Designing Convolutional Neural Network Architectures for Medical Image Classification Using Multi-Objective Evolutionary Algorithm with Zero Cost Proxies

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1 Introduction

Over the years, various methods have been proposed for automatically designing deep learning architectures, with the main goal of reducing the workforce required to manually design an architecture. A variety of methods have been proposed to automatically design deep learning architecture using Neural Architecture Search (NAS) approaches [1]. One of the key issue with NAS approaches is that they require large amount of time to search for an optimal architecture as each architecture needs to be evaluated on the dataset for fitness evaluation. To overcome this problem, multiple performance estimation strategies have been proposed which quickly estimates the performance of an individual to reduce the search time. This would not only reduces the cost time but also allows to explore large search space. Zero-Cost (ZC) proxies are an efficient performance estimation strategy which evaluates a deep learning architecture on small number of data samples to quickly estimate the performance of an individual [2]. This approach is quite effective in case of medical image classification problem as medical data consists of large number of samples and traditional NAS based methods took a lot of time for training.

Over the recent years, hardware aware NAS has gained popularity which takes into account the hardware constraints and capabilities during the search process. Considering hardware characteristics can help in designing deep learning architecture that minimize latency and the number of parameters which is critical in real-time applications especially in case of medical images where prediction time is an important factor. As the performance and hardware metrics (latency, number of parameters, size in MB) are conflicting objectives, multi-objective evolutionary algorithms have been mostly used to solve this problem. This study proposes a multi-objective NAS approach based on evolutionary algorithm for searching Convolutional Neural Networks (CNNs) architectures, which consists of sixteen different convolution and pooling operations followed by six different attention layers. Experiments on multiple MedMNIST datasets [3] were conducted to evaluate the effectiveness of the proposal, revealing that the proposal searches for an efficient lightweight architecture within one hour.

2 Methodology

In this study, we have proposed an approach for searching CNN architectures for medical image classification using NSGA-2. Non-Dominated Sorting Genetic Algorithm (NSGA-2) is a multi-objective evolutionary algorithm which maintains a diverse set of non-dominated solutions using non dominated sorting, crowding distance and elitism. For the representation of an individual, each candidate operation in the individual is represented by a real value between 0 and 1. Besides, the associated attention layer is represented by a value between 1 and 6, where 1 means no attention layer and 2-6 means different attention types. The visual representation of an encoding scheme is shown in FIG 1. Each value of the encoding scheme represents an operation and an attention layer defined in the search space (convolution or pooling layers). For performance evaluation of each individual architecture, we have used SNIP ZC proxy which multiplies the value of each parameter and its corresponding gradient for each layer.

0.15394,3	0.73577,3	0.01724,1	0.07689,5	0.89058,0	0.37734,2	0.00395,3	0.70345,4
0.69953,4	0.13817,0	0.56487,4	0.98290,3	0.59894,4	0.80453,1	0.39271,2	0.09398,2

(a) Genotype Representation

Skip Connection,CBAM	Octave Conv 5x5,CBAM	MaxPool 3x3,SE	AvgPool 3x3,Double Attention	MBConv 5x5 t1, Identity	DilConv5x5,BAM	MaxPool3x3,CBAM	Octove Conv 5x5,GE_theta-plus
Octove Conv 5x5,GE_theta-plus	Skip Connection,Identity	Inverted Residual 5x5, GE_theta-plus	MBConv 3x3 t1,CBAM	Inverted Residual 5x5,GE_theta-plus	Octove Conv 3x3,SE	DilatedConv 5x5, BAM	Avg Pool 3x3, BAM

(b) Phenotype Representation

FIG. 1: Genotype and phenotype representation of individuals consisting of 8 genes

3 Experimental Results

To evaluate the effectiveness of the proposed approach, we perform experiments on datasets from the MedMNIST benchmark [3]. The Pareto front diagram of two objectives (SNIP ZC proxy and number of parameters) is shown in FIG 2. The objective 1 is the number of parameters which needs to be minimized and objective 2 represents the ZC proxy score which we have to maximize. In Tab 1, the reported Accuracy, AUC scores and the number of paramters of best find solution is reported.

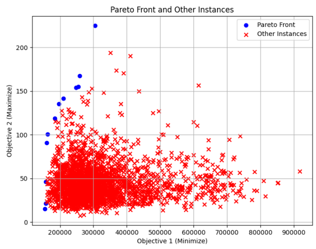

FIG. 2: Pareto front diagram of two objectives (SNIP and number of parameters)

Approach	Performance Metrics	ChestMNIST	OrganAMNIST	OrganCMNIST	OCTMnist	PenumoniaMNIST	BreastMNIST
Proposed	**Accuracy**	0.941	0.931	0.918	0.76	0.941	0.89
	AUC	0.691	0.996	**0.994**	**0.959**	0.862	**0.924**
	Number of Parameters	228598	258730	438181	270597	198058	432185
ZNMOEA [4]	**Accuracy**	**0.948**	**0.958**	0.929	**0.826**	0.941	**0.904**
	AUC	**0.797**	0.996	0.992	0.957	**0.98**	0.921

TAB. 1: Results comparison on multiple MEDMNIST datasets of proposed multi-objective NAS approach with existing approach in terms of Accuracy, AUC scores and number of parameters.

References

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