

Biological Anthropology in 2018: Grounded in Theory, Questioning Contexts, Embracing Innovation

Melanie Ann Martin

ABSTRACT Biological anthropology in 2018 encapsulated what past scholars envisioned for its future: a multidisciplinary approach to understanding human and nonhuman primate evolution and diversity using the most innovative techniques and rigorous standards available. This year also built on a tradition of introspection about what biological anthropology encompasses and by whom and how it is conducted. This review highlights research and movements in the field that reflect both of these pursuits. Studies drew on evolutionary theory to generate novel insights into human and nonhuman primate biology, behavior, and organization. Studies on hominin evolution and human biology have upended previous understandings by revealing more dynamic and context-dependent processes in our ancestry and phenotypic expressions. Across subdisciplines, biological anthropologists have advanced the use of new technologies and analytical techniques and begun to promote open, transparent, and reproducible science among a more diverse community of researchers. [*year in review, evolutionary anthropology, context and variation, emerging technologies, transparent methods, researcher diversity*]

RESUMEN La biología antropológica en 2018 encapsuló lo que investigadores anteriores imaginaron para su futuro: una aproximación multidisciplinaria para entender la evolución de primates humanos y no humanos y diversidad utilizando las técnicas más innovadoras y los estándares rigurosos disponibles. Este año también desarrolló sobre una tradición de introspección acerca de lo que la antropología biológica abarca y por quién y cómo es llevada a cabo. Esta revisión resalta la investigación y los movimientos en el campo que reflejan estas búsquedas. Los estudios se basaron en la teoría evolucionaria para generar nuevos conocimientos en la biología de primates humanos y no humanos, comportamiento y organización. Los estudios sobre la evolución de los homíninos y la biología humana han cambiado drásticamente entendimientos previos al revelar procesos más dinámicos y dependientes del contexto en nuestra ascendencia y expresiones fenotípicas. A través de las subdisciplinas, los antropólogos biológicos han avanzado el uso de nuevas tecnologías y técnicas analíticas y empezado a promover una ciencia abierta, transparente y reproducible entre una comunidad más diversa de investigadores. [*año en revisión, antropología evolucionaria, contexto y variación, tecnologías emergentes, métodos transparentes, diversidad de investigadores*]

The history of biological anthropology has been underscored by attempts to properly situate the field in relation to other natural sciences and the discipline of anthropology as a whole (e.g., Calcagno 2003; Ellison 2018; Fuentes 2010; Wiley and Cullin 2016). Today, there are three biologically and/or quantitatively oriented sections

within the American Anthropological Association (AAA)—the Biological Anthropology Society, the Evolutionary Anthropology Society, and the Society for Anthropological Sciences—which nearly every year confront their minority status within the AAA and at times larger questions about the positionality and representation of science within the

discipline (e.g., Lende 2010). This year was marked by a fresh level of introspection as another scientific anthropological organization, the American Association of Physical Anthropologists (AAPA), marked the centennial of its flagship journal (the *American Journal of Physical Anthropology*, or *AJPA*) and simultaneously began to consider changing the name of the organization. In effect, 2018 was a year for contemplating what the field has been and where it is going.

The debate about what, if any, new name might better represent the current scope of the AAPA and its members is ongoing but has parallels in earlier deliberations about the aims of the field. As reviewed by Ellison (2018) in the centennial *AJPA* issue, and earlier by Fuentes (2010), major players in the mid-twentieth century recognized the need to definitively move away from the “old” physical anthropology—with its emphasis on descriptive taxonomy—and toward a “new” multidisciplinary approach aimed at understanding “the process of primate evolution and human variation by the most efficient techniques available” (Washburn 1951, 298). Washburn’s vision of this new approach is remarkably still apt given the new perspectives and theoretical and technological developments that have come to dominate the field since its mid-century inception (Fuentes 2010; see also essays by Cartmill 2018, Grauer 2018, Leonard 2018, Richtsmeier 2018, Weiss 2018, and others in the 2018 *AJPA* centennial issue).

Inspired by this “new” definition of physical anthropology, I have chosen to highlight research published in 2018 that is strongly grounded in evolutionary theory, expands our understanding of context, variation, and dynamic process in human evolution and biology, or introduces new methods and approaches that move the field forward. Many articles highlighted in this review accomplish all of the above. Many more are not in this review but are no less exemplary in their theoretical rigor, methodological innovation, and significance to the field.

GROUNDING IN EVOLUTIONARY THEORY

One of the alternate names proposed for the AAPA was the “American Association of Evolutionary Anthropologists,” a suggestion that acknowledges both the primacy of evolutionary studies and the fact that evolutionary theory and related mechanisms are dominant and unifying frameworks for interpreting variation in all primate biology and behavior (Ellison 2018). While the descriptive does not characterize all concentrations within biological anthropology, the frequent use of evolutionary theory to generate and test predictions does distinguish our field from other anthropological subfields and social and health sciences. For example, anthropologists have long posited that life-history trade-offs in growth versus maintenance—and not merely nutritional quality—underlie epidemiological patterns of growth faltering in resource-poor environments (Blackwell et al. 2010; Bogin et al. 2018; McDade et al. 2008). Urlacher et al. (2018) provided new evidence of the etiology of this

trade-off, demonstrating that linear growth in Shuar children (Ecuador) was most adversely affected by short-term deficits related to acute inflammation. However, the effect was buffered by greater body fat, as would be predicted when growth and immune function directly compete for energetic resources.

Several studies demonstrated novel evidence of sexual selection influencing population-specific differences in mating, parental investment, biology, and economic activities. Lowe, Hobaiter, and Newton-Fisher (2018) found support for their “risky-male avoidance hypothesis” in observing that eastern chimpanzee mothers whose infants were most vulnerable to infanticide specifically avoided rising-rank males who were less likely to have previously sired infants and thus most incentivized to commit infanticide. Conversely, male mountain gorillas who indiscriminately affiliated with more infants were also shown to sire more infants, suggesting that female preference for affiliative males may drive emergent selection for more costly paternal behaviors (Rosenbaum, Vigilant, et al. 2018).

To test for evidence of sexually selected chemical communication, Spence-Aizenberg, Williams, and Fernandez-Duque (2018) examined physical and behavioral differences in olfactory traits between captive male and female owl monkeys. Hypothesizing that traits would be female-biased as a result of male selection on female quality, they found a mix of female- and male-biased dimorphic traits that were consistent with the species’ strict social monogamy, on the one hand, but inconsistent with their high paternal care, on the other hand. The authors raise the possibility that sex differences in odors may bias olfactory behaviors among males and females without corresponding to extreme dimorphism in olfactory physiology. Turning to humans, von Rueden et al. (2018) found that among the Tsimane—egalitarian forager-farmers of the Bolivian Amazon—men’s greater political influence stemmed in part from sex differences in body size, parental investment costs, and division of labor but was also due to the increased access to cooperative partners that these latter characteristics beget.

Evolutionary theory and mechanisms can also be combined with or evaluated against other frameworks for understanding human and nonhuman primate behavior. Alami et al. (2018) applied life-history theory to expand on the psychological concept of a “health locus of control” (HLC)—that is, the extent of control individuals believe they have over their own health outcomes. Alami et al. demonstrated that Tsimane adults have significantly lower HLC compared with adults in Japan and the United Kingdom—likely a reflection of higher extrinsic risks in the Tsimane environment. Lower HLC within the Tsimane also predicted lower uptake of biomedical illness treatments, with implications for health policy and interventions in high-mortality populations.

Social network theory posits that individual behavior can be explained in relation to a person’s position in a network of relationships. Ready and Power (2018) applied social network analysis to assess food-sharing patterns in a

Canadian Inuit village, demonstrating that both evolutionary mechanisms (e.g., reciprocity and kin selection) and social structural forces (e.g., local political prominence) motivated more frequent sharing. Specifically, they found that more affluent and politically influential households both shared more (rather than divesting from sharing networks) and benefitted more from sharing—evidence that sharing in the community did not serve to redistribute wealth equitably but rather reinforced existing inequalities. Koster (2018) examined reciprocal exchanges at the individual and household levels among Nicaraguan horticulturalists, simultaneously testing predictions derived from kin-selection and balance theory—the latter of which emphasizes the influence of triads and larger social structures on dyadic relationships. Koster found evidence that household members converged on similar exchange strategies, rather than maximizing pairwise benefits across households (even if kin), such that group-level reciprocity was observed at a higher rate than individual-level dyadic reciprocity. Last, while network analysis has previously shown that existing social networks shift in response to environmental pressures, it is still unclear if within-group dynamics precede major structural changes. Larson et al. (2018) examined social dynamics among female Cayo Santiago rhesus macaques in the two years prior to a rare mass-eviction event. They concluded that while rates of aggression did not increase prior to the event, subtle differences in within-group patterns of affiliative and aggressive behaviors suggested “cliquish” behaviors preceded the eviction.

Other researchers employed multiple hypothesis testing and different levels of analysis in order to examine alternative mechanisms by which behavioral and biological traits evolve and vary among species and within populations. Monson and Hlusko (2018) simultaneously tested for the influence of phylogeny and life-history variables in determining primate dental eruption sequence. Their analysis—the most comprehensive to date—supports a conserved phylogenetic sequence rather than an association with postnatal growth rates, as postulated by “Schultz’s rule” (Schultz 1960). Catalano et al. (2018) examined sex ratios from historical Swedish birth records for evidence of Trivers-Willard and Bruce effects. These hypotheses propose different mechanisms by which spontaneous abortion rates of male fetuses increase in high-risk/low-resource environments, resulting in lower male-biased birth ratios. The Trivers-Willard effect predicts reproductive suppression responds to relatively poor maternal condition or resources, whereas the Bruce effect posits that the phenomenon responds to environmental signals of higher childhood morbidity and mortality. Catalano et al. found more evidence of a Bruce effect and suggest this mechanism should be more widely considered in evaluating sex-ratio variances.

Mattison et al. (2018) examined how ultimate and proximate mechanisms—in the form of adaptive decision making and transmission of social information—have combined to influence age at last birth among the Mosuo of China.

Hypotheses derived from human behavioral ecology predict that relatively early reproductive stopping may be adaptive if it maximizes parental resources, allocare, or parental fitness given current demographic trends. Conversely, hypotheses derived from cultural evolution emphasize the role of cultural learning and norms in spreading reproductive strategies. Mattison et al. found strong evidence of temporal and village-level trends in decreasing age at last birth, suggesting that local cultural norms, and particularly kinship residence patterns, had greater influence on declining ages at last birth than did individual trade-offs or even official Chinese fertility policy.

Understanding how anthropometric measures—widely used as markers of health status—vary with genetic and environmental factors is conducive to devising appropriate policies to improve nutritional and health outcomes. Starkweather and Keith (2018) estimated the influence of shared genes and household environments on boat-dwelling Shodagor children’s and parents’ height, weight, and BMI in Matlab, Bangladesh. They found that within-household factors affecting resource distribution accounted for more variance in children’s nutritional outcomes than did genetic factors and specifically that mothers’ autonomy over resource allocation had a greater impact on these outcomes than did maternal income or education. Intriguingly, greater family size was negatively associated with paternal BMI and positively associated with children’s height, suggesting resource allocation in Shodagor households may buffer children at the expense of fathers.

CONTEXTUAL VARIATION IN BIOLOGY AND BEHAVIOR

A key tenet of biological anthropology is that human biology and behavior vary adaptively in response to socio-environmental influences. For example, skin pigmentation has evolved to balance the opposing effects of UV exposure on vitamin D requirements and folate availability at different latitudes and elevations (the “folate-vitamin D-UV hypothesis of skin pigmentation” evolutionary model; see Branda and Eaton 1978; Jablonski and Chaplin 2010). New research further supports this model by demonstrating a seasonally reciprocal relationship between vitamin D and folate, which is mediated by folate gene variation (Lucock et al. 2018). Elsewhere, research on adaptive responses in geographic extremes presented novel evidence that hormonal responses to physical activity may vary at high altitude (Sarma et al. 2018), and that supraclavicular brown adipose tissue in Yakut adults (Siberia) may play a role in nonshivering thermogenesis and, therefore, cold adaptation in this population (Levy et al. 2018).

The extent to which socio-environmental influences affect variability in human biology, behavior, or development is often underappreciated, leading to assumptions about the universality of traits that are in actuality highly culture bound (Kline, Shamsudheen, and Broesch 2018). Cross-cultural research published in 2018 evinced more nuanced aspects

of, and in some cases even upended, previous assumptions about normative, evolved human biology and behavior. Betti and Manica (2018) compared human female pelvic dimensions across 348 historic skeletal samples from twenty-four global populations. In contrast to expectations consistent with the “obstetric dilemma”—which would predict minimal variation in the size and shape of birth canals owing to tight selective constraints—they found wide geographic variation in measurements that were indicative of neutral evolutionary processes, with further implications for hominin evolution and modern obstetric practice.

In comparative research in the United States and Central Uganda, Bouterse and Wall-Scheffler (2018) observed remarkable cultural differences in solitary and group walking dynamics. When compared with their respective median solitary speeds, adults carrying children walked faster in the United States but slower in Uganda—suggesting cultural contexts influence differences in walking behavior and not necessarily the maximization of energy efficiency. Meanwhile, cross-cultural experimental field data with the Batek in Malaysia and the Tsimane in Bolivia demonstrated that taller stature compromises walking speeds through dense rainforest terrain, suggesting that short stature has been selected for better locomotor performance in these settings (Venkataraman et al. 2018). Tsimane adults were also shown to have similar average sleep durations and equally variable sleep onset times as adults in the United States, calling into question assumptions about how ancestral sleep patterns may have differed relative to those in modern, industrialized settings (Yetish, Kaplan, and Gurven 2018).

Research with polyamorous Himba pastoralists demonstrated that mate preferences differed for men and women in a manner consistent with parental investment theory but varied for formal and informal partners in a manner more in keeping with local cultural norms (Scelza and Prall 2018). Relatedly, research in rural and urban communities in Tanzania demonstrated that for children in both communities, increased schooling was associated with reduced time spent in labor activities, consistent with predictions of embodied capital theory (Hedges et al. 2018). However, boys were more likely to trade school for herding activities, whereas girls were more readily able to combine school and domestic activities. Hedges et al. suggest that these sex-biased patterns likely drive higher female school enrollment, but they caution that girls are more likely to lose important leisure time as a result of these time-allocation trade-offs.

In some cases, research published in 2018 supported findings previously only demonstrated in Western settings, providing additional evidence of universal traits. Births at a rural Argentinian hospital, in which medical interventions were minimal, were shown to peak in the early morning hours—similar to patterns seen historically in the United States—providing additional support for the hypothesis that early morning births were evolutionary favored (Chaney, Goetz, and Vallenggia 2018). Consistent with existing experimental data from Western, educated, industrial, rich, and

democratic (WEIRD) populations, field experiments carried out with sixteen globally dispersed subsistence-scale populations provided further evidence that pride is a universal human attribute that functions to help motivate cooperative behavior (Sznycer et al. 2018).

Importantly, comparative cross-cultural research investigating either divergent or universal traits depends on data collection that is both uniform and culturally salient across study populations. Yet implementing standard protocols into cross-cultural research risks producing equivocal or false evidence if protocols are not appropriately adapted. Winking et al. (2018) belabor this point in their paper using the Investment Model Scale (IMS) to examine variation in relationship quality among indigenous Mayanga/Miskito communities (Nicaragua). The IMS has been widely used to measure and predict relationship commitment among WEIRD populations (Henrich, Heine, and Norenzayan 2010) but had never previously been tested in a natural-fertility population—that is, against the reproductive pattern that would have influenced human mating behaviors and investment decisions throughout most of human evolution. Winking et al. found that while the IMS did capture real variation in the quality of relationships among the Mayanga/Miskito, specific components of the scale varied in their relevance to local commitment constructs.

Hruschka et al. (2018) review the many problems in adapting research tools, such as Likert scales, that were developed within formally educated populations for use in more culturally and economically varied settings—further noting that there has been little systematic examination of what specific tools generate meaningful or unusable responses in different contexts. Drawing from their work adapting a well-established experimental protocol for rural Bangladeshi study communities, Hruschka et al. identified several assumptions embedded in the protocol (but inapplicable to their subjects) about how respondents should perceive and respond to task stimuli. To appropriately and reliably adapt research methods to diverse populations, Hruschka et al. recommend conducting extensive preresearch engagement and piloting with study communities, cross-checking modifications with external populations, and publicly documenting protocol revisions for the benefit of other researchers. Notably, both Hruschka et al. (2018) and Winking et al. (2018) cite results from their own external cross-checks in concluding that the differences they observed in their study populations relative to standard findings likely did not derive from differences in protocol delivery.

RELATIONAL DYNAMICS INFLUENCING BIOLOGY AND BEHAVIOR

Family and group membership have emerged as key contexts influencing locally responsive variation in behavior and biology. Kramer and Veile (2018) demonstrate that infant allocare in Savanna Pumé and Yucatec Maya families provided substantial energetic savings for mothers, with alloparents' time devoted to infants offsetting maternal care by more

than double. In addition, siblings—who provided the bulk of allocare—did not significantly decrease the time spent in school, foraging, or at play, demonstrating minimal costs of allocare in traditional societies. The research demonstrates how relatively low-cost sibling care may have been favored ancestrally and continues to favor juvenile allocare in many cultures today. Jaeggi, Trumble, and Brown (2018) examined changes in urinary hormones before and after wild red-tailed monkey intergroup encounters at Ngogo. They found that, irrespective of the outcomes, cortisol rose during and shortly after encounters, suggesting anticipatory stress responses to intergroup competition. Conversely, testosterone continued to decline after outcomes, which may have reflected energetic trade-offs resulting from sustained physical stress.

Primate lactational strategies—including variation in milk composition—are another vital mechanism of maternal–infant transmission and early environment signaling. Many immunologically active milk constituents, for example, not only confer direct protection against pathogens but also modulate developing infant biology in ecologically specific fashion. In a comparative study across seven ecologically and economically diverse populations, Klein et al. (2018) demonstrated that acquired immune protein composition—which reflects both recent and lifelong maternal disease exposures—exhibited greater interpopulation variation than did innate composition. Miller (2018) similarly found differences in levels of anti-inflammatory milk bioactives between US and Kenyan (Ariaal) mothers, which further predicted differences in infant growth outcomes.

Human milk microbial composition, which may influence infant gut microbial composition, and consequently immune and metabolic development, has been shown to vary by geography, birth mode, postpartum time, and maternal obesity and antibiotic usage. Meehan et al. (2018) compared milk microbial composition in Aka hunter-gatherers and neighboring horticulturalists in the Central African Republic, finding differences in the abundance of specific taxa consistent by subsistence strategy and season. Curiously, milk microbial diversity was increased in association with larger infant allomaternal networks and frequency of allomaternal care, suggesting maternal microbial communities are influenced by bidirectional exchange of microorganisms. Research on fecal gut microbial composition among red-bellied lemurs also demonstrated modulation with social networks but found that greater social contact was associated with lower microbial alpha diversity (Raulo et al. 2018). The researchers suggest future studies to examine how diversity indices are influenced by the result of group dynamics on community microbial populations or conversely if stress is an intermediate factor influencing the statistical relationship between group interactions and microbial diversity.

Maternal cortisol is also transmitted to infants via lactation and may influence sex- and species-specific infant

behavioral development. Higher milk cortisol concentrations in rhesus macaques during the neonatal period was shown to predict more frequent play behavior in daughters, but not sons, speculated to reflect emergent personality differences that influence interactions among conspecifics (Dettmer et al. 2018). The potential for behavioral modification via adaptive “lactational programming” has implications for human infant neurobiological development in the absence of breastfeeding, though to as yet unknown effect (Dettmer et al. 2018). Notably, research with mothers in Cebu, Philippines, showed that cortisol levels of breastfeeding mothers were suppressed relative to nonbreastfeeding postpartum and nulliparous mothers. Thus, maternal postpartum metabolism and infant development may differ in breastfeeding and nonbreastfeeding dyads owing to lactation-regulated cortisol activity (Thayer, Agustin Bechayda, and Kuzawa 2018). Murray et al. (2018) observed higher concentrations of fecal glucocorticoid concentrations among lower-ranking chimpanzee mothers during pregnancy and lactation, as was predicted by their social status. However, they also observed age-related declines in the glucocorticoid concentrations of only the male offspring of low-ranking females, suggesting that offspring HPA development may be downregulated by heightened maternal prenatal stress in a sex-specific manner.

Biological anthropologists also continued to unearth fascinating new insights on father–offspring transmission and paternal biology. Eisenberg and Kuzawa (2018) reviewed human and cross-species studies in arguing that sperm telomere length progressively increases as human males age, and they advance the novel hypothesis that this effect in older fathers may serve as an adaptive intergenerational signaling mechanism to promote increased maintenance effort and later senescence in offspring. Cross-cultural and longitudinal research has previously established that human males downregulate testosterone production facultatively in response to intensive paternal care (Gettler 2016). Burke and Bribiescas (2018) found that differences in testosterone and cortisol levels between fathers and nonfathers further vary between heterosexual and gay couples, tentatively suggesting that stress, parenting experiences, and mating opportunities may differently influence hormonal responses in gay and nongay fathers. Elsewhere, preliminary research found that higher baseline and postgame changes in testosterone and cortisol in US fathers watching offspring sporting matches were more strongly associated with perceptions of referee bias than they were with the game outcomes or their perceptions of offspring performance (Alvarado et al. 2018).

Research from Cebu, Philippines, showed that temporal declines in testosterone were lower for fathers with older children or who had separated from their partners (Rosenbaum, Gettler, et al. 2018), and that prolactin may be upregulated with paternal care to a similar degree that testosterone is downregulated (Gettler, Kuo, and Agustin Bechayda 2018)—together providing additional evidence

for endocrine mediation of mating and parental effort in male human. Conversely, Tecot and Baden (2018) observed that among male red-bellied lemurs, fecal androgen levels were negatively associated with paternal carrying but positively associated with total allomaternal care behavior, which included protective behaviors such as grooming and huddling. Differences in androgen levels were unlikely to reflect mating effort, as this species exhibits long-term pair bonds and nonoverlapping seasons of infant care and breeding, suggesting that protective paternal behaviors can coexist with postnatally elevated androgen levels.

FLUIDITY IN HOMININ EVOLUTION

Several paleo- and genetic anthropology studies published this year advanced a more dynamic, complex, and nonlinear picture of hominin evolution. Challenging the prevailing view of a single population/region origin for our species, a consortium of researchers synthesized existing archaeological, fossil, genetic, and paleoenvironmental data to propose that *H. sapiens* evolved from semi-isolated, morphologically and geographically distinct populations across Africa (Scerri et al. 2018). Analysis of *H. naledi* cranial remains—dated to at least 250,000 years ago and indicating contemporaneous existence with *H. sapiens* in South Africa—also revealed an Australopithecine-sized brain with some *Homo*-like organizational features, calling into question the adaptive importance of linear increases in brain size across hominin evolution (Holloway et al. 2018).

Du et al. (2018) analyzed endocranial volumes across ninety-four hominin fossils from different taxa, arguing that brain size did not increase gradually and consistently across the hominin clade but rather via diverse, within-lineage mechanisms, including directional selection, drift, the sudden emergence of larger-brained species, and the extinction of smaller-brained ones. Tucci et al. (2018) presented genetic evidence from contemporary pygmies living on Flores Islands to suggest that dwarfism evolved independently on the island at least twice. Genomes from the living population showed admixture with Denisovans and Neanderthals but no other archaic lineages—which could have suggested an ancestral relationship with *H. floresiensis*, their famously diminutive predecessors on the island. Conversely, genomic sequencing of a Denisovan bone fragment at least 50,000 years old revealed that the individual came from a Neanderthal mother and a Denisovan father, strongly suggesting that admixture between the two archaic groups was common at the time (Slon et al. 2018).

Finally, the timeline of major migrations in *H. sapiens* history also continues to undergo revision. New skeletal remains unearthed in Israel support an out-of-Africa migration at least 220,000 years ago (Hershkovitz et al. 2018). The discovery of twenty-nine well-preserved footprints dated to 13,000 cal BP in British Columbia, meanwhile, supported growing evidence that humans occupied Pacific North America

at the end of the Last Glacial Maximum (McLaren et al. 2018).

NEW DISCOVERIES FROM OLD DATA

Notably, many of this year's major breakthroughs in hominin evolution have stemmed not from new field discoveries but from extensive collaboration, interdisciplinary synthesis, and reexamination of existing data using emerging technologies and analytical methods. Research done with multisite samples or using existing multispecies and cross-cultural databases similarly requires extensive collaboration but allows for more robust hypothesis testing through increased sample size and statistical power, greater sample diversity, information theoretic approaches, and tests of phylogenetic or spatial autocorrelation (Gavin et al. 2018).

Baker and Shackelford (2018) reviewed published primate genetic field studies to produce independent support for the use of testes size as a proxy measure for sperm competition while also advancing a more accurate formula derived directly from paternity data. Nunn and Samson (2018) examined sleep characteristics of primates in the Phylogeny of Sleep database, finding that humans sleep considerably less than expected given their phylogeny and social and environmental ecologies. They argue that sleep patterns in humans may have evolved in response to increased terrestrial living and predation risks or the learning opportunity costs of sleep (Nunn and Samson 2018).

Gleeson and Kushnick (2018) used the Standard Cross-Cultural Sample (SCCS) to test the prediction that greater self-sufficiency in females would be associated with reduced sex stature dimorphism—supporting the hypothesis that female choice for less-aggressive males can drive “self-domestication.” Ross et al. (2018) also used the SCCS in demonstrating that the predominance of monogamy in highly unequal societies (presumed to arise with the emergence of intensive agriculture) is consistent with predictions of the polygyny threshold model. They observed that while the frequency of poorer men does increase in stratified economies (favoring polygyny), the frequency of sufficiently wealthy men also substantially decreases, leading to diminished marginal returns for prospective additional wives and ultimately favoring monogamy. Colleran and Snopkowski (2018) analyzed Demographic and Health Survey (DHS) data to illuminate multiple causal pathways by which local demographics, women's employment, and contraceptive use differently influence fertility decline across populations. Readers are further directed to the forthcoming methods paper by Rosinger and Ice (under review), which describes how large-scale publicly available datasets like the DHS may be used to complement or conduct original research in human biology.

Recent biological anthropological research has also capitalized on data accumulated in longitudinal primate field studies to reveal novel patterns in primate demography and epidemiology. Feldblum et al. (2018) revisited Gombe chimpanzee data collected between 1971 and 1972, finding

evidence that male-biased sex ratios, dominance struggles, and insipient alliances preceded a famous group fission and resulting “four-year war” at the site. Analyzing more than twenty years of chimpanzee demographic data at Ngogo, Wood et al. (2017) found that the average Ngogo life expectancy was closer to that of human hunter-gatherers than to those of other chimpanzee sites, but that maximum lifespans at Ngogo and other chimpanzee sites were similar to each other, though still well below human maximums. Wood et al. suggest that ecological circumstances related to predation and food availability may uniquely favor higher survivorship at Ngogo.

Longitudinal observations of Kibale chimpanzees were used in separate studies to generate the most complete pictures to date of morbidity risks and juvenile feeding transitions. Thompson et al. (2018) found that respiratory illness was the leading cause of death at Kibale over twenty years of observations. Adults over forty and low-ranking younger adult males had the highest risks of respiratory illness, which may reflect age or testosterone-mediated declines in immunocompetence. The analysis by Bray et al. (2018) determined that solid food ingestion begins around five months and steadily increases without any decrease in suckling frequency until weaning at four to six years, by which time juveniles have acquired typically adult dietary breadth and feeding patterns. Feeding behaviors were also acquired fairly early in infancy, which is inconsistent with the “needing-to-learn” hypothesis that posits complex diets favor delayed maturation to ensure protracted learning (Ross and Jones 1999).

Last, longitudinal observations of wild baboons have revealed mechanisms underpinning reproductive variation within groups. Tinsley Johnson et al. (2018) analyzed demographic data from gelada baboons in Kenya, finding evidence of two birth peaks: a seasonal “ecological peak” coinciding with green grass availability, and a “social birth peak” coinciding with dominant male takeover events. Gesquiere et al. (2018), analyzing thirty-six years of near-daily observations of yellow and olive baboons in Kenya, found evidence supporting energetic constraint models of reproductive success, largely acting through variation in interbirth intervals. Shorter intervals were associated with several ecological, individual, and group variables consistent with greater energy availability, while body fat, which decreased across most of the duration of postpartum amenorrhea, subsequently increased prior to cycling.

INTEGRATIVE METHODS AND NEW ANALYTICAL APPROACHES

Biological anthropologists in 2018 continued to integrate more advanced technologies and biomarkers into existing methods to examine a new phenomenon or test and refine hypotheses. Finestone et al. (2018) used high-speed video recordings to examine discrete kinematic and spatiotemporal characteristics of terrestrial locomotion among chimpanzees, bonobos, gorillas, and orangutans. Their

analysis revealed similar quadrupedal gaits and postures across all four species that varied little with body size, suggesting convergent evolution related to shared anatomical features. Meanwhile, Tagg et al. (2018) used trap-camera footage to examine terrestrial nocturnal activity in wild chimpanzees—behavior that had not been systematically documented previously, owing to the logistical difficulties. Combining camera footage with ecological survey data, they concluded that nighttime terrestrial activity was widespread and flexible—occurring at all hours of the night—but infrequent, consistent with consolidated sleeping patterns. Differences in activity patterns were further influenced by temperature and absence of human activity, but not predators, rainfall, or moonlight.

The “good-genes” hypothesis posits that some aesthetic attributes are honest signals of higher biological quality (Hamilton and Zuk 1982) and has been further extended to attributes that reveal stable early developments. The hypothesis has previously been tested in humans by examining deviations in measures of bilaterally paired traits (fluctuating asymmetry, or FA) in association with measures of attractiveness or self-reported health outcomes. Expanding on this work, Pawlowski et al. (2018) hypothesized that lower FA would be associated with greater immunocompetence—stringently measured through multiple innate and postvaccine adaptive immune responses in serum. In their study of nearly two hundred healthy Polish subjects, FA measures were not associated with innate or adaptive responses, providing no support for the good-genes hypothesis and suggesting that small differences in FA among healthy individuals may be irrelevant to functional fitness outcomes.

Past years have seen an emergence of bioarchaeological studies of historical breastfeeding and weaning behaviors using stable isotopic methods. Beaumont et al. (2018) simultaneously analyzed carbon and nitrogen isotope values extracted from bone collagen and coforming dentine in individual skeletons from an Anglo-Saxon site. They concluded that carbon isotopes were more similar in bone and collagen, and more accurate in estimating smaller trophic level shifts than nitrogen. Conversely, nitrogen isotope levels in bone collagen appeared more sensitive to physiological stress, suggesting bulk bone collagen may not be an appropriate tissue for investigating historic breastfeeding and weaning patterns.

Increasingly sophisticated analytical methods, including simulated mathematical models, have also been applied to examine dynamic ecological and behavioral problems in human and nonhuman primate studies. Fuchs, Gilbert, and Kamilar (2018) applied ecological niche modeling to examine African baboon distributions and diversity. While distributions overall were best predicted by seasonal rainfall and temperature, species differed in niche breadths and the extent to which abiotic factors correlated with their distributions. Moreover, models revealed evidence of niche specialization between species that did not correlate with time since

divergence, suggesting that descriptions of baboons as ecological generalists may be inaccurate, and that ecological specialization has driven taxonomic diversity. Conversely, Scott (2018) tested for trait-dependent diversification in primates across multiple state-dependent speciation and extinction (SSE) models that made different assumptions about the rate of speciation. Of the six well-established traits considered in this analysis, only nocturnal versus diurnal activity patterns correlated with diversification across models. Scott argues that other ecological traits previously associated with diversification are likely false positives arising from comparisons against null models that assume homogenous diversification rates.

Kessler et al. (2018) tested mechanisms by which therapeutic care could have evolved in humans by simulating competing models of ineffective and effective disease care, which they tested over a range of plausible ancestral social environments. Their models predict that effective caregiving would likely evolve as an evolutionary stable strategy in small, cooperative, kin-based groups (assumed typical for most of human evolution) and in turn would have selected for increasing intelligence via returns on better disease recognition and social learning of caregiving skills. Smaldino, Flamson, and McElreath (2018) proposed that covert signaling—that is, transmitting information in a “coded” manner so that it is accurately perceived by intended recipients but obscured to a larger audience—helps facilitate cooperation by allowing intragroup assortment while avoiding conflict among the group as a whole. Their model results—which may have relevance for understanding political psychology in the industrialized West—predict that covert signaling is favored in groups with relatively low similarity, when the benefits of intragroup signaling are small but the costs of being disliked by other group members are high.

OPEN AND TRANSPARENT ANTHROPOLOGICAL SCIENCE

As quantitative social scientists whose research interests and methods often overlap with psychology, medicine, and public health, biological anthropologists are likely aware of the growing “replicability crisis” in these fields (e.g., Glenn Begley and Ellis 2012; Open Science Collaboration 2015). However, because our data are often observational and collected under dynamic, unique conditions in time and place, *reproducible methods* should be a greater concern for anthropologists than *replicable* results per se (Beheim 2016). Problems of both replicability and reproducibility, however, stem from flawed or dubious practices (e.g., insufficient sample size and power, “p-hacking,” file drawer effects, *post hoc* hypothesizing) that in turn arise from an emphasis on statistically significant versus biologically relevant findings (Kramer, Veile, and Otárola-Castillo 2016) and the academic incentives that reward them (Smaldino and McElreath 2016). The extent to which such practices affect the veracity and quality of anthropological research is unknown but is the subject of an increasingly

public conversation. Smith (2018) penned a commentary in *AJPA* calling attention to the continued misapplication of null hypothesis significance tests in biological anthropology. The 2018 annual meeting of the American Anthropological Association also hosted an executive session (“Open Science and the Anthropological Imagination”), organized by Jeremy Koster and Mary Shenk, and including several participants cited here, which highlighted current efforts to improve upon anthropological research in this regard.

Encouragingly, there is a growing contingent of researchers promoting transparency and reproducibility in anthropology directly through their own methods and publications. Two essential steps in promoting reproducible analytical methods are scripting statistical work in a standard computing language (e.g., R, Stata, SAS) and making those scripts and accompanying data publicly available (Beheim 2016). Several anthropologists have taken this initiative further and publicly preregistered hypotheses and analytical protocols prior to conducting statistical work (e.g., Gaffney and Hagen 2018; Pisor and Ross 2018; Rej et al. 2018; Tennyson and Eisenberg 2018). Others have developed or maintained open-source R packages that help facilitate reproducible and comparative anthropological methods. These include *AnthroTools*, for conducting free-list analyses and Bayesian cultural consensus modeling (Purzycki and Jamieson-Lane 2017); *AnthropMMD*, for measuring trait divergence (Santos 2018); *demogR*, for constructing and analyzing age-structured population models (Jones 2007); *local growth*, for calculating and comparing anthropometric z-scores from Tsimane, Shuar, CDC, and WHO growth references (Blackwell 2018); *rrtools*, to create compendiums for reproducible research (Marwick 2017); and the Statnet suite of packages, for conducting statistical network analysis, simulation, and visualization (Handcock et al. 2018).

Finally, in the interest of accelerating peer communication and expanding public access, anthropologists have begun expanding open-source repositories (e.g., MorphoSource) and publishing manuscripts as preprints on established servers such as bioRxiv (e.g., Snyder-Mackler et al. 2018; Su et al. 2018; Tinsley Johnson et al. 2018), PsyArXiv (e.g., Smaldino et al. 2018; Tiokhin, Hackman, and Hruschka 2018), and OSF (e.g., Sear, Sheppard, and Coall 2018). It is also worth noting that a number of peer-reviewed studies surveyed in this review were published in open-access journals (e.g., *Peer J*, *the Royal Society for Open Science*, *Scientific Reports*) or using open-access options in standard subscription-model journals.

WHO WE ARE AND WHERE WE'RE GOING

The conversation about where the field is going is not limited to the type and quality of research we do; it is also about who we are as a community of researchers. This question, incidentally, also is at the center of the debate over whether to change the name of the AAPA. One

argument for changing “physical anthropology” to another descriptor (i.e., “biological,” “biocultural,” “evolutionary”) is that the old moniker inevitably evokes the racist historical roots of the discipline. Secondarily, some proponents favor changing or dropping “American” from the name to be more inclusive of the international researchers in the organization.

The question of who we are has motivated several inquiries in the last decade of how institutional and informal norms in our field have shaped researcher experiences and opportunities (Clancy et al. 2014; Fuentes 2010; Turner et al. 2018). Finding those norms often wanting or even hostile, members have loudly called for explicit action to promote a more inclusive and diverse community across ranks, and they have been successful in implementing codes of conduct to address sexual harassment (Willermet 2016) and initiatives to recruit and retain diverse scholars (Antón, Malhi, and Fuentes 2018). But the work is ongoing.

As we grapple with evolving standards for higher-quality research, it’s worth emphasizing that the question of how we conduct research necessarily demands that we examine *who* conducts it. Calls to promote researcher diversity are not simply for diversity’s sake. Given the lingering legacy of structural inequalities in our society, it is morally correct to include more historically underrepresented voices in our field. But we also *need* to promote diversity in biological anthropology because perspective matters to the breadth and quality of the knowledge produced—especially in a field in which perspective emanates from and applies to understanding human experience. Perspective generates novel hypotheses, informs methods, and opens opportunities. Perspective influences what research gets done, to the betterment of society and human knowledge. Diversity of perspective in biological anthropology matters, and therefore diversity in our field matters.

CONCLUSION

Each new year in any scholarly field sees the emergence of new research and internal discourse that builds from or questions existing foundations. Considering the enormous breadth of inquiry within biological anthropology—spanning eras and species, molecules to social networks—it is not surprising that we intermittently struggle to define who we are and what we do. For this reason, in this year’s review I have attempted to highlight the theoretical grounding and methodological rigor that underlie the processes of discovery and innovation in the field as a whole. Biological anthropologists embrace and understand the simultaneous influences of evolutionary, ecological, and cultural mechanisms shaping human and nonhuman primate biology and behavior. We are scientists committed to the integrity of science in our research and society. We are also anthropologists critically examining the universal and the diverse, biased by our own experiences, and endeavoring to better integrate those realities to improve our field. For

these reasons, for better or worse, the questions of who we are and where we are going will perhaps always be complicated.

Melanie Ann Martin  Department of Anthropology, University of Washington, Seattle, WA 98195; martinm7@uw.edu

NOTES

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