Two Novel Performance Improvements for Evolving CNN Topologies

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Abstract
Convolutional Neural Networks (CNNs) are the state-of-the-art algorithms for the processing of images. However the configuration and training of these networks is a complex task requiring deep domain knowledge, experience and much trial and error. Using genetic algorithms, competitive CNN topologies for image recognition can be produced for any specific purpose, however in previous work this has come at high computational cost. In this work two novel approaches are presented to the utilisation of these algorithms, effective in reducing complexity and training time by nearly 20%. This is accomplished via regularisation directly on training time, and the use of partial training to enable early ranking of individual architectures. Both approaches are validated on the benchmark CIFAR10 data set, and maintain accuracy.

Introduction
Convolutional Neural Networks (CNNs) consist of a set of layers of different types to sequentially pipe and transform data with. Early convolutional layers detect edges or corners using filters, pooling layers reduce the resolution using an average or max function, allowing later layers to recombine smaller features into bigger ones. (Krizhevsky, Hinton et al. 2009; Krizhevsky, Sutskever, and Hinton 2012)

The weights of the filters can be found through back propagation and gradient descent (LeCun et al. 1998, 1989). However the overall architecture of the CNN must be stated, and many hyperparameters initialised, these are set by hand using trial and error (Simard et al. 2003; Ioffe and Szegedy 2015). This can introduce a bias towards benchmark data sets such as MNIST, which may have little relevance to real world data sets. Manual tuning of deep architectures is complicated, non-intuitive and time consuming.

A promising approach to find topologies automatically is Genetic Algorithms (GAs), heuristic algorithms that can optimise within abstract high-parameter spaces with complex or unknown interdependencies (Back 1996; Davis 1991). GAs implement a simplified model of natural selection. A population of individuals is initialised, where each individual is represented by a genome. Their fitness is measured by an objective function that maps each genome to a fitness. Fitness scores can be subjected to a penalty function (Goldenberg 1989) that punishes undesired features or behaviour with selective pressure. Individuals of higher fitness are more likely to be selected for reproduction. Genetic operators manipulate the genome stochastically: Mutation is a small random change in the genome and cross-over recombines the genome of two parents (Mooney 1995). Reproduction, genetic operations and fitness evaluation are repeated until an exit condition occurs.

CNNs can be configured through GAs by evolving network weights and topology together (Real et al. 2017). Children inherit the weights of their parents, mutations insert, alter or remove layers. CNNs are trained gradually during the course of evolution, allowing the objective fitness function to select individuals based on partially trained networks. The big drawback of this approach is that no cross-over is involved, reducing the potency of the algorithm by omitting an important operator of GAs. Introducing cross-over for weights is non-trivial and has not been achieved yet.

In this work, two novel approaches are presented. The first approach contrasts with previous work where complexity is penalised (Kouvaris et al. 2017), instead penalising evaluation wall time, allowing a more intuitive and direct effect. Additionally, a method is presented to utilise both partial training and cross-over by gradually training models through an epoch function. Both approaches maintained accuracy on the CIFAR10 image classification data set (Krizhevsky, Hinton et al. 2009).

Method
Initially a base experiment is set up, following Sun (Sun et al. 2018), with minor differences to aid computational efficiency.

The GA evolves a generational population of 20 individuals, each represented by a genome describing the topology of a CNN. Each individual is evaluated by training and testing on the respective CIFAR10 partition.

1The code is available at https://github.com/YStrauch/evolving-cnn-topologies-for-image-recognition
The initial genomes are generated by randomly concatenating skip or pooling layers with equal probability until a pooling layer would reduce the resolution to half a pixel, or the number of layers is greater than a max depth chosen randomly from $[10, 120]$. Skip layers contain two convolutional layers with quadratic filters of size $3$, unit stride, and same padding. The number of filters of each convolutional layer is chosen randomly from the set $\{64, 128, 256\}$. Pooling layers use either a max or average function chosen randomly. A Multi-Layer Perceptron (MLP) with no hidden layers followed by a softmax layer determines the output. Individuals are trained for $60$ epochs in a batch size of $50$ using stochastic gradient descent with a momentum of $0.9$ and an initial learning rate of $0.1$, which decays by a factor of $0.9$ after $1, 26$ and $43$ epochs.

CNNs are implemented using pytorch (Paszke et al. 2017) and trained on 4 GTX1080 TI on the Iridis 5 HPC. Each GPU concurrently evaluates one individual at a time. In the baseline implementation, the fitness of an individual is equal to its accuracy on the test fold. If an architecture was previously evaluated its accuracy is retrieved from a cache.

Individuals are selected for reproduction using tournament selection, i.e. two distinct individuals are chosen randomly from the population, and the individual with higher fitness is selected. With a $90\%$ chance, this individual is crossed over with a second individual selected by another tournament selection. With a $20\%$ chance, the genome is mutated. Both genetic operators can be applied cumulatively, cross-over first. Selected individuals are added to a new generation of individuals until $20$ individuals are found. If the best individual of the old generation is not in the new one, it replaces the weakest individual of the new generation (elitism). The new generation replaces the old one. This process is repeated for $20$ generations.

The one-point cross-over slices the feature detection layer stack open and re-combines them cross-wise. The Softmax-MLP classifier is not part of cross-over and is always appended once. Mutation either inserts a skip layer with $70\%$ probability, or with each $10\%$ likelihood inserts a pool layer, removes a layer, or mutates a layer. Layers are inserted at a random position. Skip layers are mutated by re-randomising the number of filters; pool layers flip their kernel function between average and max. If cross-over or mutation would produce half pixels due to too many pooling layers, the operator is aborted and restarted from the beginning.

**Regularisation**

The primary aim is to reduce the wall time taken by the algorithm. During fitness evaluation, the time required from the beginning of training to the end of testing is measured. For every hour spent, fitness is decreased linearly by $C$.

$C$ quantifies a trade-off between training time and accuracy, the bigger $C$, the higher the selective pressure towards faster individuals. This parameter was set at $C = 0.05$ which allowed a reduction in training time without loss of predictive performance.

**Partial Training**

Evolution by natural selection does not need an absolute fitness score, but rather a relative measure to rank each generation. The core idea is that earlier generations are trained for shorter durations, meaning less time is spent on earlier unfit topologies. In contrast to a previous approach (Real et al. 2017), weights are not heritable, so partial training cannot be done implicitly. Instead, an epoch function is introduced defining how long individuals are to be trained. To allow a fair comparison, partially trained individuals are stored so that they can be retrieved at a later time for further training.

The number of epochs each architecture is trained for is found using a linear function, dependent on the number of generations, ranging from a lower bound of $30$ to an upper bound of $70$, with rounding to the next integer. These bounds were chosen to make the algorithm spend less time on inferior and more time on better topologies. The learning rate decay points were scaled to come into effect after $1, 30$ and $50$ epochs.

**Results**

| Approach               | Acc. (%) | Gen. | Epochs | Batch Size | GPU Days |
|------------------------|----------|------|--------|------------|-----------|
| Evolving Topologies a  | 95.22    | 20   | 350    | 1          | 35        |
| Regularised b          | 89.06    | 20   | 60     | 50         | 14        |
| Partial Training b     | 88.70    | 20   | 60     | 50         | 12        |
| Base Experiment b      | 88.36    | 20   | 60     | 50         | 15        |
| Evolving Weights c     | 77.19    | 50   | 180    | 1          | 17        |

Table 1: Both performance improvements yielded better accuracies in less time than the base experiment.

Table 1 compares two approaches from the literature with the base experiment and performance optimisations. The best architectures found by each approach are depicted in Figure 1. The best CNN found in the base experiment (Fig. 1a) has lower accuracy than that reported by Sun, however as theirs is trained for nearly $9$ times as many epochs and over double the GPU days, this is unsurprising. As methods are being compared, not time or resources available, it is this base experiment result that is used for accuracy and time comparison.

All the best topologies found have a stack of pooling layers in the end. Initially this was suspected to be due to the initialisation logic stopping when half pixels would occur, however analysis of the distribution of layers throughout evolution (Fig. 2) found an active drift towards this phenomenon. Remarkably, the population learned to alternate
Figure 1: (a) The best of the base experiment. (b) Regularised topology with highest fitness has fewer filters, and an extra pool layer. (c) With regularisation the best has more filters in one convolutional layer and has put two pool layers together. (d) With partial training the best has fewer filters in the early layer and more later. Unlike the others, it includes a max filter.

Figure 2: The population converges to have more skip layers in the first and more pooling layers in the second half of the genome. In generation 10 and 20, all individuals start with a skip layer. In generation 20, there is a pattern of alternating skip and pooling layers at depths 1-6.

and found to be similar overall. There is a constant, short delay on the X axis. As the first generation is more complex and less accurate, it seems likely that this is rooted in random chance within the initial genome generation, and is independent of regularisation.

Networks are 1-2 layers shallower on average, with comparable accuracy, fitness evaluations are naturally lower due to regularisation. The algorithm was therefore successful in discovering deep networks that performed as well as shallower networks. The spread in fitness evaluations does not collapse, and converges reasonably, indicating a good population diversity.

The regularised run favoured having fewer filters per skip layer. In contrast to the base experiment, the number of filters converged towards 128 instead of 256 filters. This indicates that having fewer filters increases training speed and maintains accuracy, at least for the few training epochs configured.

The individual with highest fitness (Fig. 1b) and the one with highest accuracy (Fig. 1c) are very similar. The only differences are that the faster (fitter) individual uses 128 instead of 256 filters in one skip layer, and the order of this layer and its successor. These tiny changes allowed the individual to evaluate with 15 minutes difference and only sacrificed 0.0064 accuracy. Such small changes add up significantly in the course of the GA and allowed it to evaluate 8% faster than the base experiment without sacrificing accuracy of the end result, the highest accuracy found is slightly higher.

**Regularisation**

The wall time of the regularised approach was 31 hours (8%) shorter and yielded an accuracy that is slightly better than the base experiment. Convergence was compared (Fig. 3a) to regularisation. The algorithm was therefore successful in discovering deep networks that performed as well as shallower networks. The spread in fitness evaluations does not collapse, and converges reasonably, indicating a good population diversity.

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due to the regularisation. (b) The partial trained accuracy
converges more slowly in respect to generations, and catches
up in generation 17. Reduced training will give lower fitness
nearer the start.

**Partial Training**

The GA ran 70 hours (19%) faster than the base experiment. The best topology found (Fig. 1d) has a slightly higher ac-
curacy than the one found in the base experiment. Figure
3b shows a bigger spread in accuracy than the previous ex-
periment, as the population is more diverse. The population
converges more slowly in terms of generations, however this
does not mean that convergence was slower in terms of wall
time; on the contrary it actually converged much faster. As
expected, the speed-up (Fig. 4) is inversely proportional to
the number of training epochs with some noise. The first two
generations were evaluated 18 hours faster while maintain-
ing the mean fitness of the base experiment (shown in Fig.
3b), demonstrating the efficacy of this idea. The same mean
fitness as the base experiment was reached by generation
18, despite having saved more than 60 hours of computation
(70 hours in total). Speed-up occurs even after generation 15
where the epoch function passes the baseline experiment of
60 epochs.

**Discussion and Conclusion**

Two methods to speed up convergence of genetic algorithms
fnding CNN topologies for image recognition are presented.
Though results may vary depending on the hardware used,
the advantage of using wall time is that selective pressure
will drive the population to accommodate the performance
of the underlying architecture. However, care should be
taken not to mix different GPU types or individuals will
be ranked unfairly. Also one has to keep in mind that in-
dividuals may be assigned a negative fitness score, which
would complicate other genetic selection algorithms such as
roulette selection.

The second approach changed training epochs over the
course of evolution to allow removal of weak configurations
early on without excessive training. The linear function pre-
sented uses a lower and upper bound to simplify migration
from the flat value used in the base experiment. Changing
this function to a more dynamic approach, such as reacting
to previous fitness evaluations to train longer if needed could
allow adaptation to a variety of datasets.

Both approaches are demonstrated to speed up architec-
ture selection in this work. While they both introduce their
own hyperparameters, the ability of these algorithms to tune
numerous other parameters makes them very valuable, al-
lowing the wider adoption of deep learning methods.

Interestingly, combining both approaches neither results
in a combined speed-up nor a comparable accuracy. A speed-up of only 0.6% compared to partial training, and top
accuracy of 79.47% (10% worse than the base experiment)
indicate that the two methods conflict with or even oppose
another. This requires further investigation.

Further validation of the two approaches presented with
their speed-ups, extensive repetition of the two experiments,
and application to more data sets and use cases would be
worthwhile. This work sets out two approaches new to this
particular domain, and demonstrates their utility.

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