

# Genetic Convolutional Neural Network

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## I. INTRODUCTION

In recent times, CNNs have emerged as the go-to technique for image classification problems. However, they rely highly on their architecture, which needs to be hand crafted by a personnel having expertise in both, CNN and the respective problem. This makes it difficult for researchers who have no expertise in CNNs, to explore their full potential. We will try to implement an already proposed algorithm, which is capable of discovering a potentially good architecture for a CNN best suitable for image classification.

- Fitness function for GA is classification accuracy of the network.
- Select best chromosomes and repeat until convergence.

## IV. DATASET

- MNIST (60,000 training images, and 10,000 test images)
- CIFAR-10 (10 classes, 6,000 images each)

## V. RESULTS

Best chromosome=[1,1,1,0]

Accuracy on test MNIST Dataset-98.01 %

Accuracy on test CIFAR-10 Dataset-98.39%

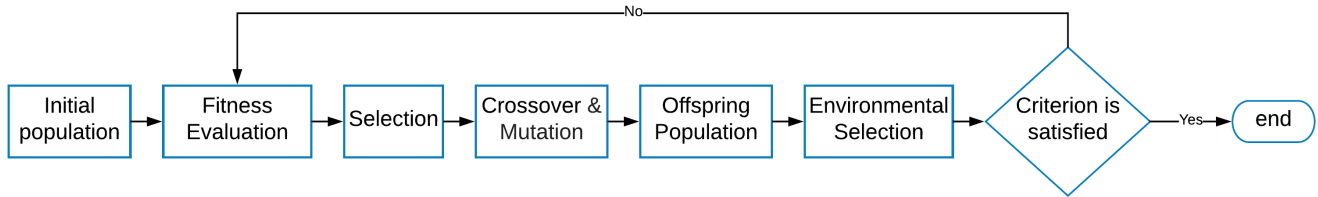


Fig. 1: Block Diagram of Algorithm

## II. LITERATURE REVIEW

L.Xie and A. Yuille proposed a fixed length encoding method to represent neural networks. By using genetic operations they automated the process of exploring better networks. Fitness of an individual is calculated by training the decoded network on MNIST dataset. Their network consists of S stages and any stage s has Ks internal nodes. All nodes in a stage are ordered and is a convolution operation. [1]

A stage with 4 internal nodes, needs  $0.5 * K_s * (K_s - 1)$  bits to represent string. A possible encoding can be 1-00-111. 1 represents that node 1 is connected to node 2, 00 means node 1 and node 2 are not connected to node 3. 111 represents, node 1, node 2 and node 3 are connected to node 4. Connections are only allowed from a low numbered to a high numbered node. They used 2 default nodes, default input which receives input from previous stage and a default output node which gives output to next stage. [2].

## III. OUR APPROACH

- Initialize a random population of 10 chromosomes in which each chromosome has four genes.
- If value of gene is 1 then it represents a convolution layer and if it's 0 then it represents a pooling layer.
- Generate a CNN model using this chromosome.
- Evaluate this CNN model based on its fitness value.

## Architecture summary of best chromosome

Layer (type)	Output Shape	No.of Params
Conv2d-1	[-1, 20, 26, 26]	200
Conv2d-2	[-1, 40, 24, 24]	7,240
Conv2d-3	[-1, 60, 22, 22]	21,660
Conv2d-4	[-1, 80, 20, 20]	43,280
Pool2d	[-1, 80, 10, 10]	-
Linear-5	[-1, 500]	4,000,500
Linear-6	[50, 10]	5,010

## VI. PROJECT STATUS

### A. Task Completed

- Implemented LeNet like Structure Encoding of chromosome.

### B. Future Tasks

- Implement ResNet or DenseNet like architectures in current encoding scheme.
- Implement one more encoding scheme.

## REFERENCES

- [1] Yanan Sun, Bing Xue, Mengjie Zhang, and Gary G Yen. Automatically designing cnn architectures using genetic algorithm for image classification.
- [2] Lingxi Xie and Alan L. Yuille. Genetic CNN.