Estimating Biological Age from Physical Activity using Deep Learning with 3D CNN

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***Abstract*—We introduce an approach to predict biological age based on a 3-dimensional deep convolutional neural network (3D-CNN), using human physical activity as recorded by a wearable device. Results on mortality hazard analysis using both the Cox proportional hazard model and Kaplan-Meier curves each show that the proposed method results in an improved performance. This work has significant implications in combining wearable sensors and deep learning techniques for improved health monitoring, for instance, in a mobile health environment.**

***Index Terms*—Age estimation, aging, deep learning, biological age, 3D CNN, physical activity, all-cause mortality.**

I. Introduction

The process of aging is complex and affects all biological systems. Age has a deep connection with health and mortality [1], [2], [3]. In general, a younger person is expected to have a better health condition, to be physically more active, and to have lower mortality hazard in comparison with a relatively older person. Although biological age is a loosely used concept and lacks precise definition, it is often viewed as the true age of an individual [4]. Thus, biological age provides a better measure of the life expectancy of an individual than his or her chronological age [5], [6]. In this work, we investigate the question of whether human physical locomotor activity as recorded using a wearable device can be used for reliable estimation of biological age in adults.

Levine [1] compared the performance of five BA estimation algorithms, and identified the Klemera and Doubal (KD) method as the most reliable predictor for mortality. The performance using BA was significantly better in comparison with using chronological age. Mitnitski *et al.* [3] compared performance of frailty index (FI) with biomarker-based measures of BA. They employed the KD algorithm in predicting mortality. Belsky *et al.* [7] compared different methods of BA estimation, including genomic, epigenetic, and blood biomarker measures. In a more recent work, Rahman and Adjeroh [8] proposed a centroid based biological age estimation method using notion of age neighborhoods.

Putin *et al.* [9] studied the use of biomarkers in a deep learning framework for chronological age prediction. They utilized an ensemble of multiple deep neural networks (DNNs) and trained on blood biomarkers. The best performance by a DNN was MAE of 6.07 years in predicting chronological age and the ensemble learning produced MAE of 5.55 years.

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Rahman and Adjeroh [10] applied deep convolutional long short term memory (ConvLSTM) on a week long physical activity data measured per minute to estimate biological age. They also compared estimated biological ages with KD method applied on biomarkers in a common dataset. Pyrkov *et al.* [11] applied a 1-dimensional convolutional neural network on the physical activity data to estimate biological age. Cole *et al.* [12] studied a deep learning framework using 3D-CNN based approach with raw MRI data. They showed their model can predict chronological age for healthy individuals. Zhavoronkov *et al.* [13] discussed recent advances in using artificial intelligence for studying aging and longevity.

In this work, we consider the use of physical activity data for reliable estimation of human biological age. In particular, we consider the temporal nature of human locomotor activity as a key element in its use for analyzing biological age. Thus, rather than using 1D CNN [11] to estimate biological age, we apply a deep learning framework using 3-dimensional Convolutional Neural Network (3D-CNN). We also consider 2D image representation of the data and apply a 2D-CNN based approach. Using the Cox proportional hazard model and Kaplan-Meier curves, we show comparative performance of our proposed biological age estimation methods with the existing deep learning approaches.

II. Methodology

A. Datasets

Activity Dataset & Preparation. We used physical activity data from the National Health and Human Nutrition Examination Surveys (NHANES) 2003 – 2004 and 2005 – 2006 as described in [10], [11].

Anthropometric & Biomarkers Dataset. We also used NHANES 2003-2006 anthropometric and biomarker datasets. These were used to study the potential relationship between human physical activity and the biomarkers (see [10]).

B. 2D and 3D CNN for Activity Data

The convolutional neural network (CNN) is the most popular deep learning networks. The convolution operation extracts patches from its input feature map and applies the same transformation to all of these patches, producing an output feature map. Convolutions are defined by two key parameters: a) size of the patch and b) number of filters. Convolution operation works by sliding these windows over the input feature map, from every accessible/possible location. Each patch is now transformed via a tensor product with learned weight matrix called convolution kernel.

Our approach to analyzing the human activity data build on the concept of finding local patterns by applying the convolution operation of an image. Two major characteristics of convolutional neural networks (CNN) are that they learn patterns in a hierarchical manner, and that the patterns learned are translation invariant. Our proposed method for estimating biological age is to apply 2D and 3D CNN. Note that this approach is different from the 1D CNN problem. Rather we take advantage of the structure in the sequence of 2D and 3D representations of the daily activities to learn valuable patterns from the activity data (which may be difficult using 1D CNN, or DNN). For 2D-CNN, we consider the features as an image of size 168×60 (DH×M) ignoring the days as temporal information. However, for 3D-CNN, we consider the features as a 3D volume with temporal information across the days, where each day has 24 hours and an hour is 60 minutes. So to break it down, we represent the features as a three dimensional information of 7×24×60 (D×H×M) minutes.

For both the proposed 2D and 3D approach, we concatenate two more fully connected dense layers and finally a single unit of neuron without activation to build up a scalar regression that estimates the biological age. Fig.1 shows the architecture of the proposed 3D-CNN model. We also apply a 1D CNN model [11], and a DNN model on the dataset to predict biological age. We compare the results from these four deep neural network models.

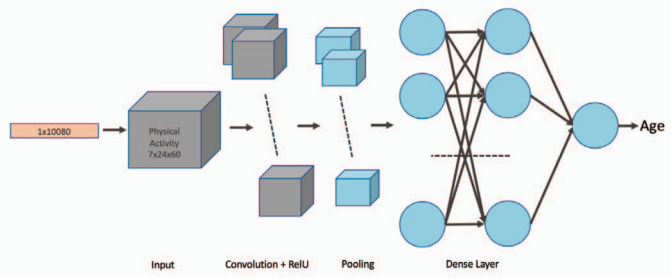


Fig. 1. Architecture of the proposed deep learning methods for biological age estimation using human locomotor activity data using 3D-CNN.

III. Results

A. Association of Locomotor Activity with Chronological Age

There exists a discernible association between physical activity and chronological age. On average, physical activity has a correlation coefficient of -0.19 (p-value = 0.00) with chronological age (see Table I). We have grouped subjects in the physical activity dataset based on their age ranging from 18 to 84, to further understand the relation between physical activity and chronological age. See Fig. 2. Average physical activity goes up from age 18 to 45. After that we observe a generally linear decline of average physical activity from age 46 to 85 years. Table I also shows the correlation between physical activity and different blood biomarkers (for individuals with both activity and biomarker data).

Mitnitski *et al.* [3] defined biological age acceleration as $\Delta = CA - BA$, where CA denotes chronological age and BA denotes biological age. However, here we used

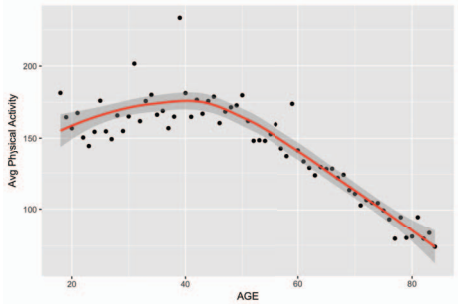


Fig. 2. Variation of average physical activity with age. Values plotted for individuals grouped by year of age.

TABLE I
CORRELATION BETWEEN AVERAGE PHYSICAL ACTIVITY, CHRONOLOGICAL AGE, AND BLOOD BIOMARKERS.

	Average Physical Activity	Age
C-reactive protein	-0.083	0.048
Glycated hemoglobin	-0.086	0.340
Serum Albumin	0.167	-0.090
Total Cholesterol	-0.034	0.182
Serum Urea Nitrogen	-0.059	0.457
Alkaline Phosphatase	-0.068	0.062
Systolic blood pressure	-0.110	0.535
Diastolic blood pressure	0.049	0.099
Pulse	-0.084	-0.211
High density lipoprotein	-0.024	-0.014
Hemoglobin	0.150	-0.024
Lymphocyte percent	0.059	-0.066
White blood cell count	-0.067	-0.053
Hematocrit	0.147	-0.011
Red blood cell count	0.151	-0.133
Platelet count	-0.038	-0.116
Chronological age	-0.193	

the normalized biological age acceleration (NBAA), denoted $\eta = \frac{\Delta}{CA} = \frac{CA-BA}{CA}$ used by Rahman and Adjeroh [10]. This normalization is performed to reduce the effect of of large Δs. For example, a Δ value of 5 could have different biological or health implications for an 18 year old ($\approx 28\%$ difference) and for a 70 year old ($\approx 7\%$ difference).

B. Estimated BA using 3D-CNN on physical activity data leads to improved modeling of all-cause mortality.

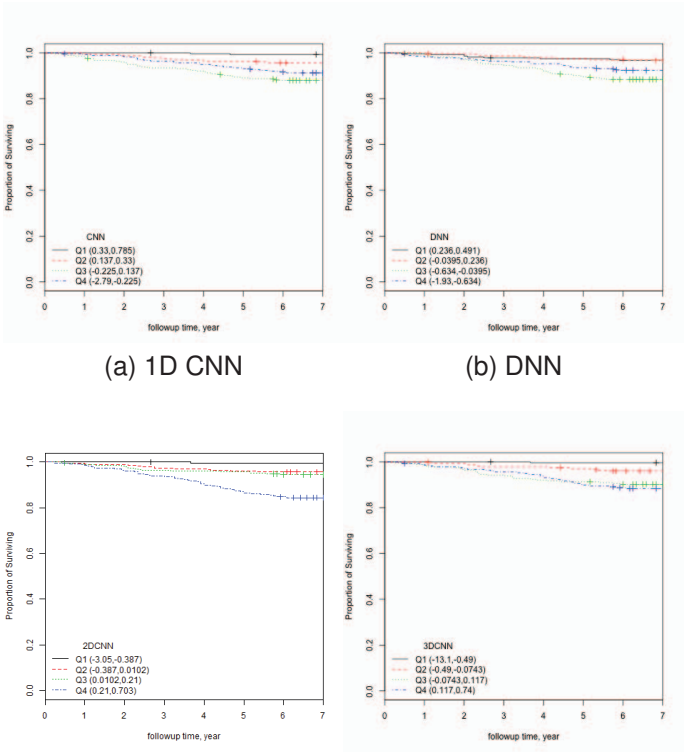
Biological age is a quantitative measure which is expected to provide some general indication of the health or functional status of an individual. Numerous approaches have used the idea of the association of physiological variables (biomarkers, activity) for estimating BA [2], [14], [11], [15]. However, given a new data modality, such as the human locomotor activity data studied in this work, a different model may be needed. The proposed network architecture is shown in Fig. 1. To evaluate how well the estimated BA using the proposed deep learning approache on locomotor activity data captures the functional status of the subjects, we considered how the estimated BA relates to health risks. In particular, we studied the association of all-cause mortality with the normalized biological age acceleration (η) using the estimated BA models.

Cox PH model. We used Cox proportional hazard modeling (Cox PH) [16], [17] and Kaplan-Meier (KM) curves [18] to

TABLE II
RESULTS OF THE COX PROPORTIONAL HAZARD (COX PH) MODEL AND LOG-RANK TEST APPLIED ON THE NORMALIZED BIOLOGICAL AGE ACCELERATION $\eta = (CA - BA)/CA$ FOR ESTIMATED BIOLOGICAL AGES.

	CoxPH		Log Rank	
	HR	p-value	Chi-Sq	p-value
1D CNN[11]	1.05	1.63E-11	33.60	2.41E-07
DNN	1.07	1.75E-19	22.10	6.22E-05
2D CNN	1.06	1.89E-14	58.13	1.48E-12
3D CNN	1.13	5.94E-20	36.79	5.09E-09

quantify the association of the proposed 2D-CNN and 3D-CNN estimated BA with all-cause mortality. Table II shows the results for all the approaches. We applied η as the covariate in the Cox model. We observe that for 1D CNN, and DNN, the HR value is 1.05, and 1.07 respectively. The 2D-CNN gives HR = 1.06 while the proposed 3D-CNN approach has the best results, with HR = 1.13.



(a) 1D CNN (b) DNN

(c) 2D CNN (d) 3D CNN

Fig. 3. The Kaplan Meier curves for estimated biological ages (BA) based on the physical activity applying $\eta = \frac{CA-BA}{CA}$ for (a) 1D-CNN, (b) DNN, (c) 2D-CNN, and (d) 3D-CNN. Q1, Q2, Q3, and Q4 denote 1st, 2nd, 3rd, and 4th quartiles, respectively. The number of individuals in each Q is 276.

KM plots and LogRank. To further study the performance of the estimated BAs, we analysed the Kaplan-Meier (KM) survival curves obtained using the quantile factored NBAA ($\eta = \frac{CA-BA}{CA}$). Fig. 3 shows the KM plots for the BA estimation algorithms. A given variable is a good mortality predictor if the Kaplan-Meier curves are easily distinguishable (more distance between them), and the variable gives a lower survival rates from low to high levels, with less crossing between curves. Among the deep learning BA estimation methods, the approach proposed by Pyrkov *et al.* [11] using 1D CNN performed better than using the direct DNN model on the 1D data. However, the proposed 2D-CNN and 3D-CNN approach produced an improved result when compared with the 1D-CNN method [11]. The differences among the biological age estimation methods is more evident using quantitative measures, e.g., the χ^2-distance between their respective KM curves, as captured by the log-rank test (see Table II). 2D-CNN estimated biological age has the highest χ^2-distance followed by 3D-CNN, 1D-CNN, and DNN.

IV. DISCUSSION

In this work we have investigated deep learning approaches on the NHANES locomotor physical activity data. We estimate biological age (BA) based on the physical activity and chronological age (CA). To quantify how well the estimated biological age captures the health risk, we apply the Cox proportional hazard model with all-cause mortality. The deep learning models (i.e., DNN, (1, 2, 3)D-CNNs) were trained to exploit the dependence of the physiological changes with age. All the deep learning approaches were trained to minimize the mean squared error (MSE) between estimated BA and CA.

For 3D-CNN we have used 128 filters, a kernel size of 3×3×3 with a "ReLU" activation function. The first dense layer has 256 filters and second has 128 filters. 30% dropout was performed after each dense layer. We have selected Adam optimizer for this work empirically. Mean square error (mse) was used as loss function.

A. Connection with General Health Status.

Another way to investigate the performance of the proposed approaches in capturing health risks is to consider their possible relationship with known indicators of health risk or how the estimated biological age differentiates between subjects with known diseases and those without. Below we consider this perspective in evaluating a BA estimation method.

TABLE III
LOG RANK RESULTS APPLYING ($\eta = \frac{CA-BA}{CA}$) FOR DIFFERENT SBSI CATEGORIES. RESULTS ARE SHOWN AS χ^2 DISTANCES. Q1, Q2, DENOTE 1ST QUARTILE, 2ND QUARTILE, ETC.

	$SBSI_{Q1}$	$SBSI_{Q2}$	$SBSI_{Q3}$	$SBSI_{Q4}$
1D-CNN	11.13	10.22	23.47	63.8
DNN	42.27	22.95	71.61	131.52
2D-CNN	13.88	18.98	31.91	78.28
3D-CNN	10.37	7.06	17.75	48.95

Relationship with Known Health Indices. For general indices of health status, we can consider the body mass index (BMI), waist to height ratio, or the more recently introduced surface based body shape index (SBSI) [19]. In particular, we studied the normalized biological age acceleration [10] (denoted η) computed using the estimated BA from CNNs with variations in the SBSI categories. Rahman and Adjeroh made an observation on the superiority of SBSI over BMI [19]. We have also observed the performance of the CNN models with respect to the surface based body shape index (SBSI [19]) quartiles. Table III shows the log-rank test on the

SBSI quartiles. The results are shown using η, for each SBSI category. We observe that, in general the χ^2 values increase from first quartile to fourth quartile (i.e., 2D-CNN, 3D-CNN). However, the increase is not monotonic for all the variations of CNN. For example, the χ^2-distance decreased from Q_1 (11.13) to Q_2 (10.22) and then increased for Q_3 (23.47) for 1D-CNN. We observe a similar trend for DNN as well. The 2D-CNN produced the best result on this metric.

B. Comparison

Pyrkov *et al.* [11] proposed a deep learning architecture for analyzing the physical activity data that is based on a one dimensional convolutional neural network (CNN) architecture. We implemented a 2-dimensional convolutional neural network (2D-CNN, our own architecture and implementation) and a deep neural network (DNN) [10] to estimate biological age. These models (DNN, 1D-CNN, and 2D-CNN) are used as comparative results. The results on mortality modeling using the Cox model and KM curves have shown the performance of the proposed 3D-CNN in comparison with DNN and 1D CNN by Pyrkov *et al.* [11]. See Tables II and Fig. 3. The results showed that the proposed 2D-CNN, and 3D-CNN methods generally outperformed the 1D CNN, or the DNN. Since the deep learning methods were trained to minimize the mean square error between the estimated and the original chronological age, we compare the methods based on their performance in CA estimation.

TABLE IV
RESULTS OF THE DEEP LEARNING AGE PREDICTION METHODS.

	MAE	RMSE	CORR	epoch
1D-CNN[11]	15.49	18.81	0.45	500
DNN	15.92	18.38	0.45	100
2D-CNN	14.19	**17.48**	**0.48**	50
3D-CNN	**14.08**	19.40	**0.48**	**10**

Table IV shows the mean absolute error (MAE), root mean square (RMSE), and correlation (CORR) for all the deep learning methods discussed. We observe that 3D-CNN has the lowest MAE (14.08) and best correlation (ρ=0.48). 2D-CNN has a correlation of 0.48 and MAE of 14.19 respectively). 3D-CNN required fewer epochs (10 compared with 50 (2D-CNN), 100 (DNN), and 500 (1D-CNN)) to converge.

V. CONCLUSION

In this work, we studied biological age estimation using human locomotor activity. We applied two deep learning based frameworks to estimate biological age (BA) using 2D-CNN and 3D-CNN. We established that these models can be used to exploit patterns in human locomotor physical activity to estimate biological age. The paper used different measures to compare performance in age estimation, including the traditional methods (namely, MAE, RMSE, and correlation). To evaluate performance in BA estimation, we considered the relation with known health indices (SBSI), in addition to traditional mortality modeling using Cox PH, χ^2-distance from the log-rank test, and KM curves. Considering different methods for quantifying the performance of the estimated BA, the 2D-CNN and 3D-CNN have the overall best results over 1D methods.

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