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Morphometric analyses of hominoid crania, probabilities of conspecificity and an approximation of a biological species constant



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ABSTRACT

Thackeray has previously explored the possibility of using a morphometric approach to quantify the “amount” of variation within species and to assess probabilities of conspecificity when two fossil specimens are compared, instead of “pigeon-holing” them into discrete species. In an attempt to obtain a statistical (probabilistic) definition of a species, Thackeray has recognized an approximation of a biological species constant ($T = -1.61$) based on the log-transformed standard error of the coefficient m ($\log se_m$) in regression analysis of cranial and other data from pairs of specimens of conspecific extant species, associated with regression equations of the form $y = mx + c$ where m is the slope and c is the intercept, using measurements of any specimen A (x axis), and any specimen B of the same species (y axis). The log-transformed standard error of the co-efficient m ($\log se_m$) is a measure of the degree of similarity between pairs of specimens, and in this study shows central tendency around a mean value of -1.61 and standard deviation 0.10 for modern conspecific specimens. In this paper we focus attention on the need to take into account the range of difference in $\log se_m$ values ($\Delta \log se_m$ or “delta $\log se_m$ ”) obtained from comparisons when specimen A (x axis) is compared to B (y axis), and secondly when specimen A (y axis) is compared to B (x axis). Thackeray’s approach can be refined to focus on high probabilities of conspecificity for pairs of specimens for which $\log se_m$ is less

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than -1.61 and for which $\Delta \log se_m$ is less than 0.03 . We appeal for the adoption of a concept here called “sigma taxonomy” (as opposed to “alpha taxonomy”), recognizing that boundaries between species are not always well defined.

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Introduction

Palaeo-anthropologists who address the challenge of alpha taxonomy, as defined by [Mayr et al. \(1953\)](#), by classifying hominins and placing them into one or other discrete species, are dependent on the assumption that there are clear boundaries between taxa. However, boundaries between species are not always necessarily clear, as recognized by Darwin in 1851 and 1854 in his studies of “varieties” of barnacles; as recognized also by Locke in 1689 when he stated that “the boundaries of the species, whereby men sort them, are made by men”; and as recognized by [de Buffon \(1749\)](#) when he noted that variation occurs “from one species to another, and often from one genus to another, with imperceptible nuances” (page 150 of the first English translation of *Histoire Naturelle, Premier Discours*). [Darwin \(1859\)](#) recognized in his concluding chapter of *The Origin of Species* that it was necessary to measure the “amount” of variation in a species. Although these comments were made prior to the current understanding of genetics, they are relevant to the question as to what constitutes a biological species. [Thackeray \(1997, 2005\)](#) explored the possibility of using a morphometric approach to quantify the “amount” of variation within species (to quote Darwin) and to assess probabilities of conspecificity when two fossil specimens are compared, instead of “pigeon-holing” them into discrete species.

Method

In this study we calculate the log-transformed standard error of the coefficient m ($\log se_m$) in regression analysis of cranial and other data from pairs of specimens of conspecific extant species, associated with regression equations of the form $y = mx + c$ where m is the slope and c is the intercept, using measurements of any specimen A (x axis), and any specimen B of the same species (y axis). The log-transformed standard error of the coefficient m ($\log se_m$) is a measure of the degree of similarity between pairs of specimens, and shows central tendency around a mean value of -1.61 for pairwise comparisons of conspecific specimens ([Thackeray, 2007](#)).

[Gordon and Wood \(2013\)](#) have criticized this approach on the basis of pairwise comparisons of cranial measurements of different species of modern primates. In this paper we tackle one of the most important weaknesses in their critique. We focus attention here on the need to take into account the range of difference in $\log se_m$ values ($\Delta \log se_m$ or “delta $\log se_m$ ”) obtained from comparisons when specimen A (x axis) is compared to B (y axis), and secondly when specimen A (y axis) is compared to B (x axis).

Results

For pairwise comparisons of measurements for specimens representing the same species of similar size (conspecific comparisons), using least squares linear regression, $\log se_m$ values do not differ substantially depending on whether specimen A is on the x axis and specimen B is on the y axis, or vice versa when specimen A (y axis) is compared to B (x axis) ([Fig. 1](#)).

By complete contrast, for pairwise comparisons of measurements for specimens representing different species of different size (“mixed genera” or inter-generic comparisons), $\log se_m$ values differ substantially depending on whether specimen A is on the x axis and specimen B is on the y axis, or vice versa ([Fig. 2](#)). In some cases where measurements of very differently-sized crania of different species are compared, relatively low $\log se_m$ values can occasionally be obtained, even as low as -1.7 (for specimen A on the x axis and specimen B on the y axis), contrasting with a substantially higher (more

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