Identification of Personality Based on the Sphenoid Sinus Structure Using Machine Learning

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Abstract
The aim of our study is to develop a new, simple, and effective method for identification of personality based on the characteristics of the sphenoid sinus structure, using machine learning for subsequent implementation into routine medical practice in Ukraine. The study involved 200 multislice computed tomography (MSCT) scans of individuals of various genders and ages. During the study, we obtained results with an accuracy exceeding 70%.

Keywords 1
Identification of personality, multislice computed tomography, deep learning

1. Introduction

The full-scale Russian invasion has had a profound impact on Ukrainian society, presenting numerous challenges and causing immense suffering for millions of Ukrainians [1]. War crimes continue to be committed in the occupied territories, and the discovery of unmarked mass graves in various locations is deeply disturbing [2]. Establishing the identities of those who have fallen victim to Russian aggression is a crucial task at hand [3]. Personal identification is particularly important during times of war, although no method can guarantee a 100% reliable result [1]. Fingerprints [4] are commonly used, but in wartime, bodies may be burned or damaged, rendering fingerprint identification impossible. Autolysis, the natural decomposition of bodies over time, can also hinder the use of fingerprints or retinas for identification. DNA identification [5] is a promising and accurate method, but obtaining DNA samples from deceased individuals' relatives is not always feasible. While global databases exist for DNA identification, Ukraine lacks such a resource. Additionally, DNA collection requires significant time, effort, and invasiveness, making implementation challenging. The proposed study aims to utilize existing data for collection and analysis. Bones are considered the most stable structures for the analysis [6], and studying cranial bones, particularly the sphenoid sinus, shows promise. Computed tomography [7] (CT) scans can be used to examine the sphenoid sinus, as it is less likely to be damaged due to its deep location within the skull. Medical image segmentation [8], a process that identifies pixels of interest in medical images, can be employed to process CT images. Convolutional neural networks (CNNs), particularly the U-Net architecture, have proven effective for medical image segmentation. CNNs offer promising potential for automated diagnostic methods and personal identification with help of deep learning [9]. While there are existing segmentation platforms, a clear workflow and necessary functions for easy

configuration are currently lacking. Therefore, CNNs present a promising approach for processing medical CT images in the context of personal identification [10].

To date, there is a relatively small amount of scientific works dedicated to the identification of personality. This can be attributed to several factors, including the complexity of developing algorithms for personality's identification, the intricate process of pre-processing medical images, and the limited size of databases used for solving this task. All of these factors can create additional barriers to the implementation of methods described by various authors into medical practice, and it appears to be a reason why these methods have not been realized.

Although the proposed method offers numerous advantages associated with accurate personal identification, there are certain aspects that may pose challenges in achieving the intended goal. The first drawback could be the lack of results from CT scans. Despite the availability of extensive X-ray data covering a significant portion of Ukraine's population, approximately 30% of individuals have not undergone CT scans according to various sources. Consequently, alternative methods should be considered for identifying this group of people.

The second drawback could be the age factor, specifically concerning children. In our proposed method, similar to other studies, children were not included in the groups of individuals whose identity was intended to be identified. Considering the age-related variability of the maxillary sinus and the infrequent use of CT scans in children due to limited indications, personal identification in pediatric age groups can be challenging.

The aim of our study is to develop a new, simple, and effective method for identification of personality based on the characteristics of the sphenoid sinus structure, using deep learning for subsequent implementation into routine medical practice in Ukraine.

2. Material and Methods

The study involved analyzing CT scans of 200 individuals of various ages and genders. Segmentation, which is the process of identifying and analyzing specific structures within medical images, is a challenging task in medical image analysis. It provides valuable information about the shape and characteristics of organs and tissues. To assist with the segmentation process, a Standard Operating Procedure (SOP) was developed specifically for creating 3D models of the sphenoidal sinus from CT images.

The procedure consists of three main steps. Firstly, the CT images are prepared, converted, and masks are created. Secondly, models for the experiment are constructed using the popular Tensorflow library. Finally, the experiment is conducted, and the results are compared. The RadiAnt software will be used to select tomographic images from a Toshiba Aquilion CT [11] scanner, which can collect data from four slices simultaneously with a high level of performance. This scanner provides high-resolution multi-slice scanning with wide bandwidth.

The data used in this study will be obtained from 2000 individuals who have undergone CT. The data was be used in accordance with the existing contract between Kharkiv Institute of Emergency Medicine and the Kharkiv National Medical University. Each scan contains patient identity data, such as name, age, sex, date of birth, occupation, referring physician, date of examination, and unique DICOM identifiers [12].

These methods require large and accurately labeled training datasets, which are created by medical experts. Therefore, it is crucial to choose an appropriate image annotation tool. The Labelme tool was selected for its high accuracy and ability to output annotations in JSON format [13].

All individuals whose CT images are included in this research have voluntarily given informed consent to participate.

The network was trained end-to-end using binary cross-entropy loss function, Adam optimizer, learning rate 0.01, and Exponential Linear Unit (ELU) as an activation function. The size of input image is 128x128x3 and its mask is 128x128. Epochs, batches sizes and validation split were customized utilizing remote server with the following configuration CPU: 2x AMD EPYC 7413 24-Core CPU, 180W, 2.65GHz, 128MB, - L3 Cache, DDR4-3200, Turbo Core max. 3.60GHz, GPU: 4x NVIDIA Tesla A100 (NVLink), 80GB, RAM: DDR4-3200512GB.
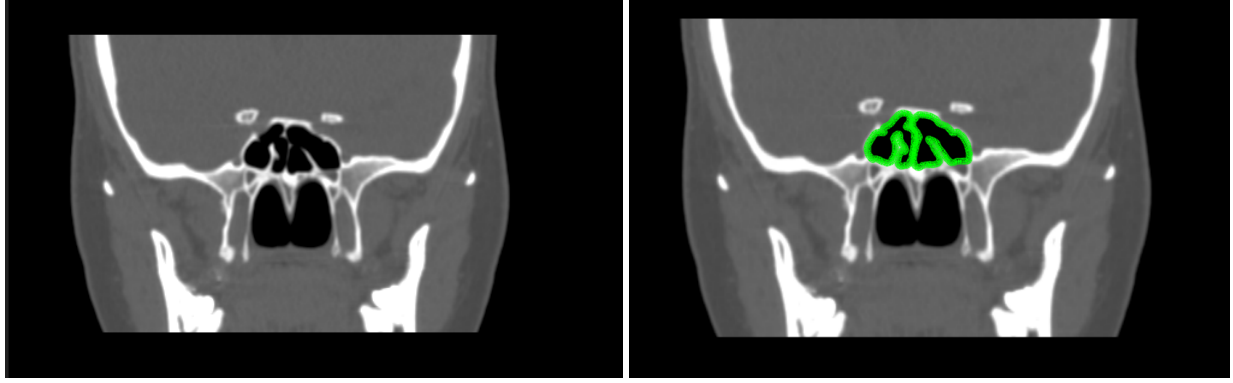
Figure 1: MSCT slice of the Sphenoid sinus and its mask

3. Results

All the results of the experiment using U-Net model with different parameters: batch size, number of epochs, validation split and with IoU (Intersection over Union) metric value are in the Table 1.

Table 1
Results of the experiment

Model name	Batch size	Number of epochs	Validation split	IoU
modelA_5_10_10	5	10	0.10	0.637
modelA_5_10_33	5	10	0.33	0.617
modelA_5_15_10	5	15	0.10	0.737
modelA_5_15_33	5	15	0.33	0.658
modelB_10_10_10	10	10	0.10	0.512
modelB_10_10_33	10	10	0.33	0.441
modelB_10_15_10	10	15	0.10	0.653
modelB_10_15_33	10	15	0.33	0.705
modelC_20_10_10	20	10	0.10	0.613

The U-Net model is composed of convolutional and transposed convolutional layers. It has the following structure: The input data, representing an image, is passed through an Input layer. The pixel values of the image are normalized using a Lambda layer, where each pixel value is divided by 255 to obtain normalized values ranging from 0 to 1.

Next, the input data is processed through a Conv2D layer with 32 filters. This layer utilizes the ELU (Exponential Linear Unit) activation function, which takes into account negative values when activating neurons.

The layer weights are initialized using the "he_normal" method, promoting more effective model training. To prevent overfitting, a Dropout layer is applied, randomly disabling a certain percentage of neurons (in this case, 10% of neurons with a dropout rate of 0.1). This helps reduce correlation among neurons and enhance the model's generalization ability. Following the Dropout layer, another Conv2D layer with 32 filters and the ELU activation function is applied. This additional convolutional layer aids in extracting higher-level features from the image. Subsequently, a MaxPooling2D layer is used to perform pooling operations, reducing the data dimensionality by removing redundant information and focusing on the most important image features. Similar operations are repeated for subsequent levels (c2, c3, c4, c5), where additional convolutional layers with an increased number of filters are applied.
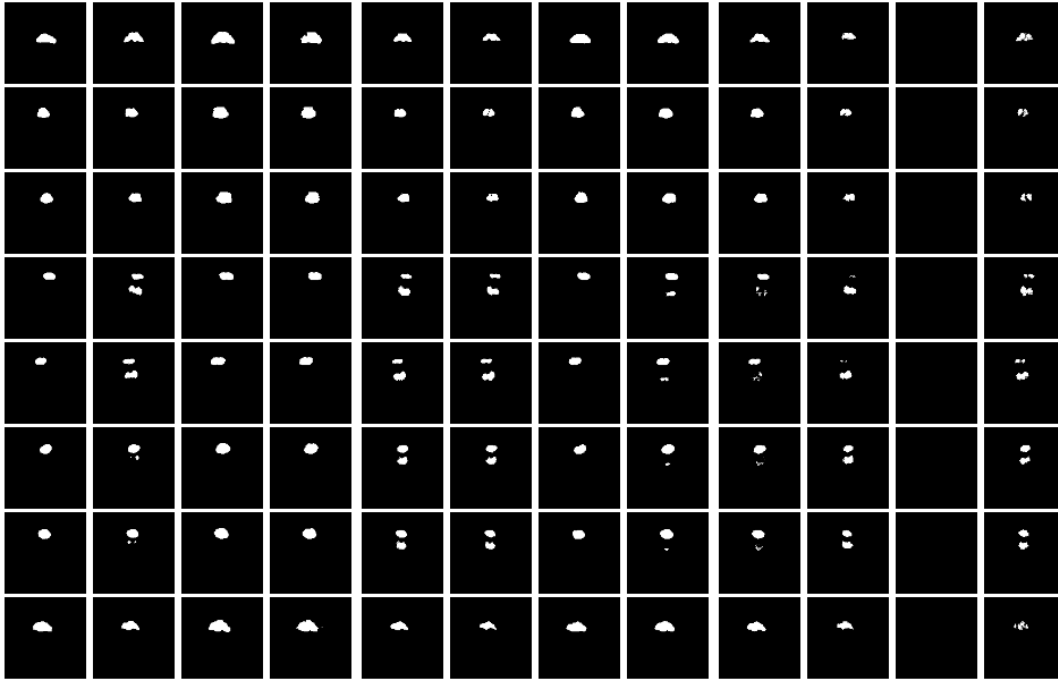
Figure 2: An example of the personality identification using various models

This allows the model to extract increasingly abstract and complex features from the image. After the final convolutional layer, c5, the decoding process begins. To increase the data size, a Conv2DTranspose layer is utilized, performing the reverse operation of convolution and expanding the spatial dimensions of the data. The output of the Conv2DTranspose layer is then concatenated with the corresponding layer (c4) using the concatenate layer. This allows for preserving spatial dependencies between features and connecting them for further decoding. Additional convolutional layers, c6, are then applied for decoding and feature extraction at different levels. The decoding operations are repeated for subsequent levels (c7, c8, c9), gradually reducing the number of filters in the convolutional layers. This enables the model to progressively restore the original data size and refine the results. Finally, a Conv2D layer with a single filter and the sigmoid activation function is used. This layer is employed to obtain the final segmented image, where each pixel takes a value from 0 to 1, representing the probability of belonging to a specific class. The model is compiled using the Adam optimizer and binary_crossentropy loss function. The Adam optimizer efficiently updates the model weights by minimizing the loss function. The binary_crossentropy loss function is employed for binary classification tasks, where the goal is to separate image pixels into two classes: background and object.

4. Discussion

Thus, we have developed a new approach to personal identity identification using machine learning. It is worth noting that the proposed method differs from similar approaches and offers several advantages.

Currently, one of the most promising research studies is the work of Wen H. et al. [14] and Dong et al. [15], The studies were conducted on a large database of subjects (732 individuals). However, it is worth noting the relatively uneven distribution between the training group and the target group (600 and 123 individuals, respectively). Furthermore, in the course of this research, all patients were categorized into ranks (from 1 to 5) based on the "complexity" of their sphenoid sinus structures. Our own experiment demonstrates that it is most challenging to identify sinuses with smaller volumes and simple configurations (lacking additional septa, bays, and cellular structure). In our opinion, such categorization could potentially distort the results.

Another negative factor in both of the presented works is the requirement for extensive pre-processing in the identification process. Given the substantial number of individuals whose identities

need to be verified in Ukraine and the shortage of medical and technical personnel capable of serving as experts for this task, the process of implementing a personal identity identification protocol into the country's healthcare system could consume a significant amount of time.

In the study presented by Soudhin et al [16], it is notable that a small number of subjects were included in the experiment (72 individuals). Thirteen of these subjects underwent CT scans twice. The inclusion of such individuals in both the target and training groups, given the relatively small number of subjects in each group, can intentionally increase the percentage of positive results.

A common drawback of other studies known to date is the limited number of subjects in the database [17, 18].

During the experiment conducted on a large dataset of 200 individuals, results were obtained that can aid in the identification of a person, whether alive or deceased. The proposed method is straightforward, and its implementation only requires the assessment of a medical expert to evaluate the quality of image labeling in the training group. This method is versatile, as it can be easily integrated into the healthcare system of any country, not limited to Ukraine. The method holds promise, as it has significant potential for improving the accuracy of identity determination. For instance, while it has been developed for 2D CT scans for now, there are plans to extend the analysis to 3D images in the future. Furthermore, the study aims to include anatomical structures (such as the optic nerve canal, internal carotid artery canal, and optic nerve canal) known for their notable variability, which has not been previously included in any similar studies [19] or even studies in an other medical fields [20, 21]. Using 3D segmentation is more rational, considering the fact that three-dimensional imaging most accurately captures the anatomical features of the area under investigation [22]. It is known that automatic and semi-automatic methods can be used for image annotation. Most authors prefer automatic research [23] methods without involving medical professionals in the annotation process. However, given the complexity and diversity of the sinus structure, physician oversight may be necessary and could enhance the effectiveness of the study.

5. Conclusions

In conclusion, our study has led to the development of a straightforward, informative, and readily applicable method for personal identity identification. This method can be seamlessly integrated into medical practice and utilized for identifying individuals, both living and deceased, not only in Ukraine but also in any country around the world. Furthermore, the inclusion of physician oversight in the annotation process adds an extra layer of reliability to our methodology.

The implications of our findings are significant, offering potential applications in various fields such as forensics, anthropology, and medical research. The simplicity and efficiency of our method make it accessible for implementation in diverse healthcare settings, promising a practical solution for personal identification challenges. As our research continues to advance, we anticipate further refinements and applications, ultimately contributing to the enhancement of identification techniques on a global scale
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6. References

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