Designing Convolutional Neural Networks using Surrogate assisted Genetic Algorithm for Medical Image Classification

Supplementary material

ABSTRACT

We present the pseudo-code, parameter settings, and necessary results to further explain our proposed methodology.

1 SUPPLIMENTARY MATERIAL

Table 1 shows the best reported parameter settings of the GA algorithm, which are shown in Table for both the MedMNIST and CIFAR-10 datasets. These parameters are selected after doing multiple trials of experiments. Futhermore, the pseudo code of proposed approach is shown in Alogrithm 1 and number of parameters, layers and size in megabytes of best performed architectures of MedMNIST datasets are shown in Table 2

Parameters	Value	
	CIFAR-10	**MedMNIST**
Number of generations	30	20
Population size	30	20
Mutation operator	Random Swapping	Random Swaping
Crossover operator	Two-Point Crossover	Two-Point Crossover
Mutation rate	0.6	0.6
Crossover rate	0.9	0.9
Tournament size	2	2
Chromosome length	32	32

Table 1: GA parameters used for experiments in CIFAR-10 and MedMNIST datasets

Dataset Name	Size in MB	Params	# of layers
Dermamnist	0.02	17569	6
Pathmnist	0.0189	16359	8
Chestmnist	0.00409	3210	8
RetinaMNIST	0.029045	26405	8
OrganAMNIST	0.00502	4545	8

Table 2: Number of parameters , model size in megabytes and number of layers of best performed architectures in MedMNIST benchmark

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Algorithm 1: Pseudo Code of Proposed NAS approach using GA

Input: Number of Generations (NoG), Population Size (P_s), Epochs, Dataset, Crossover Prob (C_P), Mutation Prob (M_P)

Output: The discovered best performing architecture

$Dataset_{train}, Dataset_{test} \leftarrow Dataset$

/*Divide the train set into train and validation set with 80/20 split */

$Dataset_{train}, Dataset_{val} \leftarrow Dataset_{train}$

$Pop_i \leftarrow$ Initialize population randomly with given P_s

Fitness_pop$_i \leftarrow Evaluate\_Model(Dataset_{val})$

Surrogate_Model $\leftarrow TrainSurrogate(Pop_i, $Fitness_pop$_i)$

$g \leftarrow 0$

while $g \leq N_g$ **do**

  /* Get Individuals using tournament selection */

  $P_1, P_2 \leftarrow Tournament\_Selection()$

  /*Apply crossover and mutation operators to generate new offsprings */

  $Q_{g1}, Q_{g2} \leftarrow Crossover(P_1, P_2, C_P)$

  $Q_{g1}, Q_{g2} \leftarrow Mutation(Q_{g1}, Q_{g2}, M_P)$

  /*Predict the estimated fitness value from offspring. 80 %∗ from Surrogate and 20 %∗ from training the individuals /

  while *80% individuals* **do**

    Fitness_Offspring $\leftarrow Surrogate\_Model.Predict(Q_1, Q_2)$

  while *20% individuals* **do**

    Fitness_Offspring $\leftarrow Evaluate\_Model(Q_1, Q_2)$

  if *Fitness of offspring is leass than worst individual in parents population* **then**

    Swap the individual with offspring

  $P_{t+1} \leftarrow P_g \cup Q_g$

  /*Retrain the surrogate model %∗ /

  Surrogate_Model $\leftarrow TrainSurrogate(Pop_i, $Fitness_pop$_i)$

  $g \leftarrow g + 1$

Return the individual having best fitness in P_t

Train the best found individual on the test set to get final accuracy.

Table 3 shows the results of MedMNIST datasets with different crossovers and encoding schemes. It shows that the overall results on two-point crossover with continuous encoding is better as compared

Type Encoding	Type Crossover		Derma MNIST	RetinaMNIST	OrganAMNIST	PathMNIST	ChestMNIST
Discreate	One Point	AUC	0.90	0.72	0.98	0.97	0.70
		ACC	0.72	0.51	0.86	0.84	0.94
		F1S	0.70	0.47	0.79	0.93	0.91
	Two Point	AUC	0.91	0.74	0.99	0.97	0.72
		ACC	0.73	0.52	0.93	0.92	0.94
		F1S	0.70	0.50	0.90	0.92	0.93
	Uniform	AUC	0.9	0.72	0.97	0.97	0.92
		ACC	0.73	0.5	0.79	0.82	0.93
		F1S	0.72	0.45	0.88	0.91	0.89
Continuous	One Point	AUC	0.91	0.69	0.97	0.94	0.71
		ACC	0.73	0.50	0.79	0.8	0.94
		F1S	0.72	0.44	0.88	0.93	0.92
	Two Point	AUC	0.92	0.77	0.99	0.99	0.99
		ACC	0.75	0.53	0.96	0.94	0.96
		F1S	0.73	0.49	0.95	0.93	0.95
	Uniform	AUC	0.92	0.72	0.98	0.94	0.93
		ACC	0.76	0.49	0.83	0.89	0.94
		F1S	0.73	0.43	0.91	0.93	0.91

Table 3: Results comparison on different encoding schemes and crossover operators on MedMNIST dataset

	Crossover		
Encoding	One-Point	Two-Point	Uniform
Discrete	95.5	96.17	95.42
Continuous	95.79	96.8	95.81

Table 4: Results comparison on different encoding schemes and crossover operators on CIFAR-10 dataset

to other crossover techniques and discrete encoding scheme. The two-point crossover preserves the information of both parents individuals effectively while uniform crossover changes the off-springs a lot which leads to offpsrings with lot of variation and degrades the performance. For MedMNIST dataset, we used f1-Score as the fitness value as the f1-score provides a better assessment of models performance and balanced measures of precision and recall. Similarly, the results with different crossovers and encoding schemes on CIFAR-10 dataset is given in Table 4