

PROJECT REPORT



॥ त्वं ज्ञानमयो विज्ञानमयोऽसि ॥

Neural Architecture Search (NAS)

Submitted To : Dr. Deepak Mishra

Preeti Dwivedi(M19DCS004)
Jitendra Chautharia (MT19CPS001)

1 Problem statement :

Create a search function to search in a NAS space for the best performing CNN architecture on fashion-mnist dataset.

2 Description of dataset

Fashion-MNIST is a dataset of Zalando's article images which consists of a training set and a test set of 60,000 and 10,000 examples respectively. Each example consist of 28x28 grayscale image which is associated with a label from 10 classes.

3 Some Basic definitions

Neural Architecture search: Neural architecture search (NAS) is a search technique for designing the artificial neural networks architecture automatically. It tune the hyperparameters so that model produced has lower number of parameters with high accuracy possible.

Fitness function: For finding trade-off we use fitness function which is define below: $f(x) = 0.8 * \text{accuracy} + (1 - 0.8) * (1 - (\text{parameters} / (\max(\text{parameters})))$

Convolutional Neural Network: This neural network is used to process the image pixel data for applications like recognition, classification and segmentation. It has number of layers. In which first layer is an input layer which take images as input in our case it is 28 x 28 x 1.

4 Algorithm

- **Step 1:** In this algorithm we are creating a search space .
- **Step 2:** According to problem we are fixing no. of RC = 2.
- **Step 3:** Number of NC =[0,5]
- **Step 4:** Now we can shuffle all the parameters.

- **Step 5:** Then we select the genome string which have accuracy greater than 75 percent.
- **Step 7:** Now applying cross over on that selected search space .
- **Step 8:**Then finally , we get the best genome string which have maximum trade-off.

5 Results

Table for Genome accuracy,parameters and trade-off with respect to 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;'
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;

$G - string$	$Accuracy$	$Parameters$	$Fitness$
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

5.1 Result after applying cross over

After applying cross over on selected genome string we get:

- Best Fitness value : 0.84
- Max accuracy : 84.5
- Number of parameters : 21952
- Best genome string : NC 10 3 tanh;RC 55 1 gelu;NC 10 4 swish;RC 18 4 gelu;NC 25 4 tanh;FL gelu;

References

Laredo, D., Qin, Y., Schütze, O. and Sun, J.Q., 2019. Automatic model selection for neural networks. arXiv preprint arXiv:1905.06010.