A48 Estimating the Number of Individuals in a Large Commingled Assemblage of Known Size

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After attending this presentation, attendees will understand the differences between methods that estimate the number of individuals in a skeletal assemblage and which method best estimates the true population size of a large commingled assemblage.

This presentation will impact the forensic science community by assessing the results of different methods that estimate population size in skeletal assemblages and highlighting a standardized method to inventory data in large commingled assemblages.

Estimating the number of individuals in a commingled assemblage is vital for planning purposes, including budgeting, resource allocation, analytical approaches, and the direction of future recovery efforts; however, the estimate is affected by factors inherent to the assemblage (e.g., fragmentation, preservation, and recovery rates) and the estimation methods themselves (e.g., variability of methods results in numerous estimates, lack of testing on assemblages of known size, and inconsistent inventory terminology).

Minimum Number of Individuals (MNI), Grand Minimum Total (GMT), and Most Likely Number of Individuals (MLNI) estimate the number of individuals in an assemblage. MNI determines the fewest possible individuals needed to account for the physical remains that are recovered and is traditionally estimated by the reported completeness of the most common element. GMT and MLNI use pair matching, with the former producing an MNI estimate based on counts of paired and unpaired bones and the latter using the maximum likelihood estimate of the total number of individuals that may have originally comprised an assemblage.[1] Previous assessments of MLNI typically have focused on smaller assemblages (<50 individuals) in which the original loss population was unknown; MLNI has not been tested on larger assemblages of known size. For all quantification methods, an accurate inventory of the assemblage is a crucial step, since this affects the accuracy of the estimate.

The December 7, 1941, attack on Pearl Harbor resulted in 429 casualties from the USS *Oklahoma*; 394 of these individuals were not identified at the time. The remains of these individuals are known to be severely commingled; the first disinterred casket, containing five “sets” of remains, yielded 95 unique mitochondrial DNA (mtDNA) sequences. The USS *Oklahoma* project, which seeks to individually identify the USS *Oklahoma* casualties, has an assemblage of nearly 13,000 skeletal elements with nearly 5,000 samples submitted for DNA analyses.

This study examines MNI, GMT, and MLNI estimates using inventoried elements and DNA results to date from the USS *Oklahoma* project. The inventory of the USS *Oklahoma* assemblage used both a descriptive system (e.g., distal portion present) and the zonation method of Knüsel and Outram, with slight modifications.[2] Part of the DNA strategy for the USS *Oklahoma* project included sampling all crania, humeri, and tibiae, enabling the calculation of both MNI and MLNI. MNI was calculated using the most frequent element, zones, and the number of duplicated elements per mtDNA sequence (n=308 mtDNA sequences to date). GMT and MLNI were calculated using visual pair matching of all humeri in the assemblage (*left*=287, *right*=293).

For the cranium, MNI is estimated as 356 individuals (Zone 5, occipital). For the postcranium, MNI is 336 (right femur, distal) and 354 (right femur, Zone 1). By duplicated element per mtDNA sequence, MNI is 394. Based on the humeri, MNI is: 289 (right humerus, distal); 298 (Zone 5); and 369 (GMT); and MLNI is calculated as 399±15 individuals.

In this assemblage, MNI by mtDNA and MLNI provide estimates that are identical or nearly identical to the original population size. GMT is the next most accurate method, followed by MNI based on zones. The least accurate estimator is MNI based on traditional descriptive inventory terms. While MNI by mtDNA sequence is currently very accurate, the sequencing is not yet complete for the project and it will likely take several years to process all 5,000 samples. Thus, this does not represent the timeliest or most cost-effective strategy. MLNI, while also very accurate in this study, has the potential to overestimate when the associated interval is considered, and both MLNI and GMT necessitate pair-matching across the entire assemblage. If this is not possible, the zonation method is more accurate than traditional MNI, and it provides a means to reliably assess fragmented remains, especially if recovery rates are poor or fragmentation is high. Finally, MLNI assessments corroborate previous findings on a larger scale than previously tested.

The views herein are those of the authors and do not represent those of the Defense POW/MIA Accounting Agency, Department of Defense, or United States government.

Reference(s):

1. Konigsberg, Lyle W., and Bradley J. Adams. Estimating the Number of Individuals Represented by Commingled Human Remains: A Critical Evaluation of Methods. In: *Commingled Human Remains: Methods in Recovery, Analysis, and Identification*, edited by Bradley J. Adams and John E. Byrd, 193–220. San Diego, CA: Elsevier, 2014.
2. Knüsel, Christopher J., and Alan K. Outram. Fragmentation: The Zonation Method Applied to Fragmented Human Remains from Archaeological Contexts. *Environmental Archaeology*. 9 (2004):85–97.

Commingled Skeletal Remains, MNI, Zonation Method

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