OncoVision

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1 PROJECT CONTEXT

Addressing health-related issues represents the next frontier of artificial intelligence. Regarding the healthcare context, several attempts have already been conducted to develop machine learning solutions, genetic algorithms and others. For instance, in the Aravind Eye Care System in India, ophthalmologists and computer scientists are working together to test and deploy an automated image classification system to screen millions of retinal photographs of diabetic patients. Since the mid-twentieth century, researchers have proposed and developed many clinical decision support systems for help the physicians. Rule-based approaches was proposed in 1970s that allow us to:

(1) diagnose diseases;
(2) choose appropriate treatments;
(3) provide interpretations of clinical reasoning;
(4) assist physicians in generating diagnostic hypotheses in complex patient cases.

It seem a good approach but it present several problems, such as:

(1) it is costly to build;
(2) it require explicit expressions of decision rules and require human-authored updates;
(3) it is difficult to encode higher-order interactions among different pieces of knowledge authored by different experts;
(4) the performance of the systems is comprehensible only by a medical knowledge;
(5) it was difficult to implement a system that integrates deterministic and probabilistic reasoning to narrow down relevant clinical context, prioritize diagnostic hypotheses, and recommend therapy.

Instead the first generation of AI systems is relied on the curation of medical knowledge by experts and on the formulation of robust decision rules. Recent AI research has leveraged machine-learning methods, which can account for complex interactions, to identify patterns from the data. Moreover, machine-learning methods enable the development of AI applications that facilitate the discovery of previously unrecognized patterns in the data without the need to specify decision rules for each specific task [5]. Therefore, the main goal of AI system in Medicine is help the physicians in the clinical process, namely detect something, cluster the patient on some criteria, etc. On the other hand, AI systems poses new risks for medicine. Failures in medical AI could erode public trust in Healthcare. For example, bias in AI can deliver erroneous medical evaluations. Moreover, AI models magnifies existing cyber-security risks, potentially threatening patient privacy and confidentiality. In general, in a software project we need three type of expert groups:

- the group developing the algorithm;
- a group of validators;
- the operational staff.

These groups are also needed in the healthcare sector to overcome the following 3 key challenges in AI:

- conceptual challenges in formulating a problem that AI can solve;
- technical challenges in implementing an AI solution;
- humanistic challenges regarding the AI social and ethical implications.

Furthermore, incapability to address these challenges could erode public trust in medical AI, which could in turn undermine trust in Healthcare institutions themselves. At the end, unlike physicians, AI cannot draw upon "common sense" or "clinical intuition" but using a good data and training algorithm the AI model can obtain a good performance [3].In this project we will focus on skin cancer, that is the melanoma. Melanoma is a malignancy of melanocytes, which are pigment-producing cells of neuroectodermal origin that can be found throughout the body (including in the skin, iris and rectum). The cutaneous form of the disease is common in the Western world causing the majority (75%) of deaths related to skin cancer, in fact its global incidence is 15–25 per 100,000 individuals. Survival rates in patients with melanoma (cumulative for all forms) have shown a huge differences between countries in Europe, ranging between <50% in Eastern Europe to >90% in northern and central Europe for 5-year survival after primary diagnosis [4]. In the Figure 1 is shown the incidence and mortality of cutaneous melanoma in the world. The biggest problem with this cancer is a lack of early detection that could aim treatments to treat the disease in a timely manner. Therefore, that is why we decided to develop a melanoma detection AI system in order to help physicians in treatment of this disease. We will compare performance obtained by our model with the proposed one by Di Biasi et al [2].

1.1 Related project

Di Biasi et al. proposed a system that combine the Genetic Algorithms (GAs) with Convolutional Neural Networks (CNNs) to detect the melanoma. They used the GA for improve the architecture of CNN not to improve the network's hyperparameters. Indeed, they defined a population of neural networks (NN) that are codified in vectors where each vector elements represents a type of layer or pre-processing routine. Whereas for the hyperparameters of each individual, they fixed them to this values: *'sgdm', 'MaxEpochs', 16, 'MiniBatchSize', 12, 'Shuffle', 'every-epoch', 'InitialLe-arnRate', 0.0001, 'ExecutionEnvironment', 'auto'.*

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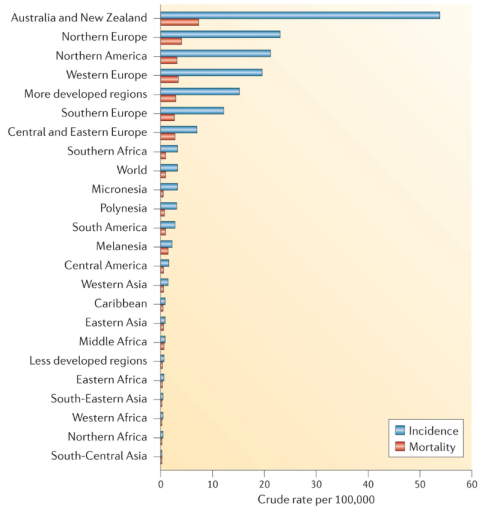

Figure 1: Incidence and mortality of cutaneous melanoma[4]

The authors defined the following constraints to the Genetic Algorithm in order to obtain a correct population of NN at each evolution step:

- the first gene of each entity must be an image input (II) or one of the pre-processing routines;
- if the gene q is a pre-processing routine, then the gene q + 1 must be a II layer or another pre-processing layer;
- the latest gene of an entity must be a classification layer.

Furthermore, they forced the possible values that the genes of an individual can take in this range: *Convolution, ReLu, Cross Channel Normalization, Max Pooling Grouped Convolution, Fully Connected Layer, Dropout and Softmax*.
The authors stopped the GA when no accuracy improvement was detected for ten consecutive evolution steps or after 100 evolutional steps. In conclusion, their dataset is composed by skin images and it is divided in two classes: melanoma (positive class) and moles (negative class). The number of instances for positive class is 70 and 100 for negative class.

2 PROJECT GOALS

The project goals are:

(1) Conduct a detailed investigation of the baseline approach selected from the literature in order to understand the performance of the approch and its limitation;
(2) Understand the problems related to the datasets, namely lack of relevant features, few samples etc;
(3) Definition of an AI pipeline that might be used for cancer detection and is not affect by the problems which the baseline approach selected from the literature suffer.

Our project is available on GitHub at this link: https://github.com/Rocco000/OncoVision

3 DETAILS OF THE CHOSEN MODEL

In this study we decided to use Convolutional Neural Network (CNN) because it represents various benefits. Before all, we must first explain how it formed and how it works. CNN is a classic artificial neural network (ANN) with input, hidden and output layers. The input layer has the role to propagate the input in the network, instead, the output layer has the role to provide the prediction of the model. Each layer can contain one or more neurons that are linked with some neurons of the previous layer and each link has an associated weight. Every neuron calculates its activation like a weighted sum of its input, then added a bias value and applies an activation function to the obtained value. CNN has a particular feature which is the convolutional layer. As stated in the paper by Kun-Hsing Yu et al[5], this type of layer is useful for extracting spatial or temporal relations and allows us to summarize and transform clusters of pixels in images to extract high-level features. Moreover, according with Albawi et al [1], CNN has these benefits:

(1) The problem that CNN solve has no spatially dependent features, therefore, it provides an opportunity to detect and recognize features regardless of their positions in the image. For example, in face detection, we do not need to pay attention to where the faces are located in the images;
(2) Each layer can detect a particular feature when input propagates toward the network. For example, the first layer detects the edges, the second detects shapes, etc;
(3) It can reduce the number of parameters to improve the computational complexity of the training process.

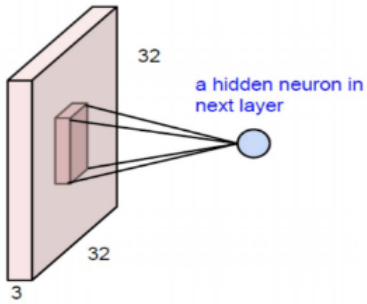

Figure 2: Example of how CNN hidden layer's neuron is responsible for a local region in the picture

To understand the third point we can use an image detection problem as an example. Consider an image 32x32x3 as input. If we use classic ANN, for connecting the input layer with a hidden layer's neuron we need 32x32x3 weight connections and this number must be multiplied by the number of neurons in the hidden layer. This amount of parameters is required only to connect the input layer with the hidden layer's neurons! Instead, in the convolutional neural network, each neuron in the hidden layer is responsible for a local region in the picture as shown in Figure 2. It means that a neuron of the next layer can only get input from the corresponding part of the previous layer (i.e. the neuron is connected only with specific neurons of the previous layer). For example, it can only be connected to 5×5 neurons. Therefore, if we want 32×32 neurons in the next layer, we will have 5×5×3 by 32x32 connections, which is 76,800 connections compared with 3,145,728 in ANN. Another assumption for simplification; is to keep the local connection weights fixed for the entire neurons of the next layer. This will connect the

neighbor neurons in the next layer with exactly the same weight to the local region of the previous layer. With this assumption, the connections between layers are similar to sliding a window of 5×5×3 in the input neurons and mapping the generated output to the corresponding place. For this reason, this type of layer is named convolutional and it looks like a filter in image processing. Therefore each layer can be associated with different filters. Other types of layers that are usually used in CNN are:

- The nonlinearity layer is usually used after the convolutional layer and it is applied to saturate the output or limit the generated output;
- The fully-connected layer where each node is directly connected to every node in both the previous and in the next layer;
- The padding layer that can resolve the loss of information that might exist on the border of the image and allow us to manage the output size;
- The pooling layer can down-sampling the image in order to reduce the complexity for further layers.

3.1 PAES Specification

The problem that we will treat has this PAES specification:

Performance	For evaluate our model we will use this metrics: accuracy, recall, precision and F1-score. In particular, we will focus on recall because we need to minimize the number of false negative.
Environment	Our model will operate in environment that has this features: (1) **Fully observable**: because the sensors provide to our model full environment state; (2) **Static**: because the environment doesn't change after an action of our model or during the time; (3) **Discrete**: because the environment limit the perceptions and actions of our model; (4) **Episodic**: because an action that our model done is independent by the previous actions; (5) **Single-agent**
Actuators	The model will interact with environment through the standard output of the machine
Sensors	The model can receive the environment input through the standard input of the machine

Table 1: PAES Specification

4 METHODICAL STEPS

Based on this goals set, the methodological step that we will conduct to address it are:

- Define a survey for physicians who are expert on the cancer disease in order to understand data problems and which features of data are relevant. We will conduct this step by using Google Forms;
- Re-implement the existing approach, because its source code is not available. We need to do this in order to compare our model performance with the performance of the existing approach;
- Study some image processing techniques in order to improve data quality;
- Search one or more new datasets in order to train our model and test the existing approach. We will conduct these researches by using Kaggle;
- Develop three genetic algorithm (GA) that produce a population of artifical neural networks (ANNs) that are optimized in three point of views:
  - The goal of the first one is to improve the hyperparameters of the network;
  - The goal of the second one is to improve the architecture of the network. After that we will select the best individual and we will apply the Grid Search algorithm on it in order to improve hyperparameters;
  - The goal of the last one is to improve both hyperparameters and architecture of the network.

  At the end of each Genetic Algorithm we will select the best individual in the last population obtained based on the evaluation metrics. For developing these alternatives we will use Python and its libraries.

Finally we will compare the results obtained by our models with the results of the baseline approach selected. Therefore the methodological steps that we will conduct, will be the steps that the follow image represents:

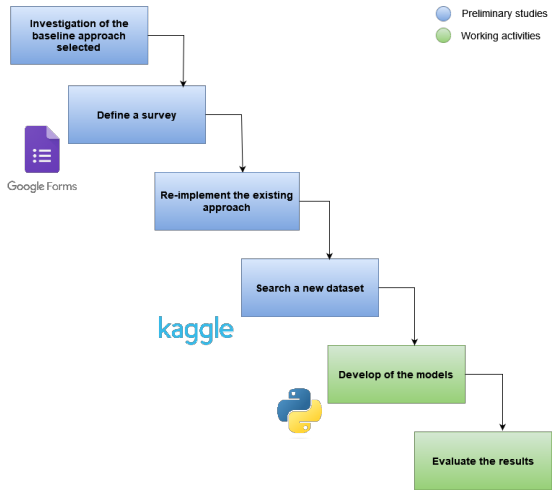

Figure 3: Methodology

5 SURVEY

6 DATA COLLECTION

After a preliminar analysis of the the existing project we have observed that this project use a very small dataset, composed only

by 170 images. Generally a DL model needs a lot of training data on witch train the model for having good performances. That is why we have researched new data. On **Kaggle** we have found several datasets related to the skin cancer problem. We have choosed two of this datasets, in particular:

- The first one, available at this link, has 10000 images divided into test and train. Each folder contains two sub-folders named *benign* and *malignant* that contains the negative and positive instances respectively.
- The second one is available at this link. Also in this case there are 10000 images, but they are classified in more category groups. Moreover there are two folders that contains all the images and `csv` file named *HAM10000_metadata* that report the matching between the image ID and the related category of problem. The categories are:
  - **akiec**, Actinic keratoses and intraepithelial carcinoma / Bowen's disease;
  - **bcc**, basal cell carcinoma;
  - **bkl**, benign keratosis-like lesions such as solar lentigines / seborrheic keratoses and lichen-planus like keratoses;
  - **df**, dermatofibroma;
  - **mel**, melanoma;
  - **nv**,melanocytic nevi;
  - **vasc**,vascular lesions such as angiomas, angiokeratomas, pyogenic granulomas and hemorrhage

  Therefore in this case we need to collapse this different categories into two classes. We will do this after we have conducted some researches to verifying if each class is benign or malignant.

7 DATA ANALISYS

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