Deep Evolution for Facial Emotion Recognition

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Abstract—Deep facial expression recognition faces two challenges that both stem from the large number of trainable parameters: long training times and a lack of interpretability. We propose a novel method based on evolutionary algorithms, that deals with both challenges by massively reducing the number of trainable parameters, whilst simultaneously retaining classification performance, and in some cases achieving superior performance. We are robustly able to reduce the number of parameters on average by 95% (e.g. from 2M to 100k parameters) with no loss in classification accuracy. The algorithm learns to choose small patches from the image, relative to the nose, which carry the most important information about emotion, and which coincide with typical human choices of important features. Our work implements a novel form attention and shows that evolutionary algorithms are a valuable addition to machine learning in the deep learning era, both for reducing the number of parameters for facial expression recognition and for providing interpretable features that can help reduce bias.

Index Terms—convolutional neural networks, evolutionary algorithms, facial expression recognition, image classification, neural network compression

I. INTRODUCTION

Humans convey their emotions across in various forms, one of which is expressed through changes in a person’s face as a consequence of their emotional state [1]. There are countless numbers of interactions between humans each day given that humans are a social species. The human face provides a lot of information in these interactions [2]. Facial Expression Recognition (FER) is the ability to recognise the expressions that are being conveyed through the changes in the face.

There has been a lot of work in this field of research given the progress in computer vision research, see [3] for a review of works from 2003 to 2012. Amongst the vast available set of machine learning algorithms, there has been a tremendous amount of recent work using deep learning [4]. Convolutional neural networks (CNN) [5] are widely used in image classification tasks. Researchers focusing on FER have since been using CNNs as they achieve higher classification performance in comparison to earlier methods.

There are existing literature reviews on the topic of machine learning and FER. Corneanu et al. [6] provides a useful taxonomy of FER and computer vision research areas such as face localisation, feature extraction, classification and multimodal fusion – these are discussed in the context of RGB, thermal and 3D images. In terms of the classification areas not a lot of CNN studies were analysed. Pramerdorfer and Martin [7] compared 6 CNN studies of depths 5 to 11 against VGG, Inception, ResNet and an ensemble on a single dataset. Pantic and Rothkrantz [8] discussed some neural network studies but did not focus on CNNs, similarly, Sarıyanidi et al. and Wu et al. [9], [10] did not describe CNN related works. Martinez et al. [11] reviewed a number of studies and described challenges and opportunities in FER research such as medical, marketing and audience monitoring as well as human computer interaction studies. They did not review studies that implemented CNNs. Ghayoumi [12] discussed a few CNN studies. Zhang [13] discussed a few deep belief networks and CNNs. Ko [14] describe a number of long short term memory CNN approaches which have been applied to FER. Latha and Priya [15] discuss 17 CNN studies which have been applied to FER.

It is clear from the existing work in the literature that CNNs achieve state-of-the-art performance on FER tasks as opposed to other machine learning methods. Training CNNs often result in a large number of trainable parameters. This in turn implies that long training times are to be expected on limited hardware. In this study, we explore a novel idea which attempts to optimise the predictive performance of CNNs for FER and simultaneously, reduce the number of neural network trainable parameters without compromising on the classification accuracy. We ask the following, can we achieve similar predictive performance when training a model on small image patches (extracted from an image) as opposed to the entire image of the face? Are certain facial features more discriminative for FER and can an evolutionary algorithm [16] discover these areas? Can an evolutionary algorithm optimise the size of small image patches to reduce the input image size and consequently the number of trainable CNN parameters?

II. PROPOSED APPROACH

Based on the literature surveyed, there have been no prior attempts at using an evolutionary algorithm to extract patches from images with the objective of reducing the number of trainable CNN parameters and to retain (or improve) classification performance. We propose Evolutionary Facial Expression Recognition (EvoFER) in this section. EvoFER extracts a number of patches from the original image and stacks the patches to form a new image.

Figure 1 illustrates an example whereby an image is input into a CNN for classification, and below, an example of four
stacked patches (extracted from EvoFER) being inputted into the same CNN. After converting to greyscale, the resolution of the original image is $281\times381\times1$ whereas the new stacked image is $50\times50\times4$. Thus, the number of trainable CNN parameters using the original image is greater than the number of parameters when using the new stacked image made up of several patches. The patches are stacked in a similar manner to a colour image having 3 colour channels (RGB).

The objective function for EvoFER is multi-objective. Firstly, EvoFER attempts to reduce the number of trainable parameters as opposed to the number of parameters which would be used when training on the full image. The second objective is to achieve the highest possible classification accuracy using the patches as opposed to using the full image. The following subsections describe EvoFER.

A. Chromosome

EvoFER chromosomes contain 2 fixed genes and then allows for a number of pair of genes to be added. The first two genes denote values $\alpha$ and $\beta$ which represent the width and height of the patches to be extracted. The remainder of the chromosome denotes $(x, y)$ pairs. Each $x$ and $y$ pair are the coordinates of the top left point of the corresponding patch to be extracted from the original image. The coordinates $x$ and $y$ are relative to the location of the nose. The nose is used as a reference point and was obtained using OpenCV and DLIB[1]. The patch is extracted by obtaining the coordinate $(x, y)$ and using $\alpha$ and $\beta$ to obtain the entire patch. A chromosome thus encodes the location and size of the patches to be extracted from the original images. A chromosome must have at least one $(x, y)$ pair. User-defined parameters specify the maximum number of $(x, y)$ pairs allowed in each chromosome. The patches are stacked on top of each other vertically which in turn creates a new image. The order of the patches is not important. Figure 2 illustrates an example of a chromosome with two patches. The width of the patches to be extracted is 10 and the height is 20. The green dotted line is the first patch and the solid blue line is the second patch. The location of the top left corner of each patch to extract relative to the coordinates of the nose are (10, 30) and (-10, -5). The figure illustrates the unstacked exacted patches.

B. Initial Population Generation

We use the standard initial population generation algorithm. We propose algorithm 1 to generate the EvoFER chromosomes. This algorithm is executed a number of times based on the number of chromosomes to create. A random value for $\alpha$ and $\beta$ is assigned to each chromosome based on a corresponding bound which is pre-defined by the experimenter. The values of $\alpha$ and $\beta$ are not modified during the evolutionary process.

Upon the creation of a chromosome, the number of patches is randomly assigned based on a user specified bound. For each patch to be created, a random value for $x$ and $y$ is created. These values are randomly generated based on the image width and height as is illustrated from lines 11 to 14 in algorithm 1. This was done so that the patches remain as closely as possible within in the bounds of the image. Initially, the evolutionary algorithm can create patches which contain redundant pixels (for example the background, hair or clothing). We do not bias the algorithm towards initialising on patches of interest, such as the mouth or eyes.

C. Mutation

We propose two mutation operators to traverse through the search space. The first is a variation of the standard mutation operator and the second is tailored to the problem domain. When the mutation function is applied one of four things can be executed depending on the number of patches in the

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1http://dlib.net/imaging.html
Algorithm 1: Creating an EvoFER chromosome.

```
begin
    Initialise an empty chromosome.
    alpha ← random[min_alpha, max_alpha ]
    beta ← random[min_beta, max_beta ]
    patches ← random[min_patches, max_patches ]
    for i = 0 to patches do
        X ← GenerateX(alpha)
        Y ← GenerateY(beta)
        Append (X, Y) to chromosome
    return chromosome.
end
```

Function `GenerateX(alpha)`

```
return random[−(image_width/2 − alpha), image_width/2 − alpha]
```

Function `GenerateY(beta)`

```
return random[−(image_height/2 − beta), image_height/2 − beta]
```

Algorithm 2: Applying shift mutation.

```
begin
    mutation_patch ← randomly select a patch from chromosome
    x_i ← x value from mutation_patch
    y_i ← y value from mutation_patch
    delta_x ← GenerateDeltaX(alpha)
    delta_y ← GenerateDeltaY(beta)
    x_i ← x_i + delta_x
    y_i ← y_i + delta_y
    return chromosome.
end
```

Function `GenerateDeltaX(alpha)`

```
return random[−alpha, alpha]
```

Function `GenerateDeltaY(beta)`

```
return random[−beta, beta]
```

The shift operation is a novel method which we describe below. Changing and shifting is always allowed, however adding and removing is only allowed under the following conditions:

- a patch can be added if the number of patches is less than the user-defined predefined maximum
- a patch can be removed if the number of patches is greater than the user-defined predefined minimum

Adding a new patch simply generates a value for x and y in a similar way to the functions presented in algorithm [1]. The new patch is appended to the chromosome. Removing a patch consists of randomly selecting a (x, y) pair to be removed. Changing a patch randomly selects one and then replaces the (x, y) pair with new values.

Algorithm 2 presents the pseudocode for applying shift mutation to a chromosome. A patch is randomly selected from the chromosome and then the x and y values are extracted from the patch. The pair is then perturbed by values ranging between [−alpha, alpha] and [−beta, beta]. This enables the algorithm to shift the patch in a random direction. The standard mutation operator allows the algorithm to take a large jump in the pixel space, whereas shift mutation restricts the jump.

Figure 3 shows an example of the shift mutation and standard mutation operators being applied to a EvoFER chromosome.

D. Crossover

The standard crossover operator is applied to the (x, y) pairs between two parent chromosomes. Specifically, let (x_1, y_1) and (x_2, y_2) be a pair of coordinates within parents P_1 and P_2. Then offspring C_1 is created by copying all of the genes in P_1 however, x_1 is replaced with x_2 and similarly, y_1 is replaced with y_2. Chromosome C_2 is created by copying all of the genes in P_2 however, x_2 is replaced with x_1 and similarly, y_2 is replaced with y_1. The offspring are evaluated and the one with the highest fitness is returned.

Figure 3 shows an example of the crossover operator being applied to two EvoFER chromosomes. The first patch from each parent chromosome is swapped to create the two offspring.

E. Chromosome Evaluation

Before executing the evolutionary process, we run a CNN model M on the image dataset and record the validation accuracy and the number of neural network trainable parameters. Once the model is trained we apply the model to the test
images and record the test performance – we denote this as the baseline model.

Each chromosome $C_i$ is evaluated on every image $X_j$ in the dataset. When determining the fitness for $C_i$, the corresponding image patches $E_k$ are extracted from $X_j$ based on the number of $(x, y)$ pairs in $C_i$. All the extracted patches $E_k$ are stacked upon each other which produce a new image $N_j$. That is, each chromosome will be applied to each $X_j$ which creates a corresponding image $N_j$. The new images $N_j$ are input into the CNN model $M$. When computing the fitness score, we make use of the baseline validation accuracy and number of trainable CNN parameters. This is done to assign a fitness score that compares relative performance of chromosomes to the baseline CNN with the ultimate goal of improving the chromosome accuracy and reducing the number of parameters.

We propose the fitness function presented in equation $1$. The function considers both the effect of the validation accuracy and the number of trainable parameters between the network produced on images $N$ and the images $X$. The objective is to maximise the fitness. When validating the fitness accuracy of the chromosome is larger than the baseline then $S_c / S_b$ is a large number. Similarly, when the number of parameters obtained by the network as a result of the chromosome is smaller than the number of parameters obtained by the baseline then $P_c / P_b$ is a large number. We allow a parameter $W_S$ to fine-tune the weight allocated to the validation accuracy. Small values (i.e., $< 1.0$) of $W_S$ will allocate greater importance to the number of parameters. This way, the experimenter can decide on the importance of the validation performance. The value of $W_S$ was determined through trial runs and we explored values ranging from $\{0.1$ to $5\}$.

$$\text{Fitness (chromosome) } = \exp \left\{ W_S \frac{S_c}{S_b} + \frac{P_c}{P_b} \right\} \tag{1}$$

where

$$W_S = \text{weight of the validation accuracy}$$

$$S_c = \text{validation accuracy for the chromosome}$$

$$S_b = \text{validation accuracy for the baseline network}$$

$$P_c = \text{number of trainable weights for the chromosome network}$$

$$P_b = \text{number of trainable weights for the baseline network}$$

We provide an example of the fitness computation of a baseline and chromosome. Suppose that a CNN is trained on a FER dataset and the validation accuracy averaged over $R$ runs is computed to be $0.65$. Assume that the number of trainable parameters for the network is $12,189,447$. Now assume that the proposed algorithm is executed and that the validation accuracy of a chromosome is $0.31$ and that the number of trainable parameters is $123,063$ (a smaller value is obtained since the input images consist of smaller stacked patches in comparison to the larger original images). Then we have $\frac{0.31}{0.65} \approx 0.48$ and $\frac{123,063}{12,189,447} \approx 0.099$. Let $W_S = 5$. The final calculation for the fitness of the chromosome is $\exp (5 \times 0.48 + 0.99) \approx 29.67$. Since the objective is to maximise the fitness then a larger value denotes a better chromosome.

For each chromosome, we execute a CNN and allow it to train on the transformed images (made up of extracted patches). We use Keras and Tensorflow to train the CNN. The pipeline of constructing patches and training the CNN is illustrated in figure $5$.

### III. EXPERIMENTAL SETUP

In this section we describe the experimental setup which was used to evaluate the performance of $EvoFER$. The rationale behind the decisions made to guide the experiments were based on preliminary implementations of CNNs to general FER.

#### A. Datasets

To evaluate the performance of $EvoFER$ we conducted a number of experiments on the datasets listed below. These datasets were selected since they are commonly used in the
literature and represent different characteristics (gender, age, ethnic diversity and image resolution).

- JAFFE [18]
- KDEF [17]
- MUG [19]
- RAFD [20]

B. Pre-processing

Pre-processing is a vital step when dealing with image data. This can be described as some method to transform original input images using some image manipulation function. The function renders new images with the ultimate goal being that the new images will help the predictive performance of the classifier. Applying a CNN directly to images which have not been pre-processed in some way can yield weaker predictive performance. For example, consider a dataset containing images of people for which the lighting conditions across the face are not consistent. It would be more suitable to attempt to correct the variation in illumination in such a way to have the same amount of lighting exposure across the entire face so that the CNN can learn useful features across the entire face. Pre-processing was shown to improve classification performance in a number of studies [21], [22], [23], [24], [25], [26], [27].

We implemented histogram equalisation on each of the images. Additionally, we converted each image into greyscale as the additional information available in colour images does not impact the performance of FER. To achieve this, we made use of OpenCV as it is commonly used in literature, for examples see [28], [29], [30].

C. Data Augmentation

The application of CNNs often require large datasets to enable good predictive performance and has been successfully used in literature, for examples see [31], [32], [33], [27], [22]. We implemented a number of augmentation techniques using the literature to guide our decisions. We augment our training images using the following techniques:

- horizontal flipping
- blurring
- noise
- rotate by -5 and -10 degrees
- rotate by 5 and 10 degrees

These augmentation techniques were only applied to the training images. The test images were kept in their original form. For each training image we generated an additional 9 images by applying two levels of blurring and noise. These were achieved by using imgaug2 – a software package for image augmentation. Table I presents the number of images which were used for training for each dataset after we applied the augmentation techniques. Figure 6 presents the augmentation techniques applied to each image.

D. Network Architecture

Figure 7 presents the CNN architecture which we propose to use for the EvoFER experiments. The architecture was inspired by our findings from existing literature, for examples see [33], [27], [34], [35]. More specifically, the reviewed works used on average 3 convolutional layers with max pooling in between them, and two fully connected layers at the end of the network. The ReLU activation function was used the most frequently in all layers except for the last where softmax was used. We thus used the literature to guide our decisions, and furthermore various modifications of the architecture were explored using preliminary runs on the JAFFE dataset by varying the depth, activation function and parameters. The last fully connected layer takes on a value of ‘C’ for the number of units as this is dependant on the number of expression classes in each dataset.

The proposed architecture consists of three convolutional and max pooling layers, along with two fully connected layers. Dropout was applied after each of the layers except for the last one. The ReLU activation function was used for all the layers except for the last fully connected layer whereby the softmax function was used. It would also be possible to optimise the network using machine learning, such as EDEN, as described in [36], however, we chose to use the findings from the literature to guide our decisions. Studies in literature (for examples see [37], [38], [39]) reveal that using an ensemble

| Dataset | Training images after augmentation |
|---------|-----------------------------------|
| JAFFE   | 1,910                             |
| KDEF    | 6,860                             |
| RAFD    | 10,152                            |
| MUG     | 2,800                             |

2https://github.com/aleju/imgaug

Fig. 6. Illustrating the different augmentation techniques which were used to increase the number of training images. Images extracted from [17].
Fig. 7. The CNN architecture which is proposed for the experiments. This network was inspired by the findings from existing literature. 'Conv2D' denotes 2D convolution and 'MaxPool2D' denotes 2D max pooling. The associated parameters are listed.

will result in superior classification performance, however, we wanted to examine the effect of using patches as input to enhance the performance.

We ran two sets of experiments. In the first, we ran EvoFER using the literature inspired network and used the patches as input to the CNN. In the second set of experiments, we ran the same literature inspired network and used the full image as input to the CNN. We denote experiments conducted on the full images as the baseline.

**E. Training and testing**

Lopes et al. [40] describe that a fair comparison is one whereby the same subjects should not be found in the training and testing sets. In their work they split the images into 8 groups containing a number of subjects each, and that the same subject is not found in more than one group. From all the studies reviewed, it was found that their work contained the most emphasis on fairness. We implemented this approach in our experiments, for which 30% of the data was used for testing and the remaining for training. We repeated the execution of EvoFER ten times and averaged our results. This was conducted for both the evaluation of the baseline and for the evolutionary process. The choice of optimiser was selected based on a literature survey. We selected the Adam optimiser and a batch size of 8.

**F. EvoFER Parameters**

Table [II] provides the details of the parameters associated with the evolutionary algorithm. The parameters associated with the training of the CNN are presented in table [III]. Finally, table [IV] presents the parameters associated with the initialisation of the chromosomes during the initial population generation and mutation operation. These parameters were chosen by performing a search on a number of values which were found in the literature and by performing a random hyper-parameter search.

**IV. RESULTS AND DISCUSSION**

Table [V] presents the average test classification accuracy results. The baseline accuracy (literature inspired CNN model with original images) and EvoFER accuracy (the same literature inspired CNN model with extracted patches from best chromosome) are presented. The CNN architecture and hyper-parameters were the same for both results. The findings reveal that on all of the datasets EvoFER was able to outperform the same CNN model which had been trained on the original images. The smallest improvement in accuracy was observed in the KDEF dataset with an improvement of 1.3%. The largest improvement in classification accuracy was obtained on the MUG dataset with a value of 20.6%. This indicates that given

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**TABLE II**

| Parameter       | Value |
|-----------------|-------|
| Population size | 100   |
| Tournament size | 7     |
| Crossover percentage | 50   |
| Mutation percentage | 50   |
| Generations     | 15    |
| Fitness function, $W_S$ | 5    |

**TABLE III**

| Parameter       | Value |
|-----------------|-------|
| Number of epochs| 10    |
| Optimiser       | Adam  |
| Batch size      | 8     |

**TABLE IV**

| Parameter       | Value |
|-----------------|-------|
| $min\_\alpha$  | 30    |
| $max\_\alpha$  | 50    |
| $min\_\beta$   | 30    |
| $max\_\beta$   | 50    |
| $min\_patches$ | 1     |
| $max\_patches$ | 4     |
The standard deviation is presented in parentheses. The findings reveal that the performance is superior when EvoFER is used.

| Dataset | Baseline Accuracy | EvoFER Accuracy | Difference |
|---------|------------------|-----------------|-------------|
| KDEF    | 61.9 (1.6)       | 65.3 (2.9)      | 3.4         |
| JAFFE   | 60.0 (4.7)       | 75.5 (4.4)      | 15.5        |
| RAFD    | 75.4 (3.4)       | 80.4 (2.3)      | 5.0         |
| MUG     | 45.8 (3.8)       | 66.4 (5.0)      | 20.6        |

The average number of trainable neural network parameters when using the original image and EvoFER extracted patches. The standard deviation is presented in parentheses.

| Dataset | Baseline Parameters | EvoFER Parameters | Difference % |
|---------|---------------------|-------------------|--------------|
| KDEF    | 1,218,944           | 145,741 (15,782)  | 88.0         |
| JAFFE   | 7,397,127           | 155,543 (0)       | 97.9         |
| RAFD    | 2,152,520           | 45,528 (6,476)    | 97.9         |
| MUG     | 2,574,279           | 47,027 (6,345)    | 98.2         |

EvoFER is able to enhance the performance by using stacked patches as input.

What is the processing time for EvoFER given that the nose has to be located prior to the application of the chromosome? We examined the time it took to perform the necessary pre-processing steps for EvoFER and in the case of the baseline CNN. These findings are presented in Table VIII. The time, in seconds, is presented for the two methods to pre-process and predict the expression for 10 images. In the case of KDEF, RAFD and MUG, EvoFER took approximately twice as long as the baseline method. This is because EvoFER has the extra overhead of needing to locate the nose to establish a reference point for the chromosome. EvoFER took less time than the baseline on the JAFFE dataset. It can be hypothesised that this is the case since the resolution of the images in the JAFFE dataset is much smaller than the other datasets. It would be of interest to reduce the resolution of images in the other datasets.
TABLE VII
A COMPARISON BETWEEN THE TRAINING TIME (SECONDS) WHEN USING THE BASELINE NETWORK ON THE ORIGINAL INPUT AND USING EvoFER ON THE EXTRACTED PATCHES INPUT. IN BOTH CASES THE SAME NETWORK ARCHITECTURE AND HYPER-PARAMETERS ARE USED. THE PRIMARY DIFFERENCE IS THE INPUT.

| Dataset | Baseline with original dataset input | EvoFER with extracted patches input |
|---------|--------------------------------------|-------------------------------------|
| KDEF    | 247                                  | 42                                  |
| JAFFE   | 61                                   | 10                                  |
| RAFD    | 112                                  | 30                                  |
| MUG     | 43                                   | 10                                  |

TABLE VIII
AVERAGE TIME TAKEN (SECONDS) TO PROCESS 10 IMAGES USING EvoFER AND THE BASELINE. THE RESULTS ARE AVERAGED OVER 10 EXECUTIONS. THE STANDARD DEVIATION IS SHOWN IN PARENTHESES.

| Dataset | EvoFER | Baseline |
|---------|--------|----------|
| JAFFE   | 0.27 (0.01) | 0.29 (0.01) |
| KDEF    | 0.42 (0.01) | 0.18 (0.01) |
| RAFD    | 0.28 (0.01) | 0.14 (0.01) |
| MUG     | 0.23 (0.01) | 0.13 (0.01) |

to determine if this could result in faster execution times for EvoFER. Despite the fact that EvoFER has an additional overhead, the processing time is not significantly large and could thus still be implemented in a real-world setting. In terms of training, EvoFER took up to 5 hours whereas training the equivalent network in a traditional setting (i.e. the baseline) took less than a minute. Once the location of the patches have been optimised, EvoFER trains faster than the baseline approach (i.e. the same network on the original dataset) - these findings are presented in table VII.

V. CONCLUSION

This study proposes a novel evolutionary algorithm to extract patches from images with the goal of transforming images into more compact representations whilst retaining the predictive performance (or increasing it) and to reduce the number of trainable parameters. We propose a chromosome representation which allows the algorithm to encode locations relative to the nose. The chromosomes also encode the width and height of the patches to be extracted at each location. We introduce a fitness function which combines the relative performance of each chromosome to a baseline execution. The baseline execution consists of running a CNN on the original images. The multi-objective fitness function attempts to optimise the validation accuracy and number of trainable parameters. To enable us to interface each chromosome to the training of a CNN we use Keras and Tensorflow.

We evaluated EvoFER and the findings revealed that it can achieve superior performance to the exact CNN architecture trained on the entire image. Furthermore, the findings revealed that EvoFER can reduce the number of trainable parameters, on average, up to 95%. EvoFER was able to optimise the search for optimal patch locations and size to enable the CNN to distinguish between the various expressions (without any insights hardcoded into the algorithm). Initially EvoFER
could select patches which did not contain parts of the face at all. In several cases there was patches which were located near people’s hair. Through the evolutionary process, EvoFER extracted patches generally around the eyes and mouth which enabled the CNN to achieve better predictive performance. We hypothesise that superior performance could be achieved by increasing the number of epochs; in this study we imposed a limit due to available computational time.

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