Application of Machine Learning to Develop a Mucormycosis Mortality Prediction Model

مشخصات نویسندگان مقاله:

A Ziaee – *Mashhad University of Medical Sciences, Mashhad, Iran*

P Arjmand – *Department of Otorhinolaryngology, Ghaem Hospital, Mashhad University of Medical Sciences, Mashhad, Iran*

M Bakhshaee – *Sinus and surgical Endoscopic Research center, Mashhad University of Medical Sciences, Mashhad, Iran*

M Arian – *Department of Infectious Diseases, School of Medicine, Mashhad University of Medical Sciences, Mashhad, Iran*

M Jabbari – *Department of Statistics, Ferdowsi University of Mashhad, Mashhad, Iran*

SH Alavi – *Department of Medical Informatics, School of Department of Otorhinolaryngology, Ghaem Hospital, Mashhad University of Medical Sciences, Mashhad, Iran*

MH Taherynejad – *Mashhad University of Medical Sciences, Mashhad, Iran*

SM Tabatabaei – *Department of Medical Informatics, School of Medicine, Mashhad University of Medical Sciences, Mashhad, Iran*

خلاصه مقاله:

Background and Aims : Mucormycosis is an emerging fungal infection associated with highmortality and morbidity. Since the disease is rare, large, randomized clinical trials are almost impossibleand most epidemiological, diagnostic, and treatment data are limited to case reports andcase series. Antifungal therapy is required promptly and at a sufficient dose to effectively manageMucormycosis. Artificial Intelligence (AI) can work as a powerful tool to fill the gaps in availabledata; machine learning (ML) as a subset of AI is commonly used on large data sets to identifyhidden patterns to create a predictive model. This study aims to test ML capabilities on a limiteddataset of mucormycosis patients to create a mortality prediction model and pave the road forfurther research regarding mucormycosis treatment choice and diagnosis assistance.Method : This study used patients′ electronic health records to develop a mortality predictionmodel based on laboratory testing and demographic data collected from ۳۲۶ hospitalized mucormycosispatients from ۲۰۱۲ to ۲۰۲۲. As part of the data cleansing process, important features areselected with RapidMiner′s automatic feature selection, and cases with a high number of missingfeatures are removed. Data imputation was also done to replace the remaining missing values,and then the data were split into train and test groups with proportions of ۲۰% and ۸۰%. Our datawere processed using ۵-fold models, including Random Forest, Support Vector Machine, NeuralNetwork, and XGBoost with their default settings; the one with the best results was selected.Models were deployed, and evaluation metrics were

collected Using R Studio software packages,including "randomForest", "caret", "e۱۰۷۱", "neuralnet", "naivebayes", and "xgboost". We thenuploaded the model to the GitHub repository for future analyses and reuse.Results : The train set included ۲۶۵ cases, and the test set included ۶۱. Eleven features wereselected : Chemotherapy, Dialysis, Brain CT Scan, ICU admission, Fever, Ptosis, OphthalmologicalSymptoms, Nasal Congestion, Epistaxis, Maxillectomy, and Ethmoidectomy. Random Forest,SVM, Decision Tree, Neural Network, Naïve Bayes, and XGBoost were ۰.۷۵۴۱, ۰.۸۰۳۳, ۰.۷۸۷۰,۰.۷۸۶۹, ۰.۷۸۶۹, and ۰.۷۵۴۱, respectively. Our ۵-fold Support Vector Machine with its defaultvalues (Cost = ۱۰; Number of vectors = ۱۶۴) reported the best accuracy of ۰.۸۰۳۳ (۹۵% CI of۰.۶۸۱۶, ۰.۸۹۴۲); model sensitivity and specificity were ۰.۸۴۶ and ۰.۷۲۷, respectively. A positivepredictive value of ۰.۸۴۶ was reported as well as a negative predictive value of ۰.۷۲۷, and a receiveroperating characteristic (ROC) diagram was drawn.Conclusion : As a result of the gratifying results of the support vector machine model, we canconclude that there is still great potential for developing mortality prediction models despite thescarce mucormycosis data availability. Machine learning models can help diagnose patients fasterand select the most effective drugs in light of the challenges associated with mucormycosis.

کلمات کلیدی:

Machine Learning; Mucormycosis; Mortality; Artificial Intelligence

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