

A Method for Comparing CT Images of the Head and its Application to Identify Examinations Belonging to the Same Person

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Abstract. The goal is to solve the problem of automatic grouping of head computed tomography (CT) examinations belonging to the same individual. This enables longitudinal analysis in the absence of personal identifiers, detection of identification errors in medical databases, and matching antemortem and postmortem CT studies of the same person based on anatomical features. A combination of an existing head CT image comparison method and hierarchical clustering algorithms is developed. Two public domain head CT datasets (CQ500 and WORC HeadNeck) are used for the study. Application of the presented method to publicly available anonymized datasets made it possible for the first time to objectively determine the number of unique patients, which is not the number of presented examinations. Five clusters of study samples were found in the CQ500 dataset, revealing that five persons have provided more than a single study therein. A private dataset of 2623 head CT examinations belonging to 1091 unique patients is used for validation. Verification on the private dataset has confirmed the effectiveness of the method: on the test set (328 patients, 793 studies), clustering accuracy is 96.5% (ARI = 0.96, AMI = 0.97). In an additional identification experiment, our method achieved Rank-1 accuracy of 90.3%, which is 18.3% higher than that of Heinrich method.

Keywords: computed tomography · forensic medicine · time series · longitudinal studies · identification · clustering · database quality control.

1 Introduction

Modern radiological databases contain large number of examinations of patients and are all along being replenished with new ones. Unfortunately, these databases are prone and actually do contain errors in patients’ identifiers. Two typical cases occur: an examined person is added to the database with novel unique ID although he/she already has got one before; a person’s examination data is linked

to other person ID. This hinders conducting longitudinal analysis, i.e. studying the dynamics of changes in a patient’s condition (e.g., disease progression, treatment efficacy assessment, tracking structural changes in the brain). Thus the method of detection that two CT images of an organ or a body part (head in this study) do belong to same individual is actual.

Person identification using computed tomography (CT) images is of paramount importance in forensic science, serving as a critical tool for identifying victims in criminal investigations and mass disasters [1]. Traditional forensic analysis relies heavily on expert interpretation, which can be influenced by human factors such as fatigue, subjectivity, and emotional involvement [2]. CT scanning provides three-dimensional data capable of revealing unique anatomical features, making them suitable for identification purposes [3,4]. Furthermore, CT allows simultaneous examination of both soft tissues and bone structures, offering more complete information compared to traditional methods [5,6]. The accuracy and reliability of CT-based identification have made it a useful tool in modern forensic practice, complementing classical approaches [7,8]. Among the anatomical structures most commonly used for identification, the dentition (dental status) [9] and frontal sinuses [10] stand out, possessing a high degree of individual variability. Algorithms using modern artificial intelligence (AI) methods enable the analysis of anatomical features without human intervention [4,11]. Convolutional neural networks (CNNs) have become effective tools capable of automatically determining cephalometric landmarks on CT scans, significantly reducing processing time [1].

The goal of this work is to solve the problem of automatic grouping of head CT studies belonging to the same patient. This enables the restoration of time series for longitudinal analysis in the absence of personal identifiers, detection identifier errors in medical databases, and matching antemortem and postmortem CT studies of the same person. For this purpose, a combination of an existing head CT image comparison method [17] and hierarchical clustering algorithms is proposed.

In publicly available medical datasets all studies are de-identified: personal identifiers (full name, date of birth, medical record number) are removed in order to exclude the possibility of direct patient identification. This is a requirement of ethics committees and personal data protection legislation [12]. Public databases lack labels indicating that several studies belong to the same patient, which prevents the automatic formation of time series. In the literature, a solution to the problem of restoring such links between de-identified CT studies based solely on the anatomical information contained in the images has not yet been described.

The proposed approach was tested on two public datasets of CT studies containing no private data: “CQ500” [18] and “WORC HeadNeck” [20]. The approach demonstrated the ability to automatically group studies. In the “CQ500” dataset, five clusters of more than one examination were found, showing that five persons contributed with more than one examination. For the “WORC HeadNeck” dataset it was confirmed that each study belongs to a separate patient.

Verification on a private dataset (2623 studies, 1091 patients) showed high effectiveness of the approach: 2555 out of 2623 studies were correctly grouped (accuracy 97.4%).

The proposed approach can be applied to head CT study datasets in forensic medical examination tasks, as well as for detecting errors and duplication of identifiers in radiological information databases (e.g., when one patient is erroneously assigned several IDs, or different patients are combined under one ID).

2 Materials

Three datasets involved in the study are briefly described in this section.

2.1 Publicly Available Datasets

A search was conducted for open datasets containing head CT images. Four datasets were identified, each with its own specific characteristics, as shown in Table 1.

Table 1. Public head CT datasets and their characteristics

Dataset name	Number of studies	Characteristics
CQ500 [18]	491	Patients with intracranial hemorrhage and head trauma
Expanded Brain CT Dataset [19]	800	Patients with intracranial hemorrhage
WORC HeadNeck [20]	136	Patients with malignant head and neck tumors
The New Mexico Decedent Image Database [21]	15000	Postmortem studies with varying degrees of tissue preservation

2.2 Private Verification Dataset

For threshold tuning and method verification, a retrospective private dataset was formed consisting of 2623 head CT studies belonging to 1091 unique patients (age > 30 years). The distribution of the number of studies per patient is as follows: 1 study – 272 patients (24.9%), 2 studies – 291 (26.7%), 3 studies – 380 (34.8%), 4 studies – 111 (10.2%), and 5 studies – 37 (3.4%). The total number of patients was 1091.

The studies were performed between 2022 and 2025 using CT scanners from Toshiba, Siemens, GE, Canon, and Philips. All images contain the necessary anatomical landmarks (eyeballs, upper cervical vertebrae C1). Some studies contain motion artifacts.

Train/test split. The dataset was randomly split on a patient basis into training (70%) and test (30%) sets. The training set included 763 patients (1,673,535 pairwise comparisons, of which 1,730 were genuine pairs). The test set included 328 patients (314,028 comparisons, of which 737 were genuine pairs). The test set comprised 793 CT studies.

Anonymization and validation labels. All images underwent an anonymization procedure: removal of all personal data (full name, date of birth, medical record number). However, de-identified surrogate IDs (random unique codes assigned to each patient) were retained in the dataset. These codes contain no personal information and do not allow the real identity of the subject to be established, but they enable objective verification of clustering quality.

2.3 Exclusion Criteria

For the application of method [17], a CT study must satisfy specific technical and anatomical requirements. A study was excluded from further processing if one or more of the following criteria were met, as summarized in Table 2.

Table 2. Exclusion criteria for CT studies

Category	Exclusion criterion
Anatomical completeness	Absence of eyeballs in the scanning field
Anatomical completeness	Absence of the upper cervical vertebra (C1) in the scanning field
Anatomical completeness	Severe soft tissue decomposition hindering eyeball localization
Integrity	Violation of the integrity of the skull bone structures
Spatial resolution	Axial slice thickness > 1.25 mm
Artifacts	Presence of motion artifacts (Figure 1c)
Artifacts	Presence of helical artifacts (Figure 1d)

Based on the exclusion criteria, two datasets were deemed unsuitable for further analysis: The New Mexico Decedent Image Database and Expanded Brain CT Dataset.

The New Mexico Decedent Image Database was excluded for the following reasons:

- Many images exhibit severe soft tissue decomposition or complete absence thereof;
- Studies obtained after gunshot wounds or road traffic accidents have violated skull integrity.

An example of an image with violated skull integrity is shown in Figure 1b. **Expanded Brain CT Dataset** was excluded due to the defacing procedure. Defacing (from the English “face de-identification”) is used to anonymize medical images by purposefully removing or distorting facial features, preventing visual or automatic person recognition. An example of defacing via insertion of foreign bodies is shown in Figure 1a.

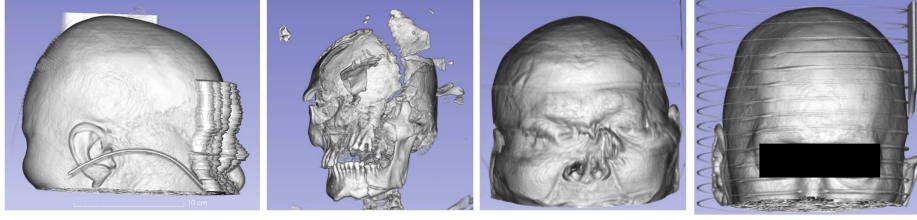


Fig. 1. Examples of CT images falling under the exclusion criteria of the applied method. (a) Defacing procedure distorting soft and bone tissues of the facial area; (b) Violation of skull integrity; (c) Motion artifacts; (d) Helical artifacts.

2.4 Ethical Considerations and Data Confidentiality

All datasets used in this study underwent an anonymization procedure.

- **Public datasets (CQ500 [18], WORC HeadNeck [20])** were originally de-identified by their authors.
- **Private verification dataset** was formed retrospectively from clinical data. All images underwent complete anonymization: personal identifiers were removed. However, de-identified surrogate IDs (random unique codes assigned to each patient) were retained in the dataset to enable objective verification of clustering quality.

Data visualization. In this article, for all frontal (en face) CT reconstructions, the eye region is masked with a rectangular overlay. No masking is applied to sagittal or axial views, as these do not contain directly identifiable facial features. This method of ensuring confidentiality complies with current recommendations in medical photography [14,15].

As discussed by Pigolkin et al. [13], the concept of personal identification in forensic medicine presupposes the existence of a known reference for comparison. In the absence of any identifying information about a sample, the task cannot be considered identification in the legal sense. Therefore, our work addresses grouping of anonymized studies rather than personal identification, which is ethically and legally distinct.

3 Methods

3.1 Automatic Matching Methods

Automatic matching methods may include the following approaches or their combinations. Some of them are listed below:

- Analysis of craniofacial points [23];
- Morphology and position of teeth, presence of dental implants and fillings [9];

- Analysis of cranial sutures [24];
- Morphology of the frontal sinus [10];
- Maxillary sinuses [25];
- Registration based on 3D-2D silhouettes [16].

In this work, the method [17] is used for automatic matching. This method creates a feature vector representation for each skull study. The pairwise comparison function based on feature vectors allows integral assessment of the degree of difference between skulls.

3.2 Authentication, Identification, and Grouping Tasks

In forensic practice using head CT studies, three distinct tasks can be distinguished: authentication (verification), identification, and grouping. They differ in input data, objectives, and results. Their clear separation is important for correct experimental design and interpretation of results.

1. Authentication (Verification)

- **Input:** Two CT studies: one belonging to a known person, the second presumably to the same person.
- **Task:** Confirm or refute that both studies belong to the same person.
- **Result:** “Yes” (same person) or “No” (different persons).

2. Identification

- **Input:** (1) A single CT study of an unknown person (corpse or patient unconscious and without documents); (2) A collection of antemortem CT studies of known persons with identifiers.
- **Task:** Determine which known person the unknown study belongs to.
- **Result:** Personal identifier (e.g., “CT belongs to Ivanov I.I.”) or a conclusion “person not identified”.

3. Grouping

- **Input:** A set of anonymized CT studies without patient identifiers.
- **Task:** Partition all studies into groups, within which the studies belong to the same person.
- **Result:** A list of groups (clusters), each corresponding to a unique individual.

The basic operation for all three tasks is the assessment of the degree of similarity between two head CT studies. In the authentication task, a single such comparison (known vs. test) is sufficient. In the identification task, sequential comparison of the unknown study with each element of the known database is required. In the grouping task, addressed in this work, it is necessary to perform pairwise comparison of all studies with each other, which allows building a distance matrix and applying clustering algorithms.

Below are listed methods for automatic matching used to assess the similarity of two head CT studies.

3.3 Modification of the Comparison Function for the Grouping Task

In the original implementation, method [17] is not commutative: $sim_{orig}(A, B) \neq sim_{orig}(B, A)$. For authentication and identification tasks, where the comparison order is fixed, this is acceptable. However, for grouping, which requires pairwise comparison of all studies with each other, a symmetric function is necessary.

Since we are interested in the maximum similarity estimate between two studies (if the algorithm shows high similarity in at least one comparison order, this supports belonging to the same person), we define the symmetric similarity measure as:

$$sim_{sym}(A, B) = \max(sim_{orig}(A, B), sim_{orig}(B, A)).$$

This ensures commutativity: $sim_{sym}(A, B) = sim_{sym}(B, A)$.

Transition from similarity to distance. Hierarchical clustering algorithms operate on a distance matrix, where a smaller value corresponds to greater similarity. We transform the obtained symmetric similarity measure into distance:

$$d(A, B) = 1 - sim_{sym}(A, B). \quad (1)$$

Given that the original values are normalized to the interval $[0, 1]$, the function $d(A, B)$ takes values in $[0, 1]$, is symmetric, and a smaller value means greater similarity. The resulting distance matrix is used for hierarchical clustering.

3.4 Solution to the Grouping Problem

The grouping of processed data consists of 4 main stages:

1. **Creation of a feature vector** describing the set of anatomical features of the CT image [17].
2. **Computation of the pairwise comparison matrix** using the symmetric distance $d(\cdot, \cdot)$ defined in (1).
3. **Analysis of the pairwise comparison matrix:** Systematic pairwise examination of all studies. Feature extraction and matching identify corresponding anatomical characteristics across all studies.
4. **Clustering result:** Partitioning of studies into groups, where each group represents studies belonging to one patient.

3.5 Mathematical Description of the Grouping Process

The input data for analysis is a set B of computed tomography (CT) studies of the head, consisting of N images. The number of patients is initially unknown and equals M . Each patient p_j (where $j \in [1, M]$) has k_j studies, $1 \leq k_j \leq N$. In public datasets, patient identifiers are not attached to the studies.

- Each study $b_i \in B$, $i \in [1, N]$

- Each patient p_j (where $j \in [1, M]$) has k_j studies: thus P_j is the set of studies of patient p_j
- $B = \bigcup P_j, 1 \leq j \leq M$

Step 1: Feature vector formation. For each image, a feature vector characterizing the anatomical region of the skull is formed:

$$F = \{x_i \in \mathbb{R}^k\} = \{f(b_i) \in \mathbb{R}^k\}, \quad i = 1, \dots, N$$

where x_i is the feature vector of the image, $x_i = f(b_i)$ is the procedure for computing the feature vector from the image [17], and k is the dimensionality of the feature vector.

Step 2: Computation of the pairwise comparison matrix $D \in \mathbb{R}^{N \times N}$:

$$D_{ij} = d(x_i, x_j),$$

where d is the function for comparing two feature vectors (1).

Step 3: Threshold-based clustering. To create an adjacency matrix A from the pairwise distance matrix D , we define the threshold function $\tau : \mathbb{R} \rightarrow \{0, 1\}$:

$$A_{ij} = \tau(D_{ij}) = \begin{cases} 1, & \text{if } D_{ij} \leq \theta \\ 0, & \text{otherwise} \end{cases}$$

where $\theta \in \mathbb{R}$ is the threshold value. That is, two studies are grouped only if their mutual distance does not exceed a predetermined value θ . The threshold θ determines the decision rule of whether two feature vectors belong to the same patient. Its value is determined experimentally.

Step 4: Construction of the adjacency graph from the binary adjacency matrix A . We define an undirected graph $G = (V, E)$ where:

- $V = \{1, 2, \dots, n\}$ are vertices with feature vectors
- E are vertices (i, j) are connected only if $A_{ij} = 1$

Step 5: Determination of the partition into unique classes. Let P denote the partition of V into connected components of G . Each connected component $P_k \subseteq V$ represents a cluster of biometric data of an individual person, satisfying the conditions:

- **Connectivity of vertices within each cluster:** $\forall i, j \in P_k$, there exists a path between vertices i and j
- **Absence of connections between clusters:** $\forall i \in P_k, j \notin P_k, D_{ij} > \theta$

The described algorithm partitions similar biometric vectors into separate clusters, each corresponding to a unique individual.

Threshold determination. The clustering threshold θ was determined on the training set as the minimum distance among “impostor” pairs (studies of different patients):

$$\theta = \min(impostor) - \varepsilon, \quad \text{where } \varepsilon = 10^{-6}.$$

This approach guarantees the absence of false merging of impostor patients (FPR = 0) on the training set.

3.6 Clustering Quality Metrics

The contingency matrix C of size $R \times C$ is defined as:

$$C_{rc} = |\{i : \text{true_labels}[i] = r \wedge \text{cluster_labels}[i] = c\}|$$

where R is the number of true patients and C is the number of obtained clusters. The Hungarian algorithm finds the optimal matching between true patients and clusters by maximizing the sum of diagonal elements of the permuted matrix.

Based on the contingency matrix, the following metrics are computed.

Adjusted Rand Index (ARI) Let $n_{i\cdot} = \sum_c n_{ic}$ and $n_{\cdot j} = \sum_r n_{rj}$. The Rand Index (RI) is defined as:

$$RI = \frac{\sum_{r,c} \binom{n_{rc}}{2}}{\binom{N}{2}}, \quad \binom{x}{2} = \frac{x(x-1)}{2}.$$

The Adjusted Rand Index corrects RI for chance:

$$ARI = \frac{\sum_{r,c} \binom{n_{rc}}{2} - \frac{(\sum_r \binom{n_{r\cdot}}{2})(\sum_c \binom{n_{\cdot c}}{2})}{\binom{N}{2}}}{\frac{1}{2} \left[\sum_r \binom{n_{r\cdot}}{2} + \sum_c \binom{n_{\cdot c}}{2} \right] - \frac{(\sum_r \binom{n_{r\cdot}}{2})(\sum_c \binom{n_{\cdot c}}{2})}{\binom{N}{2}}} \quad (2)$$

with $ARI \in [-1, 1]$, where 1 indicates perfect agreement, 0 indicates random partitioning, and negative values indicate agreement worse than random.

Adjusted Mutual Information (AMI) The Mutual Information (MI) between two partitions U and V is:

$$MI(U, V) = \sum_{r=1}^R \sum_{c=1}^C \frac{n_{rc}}{N} \ln \left(\frac{N \cdot n_{rc}}{n_{r\cdot} \cdot n_{\cdot c}} \right).$$

The Adjusted Mutual Information corrects MI for chance:

$$AMI(U, V) = \frac{MI(U, V) - \mathbb{E}[MI]}{\max(MI(U, V)) - \mathbb{E}[MI]} \quad (3)$$

with $AMI \in [0, 1]$, where 1 indicates perfect agreement.

Clustering Accuracy (Matching Accuracy) After obtaining the optimal cluster-to-patient correspondence using the Hungarian algorithm, the clustering accuracy is defined as:

$$\text{Accuracy} = \frac{1}{N} \sum_{k=1}^K n_{i_k, j_k} \quad (4)$$

where $\sum_{k=1}^K n_{i_k, j_k}$ is the sum of elements of the contingency matrix selected by the Hungarian algorithm (optimal matching), and N is the total number of studies.

4 Results

4.1 Private Dataset

Clustering Performance on the Test Set On the test set (793 studies, 328 patients), hierarchical clustering with the threshold $\theta = 0.2753$ produced **356 clusters** (vs. 328 true patients). The quality metrics showed almost perfect agreement: ARI = 0.9619 (Equation 2), AMI = 0.9660 (Equation 3), and clustering accuracy = 96.47% (765/793) (Equation 4).

The excess of 28 clusters indicates that 28 patients were “fragmented” into two or more clusters — a direct consequence of the conservative threshold $\theta = \min(impostor) - \varepsilon$, which guarantees FPR = 0. In forensic applications, this strategy is preferable: false merging of different individuals is unacceptable, whereas over-partitioning can be corrected by expert analysis. Despite the strict threshold, ARI and AMI values exceed 0.96, confirming almost ideal correspondence with the true patient distribution.

4.2 CQ500 Dataset

The CQ500 dataset contains 491 images. After applying the exclusion criteria, 171 studies were selected. Feature vectors were generated for these studies, and the pairwise distance matrix D was computed. As a result, **5 patient groups (clusters)** were found: one cluster containing 4 studies and four clusters containing 2 studies each.

The cluster containing 4 studies is shown in Figure 2. Visualization was performed using the 3D Slicer software [22]. Visual analysis of studies assigned to the same group reveals consistent matches of individual anatomical features, including the morphological pattern of the frontal sinuses and the contours of the facial and cranial vaults. This confirms the correctness of the automatic grouping. The use of dental characteristics (tooth morphology) was difficult because the dentition area is often outside the scanning field.

4.3 WORC HeadNeck Dataset

The WORC HeadNeck dataset contains CT studies of 136 patients with malignant head and neck tumors. Of these, 16 studies did not satisfy the inclusion criteria and were excluded from analysis. Thus, 120 studies were included in the analysis. As a result of grouping, **120 clusters** were obtained, each containing exactly one study. This confirms the information provided in the dataset description that each patient has only one CT study.

4.4 Summary of Results

The overall results of processing the datasets are presented in Table 3.

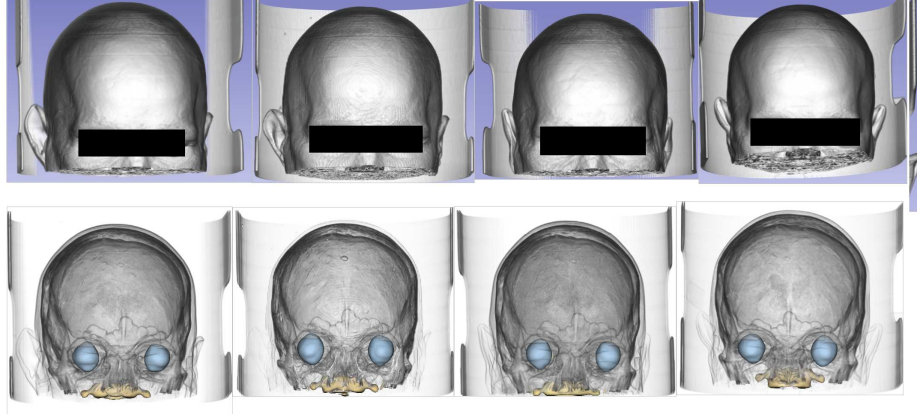


Fig. 2. Visualization of four images (00029, 00281, 00198, and 00483) belonging to the same group. First row shows volume rendering of superficial head structures. Second row presents semi-transparent volume rendering showing the frontal sinuses with segmentation results of the eyeballs (blue) and the upper cervical vertebra (yellow).

Table 3. Summary of grouping results on the test set

Dataset name	Total studies	Analyzed studies	Ground truth patients	Obtained clusters
Private (test set)	793	793	328	356
CQ500	491	171	unknown	164
WORC HeadNeck	136	120	120	120

4.5 Additional Experiment: Identification Task and Recognition Performance

To assess the generalization capability of our method, we evaluated its performance in two additional tasks: recognition (genuine vs. impostor pair classification) and identification (Rank- k accuracy).

Recognition Performance On the test set (793 studies, 328 patients), the threshold $\theta = 0.2753$ yielded the following confusion matrix: **681 true positives, 56 false negatives, 0 false positives, and 313,291 true negatives**. Consequently, Precision = 1.0, Recall = 92.4%, Specificity = 1.0, Accuracy = 99.98%, and F1-score = 0.96.

The absence of false positives (FPR = 0) confirms that no different patients were erroneously merged, which is essential for forensic applications. Figure 3 presents the distance distributions for genuine and impostor pairs (training and test sets) as well as the ROC curve with AUC = 0.989.

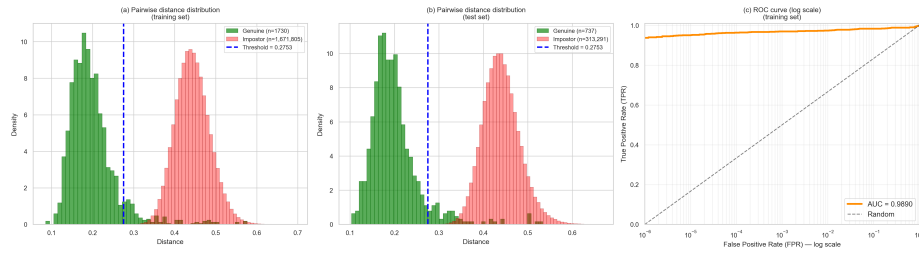


Fig. 3. Results of the test set analysis: (a) Distribution of distances for genuine and impostor pairs (training set); (b) Distribution of distances for genuine and impostor pairs (test set); (c) ROC curve (log scale) on the training set (AUC = 0.989).

4.6 Comparison with Existing Head CT Image Identification Methods

Our method, developed for grouping, was additionally evaluated in the identification task. With a gallery of all test studies (793 studies, self-match excluded), a Rank-1 accuracy of 90.3% was achieved with minimal increase with increasing rank (Rank-10 = 90.4%).

Comparison with Heinrich [25]. The most relevant for comparison is the method of Heinrich [25], which uses a single CT slice of the maxillary sinus for person identification. In Heinrich’s study, based on 722 patients, Rank-1 accuracy of 72%, Rank-5 of 80%, and Rank-10 of 87% were achieved. Thus, our method outperforms Heinrich by 18.3% in Rank-1 accuracy (90.3% vs 72%).

Moreover, in our method, the increase in accuracy from Rank-1 to Rank-10 is only 0.1% (90.3% → 90.4%), while in Heinrich this increase reaches 15% (72%

→ 87%). This difference is explained by the fact that we did not exclude most studies with motion artifacts to approximate real-world conditions, whereas in Heinrich’s work such studies were likely excluded.

The obtained results demonstrate that our method not only solves the clustering task but also surpasses specialized identification methods when working with head CT, while maintaining high robustness to artifacts and providing a zero false positive rate ($\text{FPR} = 0$).

5 Conclusion

The method successfully processes studies of patients with trauma, skull fractures, and intracranial hemorrhages. For the WORC HeadNeck dataset, the uniqueness of all processed studies was confirmed. Each one belongs to a different individual (120 clusters with one study each). For the CQ500 dataset, 5 groups of studies corresponding to the same subject were identified (i.e., 5 patients have repeated studies).

Verification on the private dataset (2623 studies, 1091 patients) with a patient-wise split of 70%/30% confirmed the effectiveness of the method. The threshold determined on the training set provided:

- Absence of false merging of different patients ($\text{Precision} = 1.0$, $\text{FPR} = 0$);
- High clustering quality on the test set: $\text{ARI} = 0.96$, $\text{AMI} = 0.97$, clustering accuracy = 96.5%.

In the identification task based on maxillary sinus CT, our method outperforms Heinrich [25] in Rank-1 accuracy: 90.3% vs 72%.

The obtained results confirm the applicability of the method for clustering anonymized head CT studies and identification, including tasks of quality control of identifiers in medical databases and the formation of longitudinal datasets.

The key limitation for using the method is the need for specific anatomical landmarks in CT images that are eyeballs and the upper cervical vertebra (C1). Furthermore, soft tissue preservation, necessary for eye localization, may not be available in some forensic scenarios (e.g., severe tissue decomposition) or in certain public datasets. Overcoming these limitations to expand the applicability of the method constitutes the subject of our future research.

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