Cost-Sensitive Machine Learning Classification for Mass Tuberculosis Verbal Screening

Ali Akbar Septiandri
Aditiawarman
Roy Tjiong
Inovasi Sehat Indonesia, Jakarta, Indonesia

Erlina Burhan
University of Indonesia, Jakarta, Indonesia

Anuraj Shankar
Oxford University, Oxford, UK

Abstract

Score-based algorithms for tuberculosis (TB) verbal screening perform poorly, causing misclassification that leads to missed cases and unnecessary costly laboratory tests for false positives. We compared score-based classification defined by clinicians to machine learning classification such as SVM-RBF, logistic regression, and XGBoost. We restricted our analyses to data from adults, the population most affected by TB, and investigated the difference between untuned and unweighted classifiers to the cost-sensitive ones. Predictions were compared with the corresponding GeneXpert® MTB/Rif results. After adjusting the weight of the positive class to 40 for XGBoost, we achieved 96.64% sensitivity and 35.06% specificity. As such, the sensitivity of our identifier increased by 1.26% while specificity increased by 13.19% in absolute value compared to the traditional score-based method defined by our clinicians. Our approach further demonstrated that only 2000 data points were sufficient to enable the model to converge. The results indicate that even with limited data we can actually devise a better method to identify TB suspects from verbal screening.

Keywords: Tuberculosis, verbal screening, machine learning

1. Introduction

In developing countries, affording state-of-the-art technology such as using polymerase chain reaction (PCR) devices to detect tuberculosis (TB) cases, e.g. GeneXpert® MTB/Rif, is still hard. Yet, these countries are the ones where the number of TB cases is still high. According to the Global Tuberculosis Report 2016 (World Health Organization, 2016), “Six countries accounted for 60% of the new cases: India, Indonesia, China, Nigeria, Pakistan and South Africa.” Recent cases of COVID-19 have shown that population-wide testing and contact tracing are necessary for deadly communicable diseases (Panovska-Griffiths et al., 2020; Matukas et al., 2020). Mass verbal screening can help to overcome this challenge in early detection of tuberculosis (Bothamley et al., 2002; Malik et al., 2018). However, this solution tends to have low specificity. This work addresses the problem by developing a machine learning model to increase the verbal screening performance.

© 2020 A.A. Septiandri, A.A. Aditiawarman, R. Tjiong, E. Burhan & A. Shankar.
Most medical diagnosis cases have to deal with the imbalanced dataset problem (Jothi et al., 2015). Since the majority of the people are healthy, the classification results are more likely to be negative. Since we want to prevent an epidemic because TB is a communicable disease, our goal is then to keep the sensitivity as high as possible while trying to increase the specificity.

We utilised several machine learning algorithms, namely support vector machines (SVM) with Gaussian (RBF) kernel (Fernández-Delgado et al., 2014) and XG-Boost (Chen and Guestrin, 2016). As a benchmark, we also employed a logistic regression model. We evaluated our models by comparing our predictions with the corresponding GeneXpert ® MTB/Rif results. We used two score-based classification methods as the baselines in this study.

2. Related Work

Automated tuberculosis (TB) detection has been studied for nearly two decades. One way to detect TB cases automatically is by using a rule-based approach from both clinical and laboratory criteria (Hripcsak et al., 1997). In a more recent approach, Shamshirband et al. (2014) were able to achieve 87.00% sensitivity and 86.12% specificity in TB diagnosis using Artificial Immune Recognition System (AIRS) learned from supporting lab results. It is also shown in (Seixas et al., 2013) that using artificial neural networks (ANN) could help them to reach more 94.5% sensitivity and 91.0% specificity in diagnosing pleural TB based on anamnesis variables and HIV status.

Although a real-time screening alert has been done in (Weng et al., 2011), machine learning was not employed in that study. Therefore, we proposed to do so in this paper aiming for a simpler but more effective tool to identify TB suspects compared to simple score or rule-based methods.

3. Dataset

Cohort The dataset in this study was collected by field workers. The data were collected from 12 November 2013 to 1 July 2016 from several sites in Jakarta, Indonesia. The dataset we are using in this experiment consists of 8732 rows where each row corresponds to an individual with 7508 TB- and 1224 TB+ from the screening process with their available GeneXpert ® MTB/Rif result. We are also focusing on people with no history of TB before our study. Due to inaccuracy, we chose to remove the rows where the height is either unavailable or less than 120 cm.

We divided our dataset into three sets, i.e. training, validation, and test sets (60:20:20). We built our models using machine learning algorithms from the training set and then evaluated them with the validation set. Eventually, we tested the best models from each algorithm on the test set.

Features The features in this study are symptoms, comorbidities, and characteristics commonly found in TB patients. Four attributes in this dataset are of numerical values, i.e. height, weight, age, and cough duration (in days). We also used the sex of the people screened as the attributes for machine learning algorithms. The statistical properties of the features can be seen in Table 1.

Aside from derived attributes like the body mass index (BMI), the attributes were acquired by verbally asking the subjects. We only marked ‘Yes’ as the value of diabetes, kidney failure, asthma, COPD, and HIV questions if the subjects had done the appropriate lab test before. We can see that breathing shortness, chest pain, diabetes, family diabetes, TB exposure, kidney fail-
ure, asthma, COPD, and HIV contain lots of unknown values. This is because they were added later in the field study. Comorbidity in particular needs to be confirmed by a lab test for our screeners to report them as a yes/no.

| Feature          | Yes   | No    | Unknown |
|------------------|-------|-------|---------|
| cough            | 5480  | 3242  | 10      |
| fever            | 1777  | 6955  | 0       |
| haemoptysis      | 646   | 7758  | 0       |
| night sweat      | 1365  | 7367  | 0       |
| weight loss      | 1890  | 6842  | 0       |
| fatigue          | 2185  | 6547  | 0       |
| breathing shortness | 189  | 1370  | 7173    |
| chest pain       | 123   | 1436  | 7173    |
| diabetes         | 969   | 5092  | 2671    |
| family diabetes  | 137   | 468   | 8127    |
| TB exposure      | 1414  | 4808  | 2510    |
| kidney failure   | 75    | 4880  | 3777    |
| asthma           | 717   | 4831  | 3184    |
| COPD             | 232   | 4710  | 3790    |
| HIV              | 251   | 4695  | 3786    |
| active smoker    | 4313  | 4419  | 0       |

### Table 1: Statistical Properties of the Features

#### 4. Methods

**Classification Algorithms** Our clinicians devised two scoring methods that were used throughout the project. When the total score of a person exceeds a certain threshold, we classify that person as a TB suspect. Those TB suspects were then tested by GeneXpert®MTB/Rif to confirm our finding. The pseudo-code for these methods can be seen in Algorithm 1 and Algorithm 2 in the Appendix. In these two algorithms, a person will be categorised as *underweight* if their BMI is lower than 18.5.

This method needs experts to define the scoring scheme, i.e. how each attribute contributes to our suspicion about whether a person is TB+. To deal with this problem, we proposed a machine learning classification which continues to learn as the number of data grows larger. We employed support vector machine (SVM) (Boser et al., 1992), XGBoost (Chen and Guestrin, 2016), and logistic regression models to classify the individuals.

**Evaluation Approach/Study Design** We trained the untuned version of each machine learning algorithm first to get an idea of how a cost-sensitive approach would later improve our models. We kept the parameters to the default settings and imputed the unknown/null values to the most frequent values. After that, we trained the models using a different weighting of positive class with the chosen hyperparameters. We tuned the hyperparameters with several different class weights, such as 10, 15, 20, 25, 30, 35, 40, 45, and 50. We did a grid search with 3-fold cross-validation using our training data to get the optimal AUC score. We chose AUC score to optimise both sensitivity and specificity.

### 5. Results

**Untuned Classifiers** The untuned classifiers tend to favour the negative class as can be seen in Table 2. The machine learning classifiers performed worse than the score-based classifiers because the training set is highly imbalanced while the score-based classifiers are optimised for sensitivity.

**Cost-sensitive Classifiers** In SVM case, we got higher sensitivity than Score-2 and higher specificity than Score-1 when we used at least 15 as the positive class weight. While the class weight is less than 20, we can also produce at least the same specificity as Score-1 with SVM. With XGBoost, we got an even better result: increasing the specificity from 20.63% to 35.78% while only reducing the sensitivity from 93.16% to 92.74%
Table 2: Classifier Performance (in %)

| Classifier   | Untuned Sensitivity | Specificity | Subsampling Sensitivity | Specificity | Test Set (Cost-sensitive) Sensitivity | Specificity |
|--------------|---------------------|-------------|-------------------------|-------------|--------------------------------------|-------------|
| LogReg       | 16.24               | 97.49       | 68.80                   | 74.74       | 98.32                                | 22.80       |
| XGBoost      | 23.93               | 97.49       | 68.80                   | 74.27       | 96.64                                | 35.06       |
| SVM-RBF      | 0.00                | 100.00      | 73.50                   | 71.03       | 96.64                                | 29.82       |
| Score-1      | 93.16               | 20.64       | -                       | -           | 95.38                                | 21.87       |
| Score-2      | 84.19               | 46.30       | -                       | -           | 88.24                                | 43.94       |

Based on Score-1’s result (class weight: 40). Yet, this specificity is still 10.45% away from Score-2 specificity (46.23%). Logistic regression also produces a quite decent result when using 20 as the class weight, i.e. 93.16% sensitivity and 34.26% specificity.

The Effect of Dataset Size

As shown in Figure 1, all the metrics seem to converge when the number of training data is ≈ 2000. Our exploration with the subsampling method also turned out to be ineffective as shown in Table 2. These results imply that using cost-sensitive classifiers is preferred to using subsampling to overcome the imbalanced class problem.

Evaluation on Test Set

Although the best specificity is achieved by the Score-2 method, the sensitivity is low despite being used for early stage TB diagnostics. Our best compromise is to use the XGBoost model where the sensitivity and specificity are the second-best overall.

6. Conclusions

We were able to increase the specificity while still keeping the sensitivity relatively high by using machine learning algorithms. We showed that using imbalanced weighting for the classes is necessary for this task. Furthermore, the best model converged after around 2000 data points. Therefore, we might use this as a reference point in further experiments.

Increasing the specificity by more than 10% as achieved in this study means saving lots of money and time to do unnecessary tests. We can achieve this without losing any sick people in the screening process. In a more practical sense, the best model from our work can be installed on smartphones where verbal screeners can rapidly identify TB suspects, especially in rural and poor areas where access to clinics might be limited. The suspects can then be taken to better health facilities to be tested further to confirm the findings.

Acknowledgments

We thank Stop TB Partnership for providing GeneXpert®MTB/Rif instruments through the TB REACH Wave 3 program.
References

- Bernhard E Boser, Isabelle M Guyon, and Vladimir N Vapnik. A training algorithm for optimal margin classifiers. In Proceedings of the fifth annual workshop on Computational learning theory, pages 144–152, 1992.

- GH Bothamley, JP Rowan, CJ Griffiths, M Beeks, M McDonald, E Beasley, C Van den Bosch, and G Feder. Screening for tuberculosis: the port of arrival scheme compared with screening in general practice and the homeless. Thorax, 57(1):45–49, 2002.

- Tianqi Chen and Carlos Guestrin. Xgboost: A scalable tree boosting system. In Proceedings of the 22nd ACM SIGKDD International Conference on Knowledge Discovery and Data Mining, KDD ’16, pages 785–794, New York, NY, USA, 2016. ACM. ISBN 978-1-4503-4232-2. doi: 10.1145/2939672.2939785. URL http://doi.acm.org/10.1145/2939672.2939785.

- Manuel Fernández-Delgado, Eva Cernadas, Senén Barro, and Dinani Amorim. Do we need hundreds of classifiers to solve real world classification problems. J. Mach. Learn. Res, 15(1):3133–3181, 2014.

- George Hripcsak, Charles A. Knirsch, Nilesh L. Jain, and Ariel Pablos-Mendez. Automated tuberculosis detection. Journal of the American Medical Informatics Association, 4(5):376, 1997. doi: 10.1136/jamia.1997.0040376. URL http://dx.doi.org/10.1136/jamia.1997.0040376.

- Neesha Jothi, Wahidah Husain, et al. Data mining in healthcare—a review. Procedia computer science, 72:306–313, 2015.

- AA Malik, F Amanullah, AJ Codlin, S Siddiqui, M Jaswal, JF Ahmed, S Saleem, A Khurshid, and H Hussain. Improving childhood tuberculosis detection and treatment through facility-based screening in rural pakistan. The International Journal of Tuberculosis and Lung Disease, 22(8):851–857, 2018.

- Larissa M Matukas, Irfan A Dhalia, and Andreas Laupacis. Aggressively find, test, trace and isolate to beat covid-19. CMAJ, 2020.

- Jasmina Panovska-Griffiths, Cliff C Kerr, Robyn M Stuart, Dina Mistry, Daniel J Klein, Russell M Viner, and Chris Bonell. Determining the optimal strategy for re-opening schools, the impact of test and trace interventions, and the risk of occurrence of a second covid-19 epidemic wave in the uk: a modelling study. The Lancet Child & Adolescent Health, 2020.

- JM Seixas, J Faria, Filho Souza, AFM Vieira, A Kritski, A Trajman, et al. Artificial neural network models to support the diagnosis of pleural tuberculosis in adult patients. The International Journal of Tuberculosis and Lung Disease, 17(5):682–686, 2013.

- Shahaboddin Shamshirband, Somayeh Hessam, Hossein Javidnia, Mohsen Amiribesheli, Shahgayegh Vahdat, Dalibor Petković, Abdullah Gani, and Miss Laiha Mat Kiah. Tuberculosis disease diagnosis using artificial immune recognition system. Int J Med Sci, 11(5):508–14, 2014.

- Chunhua Weng, Candido Batres, Tomas Borda, Nicole G Weiskopf, Adam B Wilcox, J Thomas Bigger, and Karina W Davidson. A real-time screening alert improves patient recruitment efficiency. In AMIA Annual Symposium Proceedings, volume 2011, page 1489. American Medical Informatics Association, 2011.
World Health Organization. Global tuberculosis report 2016. 2016.
Algorithm 1: Score-1

score ← 0;
for $s \in \{\text{cough, fever, night_sweat, weight_loss, fatigue}\}$ do
    if $s = \text{true}$ then
        score ← score + 1;
    end
end
if hasKidneyFailure||hasAsthma||hasCOPD||hasHIV then
    score ← score + 1;
end
if hasTBExposure then
    score ← score + 1;
end
if hasDiabetes then
    score ← score + 1;
end
if isUnderweight then
    score ← score + 1;
end
if isActiveSmoker then
    score ← score + 1;
end
if coughDuration $\geq 14$ then
    score ← score + 2;
end
if hasHaemoptysis then
    score ← score + 3;
end
return score $\geq 2;$
Algorithm 2: Score-2

\[
\text{score} \leftarrow 0;
\]
\[
\text{for } s \in \{\text{cough, fever, night_sweat, weight_loss, fatigue, breathing_shortness, chest_pain}\}
\]
\[
\text{do}
\]
\[
\quad \text{if } s = \text{true} \text{ then}
\]
\[
\quad \quad \text{score} \leftarrow \text{score} + 2;
\]
\[
\quad \text{end}
\]
\[
\text{end}
\]
\[
\text{if hasKidneyFailure} || \text{hasAsthma} || \text{hasCOPD} || \text{hasHIV} \text{ then}
\]
\[
\quad \text{score} \leftarrow \text{score} + 1;
\]
\[
\text{end}
\]
\[
\text{if hasTBExposure} \text{ then}
\]
\[
\quad \text{score} \leftarrow \text{score} + 1;
\]
\[
\text{end}
\]
\[
\text{if hasDiabetes} \text{ then}
\]
\[
\quad \text{score} \leftarrow \text{score} + 1;
\]
\[
\text{end}
\]
\[
\text{if isUnderweight} \text{ then}
\]
\[
\quad \text{score} \leftarrow \text{score} + 1;
\]
\[
\text{end}
\]
\[
\text{if isActiveSmoker} \text{ then}
\]
\[
\quad \text{score} \leftarrow \text{score} + 1;
\]
\[
\text{end}
\]
\[
\text{if coughDuration} \geq 14 \text{ then}
\]
\[
\quad \text{score} \leftarrow \text{score} + 4;
\]
\[
\text{end}
\]
\[
\text{if hasHaemoptysis} \text{ then}
\]
\[
\quad \text{score} \leftarrow \text{score} + 4;
\]
\[
\text{end}
\]
\[
\text{return } \text{score} \geq 4
\]