Research Square

Preprints are preliminary reports that have not undergone peer review.
They should not be considered conclusive, used to inform clinical practice,
or referenced by the media as validated information.

A Robust Forensic Reasoning To Estimate The Minimum Number Of Individuals: The Certain Exclusion

Siam Knecht

siam.knecht@univ-amu.fr

Aix Marseille Univ, CNRS, EFS, ADES

Lucie Biehler-Gomez

University of Milan

Gabriele Krüger

University of Pretoria

Leandi Liebenberg

University of Pretoria

Mustapha Ouladsine

LIS UMR 7020 CNRS, Aix Marseille Université

Cristina Cattaneo

University of Milan

Christophe Roman

LIS UMR 7020 CNRS, Aix Marseille Université

Pascal Adalian

Aix Marseille Univ, CNRS, EFS, ADES

Research Article

Keywords: MNI, forensic anthropology, exclusion, regression, skeletal assemblage, commingling, osteometry

Posted Date: June 18th, 2026

DOI: https://doi.org/10.21203/rs.3.rs-9940913/v1

License: This work is licensed under a Creative Commons Attribution 4.0 International License.
Read Full License

Additional Declarations: No competing interests reported.

Version of Record: A version of this preprint was published at International Journal of Legal Medicine on June 20th, 2026. See the published version at https://doi.org/10.1007/s00414-026-03884-0.

Abstract

Estimating the Minimum Number of Individuals (MNI) in commingled skeletal assemblages is a core task in forensic and archaeological anthropology. Traditional methods, based on the frequency of lateralized elements, often suffer from underestimation due to fragmentation and morphological similarity. This study introduces a new MNI estimation method grounded in the principle of certain exclusion (with a 99% confidence interval), which focuses on detecting osteometric incompatibilities between elements rather than identifying matches. We developed linear regression models based on a large international dataset (n = 2,969 individuals) to generate 99% prediction intervals between long bone measurements. A recursive protocol, termed Allometric Research by Exclusion (RAE), was implemented to isolate bones that cannot belong to the same individual. The method was validated via bootstrap simulations using independent samples from the Milano and Pretoria Bone collections. Across all assemblages, the exclusion-based MNI estimates were consistently higher than those obtained by frequency-based methods, and more closely approximated the real number of individuals. This trend was especially clear in small to mid-sized assemblages, where precise MNI estimation is most critical. The exclusion method offers a statistically grounded, replicable, and conservative approach to MNI estimation. Its integration into forensic and archaeological workflows may enhance the accuracy and defensibility of population reconstruction in complex contexts.

Introduction

The estimation of the Minimum Number of Individuals (MNI) is a fundamental step in both archaeological and forensic anthropology when analyzing assemblages of commingled human remains. Defined as the smallest number of individuals necessary to account for all present, identified skeletal elements, the MNI provides a critical metric for contextualizing mortuary practices, reconstructing past populations, or managing mass fatality incidents. Its importance spans a wide range of applications, from documenting funerary assemblages to identifying victims in forensic scenarios, where legal and ethical obligations request the highest possible standards of accuracy and reproducibility [1, 2].

Over the past decades, several methodological approaches have been developed to estimate the MNI, each reflecting different disciplinary applications, levels of preservation, and types of assemblages. The most widely used method, often referred to as determining the MNI frequency, involves identifying the most frequently occurring lateralized element, under the assumption that a single individual cannot contribute more than one instance of the same-sided element (e.g., left or right femur) [3, 4]. While this approach is the most conservative, straightforward and widely applicable, it often suffers from significant limitations. Its accuracy is highly sensitive to differential preservation, recovery bias, and fragmentation, all of which can artificially lower the MNI and obscure the true demographic or forensic significance of the assemblage.

In addition to frequency-based MNI estimates, probabilistic methods have been developed to estimate the Most Likely Number of Individuals (MLNI), which explicitly account for uncertainty and preservation

bias [3, 5]. More refined methods have incorporate aspects such as the spatial distribution of remains, taphonomic signatures, or osteometric and morphological variation [6]. Quantitative approaches, such as pair-matching, template-based reconstructions, and statistical models, have also been introduced, particularly in forensic contexts where the stakes of underestimating the number of individuals are especially high [7–16]. Nevertheless, these techniques often require complete or nearly complete bones, access to reference populations, or complex computational tools, which may not always be available or feasible, especially in forensic context where methods must be as easy to use and efficient as possible. In addition, the expert-based interpretation may introduce variability in the results, potentially reducing the method's reliability. To our knowledge, no studies have yet assessed the variability in expert interpretation for this type of method.

A particularly challenging issue in MNI estimation is the presence of fragmentary remains, which can neither be definitively paired nor confidently assigned to a known individual. In such cases, traditional methods tend to default to conservative estimates, prioritizing minimal assumptions at the expense of potential underestimation. This conservative bias, while methodologically cautious, can lead to substantial discrepancies between the actual and estimated number of individuals, especially in cases involving highly commingled or poorly preserved assemblages. Recent computational approaches have sought to address this limitation by developing automated pair-matching methods specifically designed for fragmented skeletal remains, including two-dimensional form registration techniques [17].

An additional and critical limitation arises when attempting to associate skeletal fragments between individuals with closely similar morphological characteristics. In contexts where individuals are biologically or demographically homogeneous—such as mass graves involving young adult males from the same population—morphometric differences between elements can be minimal, increasing the risk of incorrect positive associations. Osteometric sorting approaches have shown that size disparity between individuals is a key factor limiting the effectiveness of such associations and that these methods are more reliable for identifying metric incompatibilities than for establishing positive matches [18, 19]. In this perspective, prioritizing exclusion by identifying elements that cannot belong to the same individual rather than probabilistic association reduces the risk of over-aggregation and improves the robustness of MNI estimation.

Consequently some researchers have explored alternative strategies that focus not on identifying matches between elements, but on detecting exclusive anatomical features, remains that could not possibly originate from the same individual. The logic of exclusion, rather than inclusion, thus offers a promising conceptual shift. Notably, Parmentier et al. [20] proposed a methodology grounded in identifying "certain exclusions" between elements based on morphometrical incompatibility. This approach has the advantage of generating robust lower-bound estimates of MNI that are less sensitive to fragment size or preservation state.

Building on this framework, the present study introduces an extension or validation of a previously proposed approach to MNI estimation based explicitly on the principle of certain exclusion. Our method

formalizes and expands the concept by providing a systematic, reproducible, and scalable protocol for identifying mutually exclusive skeletal elements, even in highly fragmented assemblages. Through a combination of anatomical assessment, logical structuring, and computational implementation, we aim to offer a more reliable tool for estimating the minimum number of individuals represented in complex assemblages. This contribution is particularly relevant for forensic and bioarchaeological contexts where accuracy, transparency, and methodological rigor are paramount.

Material and methods

Data

This study draws on an extensive dataset of long bone measurements from 3,302 adult individuals, including 1,379 females and 1,923 males, encompassing a wide chronological and geographical diversity (Table 1). The data were compiled from eight distinct osteological collections and merged into a shared database used to train regression models. To ensure robust external validation, two contemporary collections—the CAL Milano and Pretoria Bone Collections (PBC) —were deliberately excluded from the modeling phase and used solely for testing.

The training dataset includes both archaeological and anatomical series. The Goldman dataset, curated by Dr. Benjamin Auerbach, contributed the largest sample (n = 1,528) and includes postcranial measurements from European individuals spanning antiquity to the present day. Three archaeological collections from southern France—Laudun (5th–13th century), La Ciotat (LC-HOP, 16th–19th century), and Marseille Petites Crottes (MPC, 18th–20th century)—provided an additional 485 individuals. These collections are curated at the UMR ADES osteological library and the "Ostéothèque DRAC PACA" in Marseille. The Robert J. Terry Anatomical Collection (n = 454), held at the Smithsonian Institution's National Museum of Natural History in Washington D.C., offered well-preserved 20th-century skeletons with detailed documentation [21]. Two modern French anatomical collections were also included: the Nice Collection (n = 40), composed of body donations for research and education in accordance with French legislation, and the Olivier Collection (n = 102), housed at the Muséum national d'Histoire naturelle (MNHN) in Paris, which includes biological profiles such as sex, age at death, and stature.

Validation was carried out using two independent, demographically documented collections. The CAL Milano Cemetery Skeletal Collection, curated by the Laboratory of Forensic Anthropology and Odontology (LABANOF) at the University of Milan, consists of over 2,000 unclaimed individuals born between 1866 and 2000, of whom 333 were selected for this study [22]. The Pretoria Bone Collection (PBC), housed in the Department of Anatomy at the University of Pretoria, was established in 1942 with the creation of the medical school [23, 24]. Initially conceived as a teaching aid, the collection was reorganized in 2000 into a research-oriented resource with well-documented demographic information. The majority of individuals are Black South African males, reflecting both the demographic profile and historical labour migration patterns in Pretoria. All remains derive from whole-body donations or unclaimed bodies, in accordance with the South African National Health Act, and include metadata such

as sex, age, cause of death, and population affinity. Since 2018, a subset of the collection has been integrated into the Bakeng se Afrika digital repository, where selected cranial and postcranial elements have been scanned using micro-XCT, thereby expanding research opportunities and international accessibility. 360 post cranial skeletons were selected from PBC for this study.

Table 1: Collections selected for this study.

	Collection	Location	Time period	Sex	Females	Males	Total
Training sample	Goldman	Europe	Antiquity to the present day	Estimated	543	985	1528
	Laudun	France	5^{th} – 13^{th} century	Estimated	54	113	167
	LC-HOP	France	16^{th}-19^{th}	Estimated	105	109	214
	MPC	France	18^{th} – 20^{th} century	Estimated	57	47	104
	Nice	France	21^{st} century	Known	21	19	40
	Terry	USA	20^{th} century	Known	207	247	454
	Olivier	France	20^{th} century	Known	40	62	102
Test sample	CAL Milano	Italy	21^{st} century	Known	172	161	333
	PBC	South Africa	21^{st} century	Known	180	180	360
Total			Antiquity to the present day	Estimated and known	1379	1923	3302

Measurements

A total of 16 documented long bone measurements common to all collections were selected for this study (Table 2). These measurements encompass key anatomical dimensions, including maximum

lengths, measurements taken at the proximal and distal epiphyses, and midshaft regions [25, 26]. Measurements were conducted using calipers or osteometric boards to ensure precision and consistency. Data were primarily collected from the left side of the skeleton; in cases where the left side was absent, measurements were taken from the right side.

***Table 2**: Long bones measurements selected for this study.*

Anatomical localization	Bone	Code	Measurement
Upper limb	Humerus	humxln	Maximum length
		humebr	Distal epicondylar breadth
		humhhd	Maximum vertical diameter of the head
		hummxd	Maximum diameter midshaft
		hummwd	Minimum diameter midshaft
	Radius	radxln	Maximum length
		radtvd	Transverse diameter at midshaft
		radapd	Antero-posterior diameter at midshaft
Lower limb	Femur	femxln	Maximum length
		fembln	Physiological length
		femebr	Epicondylar breadth
		femhhd	Maximum diameter of the head
		femmtv	Medio-lateral diameter of the midshaft
		femmap	Antero-posterior diameter of the midshaft
	Tibia	tibxln	Lateral condyle - medial malleolus length
		tibpeb	Maximum proximal epiphyseal breadth

Modeling allometric relationships

Although the reference dataset is mostly composed of complete skeletal elements, the analytical framework predicts one osteometric measurement from another across different bones, thereby effectively simulating conditions of pronounced fragmentation. In this study, we propose an innovative method for estimating the Minimum Number of Individuals (MNI), based on the principle of certain exclusion, which relies on allometric relationships between different long bones. Rather than seeking to associate fragments with each other, this approach focuses on detecting morphometric incompatibilities, thus enabling the identification of bones that cannot belong to the same individual.

We developed a series of linear regression models using a **large and diverse reference database** composed from multiple anthropological collections (Table 1). Importantly, the **Milano (Italy) and Pretoria (South Africa) collections were intentionally excluded from the modeling phase** to serve as **independent datasets for validation.**

We have built a set of linear regression models from a common database containing over 2,609 individuals from a variety of anthropological collections (Table 1). This diversity is a major asset of our approach, increasing the morphological representativeness and statistical robustness of the models. The models were aggregated in an ensemble framework: for each anatomical pairing, several models predict one osteometric measurement from another, and their outputs are combined to assess compatibility. This ensemble strategy increases robustness by integrating multiple morphometric relationships rather than relying on a single regression equation.

Each model predicts one osteometric measurement from another (see Annex 1), and generates a 99% prediction interval. This threshold was chosen to promote exclusion reliability: while it reduces the total number of exclusions identified, it also reduces the risk of error, which is crucial in forensic or bioarchaeological contexts.

For each pair of osteometric measurements available in the sample, the observed value is compared with the expected prediction interval. If the target measurement lies outside the interval, we consider that the incompatibility is sufficient to exclude the possibility that the two bones come from the same individual. This process forms the basis of iterative exclusion testing.

Allometric Research by Exclusion (RAE)

The MNI estimation protocol is based on a series of iterations:

- Identification of improbable compatibilities: for a given measurement, all available measurements of another bone are compared. Improbable compatibilities between measurements are set aside in a sub-sample.
- Recursive exploration: this sub-sample is then analyzed in turn. Each new exclusion feeds a logical chain: at each stage, improbable compatibilities between elements are isolated and analyzed, until no new exclusion is detected.
- MNI calculation: at the end of the process, each exclusion chain identifies at least one distinct individual. The final MNI is then the maximum of the MNIs calculated from all the variables tested.
- This reasoning applies to all variables available in the sample. The aim is to provide a robust estimate of MNI, less sensitive to fragmentation or lateralization bias than conventional frequency-based methods.

This approach overcomes the limitations of conventional methods based on the frequency of lateralized elements, by integrating biological variability in a quantitative way.

Bootstrap validation

To evaluate the effectiveness of our method, we conducted a **bootstrap-based validation** using only the **Milan and Pretoria collections,** which were **excluded from model training**. At each iteration, a subsample of complete individuals is drawn at random from the test database, then fragmented to simulate a real assembly. We then compare: MNI by frequency, MNI by exclusion (RAE), and the real MNI (exact number of individuals in the draw).

Results

Across both validation samples, the Real Number of Individuals (RNI) consistently exceeded both the Minimum Number of Individuals estimated by frequency (Frequency MNI) and that estimated by certain exclusion (Exclusion MNI), confirming the conservative nature of both methods. However, the MNI derived from certain exclusion systematically provided closer estimates to the frequency-based approach, which generally improve the accuracy of an additional individual.

Table 3 presents the detailed results for each validation context (Milan and PBC), covering assemblages of increasing complexity. For the smallest assemblages (e.g., Milan 1 or PBC 1), both frequency and exclusion methods underestimated the RNI, but the gap was narrower using the exclusion approach. This trend became more pronounced as the number of individuals increased, in which we observed a sharp divergence from the RNI.

This systematic underestimation by frequency-based methods was especially evident in larger, more commingled samples. The exclusion method, while still conservative, showed a stronger capacity to approximate the actual population size by accounting for elements that could not possibly belong to the same individual, thus reducing the risk of erroneously aggregating fragments. Overall, these results support the validity of the certain exclusion method as a more accurate and operationally effective approach to estimating the MNI, particularly in complex or fragmentary assemblages.

***Table 3**: MNI estimation results by frequency, exclusion and real number of individuals.*

Validation sample	Frequency MNI	Exclusion MNI	Real Number of Individuals
Milan 2	1	1	2
PBC 3	1	3	3
Milan 5	3	4	5
PBC 7	3	5	7
Milan 8	4	5	8
PBC 9	5	6	9
Milan 10	6	6	10
PBC 11	3	6	11
Milan 15	7	8	15
PBC 18	6	8	18
Milan 23	10	12	23
PBC 25	9	11	25
Milan 29	11	14	29
PBC 31	12	15	31
Milan 38	11	13	38
PBC 44	16	18	44
Milan 48	17	18	48
PBC 50	19	20	50
Milan 58	18	19	58
PBC 70	25	26	70
Milan 79	27	28	79
PBC 95	40	42	95

Discussion

Estimating the Minimum Number of Individuals (MNI) in commingled assemblages remains a major methodological challenge in both forensic anthropology and bioarchaeology. Traditional approaches, particularly the frequency-based method, have remained dominant due to its simplicity and accessibility. However, these methods are known to be highly sensitive to fragmentation, preservation bias, and lateralization artefacts. As multiple studies have emphasized frequency approaches tend to

systematically underestimate MNI when remains are incomplete or demographically homogeneous, leading to distorted interpretations of assemblage composition (e.g., [1, 27]).

To overcome these limitations, researchers have explored alternative strategies, each with its own strengths and constraints. Alternative techniques, such as pair-matching, osteometric sorting [28], template reconstruction, and more recently, computational reconstructions using Bayesian models [29] or deviation analysis [30] offer refined tools but often require high data integrity and are sensitive to observer bias or missing data. For example, visual matching, while potentially powerful, can be subjective and time-consuming in the case of large sets [31]. Similarly, osteometric sorting methods [32], which use statistical models to compare measurements of even elements, can be affected by bone fragmentation and size disparity between individuals [19].

In contrast, the exclusion principle introduced by Parmentier et al. [20], marked a conceptual shift: rather than searching for matches (which are uncertain), the method emphasizes identifying incompatibilities, which can be stated with greater confidence. This approach is based on the fact that, in certain circumstances, it is possible to demonstrate definitively that two specimens could not belong to the same individual. In addition, the power of exclusion is particularly useful when faced with extremely fragmented remains or a partial body representation, where articular surfaces are missing or incomplete.

Our study builds upon and extends this exclusion-based framework by incorporating a systematic, regression-driven approach to identify allometric incompatibilities using a robust and diverse international reference dataset. Critically, by excluding the Milano and Pretoria samples from model training and using them solely for validation, we ensure that our results are not biased by overfitting or circular inference—a methodological shortcoming occasionally observed in previous literature when reference and test data are not sufficiently separated.

The results from our bootstrap validation clearly demonstrate the added value of this approach. As shown in Table 3 and Fig. 2, the exclusion-based method consistently outperforms frequency-based estimation, even if only in one case. While both methods remain conservative (i.e., systematically below the Real Number of Individuals, RNI), the exclusion method provides closer approximations to ground truth. This is particularly evident in small to mid-sized assemblages, where a discrepancy of even a single individual may drastically alter demographic or forensic interpretations. The fact that the exclusion-based MNI tends toward the frequency-based MNI is logically explained by the increasing number of individuals smoothing out the distribution, thus making separation between data points impossible. This tends toward a continuum, where discrete distinctions become unfeasible.

Importantly, the exclusion method demonstrates stability across a wide range of assemblage sizes, avoiding both the over-aggregation pitfalls of frequency counting and the data dependencies of more computationally intensive methods. The use of 99% prediction intervals provides an additional safeguard, ensuring high reliability even when precision is slightly sacrificed, which represents a trade-off that is fully justified in forensic or legal contexts. We opted for a 99% confidence interval after testing lower thresholds (e.g., 95%, 98%), which failed to encompass the full variability observed in the data;

given the stakes of forensic or sensitive bioarchaeological contexts, it is crucial to minimize the risk of underestimation and prioritize robustness over overly narrow precision.

Furthermore, this approach is scalable and reproducible. It does not rely on subjective assessments or complete elements but can operate on fragmented material with minimal input, making it especially suitable for real-world applications, including mass graves, secondary burials, or disaster victim identification (DVI) scenarios. Its computational implementation also opens the door for future integration into automated or semi-automated pipelines for assemblage analysis.

The exclusion method not only provides higher MNI values than the frequency approach, but also introduces an internal logic that justifies each additional individual. By only counting elements that cannot, with 99% certainty, originate from the same individual, each step of the MNI increase is methodologically grounded—addressing a long-standing need in the field for transparent and defensible reasoning in quantitative estimations.

Limitations and Perspectives

While the exclusion-based method demonstrates promising results and clear advantages over traditional approaches, several limitations should be acknowledged.

A key methodological consideration concerns the composition of the reference dataset used to train the allometric models. Osteometric sorting approaches are known to be sensitive to population-specific variation, and their performance may be affected when reference and target assemblages differ in chronology or biological background. In the present study, the use of a large and heterogeneous reference sample spanning multiple populations and time periods was a deliberate choice. Rather than aiming to optimize population-specific reassociation, our objective was to identify robust allometric incompatibilities that remain valid across a broad range of human variation. Importantly, the Milano and Pretoria collections were entirely excluded from model training and used exclusively for validation, ensuring that model performance was assessed under conservative conditions where reference and test samples do not overlap. This design provides a stringent test of the exclusion-based framework, although future work should explore the benefits of population-specific calibration when such information is available.

In addition to this population-related consideration, the method is dependent on the quality and completeness of osteometric data. Although designed to handle fragmented remains, it still requires the availability of at least one reliable measurement per bone, limiting its application in extremely degraded or burned assemblages. Furthermore, the models rely on linear allometric relationships, which may not fully capture the complexity of human skeletal variation, particularly in non-adult populations, which were not considered in this study. A further limitation relates to bilateral asymmetry: skeletal remains often display differences between left and right elements, which may influence the accuracy of MNI estimates even when applying exclusion rules. Since the reference databases used in this study include only one

side (left or right), future work should assess the impact of asymmetry and ideally incorporate paired data. From an operational perspective, the next step is already underway, with the development of a dedicated tool currently in progress on the ADES laboratory website (https://ades.univ-amu.fr/fr), which will allow forensic anthropologists and archaeologists to apply the protocol in field or lab settings without advanced statistical training.

Conclusion

This study presents a novel approach to estimating the Minimum Number of Individuals (MNI) based on the principle of certain exclusion, offering a reliable, systematic alternative to conventional frequency-based methods. By focusing on morphometric incompatibilities rather than uncertain associations, our method significantly reduces aggregation bias while remaining conservative in its estimates.

The use of allometric models trained on a large, diverse database and validated through independent bootstrap simulations provides strong support for the robustness and generalizability of the approach. The exclusion method consistently outperformed traditional techniques across a range of assemblage complexities, particularly in small to mid-sized samples where individual identification is most sensitive.

While limitations remain, such as the need for osteometric data and the simplification of skeletal relationships into linear regressions, this method lays the groundwork for more transparent, replicable, and biologically grounded MNI estimation. The creation of dedicated computational tools is currently developed to facilitate its broader application in forensic anthropology, bioarchaeology, and humanitarian investigations.

Declarations

Ethical approval

Not applicable.

Clinical trial number

Not applicable.

Conflict of interest

The authors declare no competing interests.

Funding declaration

Not applicable.

Author Contribution

Conceptualization: SK and AP; Methodology: SK, CR and AP;Formal analysis and investigation: SK, LB-G, PA and CR ; Writing - original draft preparation:SK and LBG; Writing - review and editing: SK, LB-G, GK, LL CR, CC and PA; Resources:LB-G, GK, LL; Supervision: MO, PA, CR and CC.

Acknowledgement

We would like to thank the Laënnec Institute for supporting this project.

References

1. Adams BJ, Byrd JE (2008) Recovery, Analysis, and Identification of Commingled Human Remains. Humana, Totowa, NJ
2. Blau J (2016) Handbook of forensic anthropology and archaeology. Routledge
3. Adams BJ, Konigsberg LW (2004) Estimation of the most likely number of individuals from commingled human skeletal remains. Am J Phys Anthropol 125:138–151. https://doi.org/10.1002/ajpa.10381
4. Knüsel CJ, Outram AK (2004) Fragmentation: The Zonation Method Applied to Fragmented Human Remains from Archaeological and Forensic Contexts. Environ Archaeol 9:85–98. https://doi.org/10.1179/env.2004.9.1.85
5. Konigsberg LW, Adams BJ (2014) Estimating the Number of Individuals Represented by Commingled Human Remains. Commingled Human Remains. Elsevier, pp 193–220
6. Osterholtz AJ, Baustian KM, Martin DL (2014) Commingled and Disarticulated Human Remains: Working Toward Improved Theory, Method, and Data. Springer, New York, NY
7. Christensen AM, Crowder CM (2009) Evidentiary Standards for Forensic Anthropology*. J Forensic Sci 54:1211–1216. https://doi.org/10.1111/j.1556-4029.2009.01176.x
8. Dirkmaat DC, Cabo LL, Ousley SD, Symes SA (2008) New perspectives in forensic anthropology. Am J Phys Anthropol 137:33–52. https://doi.org/10.1002/ajpa.20948
9. Karell MA, Langstaff HK, Halazonetis DJ et al (2016) A novel method for pair-matching using three-dimensional digital models of bone: mesh-to-mesh value comparison. Int J Legal Med 130:1315–1322. https://doi.org/10.1007/s00414-016-1334-3
10. McWhirter Z, Karell MA, Er A et al (2021) Exploring the Functionality of Mesh-to-Mesh Value Comparison in Pair-Matching and Its Application to Fragmentary Remains. Biology 10:1303. https://doi.org/10.3390/biology10121303

11. Fancourt HSM, Lynch JJ, Byrd JE, Stephan CN (2021) Next-generation osteometric sorting: Using 3D shape, elliptical Fourier analysis, and Hausdorff distance to optimize osteological pair-matching. J Forensic Sci 66:821–836. https://doi.org/10.1111/1556-4029.14681
12. Anastopoulou I, Karakostis FA, Harvati K, Moraitis K (2021) Accurate and semi-automated reassociation of intermixed human skeletal remains recovered from bioarchaeological and forensic contexts. Sci Rep 11:20273. https://doi.org/10.1038/s41598-021-99962-x
13. Palamenghi A, Mazzarelli D, Cappella A et al (2023) Digital pair-matching of iliac bones: pilot study on a three-dimensional approach with models acquired through stereophotogrammetry. Int J Legal Med 137:105–113. https://doi.org/10.1007/s00414-022-02895-x
14. Palamenghi A, Cappella A, Cellina M et al (2022) 3D-3D Superimposition of Pubic Bones: Expanding the Anthropological Toolkit for the Pair-Matching of Commingled Skeletal Remains. Biology 12:30. https://doi.org/10.3390/biology12010030
15. Cappella A, Palamenghi A, Solazzo R et al (2024) An exclusionary screening method based on 3D morphometric features to sort commingled atlases and axes. Sci Rep 14:13149. https://doi.org/10.1038/s41598-024-63029-4
16. Litavec H (2025) An examination of commingled first tarsometatarsal and atlantoaxial joints by deviation analysis. J Forensic Sci 70:649–668. https://doi.org/10.1111/1556-4029.15696
17. Lynch JJ (2018) An Automated Two-dimensional Pairwise form Registration Method for Pair-matching of Fragmented Skeletal Remains. J Forensic Sci 63:1790–1795. https://doi.org/10.1111/1556-4029.13787
18. Byrd J, Adams B (2003) Osteometric Sorting of Commingled Human Remains. J Forensic Sci 48:1–8. https://doi.org/10.1520/JFS2002189
19. Byrd JE, LeGarde CB (2018) Evaluation of method performance for osteometric sorting of commingled human remains. Forensic Sci Res 3:343–349. https://doi.org/10.1080/20961790.2018.1535762
20. Parmentier S Une nouvelle méthode d'estimation du Nombre Minimum d'Individus (N.M.I.) par une approche allométrique: le NMI par exclusions (2010). Applications aux séries ostéologiques de la région Provence-Alpes-Côte d'Azur. Anthropologie biologique. Université de la Méditerrannée, Français
21. Hunt DR, Albanese J (2005) History and demographic composition of the Robert J. Terry anatomical collection. Am J Phys Anthropol 127:406–417. https://doi.org/10.1002/ajpa.20135
22. Cattaneo C, Mazzarelli D, Cappella A et al (2018) A modern documented Italian identified skeletal collection of 2127 skeletons: the CAL Milano Cemetery Skeletal Collection. Forensic Sci Int 287. https://doi.org/10.1016/j.forsciint.2018.03.041. :219.e1-219.e5
23. L'Abbé EN, Krüger GC, Theye CEG et al (2021) The Pretoria Bone Collection: A 21st Century Skeletal Collection in South Africa. Forensic Sci 1:220–227. https://doi.org/10.3390/forensicsci1030020
24. L'Abbé EN, Loots M, Meiring JH (2005) The Pretoria Bone Collection: A modern South African skeletal sample. HOMO 56:197–205. https://doi.org/10.1016/j.jchb.2004.10.004

25. Langley NR, Jantz LM, Ousley SD, Jantz RL, Milner G (2016) Data collection procedures for forensic skeletal material 2.0. University of Tennessee and Lincoln Memorial University
26. Moore-Jansen PH, Ousley SD, Jantz RL (1994) Data collection procedures for forensic skeletal material. Department of Anthropology, The University of Tennessee, Knoxville, TN, p 48. Report No
27. Ubelaker DH (2008) Forensic Anthropology: Methodology and Diversity of Applications. In: Katzenberg MA, Saunders SR (eds) Biological Anthropology of the Human Skeleton, 1st edn. Wiley, pp 41–69
28. Bertsatos A, Chovalopoulou M (2019) Validation study of osteometric techniques for sorting commingled human skeletal remains in archaeological samples. Intl J Osteoarchaeology 29:253–259. https://doi.org/10.1002/oa.2733
29. McCormick K (2019) A Novel Method for Osteometric Reassociation Using Hamiltonian Markov Chain Monte Carlo (MCMC) Simulation. https://doi.org/10.5744/fa.2019.1000. FA 2:
30. Lynch JJ (2018) The Automation of Regression Modeling in Osteometric Sorting: An Ordination Approach. J Forensic Sci 63:798–804. https://doi.org/10.1111/1556-4029.13597
31. Anastopoulou I, Karakostis FA, Borrini M, Moraitis K (2018) A Statistical Method for Reassociating Human Tali and Calcanei from a Commingled Context. J Forensic Sci 63:381–385. https://doi.org/10.1111/1556-4029.13571
32. Lynch JJ, Byrd J, LeGarde CB (2018) The Power of Exclusion using Automated Osteometric Sorting: Pair-Matching. J Forensic Sci 63:371–380. https://doi.org/10.1111/1556-4029.13560

Figures

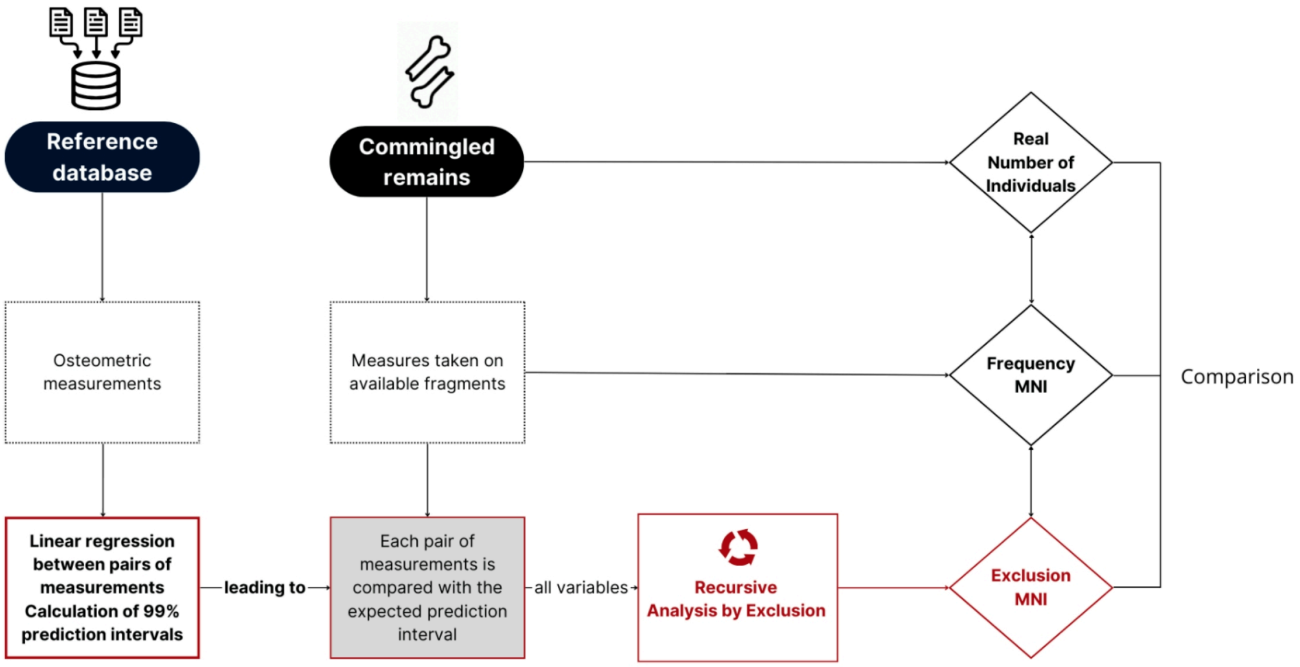


Figure 1

Diagram of the methodology used in this study.

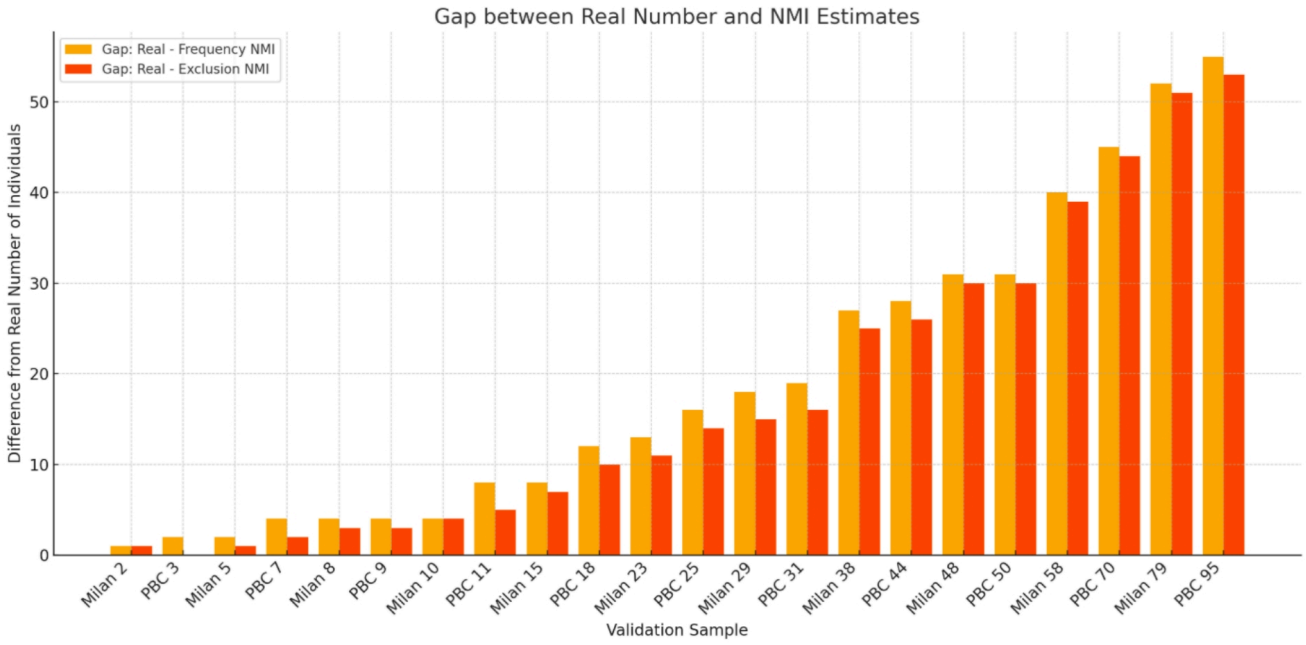


Figure 2

Gap between the Real Number of Individuals and MNI estimates.