A Novel Approach of Deep Learning on Detection and Classification of Leukemic Cells and BCR-ABL1 Gene

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The American Cancer Society estimates that 23,660 Americans will die of leukemia in 2022. It is the eighth-most lethal form of cancer and the second among children. Accurate and early diagnosis is of the essence. While misdiagnosis is a universal concern, it is particularly critical in underdeveloped regions. Therefore, an inexpensive and easily available diagnostic technology could save the lives of millions of people. Machine learning (ML) and deep learning (DL) were used to improve upon an inexpensive technology (C-3BO), developed in a previous project to identify and predict leukemia. The goal was to use them to diagnose leukemia with peripheral blood smear (PBS) images and predict ABL1-BCR gene mutation in chronic myeloid leukemia (CML) with gene expression profile (GEP). First, 549 labeled images were downloaded from different diverse sources. Because that amount was insufficient, preprocessing techniques were applied to increase the variety and quantity of data. C-3BO was refined to find underlying patterns of certain types of leukemia using a custom neural network superior to other used ML algorithms. Information was extracted from ABL1-BCR genetic data and translated into a data frame. When that data was meticulously refined, a polynomial regression model was fine-tuned to predict the clinical classification of variant genomes. An app was developed once accuracy was 86% and 97% for PBS and GEP respectively. These statistics illustrate C-3BO's proficiency in diagnosing and predicting leukemia, as its methods are unavailable in many underdeveloped regions; this inexpensive software is perhaps the future of diagnosis in these regions.

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