

# Skin Cancer Survival Prediction Using Artificial Intelligence Techniques

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The advancement in cancer research using high throughput technology and artificial intelligence (AI) is gaining momentum to improve disease diagnosis and targeted therapy. However, the complex and imbalanced data with high dimensionality pose significant challenges for computational approaches and multi-omics data analysis.

Keywords: skin cancer ; melanoma ; machine learning ; ensemble technique ; feature selection

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## 1. Introduction

In recent years, the alarming surge in malignant diseases has become a critical global health concern. Among these malignancies, skin cutaneous melanoma cancer (SKCM) is one of the most aggressive variants, demanding thorough investigation and understanding <sup>[1]</sup>. According to an International Agency for Research on Cancer (IARC) report, cancer is the leading cause of mortality. The report exhibits that nearly 10 million deaths have resulted from various types of cancer <sup>[2]</sup>. The World Health Organization (WHO) 2023 report illustrates that cancer is the second leading cause of death (16%), followed by cardiovascular disease (27%) <sup>[3]</sup>. In such a situation, the early diagnosis of a disease can cure and prevent the patients from further jeopardy. In general, there are two main forms of skin cancer: melanoma (cancers resulting from melanocyte malfunction) and non-melanoma skin cancers (from cells generated from the epidermis) <sup>[4]</sup>. Among various types of cancers, SKCM has become one of the most prevalent cancers in the last ten years <sup>[5]</sup> with tumors made of melanocyte cells. It is currently a major public health issue worldwide, and the increasing prevalence of the disease might significantly impact the world's population and economy <sup>[6]</sup>. However, early diagnosis and effective tumor therapy lead to a cure rate of over 90% in individuals with incipient melanoma <sup>[7]</sup>. There are several factors for an increased number of skin cancers. One of the most common occurrences of skin cancer is due to ultraviolet (UV) rays <sup>[8]</sup>. Other reasons include sun exposure, depletion of the ozone layer, genetic predisposition, and so on.

Several studies have shown that SKCM results from abnormalities in transcriptional and epigenetic factors, including the expression of messenger ribonucleic acid (mRNAs) and micro ribonucleic acid (miRNAs), the aberration in methylation patterns of CpG islands of genes, and histone modifications, which opens the door for the development of potential molecular biomarkers in melanoma <sup>[9][10]</sup>. As predictive indicators for cutaneous melanoma, miRNA expression has been implicated in several past studies.

## 2. Artificial Intelligence Technologies and Skin Cancer

In recent years, cancer has been a very undeniable global health challenge. There are various cancer types, such as lymphoma, leukemia, breast cancer <sup>[11]</sup>, lung cancer, skin cancer, and so on. Early skin cancer detection significantly impacts prognosis, and various techniques have been exploited. From histopathological examination to advanced imaging modalities <sup>[12]</sup>, the quest for optimizing predictive models has given rise to the integration of ensemble techniques. This literature review delves into the multifaceted landscape of skin cancer detection methodologies, focusing on the evolving role of ensemble techniques in enhancing survival prediction accuracy. On the other hand, ML is greatly contributing to anomaly detection in various fields, including health care, vehicular networks <sup>[13][14]</sup>, the Internet of Things (IoT), E-commerce, and so on. ML and DL algorithms significantly aid in identifying skin cancer, with early detection potentially leading to successful treatment, making melanoma a significant health concern <sup>[15][16][17][18]</sup>. Various ML and DL techniques have been applied in existing literature, such as in <sup>[19]</sup>, where the authors presented a convolutional neural network (CNN) based DL stacked ensemble framework for melanoma skin cancer detection using transfer learning. The model uses multiple CNN sub-models and a meta-learner to predict malignant melanoma moles. The model achieves a high accuracy of 95.76%, precision of 95.60%, recall of 96.67%, specificity of 94.67%, F1 score of 94.67%, and area under the curve (AUC) of 0.957% identifying both benign and malignant melanoma. Although this research is important, it

could not achieve better accuracy. Similarly, another work in [20] proposed a DL-based skin cancer detection system on an imbalanced dataset. The authors employed the MNIST: HAM10000 dataset that contains seven classes of skin lesions. In order to classify the skin cancer, the authors utilized AlexNet, InceptionV3, and RegNetY-320 techniques. However, the achieved accuracy (91%), F1-score (88.1%), and ROC curve (95%) reflect a poor accuracy as compared to the proposed study.

Moreover, the authors in [21] proposed a CNN-based skin cancer detection system using a publicly available dataset, HAM10000, that includes seven skin cancer types. The authors achieved the following: accuracy (86%), precision (84%), recall (86%), and F-1 score (86%). Thus, all the achieved results fall in the 80s, which reflects the poor performance of the proposed study. Authors in [22] employed a CNN-based approach using a HAM10000 dataset that comprises 6705 benign and 1113 malignant samples and 2197 unknown lesion samples. The proposed model achieved an accuracy of 93.16% on training and 91.93% on testing. Moreover, the authors balanced the dataset of both classes, resulting in an enhanced accuracy of categorization. Despite training several transfer learning models on the same dataset, the outcomes did not surpass those of their proposed model. Another similar work in [23] proposed a CNN-based skin cancer diagnosis that is evaluated using the ISIC 2019 dataset. This work is based on multiclassification system that classifies the cancer types including benign keratosis, melanoma, melanocytic nevi, and basal cell carcinoma. The achieved results depicted an accuracy of 96.91%, which is inefficient as compared to the proposed study. Similar to the research, authors in [2] studied three immune-related mRNAs (SUCC, BTN3A1, and TBC1D2) linked to melanoma prognosis. This study used univariate Cox regression and Kaplan–Meier analysis to compare the overall survival probability between high-risk and low-risk groups, analyzing the time-dependent ROC curve. However, the accuracy of various classifiers is lower as compared to researchers' achieved results.

Furthermore, reference [10] developed a combination of ML and DL-based tools to predict the short-term survival of cutaneous malignant melanoma (CMM), a common malignancy. The study found that additional clinical variables such as sex, tumor site, histotype, growth phase, and age were significantly linked to overall survival, with DNN and RF models showing the best prognostic performance with an accuracy of 91% and 88%, respectively. Reference [24] analyzed mRNA expressions of m5C regulators in colorectal cancer tissues and identified high mutation frequency. NOP2 and YBX1 were highly expressed in prostate, gallbladder, lung, and renal cancers. NSUN6 functions as a tumor suppressor in pancreatic cancer. UV radiation was identified as the primary environmental driver. The authors in [25] trained a HAM10000 ISIC dataset using DL for multiclass skin cancer diagnosis. The proposed model detects the skin lesion with an accuracy of 96.26%.

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