RESEARCH ARTICLE

Estimating intralimb proportions for commingled remains

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Abstract

Intralimb proportions provide insights into growth, development, populations history, and adaptation across human groups. However, the conventional approach of calculating brachial and crural indices for individual skeletons and comparing assemblages using sample means is not feasible in commingled remains. This study aims to assess the reliability of an "aggregate method" based on the ratio of sample means of limb bone lengths as an alternative to conventionally calculated indices. We examined the correlation between the aggregate and conventional indices using data from ≥124 worldwide groups (≥2000 adults). The impact of sample size, commingling degree, and within-group variation on the correspondence between conventional and aggregate indices was further evaluated using simulated datasets. Reliability was measured using the absolute differences between the aggregate and "true" population mean indices and the proportion of simulations producing large errors (>0.02, the average within-group variation among observed populations). Strong correlations are observed between the aggregate and conventional indices across groups in the empirical dataset. Simulation analyses indicates that larger samples improve prediction reliability, while increased commingling and within-group variation reduce accuracy. The aggregate method is robust when upper limb samples contain >30 bones (lower limb >50), with more than half of the bones representing proximal and distal elements from the same individuals, and the standard deviation in the index is smaller than 0.02. With sufficient sample sizes, the "aggregate method" is a reliable alternative for estimating average intralimb proportions in commingled and poorly preserved skeletal assemblages, enhancing the research potential of such collections.

KEYWORDS

aggregate method, brachial index, commingled remains, crural index, intralimb proportions

1 | INTRODUCTION

Commingled remains refer to human skeletal assemblages containing multiple individuals that are mixed, incomplete, and disarticulated, making it difficult to attribute specific bones to a particular individual (Adams & Byrd, [2014](#page-8-0); Byrd & LeGarde, [2014,](#page-9-0) [2019;](#page-9-0) Nikita, [2014,](#page-10-0) [2017;](#page-10-0) Nikita & Karligkioti, [2019;](#page-10-0) Osterholtz, [2018](#page-10-0); Ubelaker, [2014](#page-10-0); Vaduveskovic & Djuric, [2020](#page-10-0)). In bioarchaeological and forensic research, these assemblages are often encountered in contexts involving mass fatalities, such as earthquakes, fires (Naji et al., [2014;](#page-10-0) Warren & Van Deest, [2014\)](#page-10-0), wars (Adams & Byrd, [2006;](#page-8-0) Holland et al., [1993;](#page-9-0) Jin et al., [2014\)](#page-9-0), terrorist attacks (de Boer et al., [2019;](#page-9-0) Holland et al., [2003](#page-9-0)), secondary and collective burials (Mohd Noor et al., [2017;](#page-9-0) Siebke et al., [2019;](#page-10-0) Willmott et al., [2020\)](#page-11-0), accumulated

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refuse (Bushozi & Jilala, [2022;](#page-9-0) Campbell, [2018](#page-9-0)), and/or looted cemeteries (Trammell et al., [2018](#page-10-0)). Taphonomic processes, including animal scavenging, postdepositional disturbance, or intentional human intervention, can also contribute to commingling (Adams & Byrd, [2006](#page-8-0); Conlon, [2014;](#page-9-0) Jin et al., [2014;](#page-9-0) Meyer et al., [2020;](#page-9-0) Mundorff, [2014](#page-10-0); Nikita & Karligkioti, [2019;](#page-10-0) Osterholtz, [2018](#page-10-0); Steadman et al., [2014](#page-10-0); Vaduvesković & Djuric, [2020\)](#page-10-0). The challenge of identifying specific individuals within commingled assemblages hinders the reconstruction of the biological profile and subsequent analyses.

The study of the intralimb proportions (the relative lengths of different bones within the same limb) provides key insights into human development and adaptation to diverse environments (Bailey et al., [2007;](#page-9-0) Bogin & Varela-Silva, [2009](#page-9-0); Cowgill et al., [2012;](#page-9-0) Holliday, [1997;](#page-9-0) Pomeroy, [2023;](#page-10-0) Pomeroy et al., [2021](#page-10-0); Savell, [2020;](#page-10-0) Savell et al., [2022](#page-10-0); Tilkens et al., [2007;](#page-10-0) Waxenbaum et al., [2019\)](#page-10-0). Intralimb proportions are thought to reflect both genetic and plastic responses to the environment, as well as population history. Factors such as climate (Auerbach & Ruff, [2010](#page-9-0); Pomeroy et al., [2021](#page-10-0); Ruff, [1993,](#page-10-0) [1994,](#page-10-0) [2018;](#page-10-0) Savell, [2020;](#page-10-0) Savell et al., [2022;](#page-10-0) Waxenbaum et al., [2019](#page-10-0); Weaver et al., [2016](#page-10-0); Yim et al., [2023](#page-11-0)), nutritional status (Bogin et al., [2002](#page-9-0); Leonard et al., [2000;](#page-9-0) Stinson, [2009\)](#page-10-0), and oxygen intake (Bailey et al., [2007](#page-9-0); Bogin & Varela-Silva, [2009](#page-9-0); Payne et al., [2018](#page-10-0); Pomeroy et al., [2012](#page-10-0); Weitz & Garruto, [2004](#page-10-0); Weitz et al., [2000\)](#page-11-0) may shape intralimb proportions, while genetics and populations history also play a role (Betti et al., [2012;](#page-9-0) Cowgill et al., [2012](#page-9-0); Pomeroy et al., [2021;](#page-10-0) Roseman & Auerbach, [2015;](#page-10-0) Savell, [2020;](#page-10-0) Savell et al., [2016,](#page-10-0) [2022](#page-10-0); Temple et al., [2008](#page-10-0)). For instance, groups inhabiting relatively isolated and extreme environments, such as the Arctic, exhibit intralimb proportion variations that are consistent regionally yet distinct from other populations (Auerbach, [2012,](#page-8-0) [2014](#page-8-0); Auerbach & Ruff, [2010;](#page-9-0) Holliday & Hilton, [2010\)](#page-9-0), likely due to shared ancestry and/or convergent evolution.

Conventionally, intralimb proportions are reported using the crural index (CI) and the brachial index (BI). The CI, measuring intra-lower limb proportions, is calculated by dividing the maximum tibial length (TML) by the bicondylar femoral length (FBL) and then multiplying by 100. Similarly, the BI, for intra-upper limb proportions, is determined by dividing the maximum radial length (RML) by the maximum humeral length (HML), also multiplied by 100 (Auerbach & Ruff, [2010](#page-9-0); Payne et al., [2018;](#page-10-0) Pomeroy et al., [2012;](#page-10-0) Ruff, [2018\)](#page-10-0). Assemblages are typically described and compared using mean values computed from the CI and BI of individual skeletons. However, for commingled remains or poorly preserved assemblages, it can be difficult to identify distinct individuals. Although several techniques exist for reuniting bones from the same individuals from such contexts, they tend to be more effective in small-scale rather than large-scale commingled assemblages, require extensive measurements or 3D models of bones, and are not always successful (Adams & Byrd, [2006,](#page-8-0) [2014](#page-8-0); Anastopoulou et al., [2019;](#page-8-0) Bourgeois et al., [2021](#page-9-0); De Simone & Hackman, [2019](#page-9-0); Sgheiza, [2021](#page-10-0)). Additionally, a common challenge is the frequent incomplete preservation of both proximal and distal limb bones from the same individual, which complicates the assessment of individual limb proportions.

In order to compute CI and BI for commingled or incomplete assemblages, a simple alternative approach is an aggregate method, which involves computing the sample means of relevant measurements of unfragmented long bones (femur or tibia lengths for the aggregate CI [aCI] or humerus and radius lengths for the aggregate BI [aBI]) and then calculating the appropriate indices from these means (Table 1). This simple method may facilitate the estimation and comparison of mean intralimb proportions across assemblages without the need for individual skeleton identification or completeness of all elements from individuals, provided that some intact, unfragmented long bones are available. However, the validity and comparability of aggregate indices to the conventional CI (cCI) and BI (cBI), either as conventionally calculated for groups as sample means (cCIgroup or cBIgroup) or as an approximation of the true population value of the indices (μCI or μBI), remain unexplored. The relationships could be influenced by several factors, such as sample size, the degree of commingling (i.e., the extent to which bones originate from the same or different individuals), and the variability of limb proportions within the studied population.

Thus, our research is centered on a key question: How effective is the aggregate method in estimating BI and CI for assemblages of commingled and incomplete human remains? To investigate this, we

Abbreviations: Σ , the sum from 1 to *n*; *aBI*, aggregate brachial index on group level; aCl , aggregate crural index on group level; Bl_i , the brachial index for the ith individual; cBI, conventional brachial index on group level (i.e., sample mean of individual BI); cCI, conventional crural index on group level (i.e., sample mean of individual CI); CI_i, the crural index for the ith i ndividual; FBLi, the bicondylar femoral length for the ith individual; HML_{i} the humeral length for the ith individual; i, the ith individual in the group; n , the total number of individuals in the group; RML_i , the radial length for the ith individual; TML_i, the tibial length for the ith individual.

carried out two sets of analyses. First, we compared the cCIgroup and cBIgroup measurements from various global skeletal assemblages to their corresponding aggregate indices (aCIgroup and aBIgroup). Second, we generated simulated commingled datasets, with parameter ranges based on the empirical global data, to evaluate these against the μCI and μBI benchmarks. The simulation within the study was designed to validate the applicability of the aggregate method under certain constraints, recognizing that it may not accurately replicate every aspect of complex conditions in reality. In practical analysis, it is crucial to evaluate relevant factors to identify circumstances when the proposed solution is sufficiently reliable. In adopting this pragmatic perspective, this research seeks to enhance the analysis of data from commingled and incomplete skeletal assemblages, contributing to improved methodological practices in skeletal remains analysis.

2 | MATERIALS AND METHODS

2.1 | Materials

Two published datasets were combined to create a global reference dataset: Ruff's European dataset (Ruff, [2018](#page-10-0); [https://fae.](https://fae.johnshopkins.edu/chris-ruff/) [johnshopkins.edu/chris-ruff/](https://fae.johnshopkins.edu/chris-ruff/)) and the Goldman Osteometric dataset (Auerbach & Ruff, [2006](#page-8-0); [http://web.utk.edu/](http://web.utk.edu/~auerbach/GOLD.htm)~[auerbach/GOLD.htm](http://web.utk.edu/~auerbach/GOLD.htm)). Ruff's European dataset includes limb bone measurements from 2177 adults from 272 groups in seven regions of northern and southern Europe, spanning the Paleolithic to modern periods. The Goldman dataset contains measurements from 1538 archaeological and contemporary human adult skeletons pertaining to 208 groups worldwide. Both datasets include measurements that can be used to calculate the BI and CI. To ensure data integrity, individuals of unknown origin were excluded from the analysis, while for overlapping groups in both datasets, those from Ruff's European dataset were mainly retained due to its larger data size. In this context, the term "group" refers to the population origin or site from each sample, labelled as "SITE" in Ruff's dataset and "NOTE" in Goldman's. The different "groups" analyzed in this study are, therefore, the result of varied levels of aggregation in terms of temporal variability or social differentiation, which are additional factors influencing the variability within groups. Notably, skeletons belonging to the Harman Todd Skeleton Collection were separated into seven groups according to their labelled geographical origin.

2.2 | Methods

2.2.1 | Data selection

Measurements used in this study include the maximum lengths of the humerus (HML), radius (RML), tibia (TML), and bicondylar femur length (FBL). When available, the mean of measurements from the left and right sides of an individual skeleton was used to give a single measurement per individual. Differences between the left and right sides were

relatively small: Paired t-tests showed no significant difference in left and right side lengths for the 1210 paired femora (Cohen's $d = 0.06$, $p > 0.05$) and 1190 paired tibiae (Cohen's $d = 0.02$, $p > 0.05$) within each assemblage from the Goldman dataset. For the humerus (1163 pairs from the Goldman dataset and 1227 pairs from Ruff's dataset) and the radius (1063 pairs from the Goldman dataset and 1093 pairs from Ruff's dataset), despite t-tests showing significant differences (p < 0.05), the effect size was small (Cohen's $d = -0.16$ for the humerus and -0.1 for the radius) suggesting a relatively minor magnitude of these differences. The origin and sex information of sample groups were retained to enable analyses of within-group variation in limb proportions. Groups with fewer than five individuals providing BI or CI data were excluded from the analysis. Additionally, one individual with a BI over 1 from the Mobridge site, South Dakota, United States, from the Goldman dataset was excluded, as such a ratio is biologically implausible (Aitken, [2021;](#page-8-0) Bogin & Rios, [2003](#page-9-0)). Consequently, the BI dataset included data from 1407 males and 941 females from 124 groups, while the CI dataset included 1561 males and 1062 females from 132 groups (see Data [S1](#page-11-0), Lists 1 and 2).

Notably, this study adopts a practical approach by pooling data from both sexes, a strategy that simplifies the analysis and also reflects the complexities encountered in commingled remains scenarios. While methods exist to estimate sex from individual limb bones that can be equally or more reliable than methods based on the pelvis or skull (e.g., Spradley & Jantz, [2011\)](#page-10-0), disparities between the characteristics of the examined remains and those of reference populations, particularly in cases of extensive commingling (Duangto & Mahakkanukrauh, [2020;](#page-9-0) Verma et al., [2020\)](#page-10-0), mean that the reliability of these methods across different populations, both temporally and geographically, is unclear. Furthermore, while previous studies have reported sex differences in BIs (e.g., Auerbach, [2007\)](#page-8-0), such differences appear minimal in the datasets under examination. This observation holds true when considering both group-level comparisons (as indicated by the t-test in Figure [S1,](#page-11-0) where 71 out of 95 groups, each comprising more than three individuals of both sexes, exhibit no statistically significant sex differences for BI and 100 out of 105 for CI) and when analyzing the pooled sample (Figure [1](#page-3-0)). The parameters for simulations were, therefore, based on observed values that did not separate the sexes.

It is also noteworthy that within the groups exhibiting significant sex differences in BI (Data [S1,](#page-11-0) List 3), six had a notable disproportion in the numbers of males and females, while three had small sample sizes (fewer than five individuals of each sex). Similarly, among the groups demonstrating significant sex differences in CI (Data [S1,](#page-11-0) List 4), two exhibited uneven distributions of male and female individuals. The nature of such an unbalanced and limited sample may have introduced potential biases affecting the observed sex differences in intralimb proportions. Nonetheless, two groups from each of the Jomon period Japanese (Tsugumo Shell Mound and Yoshigo Shell Mound groups) and Arctic populations (Tigara and Ipituaq groups) in the Goldman dataset displayed significant sex differences in BI, while only one group in each of the other populations had significant sex differences. Therefore, it is advisable to account for potential BI sex differences when conducting studies involving both of these populations.

FIGURE 1 Distribution of male and female intralimb proportions in the global dataset. cBI, conventional brachial index; cCI, conventional crural index. [Colour figure can be viewed at [wileyonlinelibrary.com\]](http://wileyonlinelibrary.com)

cCI - Female

2.2.2 | Comparison of group conventional and aggregate indices

For each group, the conventional indices (cBI $_{\rm group}$ and cCI $_{\rm group}$) were calculated as the mean of all the individual indices within each group. To assess the variation in limb proportions within each group, the standard deviations of the cBIgroup and cCIgroup were calculated. The aggregate indices (of each group aBIgroup and aCIgroup) were calculated as the ratio of the mean lengths of the radius (RML) and humerus (HML) within the group for aBI or mean tibial (TML) and femoral lengths (FBL) within the group for aCI.

A preliminary evaluation of the validity of the aggregate method was conducted by measuring the Pearson correlation between the two sets of indices in R version 4.1.3 (R Core Team, [2022](#page-10-0)). The validity of the use of parametric methods with ratio data is discussed further below. A p-value of less than 0.05 was considered statistically significant.

2.2.3 | Simulating the virtual commingled remains

Two functions, "simFun bi" and "simFun ci," were written and executed in R version 4.1.3 (R Core Team, [2022](#page-10-0)) to simulate virtual commingled assemblages in order to evaluate the performance of the aggregate indices. The scripts and detailed illustrations can be accessed on the GitHub repository [\(https://github.com/](https://github.com/CarolDoudouCao/Aggregate_IntraLimb_Proportions_for_Commingled_Remains) [CarolDoudouCao/Aggregate_IntraLimb_Proportions_for_Commingled_](https://github.com/CarolDoudouCao/Aggregate_IntraLimb_Proportions_for_Commingled_Remains) [Remains\)](https://github.com/CarolDoudouCao/Aggregate_IntraLimb_Proportions_for_Commingled_Remains). Both functions require the following input parameters: (1) the number of matched and unmatched bones (which allows for control over the sample size and commingling degree); (2) the population mean and standard deviation of the humeral (or femoral) length, obtained from the grand mean of the means and standard deviations of empirical dataset; (3) the true mean of the indices (μBI or μCI) and their respective standard deviations; and (4) the number of repetitions to be performed. Note that the sample size refers here to the total number of limb bones rather than the number of individuals. This approach is also more applicable to real commingled contexts, as estimating the number of individuals can be sometimes challenging when dealing with disarticulated skeletons.

Although the application of parametric methods to ratio data may be problematic (e.g., Cowgill et al., [2012](#page-9-0)), we use parametric analyses

throughout this study for several reasons. First, this choice aligns with the empirical data encountered in most real-world scenarios. Shapiro tests were used to examine the distribution of limb lengths and indices within each group. We found no evidence suggesting that long bone lengths were not normally distributed. As for two indices (Figures [S2](#page-11-0) and [S3](#page-11-0)), only less than 10% of the groups rejected the null hypotheses (9 out of 124 for BI and 12 out of 132 for CI), even without the multiple testing correction (which, if introduced, would result in only one group rejecting the hypothesis for each of the two indices). Moreover, previous studies have also demonstrated the reliability and comparability of ratios of data means under certain conditions, particularly when the numerators and denominators are normal, their mean is positive, and certain criteria regarding the coefficient of varia-tion are met (Cho et al., [2022;](#page-9-0) Díaz-Francés & Rubio, [2013](#page-9-0); Hayya et al., [1975;](#page-9-0) Hedges et al., [1999;](#page-9-0) Hinkley, [1969](#page-9-0); Merrill[,1928;](#page-9-0) Marsaglia, [2006\)](#page-9-0). It is also suggested that Gaussian models generally exhibit robustness and are mainly affected by extreme outliers, whereas certain non-Gaussian models and randomization techniques may increase the risk of higher false-positive rates (Knief & Forstmeier, [2021](#page-9-0); Lumley et al., [2002;](#page-9-0) Zuur et al., [2010\)](#page-11-0). In addition, by assuming a normal distribution for limb lengths and indices, this approach helps enhance the ability to manage the commingling degree (especially the variability in intralimb proportions) throughout the simulation.

Our simulation functions operate by creating a series of artificial datasets with specified sample sizes, commingling degrees, and userdefined variation in the limb length as well as the relevant index. For instance, with a sample size of 100 bones and a commingling degree of 0.5, there would be 50 humeri and 50 radii in the dataset, with half of the humeri matched to their corresponding radii (i.e., from the same "individual") and the other half unmatched. In each dataset, the number of humeri (or femora) is equal to the number of radii (or tibiae). While the number of different limb bones can be uneven in real contexts of commingling, here, the equal number was maintained to ensure a consistent and balanced representation of limb bones throughout the simulation. For the example scenario outlined, the simulation process consists of the following steps:

- 1. Sample 25 humeral lengths from the normal distribution N (μhumerus and σhumerus).
- 2. Sample 25 BIs from the normal distribution N (μBI and σBI).
- 3. Calculate corresponding radial length for each humeral length based on the BI sampled in step 2.
- 4. Repeat steps 1–3 as above, but remove the initial set of 25 humeral lengths.
- 5. Repeat steps 1–3 as above, but remove the radial lengths.

This process generates 25 pairs of matching humeral and radial lengths (steps 1–3), 25 unmatched humeri (step 4), and 25 unmatched radii (step 5), with a total of 100 measurements. The mean of the 50 humeral lengths and radial lengths is then computed from these sampled values, and the aBI is calculated. This process is repeated 10,000 times for each parameter combination.

After executing each simulation, an output list was generated, containing the aggregate index and its corresponding error in relation to the μBI or μCI as appropriate (see above and Table 2). To calculate the error, the μBI or μCI was subtracted from the aBI or aCI, respectively, and the mean, median, and standard deviation of the errors for the 10,000 simulations conducted on each set of parameters were used to assess the performance of the aggregate index. The 75th percentile error was also calculated to capture the presence of larger errors in the long tail of the highly right-skewed error distribution. This percentile represents the value below which 75% of the errors fall, providing a measure of the upper end of the error distribution and quantifying the extent of larger errors. The margin of computed errors was determined using a threshold of 0.02, which corresponds to the representative value of the standard deviation in both BI and CI for each group within the global dataset. Errors exceeding this threshold were considered "large" errors, and the proportion of simulations with large errors was calculated as an additional measure of the accuracy of the aggregate indices.

We examined the following parameters settings:

TABLE 2 Summary statistics for group means of limb lengths and intralimb indices.

Lengths/indices	Mean	Max	Min	Standard deviation
HML_{group} (in mm)	308.8	344.6	271.3	13.2
RML_{group} (in mm)	234.5	259.9	209.3	10.2
FBL_{group} (in mm)	426.8	467.7	383.8	16.5
TML _{group} (in mm)	356.2	399.7	314.1	15
cBl_{group}	0.760	0.808	0.719	0.019
cCl _{group}	0.835	0.869	0.793	0.015
σBl_{group}	0.024	0.072	0.002	0.009
$\sigma C I_{\rm group}$	0.023	0.044	0.009	0.006

Abbreviations: cBl_{group} , the conventional brachial index within the group; cCl_{group} , the conventional crural index within the group; FBL_{group} , the mean bicondylar length of the femur within the group; HML_{group} , the mean maximum length of the humeral length within the group; Max, maximum value; Min, minimum value; RML_{group}, the mean maximum length of the radial length within the group; TML_{group} , the mean maximum length of the tibial length within the group; σBl_{group} , the standard deviation of the conventional brachial index within the group; σCl_{group} , the standard deviation of the conventional crural index within the group.

- Sample size, 30 different settings between 10 and 300 bones.
- Commingling degree, defined as the proportion of bones with matching pairs (i.e., 0 when all bones are matched and 1 when no two bones in the sample originated from the same individual); 30 different settings between 0 and 1.
- Within-group variation in the limb index (i.e., σ BI and σ CI), 0.01, 0.02, and 0.05 for CI and 0.01, 0.02, and 0.08 for BI, representing the minimum, mean, and maximum variabilities observed in the empirical dataset and rounded to two decimal places.

3 | RESULTS

3.1 | Correlation between aggregate and conventional indices in the empirical data

A strong correlation was observed between the conventional indices and their corresponding aggregate indices across groups (Figure [2](#page-5-0) and Table [3\)](#page-5-0). The correlation between aBI and cBI ($r = 0.9995778$, p < 0.001) as well as aCI and cCI ($r = 0.9996425$, p < 0.001) was exceptionally high, with confidence intervals (95%) exceeding 0.99 at both ends. These findings provide preliminary support for considering the aggregate indices as reliable proxies for the conventional indices.

3.2 | Summary statistics

Table 2 presents the mean, maximum, and minimum values, as well as corresponding standard deviations of the mean limb lengths and indices of the groups in the empirical dataset (the "population" values). As described in the methods, the minimum, mean, and maximum values for within group variability used in the subsequent analyses for BI were 0.01, 0.02, 0.05, and 0.08, while for CI, the respective values were 0.01, 0.02, and 0.05.

3.3 | Simulating commingling conditions

The results of simulating the impact of three conditions on the reliability of the aggregate indices are presented in Figures 3–[5.](#page-6-0) Figures [3](#page-6-0) and [4](#page-6-0) show the mean, median, and 75th quantile of absolute errors for BI and CI. Figure [5](#page-7-0) illustrates the frequency of simulations with large errors (>0.02). The aggregate indices consistently demonstrate a high level of accuracy, with the majority of mean and median errors below 0.001 and none exceeding 0.02, despite the variation in the variability of the indices as well as the commingling degree. However, a few errors at the 75th quantile exceed the threshold of 0.02, primarily occurring (prevalence >5%) when the sample size (i.e., the number of sampled bones) is below 30 for aBI (or 50 for aCI), the within-group variation is above 0.02 (the mean within-group variation across worldwide populations), and the commingling degree exceeds 0.5 (indicating a higher number of unmatched bones compared with matched bones).

TABLE 3 Correlation between aggregate and conventional indices.

Abbreviations: aBI, aggregate brachial index; aCI, aggregate crural index; cBI, conventional brachial index; cCI, conventional crural index.

The findings highlight the influence of all three conditions: sample size, within-group variation in intralimb proportions, and comingling degree on the performance of aggregate indices. As the variation as well as commingling increases, a larger sample size is required to mitigate the likelihood of encountering large errors. To achieve accurate estimations with minimal occurrences of large errors in the aggregate indices, a sample size exceeding 100 bones is required when the variation is up to 0.05, and the commingling degree is less than 0.5. Moreover, under extreme conditions where the commingling degree is 1 (implying no two bones in the assemblage are from the same individual) and the within-group variation reaches its highest (0.08 for BI and 0.05 for CI), an even larger sample size exceeding 150 bones (75 humeri and 75 radii or 75 femora and 75 tibiae) is required to reduce the occurrence of large errors. Nevertheless, such extreme levels of bone mixture and variation are highly improbable in realworld scenarios.

4 | DISCUSSION

This study investigated the reliability and robustness of an aggregate method for estimating mean CI and BI from commingled skeletal assemblages. Comparison between conventional approaches based on sample means and the aggregate method proposed here show high levels of positive correlation in the global empirical dataset, suggesting close agreement between the two measures. Our simulation experiments with different commingling conditions (sample size, commingling degree, and within-group variation in the intralimb proportions) further support our conclusions and the robustness of the

FIGURE 2 Correlation between the aggregate and conventional indices for a diverse worldwide sample of human groups. aBI, aggregate brachial index; aCI, aggregate crural index; cBI, conventional brachial index; cCI, conventional crural index. [Colour figure can be viewed at wileyonlinelibrary.com]

aggregate method under a wide range of conditions. The accuracy of the aggregate method is influenced by all three parameters in a predictable way. Closer approximations to the population mean (μ) CI and BI can be obtained when a greater number of limb bones in the sampled skeletons derive from the same individuals, while, in contrast, greater variation in intralimb proportion within the group leads to lower accuracy of the aggregate indices. Nevertheless, the discrepancies between sample and population means were consistently small, affirming the utility of the aggregate method as an alternative estimation approach.

Notably, with a sample comprising over 30 upper limb bones (humerus plus radius) or 50 lower limb bones (femur plus tibia), a commingling degree below 0.5, and a within-group variation in the index restricted to 0.02 (the average value from the empirical dataset), the occurrence of large errors (>0.02) is effectively limited to approximately 5% or less. Although extreme conditions of commingling or within-group variation in limb proportions require a much larger sample size exceeding 150 limb bones to obtain reliable estimates, such situations are unlikely to occur. These findings highlight the critical role of sample size in achieving accurate predictions using the aggregate method. While accurate estimates of the commingling degree and variation in intralimb proportions within the assemblage may be elusive, the number of sampled bones is always quantifiable. Thus, collecting an adequate number of bones from the assemblage can serve as a practical benchmark for employing the aggregate method as a reliable alternative to conventional intralimb indices, effectively compensating for uncertainties associated with commingling and variation in limb proportions.

5 | LIMITATIONS OF THE STUDY

It is also important to acknowledge the limitations and context-specific considerations in the application of the aggregate method, as well as the potential challenges in ratio-based analyses and sample comparability. Caution should be exercised when dealing with highly commingled assemblages or groups with significant variation in intralimb proportions. Particularly, in cases where remains are limited in number or highly mixed, the feasibility and reliability of the method may be

FIGURE 3 Mean, median, and 75th percentile of absolute errors in the aggregate brachial index (BI). The standard deviation (σ cBI) is set as 0.01, 0.02, and 0.08, respectively in the left, middle and right panels. [Colour figure can be viewed at [wileyonlinelibrary.com\]](http://wileyonlinelibrary.com)

FIGURE 4 Mean, median, and 75th percentile of absolute errors in the aggregate crural index (CI). The standard deviation (σ cCI) is set as 0.01, 0.02, and 0.05, respectively in the left, middle and right panels. [Colour figure can be viewed at [wileyonlinelibrary.com\]](http://wileyonlinelibrary.com)

FIGURE 5 Proportion of simulations with large errors (>0.02) across varied within-group variations. Left column shows the results of the brachial index (BI) simulation and right column shows the results of the crural index (CI) simulation. The standard deviation of the brachial index $(\sigma$ cBI) is set at 0.01, 0.02, 0.05, and 0.08 moving from top to bottom. The standard deviation for the crural index (σ cCI) is set at the 0.01, 0.02, and 0.05 moving from top to bottom. [Colour figure can be viewed at [wileyonlinelibrary.com\]](http://wileyonlinelibrary.com)

compromised, especially if there is any preservation bias due to body or bone size. By contrast, a relatively small sample size may be acceptable if the intralimb proportion in the population, from which the sampled bones originate, is known to be highly consistent and/or if the

commingling degree of the assemblage is minor. In this study, a threshold of 0.02 was used to define a large error in the aggregate method, representing the average within-group variation in intralimb proportions observed across worldwide groups. This threshold can be tailored to the specific context and goals of the analysis using the scripts provided. For instance, a smaller value can be used to accommodate a higher accuracy requirement, allowing for the determination of appropriate sample size requirements and power calculations.

Also notably, the aggregate method provides estimates of the intralimb proportion using mean measurements of the group without precise individual identifications. While it provides valuable insights into the group-level profile, it will not be suitable for addressing questions at the individual level. Additionally, it still falls short in adequately approaching intergroup comparisons, given the uncertainty associated with the estimate, and the variance within each group's metric cannot be estimated. In any case, where articulated skeletons are available, the conventional method should be chosen over the aggregate method or other alternatives. Moreover, the impact of variation in the sex ratio of the assemblage was not assessed, as sex cannot always be reliably estimated for individual commingled bones. However, sex ratio may have an impact on the aggregate approach given that BI and CI may differ between the sexes. While sexual dimorphism can increase the within-group variance in the index, its impact on the aggregate index is limited, especially in cases with adequate sample sizes (notably in datasets with more than 150 bones, where the influence of variability is negligible). Nevertheless, significant sex differences in BIs or CIs may exist in certain populations, possibly reflecting specific environmental contexts or population history (Allen, 1877; Auerbach & Ruff, 2006; Bailey et al., [2007;](#page-9-0) Bogin et al., [2002](#page-9-0); Holliday, [1999;](#page-9-0) Pomeroy, [2023;](#page-10-0) Pomeroy et al., [2021](#page-10-0); Roseman & Auerbach, [2015;](#page-10-0) Temple et al., [2008](#page-10-0)). Thus, it is important to be cautious when applying the proposed aggregate approach to these groups (such as the Jomon period Japanese and Arctic populations), as large sex differences may increase the heterogeneity within the population and thus affect the accuracy of the result negatively.

Despite these limitations, this research suggests that the aggregate approach presents a practical and simple alternative to the conventional method of estimating mean intralimb proportions of skeletal assemblages. This alternative method not only addresses some of the challenges posed by commingled skeletal remains (Adams, 2014; Osterholtz, [2018;](#page-10-0) Ubelaker & Wu, [2020\)](#page-10-0) but also provides valuable insights for assemblages with variable preservation and incomplete limbs. The high correlation between conventional and aggregate methods across different groups in the empirical dataset suggests that assemblage-mean intralimb indices can be reliably calculated where individual measurements for a dataset are missing, but mean long bone lengths have been published. By examining the validity of the aggregate method and considering its performance under different conditions of commingling, this research expands the repertoire of techniques available for studying commingled assemblages and increases their potential for informing us about the lives and adaptations of past populations.

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CONFLICT OF INTEREST STATEMENT

The authors declare that they have no conflicts of interest regarding the publication of this paper.

DATA AVAILABILITY STATEMENT

The code required for reproducible analysis can be accessed in the GitHub repository ([https://github.com/CarolDoudouCao/Aggregate_](https://github.com/CarolDoudouCao/Aggregate_IntraLimb_Proportions_for_Commingled_remains) [IntraLimb_Proportions_for_Commingled_remains\)](https://github.com/CarolDoudouCao/Aggregate_IntraLimb_Proportions_for_Commingled_remains).

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SUPPORTING INFORMATION

Additional supporting information can be found online in the Supporting Information section at the end of this article.

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