A Robust and Interpretable Deep Neural Network Algorithm for Leukemia Identification in Peripheral Blood Smear Cells

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The American Society of Clinical Oncology estimates a national shortage of over two-thousand hematologists and oncologists by 2025, yet leukemia is consistently among the ten most prevalent forms of cancer worldwide. Deep learning (DL), through the utilization of neural networks, offers considerable promise to these rampant issues. Unfortunately, the biggest barrier to the usage of DL in healthcare is echoed by the black box problem, where a model is too complex to be easily explained or visually interpreted. In lieu of such a problem, this project aimed to expand upon Cancer-3 Blood Oncologist (C-3BO), a previously developed program that accurately detects leukemia, to interpret its diagnoses. First, images of leukemia subtypes were sourced from various hematology databases and applied to preprocessing functions for data augmentation. A deep custom convolutional neural network was meticulously trained to accurately diagnose leukemia and its subtypes. Then, a novel algorithm was developed to recursively reverse-propagate a predicted output value to the original image, in which the most significant features are accentuated. Significantly, this algorithm produces a higher average confidence per image than both experimental patching and Taylor decomposition, two popular techniques in explainable DL. To increase the accessibility of C-3BO, a multilingual website was developed for hematologists to use and provide a personal evaluation of interpretability. Experimental results and examinations suggest that not only is C-3BO a robust and available model, but it also interprets its diagnoses visually.

Awards Won:
Central Intelligence Agency: Second Award: $300