CSL 7540 - Course Project

Neural Architecture Search

Instructor

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Problem Statement

We have to develop a Neural Architecture Search that will generate a neural network by genome-string with low number of parameters used and should give high accuracy (more than 75%) on a Classification task performed on MNIST Fashion dataset. The dataset has 10 classes.

Introduction

Neural Architecture Search (NAS) is a technique used to automating the design of Artificial Neural Network(ANN).

NAS can be categorized according to the search space, search strategy and performance estimation strategy used:

- The **search space** defines the type of ANN that can be designed and optimized.
- The **search strategy** defines the approach used to explore the search space.
- The **performance estimation strategy** evaluates the performance of a possible ANN

Introduction

Convolutional Neural Network(CNN)

Building a CNN involves multiple choices

- Type of layer
- Number of layers
- Number of neurons
- Activation functions
- Regularization/Dropout
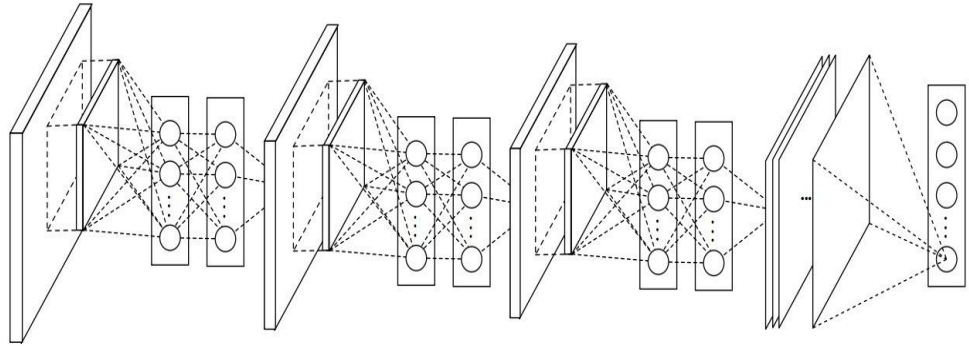
Approach

- Generating random length of the genome string.
- Taking RC exactly = 2.
- Taking NC =[0,5].
- By shuffling the parameters , get some genome strings .
- Now, Updating the string with the help of previous layer and parameters
- Storing the genome string which have more than 75% accuracy.

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Fitness Function :

$$F = 0.8 * accuracy + (1-0.8)(1-parameters/(max(parameters)))$$

With the help of fitness function we calculate trade-off .

Crossover: Crossover is a genetic operator used to vary the programming of a chromosome or chromosomes from one generation to the next . In this process, two strings are picked from the mating pool at random to crossover in order to produce superior offspring. It is used to combine the genetic information of two parents to generate new offspring.

Now applying crossover to updated genome string to get the best genome string which have max trade-off.

Results

- Generated Genome-Strings using local Best First Search algorithm which have more than 75% accuracy.

Index	Genome-String
S1	NC 28 6 gelu;NC 26 2 sigmoid;NC 1 4 swish;NC 23 2 relu;RC 50 6 relu;RC 38 4 sigmoid;FL gelu;'
S2	NC 5 4 gelu;NC 31 6 sigmoid;RC 13 7 gelu;NC 24 6 tanh;NC 7 3 tanh;RC 64 7 relu;NC 19 6 relu;FL tanh;'
S3	RC 13 6 relu;NC 1 7 swish;RC 18 4 gelu;NC 25 4 tanh;FL gelu;
S4	RC 40 6 relu;RC 52 3 swish;FL sigmoid;'
S5	NC 21 6 tanh;NC 10 4 sigmoid;RC 52 7 gelu;NC 4 6 relu;NC 3 7 sigmoid;NC 3 2 tanh;RC 16 3 sigmoid;FL gelu;
S6	NC 32 7 relu;NC 31 5 tanh;NC 12 4 tanh;NC 20 3 swish;NC 8 2 gelu;RC 16 7 gelu;RC 48 6 tanh;FL sigmoid;
S7	NC 10 3 tanh;RC 55 1 gelu;NC 10 4 swish;RC 57 2 swish;NC 4 5 relu;NC 1 5 gelu;NC 23 3 tanh;FL swish;
S8	RC 64 6 tanh;RC 28 6 tanh;NC 6 2 sigmoid;NC 13 1 sigmoid;NC 22 5 sigmoid;NC 21 3 relu;NC 19 7 sigmoid;FL gelu;

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Comparison among the number of parameters, accuracy and fitness score of the Genome-Strings

Index	Parameters	Accurancy	Fitness
S1	79540	0.8310999870300293	0.7147648648740895,
S2	105972	0.849399983882904	0.6795199871063233,
S3	10964	0.8188999891281128	0.8344277329701006,
S4	24294	0.7513999938964844	0.7552701479877577,
S5	39987	0.775600016117096	0.7450129083755023,
S6	72993	0.8802000284194946	0.7664009920482444,
S7	20073	0.8277999758720398	0.8243563888054339,
S8	100528	0.8109999895095825	0.659074403716525

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- Genome string after using crossover

S1	NC 28 6 gelu;NC 26 2 sigmoid;NC 1 4 swish;NC 23 2 relu;RC 50 6 relu;RC 38 4 sigmoid;FL gelu;
S2	NC 5 4 gelu;NC 31 6 sigmoid;RC 13 7 gelu;NC 24 6 tanh;NC 7 3 tanh;RC 64 7 relu;NC 19 6 relu;FL tanh;
S3	RC 13 6 relu;NC 1 7 swish;RC 18 4 gelu;NC 25 4 tanh;FL gelu;
S4	RC 40 6 relu;RC 52 3 swish;FL sigmoid;
S5	NC 21 6 tanh;NC 10 4 sigmoid;RC 52 7 gelu;NC 4 6 relu;NC 3 7 sigmoid;NC 3 2 tanh;RC 16 3 sigmoid;FL gelu;
S6	NC 32 7 relu;NC 31 5 tanh;NC 12 4 tanh;NC 20 3 swish;NC 8 2 gelu;RC 16 7 gelu;RC 48 6 tanh;FL sigmoid;
S7	NC 10 3 tanh;RC 55 1 gelu;NC 10 4 swish;RC 57 2 swish;NC 4 5 relu;NC 1 5 gelu;NC 23 3 tanh;FL swish;
S8	RC 64 6 tanh;RC 28 6 tanh;NC 6 2 sigmoid;NC 13 1 sigmoid;NC 22 5 sigmoid;NC 21 3 relu;NC 19 7 sigmoid;FL gelu;'
S9	RC 13 6 relu;NC 1 7 swish;RC 57 2 swish;NC 4 5 relu;NC 1 5 gelu;NC 23 3 tanh;FL swish;'
S10	NC 10 3 tanh;RC 55 1 gelu;NC 10 4 swish;RC 18 4 gelu;NC 25 4 tanh;FL gelu;
S11	NC 5 4 gelu;NC 31 6 sigmoid;RC 13 7 gelu;NC 24 6 tanh;RC 16 3 sigmoid;FL gelu;
S12	NC 21 6 tanh;NC 10 4 sigmoid;RC 52 7 gelu;NC 4 6 relu;NC 3 7 sigmoid;NC 3 2 tanh;NC 7 3 tanh;RC 64 7 relu;NC 19 6 relu;FL tanh
S13	NC 28 6 gelu;NC 26 2 sigmoid;NC 1 4 swish;NC 23 2 relu;RC 50 6 relu;RC 28 6 tanh;NC 6 2 sigmoid;NC 13 1 sigmoid;NC 22 5 sigmoid;NC 21 3 relu;NC 19 7 sigmoid;FL gelu;
S14	RC 64 6 tanh;RC 38 4 sigmoid;FL gelu;'
S15	RC 40 6 relu;RC 48 6 tanh;FL sigmoid;'
S16	NC 32 7 relu;NC 31 5 tanh;NC 12 4 tanh;NC 20 3 swish;NC 8 2 gelu;RC 16 7 gelu;RC 52 3 swish;FL sigmoid;

Comparison

$G-string$	$Accuracy$	$Parameters$	$Fitness$
S1	0.83109	79540	0.8310
S2	0.84939	105972	0.8493
S3	0.81889	10964	0.8493
S4	0.7513	24294,	0.751
S5	0.7756	39987	0.775
S6	0.8802	72993	0.8802
S7	0.8277	20073,	0.8277
S8	0.8109	100528	0.81099
S9	0.7850	9625	0.7850
S10	0.8493	21952	0.84930
S11	0.8381	41922	0.8381
S12	0.80430	105738	0.8043
S13	0.8119	130004	0.8119
S14	0.7899	44464	0.78990
S15	0.8457	74434	0.84579
S16	0.85350	53093	0.8535

Conclusion

- Using local BFS , we get two type of best genome string :

  (i) First one is with respect to accuracy which have ,
      Best accuracy : 88.02%
      No. of params : 72993
      Fitness value   : 0.79
      Genome string : NC 32 7 relu; NC 12 4 tanh; NC8 2 gelu;RC 16 7 gelu;RC 48 6   tanh;FL sigmoid

  (ii) Second one is with respect to parameters which have ,
       Accuracy   : 78.5%
       Best params : 9625
       Fitness value : 0.81
       Genome string : 'RC 13 6 relu;NC 1 7 swish;RC 57 2 swish;NC 4 5 relu;NC 1 5 gelu;NC 23 3 tanh;FL
  swish;'

- Using crossover , we get best genome string which have maximum trade-off,

    Accuracy   : 84.5%
     No. of params   : 21952
     Best Fitness value : 0.84
     Genome string   : ' NC 10 3 tanh;RC 55 1 gelu;NC 10 4 swish;RC 18 4 gelu;NC25 4 tanh;FLgelu;'

Thank You