ORGAN-BASED AGE ESTIMATION BASED ON 3D MRI SCANS

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ABSTRACT

Individuals age differently depending on a multitude of different factors such as lifestyle, medical history and genetics. Often, the global chronological age is not indicative of the true ageing process. An organ-based age estimation would yield a more accurate health state assessment. In this work, we propose a new deep learning architecture for organ-based age estimation based on magnetic resonance images (MRI). The proposed network is a 3D convolutional neural network (CNN) with increased depth and width made possible by the hybrid utilization of inception and fire modules. We apply the proposed framework for the tasks of brain and knee age estimation. Quantitative comparisons against concurrent MR-based regression networks illustrated the superior performance of the proposed work.

Index Terms— Age estimation, deep learning, magnetic resonance imaging, convolutional neural networks

1. INTRODUCTION

Age estimation is an integral part of biological profile assessment, especially in the medical and forensic domains. In recent years, age estimation has become an important factor for a variety of legal proceedings like immigration, unknown birth date and other criminal/civil disputes [1]. There are several methodologies for age estimation based on magnetic resonance (MR) images of the foot, elbow, wrist and teeth [2–4].

Within the context of age estimation, it is important to distinguish the difference between the chronological and biological ages. The chronological age (CA) is defined as the amount of time passed since birth to a given date. However, the actual age of various organs could be healthier or more damaged owing to different factors such as lifestyle, genetics, medical history and food habits. Thus, an individual’s BA could deviate from his/her CA. Even more, different organs of the same person may have different BAs. Consequently, age estimation of MRI scans could be used to gather important clinical information when observing discrepancies between the predicted BA and the actual CA [5]. However, since there is no solid definition of BA, in this preliminary study we consider the CA as the ground-truth label.

For instance, the human brain undergoes morphological changes owing to the ongoing aging process. More specifically, the gray matter (GM) mass is a strong indicator for the biological brain age [6]. It was found that the GM mass declines linearly with age [7]. In a previous work, T1-weighted MRI scans of the GM mass were utilized to estimate the brain age of the test subject. This could help in the early diagnosis of neurogenerative disorders such as Alzheimer and Parkinson [8, 9].

Classical approaches for MRI-based brain age estimation involve the manual extraction of features such as cortical thickness and surface curvature [10]. This is followed by traditional machine learning algorithms such as kernel methods [11] or support vector machines (SVM) [12]. A major downside of feature extraction is that the features may not fully represent the contents of the input scan. With the advent of deep learning (DL), neural networks greatly increased the accuracy of prediction tasks without manual feature engineering. For example, convolutional neural networks (CNNs) were utilized to predict the brain age from 2D input MR slides [13, 14]. More notably, shallow 3D CNN architecture were used to predict the brain age using T1-weighted MRI volumes [15, 16].

In this paper, we propose a hybrid 3D-CNN architecture for organ-specific age estimation from MRI scans. The proposed network utilizes recent advances from the deep learning community such as Inception and SqueezeNet architectures [17, 18]. We apply the proposed framework on two open source MRI datasets for estimation of the brain and knee-joint ages, respectively. Additionally, two approaches utilizing the MRI volume are investigated. The first approach utilizes the entire field of volume while in the second approach the data is split into more localized 3D chunks. A 2D variant of the proposed network is also presented for computational efficiency purposes. Finally, a quantitative comparison is carried out against prior 2D and 3D age estimation approaches.

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2. METHODS

In this section, the utilized pre-processing steps required for the brain age estimation will be outlined. Furthermore, the proposed architecture and different methods for feeding the input data will be explained. An outline of the utilized network is shown in Fig. 1.

2.1. Pre-processing of Brain MRI

The GM is a strong representation of the brain age [13]. Thus, we utilize the pre-processing steps recommended in [7]. First, the GM tissues are segmented from the input brain volumes using the statistical parameter mapping 12 (SPM12) software [19]. The resultant segregated tissues are then spatially normalized according to the international consortium for brain mapping (ICBM) 152 template. Using DARTEL [20], the GM volumes are non-linearly registered and resampled using a 4 mm smoothing kernel which results in a final volume size $121 \times 145 \times 121$ voxels. Examples are depicted in Fig. 2.

2.2. Architecture

The proposed 3D-CNN regression is a combination of Inception v1 [17] and Squeezenet [18] architectures. The inception modules enable learning deeper feature representations by convolving the input volumes with filters of different kernel-dimensionality. This allows the creation of deeper and wider networks while maintaining the same computational budget. Additionally, squeeze and expand layers are also utilized. They together form the fire module which is the prime architectural component of the Squeezenet. These blocks consist primarily of $1 \times 1 \times 1$ kernels and help to downsize the number of parameters even further.

The final architecture consists of a stem network utilizing $3 \times 3 \times 3$ convolutions and max pooling layers followed by 4 modules, each composed of 2 inception blocks and a single fire module [17]. Afterwards, a global average pooling (GAP) is applied which acts as a structural regularizer. This reduces the four-dimensional input tensor to a one-dimensional vector of 512 features which is then connected to three dense layers. Finally, a regression layer outputs the predicted age.

2.3. 3D Input Pipeline

The manner of feeding the input 3D volumes can have a significant effect on the resultant regression result. In this work, we investigate two different approaches of feeding the input data. The first approach is based on feeding the entire 3D volume as input which results in a single age for each estimated test subject. In order to prevent overfitting, additional data augmentation is also applied such as horizontal flipping and translating the volume within a defined voxel-range. In terms of training efficiency, training on the whole 3D volume demands huge memory space as well as increased training time owing to the on-the-fly data augmentations.

The second approach consists of dividing the MRI volume of each patient into smaller 3D chunks (of 12 slides in the axial-plane) which serve as individual input samples. This implicitly expands the dataset size without further data augmentation. As a result, the network outputs multiple age estimations for each test subject with the final age given as the mean of the predicted age of all the input chunks. This could enable more detailed subjective analysis of the predicted age of each input chunk.

For lower computational complexity, a 2D variant (2D-CNN) of the proposed 3D framework is introduced. This network utilizes 2D convolution operations instead of the 3D counterpart while using the same design as in Fig. 1. For the input pipeline, 2D axial slides are fed with pixel dimensions $121 \times 145 \times 12$.

3. EXPERIMENTAL EVALUATIONS

The proposed 3D CNN architecture is evaluated for the task of brain age estimation using the open source IXI Brain Dataset [21]. T1-weighted MR scans from 425, 90 and 45 subjects...
Fig. 2. Examples for the input MR images. First, segmented GM from axial 3D T1-weighted scans for (a) 23 year old subject, (b) 86 year old subject, followed by T2-weighted sagittal images for the knee in a (c) 25 year old subject, (d) 88 year old subject.

Fig. 3. The distribution of subjects from both genders in the utilized brain dataset with $\mu$ representing the mean age. Were used for training, cross-validation and testing, respectively. The data distribution of the training dataset is depicted in Fig. 3. For the first 3D input pipeline approach (3D-CNN-full), the entire pre-processed GM volumes, each of size $121 \times 145 \times 121$, are fed to the network. For the second approach, individual 3D chunks from each test subject, of size $121 \times 145 \times 12$, are fed instead (3D-CNN-chunk). Additionally, for the 2D variant of the proposed network (2D-CNN), only individual 2D axial slices of $121 \times 145$ pixels are fed into the network.

To demonstrate the performance of the proposed network, we quantitatively compare against other competing approaches for MRI-based brain age estimation. First, the 2D framework from [13], which consists of a modified VGGNet, was compared to the 2D variant of our proposed framework. Additionally, we compare our 3D models (3D-CNN-full and 3D-CNN-chunk) against the recent state-of-the-art 3D network in [16]. To ensure a fair comparison, the models were trained using the original recommended hyperparameters. For the quantitative metrics, the mean absolute error (MAE), standard deviation (SD) and root mean square error (RMSE) are utilized.

Table 1. Quantitative comparisons.

| Method                  | Brain dataset | Knee dataset |
|-------------------------|---------------|--------------|
|                         | MAE   | SD   | RMSE | MAE   | SD   | RMSE |
| 2D-CNN (Huang [13])    | 3.83  | 4.79 | 4.89 | 4.28  | 6.07 | 6.17 |
| 3D-CNN (Ueda [16])     | 3.84  | 4.3  | 4.48 | 5.36  | 6.93 | 7.12 |
| 2D-CNN                  | 3.21  | 4.16 | 4.48 | 3.72  | 5.35 | 5.53 |
| 3D-CNN-full             | 2.98  | 3.9  | 4.06 | 3.35  | 4.36 | 4.47 |
| 3D-CNN-chunk            | **2.76** | **3.7** | **3.93** | **2.98** | **3.97** | **4.16** |

4. RESULTS OF BRAIN AGE ESTIMATION

The quantitative comparison between MR-based regression networks for the task of brain age estimation is presented in Table 1. The 2D VGG-based network by Huang [13] resulted in the worse RMSE score and the highest standard variation. The 3D network proposed by Ueda in [16] yielded a better RMSE score albeit with no improvement to the MAE. We hypothesize that this is the result of reducing the depth of the 3D network, in comparison to the 2D VGGNet, to accommodate the memory requirements and complex operations necessary for voxel-based training.

The 2D variant of our proposed network outperforms the previous approaches across the utilized metrics. This is due to the increased network depth and width, and thus learning capability, made possible by the utilization of inception and fire modules. Furthermore, the proposed 3D network resulted in the best quantitative scores. However, the manner of feeding the input 3D data had a significant effect on the regression performance. Feeding smaller 3D chunks as inputs via the 3D-chunk network culminated in an MAE of 2.76 years instead of 2.98 years for feeding the whole patient volumes. This allows us to hypothesize that chunk-specific age estimation from 3D volumes enables a better CA estimation and can lead to a possible organ-specific BA estimation which encourages more in-depth studies in the future.

5. KNEE AGE ESTIMATION

Apart from the brain, other anatomical regions of the human body also display ageing traits such as the joints and knees...
Thus, to demonstrate the generalization capability of our framework to different body organs, we investigate the task of MR-based knee age estimation. This could benefit the early diagnosis of knee ailments such as predicting the risk of Arthritis caused by degeneration of the cartilage in the knee and specifically Osteoarthritis in case of athletes [23].

For this purpose, we utilize the open-source NYU fastMRI dataset [24] demonstrated in Fig. 2. The dataset consists of T2-weighted scans with fat suppression for 550 subjects. For pre-processing, the voxels of the MR scans were normalized to have zero mean and unit variance with a final volume size of $320 \times 320 \times 28$. The subjects were split into 415, 90 and 45 for training, cross-validation and testing, respectively. To train the 3D-CNN-chunk network, each input volume was split to a chunk size of $320 \times 320 \times 4$.

The quantitative results are presented in Table 1. In this case the shallow 3D network proposed in [16] is outperformed by the deep 2D VGGnet which exhibits an MAE improvement of 1.08 years. On the other hand side, our proposed networks have significantly better performance with an MAE score of 2.98 years by the 3D-CNN-chuck network in comparison to 4.28 years by the 2D-CNN network in [13].

6. CONCLUSION

In this work, we present a new network architecture for MR-based organ age estimation. The proposed architecture is based on a combination of inception and fire modules which enables increased network depth and width while maintaining the computational complexity and number of parameters. To showcase the performance of the presented framework, quantitative comparisons are carried out against current state-of-the-art MR regression networks for the tasks of brain and knee age estimation. The proposed architecture resulted in a significantly improved performance.

In the future, we would like to explore the tasks of age estimation for additional organs which may exhibit age-related changes such as spine, kidneys and liver. Additionally, we plan to conduct clinical analysis by radiologists for the cases were the estimated age deviates remarkably from the ground-truth chronological age in order to infer the BA.

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