

Abstract

Artificial intelligence (AI) is a fundamental technology useful in many fields, ranging from finance, weather forecast, to medicine. Positive results are reached especially in the diagnostic field, where AI provides a great support to the physician's assessments. The goal of this thesis is to support biomedical data analysis by means Artificial Intelligence methods and techniques. To this aim I define processes based on Machine Learning capable of improving diagnoses, by identifying the schematics of a well-determined pathology. These tools will be available to clinicians, in order to be able to intervene on patients through countermeasures adapted to their specific needs. I have concentrated my attention on the detection two kinds of diseases: (i) the degenerative disease, such as Parkinson and Coloboma, and (ii) the oncological disease, such as Leukemia and Melanoma.

In particular, in the case of Parkinson, it is difficult to formulate a clinical diagnosis because there are neither objective tests nor specific biochemical and neuro-radiological markers. I apply IR techniques to patient records belonging to a standard dataset for classifying Parkinson patients on the base of the reports produced during the different visits. The obtained results are very promising on the use of this tool in the clinical practice. I also investigate how traditional biometric techniques may fail in presence of a iris pathology, such as Coloboma. Thus, I adopted Artificial Intelligence techniques for detecting irises affected by Coloboma, I demonstrated that traditional biometrics algorithms fail in presence of this disease, such as the ones proposed by Daugman and Canny. Thus, I develop an algorithm which extends the largely adopted Daugman's algorithm and allows also the people affected by this disease to be recognized by biometrical systems. In this way, they are not excluded by the access a services secured by iris detection. I also experiment Artificial Intelligence models and technique to detect in the case of the detection of oncological disease. In particular, concerning Leukemia I define a process aiming at detecting a set of differentially expressed genes in terms of methylation level, i.e., genes that in different conditions have an expression level significantly different in the Acute Myeloid Leukemia (AML) and Acute Lymphoblastic Leukemia (ALL) cases, and their characteristic pathways. The detection of gene expression data samples involves feature selection and classification. To this aim, Deep Learning models have been adopted (e.g., feature selection techniques and classifiers methods). A methodology is also proposed for the classification of melanoma by adopting different Deep Learning techniques applied to a common image dataset extracted from the ISIC dataset and consisting of different types of skin diseases, including melanoma on which is applied a specific pre-processing phase. The results of the adopted techniques (i.e., ResNet, 2D CNN, and SOM) are compared to select the best effective neural network for the recognition and classification of melanoma and evaluate the impact of the pre-processing phase. I also propose an augmented reality applica-

tion for to support of the diagnosis of melanoma. It exploits both Artificial intelligence and image processing techniques. I describe in detail the real-time process proposed to display the augmented nevus information and evaluated the real-time performances and the app usability. The main results of the proposed approaches are encouraging and suggest that they may be considered in the practical clinical. In the future, I plan to use artificial intelligence models and techniques and image processing to analyze Magnetic Risonance Images of the brain to detect progression of Parkinson's disease. Furthermore, the results obtained in the case of Coloboma of the eye could be extended and studied in other ophthalmic diseases.