

Performing Melanoma Diagnosis by an Effective Multi-view Convolutional Network Architecture

Eduardo Pérez^{1,2} · Óscar Reyes³

Received: 20 August 2020 / Accepted: 26 June 2023 / Published online: 28 July 2023 © The Author(s), under exclusive licence to Springer Science+Business Media, LLC, part of Springer Nature 2023

Abstract

Despite the proved effectiveness of deep learning models in solving complex problems, the melanoma diagnosis remains as a challenging task mainly due to the high levels of inter and intra-class variability present in images of moles. Aimed at filling this gap, in this work we propose a novel architecture for melanoma diagnosis which is inspired on multi-view learning and data augmentation. In order to make the model more transformation-invariant, the proposed architecture creates different independent and specific views of an image. The transformations applied on the original images are learned by genetic algorithms which find the best set of transformations. Also, the final predictions are yielded by aggregating information that comes from independent views. To evaluate the suitability of the proposal, an extensive experimental study on fifteen public melanoma-image datasets was conducted. The impact of the parameters of the genetic algorithms on the proposed architecture were analyzed, and it was also demonstrated that the proposed architecture attained better results when using transformations derived from the genetic algorithm than using random transformations. Finally, the results showed the suitability of the proposed model, where four state-of-the-art data augmentation techniques were significantly outperformed.

Keywords Convolutional neural networks \cdot Melanoma diagnosis \cdot Multi-view learning \cdot Genetic algorithm \cdot Data augmentation

1 Introduction

Melanoma is a skin cancer which commonly propagates to nearby tissues, and nowadays it presents the highest levels of mortality among the different types of skin cancer (Siegel et al., 2019; Miller et al., 2019). Global actions, therefore,

Communicated by Jan Kybic.

This research was supported by the i-PFIS contract no. IFI17/00015 granted by Health Institute Carlos III of Spain. E. Pérez and Ó. Reyes have equally contributed to this work and should be considered joint first author.

 Óscar Reyes oscar.reyes@healios.io; ogreyesp@gmail.com
Eduardo Pérez

eduardo.perez@imibic.org

- ¹ Knowledge Discovery and Intelligent Systems, Maimónides Biomedical Research Institute of Córdoba, Córdoba, Spain
- ² Department of Computer Science and Numerical Analysis, University of Córdoba, Córdoba, Spain
- ³ Healios AG, Basel, Switzerland

are needed to revitalize efforts for melanoma control and prevention. The early diagnostic of melanoma is, however, a tough task even for expert dermatologists, mainly because the complexity, variability and dubiousness of the symptoms (Geller et al., 2007). There are a great variety of morphologies in moles of patients (both in healthy and sick people), such as the asymmetry, border irregularity, color variegation, and the positions of different zones having specific shade of colors, that largely hamper the early diagnosis of melanoma, as can be seen in Fig. 1. Consequently, the melanoma diagnosis problem poses the challenge of developing efficient methods that ease the diagnostic and, therefore, aid dermatologists in decision-making.

Several studies have shown that the early diagnosis of melanoma from skin images can be greatly benefited using computational methods (Lee et al., 2018; Haenssle et al., 2018; Pérez et al., 2021), and such techniques may even overcome the diagnosis made by a committee of expert dermatologists (Haenssle et al., 2018). In this sense, in the recent years there has been an increasing attention in developing deep learning models for diagnosing melanoma, more specifically Convolutional Neural Networks (henceforth, CNNs)