



Cross-platform program for likelihood-based statistical comparisons of mortality profiles on a triangular graph

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ABSTRACT

The construction of mortality profiles to investigate age-at-death patterns is a typical component of most faunal analyses. While many methods exist for constructing and comparing mortality profiles, plotting the percentages of juvenile, prime, and old individuals on a triangular graph, or ternary diagram, remains a popular method for making comparisons. Typically, these comparisons are made visually, but because sample sizes are often small, any differences may be the product of sampling rather than meaningful contrasts in depositional history. To overcome this problem, here we present a likelihood-based method for making statistical comparisons of mortality profiles on a triangular graph, and we make available a cross-platform computer program that implements the method. Although we developed the method with mortality profiles in mind, in principle, it can be used to analyze any kind of artifact for which there are three distinct categories.

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1. Introduction

The construction of mortality profiles to investigate age-at-death patterns is a typical component of most faunal analyses. These age profiles, or distributions, are used, in conjunction with other evidence, to reconstruct aspects of a sample's pre- and post-depositional history, including prey selection, herding strategy, mode of accumulation, and differential preservation. Mortality distributions are often compared to two theoretical models, the "living," or "catastrophic," profile and the "attritional" profile (see Klein, 1982b; Stiner, 1990). The living profile represents the age structure of a live herd on the landscape, and in a faunal assemblage, it could be created when an entire herd died at once or when non-selective hunting occurred. The natural attrition of a population occurs through the deaths of the most vulnerable individuals, the youngest and oldest individuals, by predation, disease, and starvation. The attritional profile is related to the living profile, as it reflects the animals that die between each age class in the living population or profile. These model profiles provide a baseline for comparisons with the actual profiles found in faunal assemblages, which are expected to show a variety of age distributions, perhaps

reflecting the targeting hunting of specific age classes, the management of domesticated herds, or other factors.

While many methods exist for constructing and comparing mortality profiles (reviewed in Steele, 2005), triangular graphs, or ternary diagrams, remain a popular method for making comparisons. These graphs are straightforward to create; they allow researchers to easily compare multiple samples or multiple species on a single graph; and they can be used with a variety of methods for determining age-at-death and with coarse-grained age data. Greenfield (1986, 1988) was the first to use triangular graphs to compare mortality profiles. He investigated variation in the percentages of very immature, sub-adult, and adult animals, as the result of shifts in herd management from exclusively meat production to also including milk and wool production. Following Stiner (1990), most applications of the method have plotted the percentages of juvenile, prime, and old individuals relative to five interpretive zones: the lower-left corner for juvenile dominated assemblages, the lower-right corner for prime-dominated assemblages, the top portion for old-dominated assemblages, the right-of-center portion for assemblages with a living structure, and the left-of-center portion for assemblages with the attritional age structure. Subsequently, these three age classes sometimes have been redefined to address specific research questions. For example, like Greenfield (1986, 1988), Lubinski (2000) was mainly interested in younger pronghorn, so he plotted the percentages of fawn,

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yearling, and mature animals. Bunn and Pickering (2010a, 2010b) recommend excluding the youngest juveniles from the juvenile category and redefining the old category. The five interpretive zones can also be modified to reflect alternative mortality models (e.g., Rendu et al., in press).

While triangular graphs facilitate useful visual comparisons, differences in sample size are not apparent and there is no straightforward way to make statistical comparisons. In principle, the commonly used chi-square test of independence, or perhaps the somewhat less well-known G-test, could be used to compare the proportions of juvenile, prime, and old animals found in two or more assemblages, but the p -values are only accurate for fairly large samples (Agresti, 2002; McDonald, 2009; Sokal and Rohlf, 1995). Additionally, because one of the strengths of triangular graphs is to facilitate visual comparisons, a way to visually represent the level of confidence in the placement of assemblages on the graph is desirable. To address these problems, Steele and Weaver (2002) proposed a modified triangular graph method where bootstrapping was used to create 95% density contours around samples, which approximate 95% confidence intervals. The size of the 95% density contour reflects sample size, and samples with non-overlapping contours are likely to have had different pre- or post-depositional histories (i.e., they are significantly different in the conventional statistical sense). This modified triangular graph method has proven useful to multiple researchers (Adler et al., 2006; Bunn and Pickering, 2010a, 2010b; Monchot and Aouraghe, 2009; Norton and Gao, 2008), but some shortcomings remain with the approach. Of particular importance, the bootstrapping approach does not work with samples for which one age class is empty (e.g., 40% young, 60% prime, and 0% old). Because this is a common situation, we sought to further update the modified triangular graph program to accommodate such samples.

As an alternative to the bootstrapping method of Steele and Weaver (2002), here we present a likelihood-based method for making statistical comparisons of mortality profiles on a triangular graph. This new method works with samples for which an age class is empty. We first present the mathematical and computational details of the method. Then, we compare the bootstrapping and likelihood approaches. Finally, we describe the cross-platform computer program that implements the new method.

2. Likelihood method

The joint probability mass function for the multinomial distribution (Casella and Berger, 2002) gives the probability of observing counts of x_j , x_p , and x_o for juvenile, prime, and old individuals respectively of a particular taxon in an archaeological assemblage, given that the human group that created the assemblage tended to obtain proportions of juvenile, prime, and old individuals of θ_j , θ_p , and θ_o respectively:

$$P(x_j, x_p, x_o | \theta_j, \theta_p, \theta_o) = \frac{(x_j + x_p + x_o)!}{x_j! x_p! x_o!} \theta_j^{x_j} \theta_p^{x_p} \theta_o^{x_o}. \quad (1)$$

Given that an assemblage contains counts of x_j , x_p , and x_o , the likelihood of particular values for the parameters θ_j , θ_p , and θ_o can be obtained by holding x_j , x_p , and x_o constant in Eq. (1) and changing θ_j , θ_p , and θ_o , with the restriction that $\theta_j + \theta_p + \theta_o = 1$:

$$L(\theta_j, \theta_p, \theta_o | x_j, x_p, x_o) = \frac{(x_j + x_p + x_o)!}{x_j! x_p! x_o!} \theta_j^{x_j} \theta_p^{x_p} \theta_o^{x_o}. \quad (2)$$

The likelihoods given by Eq. (2) measure how much the data support particular parameter values. The maximum likelihood estimates for the parameters are the values of θ_j , θ_p , and θ_o that

maximize Eq. (2), which in the case of the multinomial distribution are simply $\theta_j = x_j$, $\theta_p = x_p$, and $\theta_o = x_o$.

Based on Eq. (2), we used the following steps to draw 95% confidence intervals on a triangular graph. First, given the observed counts for the particular assemblage, we evaluated Eq. (2) to determine the likelihood for the proportions of juvenile, prime, and old that corresponded to every location on the triangular graph. In principle, there are an infinite number of locations, but, in practice, the number of locations is finite, and it depends on the user-specified size of the graph. Second, we found the likelihood value that would produce a contour that encompasses 95% of the total likelihood mass. The total likelihood mass is the sum of the

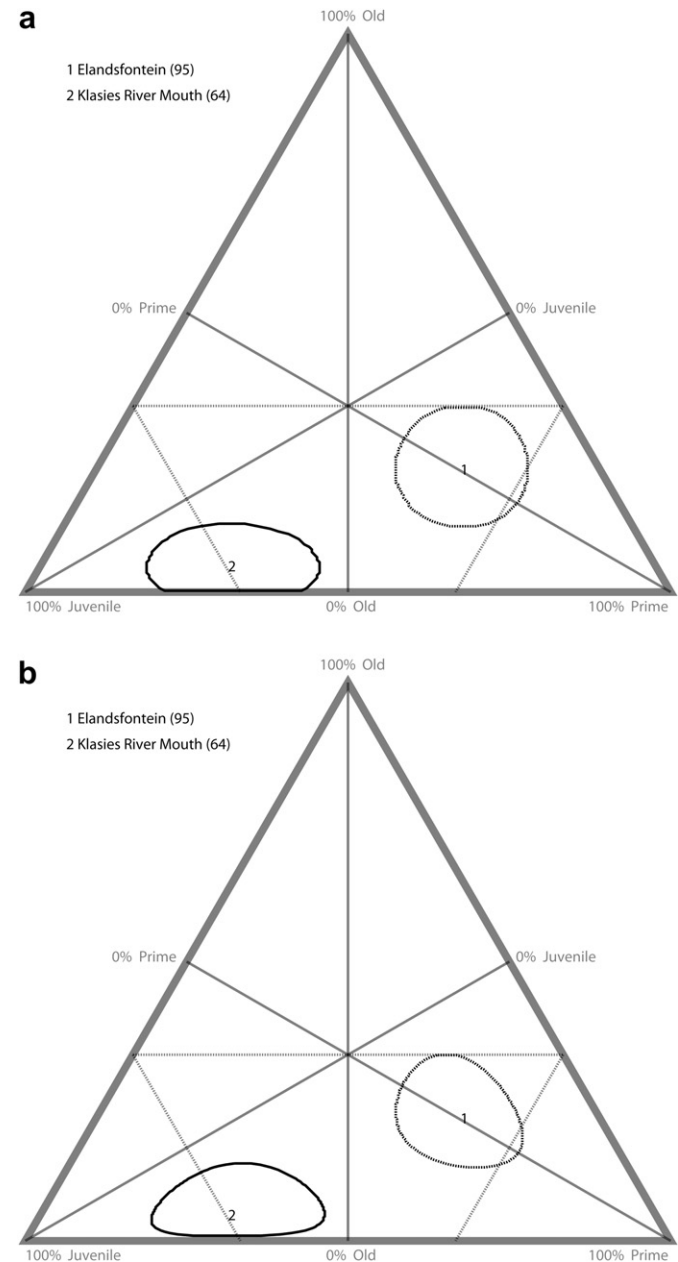


Fig. 1. Comparison of bootstrap (a) vs. likelihood (b) confidence intervals. The data are from Klein (1982a) and Lyman (1994). The non-overlap of the confidence intervals indicates that there is a statistically significant difference in age structures of the extinct giant African buffalo found at Elandsfontein (dotted) and Klasies River Main (Mouth) (solid). The bootstrap and likelihood confidence intervals differ somewhat in size and shape, but both approaches would lead to similar interpretations.

likelihoods for all the locations: $L_T = \sum_{i=1}^n L_i$, where n is the number of locations and L_i is the likelihood for location i , so a 95% confidence interval corresponds to contour that encompasses $0.95L_T$. The confidence interval contours are analogous to the contours on a topographic map, except that the former connect points of equal likelihood and the latter connect points of equal elevation.

3. Comparison of bootstrap vs. likelihood confidence intervals

The bootstrap and likelihood confidence intervals differ somewhat in size and shape (Fig. 1). The more symmetrical shape of the bootstrap confidence intervals does not seem to be a consequence of the bootstrap resampling procedure itself; it appears to be an artifact of the Gaussian kernel smoother used by Steele and Weaver (2002) to make the contours less ragged. The likelihood approach has three additional advantages over the bootstrapping approach. First, the accuracy of the likelihood confidence intervals does not depend on sample size, whereas the bootstrap confidence intervals would be expected to become more accurate with increasing sample size (Efron and Gong, 1983). Second, even with small sample sizes, the likelihood contours are never ragged. Kernel smoothing reduces the raggedness of the bootstrap contours somewhat, but does not completely remove it, particularly with small sample sizes (see figures in Steele and Weaver, 2002). Third, the likelihood approach can handle counts of zero for an age class (Fig. 2). The bootstrapping approach performs poorly when any of the age classes have counts of zero. Nevertheless, in most cases, both approaches would lead to similar interpretations (Fig. 1). Table 1 gives the data used to generate Figs. 1 and 2.

4. Cross-platform program

A stand-alone Macintosh OS X and Windows program that implements the likelihood approach described here is available at

Table 1

Data used to generate Figs. 1 and 2.

Sample	Sample size	Juvenile	Prime	Old
Elandsfontein	95	20	54	21
Klasies River Main	64	42	19	3
Sample size 40	40	16	24	0
Sample size 20	20	8	12	0
Sample size 10	10	4	6	0
Sample size 5	5	2	3	0

<http://anthropology.ucdavis.edu>. Data are read from text (ASCII) files or can be entered (and saved) with the program. The line width, style, and color of the confidence interval can be specified for each sample that is plotted on the triangular graph. The user can also set various aspects (e.g., confidence interval percentage) of the graph and save completed analyses as Portable Network Graphics (.PNG), Portable Document Format (.PDF), or Postscript (.PS) files.

5. Conclusions

Faunal analysts commonly compare the age profiles of taxa within or between assemblages to reconstruct pre- and post-depositional histories. Typically, these comparisons are made visually, but because sample sizes are often small, any differences may be the product of sampling rather than meaningful contrasts in depositional history. Following conventional statistical practice, differences that may be the product of sampling should not be interpreted. Because general statistical packages do not provide ways to statistically compare age structures, we make available a cross-platform computer program for making statistical comparisons on a triangular graph using the likelihood-based method presented here. Although we developed the method with mortality profiles in mind, it potentially has many applications beyond age profiles. In principle, it can be used to analyze any kind of artifact for which there are three distinct categories, which could include breakage or surface modification categories for faunal analyses or tool types for lithic analyses.

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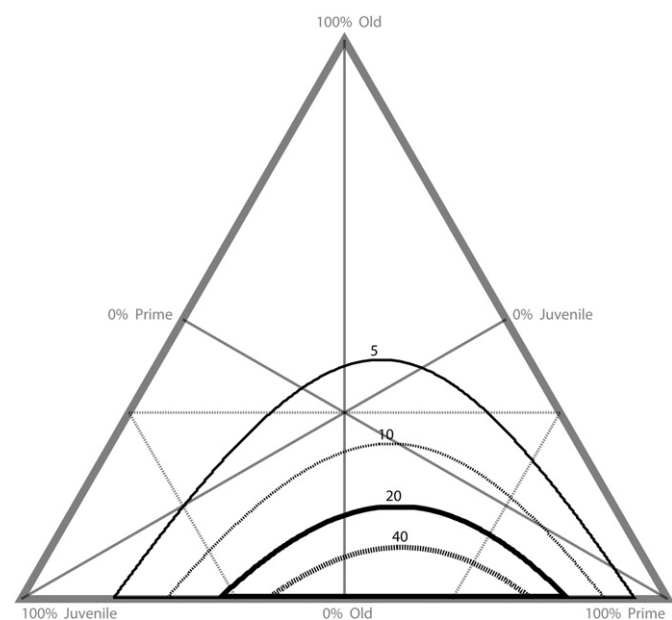


Fig. 2. Example illustrating confidence intervals when one age class has a count of zero, and the effects of sample size on confidence. All of the confidence intervals are based on 40% juvenile, 60% prime, and 0% old individuals, but they encompass different areas of the triangular graph because of differences in total sample size. The total sample sizes are 5, 10, 20, and 40 for the thin-dotted, thin-solid, thick-solid, and thick-dotted lines respectively.

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