

4. Experimental results

4.1. Experimental setup

Here we describe our experimental setup, which is summarized in Fig. 2.

*Feature sets.* We examine three different combinations of the features mentioned in Section 2.2.
Feature set #1 (FS1, without assessment): Demographics, ICD-10 and MHDGs: Our first feature set consists of features commonly available in most hospital setting. It includes three groups: demographics, ICD-10 and MHDGs. There are total 415 features from these three groups. We filter out the features that are active for less than 1% of data points resulting in 109 features.

Feature set #2 (FS2, with assessment): Demographics, ICD codes, MHDGs and assessments: In the second setting, we use all available features to form feature set #2. These features include demographics, ICD-10, MHDGs and assessments. This feature set differs from the feature set #1 in the assessments. There are total 440 features. We filter out the features that are active for less than 1% of data points resulting in 109 features.

Figure 2: Our experimental setup.
points resulting in 134 features.

- **Feature set #3 (FS3, mental health information only):** MHDGs and assessments: In the third setting, we use only two groups of mental health features (MHDGs and assessments) to form feature set #3. This feature set includes 85 features in total. We filter out the features that are active for less than 1% of data points resulting in 37 features.

*Data splitting.* The patients are randomly split into a training set of 3,700 patients (8,466 assessments) and a validation set of 3,699 patients (8,392 assessments).

*Baseline prediction models.* We compare the randomized methods described in Section 3 against baselines. Three baseline techniques are: clinician assessments, lasso regularized logistic regression (lasso-LR) [41], and CART [42]. Clinician assessment produces an overall score of risk based on the 18-item checklist (see also Sec. 2.2). CART generates interpretable decision trees [42]. Logistic regression enjoys wide popularity in medical statistics due to its simplicity and interpretability [43]. Though simple, it has proven to be very effective in many studies [44], and has been used to investigate suicide in many recent studies [45, 46]. We use lasso regularized logistic regression to find a compact subset of features from that best represents suicide risk [41]. Lasso has one tuning parameter – the penalty factor, which is tuned to obtain the best performance.

Details of the experimental setup for Random Forests, Gradient Boosting Machine and Deep Neural Network with Dropout are presented in Appendix A.2.

*Validation.* We consider the suicide risk prediction as a binary classification: risk versus non-risk. Each assessment for a patient is treated as a data point to predict future suicide risk. Each model is used to predict the suicide risk at six different horizons: (i) 15 days (ii) 30 days (iii) 60 days (iv) 90 days (v) 180 days and (vi) 360 days. The classification performance of each model is evaluated using (a) Recall $R$ (a.k.a. sensitivity), (b) Precision $P$ (a.k.a. positive predictive value or PPV), (c) F-measure, computed as $2RP/(R+P)$,
which is a balance between recall $R$ and precision $P$, and (d) area under the ROC curve (AUC, a.k.a. $c$-statistic) with confidence intervals based on Mann-Whitney statistic $^{47}$.

4.2. Results

We test 5 machine learning methods with 3 different feature sets. The training set and validation set are split as discussed in the experimental setup section. We feed the training set to each method and obtain the learned models. We then use these models to predict the output on validation set to compute recall, precision, F-measure and the Area under ROC curve (AUC).

4.2.1. Feature set #1: Demographics, ICD-10 and MHDGs

Recall and precision of all 6 methods are presented in Figs. 3(a,b). Clinician assessments tend to detect more short-term risk within short terms (high recall/sensitivity) at the cost of low precision. Machine learning methods, on the other hand, tend to be more conservative and strike the balance between recall and precision. This is reflected on F-measures reported in Table 3. On this measure, CART performs poorly compared to prediction of clinician and other methods. Its F-measure is lower than that of clinician prediction at almost all horizons (except at 360-days horizon). Lasso-LR performs better than clinician at mid-term horizons (60-360 days) but short-term horizons (15-30 days). On the other hand, the randomized methods (RF, GBM and DNND) performs better than the remaining methods and clinician, except for the GBM at 15-days horizon. Out of these three methods, DNND always gives the highest F-measure at all horizons and the margin compared to lasso-LR is significant.

A comparison of AUC obtained from this feature set over multiple predicting horizons is presented in Figure 4. Except CART, all predictive methods outperforms clinician with significant margins (from 6% for 15-days horizon to 25% for 360-days horizon). Among predictive methods, the randomized methods always perform the best.
Figure 3: Recall and precision on Feature set #1: Demographics, ICD-10 and MHDGs.

Figure 4: Comparison of AUC (95% CIs) from feature set #1: Demographics, ICD-10 and MHDGs.

Table 3: Comparison of F-measure obtained from Feature set #1: Demographics, ICD-10 and MHDGs.
4.2.2. Feature set #2: Demographics, ICD codes, MHDGs and assessments

In this experiment, we investigate whether adding assessments would improve the predictive performance. Figs. 5(a,b) show recall and precision. Overall, the results look qualitatively similar to those found earlier using just clinical information. More quantitatively, Fig. 6 plots the F-measures of feature set #2 against F-measures of feature set #1 for all machine learning methods and all predictive horizons. There are 22 out of 30 cases where adding assessments improve the F-measure indicating that assessments may hold extra risk information that is not readily available in the medical records. However, the mean difference in F-measures due to assessment is merely 0.02, suggesting that the extra risk information is not very critical.

Table 4 reports the F-measures in detail. DNND is still the best predictive method on this feature set. A comparison of AUC obtained on feature set #2 is plotted in Figure 7. Overall, AUC figures increase compared to those of feature set #1. Especially, AUCs obtained by 3 randomized methods are greater than 70% (from 71% for 15-days horizon to the highest of 74%). These methods outperform lasso-LR at short-term and mid-term horizons.

Figure 5: Recall and precision on Feature set #2: Demographics, ICD-10, MHDGs and assessments.
Figure 6: Values of adding assessments on F-measures over all methods and all predictive horizons. Points above the diagonal indicate improvement due to assessments.

| Horizon    | Clinician | CART | Lasso-LR | RF | GBM | DNND |
|------------|-----------|------|----------|----|-----|------|
| 15 days    | 0.149     | 0.046| 0.075    | 0.101| 0.161| **0.177** |
| 30 days    | 0.195     | 0.152| 0.189    | 0.185| 0.224| **0.276** |
| 60 days    | 0.232     | 0.201| 0.290    | 0.251| 0.313| **0.343** |
| 90 days    | 0.248     | 0.264| 0.316    | 0.325| 0.340| **0.379** |
| 180 days   | 0.277     | 0.294| 0.402    | 0.413| 0.411| **0.434** |
| 360 days   | 0.293     | 0.345| 0.464    | 0.484| 0.467| **0.487** |

Table 4: Comparison of F-measure obtained from feature set #2: Demographics, ICD-10, MHDGs and assessments.
Figure 7: Comparison of AUC (95% CIs) from feature set #2: Demographics, ICD-10, MHDGs and assessments.

| Horizon   | Clinician | CART | Lasso-LR | RF  | GBM  | DNND |
|-----------|-----------|------|----------|-----|------|------|
| 15 days   | 0.149     | 0.130| 0.013    | 0.118| 0.110| **0.183** |
| 30 days   | 0.195     | 0.129| 0.030    | 0.239| 0.211| **0.222** |
| 60 days   | 0.232     | 0.197| 0.124    | 0.269| 0.250| **0.323** |
| 90 days   | 0.248     | 0.254| 0.177    | 0.350| 0.281| **0.360** |
| 180 days  | 0.277     | 0.288| 0.295    | 0.416| 0.407| **0.425** |
| 360 days  | 0.293     | 0.337| 0.330    | 0.466| 0.441| **0.469** |

Table 5: Comparison of F-measure obtained from feature set #3: MHDGs and assessments.

4.2.3. Feature set #3: MHDGs and assessments

Recall and precision are reported in Fig. 8(a,b). A comparison of F-measure obtained on feature set #3 is presented in Table 5. Leaving out two groups of features (demographics and ICD-10), F-measure metrics drop by a little amount. However, DNND is still the best predictor, as previous two settings.

A comparison of AUC obtained on feature set #3 is plotted in Figure 9. On this feature set, AUCs of three randomized methods increase by a significant amount on short-term and mid-term horizons. For 15-days horizon, the highest AUC is of DNND (0.736, CIs: [0.710, 0.762]). AUCs other short-term and mid-term horizons are greater than 74%. On the other hand, AUCs obtained by lasso-LR on this feature set drop significantly, ranges from 30% to 55%.
Figure 8: Recall and precision on feature set #3: MHDGs and assessments.

Figure 9: Comparison of AUC (95% CIs) from feature set #3: MHDGs and assessments.
5. Discussion

Predicting suicide is extremely challenging due to the rarity of the event and absence of reliable and consistent risk factors. Ensemble learning and model averaging combines several weak learners and improves prediction accuracy. In this paper, we attempt to improve accuracy of suicide risk prediction by using randomized machine learning techniques, and compare their performance with traditional methods and clinician assessments.

Findings. In terms of predictive power (measured by F-measure and AUC), predictive machine learning methods outperform clinician prediction. This resembles findings in previous work using linear lasso-based methods [8]. The new finding is that randomized machine learning methods (RF, GBM and DNND) outperformed linear models over feature sets studied. Among the three feature sets used to build the model, demographics and ICD-10 features had significant impact on lasso-penalized logistic regressions, while the randomized methods only needed MHDG and assessments to make good predictions. This could be explained by the linearity of logistic regression, which tends to work better when more features are available to separate the classes. Nonlinear methods can exploit the data structure better to find nonlinear regions that correspond to risky outcomes.

While it is widely acknowledged that the final clinician rating in risk assessments has limited predictive power [23] and is highly variable among clinicians [48], we found that the knowledge generated by the assessment process is rich, provided that there exist powerful learning methods to exploit it. This also suggests that combining multiple assessment instruments may offer improved accuracy [19].

High dimensionality and redundancies are major issues in medical records that have led to feature selection and sparsity-inducing techniques. Our results demonstrate that randomized methods are, by design, robust against these properties.

Suicide risk prediction. This work contributes to the literature of suicide prediction and prevention. At present the understanding of risk factors and how they interact is rather poor. Improving the situation is a major goal in “A Prioritized Research Agenda for
Suicide Prevention: An Action Plan to Save Lives”, 2014 by National Action Alliance for Suicide Prevention.  Most existing work, however, is focused on identifying individual risk factors. The suicide risk factors are, however, rather weak. Individual identification will generally over-estimate the power of each factor. Further, these factors have complicated interactions with patient characteristics causing their predictive power to be distributed over many aspects of patient health.

Earlier studies focused on using statistical techniques to select a small subset of risk factors based on their predictive power [32, 50, 33]. These methods however returned a huge number of false positives. Again, this can be attributed to the low prevalence of suicide. A later study using multivariate analysis of 21 common predictors failed to identify patients who committed suicide [51]. A recent study of predicting deliberate self harm (DSH) was able to detect high risk patients using clinical decision rules [52]. However, in the absence of data for the specific rules, the study performed poorly.

Deep learning. Among randomized methods, we found that Deep Neural Networks with dropout and multitask learning work best. Deep Neural Networks with dropout have been recently shown to work well for 30-readmission prediction [40]. It suggests that with recent advances, deep learning has a great potential to play a leading role in biomedical settings [53]. Deep learning has multiple desirable properties that fit biomedical data well. First, features can be learnt, rather than designed by hand. Second, features can be learnt for multiple tasks, as demonstrated in this paper. This can be readily extended to multiple cohorts or transferring between domains (sites and cohorts). Second, multiple modalities and views (such as EMR, clinical text and medical imaging) can be integrated easily at multiple levels of abstraction rather than at the feature levels. Third, structured data such as temporal dynamics of disease progression or spatial imaging can be modeled using existing techniques such as Recurrent Neural Networks and Convolutional Networks.

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Limitations. We acknowledge the following limitations in our work. We used only a single retrospective cohort and confined to a single location for our experiments. The use of future ICD codes as proxy of suicide risk is based on experience not internationally recognized. The use of randomized methods is critical to obtain higher predictive accuracy than standard logistic regression, but they are harder to tune and interpret. However, it is possible to derive feature importance from Random Forests, Gradient Boosting Machine and Deep Neural Networks, and thus enables quantification of risk factor contribution.

6. Conclusion

As demonstrated in the experiments, randomized methods significantly improve predictive accuracy over traditional methods. Hence they provide valuable information to clinicians in eliminating false positives and focusing care and resources for high risk patients. It is therefore advisable that randomized techniques to be used for complex data and nonlinear relationships. Concurring with [40], we believe that deep learning techniques are likely to play a greater role in the coming years in biomedical settings.

Data from EMR has been successfully used to identify suicidal patients with high risk [54,8]. The models described in our work are derived from routinely collected EMR data. Such models can be easily generalized to sites with similar EMR systems. The models based on EMR could be updated in real-time, and make use of data that are routinely collected. The predictors derived from the EMR data were standardised, and thus the tools can be generalizable to sites with similar EMR systems.

Appendix A. Appendix

Appendix A.1. Details of dropout

Consider a simple scenario of a neural network with one hidden layer containing $K$ units. For $m$ training examples, the dropout training and testing of the network is illustrated in Fig [A.10]. For every training example at a updating step, we randomly drop (or disconnect) each hidden unit with a probability $r_1 = 0.5$. Hence, every example trains
Figure A.10: Illustration of dropout in a single layer neural network with dropout rate = 0.5

Figure A.11: Illustration of dropout in layer $\ell$ of a multilayer deep net.

A different network model. This is equivalent to randomly sampling from $2^K$ possible models. At the end of the training phase, many of the $2^K$ models will be trained from a single training example. The weights of the hidden units are shared among models, making it an extreme form of bagging.

The testing phase requires to average these $2^K$ models. An alternative is to use all the hidden units and multiply their weights by the dropout rate $r_1 = 0.5$ (Fig. A.10). For a neural network with a single hidden layer and a logistic regression output, this exactly computes the geometric mean of $2^K$ model predictions [38].

In general, a neural network with more than one hidden layer can be trained using a
dropout rate \( r_1 \) for every layer. During testing, all hidden units are retained and their outgoing weights are scaled by a factor of \( r_1 \) (see Fig. A.11). We describe the modified feed-forward and backpropagation equations using dropout technique as follows. Consider a neural network with \( L \) hidden layers. For each layer \( \ell \), where \( \ell \in (1, 2, \cdots, L) \), let \( h^{(\ell)} \) denote the hypothesis output, \( z^{(\ell)} \) denote the input to the layer and \( b^{(\ell)} \) denote the bias. If the dropout rate for the hidden layer is \( r_1 \), we generate \( m^{(\ell)} \) – a vector of independent Bernoulli random variables where each element is 1 with a probability \( r_1 \) and 0 with a probability \( (1 - r_1) \). Hidden units in layer \( \ell \) are dropped by element-wise multiplication of \( z^{(\ell)} \) and \( m^{(\ell)} \). The modified feed-forward step becomes:

\[
m^{(\ell)} = \text{Bernoulli}(r_1) \\
\tilde{h}^{(\ell)} = m^{(\ell)} \odot h^{(\ell)} \\
z^{(\ell+1)} = W^{(\ell+1)} \tilde{h}^{(\ell)} + b^{(\ell+1)} \\
h^{(\ell+1)} = f(z^{(\ell+1)})
\]

where \( f(z^{(\ell+1)}) \) is the activation function of the hidden unit.

Appendix A.2. Experiment settings for randomized methods

The randomized methods are: Random Forests (RF), Gradient Boosting Machine (GBM), and Deep Neural Networks with Dropout (DNND). Let \( n \) be the size of training data, \( p \) be the number of features, the settings are as follows:

- **RF**: Number of trees is set at 25. Number of features per split is \( \sqrt{p} \), as often recommended in the RF literature. Leave size is set at \( \frac{n}{64} \), that is, there are maximally 64 leaves per tree.

- **GBM**: Number of weak learners is fixed at 200. Learning rate \( \lambda \) is not fixed for each learner, but starts from a small value then increases until there is no improvement in the loss or it reaches 0.1. Data portion per weak learner is \( \rho = 0.5 \), that is, only
50% of training data is used to train a weak learner. Each weak learner uses a random feature subset of size \( m = \min \left( \frac{p}{3}, \sqrt{n} \right) \). We use regression tree as weak learner, where the leave size is limited to \( \frac{n}{64} \). Following RF, at each node split, only a random subset of features of size \( \frac{m}{3} \) is considered.

- **DNND**: We use a network with 2 hidden layers, 50 units each. Although network sizes can be changed to fit the feature complexity, we use the same architecture for all experiments to test its robustness. Training is based on stochastic gradient descent in that parameter is updated after every mini-batch of size 64. Learning rate starts at 0.1 and is halved when the loss stops improving. Learning stops when the learning rate falls below \( 10^{-4} \). Momentum of 0.9 is used, and it appears to speed up the training. Regularization is critical. We use three regularization methods: (i) Weight decay of \( 10^{-4} \), which is equivalent to placing a Gaussian prior on the weight; (ii) Max-norm of 1 for weights combing to a hidden unit. If the norm is beyond the prespecified max-value, the entire weight vector is rescaled; (iii) Dropout rate of 0.5 for both hidden units and features. Applying dropout at feature level is critical to combat against redundancy.

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