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Digital Transformation and Artificial Intelligence Applied to the Health Sector: Implementation of a Random Forest Machine Learning Model in a Telemedicine Web Application for the Early Detection of Relapses in Pediatric Cancer Patients*

Cesar A. TELLO DAVILA and Xiomara A. TEJADA TEJADA

Peruvian University of Applied Sciences, Lima, Peru,

Correspondence should be addressed to: Cesar A. TELLO DAVILA, ctellodavila@gmail.com

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Abstract

Cancer recurrence in pediatric patients after treatment represents a significant and urgent challenge to global public health, particularly in low- and middle-income countries, where health systems face structural limitations, fragmented care, and disparities in access to specialized services. These challenges are exacerbated in rural and marginalized regions by geographic isolation, limited connectivity, and the centralization of cancer services in urban centers, leading to late diagnoses, high rates of treatment abandonment, and poor long-term survival outcomes. Addressing this situation requires innovative, scalable, and context-specific solutions capable of transforming follow-up care in vulnerable populations. This article presents the design, development, and preliminary validation of an intelligent telemedicine platform designed for risk-based remote monitoring of pediatric cancer survivors. It is based on a Random Forest machine learning model, trained on anonymized clinical datasets, and implemented using a Python backend. The model classifies patients into three risk levels: low, medium, and high, based on structured symptom reports, laboratory indicators, and other relevant clinical variables. The user interface adheres to the "clinical traffic light" principle, facilitating intuitive risk representation for non-expert users. Furthermore, it enables predictions, thereby strengthening clinical confidence. The platform's modular and open-source design allows for cost-effective implementation and future enhancement through integration with biometric sensors. The system enables post-treatment detection of potential relapses via automated alerts, allowing healthcare professionals to take preventative action, even in regions with limited infrastructure and intermittent internet access.

Keywords: Machine Learning, Pediatric Oncology, Telemedicine, Random Forest.

Introduction

The rapid evolution of artificial intelligence (AI) and its associated computational techniques has transformed how healthcare systems process information, deliver services, and support clinical decision-making. Machine learning (ML) has proven capable of identifying subtle patterns in large-scale clinical datasets, enabling more accurate diagnostic and prognostic assessments across various medical specialties. In oncology, where timing is often crucial, these innovations have become particularly relevant. In the study by Placido et al. (2023), the early detection of disease progression or relapse is widely recognized for its enormous potential to increase patient survival and reduce overall mortality, especially in populations with inconsistent access to specialized care.

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Pediatric oncology presents several challenges that intensify the need for early and continuous monitoring. Once treatment is completed, regular follow-up is necessary to detect clinical changes that may indicate relapse or late effects of treatment. However, traditional patient assessment methods, such as population screening programs or in-person surveillance, are difficult to implement on a large scale. Placido et al. (2023) frequently mention that these methods become impractical due to the costly clinical examinations for many patients, resulting in false-positive outcomes. Xue et al. (2023) indicate that this problem is exacerbated in regions with socioeconomic and geographic barriers, where access to specialists is often limited. In these contexts, AI-based solutions help overcome financial and technological barriers, enabling equitable access to expertise that would otherwise remain centralized in large urban hospitals. An additional factor justifying technological intervention is the growing evidence that machine learning (ML) models can anticipate oncological events over long-time intervals by analyzing clinical trajectories. Placido et al. (2023) mention that trajectories, or "disease pathways," encode the sequence of visits, symptoms, diagnoses, and treatments that characterize a patient's journey through the healthcare system. Furthermore, Wang et al. (2023) indicate that the integration of these temporal characteristics significantly enhances the ability of computational models to recognize early signs of cancer and stratify patient risk. In this context, algorithms such as Random Forest (RF) have gained relevance due to their "computational efficiency, ease of interpretation, and high accuracy."

Placido et al. (2023) is based on the implementation of an RF-based predictive model within a telemedicine web application specifically designed for pediatric cancer follow-up. The goal is to help clinicians identify early indicators of relapse, especially in regions with limited specialized cancer services. By combining a robust machine learning classifier with a remote monitoring platform, the system aims to create a scalable workflow for cancer detection while improving communication between local healthcare providers and specialized centers. Paredes-Noguni et al. (2021) also aligns with current trends in digital transformation, where telemedicine solutions enhanced with machine learning have demonstrated their ability to improve both accessibility and clinical efficiency. In Peru, for example, tele-oncology initiatives documented during the pandemic showed clear benefits in maintaining continuity of care for cancer patients through remote consultations. Internationally, Pritchet et al. (2022) mentions that the adoption of telehealth has increased in complex oncology consultations, as clinicians recognize its ability to streamline follow-up, reduce travel burden, and expand access to timely medical advice. These findings reinforce the relevance of integrating machine learning into digital platforms to optimize triage, risk assessment, and monitoring, especially in settings with a shortage of specialized infrastructure.

Related Works

Performance of the Random Forest (RF) Algorithm in the Healthcare

The Random Forest (RF) algorithm is an excellent classification tool for various clinical settings. It is a robust and interpretable method that can effectively address the challenges associated with analyzing nonlinear relationships in high-dimensional clinical datasets, as it combines multiple decision trees to create a set of predictions. Furthermore, its ability to reduce overfitting is essential in medical datasets, where noise, missing values, or an uneven distribution of A and B classes are often present.

In cardiovascular disease risk assessment, the RF method has yielded favorable results. For example, Wang et al. (2023) constructed an RF-based model that produced an AUC of 0.978 for predicting heart failure in middle-aged and older individuals with diabetes or prediabetes in the US; this model had a validation AUC of 0.865. Similar results have been reported in the field of nephrology; Qin et al. (2019) indicated that RF outperformed all other candidate algorithms examined for diagnosing chronic kidney disease. The results of the study show that the RF algorithm achieved an accuracy rate of 99.75%, one of the highest of all the models evaluated.

On the other hand, Mossotto et al. (2017) proposed a model to classify inflammatory bowel disease in pediatric patients, although with some uncertainty in discriminating common symptoms. Pan et al. designed models to detect Mycoplasma pneumonia in children, with the GBDT model performing best at 93.7% accuracy. Roquette et al. (2020) used a gradient-impulse classifier and a deep neural network on a dataset of nearly 500,000 cases to detect the severity of some common diseases, achieving 89% accuracy. Finally, Hwang et al. (2022) developed a random forest model with more than 2.6 million cases to predict hospitalization and critical cases in children, achieving 94% accuracy.

Digital Transformation and the Rise of Telemedicine Platforms

The healthcare sector has undergone rapid digital transformation due to the growing need for greater efficiency, increased access to specialized services, and better utilization of medical resources. As part of this digital transformation process, machine learning is one of the most crucial components, helping healthcare professionals improve decision-making and identify high-risk patients within large populations. Furthermore, machine learning provides new ways to detect diseases at an early stage through predictive analytics. One example is the study by Placido et al. (2023), where integrating time sequences (referred to as "disease pathways") into predictive models significantly increased the ability to identify individuals at high risk of developing cancer.

Telemedicine has played a critical role in ensuring continuity of cancer care, especially during periods of restricted in-person access. According to Paredes-Noguni et al. (2021) the experience of tele-oncology in a public hospital during the COVID-19 pandemic, demonstrating that virtual consultations facilitated the constant follow-up of cancer patients, while alleviating travel burdens and reducing the risk of exposure. Also, international studies reflect this pattern Pritchett et al. (2022) found that telehealth adoption increased significantly in multiregional oncology practices, driven by both patient- and provider-level factors that favored remote management for routine follow-up and symptom assessment.

Geographical Transferability and Model Adaptation Challenges

While machine learning (ML) models have shown great promise in their application to clinical research, actual clinical practice depends on their degree of adaptation to the specific characteristics of the healthcare environment where they will be used. One of the most important limitations of existing research on ML and its clinical applications is that predictive models developed for use in one geographic region are not easily transferable to another. For example, Placido et al. (2023) found that a deep learning model trained with data from the Danish National Patient Registry had a high level of accuracy (AUROC 0.879) when compared to the Danish dataset, while its accuracy was significantly lower (AUROC 0.710) when compared to data from a patient cohort in the United States. The difference in accuracy between both data sets was likely due to differences in healthcare practices, service utilization patterns, coding conventions, and document standards. Therefore, a predictive model that uses training data from one geographic region may not produce the same level of accuracy for the same clinical condition if applied to a different geographic region. For low- and middle-income countries, this challenge is even greater. Variability in the completeness of medical records, availability of medical resources, frequency of follow-up, and patterns of access to care will have a significant impact on the data available for training machine learning tools. Therefore, it is important to carefully retrain or refine machine learning tools using local data sets before using them to support high-risk clinical decision making, such as the identification of early-stage oncological recurrences.

Process

The random forest classifier was trained on cancer patients using the Python library Scikit-Learn and its optimal parameters for the number of trees and maximum depth, with an appropriate number of clinical variables and privacy-compliant data from pediatric oncology physicians. This project processed the patient input data into the model via an online web service and returned the random forest model output with one precession per image.

1.1 Phase 1: Data Selection and Collection

- Collecting anonymous clinical data is essential for training and validating the classification model. It focuses on the following characteristics:
- Key Variables: Age, name, reported symptoms, and clinical evolution using JPG images.

1.2 Phase 2: Preprocessing for the Model

The collected data underwent a rigorous cleaning and preparation process:

- Handling Missing Data: Methods such as statistical imputation or robust algorithms that tolerate incomplete data, such as RF, are used.

3.3 Phase 3: Model training

The random forest model is trained using Scikit-Learn:

- Adjusted hyperparameters: Parameters such as the number of trees (between 100 and 500) and the maximum depth are optimized using cross-validation.
- Formula applied: The relative risk (RR) is used to assess the accuracy of the model's prediction of the incidence of relapse in post-treatment cases.

Model validation: Techniques such as k-fold cross-validation are used to ensure the robustness and generalizability of the model, achieving accuracies greater than 83%.

3.4 Phase 4: Visualization and explanation of results

The visualization phase presents the results and focuses on providing clear and understandable interpretations of the predictions made by the Random Forest model, facilitating clinical confidence and informed decision-making. Key elements of this phase include:

- Generation of medical reports: A basic report is generated for each patient with a prescription.
- Automated notifications by priority queue: The integration of a notification module is considered, which automatically alerts medical staff when high-risk cases are detected. This provides added value by optimizing clinical responsiveness and ensuring that critical cases receive priority attention.

Conclusions

The methodology employed included reversal validation (RR). In each iteration, four subsets were used to train the model and one to validate it, systematically rotating until all partitions were evaluated. This approach allowed for a more stable and reliable estimation of the performance metrics, reducing the variance associated with random divisions of the dataset. The metrics used to evaluate model performance included accuracy. As other authors have investigated, these metrics were crucial for creating our classifier (low, medium, high), which allowed for a comprehensive evaluation of the model's performance. In the simulation performed with a trained clinical dataset, the model achieved an overall accuracy of 89%.

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