



University of Dundee

Automated Identification from Dental Data (AutoIDD)

Reesu, Gowri Vijay; Woodsend, Brenainn ; Manica, Scheila; Revie, Gavin F.; Brown, Nathan L.; Mossey, Peter A.

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1 **Title: Automated Identification from Dental Data (AutoIDD): A New Development in**
2 **Digital Forensics.**

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7 **ABSTRACT:**

8
9 There has been a significant expansion in the use of 3-dimensional (3D) dental images in recent years. In the field
10 of forensic odontology, an automated 3D dental identification system could enhance the identification process.
11 This study presents a novel method for automated human dental identification using 3D digital dental data by
12 utilising a dental identification scenario. The total study sample was divided into two groups: Group A (120 dental
13 models) and Group B (120 Intra-oral scans-IOS). Group A data was composed of 3D scanned dental models of
14 post-orthodontic treated patients (30 maxillary and 30 mandibular). This data was considered as AM digital data.
15 To generate an identical sample, the dental casts (60) of the same patients were retrieved and laser scanned. These
16 models were considered as PM digital data. Group B data (IOS) was obtained from 30 study participants. To
17 reconstruct a dental identification scenario 30 maxillary and 30 mandibular IOS were obtained from 30
18 participants and were considered as IOS-AM. After one year, another set of IOS (60) were acquired from the same
19 participants and were considered as IOS-PM. The results showed that the AutoIDD (Automated Identification
20 from Dental Data) software was consistent in accuracy; capable of differentiating “correct matches” (high match
21 percentage) from “non-matches” (very low percentage) by 3D image superimposition. The match percentage of
22 the maxillary and mandibular IOS ranged from 64-100% and 81-100%, with a mean percentage of 96.7 and 96.4
23 respectively. This study demonstrated the feasibility of using 3D scans through a new automated software -
24 AutoIDD in digital forensics to assist the forensic expert in confirming the identity of a deceased individual from
25 the available AM dental records.

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28 **KEYWORDS:** Forensic odontology; Automated Identification; Dental data; 3-dimensional models; Intra-oral
29 scans.

43 **1. Introduction**

44 Forensic human identification by dental means has proved to be extremely useful and reliable over the years. This
45 can be achieved with the availability of accurate and comprehensive ante-mortem (AM) dental records which are
46 essential for a positive identification [1,2]. Several dental data coding systems have been proposed for the use in
47 reports and computer-assisted identifications in the field of forensic odontology. The most well-known
48 identification applications in the electronic management of dental records were CAPMI [3], WinID3 [4], Disaster
49 And Victim Identification ‘‘DAVID’’ [5], and the Plass Data system - The DVI System International [6]. All have
50 been recommended by INTERPOL to its member countries as they share a common purpose. These systems have
51 primarily automated the text searching of records and require manual processing of data.

52
53 Dental radiographs are one of the key components of dental records which assists in the process of human
54 identification. Studies on semi-automatic [7,8] and automatic dental identification based [9] on two-dimensional
55 (2D) radiographs have been proposed over the last two decades. However, 2D radiograph based approaches had
56 several limitations. The tooth segmentation process was time consuming and inaccurate due to the low image
57 quality from blurred dental radiographs. Distortions in tooth shape and arch arising from different imaging angles
58 are significant, which renders automated 2D radiographic retrieval and identification inaccurate [8,10,11].

59
60 To overcome the inherent limitations of 2D based methods, a feasible and an efficient automated 3D dental
61 identification system that would enhance the identification process is essential. The application of 3-dimensional
62 (3D) imaging in dentistry has widely expanded in recent years. As a result, clinical practices and laboratory
63 techniques are shifting to digital workflows [12]. The introduction of intra-oral scanners for direct digitalisation
64 of the patient’s dental arches were developed as an alternative to the use of conventional impression materials
65 [13,14]. This digital system has important advantages in reducing impression time, patient burden, efficient
66 storage and retrieval, higher accuracy, rapid access to 3D diagnostic information, and easy transferability of digital
67 data [15,16]. Using a laser scanner, dental casts can be converted into 3D models that may be used in alignment
68 and matching which can be subjected to automated comparative dental analysis [17].

69 This study proposes a new automated system in digital forensics to assist the forensic expert in accurately
70 identifying the correct dentition of the deceased individuals using AutoIDD (Automated Identification from
71 Dental Data), from the available AM dental records. The objective was to test the performance of the AutoIDD
72 software using AM and PM (post-mortem) 3D scans for accuracy and validity.

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74 **2. Materials and Method**

75 This study was approved by the East of Scotland Research Ethics Service, REC reference: 17/ES/0144. A
76 new automated software was designed that uses a combination of techniques including Iterative Closest Point
77 (ICP) and Principal Component Analysis (PCA) for accurate identification using 3D dental models and intra-
78 oral scans (IOS). An overview of the automated alignment and matching process is shown in Fig. 1.

79 **2.1 Data Acquisition**

80 The total study sample consisted of 240 3D maxillary and mandibular dental data. The data was divided into
81 two groups: Group A (60AM & 60PM =120 dental models) and Group B (60AM & 60PM =120 IOS).

82 The data collected for Group A consisted of 60 dental casts of 30 patients (30 maxillary and 30 mandibular
83 dental models) which were all of post-orthodontic patients. According to the clinical data storage protocol,
84 all the patients' dental casts, who had their treatment completed, were laser scanned to create indirect 3D
85 digital images of dental models by the laboratory technicians for digital storage. The dental casts were scanned
86 using R700 3Shape Orthodontic Study Model Scanner (Copenhagen, Denmark) and the images were saved
87 in stereolithography (.STL) format. Patients who had consented for their records to be used for research
88 purposes were identified through the clinic registry by the principal investigator (PI). All the patient
89 identifying information was removed and a unique study code was assigned to each 3D dental model by the
90 PI. For the purposes of this study these 3D models were considered as **"AM digital data"**.

91 To generate an identical sample, 60 dental casts (30 maxillary and 30 mandibular) of the same patients were
92 retrieved and laser scanned by the PI and were considered as **"PM digital data"**. Any dental casts that were
93 found to be damaged during the storage process were excluded from the AM and PM data. This is to determine
94 whether different scans obtained from the same patient's casts were identifiable. The rationale for using the
95 post-orthodontic data was to investigate the performance of the software in identifying the correct AM-PM
96 3D dental model matches within an orthodontic treated sample.

97 The data collected for Group B consisted of 120 IOS in total. The dental school staff and students were invited
98 to participate in this research, where 30 participants were recruited. To reconstruct a dental identification
99 scenario, 30 maxillary and 30 mandibular dental arches scans were obtained using 3Shape TRIOS Intraoral
100 Scanner (Copenhagen, Denmark) by the PI and were considered as IOS-AM. After one year, another set of
101 IOS (60) were acquired from the same participants and were considered as IOS-PM. The purpose of this
102 process was to determine the sensitivity of AutoIDD software towards any variations in an individual's
103 dentition; morphological and restorative features.

104 In total, the two groups of data comprised of four types of data sets (two sets of maxillary and mandibular 3D
105 dental models and IOS). On examination of the AM and PM IOS data, the following dental characteristics
106 were observed; restorations, missing tooth, occlusal cavities-unrestored and anterior crowding of teeth.

107 The study hypothesis is that an accurate dental identification can be facilitated through the use of AutoIDD
108 software. The identification process is based on dental characteristics, shape and alignment of the 3D dental
109 arches and any dental treatment interventions which can comprise a unique set.

111 **2.2 3D dental scans - STL files**

112 All the scans were in .STL format (standard open-source 3D file format). Once read from file a .STL is often
113 referred to as a 'mesh'. It is composed of numerous triangles (Fig. 2) where each triangle is represented by
114 the (x, y, z) values of each corner. Rather than considering the corners of the triangles, AutoIDD software
115 looks at the centre of each triangle. This is mainly for the benefit of speedy process and for the convenience
116 of having one point per outward normal.

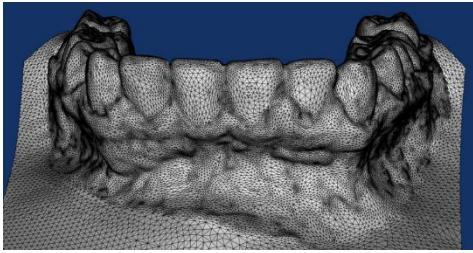


Fig. 2. 3D Mesh of a 3D scanned dental model.

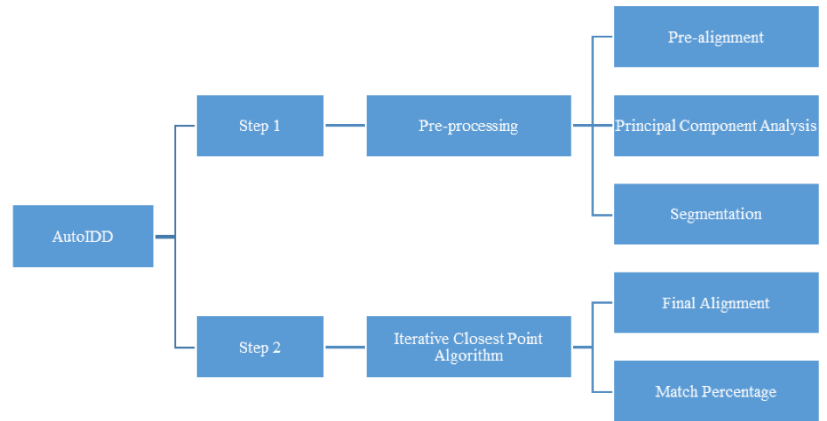


Fig. 1. An overview of the automated alignment and matching process of AutoIDD.

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2.3 Pre-processing

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2.3.1 Pre-alignment

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An overview of the steps involved:

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- Use PCA to obtain three basis vectors (x, y, & z).
- Check the signs of each basis vector.
- Fit a plane through all the tips of the teeth to gain a more accurate “up” basis vector.
- Adjust the “forwards” vector to maintain orthogonality with the new “up”.

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2.3.2 Principle Component Analysis

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The most well-known approach computing the alignment of 3D objects is the PCA method [18]. The goal was to find a method that best aligns any 3D dental scan and will consequently align two similar 3D scans in the same way. The 3D scan has symmetries and it is aligned with particular axes or symmetry planes [19]. So the output of PCA on a dental scan should yield up/down (Z-axis) as the first unit vector, forwards/backwards (Y-axis) as the second and left/right as the third (X-axis). The occlusal surfaces were compared to the PCA’s “up” according to the dental scan, i.e. maxillary or mandible which is determined by the filename (AM/PM-Maxi.stl, AM/PM-Mand.stl) and adjusted if needed. The comparison of unit vectors is completed using the scalar product. The AutoIDD software uses the following basis vectors after a series of computations:

- The “up” (regardless of it being maxillary or mandibular arch) vector of the scan is parallel to the z-axis.
- The “right” (patient’s right) vector of the model is parallel to the x-axis.
- “Forwards” is parallel to the y-axis.

147 **2.3.3 Segmentation**

148 Segmentation, also referred to as cropping is defined as the process of separating the 3D model into segments
149 that are representative of the model shape, calculated by edge detection. The goal of segmentation is to
150 simplify the representation of a model/mesh into something that is more tangible and easier to analyse [20].
151 Manual segmentation is very time-consuming for large datasets to eliminate the non-dental/ plaster part of
152 the dental model which does not contain information of the teeth. Therefore, many automated [21] and semi-
153 automated [22] computer based systems have been developed that can accurately demarcate the desired dental
154 component in the model.

155
156 In this software, once the pre-alignment of the model was attained, an automated segmentation plane
157 dissecting the dental cast was executed. In Python™, which is an open source programming language (Python
158 Software Foundation, version 3.8.0, Beaverton, USA) [23], arch meshes can be sampled according to a
159 specific instruction i.e. “to include all points above a certain height”. AutoIDD finds the highest point in the
160 direction [0, 1, 1] if mandibular mesh or [0, 1, -1] if maxillary mesh. This point should approximately be the
161 midpoint of the incisal edge. Then the mesh was cropped so that anything more than 9 mm below or 45 mm
162 behind the incisal edge midpoint was eliminated (Fig. 3). Additionally the test model was cropped by another
163 1mm vertically and 3mm horizontally just before the ICP process. This step was to ensure that the test scan
164 includes areas that the reference scan contain and make certain that each point on the test scan is paired with
165 the corresponding point on the reference model.

166 Standardisation of the methodology is an important element of minimising soft tissue influence and increasing
167 accuracy. Hence, the height and length of the segmentation plane was chosen with an intension to include
168 just the dental components in the scan. These values can be adjusted to obtain a desired plane with a goal to
169 limit gum area. The same segmentation procedure was applied to the intra-oral scans.

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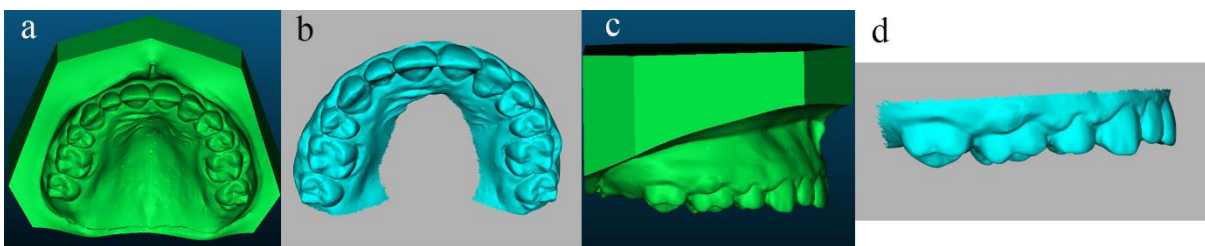


Fig. { SEQ Figure * ARABIC }. Images of the 3D dental models before (a, c) and after (b, d) after the

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173 **2.4 Iterative Closest Point (ICP)**

174 A method for an accurate and computationally efficient registration of 3D shapes was developed based on the
175 ICP algorithm which is to find the closest point on a geometric entity to a given point [24]. The algorithm
176 finds 3D correspondences between two point sets (a reference and a test set) and tries to determine the best
177 match on the “reference” set in terms of minimum distance. This whole process is considered as one iteration
178 and it continues until the alignment of the models is deemed either satisfactory or unlikely to improve.

179 Generally, a well matching model pair will converge quickly in 10 - 20 iterations, then improvement rates will
180 rapidly drop. Whereas a poorly matched pair will gradually decline down to a minimum error. To give a good
181 balance between performance and speed, AutoIDD will continue to iterate until the errors cease to improve by

182 at least 0.1% or when the iterations reach 100. ICP moves the test model in small steps per iteration and will
183 always seek to make an improvement on every iteration. It is of utmost importance that the plaster base of the
184 dental models and other non-dental features are removed and the meshes are trimmed to consistent
185 measurements. Failure to do so leads to misleadingly high error scores and instability within ICP.

186 The ICP aims to find the ‘best’ superimposition of a ‘test model’ upon a similar ‘reference model’ where the
187 correspondence between the test points and the reference points is unknown. For an ICP to reliably give
188 satisfactory results, it is required that:

- 189 • the models were pre-aligned to attain the most approximate position.
- 190 • the models must go through the segmentation process, which is to remove everything below the teeth
191 area and the posterior part of the model as per the desired measurements.
- 192 • the test model should undergo an extra cropping stage to ensure that the boundaries of the model are
193 within the reference model.

194

195 **2.5 Data processing using AutoIDD**

196 This study was conducted by simulating a dental identification scenario. The user-interface has four sections.
197 It was designed to import digital dental data into “Reference section” (AM) and “Unknown section” (PM)
198 which allows the operator to align the entire datasets to produce results, see Fig. 4. The results will be
199 displayed in the “Results section” and a “viewing section” for inspection of the 3D scans. Thirty AM and 30
200 PM maxillary dental models (Group A data) were imported into the “reference” and “unknown” sections of
201 the AutoIDD interface respectively. These were aligned for automated comparison (superimposed) and
202 identification of correct matching pairs. This was followed by 30 AM and 30 PM mandibular dental models.
203 The same process was repeated with the 30 sets of IOS (Group B data) and results were obtained. Initially,
204 all the maxillary and mandibular dental models and intra-oral scans were analysed separately to determine
205 the accuracy of AutoIDD software within a specific type of dataset.

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207 To determine the robustness of the software with different scanning methods (laser scanned models and IOS)
208 another 10% of data from each PM dataset (3 from each of 30 3D models/IOS) were selected at random using
209 online random number generator tool [25]. This sample comprised to a total of 12 maxillary and mandibular
210 dental models and IOS (six dental models and six IOS). For the purposes of the experiment, this sample was
211 considered as “test” data. Twelve corresponding/matching 3D models and IOS were retrieved from the
212 respective “reference” data. Additionally, 12 3D models and IOS were also selected at random and included
213 with the 12 corresponding reference data totalling to 24. The 12 “test” data was aligned with 24 “reference”
214 3D models and IOS.

215 Once the data is processed, the results were displayed in a tabular form for all the automated alignments. The
216 results sections features a tool bar for data interpretation; such as match score percentage, mean distances and
217 detailed view of the pair-wise alignments. The software generated excel sheets and histograms to export the
218 results. It also generates two colour maps for each 3D pair for qualitative and quantitative evaluation; one for
219 the alignment (qualitative), which shows any discrepancies in the alignment of the arches (in case of a non-
220 match) and one for superimposition (quantitative), to identify the amount of match/non-match areas between

221 that pair, see Fig. 7. The reference model (AM) is depicted in red while the unknown model (PM) in green
 222 for visual differentiation. This software is compatible on a windows laptop/desktop or mac operating system.
 223 The statistical analysis of the study groups were assessed using IBM® SPSS Package Version 22 (New York,
 224 USA).

225
 226 **3. Results**

227 The results of Group A data showed that the AutoIDD was able to correctly distinguish the matching dental models
 228 from the non-matches in all cases. In both the experimental studies (maxillary and mandibular models), all of the
 229 matching AM-PM 3D pairs were scored as 100%. This process validates the function of AutoIDD software. The
 230 mean distance, standard deviation and RMS (root mean square) of the “correct 3D dental model matches”
 231 (maxillary and mandibular) are shown in Table 1. The results of group B data also indicated that the software
 232 accurately identified the matching AM-PM IOS from the non-matches in all cases. The match percentage of the
 233 maxillary and mandibular intra-oral scans ranged from 64-100% and 81-100%, with a mean percentage of 96.7
 234 and 96.4 respectively. A noteworthy difference in the match percentage between a matching and non-matching
 235 pair was observed (Fig. 5). The maximum non-match percentage of the dental models and the scans is shown in
 236 Table 1.

Dental Arches	3D scans	AM Data (n)	PM Data (n)	Minimum Match percentage	Maximum Match percentage	Maximum Non-match percentage	Mean Distance (mm) of Correct matches	Mean Distance (mm) of Non-matches	Standard Deviation (mm) of Correct matches	RMS (mm) of Correct matches	RMS of (mm) Non-matches
Maxillary	Dental Models	30	30	-	100	7.7	0.075	0.76	0.006	0.03	1.00
	Intra-oral scans	30	30	64	100	6.0	0.094	0.87	0.031	0.10	1.11
Mandibular	Dental Models	30	30	-	100	8.6	0.076	0.80	0.013	0.06	1.04
	Intra-oral scans	30	30	81	100	6.3	0.093	1.00	0.027	0.11	1.30

Table { SEQ Table * ARABIC } shows the results obtained from the automated comparison of AM-PM 3D datasets; Group A data (Dental Models) and Group B data (Intra-oral scans).

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 238 Analysis of the 3D models/IOS displayed a total of 900 automated comparisons and alignments (30 AM x 30 PM)
 239 for each data set. Every “Unknown” model (PM) aligned with the given “Reference” (AM) models. This resulted
 240 in 30 correct matches based on “best fit alignment” and 870 non-matches. The match percentage of the
 241 corresponding AM and PM maxillary and mandibular IOS were indicated in green as shown in Fig. 5 and 6. The
 242 results of the “test” data revealed that the AutoIDD clearly differentiated maxillary and mandibular arches and
 243 accurately identified correct matching pairs among other non-matches, see Fig. 4. The results (match percentage
 244 and mean distances) were consistent with the previous outcomes.

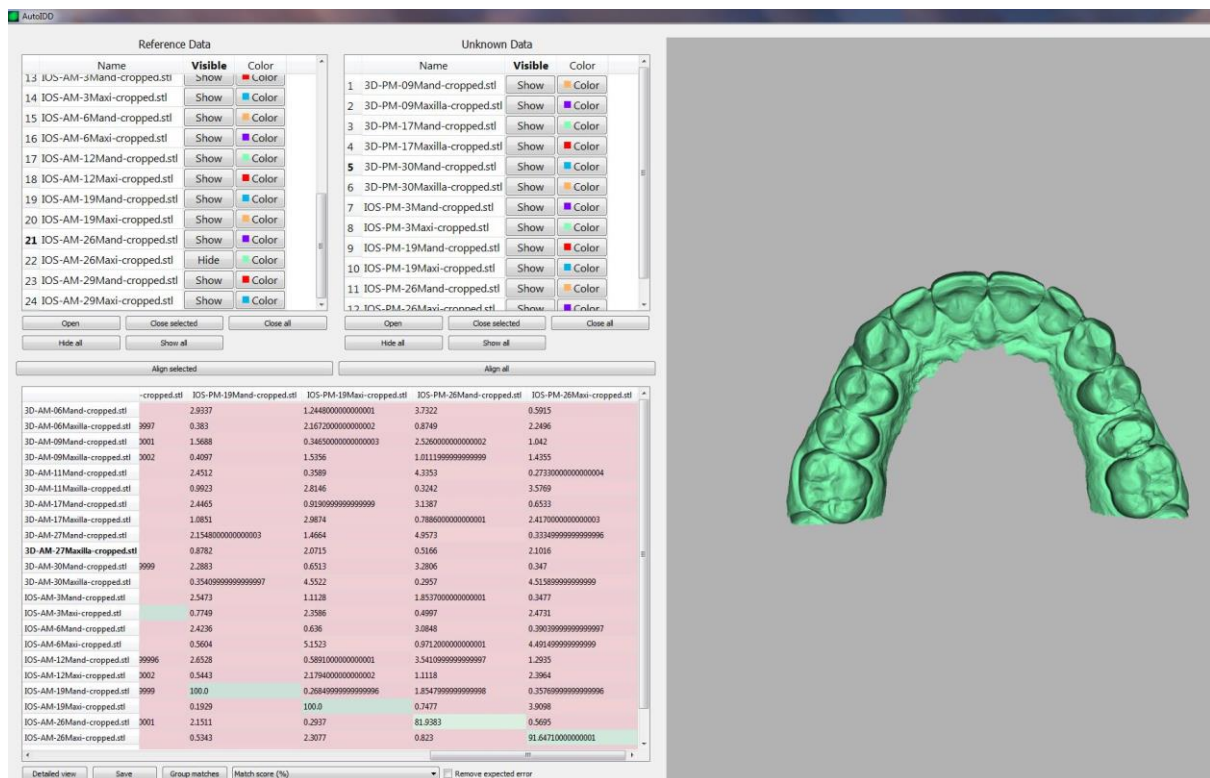


Fig. { SEQ Figure * ARABIC }. shows the user-interface of the AutoIDD software displaying the results of a processed data and 3D dental scan in the viewing section.

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The match percentage is computed by the mean distance and the measured error. The mean distance is the distance measured between each reference point on the “unknown” model relative to the corresponding point on the “reference” model. Therefore, pairs with least mean distance between the 3D meshes, have a better alignment and superimposition, and a higher probability of being a “positive identification”. This quantitative measure provides an estimate of the similarity between the two models/scans.

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The evaluation of the 3D pairs was performed through the colour maps. Areas with high degree of match in the arches is shown in green with some shades of yellow. Shades of blue and red represent extreme overlaps. Alterations or changes in the dentition (occlusal or any tooth surface) were illustrated in red. For example, a restoration present in the “unknown” scan and not in the “reference” scan is depicted in areas of red, see Fig. 7 (b,d), while an incorrect alignment of a non-match is shown in Fig. 8 a. A colour scale on the superimposition map displays the quantitative differences between the reference points of arches. These coloured maps can be saved in any preferred orientation as JPEG (Joint Photographic Experts Group) images.

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Analysis of the total comparisons in each group (maxillary and mandibular 3D models and intra-oral scans) shows the match percentage and histogram of data distribution, see Fig. 9 & 10. Overall, it was possible to identify all the correct matching pairs through the AutoIDD software. The results from the automated comparison and alignment of different types of scans were consistent. There were no scans or matching pairs with similar or close match percentage or mean distance within the processed dataset.

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	MAX-PM-01	MAX-PM-02	MAX-PM-03	MAX-PM-04	MAX-PM-05	MAX-PM-06	MAX-PM-07	MAX-PM-08	MAX-PM-09	MAX-PM-10	MAX-PM-11	MAX-PM-12	MAX-PM-13	MAX-PM-14	MAX-PM-15	MAX-PM-16	MAX-PM-17	MAX-PM-18	MAX-PM-19	MAX-PM-20	MAX-PM-21	MAX-PM-22	MAX-PM-23	MAX-PM-24	MAX-PM-25	MAX-PM-26	MAX-PM-27	MAX-PM-28	MAX-PM-29	MAX-PM-30
MAX-AM-01	100	2.6	2.8	2.2	4.8	2.2	3.9	3.1	2.6	5.0	3.4	2.8	2.7	3.3	3.5	2.5	2.3	2.3	2.0	4.9	4.9	2.6	3.1	2.4	2.5	2.1	3.0	1.9	3.2	1.9
MAX-AM-02	2.8	100	2.6	2.7	2.5	4.1	2.9	3.0	3.6	3.0	2.3	2.9	2.0	2.5	3.4	1.8	2.6	3.7	3.0	2.5	2.5	5.2	3.9	2.4	4.9	2.9	3.1	1.9	2.9	2.3
MAX-AM-03	3.3	2.9	100	2.6	3.1	2.5	3.7	2.8	2.7	3.4	2.2	2.7	2.0	2.4	4.2	2.1	2.5	3.1	2.4	2.7	2.9	3.7	3.7	2.5	3.2	2.5	3.0	2.1	2.8	2.3
MAX-AM-04	2.4	2.9	2.7	100	2.3	2.6	2.5	2.5	2.3	2.8	2.2	2.2	1.7	2.5	2.6	1.8	2.7	3.2	2.4	2.2	2.4	3.1	2.7	2.5	2.7	2.6	3.5	2.3	2.9	2.7
MAX-AM-05	6.0	2.7	2.8	1.9	100	2.2	5.0	3.3	2.4	4.6	4.2	4.7	2.4	3.4	4.3	2.8	2.2	2.0	1.9	4.1	4.9	2.7	3.2	2.3	2.5	2.0	2.8	1.8	2.9	1.9
MAX-AM-06	2.1	4.6	2.3	2.3	2.1	100	2.7	2.2	3.7	2.3	2.2	2.5	1.6	2.0	3.3	1.7	3.4	3.7	5.2	1.8	2.0	3.4	2.6	3.8	3.1	4.5	2.7	4.9	3.7	2.8
MAX-AM-07	4.4	3.3	2.9	2.0	5.0	2.3	100	4.0	2.7	4.3	4.0	5.1	2.8	3.1	4.7	2.7	2.0	2.5	2.1	4.3	4.2	3.6	6.0	2.3	4.0	2.0	2.7	2.1	2.8	1.9
MAX-AM-08	3.0	3.2	2.1	2.0	2.8	2.0	3.2	96.1	2.3	3.7	2.6	2.8	2.7	3.5	2.8	2.1	1.9	2.3	1.9	3.1	3.9	3.3	3.3	2.1	2.9	1.8	2.6	1.9	2.2	1.8
MAX-AM-09	2.7	3.1	1.9	2.1	2.6	3.5	3.0	2.2	100	2.6	2.7	3.3	1.7	2.5	4.3	1.8	2.9	2.4	2.3	2.0	2.3	1.8	1.8	3.2	4.7	3.1	1.8	1.6	3.2	2.3
MAX-AM-10	4.7	3.2	2.7	2.1	3.9	2.2	3.6	4.3	2.9	100	3.3	3.4	2.6	2.8	3.2	2.3	2.0	2.3	1.9	3.6	4.7	2.6	2.9	2.4	2.5	2.1	2.4	1.8	2.3	1.9
MAX-AM-11	3.6	2.5	2.6	2.4	3.9	2.3	4.3	3.1	2.4	3.9	100	4.2	2.4	2.7	3.4	2.4	2.0	2.2	1.9	3.4	3.8	3.2	3.5	2.6	2.9	2.1	3.1	1.9	2.4	1.9
MAX-AM-12	3.5	3.9	2.7	2.3	3.9	2.8	4.8	3.5	3.4	4.1	4.2	79.4	2.1	2.9	5.2	2.4	2.3	2.8	2.2	3.0	3.6	4.0	4.7	3.1	4.4	2.4	3.0	1.9	2.9	2.3
MAX-AM-13	2.7	2.1	1.8	1.6	1.9	1.6	2.3	2.8	2.2	2.7	2.4	2.2	99.5	2.1	2.0	2.0	1.4	1.6	1.6	2.6	2.8	1.9	2.1	1.8	1.9	1.5	1.9	1.3	1.7	1.3
MAX-AM-14	3.0	2.7	2.2	2.0	2.9	2.2	2.9	3.5	2.3	2.8	2.7	2.7	2.6	100	3.0	2.9	2.2	2.2	1.9	2.8	3.2	2.5	2.8	2.0	2.6	2.2	2.9	1.8	2.5	1.9
MAX-AM-15	3.3	3.2	2.9	2.4	3.9	3.2	4.7	3.7	3.8	3.3	3.8	4.8	1.9	3.0	100	2.2	2.9	2.8	2.5	2.7	2.9	3.3	4.0	3.0	3.7	2.7	2.4	2.2	3.6	2.6
MAX-AM-16	1.3	1.5	1.9	1.6	1.7	1.1	1.5	1.2	1.3	1.1	1.1	1.2	1.5	1.3	98.6	1.1	1.5	1.2	1.4	1.6	1.8	1.9	1.1	1.8	1.0	2.1	1.6	1.2	1.1	1.1
MAX-AM-17	2.6	3.0	2.0	2.3	2.8	3.4	2.4	2.1	3.1	2.4	2.3	2.5	1.5	2.3	3.0	1.9	100	3.2	2.3	1.8	2.1	2.5	2.6	3.2	2.2	3.4	2.7	2.9	3.7	2.3
MAX-AM-18	2.5	3.8	2.6	2.7	2.1	3.9	2.6	2.3	3.5	2.5	2.2	2.4	1.5	2.1	2.9	1.7	3.1	93.8	2.6	1.9	2.1	3.0	2.6	3.2	2.6	3.9	2.7	2.0	3.2	2.4
MAX-AM-19	2.0	3.9	2.5	2.7	2.0	5.8	2.5	2.1	3.2	2.2	2.2	2.3	1.6	2.0	3.0	1.6	3.0	3.3	100	1.8	1.8	3.0	2.4	2.9	2.7	3.9	2.4	4.1	3.3	4.8
MAX-AM-20	5.6	2.8	2.2	1.8	4.2	2.1	3.2	3.6	2.6	4.8	3.6	3.6	3.3	3.2	3.1	2.3	2.0	2.1	2.1	100	4.0	2.7	3.7	2.3	2.7	1.9	3.2	1.7	2.5	1.7
MAX-AM-21	4.9	2.8	2.1	2.0	4.2	1.9	3.1	4.3	2.2	4.7	3.7	3.4	3.0	3.7	3.1	2.9	1.8	2.2	1.8	4.0	100	3.2	3.8	2.2	3.2	1.8	3.4	1.8	2.3	1.9
MAX-AM-22	2.3	4.7	3.0	2.9	3.0	3.1	3.6	3.5	3.1	3.1	2.8	3.6	2.0	1.9	4.4	2.1	2.5	3.3	2.6	2.7	2.9	98.9	1.6	4.7	2.6	4.1	2.2	2.9	2.6	2.6
MAX-AM-23	3.6	3.5	2.9	2.5	3.8	2.9	5.3	3.4	3.6	3.5	3.2	4.3	2.4	3.0	5.5	2.2	2.4	2.8	2.4	3.4	3.4	4.8	89.7	3.1	4.6	2.5	2.7	2.0	3.2	2.3
MAX-AM-24	2.5	3.9	2.5	2.6	2.5	4.1	2.7	2.4	3.4	2.5	2.5	2.8	1.8	2.2	3.0	1.8	3.1	3.5	2.3	2.1	2.2	3.1	3.1	100	3.1	5.1	3.1	2.1	3.2	2.2
MAX-AM-25	3.2	5.1	2.5	2.4	2.9	2.8	3.7	3.1	3.2	2.8	2.5	3.7	2.0	2.8	4.1	2.0	2.2	3.0	2.3	2.9	2.9	5.0	4.4	2.9	91.1	2.3	3.4	2.2	2.7	2.4
MAX-AM-26	2.3	3.8	2.3	2.4	2.3	4.7	2.6	2.1	3.4	2.3	2.1	2.3	1.7	2.3	2.9	1.9	3.2	4.2	2.3	1.9	2.1	3.2	2.9	4.4	2.6	91.6	3.0	3.3	3.3	3.9
MAX-AM-27	3.7	3.5	2.4	2.8	3.3	2.6	3.4	3.2	2.7	3.0	3.0	3.0	2.3	3.3	3.6	2.4	2.5	2.7	2.4	3.1	3.2	4.3	2.6	3.3	2.6	100	2.3	3.4	2.7	2.7
MAX-AM-28	2.5	3.8	2.4	2.7	2.3	6.1	2.7	2.2	3.2	2.2	2.5	2.8	1.6	2.4	3.1	2.1	4.0	3.5	3.8	2.0	2.3	2.9	2.6	3.4	2.7	4.3	3.1	64.6	3.3	3.0
MAX-AM-29	2.7	2.9	2.3	2.4	2.6	3.5	2.6	2.3	3.1	2.5	2.6	2.7	1.5	2.2	2.9	1.6	2.8	2.5	2.9	2.0	2.2	2.2	2.3	3.0	1.9	3.1	2.2	2.3	100	2.6
MAX-AM-30	2.2	4.7	2.5	2.8	2.4	3.3	2.7	2.3	3.4	2.5	2.1	2.5	1.5	2.2	3.4	1.9	4.0	5.0	4.9	1.8	2.1	3.5	2.6	3.5	3.3	4.9	2.9	5.1	3.5	100

Fig. { SEQ Figure * ARABIC }. Match percentages of AM – PM maxillary intra-oral scans. The correct matching pairs

⬇️⬆️

	MAND-PM-01	MAND-PM-02	MAND-PM-03	MAND-PM-04	MAND-PM-05	MAND-PM-06	MAND-PM-07	MAND-PM-08	MAND-PM-09	MAND-PM-10	MAND-PM-11	MAND-PM-12	MAND-PM-13	MAND-PM-14	MAND-PM-15	MAND-PM-16	MAND-PM-17	MAND-PM-18	MAND-PM-19	MAND-PM-20	MAND-PM-21	MAND-PM-22	MAND-PM-23	MAND-PM-24	MAND-PM-25	MAND-PM-26	MAND-PM-27	MAND-PM-28	MAND-PM-29	MAND-PM-30	
MAND-AM-01	97.9	2.5	2.0	2.9	1.7	1.4	2.5	2.8	1.8	3.7	2.8	1.8	2.1	1.9	3.7	2.4	1.9	1.8	1.8	3.2	3.2	2.5	1.6	1.5	2.9	2.6	3.2	1.9	2.9	2.5	
MAND-AM-02	2.6	88.5	2.3	2.4	1.4	3.7	2.7	2.5	4.3	2.2	2.2	3.6	1.7	2.4	3.4	3.1	3.2	3.1	2.8	2.1	2.5	3.7	5.3	2.5	3.4	5.0	3.3	1.9	3.9	6.0	
MAND-AM-03	2.4	2.2	99.9	2.8	2.0	2.0	3.4	1.9	2.1	3.2	2.3	2.8	1.3	1.7	3.0	2.4	1.5	1.7	2.5	2.6	2.2	3.4	2.6	2.2	3.6	1.9	3.0	2.1	2.1	2.3	
MAND-AM-04	2.1	2.2	2.2	91.0	2.0	1.6	2.2	2.1	2.0	3.5	3.3	2.7	2.3	2.2	3.5	2.7	1.7	2.0	2.6	2.7	2.9	2.5	1.8	1.4	4.2	1.2	2.4	1.4	2.4	2.2	
MAND-AM-05	1.5	2.4	2.3	1.4	87.3	2.3	3.0	1.8	3.1	1.7	2.8	3.1	1.2	1.8	1.8	3.2	2.5	1.9	2.4	1.2	3.3	2.2	2.6	2.3	2.7	2.2	1.7	1.1	2.2	2.4	
MAND-AM-06	2.3	5.0	2.0	2.2	1.7	100	2.4	2.3	2.8	2.1	1.9	2.3	1.8	1.9	2.7	2.5	2.4	2.8	2.1	1.9	2.2	3.3	3.2	1.7	2.8	4.2	3.0	1.8	3.0	5.6	
MAND-AM-07	3.2	2.7	3.3	2.6	0.3	2.4	100	2.0	3.8	4.7	3.3	3.6	1.3	1.8	5.0	2.4	2.3	1.9	3.2	4.4	2.9	4.1	3.3	3.3	4.9	2.0	4.0	1.8	2.7	2.7	
MAND-AM-08	1.9	2.4	1.5	2.6	1.2	1.8	1.6	100	2.3	1.9	2.3	2.1	3.6	2.5	2.3	3.6	2.4	2.4	1.7	1.9	2.7	1.8	1.6	1.5	2.0	3.0	2.1	1.8	3.2	2.2	
MAND-AM-09	1.2	2.4	2.2	1.0	1.1	3.0	2.3	1.3	100	1.3	1.2	2.2	1.5	2.0	1.6	1.5	3.1	2.2	2.5	1.4	1.3	2.1	2.5	2.6	4.9	2.6	1.7	1.3	2.3	2.4	
MAND-AM-10	3.9	2.1	3.0	3.0	1.1	1.5	3.9	1.8	2.7	100	3.2	2.1	1.3	1.5	3.5	2.9	1.7	1.6	2.9	4.0	3.9	2.8	2.1	1.8	3.6	1.9	3.0	1.5	2.2	2.2	
MAND-AM-11	1.7	2.2	2.0	2.1	1.4	1.6	2.4	2.1	2.3	2.0	100	2.1	1.8	1.7	1.9	2.8	1.9	1.7	2.2	2.2	3.8	2.2	2.0	1.8	2.5	2.0	1.7	1.2	2.0	2.0	
MAND-AM-12	2.5	4.2	2.7	3.1	0.3	3.1	3.5	2.6	3.5	2.5	2.4	100	1.7	2.6	3.7	3.8	2.4	2.6	2.7	2.7	2.6	3.3	3.6	2.9	3.6	3.5	3.2	1.4	4.0	3.6	
MAND-AM-13	1.5	1.4	1.2	2.3	1.1	1.4	1.2	2.7	1.7	1.9	1.2	1.2	89.3	1.9	2.2	1.9	1.4	1.6	1.2	1.3	1.0	1.3	1.4	1.3	1.2	2.0	1.6	2.9	1.8	1.4	1.4
MAND-AM-14	2.0	2.8	1.8	2.4	0.6	2.3	2.1	2.7	2.4	1.6	1.9	2.4	2.2	98.4	2.1	2.4	2.3	2.3	2.1	1.7	2.0	2.3	2.4	1.7	2.4	2.7	2.2	2.6	3.8	2.5	
MAND-AM-15	3.2	3.1	2.7	2.6	1.4	2.1	4.9	2.1	4.4	3.4	3.1	3.2	1.4	2.2	99.2	2.4	2.2	3.0	3.1	3.2	1.6	3.2	2.2	4							

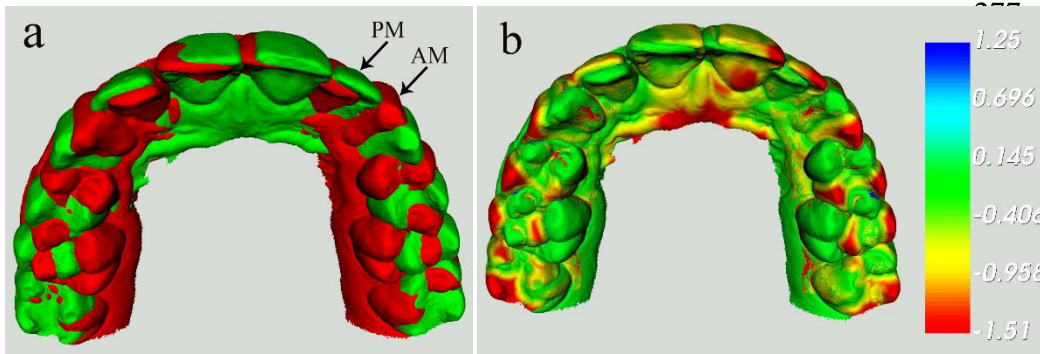


Fig. { SEQ Figure * ARABIC }. Example of an incorrect alignment (a) and superimposition (b) of a non-matching AM (Red)

285

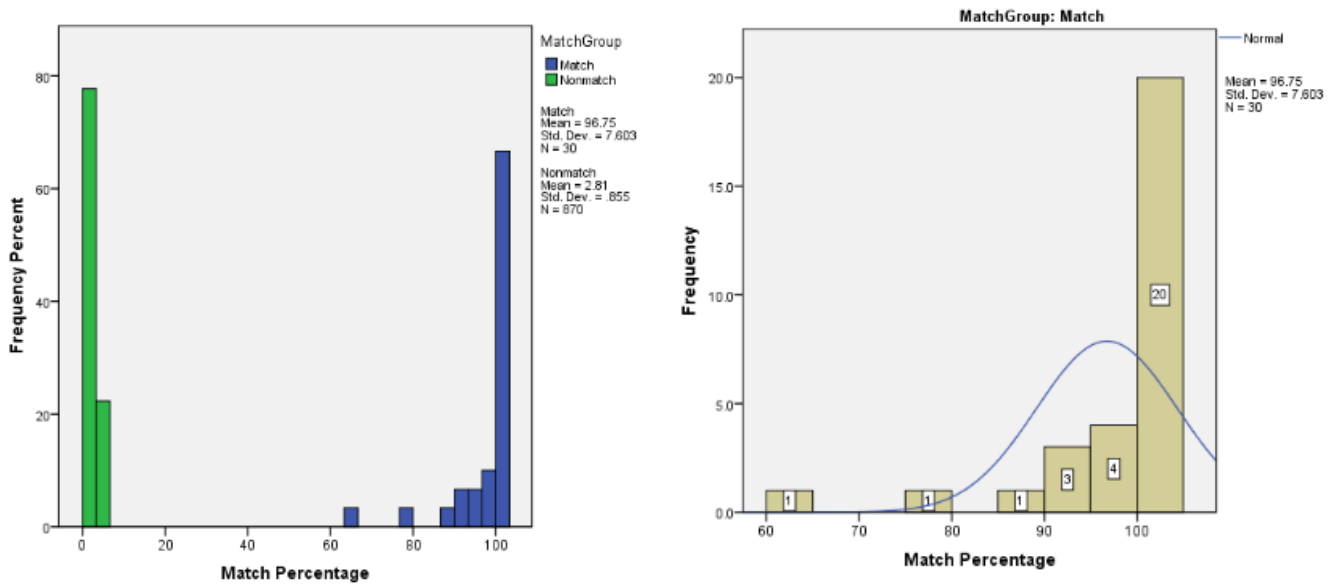


Fig. 9. Histogram of the distribution of percentage of matches and non-matches of maxillary IOS.

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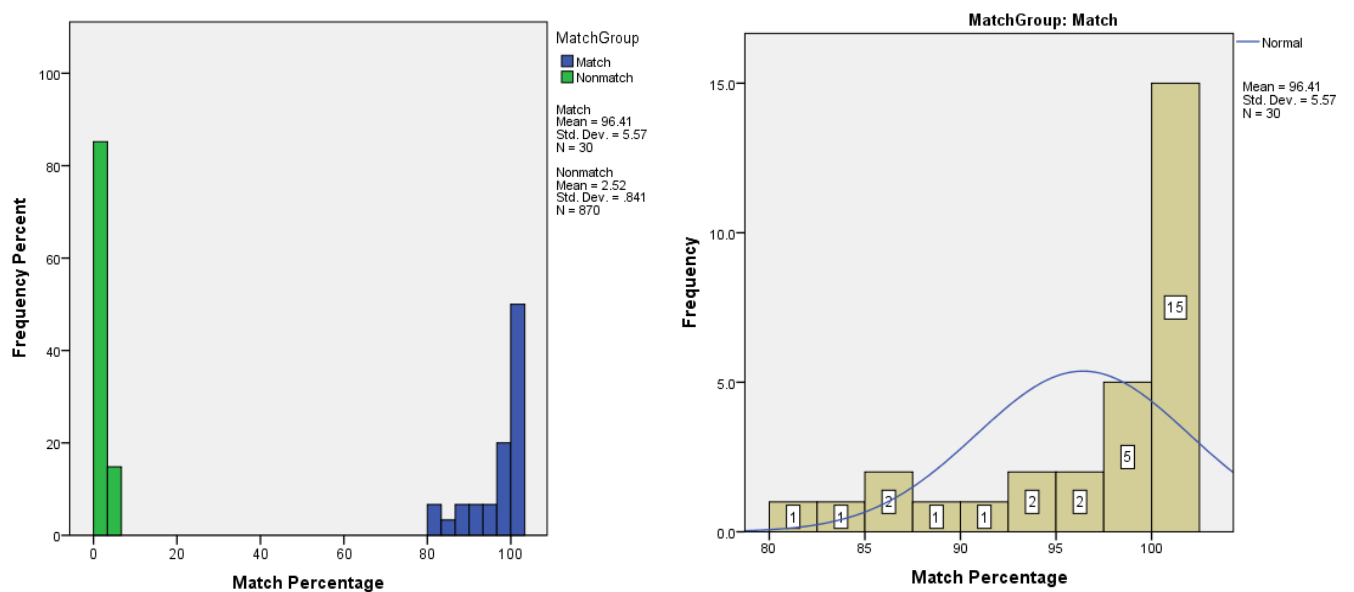


Fig. 10. Histogram of the distribution of percentage of matches and non-matches of mandibular IOS.

290

291 **4. Discussion**

292 This study demonstrates on the feasibility of using 3D dental models and IOS in the new automated system for
293 accurate dental identification. There is a shift towards digital storage of dental records, facilitated by affordable
294 3D scanners which can digitise the patient's dental casts [17]. Through the increasing use of 3D scanners and
295 chairside intraoral scanners [12-16], 3D dental models may be considered as a useful source of AM information.
296 All the scientific primary methods of human identification (fingerprint, DNA analysis, and dental) involve the
297 comparison of the AM data to PM evidence to establish a positive identification [2]. Furthermore, the dental
298 characteristics; their alignment and orientation within the arch, tooth shape and dental treatment interventions
299 were considered for a dentition to be unique [26].

300 Using registration techniques, the likelihood of finding matching dentitions in a given population were conducted
301 in 2D [27-29]. In the process of investigating the uniqueness of the human dentition, few attempted matching
302 studies on 3D scanned dentitions [30,31], while orthodontically treated samples were evaluated in 3D using semi-
303 automatic methods [32,33] which were all landmark based. All of these studies examined only the upper and
304 lower anterior teeth. A pilot study [34] analysed the incisal edges (2 mm) of the six anterior teeth of post-
305 orthodontic treated dentitions using 3D software packages for identifying matching set of dentitions. Though, the
306 study concluded that the human anterior dentition is unique and encouraged 3D approach, it required manual
307 segmentation and lacked complete automation. Another study [35] presented an algorithm for automatic matching
308 using scanned mandibular 3D models. The study was based on feature extraction and description points from the
309 models and concluded that the accuracy was highest with manual-segmented models than auto-segmented PM
310 models.

311
312 The present study is unique from the above studies. The main purpose of the AutoIDD software is to align and
313 identify matching dental patterns from the reference data. The entire scan area is considered in the registration
314 process mainly focussing on the dental components. All the previous studies used existing softwares which have
315 some limitations. The major advantage of AutoIDD software is that it was designed and developed to be fully
316 automated and no manual intervention is required. The target scan in a large dataset was efficiently identified
317 without any false positives. It also eliminates the need for surface registration and manual segmentation.

318 Though various studies proposed similar methods in the recent past, there are no reported studies which presented
319 a fully automated system to assist forensic experts with dental identification. A clear distinction between match
320 and non-match, robustness with different scan types and overall efficiency and accuracy in achieving the results
321 makes this study novel. The software assigns a match percentage to any given comparison and with multiple
322 different data and scenarios being executed.

323 Gibelli et al. also proposed similar procedures of 3D-3D superimposition, one that analysed anatomical differences
324 between dental elements [36] and another verifying the uniqueness of 3D models of the palatal rugae [37]. The
325 superimposition was based on the surface registration, where the software used calculated the least point-to-point
326 distance between the two superimposed surfaces, expressed as RMS. As the AutoIDD software considers the
327 centre of each triangle in the mesh/scan surface, all the points on the test scan are compared to the nearest
328 corresponding points on the reference scan. The mean of all the point-to-point (minimum) distance is
329 referred to as 'mean distance' in the results. There are no specific landmarks involved in the process.

330

331 It was observed that the orthodontic treatment increased the similarity and reduced the uniqueness of the human
332 anterior dentition between different patients. These similarities may cause the dentitions to be less distinguishable
333 than before treatment [33]. The study data used in group A were all 3D dental models of post-orthodontic treated
334 patients. The results of the experimental study indicate that the software has correctly distinguished the matching
335 dental models from the non-matches and all the models were found to be a 100% match. This also shows that
336 there were no changes detected in the AM-PM matching pairs. No false positives were observed. This part of the
337 study validated the function of AutoIDD. The group B data consisted of random individuals from general
338 population relevant only to the locality. In a forensic context, though equal number of corresponding or matching
339 3D reference scans were considered during the automated process, there was only one correct AM match in the
340 reference data for every PM case. The remaining 29 were non-matches. The AutoIDD was found to be consistent
341 in accuracy; capable of identifying “correct matches” from “non-matches” by assigning a high match percentage
342 for correct match and a very low for a non-match.

343 There may be more than one ante-mortem dental record, compared to one post-mortem dental record, if a number
344 of individuals are missing and the authorities suspect that the unidentified deceased could be any one of the
345 indicated missing persons. Therefore, the automated process was subjected to test the performance with an
346 increased number of AM non-matches/cases with a “test” data. The software demonstrated its robustness in
347 efficiently performing with different types of 3D scans, see Fig. 4.

348 The important outcome of the AutoIDD software is that, for a correct match the match percentage is higher than
349 other scores and it narrows down to the correct AM correspondence (indicated in green), see Fig. 5, 6. Hence, low
350 or high match percentage is not only the point, but needs to be discriminatory. For example when a 64% is assigned
351 to a PM-1 and AM-1 3D pair and the next nearest match percentage for PM-1 and AM-2 is approximately 3%,
352 and no other pair has a higher match percentage, it indicates that PM-1 and AM-1 is the best matching pair for
353 that PM model. All these numbers are content dependant; variations in the dentitions, see Fig. 7. Similarly, 100%
354 means that within the precision of the software and within the boundaries of its margin for error, it is able to
355 determine that it is an exact match, i.e. best fit match.

356
357 The intraoral scan data had some dental alterations (therapeutic and non-therapeutic) during the scan interval.
358 Many of the changes a tooth can undergo are by their nature irreversible. These discrepancies are significant
359 during the comparison process and must be evaluated by the forensic expert as to whether they are explainable or
360 unexplainable [2]. An ‘explainable discrepancy’ is one where an unrestored tooth/teeth surface(s) in AM model
361 is found to be restored in the PM model. While a tooth/teeth present in the PM model and missing in the AM
362 model is considered as an ‘unexplainable discrepancy’. The sensitivity towards any changes in the dentition can
363 be appreciated with the help of colour maps generated for every 3D pair. It was also noticed that the influence of
364 soft tissues on the overall result/score was negligible when compared to the dental component.

365
366 The evidence presented in this paper strongly suggests that for a given comparison, the correct match will be the
367 one with the highest match percentage and lowest mean value. It was observed that the accuracy of the alignment
368 process and the match percentage increased when there was greater similarity between the dentitions being
369 compared. Where changes in the dentition had occurred between scans, the match percentage was reduced. In
370 addition, the whole arch presentation may enhance the overall reliability of the identification process. The

371 advantage of 3D format is the dimensional stability; correct size proportions, which is a limitation for the
372 radiographs.

373 With the rapidly advancing 3D technologies, computerized tomography data and 3D scan data are considered
374 more reliable AM records than written dental charts. The availability of AM 3D data can allow for an accurate
375 digital comparison with the PM 3D data which can be applied in single identification cases. The process of 3D
376 comparison may potentially be considered in the Disaster Victim Identification techniques in future with the
377 increased accessibility and use of 3D datasets [38]. Henceforward, the dentists are recommended to treat
378 diagnostic casts as part of the dental record and preserve them for several years following the completion of the
379 dental treatment depending on the residence countries dental association's regulations and guidelines. This study
380 supports the storage of dental casts as a component of AM records. The forensic odontologists are also encouraged
381 to obtain PM dental impressions whenever possible which may facilitate a process of automation in forensic
382 identification.

383 This is the first fully automated system which is intended to assist forensic experts in the process of dental
384 identification. The performance of the AutoIDD has so far been tested only with full arch dental scans. Through
385 this study it is established that this automated identification system is consistent with the construct it is supposed
386 to be measuring, which is a "proof of concept" and very encouraging at the early stages of development. Moreover,
387 AutoIDD may also be used in the digital retrieval of patient dental records from digital dental databases and in
388 dental practices. Further research is required in the investigation of partial remains, pre- and post-orthodontic
389 samples and single tooth PM 3D models.

390 391 **5. Conclusion**

392 In summary, AutoIDD was able to demonstrate the identification of correct matches with a match percentage that
393 clearly differentiates the matches from non-matches. This software also enables recognition of the changes in the
394 human dentition, such as restorations and missing teeth. The match percentage is a combination of the best fit
395 alignment and the morphological changes identified by the software. A low match percentage may also infer that
396 there has been significant changes to that individual's dentition usually due to dental intervention. These changes
397 are also visible on the superimposition heat maps produced by the software.

398 This study presents a novel method for automated human dental identification using 3D scans to record digital
399 data, the innovative utility of python software, match percentage algorithm and image superimposition.

400
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402
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404 405 406 **6. References**

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