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A Dental Anthropological Databank for Use in the Statistical Estimation of Ancestry and Sex in Forensic Anthropology

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Summary of the Project

Major Goals and Objectives

The goal of this research was to establish a large dataset of dental data to improve estimations of sex (assigned at birth) and ancestry/population affinity in forensic anthropology. Teeth have traditionally been overlooked in this discipline, despite their wide use in biological anthropology. This project accomplished five main objectives: (1) **collect data** on standard and novel morphological traits and metric dental data in modern populations across the globe to identify their utility in sex (assigned at birth) and ancestry/population affinity estimation; (2) **create a large databank** of dental data that will be *publicly* available for research in applied forensic anthropology and biological anthropology; (3) **make available a free web-based computer application** to provide statistical estimates of ancestry/population affinity that can be used in forensic anthropological casework, (4) **explore methods to estimate sex** (assigned at birth) using dental data from modern collections, and (5) **provide a free database** in which to collect dental morphological and metric data..

Throughout the duration of this project, these goals were achieved. Data were collected in South Africa and the United States on donated cadaveric collections to create a large databank of dental data that will be made available to other researchers for data collection. A web-based application for the estimation of population affinity is available (rASUDAS2). A model for estimating biological sex assigned at birth using dental metric data is provided in this report. Finally, a database (Dentabase) and accompanying manual were created to collect dental morphological and metric data and perform preliminary data analyses.

Research Questions

In the last two decades, forensic anthropology has relied heavily on skeletal variables of the skull to explore population variation (e.g., Berg and Kenyhercz 2017; Hefner 2009; Hefner 2018; Jantz and Ousley 2005). While the methods developed have proved to be powerful tools for calculating probabilities associated with ancestry/population affinity estimation, they have their limitations. For example, largely intact skulls are required and methods may be somewhat limited in their available reference sample. Similarly, methods for sex estimation have relied heavily on long bone breadth measurements, and cranial and pelvic morphology. Researchers have long recognized the need for alternative and/or supplementary methods for estimating population affinity and/or sex of remains found in a forensic context that utilize additional elements of the skeleton and alternative statistical parameters. Teeth provide this additional system as the dentition: (1) preserves well in forensic contexts, (2) exhibits a wide range of metric and nonmetric variables under strong genetic control (Pilloud et al. 2016; Pilloud and Kenyhercz 2016), (3) shows patterned geographic variation (Scott and Turner 1997; Scott et al. 2018), and (4) demonstrates sexual dimorphism (Pilloud and Scott 2020).

One limitation to the analysis of dental morphological variation fifty years ago was the lack of standard methods of observation. This problem was resolved to a considerable extent by the work of C.G. Turner II and his students who developed descriptions and standardized plaques for over three dozen crown and root traits, which have been defined and illustrated in articles and books (Edgar 2017; Scott and Irish 2017; Turner, Nichol, and Scott 1991). Turner personally collected data on over 23,000 individuals (from mostly archaeological contexts) in the Americas, Asia, the Pacific, and Europe. His students have also been very prolific in data collection across the globe (e.g., Haeussler et al. 1989; Harris 1977; Hawkey 1998; Irish 2005; Irish 2006; Scott et

al. 2018). Dental metric data collection has been standardized for some time and has been used for decades to explore human evolution (e.g., Brace, Rosenberg, and Hunt 1987; Wolpoff 1971), population variation (e.g., Kieser 1990), and sexual dimorphism (e.g., Brace and Ryan 1980; Garn et al. 1967).

While there have been attempts to incorporate dental morphological data into forensic anthropology methods to estimate population affinity (e.g., Edgar 2005; Edgar 2013; Irish 2015; Kenyhercz, Klales, and Kenyhercz 2014; Pilloud et al. 2014) and sex assigned at birth (e.g., Harris and Foster 2015; Hassett 2012; Viciano, López-Lázaro, and Alemán 2013) these methods all suffer limitations. Sample sizes may be small or reference samples are limited, thereby limiting their broad applicability to forensic casework.

This project has expanded on these research efforts to understand modern human variation through data collection and analysis on dental morphology and metrics on a large modern sample incorporating several novel variables. Our fundamental research question is how can we take genetically controlled and geographically variable dental traits to develop and refine methods to identify and understand sexual dimorphism and modern human variation.

Research Design, Methods, Analytical, and Data Analysis Techniques

The web-based application, rASUDAS, for estimating ancestry from tooth crown and root morphology was first developed from samples and trait frequencies in *The Anthropology of Modern Human Teeth* (Scott and Turner 1997). The alpha version included twenty-one populations and the following seventeen traits:

- | | |
|-----------------------------|--------------------|
| 1. UI1 Winging | 10. LM2 Y-pattern |
| 2. UI1 Shoveling | 11. LM1 cusp six |
| 3. UI1 Double shoveling | 12. LM1 cusp seven |
| 4. UI2 Interruption grooves | 13. 3-rooted UM2 |
| 5. UC Bushman canine | 14. 2-rooted LC |
| 6. Premolar odontomes | 15. LP1 Tomes root |
| 7. UM1 Enamel extensions | 16. 3-rooted LM1 |
| 8. 4-cusped LM1 | 17. 1-rooted LM2 |
| 9. 4-cusped LM2 | |

The beta version developed by D. Navega and J. Coelho, in conjunction with G.R. Scott, reduced the number of populations from twenty-one to seven (i.e., Western Eurasia, Sub-Saharan Africa, East Asia, American Arctic & Northern Asia, Southeast Asia & Polynesia, Australo-Melanesia & Micronesia, North and South America). For the alpha version, all traits were dichotomized following the breakpoints in Scott and Turner (1997). For the beta version, several new traits were added, and four variables were trichotomized (i.e., shoveling, Carabelli's trait, hypocone, protostylid). Two traits from the alpha version were dropped (UI1 double shoveling and UC Bushman canine). The changes and additions were:

- UI1 shoveling (0-1, 2-3, 4+)
- UM2 hypocone (0-1, 2-3, 4+)
- UM1 Carabelli's trait (0-1, 2-4, 5+)
- UM1 cusp five
- LP2 multiple lingual cusps
- LM1 Protostylid (0, 1, 2-7)
- LM1 deflecting wrinkle
- UP1 2-rooted

The beta version included fifteen crown and six root traits. Although an improvement over the alpha version, there was still an issue. Shoveling, for example, could only be scored on UI1 and if that tooth was not present, shoveling was not part of the calculation despite its power in distinguishing populations. The same issue applied to other traits. To accommodate this problem, trait frequencies were calculated for backup traits in the same tooth class. The current

version of the application, dubbed rASUDAS2, includes four new traits (two of which were present in the alpha version but dropped in the beta version):

1. UI1 Double shoveling
2. UC *tuberculum dentale*
3. UC Bushman canine
4. LC Distal accessory ridge

And seven backup traits:

1. UI2 Shoveling
2. UI1 *Tuberculum dentale*
3. UM2 Cusp 5
4. LM1 Enamel extensions
5. LP1 Multiple lingual cusps
6. 4-cusped LM1
7. LM2 Cusp 6

In total, rASUDAS2 includes eighteen crown and seven root traits. It is possible to enter both the key trait and the backup trait, but to avoid issues of within-field correlations, we recommend that a trait is scored only on the key tooth; the backup is used when the key tooth cannot be scored for trait expression.

rASUDAS2 is based on a naïve Bayes algorithm. To compute posterior probabilities by individual, this requires point estimates of trait frequencies. Table 1 includes the frequencies for twenty-five traits and seven backup traits for the seven major populations (i.e., geno-geographic groups) used in calculating probabilities (new traits highlighted in green; backup traits highlighted in yellow). To explore how well rASUDAS2 worked with modern data, the data collected in this study were input into the program to test its suitability.

Table 1. Trait frequencies used in rASUDAS2 to compute posterior probabilities.

Trait and tooth	Breakpoints	American Arctic & NE Siberia	Australo-Melanesia & Micronesia	East Asia	American Indian	Southeast Asia & Polynesia	Sub-Saharan Africa	Western Eurasia
Winging UI1	0	0.773	0.860	0.746	0.500	0.773	0.967	0.938
	1+	0.227	0.140	0.254	0.500	0.227	0.033	0.062
Shoveling UI1	0 + 1	0.027	0.370	0.026	0.005	0.336	0.443	0.817
	2 + 3	0.811	0.606	0.654	0.542	0.589	0.558	0.181
	4+	0.162	0.024	0.319	0.453	0.074	0.000	0.002
Shoveling UI2	0+1	0.093	0.694	0.062	0.025	0.458	0.845	0.891
	2+3	0.646	0.277	0.473	0.448	0.477	0.155	0.109
	4+	0.261	0.029	0.465	0.527	0.065	0.000	0.000
Double-shov UI1	0-1	0.449	0.896	0.576	0.227	0.746	0.981	0.860
	2+	0.551	0.104	0.424	0.773	0.254	0.019	0.140
Interruption grooves UI2	0	0.376	0.804	0.587	0.490	0.703	0.916	0.629
	1+	0.624	0.196	0.413	0.510	0.297	0.084	0.371
Bushman Canine	0-1	1.000	0.972	0.992	0.994	0.980	0.771	0.972
	2+	0.000	0.028	0.008	0.006	0.020	0.229	0.028
Canine tubercle	0-1	0.691	0.617	0.836	0.699	0.522	0.449	0.690
	2+	0.309	0.383	0.164	0.301	0.468	0.551	0.310
New and back up UI1 TD	0-1	0.649	0.559	0.651	0.551	0.674	0.533	0.563
	2+	0.551	0.441	0.349	0.449	0.326	0.467	0.437
Hypocone UM2	0+1	0.145	0.059	0.097	0.115	0.018	0.086	0.253
	2+3	0.612	0.210	0.320	0.417	0.200	0.167	0.255
	4+	0.243	0.731	0.583	0.468	0.692	0.747	0.492
Carabelli's trait	0+1	0.845	0.606	0.690	0.620	0.647	0.460	0.450
UM1	2+3+4	0.134	0.213	0.165	0.325	0.168	0.426	0.288
	5+	0.021	0.182	0.145	0.055	0.185	0.144	0.262
Cusp 5 UM1	0	0.824	0.415	0.809	0.833	0.705	0.725	0.853
	1+	0.176	0.585	0.191	0.167	0.295	0.275	0.147
Cusp 5 UM2	0	0.802	0.656	0.916	0.864	0.878	0.686	0.892
	1+	0.138	0.344	0.089	0.136	0.122	0.314	0.108
Enamel extensions UM1	0+1	0.569	0.932	0.585	0.563	0.735	0.993	0.978
	2+3	0.431	0.068	0.415	0.437	0.265	0.007	0.022
Enamel extensions LM1	0-1	0.448	0.881	0.458	0.630	0.669	0.997	0.959
	2+	0.552	0.119	0.542	0.370	0.231	0.003	0.041
Lower canine distal accessory ridge	0-1	0.482	0.853	0.602	0.364	0.863	0.619	0.889
	2+	0.518	0.147	0.398	0.636	0.137	0.381	0.111
Multiple lingual cusps LP2	0+1	0.604	0.253	0.300	0.602	0.191	0.333	0.371
	2+3	0.396	0.747	0.700	0.398	0.809	0.667	0.629
Multiple lingual cusps LP1	0-1	0.803	0.604	0.654	0.675	0.592	0.752	0.867
	2+	0.197	0.396	0.346	0.325	0.408	0.248	0.132
Groove pattern LM2	X and +	0.721	0.666	0.750	0.902	0.703	0.640	0.735
	Y	0.279	0.334	0.250	0.098	0.297	0.460	0.265
4-cusped LM2	5	0.943	0.647	0.697	0.914	0.679	0.744	0.254
	4	0.057	0.363	0.303	0.086	0.321	0.256	0.746
4-cusped LM1	5	1.000	0.945	1.000	0.996	0.990	0.975	0.863
	4	0.000	0.055	0.000	0.004	0.010	0.025	0.137
Cusp 6 LM1	0	0.525	0.586	0.633	0.449	0.521	0.890	0.935
	1+	0.475	0.414	0.367	0.551	0.479	0.110	0.065
Cusp 6 LM2	0	0.782	0.864	0.858	0.746	0.915	0.902	0.983
	1+	0.218	0.136	0.142	0.254	0.095	0.098	0.017

Table 1. continued.

Trait	Breakpoints	American Arctic & NE Siberia	Australo-Melanesia & Micronesia	East Asia	American Indian	Southeast Asia & Polynesia	Sub-Saharan Africa	Western Eurasia
Cusp 7 LM1	0	0.962	0.931	0.945	0.939	0.945	0.674	0.956
	1+	0.038	0.069	0.055	0.061	0.055	0.326	0.044
Protostylid LM1	0	0.815	0.928	0.758	0.621	0.843	0.891	0.901
	1	0.169	0.061	0.137	0.321	0.231	0.100	0.091
	2+	0.016	0.011	0.106	0.060	0.012	0.009	0.008
Deflecting wrinkle LM1	0+1+2	0.426	0.737	0.637	0.335	0.641	0.950	0.871
	3	0.574	0.263	0.363	0.665	0.359	0.050	0.129
UP1 root number	1	0.942	0.612	0.744	0.857	0.644	0.359	0.501
	2+3	0.058	0.388	0.256	0.143	0.356	0.641	0.499
UM2 root number	1+2	0.624	0.301	0.355	0.441	0.386	0.189	0.391
	3	0.376	0.699	0.645	0.559	0.614	0.812	0.609
LC root number	1	1.000	0.999	0.988	0.993	0.993	0.957	0.939
	2	0.000	0.001	0.012	0.007	0.007	0.043	0.061
Tomes root LP1	1+2+3	0.985	0.815	0.842	0.801	0.809	0.823	0.885
	4+	0.015	0.185	0.158	0.199	0.191	0.177	0.115
3-rooted LM1	1+2	0.773	0.967	0.803	0.934	0.899	0.963	0.995
	3	0.227	0.033	0.197	0.066	0.101	0.037	0.005
LM2 root number	2	0.686	0.871	0.700	0.672	0.722	0.943	0.752
	1	0.314	0.129	0.300	0.328	0.278	0.057	0.248
Pegged-reduced- missing UM3	0	0.786	0.936	0.641	0.842	0.792	0.950	0.835
	1	0.232	0.064	0.359	0.158	0.208	0.050	0.165

Dental metric data were collected on the maximum crown diameters in the buccolingual and mesiodistal dimensions (Hillson, FitzGerald, and Flinn 2005; Moorrees and Reed 1964). Additionally, and unique to this study, data were collected on the cervical dimensions of the crown in the mesiodistal and buccolingual dimensions, following Hillson and colleagues (2005). These data were analyzed to explore sexual dimorphism. Data were subject to independent sample *t-tests* to identify differences between the male and female groups. Additionally, sexual dimorphism for each dental measurement was calculated according to Garn et al. (1967). In which the male:female ratio is calculated as a percentage (male/female-1.00). Positive values indicate males are larger; negative values indicate females are larger. Sectioning points for each dental measurement were also identified that can be used in sex estimation methods, in much the same way postcranial measurements are used (e.g., Spradley and Jantz 2011).

Statistical analyses were conducted using the R statistical computing environment (R Core Team 2019), Microsoft Excel, and SPSS v. 26 (SPSS Inc. 2019). All results are presented in “Results and Findings.”

Expected Applicability of the Research

To collect data on any biological variable requires training augmented by experience. To make observations on tooth crown and root morphological traits or to measure the dimensions of teeth are no exception. Workshops are a useful tool to introduce forensic practitioners to the basics of collecting data on tooth morphology and size; we have been actively engaged in training forensic anthropologists through workshops. Plus, there are written descriptions of crown and root traits (e.g., Edgar 2017; Scott and Irish 2017) that can be augmented by the standard plaques for crown traits distributed by Bone Clones (i.e., Turner-Scott Dental Anthropology System). Moreover, the Dentabase we created and its accompanying manual with trait descriptions can serve as a means to standardize data collection.

Once individuals have gained familiarity and experience with making dental observations, the application for estimating ancestry – rASUDAS2 – is available as freeware and can be used on a phone, tablet, or computer, making its use in the field or lab equally accessible. Work is ongoing to incorporate the metric data to understanding human variation. However, the metric data can be incorporated into estimations of sex assigned at birth using the tables herein and through additional work to develop methods.

We expect forensic anthropology practitioners to employ rASUDAS in casework as well as to incorporate information on sexual dimorphism on dental metrics. The Dentabase will be

used by students and professionals for additional data collection and can be used to better understand dental morphological and metric data collection and analysis.

Participants and Other Collaborating Organizations

Data were collected at several institutions in South Africa (Stellenbosch University, Pretoria University, and Witwatersrand University) and the United States (University of Tennessee, Knoxville and Texas State University, San Marcos). Graduate students, Dorottya Kenessey and Tatiana Vlemincq-Mendieta, were trained by the two PIs in dental data collection and data analysis and assisted in all phases of the project. Additionally, an undergraduate researcher and McNair scholar, SaMoura Horsley, as well as an additional graduate student at the University of Nevada, Reno, Cassie Skipper, have conducted analyses with the data collected. Dr. Rebecca George, while a doctoral student at the University of Nevada, Reno, assisted with database management. Dr. Casey Philbin of UNR created the Dentabase and worked on the manual explaining its use. David Navega and Joao Coelho, of the University of Coimbra, created the rASUDAS2 application that provides estimates of ancestry/population affinity and is being updated with the data collected as part of this project.

Changes in Approach from Original Design and Reason for Change

The PIs originally planned to validate the programs using data collected from Medical Examiner's Offices in the western United States. Further, they planned to collect data in South America to augment the sample. Due to COVID and travel restrictions imposed by the University of Nevada, Reno and other countries, such travel was not taken. This situation modified the outcomes of the project slightly but did not alter the overall project itself.

Outcomes

Activities/Accomplishments

Several conference presentations were given based on the data collected as part of this project. A dissertation, a master's thesis, and an undergraduate McNair scholar research project all utilized data from this project, thus far. Two workshops were given based on this research. An updated web-based application for ancestry/population affinity estimation is underway. Finally, a database was created (Dentabase) in which dental morphological and metric data can be collected. This database is queryable and works to assist the researcher in data analysis. A manual was also created for this database. Both the database and manual as well as the web-based application are freely available to researchers. All of these activities and accomplishments are outlined below under "Artifacts." Finally, the data collected for this project will be made publicly available to scholars for additional research.

Results and Findings

Dental Morphology

Trait frequencies used in the Bayes algorithm to calculate posterior probabilities within rASUDAS2 were derived from archaeological samples examined by C.G. Turner II, J.D. Irish, and G.R. Scott. To test applicability to modern samples, modern data collected for this project from self-identified individuals from South Africa and the United States (South African Black, European/White, South African Coloured, American Black/African American) were input into rASUDAS2 using between 12 and 25 traits. Scott et al. (2021) used the application to address a bioarchaeological problem and found that results could be obtained when twelve or more traits were scored. Table 2 illustrates group assignment for each sample in this study.

Table 2. Group assignment for study samples in rASUDAS2.

	South African Black	European White	South African Coloured	American Black/ African American
n	159	161	58	25
Western Eurasia	0.220	0.752	0.293	0.320
East Asia	0.006	0.000	0.034	0.000
American Arctic	0.044	0.019	0.086	0.000
Non-Arctic American	0.006	0.000	0.000	0.000
Southeast Asia	0.006	0.025	0.069	0.120
Austral-Melanesia	0.031	0.075	0.103	0.150
Sub-Saharan Africa	0.686	0.130	0.414	0.400

Overall, group assignment accuracy has improved in the new version of the application. Although the trait frequencies used in the Bayes algorithm are mostly from archaeological remains, the application works well with modern populations. Individuals who self-identified as European and African were not often assigned to an Asian or Asian-derived group. To better distinguish these populations, additional traits will be added to the current rASUDAS2 trait list (e.g., crenulations, mid-line diastemas, shouldered upper premolars) once population frequencies have been estimated for the seven major geno-geographic groups.

Dental Metrics

Every metric variable in the dataset for every tooth under investigation was found to be significantly different between males. The percent dimorphism was positive in every case, indicating that males were larger. Tables 3 and 4 summarize these results; they also provide a sectioning point that can be used to estimate the sex of an individual.

Table 3. Statistical analyses of measurements of the crown.

		FEMALE (n=268)			MALE (n=552)			<i>t-test</i>	Mean Difference	%dimorphism	Sect. pt
		Mean	St Dev	<i>p-value</i>	Mean	St Dev	St Error	<i>p-value</i>	M-F	(M/F-1.00)	(M+F)/2
Maxilla	I1_MD	8.45	0.53	0.04	8.69	0.63	0.04	<.001	0.24	2.84	8.57
	I1_BL	6.98	0.44	0.03	7.28	0.45	0.02	<.001	0.30	4.30	7.13
	I2_MD	6.59	0.64	0.05	6.86	0.64	0.03	<.001	0.27	4.10	6.73
	I2_BL	6.25	0.47	0.03	6.57	0.51	0.03	<.001	0.32	5.12	6.41
	C_MD	7.41	0.91	0.06	7.81	0.50	0.02	<.001	0.40	5.40	7.61
	C_BL	7.98	0.53	0.03	8.59	0.58	0.03	<.001	0.61	7.64	8.29
	P3_MD	6.90	0.53	0.04	7.08	0.51	0.02	<.001	0.18	2.61	6.99
	P3_BL	9.12	0.67	0.04	9.43	0.76	0.03	<.001	0.31	3.40	9.28
	P4_MD	6.49	0.52	0.04	6.66	0.55	0.03	<.001	0.17	2.62	6.58
	P4_BL	9.17	0.64	0.04	9.52	0.67	0.03	<.001	0.35	3.82	9.35
	M1_MD	10.26	0.71	0.05	10.54	0.86	0.04	<.001	0.28	2.73	10.40
	M1_BL	11.15	0.61	0.04	11.66	0.59	0.03	<.001	0.51	4.57	11.41
	M2_MD	9.76	0.75	0.05	10.03	0.80	0.04	<.001	0.27	2.77	9.90
	M2_BL	11.35	0.76	0.05	11.93	0.83	0.04	<.001	0.58	5.11	11.64
	M3_MD	8.81	0.88	0.09	9.14	0.85	0.05	0.001	0.33	3.75	8.98
M3 BL	10.91	1.07	0.10	11.47	1.12	0.07	<.001	0.56	5.13	11.19	
Mandible	I1_MD	5.22	0.42	0.03	5.37	0.44	0.02	<.001	0.15	2.87	5.30
	I1_BL	5.66	0.37	0.03	5.90	0.39	0.02	<.001	0.24	4.24	5.78
	I2_MD	5.79	0.41	0.03	5.97	0.47	0.02	<.001	0.18	3.11	5.88
	I2_BL	6.08	0.38	0.03	6.29	0.45	0.02	<.001	0.21	3.45	6.19
	C_MD	6.57	0.43	0.03	7.03	0.48	0.02	<.001	0.46	7.00	6.80
	C_BL	7.35	0.47	0.03	8.05	0.59	0.03	<.001	0.70	9.52	7.70
	P3_MD	6.93	0.50	0.03	7.17	0.53	0.02	<.001	0.24	3.46	7.05
	P3_BL	7.71	0.59	0.04	8.06	0.59	0.03	<.001	0.35	4.54	7.89
	P4_MD	7.04	0.55	0.04	7.23	0.60	0.03	<.001	0.19	2.70	7.14
	P4_BL	8.26	0.61	0.04	8.55	0.58	0.03	<.001	0.29	3.51	8.41
	M1_MD	10.79	0.67	0.05	11.17	0.67	0.03	<.001	0.38	3.52	10.98
	M1_BL	10.25	0.60	0.04	10.60	0.66	0.03	<.001	0.35	3.41	10.43
	M2_MD	10.58	0.76	0.06	10.95	0.81	0.04	<.001	0.37	3.50	10.77
	M2_BL	10.10	0.77	0.06	10.52	0.70	0.03	<.001	0.42	4.16	10.31
	M3_MD	10.68	0.96	0.10	11.20	1.01	0.06	<.001	0.52	4.87	10.94
M3 BL	10.07	0.88	0.09	10.49	0.77	0.04	<.001	0.42	4.17	10.28	

Table 4. Statistical analyses of measurements of the cervix.

		FEMALE (n=268)			MALE (n=552)			<i>t</i> -test	Mean Difference M-F	%dimorphism (M/F-1.00)	Sect. pt (M+F)/2
		Mean	St Dev	St Error	Mean	St Dev	St Error	<i>p</i> -value			
Maxilla	I1_MD	6.19	0.55	0.04	6.46	0.59	0.03	<.001	0.27	4.36	6.33
	I1_BL	6.29	0.45	0.03	6.63	0.45	0.02	<.001	0.34	5.41	6.46
	I2_MD	4.73	0.56	0.04	5.04	0.52	0.03	<.001	0.31	6.55	4.89
	I2_BL	5.80	0.43	0.03	6.23	0.50	0.03	<.001	0.43	7.41	6.02
	C_MD	5.36	0.40	0.03	5.85	0.45	0.02	<.001	0.49	9.14	5.61
	C_BL	7.43	0.51	0.03	8.17	0.61	0.03	<.001	0.74	9.96	7.80
	P3_MD	4.65	0.50	0.03	4.91	0.44	0.02	<.001	0.26	5.59	4.78
	P3_BL	8.19	0.67	0.05	8.65	0.68	0.03	<.001	0.46	5.62	8.42
	P4_MD	4.74	0.67	0.05	4.94	0.47	0.02	<.001	0.20	4.22	4.84
	P4_BL	8.17	0.78	0.05	8.76	0.70	0.03	<.001	0.59	7.22	8.47
	M1_MD	7.49	0.66	0.05	7.86	0.61	0.03	<.001	0.37	4.94	7.68
	M1_BL	10.13	0.65	0.05	10.60	0.64	0.03	<.001	0.47	4.64	10.37
	M2_MD	7.35	0.82	0.06	7.84	0.78	0.04	<.001	0.49	6.67	7.60
	M2_BL	10.18	0.75	0.05	10.74	0.79	0.04	<.001	0.56	5.50	10.46
	M3_MD	6.73	1.04	0.11	7.14	0.79	0.05	<.001	0.41	6.09	6.94
M3 BL	9.54	1.00	0.10	10.13	0.96	0.06	<.001	0.59	6.18	9.84	
Mandible	I1_MD	3.56	0.34	0.02	3.69	0.34	0.02	<.001	0.13	3.65	3.63
	I1_BL	5.38	0.43	0.03	5.68	0.41	0.02	<.001	0.30	5.58	5.53
	I2_MD	3.90	0.36	0.02	4.10	0.41	0.02	<.001	0.20	5.13	4.00
	I2_BL	5.81	0.42	0.03	6.08	0.41	0.02	<.001	0.27	4.65	5.95
	C_MD	5.01	0.41	0.03	5.60	0.49	0.02	<.001	0.59	11.78	5.31
	C_BL	7.10	0.49	0.03	7.85	0.58	0.03	<.001	0.75	10.56	7.48
	P3_MD	4.84	0.39	0.03	5.15	0.43	0.02	<.001	0.31	6.40	5.00
	P3_BL	6.83	0.55	0.04	7.26	0.57	0.03	<.001	0.43	6.30	7.05
	P4_MD	5.06	0.44	0.03	5.37	0.49	0.02	<.001	0.31	6.13	5.22
	P4_BL	7.16	0.59	0.04	7.60	0.59	0.03	<.001	0.44	6.15	7.38
	M1_MD	8.87	0.60	0.05	9.24	0.63	0.03	<.001	0.37	4.17	9.06
	M1_BL	8.74	0.59	0.05	9.16	0.65	0.03	<.001	0.42	4.81	8.95
	M2_MD	9.13	0.70	0.06	9.51	0.72	0.04	0.000	0.38	4.18	9.32
	M2_BL	8.73	0.70	0.05	9.18	0.70	0.03	<.001	0.45	5.15	8.96
	M3_MD	9.10	1.18	0.17	9.72	1.11	0.09	<.001	0.62	6.81	9.41
M3_BL	8.65	0.79	0.10	9.12	0.84	0.05	<.001	0.47	5.43	8.89	

The cervical measurements of the teeth exhibit much higher levels of sexual dimorphism than do those of the crown. Cervical measurements of the upper and lower canine show the highest levels of dimorphism (between 9.14% and 11.78%); however, the mesiodistal crown measurement of the lower canine is also in this range with 9.52% dimorphism. In a simple discriminant function analysis to estimate sex using only these five variables, the cross-validated model was able to correctly estimate sex in 81.0% of cases (Table 5).

Table 5. Confusion matrix results of cross-validated results of discriminant function analysis.

	Female	Male	Total
Female (n)	123	68	191
Male (n)	42	346	388
Female (%)	64.4	35.6	100.0
Male (%)	10.8	89.2	100.0

These preliminary analyses indicate discriminatory power using the dentition to estimate sex (assigned at birth), particularly when the canine teeth can be used. Future work on dental metrics will incorporate more advanced statistical methods (e.g., fuzzy logic and machine learning techniques) with the ultimate goal of combining the dental and metric data to explore modern dental human variation further.

Limitations

Due to COVID restrictions, data could not be collected to create a more global sample. Therefore, the current dataset is somewhat limited in that it only represents the United States and South Africa; although, it is augmented with data previously collected from Asia. Further, the PIs were unable to travel to collect data within the United States at Medical Examiner’s offices

as originally planned. As such, the results presented herein, have not yet been fully validated with data from forensic cases.

Artifacts

List of products (e.g., publications, conference papers, technologies, websites, databases), including locations of these products on the Internet or in other databases

Conference Presentations

- 2022 Scott, G. Richard, David Navega, Joao Coelho, Dori E. Kenessey, Tatiana Vlemincq-Mendieta, Marin A. Pilloud. *Tooth morphology and population affinity: testing rASUDAS2 on modern African and European-derived samples*. American Association of Biological Anthropologists: contributed poster presentation.
- 2022 Horsley, SaMoura L., Cassie Skipper, Marin A. Pilloud. *The Combined Use of Craniometrics and Odontometrics to Estimate Parameters of the Biological Profile*. American Academy of Forensic Sciences: contributed poster presentation.
- 2021 Skipper, Cassie E., SaMoura L. Horsley, Dori Kenessey, Tatiana Vlemincq-Mendieta, G. Richard Scott, Marin A. Pilloud. *Population variation in the occurrence of midline and canine diastemata*. American Academy of Forensic Sciences: contributed poster presentation.
- 2021 Scott, G. Richard, David Navega, Joao Coelho, Dori Kenessey, Tatiana Vlemincq-Mendieta, Marin A. Pilloud. *Tooth morphology and population affinity: testing rASUDAS2 on modern African and European-derived samples*. Virtual presentation at XV Jornadas Nacionales De Antropología Biológica, Buenos Aires, Argentina.
- 2021 Scott, G. Richard, D. Navega, Joao Coelho. *The evolution of rASUDAS and its application to bioarchaeological problems*. Invited lecture (virtual): Cycle of Conferences of CIAS, Coimbra, Portugal.
- 2020 Kenessey, Dori E., Tatiana Vlemincq-Mendieta, G. Richard Scott, and Marin A. Pilloud. *Global variation in dental crowding*. American Association of Physical Anthropologists: contributed poster presentation.
- 2020 Kenessey, Dori E., Tatiana Vlemincq-Mendieta, G. Richard Scott, Marin A.

Pilloud. *Odontometric variation of male skeletal samples from the United States and South Africa*. American Academy of Forensic Sciences: contributed poster presentation

- 2018 Scott, G. Richard, Rose Perash, Laura E. Cirillo, Cortney H. Hulse, M.J. Schroeder, Cassie E. Skipper, and Samantha Gonzalez. *Testing the Beta version of rASUDAS: promises and pitfalls*. American Association of Physical Anthropologists: contributed poster presentation.

Publications

- In progress. Scott, G. Richard, David Navega, Joao Coelho, Marin A. Pilloud, Eugenia Cunha, and Joel D. Irish. rASUDAS2: updated application for estimating population affinity from tooth crown and root morphology. To be submitted to *Forensic Anthropology*
- 2021 Scott, G. Richard, Dennis H. O'Rourke, J.A. Raff, J.C. Tackney, Leslea J. Hlusko, Scott A. Elias, L. Bourgeon, O. Potapova, E. Pavlova, V. Pitulko, and John F. Hoffecker. Peopling the Americas: Not "Out of Japan." *Paleoamerica* 7:309-332.
- 2018 Scott, G. Richard, David Navega, Joao Coelho, Marin A. Pilloud, Eugenia Cunha, and Joel D. Irish. rASUDAS: a new web-based application for estimating ancestry from tooth morphology. *Forensic Anthropology*, 1:18-31.

Dissertations/Theses

- Summer 2022 Andrea Sbei. *Odontometric Sex Estimation Using a Modern Forensic Skeletal Collection*. University of Nebraska, Lincoln; Department of Anthropology. Master's thesis.
- 2022 Cassie Skipper. *Investigating the Utility of Metric and Morphological Cranial and Dental Ancestry Estimation Methods on Modern Japanese, South Korean, and Thai Populations*. University of Nevada, Reno; Department of Anthropology. Doctoral dissertation.
- 2022 SaMoura Horsley. *Use of Craniometrics and Odontometrics to Estimate Parameters of the Biological Profile*. University of Nevada, Reno; Department of Anthropology. McNair Scholar Undergraduate Research Project.

Workshops

- 2019 Marin A. Pilloud. *Dental Morphology and Development in Forensic Anthropology*. Three-day workshop (25-27 June) given to the Defense POW/MIA Accounting Agency; Joint Base Pearl Harbor Hickam; Hawaii
- 2019 Marin A. Pilloud, G. Richard Scott, Christine Pink, and Rebecca George. *The Use of Dental Morphology in Forensic Anthropology*. Full-day workshop given at the American Academy of Forensic Sciences annual scientific meeting (19 February); Baltimore, Maryland

Application

rASUDAS2

<https://osteomics.com/rASUDAS2/>

Database

Dentabase. Access database to collect dental morphological and metric data. Available via request to PI Marin Pilloud (mpilloud@unr.edu).

Dentabase Manual

Pilloud, M.A., Kenessey, D.D., Vlemincq-Mendieta, T., Scott, G.R., Philbin, C.S. 2022 *Dentabase Manual*. Reno, NV. University of Nevada, Reno.
<https://sites.google.com/view/pilloudlab/dentabase?authuser=0>

Data sets generated (broad descriptions will suffice)

Dental metric and morphological data were collected on 708 individuals and data on dental morphology were collected on an additional 124 individuals (n=832) in South Africa and the United States (Table 6). These data will be made available to the public for research projects. Researchers may contact the PI, Marin Pilloud (mpilloud@unr.edu) for access to these data.

Table 6. Total data collected during project duration.

Collection	Metric data	Morphological data
Pretoria University, South Africa	148	272
Stellenbosch University, South Africa	106	106
University of the Witwatersrand, South Africa	99	99
University of Tennessee, Knoxville	253	253
Texas State University, San Marcos	102	102
TOTAL	708	832

Dissemination activities

The web-based application, rASUDAS, and the Dentabase database and manual are freely available to researchers on the internet. The PIs and collaborators will continue to work on these data and to share them with other researchers to advance our understanding of dental variation.

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