basicranial length, drawing on consistent proportional relationships in apes and humans. *Ar. ramidus* is confirmed to have a relatively short basicranium. A short, broad cranial base with an anterior foramen magnum is otherwise found exclusively in *Homo* and *Australopithecus* among catarrhines, warranting identification of *Ar. ramidus* as a hominin/d. Reorganization of the cranial base is among the earliest morphological markers of this clade.

Aging methods across populations: Focus in Nigeria.

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Building on a body of work by Jantz, Konigsberg, and Kimmerle (2008) which addressed questions about population variation in human identification, models for aging Nigerian populations are investigated. Demographic data for n=2,590 cases and biometric scores (n=356) for the pubic symphysis and fourth ribs, scored in the manners of Suchey-Brooks and Iscan and co-workers, were collected for identified individuals autopsied at LASUCOM, Nigeria. Overall the average ages and general age ranges for each phase are lower than that of the original methods. The Nigerian samples have a lower mean age at death, though the overall range is consistent, whereas the American sample tends to be slightly older. Comparing the distributions of the samples through independent sample t-tests, reveals they are significantly different, for both male and female groups, well below the 0.05 level. Interestingly, the mean difference is far less between Nigerians and Americans, 4.35 years, than it is among Nigerian and Balkan samples, 13.6 years. To calculate age-at-death parameters that can be used by investigators in the field – a Bayesian statistical approach is used. Combined parameters for both traits are calculated. For the 321 Nigerian individuals having both rib and pubic symphysis data, an "R" script "lrage.viewer.biv" applies single trait models for the rib and pubic symphysis stages and combines these with the total Nigerian age-at-death distribution (n=2,461). Of the 296 individuals in a bootstrap sample, 141 (47.63%) had ages that fell within their stated 50% HPD. This is not significantly different from the 50% expected (p=0.4158).

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Age-related trauma incidence in the Gombe chimpanzees.

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Previous research indicates that adult chimpanzees accumulate injuries as they age, so that older chimpanzees have more skeletal traumata compared to younger conspecifics. We tested whether this same trend is apparent in sub-adults versus adults in an expanded skeletal sample of wild chimpanzees from Gombe National Park, Tanzania. We examined 30 chimpanzee skeletons (16 female, 14 male) for skeletal trauma, all with known sex and age (or a reliable age estimate), and represented by complete or near complete skeletons. Trauma incidence is the percent of observable bones affected by trauma, allowing for some broad comparisons between skeletons with differing numbers of bones (e.g. adults versus sub-adults, or in cases of a few missing hand or foot bones). We analyzed the relationship between trauma incidence and age using the statistical software Arc. This study confirms that number of traumata increases with age in adult chimpanzees. In the sample that includes chimpanzees of all ages, we did not find a linear relationship between age and trauma incidence (R^2 = -0.065, p = 0.17). This is due to 4 influential cases whose trauma incidences are an order of magnitude larger than the other chimpanzees in the sample. We argue that the influential cases should not be considered outliers because cause of death is conspecific aggression, one of the leading causes of death for chimpanzees at Gombe, and because in a sub-sample including only adult chimpanzees, cause of death did not affect trauma incidence (chi-square = 0.868, df = 1, p > 0.1).

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Culture-Genetic models of information exchange among Pleistocene human populations.

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Homo sapiens have a significantly larger census population size than any of the other hominoids and thus should show a greater level of genetic variation. Yet this is not the case, as ape species possess much more diversity than humans do at genetic loci (Charlesworth 2009). Here, I test models which explain this lack of genetic diversity as a result of a significantly low amount of gene flow between small regional populations of early humans during the Pleistocene (i.e. Premo and Hublin 2009). I derive predictions from these models by computer simulations and compare the results to the physical variability of fossil humans and Middle Paleolithic lithic traditions. This method utilizes a new application of Information Theory to allow for the comparison of paleoanthropological data and genetic models. By building a database of both fossil data and cultural material from archaeological sites in Europe, assumptions about an increase in the amount of information concomitant with the introduction of a new human group to Europe during the Middle Pleistocene are tested. Results fail to falsify the null hypothesis that there is no change in the amount of information throughout the Middle Pleistocene, suggesting that many of these models are faulty. I argue that effective population size may be partially explained by patterns of human culture, but that we need to take into account other aspects. In fact, low effective population size may not be a good indicator of census size in the Pleistocene.

Structural asymmetries in the human brain assessed via MRI.

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The human brain is structurally and functionally different between hemispheres. Developmental, evolutionary, and genetic factors are thought to influence these asymmetries. Behavioral traits such as manual dexterity, motor control, and aspects of language are usually lateralized in the brain, but the extent to which these can be directly linked to specific anatomical asymmetries has been the subject of debate. Analyses of fossil hominin endocasts have revealed anatomical asymmetries that are assumed to reflect asymmetries in underlying brain regions. Clarifying where - and by how much - extant human brains are asymmetrical will allow better interpretations of these fossil asymmetries, both with respect to suspected brain asymmetries as well as possible functional/behavioral implications. Two areas of particular interest are Broca's and Wernicke's areas, because they play key roles in language production in modern humans. Previous research has suggested that these areas are asymmetric, but studies to date have had small sample sizes and often use brain scans of unhealthy patients. To this end, we investigated the various left-right differences of the human brain through a voxel-based morphometric analysis of MRI scans of 72 healthy, female subjects. Left-right reversed versions of individual brains were mapped into their corresponding original versions, using non-rigid deformation methods. These mappings were then registered to a common atlas, and average degrees of left-right asymmetry were calculated for each voxel. Our results showed both Broca's and Wernicke's areas to have significant leftward asymmetry at the p-value of 0.001. Implications of this work for hominin evolution will be discussed.

Revealing the evolutionary dynamics of pathogens in primate populations.

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Recent advances in DNA/RNA sequencing technology, combined with newly