

Patterns of integration and modularity in the primate skeleton: a review

Noreen von Cramon-Taubadel

Buffalo Human Evolutionary Morphology Lab, Department of Anthropology, University at Buffalo, Buffalo, NY 14226

e-mail: noreenvo@buffalo.edu

Summary - *The question of how complex morphologies evolve, given constraints imposed by genetic, developmental and functional factors, has been a topic of inquiry for many decades. In the mid-twentieth century the study of morphological trait covariation, and the implications of this for evolutionary diversification, was developed under the general concept of “morphological integration”. Given the polygenic inheritance model underlying quantitative skeletal traits, and the existence of differential pleiotropic effects, it is assumed that variation in the genotype to phenotype map will lead to the emergence of semi-autonomous “modules” that share relatively stronger covariance (integration) among traits within them. Understanding these potential patterns of modularity in the primate skeleton is important for clarifying the seeming inconsistencies presented by “mosaic” morphologies found in fossil taxa, as well as providing hypothetical units of morphological evolution that can be compared across the primate order. A review of the primate skeletal integration and modularity literature was conducted with the aim of assessing (i) the general nature of primate skeletal integration patterns, and (ii) the extent to which any identified modularity patterns are ubiquitous across primates. The vast literature on cranial integration reveals some consistency in suggesting that the face and the neurocranium (and in some cases, the basicranium and vault) form distinct modules, but the intensity of this modular pattern varies across taxa. The much more modest postcranial integration literature suggests that apes show overall reduced covariation among skeletal regions compared with other anthropoid taxa, but the extent to which any identified modularity patterns hold true across primates is still very unclear. While much has been learned about primate skeletal integration in the past two decades, we still need more studies that establish benchmarks as to what constitutes an integrated modular structure, and that empirically test these potential modules across a wider range of primate taxa.*

Keywords - *Characters, Modules, Mosaic Evolution, Cranium, Postcranium.*

Introduction: On the evolution of “characters”

At the heart of the evolutionary process of descent with modification via natural selection lies the concept of “divergence of character” (Darwin 1859) or the accumulation of heritable variation such that new taxa (be they sub-species, species or genera) are eventually formed. However, Darwin did not understand precisely how such characters were inherited or how their variability was maintained over time. Furthermore, as noted by Huxley (1942), Darwin’s insights were born out of a blend of

induction and deduction, rather than based on the results of mathematical analyses of theoretical or empirical data. As such, a detailed understanding of the inheritance of “characters” was not developed until the early 20th century, when Fisher (1918) showed mathematically that the inheritance of quantitative characters was compatible with the recently re-discovered Mendelian principle of particulate genetics (Wijsman 2005). Under a mathematical model of polygenic inheritance, quantitative characters (i.e., characters whose variance can be quantified on a continuous scale) are coded for by a number of genetic loci, each with alleles segregating and

assorting according to typical Mendelian “rules” (Lynch and Walsh 1998; von Cramon-Taubadel and Schroeder 2018). The polygenic inheritance model for quantitative characters assumes that each polygene contributes to the ensuing phenotypic variation with equal and additive effects (i.e., additive genetic variation or the combined effects of multiple genes that exert influence on the phenotype in a linear fashion), while the non-additive variation introduced due to dominance effects (within-locus interaction), epistasis (between-locus interaction), and environmental factors must also be taken into consideration, even if it is often difficult to quantify directly.

Indeed, while more is now known about the genomic location of some major polygenes contributing to some complex quantitative characters (e.g., Leamy et al. 1999; Rogers et al. 1999; Blue 2018; Wainschtein et al. 2022), the precise genetic architecture of most quantitative characters remains elusive. This is partly due to the complexity of such genetic architectures, but has more to do with the fact that quantitative characters are not “real” units of evolutionary change (von Cramon-Taubadel 2019). Huxley (1942, p. 18) acknowledged this when stating that “characters as such are not and cannot be inherited. For a character is always the joint product of a particular genetic composition and a particular set of environmental circumstances”. This succinctly describes a fundamental paradox in the study of morphological evolution. We empirically and statistically analyze phenotypic “characters”, or what we think are the quantifiable manifestations of the inherited information on which natural selection works, yet we do not know exactly how these empirical characters map back on to the genetic loci that are actually inherited (Lewontin 1974; Atchley and Hall 1991; Marroig and Cheverud 2004; von Cramon-Taubadel 2019).

Moreover, while we tend to conceptualize whole organisms as being composed of collections of characters, it has long been recognized that analyzing any one character, or even a few characters, in isolation, leads to a rather limited view of the overall picture of organismal form

(e.g., Thompson 1917). Nevertheless, as Olson and Miller (1958) note, in order for the totality that is an organism to be effectively conceptualized, it is necessary to decompose that organism into a finite number of single characters, which, in the study of morphology, are typically expressed as linear dimensions of particular body parts. While the process of reducing the morphology of a complex organism to a limited set of numbers might represent a loss compared to detailed qualitative morphological description, what is gained is the ability to produce objective mathematical representations of sample *populations* of organisms that can be probed using a myriad of multivariate statistical approaches. The primary purpose of this review is to situate the multivariate analysis of primate skeletal “characters” in the wider context of evolutionary morphology. First, I will review the basics of how the coordinated growth of organismal form leads to patterns of integration and modularity among body parts, then consider the implications of this for understanding “mosaic” patterns of morphological evolution, and finally review what we think we know about patterns of integration and modularity across the primate cranial and postcranial skeleton.

Morphological integration, modularity, and evolution

It has long been recognized that different regions or parts of an organism are coordinated in terms of their size and shape properties to varying degrees, going back to early studies of morphology in the 18th and 19th centuries (Klingenberg 2013). However, in 1958 this was formalized as a statistical endeavor under the concept of “morphological integration” by Olson and Miller. They argued that understanding why some phenotypic characters (or “traits”) tended to covary more strongly with one another during ontogeny or throughout evolutionary history was key to a better understanding of phenotypic evolution (Magwene 2001). They set the precedent of using statistical correlation among quantified traits as a means of measuring the degree of

correspondence (or “integration”) among them, and in turn relating these degrees of correlation with particular groups of traits, identified *a priori* based on hypotheses of functional or developmental connectivity (Olson and Miller 1958). Their empirical studies confirmed the notion that some traits were more tightly integrated with each other than others, and that this degree of integration was directly related to the extent to which traits share the same developmental origins and/or functions within an organism.

While Olson and Miller’s (1958) insights were not immediately subsumed within the broader study of morphological evolution, their ideas were subsequently married with theoretical ideas from quantitative genetics and developmental biology to generate a more sophisticated framework for analyzing morphological integration in an evolutionary context (e.g., Lande 1979, 1980, 1984; Cheverud 1982; Chernoff and Magwene 1999; Magwene 2001). In this regard, James Cheverud’s 1982 study of morphological integration in the macaque cranium, in which he calculated basic quantitative genetic parameters such as additive genetic variance and trait heritability using cranial measurements from the Cayo Santiago skeletal collection, was instrumental in forging connections between quantitative genetic theory and morphological integration in the anthropological literature. He highlighted that genetic correlation must underlie phenotypic correlation via the processes of polygeny, pleiotropy and linkage disequilibrium (see Figure 1), such that, at a proximate level, traits that are more genetically correlated will tend to covary and evolve together. Using this logic, he considered groups of traits that are highly genetically correlated to be part of “genotypic sets” (*G*-sets) and argued that it is reasonable to assume that developmentally or functionally related traits will likely be found in the same *G*-sets. Based largely on the clinical developmental work of Moss and colleagues (e.g., Moss and Young 1960), cranial traits from macaque mother-offspring dyads were divided into so-called *F*-sets, reflecting *a priori* defined developmental and functional cranial units, such

as, for example, the neurocranial, orofacial, nasal, and masticatory units (Cheverud 1982). Due to the artificial provisioning of the macaque colony at Cayo Santiago, it was argued that correlations among traits due to environmental effects were likely minimal, suggesting that most of the familial trait correlations reflected shared additive genetic variance. The results confirmed Olson and Miller’s (1958) findings in showing that the average correlations among traits within *F*-sets were higher than those found among traits in different *F*-sets. However, the results also illustrated that *F*-sets did not behave as completely independently evolving units, with a fair amount of integration connecting traits across *F*-sets. Cheverud (1982) also noted that, while stabilizing selection is important for generating genetic correlations among traits, stochastic processes, such as genetic drift, are equally important in generating non-functional correlations among traits in ways that influence the empirical patterns of integration that we observe in the phenotype.

Although Cheverud (1982) did not use the term, the *F*-sets used in his study could also be referred to as “modules”. As Wagner and Altenberg (1996) so eloquently point out, “modularity” refers to a variational property of the phenotype, or more fundamentally, a property of the genotype-phenotype map (Wagner 1996; Fig. 1a). In most cases, we have no idea what that genotype-phenotype map looks like for any given quantitative trait, yet it lies at the heart of many topics within evolutionary biology (Wagner and Altenberg 1996). While extensive pleiotropy is necessary to create a genotype-phenotype map for a functioning, integrated organism, pleiotropy is not unbounded (Wright 1968; Wagner and Altenberg 1996; Welch and Waxman 2003; Stearns 2010), but rather differential patterns of pleiotropy within and between units of phenotype termed “modules” helps to explain how complex morphology evolves (Hansen 2003). The concept of modularity is predicated on the idea that the development of complex morphologies is semiautonomous, such that an organism can be decomposed into overlapping but somewhat independent units or “modules”, each of which

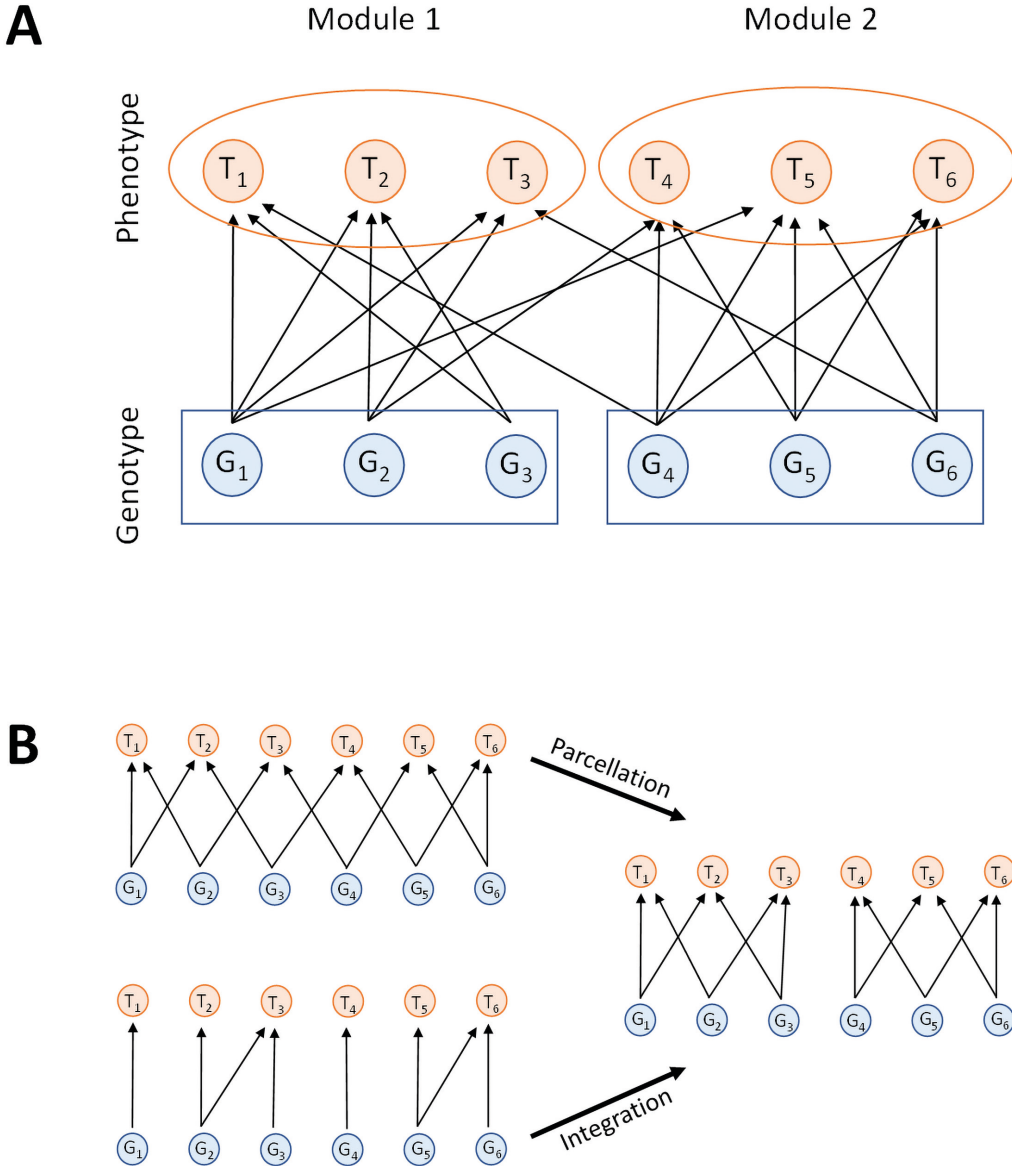


Fig. 1 - Integration and modularity are properties of the underlying genotype to phenotype map, the precise architecture of which is largely invisible to us. Following [Wagner \(1996\)](#), modules emerge as trait complexes (T_1 - T_3 and T_4 - T_6) exhibit tighter morphological integration due to varying pleiotropic effects from the underlying polygenes (G_1 - G_6). (A) While all genes contribute to the inheritance of multiple traits, there are stronger pleiotropic effects within modules than there are between modules. (B) Modularity can evolve and change over time due to tighter genetic integration or parcellation. Following [Wagner \(1996\)](#), parcellation involves the elimination of pleiotropic effects between traits in, what will become, different modules, while maintaining or strengthening pleiotropy within modules. Conversely, integration involves the creation of new pleiotropic effects among traits that were previously relatively genetically independent from each other.

are underlain by a genotypic map with greater genetic correlation (i.e., more pervasive pleiotropy) within modules than between modules (e.g., Wagner 1996; Wagner et al. 2007; Hallgrímsson et al. 2009). Hence, modularity and integration are fundamentally intertwined and somewhat hierarchical concepts, whereby morphological integration is the empirical manifestation of the genotype-phenotype map in terms of trait covariance or correlation, while modularity can be theoretically conceived of as describing the basic units of morphological evolution, even if “modules” can be difficult to define or describe empirically (Hansen 2003; Klingenberg 2008, 2014; Wagner et al. 2007; Hallgrímsson et al. 2009; Armbruster et al. 2014).

Why is the consideration of patterns of trait integration and modularity important in the study of morphological evolution? Most fundamentally, the covariation among traits (i.e., the extent to which they are integrated) can have a profound effect on the nature of their evolvability, or their potential ability to respond to a selective pressure (Hansen 2003; Hansen and Houle 2008). As Lande (1979) illustrated via his multivariate extension of the classic Breeder's equation, the predicted response to selection (Δz) is a direct function of the underlying additive genetic variance-covariance matrix (known as the G-matrix) and the selection gradient (β). Therefore, the nature of the covariance of traits within the G-matrix will directly influence the possible morphological response to any given selection pressure (Steppan et al. 2002). If a group of traits are not strongly integrated (weak covariance), then individual traits have greater potential to evolve in the direction(s) dictated by selection pressure, ultimately increasing the possibility that new morphologies arise (Hansen 2003). However, if traits are more strongly integrated and/or if strong modularity exists, then the possible outcomes of any given selection pressure are more variable (Hansen 2003; Hansen and Houle 2008). As illustrated in Figure 2, this is best understood using a simple two-trait example, where two traits either covary strongly (scenario A) or do not covary (scenario

B). In both cases, the same selection gradients (β_1 - β_3) are applied, but the nature of the potential morphological response differs between the two scenarios. In the case of little covariation (scenario B), responses (ΔZ_{1-3}) are in the same direction as the selection gradients, while in the case where the two traits are integrated, the responses vary in intensity and direction depending on how the selection pressure aligns with the pattern of covariation (Hansen and Houle 2008). This simple example illustrates that, even with just two traits, the effects of trait integration on morphological evolution can be profound. Expanding this to a more complex model incorporating multiple modules with varying degrees of connectivity (i.e., pleiotropy) between and among modules makes clear that the degree to which morphology can and will respond to selection pressure will largely depend on the underlying genetic architecture, and the nature of constraints imposed by particular pleiotropic effects (Hansen 2003).

However, patterns of integration and modularity are not static states of being (Fig. 1b; Hallgrímsson et al. 2009) and can be created or dismantled by stabilizing or directional selection (e.g., Wagner 1996; Cheverud 1996a; Steppan et al. 2002; Wagner et al. 2007). Indeed, most studies of morphology in anthropology must infer the actions of past evolutionary forces from the observable patterns of trait variation in extant or extinct taxa. Therefore, anthropologists tend to measure the outcomes of past evolutionary pressures on morphology rather than experimentally test the future outcomes of different evolutionary scenarios (Klingenberg 2013; Conaway et al. 2018). In most cases, the structure of the underlying additive genetic matrix (G-matrix) cannot be directly measured and is instead substituted with a matrix describing the variances and covariances among a set of quantitative traits (P-matrix). This approach is justified based on the results of Cheverud (1988), which showed that G- and P-matrices based on reasonably large sample sizes ($n \geq 40$) had similar patterns of correlation. Cheverud's conjecture regarding the proportionality of the G- and P-matrix has

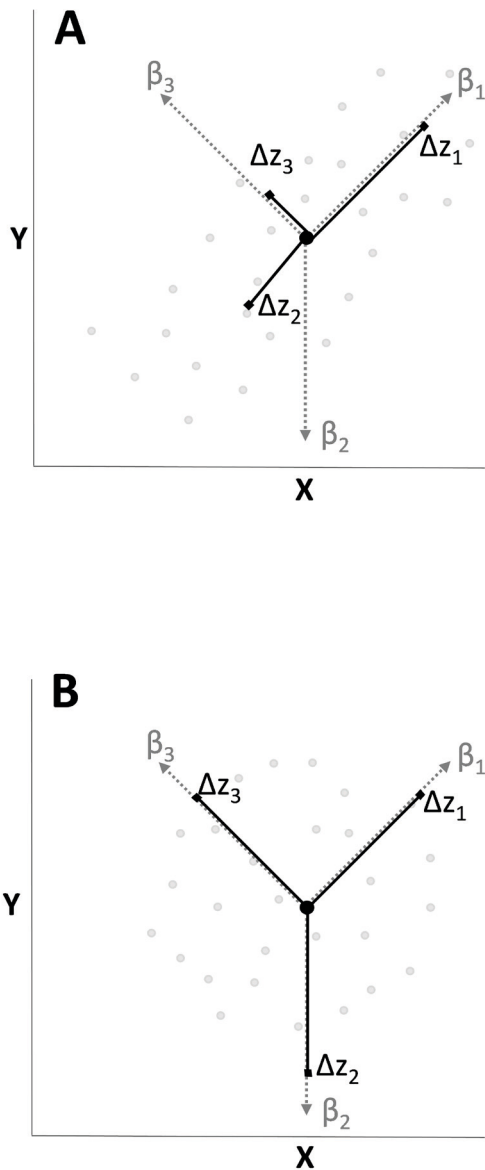
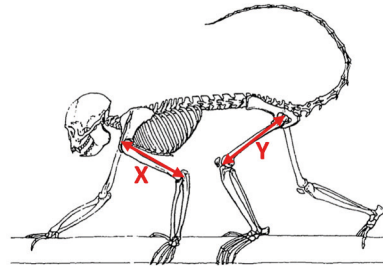


Fig. 2 - The relationship between trait covariation and the ability to respond to selection (after Rolian 2014). In scenario A, two hypothetical traits, humerus length (Trait X) and femoral length (Trait Y), are positively and strongly correlated, while in scenario B, they are uncorrelated. In both scenarios, the same three selection gradients (β_1 -3) are applied with the same magnitudes but favoring different directions in morphospace. The responses (Δz_1 -3) differ substantially depending on how the selection gradients align with patterns of covariation. In scenario A, β_1 aligns with the major axis of trait covariance and, therefore, also elicits the greatest coordinated morphological response, while in the case of β_2 , the response is much smaller and not aligned with the direction of the selection gradient. Similarly, β_3 is perpendicular to the major axis of covariation and elicits a minor response due to the constraint imposed by the strong positive covariance between the two traits. In scenario B, all responses are parallel to the direction of the selection gradients, as the lack of covariance between the two traits does not impose any constraint on evolution into any part of morphospace.



subsequently been validated using morphological traits in tamarins (Ackermann and Cheverud 2002), as well a large sample of matched human genetic and phenotypic data (Sodini et al. 2018). While caution should be exercised when substituting the P-matrix for the underlying G-matrix

(particularly for traits with low heritability; Love et al. 2022), it does open up the possibility of applying quantitative evolutionary theory “even when one is so unfortunate as to only have phenotypic data available” (Cheverud 1988, p. 966). This unfortunate situation is the one faced by

the majority of paleoanthropologists interested in reconstructing evolutionary history based on fossil anatomy, as well as many bioarchaeologists, who, for practical, ethical (e.g., the desire to avoid destructive analysis), and financial reasons, may not be able to glean genetic data from skeletal remains. As such, Cheverud's conjecture, and the empirical data underlying it, have been instrumental in facilitating the study of primate evolutionary morphology in an explicit quantitative genetic evolutionary framework.

Integration and the emergence of "mosaic" morphologies

The term "mosaic" evolution is often used in paleoanthropology to describe the seemingly piecemeal changes seen in morphology throughout the hominin fossil record (e.g., [Foley 2016](#); [Parravicini and Pievani 2019](#)). For example, the relatively complete skeletal remains assigned to the taxon *Australopithecus sediba* appear to possess a "mosaic" of primitive characteristics, shared with earlier australopithecine taxa, alongside more derived features typically found in later examples of the genus *Homo* ([Berger et al. 2010](#); [Berger 2013](#)). The degree to which mosaicism confounds skeletal analysis is apparent even in the recently discovered hominin taxon named *Homo naledi* ([Berger et al. 2015](#)). For example, *H. naledi* has been dated to between 236–335 Kya ([Dirks et al. 2017](#)), has a small brain in the range typical of australopithecines ([Schroeder et al. 2017](#)), yet with cranial features shared with other members of the genus *Homo* ([Laird et al. 2017](#)). This mirrors the combination of a young date, small brain and *Homo*-shaped cranium also found in *Homo floresiensis* ([Aiello 2015](#)). These examples of fossil mosaicism consistently lead to major debates about the taxonomic and phylogenetic position of any given fossil, as there is no clear agreement on how to weigh the relative importance of different skeletal elements, which may display distinct combinations of primitive and derived characteristics.

If we situate the evolution of mosaic morphology in the context of integration and modularity, then the degree of mosaicism can be quantified

by the strength of genetic correlation within and between parts ([Cheverud 1982](#); [Young et al. 2010](#)). In order for parts of an organism to evolve relatively independently, the degree of genetic correlation between parts must be low and/or the correlation within parts must be sufficiently strong to counteract the effects of direct selection on other parts ([Falconer and Mackay 1996](#)). This is precisely what the concept of modularity describes, whereby an organism can be conceived of as comprising a set of loosely articulated modules, each of which is more likely to evolve as a single morphological unit somewhat independently of other modules. Therefore, gaining a better understanding of patterns of modularity and integration across primate taxa would also help put into context the seemingly mosaic patterns of morphological change we see in the fossil record.

Having said that, there are some fundamental problems with the way that morphological traits or "parts" have been conceptualized within anthropology, that cause major stumbling blocks for the evolutionary analysis of mosaicism in the fossil record. Firstly, there is a long history within anthropology of separating the craniomandibular complex from the postcranium, that has led to the empirical disassociation of potentially integrated morphologies (or "modules"). This body-head separation is obvious in the structure and organization of most major natural history collections, with cranial material being more well represented and stored separately from postcrania. In addition, craniodental fossil remains are more prevalent than postcrania in the primate (including hominin) fossil record, necessitating a more intense focus on comparative cranial collections. Studies of primate craniodental variation are also more numerous, presumably because of the long-held emphasis on cranial size and shape variation for understanding the evolution of humans ([von Cramon-Taubadel and Weaver 2009](#)), as well as the assumption that craniodental data more faithfully record the phylogenetic relationships among taxa (e.g., [Pilbeam 1996](#); [Young 2005](#); [von Cramon-Taubadel and Lycett 2014](#); [Keyon-Flatt et al. 2020](#)). Conversely, variation in the postcranium is presumed to better

reflect past adaptation across species (especially as it relates to locomotion and positional behavior), as well as reflect the action of phenotypic plasticity via extensive bone remodeling (Ruff et al. 2006; Agostini et al. 2018). Secondly, and related, we lack a good understanding of what the morphological units of evolution might be for primates (i.e., are there specific groups of traits or “modules” that tend to evolve together?). Much of our existing research on the evolution of primate morphology treats individual morphological traits as if they are units of evolution like genetic loci (von Cramon-Taubadel 2019), when it is clear that morphology evolves as a coordinated system of “traits”, which covary to a greater or lesser extent depending on underlying proximate sources of variation (additive polygenic variation, epistasis and pleiotropy; Fig. 1a). However, criteria based on anatomy (e.g., hindlimb), development (e.g., regions with similar ossification patterns), and function (e.g., mastication) can be employed to create hypothetical modules (similar to Olson and Miller’s F-sets), which can then be subjected to tests of within- and between-module integration. In recent years, there has been an increase in the number of studies of integration and modularity within and among skeletal regions in primates, yielding new insights into patterns of skeletal trait covariation that are important for furthering our understanding of primate (and hominin) morphological diversification.

What we currently know (or think we know) about primate skeletal integration patterns

Esteve-Altava (2017) presented a review of 205 research articles that sought to test or validate hypotheses of morphological modularity in animal and plant taxa. In so doing, they wanted to assess the extent to which there are consistencies or biases in the way such studies are conducted in terms of methods used to quantify modules, and the biological factors thought to be important in generating patterns of

modularity observed. The results revealed that the large increase in publications on morphological modularity in the past 25 years comes mainly from the study of mammals, with particular focus on humans and mice. Despite the fact that delimiting hypothetical modules in the vertebrate head is challenging due to the presence of overlapping developmental and functional interactions that might obscure covariation patterns (Lieberman 2011; Hallgrímsson et al. 2009), the head is the most studied body region, with a bias towards analyses of cranial hard tissue (as opposed to dentition or brain anatomy). Typically, such modularity studies begin by proposing hypothetical modules based on functional, developmental, genetic or evolutionary criteria (Klingenberg 2008, 2013), and then analyses of trait integration (covariance and/or correlation) within and between modules are used to test the validity of these hypotheses. The traits used to empirically test hypotheses are typically quantified using either traditional (i.e., linear metrics) or geometric morphometric (i.e., landmark-based) methods.

The trends identified by Esteve-Altava (2017) clearly show that studies of modularity and integration in biological anthropology have been key contributors to the overall body of literature on this important topic. The results also confirm the cranial-postcranial bias in anthropology mentioned earlier, although it is worth noting that there have been several key studies of primate postcranial integration (reviewed below) published since 2017. Also, while Esteve-Altava (2017) illustrates some trends in the quest to identify potential modules and test the factors underlying them, it does not specifically review papers that seek to compare patterns and magnitudes of integration (or modularity) across taxa. Hence, what follows here is an attempt to review what we know, or think we know, about integration and modularity in the primate skeleton, with two specific questions in mind:

- 1) What is the nature of within-skeletal integration patterns?
- 2) How universal are skeletal integration patterns across primate taxa?

The first question is concerned with the identification of “modules” within the skeleton, based on developmental, functional, genetic, or anatomical criteria. The second question concerns the extent to which, should such modules exist, patterns of integration and modularity are ubiquitous across primate taxa. Alternatively, if systematic differences are found among taxa, do these fall down phylogenetic lines, or are they related to other factors such as similarities in feeding or locomotor behaviors? As such, assessing what we know in light of these two questions will provide important context for the study of mosaic morphological evolution, both in extant and fossil primates. For organizational purposes, the review will follow a “head-to-toe” structure, starting with the more extensive literature on craniomandibular integration, and moving to the less well studied postcranium, although special note of studies incorporating multiple skeletal regions will also be made. It should also be noted that only studies of bone morphological integration will be considered here, but the reader is referred to the following studies for examples of analyses of dental integration (e.g., Hlusko et al. 2009, 2011, 2016; Gómez-Robles and Polly 2012; Grieco et al. 2013; Delezené 2015; Lawrence and Kimbel 2021).

Integration and modularity in the primate skull

The skull is a complex skeletal region to unpack in terms of integration and modularity as it comprises many closely aligned units surrounding the sensory organs and the brain that share bony walls, as well as being dynamically affected by multiple mechanical forces related to mastication, locomotion, and other behaviors (e.g., Hallgrímsson et al. 2007; Lieberman 2011; Klingenberg 2013). Nevertheless, three major units are typically identified based on embryological and functional criteria; the basicranium (deriving from the endochondrally ossifying chondrocranium), the neurocranium (i.e., the intramembranously ossifying bones of the cranial vault) and the face (derived from the splanchnocranium with a combination of endochondral and intramembranous ossification) (Cheverud 1996a; Bastir 2008;

Lieberman et al. 2008; Lieberman 2011). There is also a fundamental distinction between bones that derive from neural crest cells (facial bones) and those that derive from paraxial mesoderm cells (neurocranial vault and base) (Moore 1981). The basicranium is often thought of as the “central integrator” of the cranium (e.g., Lieberman et al. 2000, 2008), due both to its central location as a platform on which the face and neurocranium rest, and its pattern of earlier growth, attaining adult size and shape before the rest of the cranium. These larger units (particularly the face) are then sometimes divided into smaller subunits based on developmental and/or functional criteria, relating to mastication, vision or other functions such as respiration (e.g., Cheverud 1982, 1995; Marroig and Cheverud 2001). As noted by Klingenberg (2013), the literature on primate (including human) cranial integration is extensive and varies greatly in terms of the methods used to quantify traits, as well as the underlying biological concepts applied. What follows is a review of some of the major studies, particularly as they relate to the two questions posed earlier. Therefore, I focus here on studies that seek to determine the extent of modularization in the primate cranium (i.e., are these developmental and functional units actually representative of integrated modules?), as well as focus on studies that provide some degree of cross-taxon comparison.

Early studies by Cheverud (1982, 1989, 1995, 1996b) of pedigreed papionins and tamarins found genetic integration in the masticatory region of the face and the cranial vault, showing modularization of the braincase and the face across both catarrhine and platyrrhine taxa. In a comparison of cranial covariance patterns across tamarin species (genus *Saguinus*), Ackermann and Cheverud (2000) found some correspondence between covariance and phylogenetic relationships, suggesting that covariance patterns can diverge over time. Marroig and Cheverud (2001) examined the nature of cranial patterns across a broad sample of platyrrhine taxa and found that covariance structure was relatively consistent across taxa, suggesting that functional or developmental integration may have kept cranial

covariances stable throughout the diversification of platyrrhine lineages. In terms of integration patterns, they found that functionally and developmentally related traits were more strongly correlated than unrelated traits, that facial traits were more strongly intercorrelated than neurocranial traits, and traits specific to the oral region were the most highly integrated. However, there was not much evidence for higher levels of integration within other “modules” such as the orbital, nasal, cranial vault or basicranium. In a later study, Marroig et al. (2004) found similar results for an expanded cranial dataset for saki (genus *Pithecia*) species, with the additional finding of strong integration in the nasal region. Despite the relative consistency of patterns among species, some taxonomic differences in the relative magnitude of integration of the face and neurocranium were apparent, with some Callitrichids (marmosets and tamarins) and night monkeys (genus *Aotus*) showing stronger neurocranial integration than facial integration, relative to the other taxa. These differences cannot be explained on phylogenetic grounds, but Marroig and Cheverud (2001) suggest they may reflect independent evolutionary changes in the relative modularity of pleiotropic effects on the face versus the neurocranial in these taxa. Taken together, the results for platyrrhines suggest substantial modularization of the cranium, with the oral region within the face being the most distinct module across taxa, assumed to reflect the importance of dietary behaviors in driving taxonomic diversification (Shirai and Marroig 2010).

A number of studies have investigated patterns of cranial integration and modularity in catarrhines, particularly focusing on hominoids (e.g., Ackermann 2002, 2005; Polanski and Franciscus 2006; Mitteroecker and Bookstein 2008; de Oliveira et al. 2009; Singh et al. 2012; Neaux 2017). Ackermann (2002) found patterns of variance-covariance in facial traits of humans, chimpanzees and gorillas were broadly similar, although some differences were apparent (see also Bastir and Rosas 2004). A later study found patterns of facial trait integration across ontogenetic stages to be similar across these ape taxa

(Ackermann 2005), although some differences, particularly between humans and other hominids were present. Polanski and Franciscus (2006) highlight taxonomic differences in the magnitude of modularization, finding that humans were less integrated in facial traits relative to other African apes, suggesting that human faces and neurocrania are relatively more “uncoupled”. However, this interpretation has been questioned, on methodological grounds, by Mitteroecker and Bookstein (2008), whose analysis of developmental integration found similar (but not identical) patterns in humans, chimps and gorillas, consistent with the results of Ackermann (2002, 2005) and those found for other primate groups (e.g., Cheverud 1996b; Marroig and Cheverud 2001; Marroig et al. 2004; de Oliveira et al. 2009). Singh et al. (2012) included orangutans in their analyses and also found consistent patterns of integration between the face and basicranium, and between the face and vault, across all taxa, despite the relatively large morphological distinction between them. Similar patterns of integration between the face and basicranium have also been shown in hominids and *Hylobates* species (Neaux 2017), suggesting that the pattern appears to hold true at higher taxonomic levels across hominoids. Using a broad sample of catarrhine taxa, de Oliveira et al. (2009) found a significant association between phylogenetic distance and the similarities in integration among genera. However, the overall pattern of trait association is remarkably consistent across taxa, while the overall magnitudes of inter-trait correlations varied substantially among catarrhine lineages. Profico et al. (2017) found support for the face and basicranium acting as relatively distinct modules in a sample of hominoid and cercopithecoid taxa, cautioning that these morphological modules may reflect responses to different evolutionary pressures when compared across catarrhines. This accords with the patterns of modularity found by Jung et al. (2021a) in an ontogenetic study of macaques, whereby the basicranium and face formed a single integrated module during juvenile growth stages, but were relatively “dis-integrated” by the time adulthood had been reached. In contrast, the vault and

basicranium were found to act as an integrated module throughout all ontogenetic stages tested (Jung et al. 2021a).

Many studies have focused specifically on investigating craniofacial integration patterns within humans (e.g., Lieberman et al. 2000; Bookstein et al. 2003; Bastir and Rosas 2006; Martínez-Abadías et al. 2012). It is widely assumed that the evolution of the highly derived human cranium is linked with increased basicranial flexion, presumably related to the wider skeletal changes accompanying the evolution of bipedalism in the hominin lineage (e.g., Ross and Ravosa 1993; Ross and Henneberg 1995; Lieberman et al. 2000, 2008; Bastir et al. 2010). Bastir and colleagues have shown evidence for strong covariation between the basicranium (particularly the lateral basicranium) and the face, lateral cranial vault, and mandible (e.g., Bastir et al. 2004; Bastir and Rosas 2005, 2006; Bastir et al. 2006). According to Enlow's counterpart growth hypothesis (Enlow and Hans 1996), individual functional units within the cranium (*sensu* Moss and Young 1960) are integrated at a higher level, due to the need for one cranial region to compensate for the growth of another region. However, there is an ontogenetic dimension to these modularity and covariance patterns (e.g., Bastir et al. 2006) with the midline basicranium ceasing growth earlier than the lateral basicranium, which continues to grow in concert with the face for an extended period. As such, this suggests that patterns of modularity and integration are not static across ontogeny, further complicating the identification, and comparison, of morphological modules (see also Bastir and Rosas 2009). Moreover, these results suggest that the human basicranium is composed of two modules, midline and lateral basicranium, that possess different patterns of integration with the face during growth and development (Bastir and Rosas 2006; Gkantidis and Halazonetis 2011; Neaux et al. 2013). Neaux et al. (2013) demonstrated that the shape of the lateral basicranium in chimpanzees also plays a significant role in the integration of the face and cranial base, but that the patterns of integration between the face and

basicranium are different for chimpanzees compared with humans.

In the first study to do so, Martínez-Abadías et al. (2012) used a sample of human crania of known pedigree to estimate genetic and phenotypic integration in human skull shape. They found strong genetic integration across all cranial regions, suggesting that the face, cranial vault and basicranium did not behave as independent modules, but rather that past selection on only one trait or cranial region may have driven the differentiation of the entire cranial complex in humans. This finding challenges the traditional view of three major cranial modules (face, basicranium and neurocranium) typically accepted based on developmental and morphological criteria (Bastir 2008). Using a very different approach based on anatomical network analysis, Esteve-Altava et al. (2013) found that the human skull is composed of an anterior facial module (centered around the ethmoid bone) and posterior cranial module (centered around the sphenoid). These units cut across traditional developmental-functional module definitions and are theorized to reflect the numbers of connections around central bones (ethmoid, sphenoid and frontal) that originate as fusions between a number of bones in early mammalian evolution. However, Esteve-Altava et al. (2013) note that the seeming inconsistencies between their results and those of Martínez-Abadías et al. (2012) are explicable under the concept of the palimpsest model of covariation (Hallgrímsson et al. 2009), whereby it is difficult (if not impossible) to determine the factors underlying observed patterns of phenotypic covariation given the layering of different influences (pleiotropic, developmental, ontogenetic etc.) over time (see also Barbeito-Andrés et al. 2015). Esteve-Altava and colleagues (2013) do not assume the existence of modules defined *a priori*, but rather use patterns of morphological connectivity among anatomical landmarks to decipher the existence of modules and sub-modules. The fact that their analyses reveal "modules" that accord with some traditionally identified developmental units (e.g., Lieberman 2011) suggests that skull modules

(at least the facial and cranial ones) are “real” in humans, while the results of [Martínez-Abadías et al. \(2012\)](#) suggest that the distinction between these modules is relatively slight, compared to the degree of integration among modules. In that sense, the human skull can be characterized as being “both integrated and modular” ([Martínez-Abadías et al. 2015, p. 46](#)).

Despite differences in the methods used to quantify cranial shape and the statistical methods used to assess patterns of modularity and integration, some common themes emerge from all of these cranial studies. The most obvious distinction among cranial regions in terms of potential modularity is between the anterior face and cranial vault (including the basicranium). Under the “spatial packing” hypothesis ([Biegert 1963](#)), increased basicranial flexion in primates is predicted to be directly related to enlarged brain size. The basic logic behind this hypothesis is that a more flexed cranial base allows for a larger brain to be carried above it, without the need to increase the width or length of the basicranium ([Lieberman et al. 2008](#)). Early tests of the spatial packing hypothesis in primates found a strong correlation between cranial base angle (CBA) and relative encephalization ([Ross and Ravosa 1993](#)), a general conclusion that has been supported by several subsequent studies (e.g., [Lieberman et al. 2008](#)). However, encephalization only explains about 40% of the variation in CBA across primates, even accounting for phylogenetic differences, suggesting that basicranial flexion may also be related to other factors such as facial growth and orientation. Studies of craniofacial variation using mouse strains with varying craniofacial shapes, including strains with mutations that affect CBA in a predictable way, have also found support for the spatial packing hypothesis ([Lieberman et al. 2008](#)). The results of this and other studies of primates and mice models support the idea that basicranial flexion is linked to both increased brain size and also to facial size and orientation (e.g., [Lieberman et al. 2008](#); [Bastir et al. 2010](#); [Lieberman 2011](#); [Bastir and Rosas 2016](#); [Schroeder and von Cramon-Taubadel 2017](#)).

Relatively few studies have investigated patterns of craniofacial integration and modularity across all primates. As an example of one of the few that has, [Makedonska \(2014\)](#) did not find strong support for the existence of distinct modules using a sample of platyrrhine and cercopithecoid taxa. Similarly, [Neaux et al. \(2018\)](#) also found significant integration between the basicranium and the face across a broad sample of primate taxa (including strepsirrhines), but found differences in the patterns of integration between major primate groups (see also [Neaux et al. 2019](#)). In the study by [Neaux and colleagues \(2018\)](#), the influence of integration on rates of evolution was tested across primate taxa, and they found that, despite pervasive integration between these modules, the face showed higher rates of evolution than the basicranium across lineages, suggestive of some degree of modular “decoupling”. This helps to explain the apparent paradox (and the sometimes conflicting results obtained from different studies) that primates have a skull structure that is both highly integrated but with distinct modularity, especially between the basicranium and the face (or between the face and cranium; [Esteve-Altava et al. 2015](#)). A recent study of cranial integration in a broad sample of catarrhine and strepsirrhine taxa ([Villamil 2021](#)) found a highly conserved pattern of trait covariation among all species, but with evidence of distinct modularity between the cranial base and face. Moreover, based on these results, it was suggested that the magnitude of cranial base integration is associated with differences in developmental rates across species, while facial integration is associated with body size variation. If this is indeed the case, one implication is that the generally lower cranial covariation observed in humans (and in other hominoids) is related to separate evolutionary trends in the face and basicranium, each evolving in a semi-independent manner, rather than an overall shift towards reduced integration of the whole cranium in the ape lineage.

It is also useful to set the overall results for primates in their wider mammalian context, where studies have found that mammalian skull

diversity is based on a largely shared pattern of trait covariance structure, that has remained relatively constant for at least 65 million years (Porto et al. 2009). These findings are in line with the notion that while morphological integration affects the evolution of shape disparity (Goswami and Polly 2010), it does not necessarily affect rates of evolution (Goswami et al. 2014). It is important to note, however, that while the *pattern* of trait covariance is similar across mammals, this does not preclude the production of large amounts of cranial form variation (as seen even within primate lineages). This is because *magnitudes* of integration vary substantially among mammals, with more derived placental lineages having generally lower cranial integration than marsupials. Marsupials also exhibit specific patterns of integration, particularly in the face, presumably reflecting the precocious development of the orofacial anatomy to support suckling behaviors (Porto et al. 2009; Shirai and Marroig 2010). In contrast, most eutherian lineages have relatively stronger cranial integration overall, given that longer intra-uterine gestation allows for greater investment in neurocranial growth, at the expense of early facial development. Porto et al. (2009) also found that humans had the lowest magnitude of overall cranial integration, but with relatively distinct modules, particularly in the cranial vault (but see also Villamil 2021). Distinctive patterns of modularity were also found for gorillas and chimpanzees, which, when viewed against the general trend of decreasing overall magnitudes of integration and increasing modularity across eutherian mammals (Porto et al. 2009), helps contextualize the apparent paradox noted earlier, whereby hominids possess both pervasive integration across the cranium, that is nevertheless modularized to some extent. Therefore, it is possible that all primates possess a similar cranial modular structure centered around semi-autonomous facial and neurocranial modules, but distinct patterns and magnitudes of integration categorize different primate groups. The extent to which modular patterns described here are shared across primate lineages will necessitate further study with

a broader range of strepsirrhine and haplorrhine taxa, using an internally consistent methodological approach to quantify cranial form and compare patterns and magnitudes of integration.

Integration and modularity in the primate axial skeleton

While the literature on the assessment of magnitudes of integration and patterns of modularity in the primate cranium is immense, there are relatively few studies assessing patterns of integration among different elements of the axial skeleton. In a study of postnatal growth in the face and mandible of humans and chimpanzees, Bastir and Rosas (2004) found support for two major units of integration; a facial component (including the maxilla and mandible) and a combination of the neuro- and basicranium. Despite the fact that the mandible only articulates with the cranium via the temporo-mandibular joint (TMJ), relatively strong covariance between the maxilla and the mandible is expected given the need to maintain active occlusion of the associated dentition during mastication (Cheverud 1996a). Bastir et al. (2006) also note that the mandible and maxilla achieve adult size in humans at approximately the same time (usually around age 16), and several years later than the cessation of basicranium growth. Moreover, the mandibular and maxillary processes are derived, developmentally, from similar groups of neural crest cells, ensuring that they share multiple molecular interactions during growth (Szabo-Rogers et al. 2010; Neaux et al. 2015). Bastir and Rosas (2006) also highlight the integration between the mandibular ramus and the lateral basicranium in a human sample, indicative of the need to maintain functional connectivity between the mandible and the basicranium. Hence, given the developmentally and functionally mediated connections between the cranium and the mandible, some degree of integration is expected among these skeletal regions across primates.

In terms of modularity within the mandible itself, the most obvious identifiable sub-units are the ramus and the corpus, reflecting the dual functions of housing the dentition and attaching

the masticatory muscles, both of which interact with the cranium in significant ways (Polanski 2011). Neaux et al. (2015) provide an assessment of patterns of integration between the face and mandible of extant hominids, and find that while orangutans (genus *Pongo*) exhibit relatively high covariance between the face and mandibular ramus, humans, chimpanzees and gorillas do not, instead showing stronger covariation between the face and mandibular corpus. Using a sample of adult and juvenile macaque skulls, Jung et al. (2021a) found relatively strong integration between the face and both the mandibular ramus and corpus throughout macaque ontogeny, even though the magnitude of integration varied across different developmental stages.

A recent study by Jung and von Cramon-Taubadel (2022) allows the modularity of the cranium and mandible to be set in the wider context of integration patterns across the primate axial skeleton. For the majority of anthropoid taxa, the cranium and mandible were not particularly well integrated, forming a modular structure comparable to, or weaker than, that seen among adjacent vertebral elements. The exception to this pattern was for the human data, where the magnitude of integration between the cranium and mandible was both absolutely stronger compared with other taxa, and also was substantially stronger than the integration among vertebral elements in general. This indicates that, although the cranium and mandible form a tightly integrated unit among primates in general, the human mandible and cranium constitute a particularly strongly integrated module.

On the basis of shared developmental-genetic systems and functional considerations, it is reasonable to assume that the vertebral column will be integrated with the occipital region of the cranium (Villamil 2018; Arlegi et al. 2020). In particular, given that the occipital and the first five cervical vertebrae are patterned by the expression of the *Hoxa-1* and *Hoxb-1* genes, some degree of modularity between the cervical spine and the basicranium is expected across primates (Wellik 2007). Villamil (2018) found that humans, chimpanzees and gibbons shared common patterns

of integration within the cervical portion of the vertebral column, with modularity patterns that generally followed those found in other mammalian groups (e.g., Arnold et al. 2016; Randau and Goswami 2017) despite the different postural and locomotory behaviors of these three hominoid taxa. Similar results were also obtained for an analysis of cervical vertebrae in humans, gorillas, and chimpanzees (Arlegi et al. 2018), but Arlegi et al. (2022) found differences between gorillas, chimps and humans in the patterns of integration between the cervical spine and the cranium as a whole. In particular, they noted that the precise cranial traits that are tightly integrated with the vertebrae differed among taxa (see also Villamil and Santiago-Nazario 2022), and gorillas were found to have overall greater magnitudes of integration compared with humans and chimpanzees. Nevertheless, it appears that aspects of cranial base shape are tightly integrated with all cervical vertebrae (particularly the atlas, C1), the third through to the sixth cervical vertebrae (C3–C6) form a module, and C2 and C7 are relatively weakly integrated with other elements, possibly reflecting their transitional status (Villamil 2018).

Only a handful of studies have investigated patterns and magnitudes of integration throughout the entire vertebral column. Arlegi and colleagues (2020) found that the mid-thoracic region (T4–T9), followed by the mid-lumbar region (L2–L3) were the most tightly integrated in modern humans. These results indicate that central vertebrae are more integrated with magnitudes of integration decreasing towards peripheral vertebrae (C1 and L5) and towards the boundaries between vertebral regions. Looking at a broader taxonomic picture, it has been shown that hominoids, in general, display lower magnitudes of integration across different elements of the vertebral column when compared with other catarrhine (Jung et al. 2021b) and anthropoid (Jung and von Cramon-Taubadel 2022) taxa. Humans have lower magnitudes of integration in the more caudal thoracic and lumbar vertebrae compared with other apes, suggesting fewer constraints on the evolution of the unique hominin lumbar spine shape (presumably) in

response to bipedalism. While the precise pattern of vertebral element integration varies among cercopithecoids and hominoids, some general morphological patterns are noteworthy (Jung et al. 2021b). The first cervical vertebra is consistently the least or second least integrated vertebrae across all taxa, in agreement with the pattern noted by Arlegi et al. (2020) for humans. Additionally, the sacrum was amongst the most strongly integrated element in most taxa, a pattern that is independent of whether the lumbar region was relatively less (as in humans and chimpanzees) or more integrated. While the reason for this is not yet clear, it may be related to the fact that the sacrum must articulate with the ossa coxae to form the pelvic girdle and, in the case of non-hominoids, articulate with the tail. When compared against a broader taxonomic sample of anthropoids, hominoids show weaker patterns of integration among all vertebral elements, instead showing stronger patterns of modularity within the axial skeleton (Jung and von Cramon-Taubadel 2022). However, the precise morphological nature of these modularity patterns varied considerably among taxa. Interestingly, there was convergence between apes and the Howler monkeys (genus *Alouatta*) in terms of shared patterns of increased modularity (Jung and von Cramon-Taubadel 2022), which suggests a relatively strong influence of biomechanical factors related to positional behaviors on vertebral modularity, that cuts across phylogenetic patterns.

Integration and modularity in the primate appendicular skeleton

Young et al. (2010) were the first to assess the relationship between limb proportion variability across anthropoids and magnitudes of integration among limb segments (e.g., the femur, tibia and metatarsals as representative of the hindlimb) and among developmentally homologous limb bones (e.g., the femur and humerus). This elegant study sought to address the seemingly simple question of how and why primates vary so substantially in limb proportions, when quantitative theory predicts that limbs should evolve in parallel due to their shared developmental

and genetic basis (Hallgrímsson et al. 2002). As such, the situation we observe among apes, where we have both hindlimb (i.e., humans) and forelimb (i.e., gibbons) dominated taxa, is rather unusual, given the developmental constraints on independent limb evolution. Young et al. (2010) suggest that selection for independence of limb function led to changes in limb covariance structure, such that homologous modules of the fore- and hindlimb became “dis-integrated”, opening up the possibility of the evolution of new limb proportions. Their results support this hypothesis, in showing that ape taxa have relatively lower integration, both between bones within limb complexes, and between developmentally homologous bones, when compared with catarrhine and platyrrhine monkey taxa. This helps explain how it was possible for the unusual mode of locomotion of human bipedalism to evolve, alongside the more diverse postural and locomotory behaviors seen in extinct and extant hominoids. It also puts into context the more limited diversification in general skeletal “bauplan” seen in monkey taxa, whereby strong genetic and developmental integration constrained postcranial evolution towards size-scaled variants with more similar limb proportions (Young et al. 2010; Rolian 2020).

A similar analysis conducted for strepsirrhine taxa (Villmoare et al. 2011) found a stronger signal of integration between the fore- and hindlimb for arboreal quadrupeds than for non-quadrupeds (primarily vertical leapers). However, no difference was found among locomotor categories in terms of within-limb integration (see also Lawler 2008). These results point to the fact that inter- and intra-limb integration can be shaped by selective pressures in relation to specific locomotor adaptations, given that locomotor categories in strepsirrhines cut across phylogenetic groups. Similarly, the fact that Young et al. (2010) found shared patterns of limb integration among phylogenetically distant catarrhine and platyrrhine monkeys suggests that primate limb proportions are sufficiently unconstrained so as to allow their independent evolution in response to specific locomotor

selective pressures. However, *Hox* gene expression domains affect both the vertebral column and limb elements (Wellik 2007; Rolian 2014), ensuring that similar developmental mechanisms may be responsible for the dissociation between limb elements (as seen in Young et al. 2010), as well as among vertebral elements (as seen in Jung and von Cramon-Taubadel 2022) in hominoids, thus allowing for an additional lifting of constraint on the evolution of novel postcranial morphologies across ape taxa. However, when viewed through a slightly different lens, it appears that once disparate and more specialized limb proportions evolved (as was the case for apes), evolvability¹ was reduced in terms of the ability to respond to selection in favor of new adaptive niches (Rolian 2020). In other words, while a decrease in covariance between fore- and hindlimbs facilitated the evolution of specialized modes of locomotion in hominoids, it also resulted in apes occupying “ecomorphological cul-de-sacs” (Rolian 2020, p. 702), increasing the probability that ape populations face extinction due to the inability to evolve into new, more generalized, regions of morphospace.

Primate autopods (hands and feet) also provide an interesting case-study for the comparison of patterns of integration as they are serially homologous skeletal structures that evolved via genetic duplications (Ruvinsky and Gibson-Brown 2000; Rolian 2009). As such, it is expected that primate autopods are developmentally integrated, yet primates also exhibit key differences in the extent to which their hands and feet are morphologically or functionally similar (Young and Hallgrímsson 2005; Lawler 2008; Rolian 2009). As expected, catarrhine taxa with functionally convergent autopods (primarily cercopithecoids) were found to have stronger integration between

hands and feet, while hominoid species with more functionally divergent autopods showed much lower magnitudes of covariation (Rolian 2009; see also Young and Hallgrímsson 2005). This hominoid-cercopithecoid dichotomy in magnitudes of integration mirrors that found by Young et al. (2010) for homologous limb bones. Having said that, covariances between homologous phalanges in humans were found to be strong enough such that selection pressure on the human foot in relation to bipedalism could have caused a correlated evolutionary response in the human hand (Rolian et al. 2010). This opens up the possibility that the long robust thumb and shorter fingers of the human hand evolved not in response to a selection pressure favoring certain manipulatory abilities, but rather as an evolutionary side-product of selection for a strong adducted hallux in relation to bipedalism (Rolian et al. 2010; Rolian 2014). This interpretation contrasts, however, with the results of anatomical network analyses of the entire musculoskeletal anatomy of the chimpanzee and human fore- and hindlimbs (Diogo et al. 2018), which suggest that bipedal humans do not have greater limb dissimilarity than chimpanzees (at least in terms of musculoskeletal organization), despite their functional divergence.

A few studies have tested the link between locomotor behaviors and patterns of integration in primate hands and/or feet. Lawler (2008) found relatively strong integration between the hands and feet of wild sifaka. Williams (2010) found no evidence of stronger integration between the capitate and third manual ray (metacarpal and associated phalanges) of knuckle-walking and non-knuckle-walking hominoids, arguing against the existence of a morphological “complex” (or module) associated with this form of locomotion. A recent study by Komza et al. (2022) found support for the hypothesis that magnitudes of integration among medial elements of the hominoid midfoot should be lower for great apes than for humans due to their abducted halluces. The human foot was also found to have a distinctive pattern of stronger integration between the first metatarsal and the

¹ Note that “evolvability” can be defined to mean slightly different phenomena, depending on the context. Rolian (2020, p.706) defines evolvability as the number of generations it takes to evolve into new areas of morphospace, given a particular fitness landscape. This differs from the more typically used definition of evolvability as the ability of a multivariate phenotype to respond to a particular selection pressure (Hansen and Houle 2008).

medial cuneiform, relative to the magnitude of integration between the other metatarsals and their articulating tarsals. Furthermore, the results of Komza et al. (2022) also found overall lower magnitudes of integration in the human mid-foot, despite a common pattern of integration among all of the hominoid taxa tested.

Lower overall magnitudes of integration have also been found for the human pelvis (Grabowski et al. 2011), suggesting a lower level of constraint on pelvic evolution compared to other hominids (Conaway and von Cramon-Taubadel 2022). This is particularly evident in pelvic traits related to bipedalism (Grabowski and Roseman 2015) and obstetrics (Grabowski 2013), suggesting that strong natural selection drove the morphological diversification of the human (and hominin) pelvic girdle (see also Mallard et al. 2017). Lewton (2012) found a common pattern of integration and modularity in the pelvis across all primates, with additional support for the existence of internal modularity centered around the ilium and the ischiopubis, which may reflect the genetic control of early pelvigenesis in tetrapods (Young et al. 2019). On the basis of these findings, it was suggested that primates are characterized as having overall low levels of pelvic integration and associated high levels of evolvability relative to other postcranial regions (Lewton 2012).

The torso integration model (Schultz 1960) posits a direct relationship between the relative width and curvature of the thorax, and the width and curvature of the iliac blades in apes, such that it is thought to be possible to reconstruct the thorax morphology for fossil hominins if evidence of pelvic morphology is available. In a test of the presumed integration between the human thorax (shape of the middle thoracic spine and associated ribs) and the pelvis, Torres-Tamayo et al. (2018) found that sexual dimorphism confounded the correspondence between thoracic and pelvic widths in two human populations, thereby calling in question the extent to which the morphology of the thorax and pelvic covary. In a later study incorporating data from 3D torso models of humans and chimpanzees, Torres-Tamayo et al. (2020) found that some aspects of

thoraco-pelvic covariation were common to both species, but species-specific patterns were also evident, related primarily to sexual dimorphism and allometry. As such, the extent to which thoracic and pelvic morphology is integrated across primates more broadly is still unclear, and will require further analyses based on abdominopelvic CT scans of a range of primate species.

Relatively few studies have investigated patterns of integration in the primate pectoral girdle. In the first study of modularity and integration in the scapula, Young (2004) found similar patterns of integration among hominoids, with some evidence of modularity around the blade and acromion (and to a lesser extent the glenoid), distinct from the coracoid. This suggests that the primate scapula may comprise at least two distinct modules, a pattern that appears to be shared across placental mammals (Sears et al. 2013). It is currently unclear to what extent we should expect the pectoral and pelvic girdles to covary, given the quite different developmental genetic basis of each structure, as well as their somewhat disjointed evolutionary histories (Sears et al. 2015; Young et al. 2019). Agosto and Auerbach (2021) found covariation between traits of the shoulder girdle and the basicranium in a sample of colobines (genus *Colobus*), which was expected based on shared developmental and functional factors, and also between the shoulder and pelvic girdles. Therefore, while the serial homology of the girdles is unclear (Sears et al. 2015), they are, nevertheless, analogous anatomical structures in terms of their function in linking limbs with the axial skeleton (Sears et al. 2015; Young et al. 2019), which may have generated greater covariance throughout mammalian (and primate) evolution.

As the preceding review makes clear, the volume of studies investigating patterns of integration in the primate postcranium is dwarfed by the literature on cranial integration. While more postcranial studies are now being carried out, there still remains a dearth of basic information on how magnitudes of integration compare within and across skeletal regions, and to what extent any hypotheses of modularity (based on

developmental and functional criteria) are actually supported by patterns of covariation across traits. In an attempt to address this latter question, [Conaway et al. \(2018\)](#) compared distributions of integration values obtained from resampled traits across the scapula, os coxa, femur, tibia, fibula, humerus, ulna and radius of a sample of macaque skeletons (*Macaca fascicularis*). Subsets of traits from these bones were also used to construct hypothetical modules based on anatomical, developmental, and functional criteria, which could be compared against a null hypothesis of no modularity (i.e., where inter-trait covariance is randomly spread throughout the postcranium). The results found that most hypothetical modules were more strongly integrated than taking random traits from across the skeleton, with girdle elements (scapula and os coxa) being less strongly integrated than limb bones. Moreover, the combined forelimb was less strongly integrated than the hindlimb, suggesting some degree of limb independence, even for quadrupedal macaques ([Conaway et al. 2018](#)). If this pattern is borne out for other primates, it suggests that the primate forelimb may be less subject to constraint and may show higher evolvability (*sensu* [Hansen and Houle 2008](#)) than the hindlimb, due to its involvement in several locomotory, feeding and social behaviors (e.g., grooming and infant handling).

Many of the postcranial integration studies carried out to date suggest reduced magnitudes of integration in hominoids relative to other primates ([Young et al. 2010](#); [Rolian, 2009](#)), and in humans relative to other hominoids ([Porto et al. 2009](#); [Grabowski et al. 2011](#); [Komza et al. 2022](#)), indicating a reduction in constraint, and greater potential to evolve in the direction of selection pressures ([Marroig et al. 2009](#)). This is also supported by a recent study comparing magnitudes of integration across the appendicular skeleton of a wider sample of hominoids and two cercopithecoid taxa ([Conaway and von Cramon-Taubadel 2022](#)). However, this latter study also found differences in the patterns of integration across skeletal regions within hominoids, with gorillas generally showing higher magnitudes of

integration across all skeletal elements, and gibbons showing lower magnitudes of integration. In addition, the results found that girdle elements (i.e., scapula and os coxa) were consistently less strongly integrated than limb elements among all catarrhine species ([Conaway and von Cramon-Taubadel 2022](#)), mirroring the results found by [Grabowski et al. \(2011\)](#) and [Lewton \(2012\)](#) for the pelvis. The only exception to this pattern was for the gibbon os coxa, which was found to be as strongly integrated as limb elements (albeit in the context of overall low magnitudes of integration). Hence, it is not clear whether gibbons differ from other hominoids in having an unusually strongly integrated pelvis (see [Conaway and Adams 2022](#)) or a particularly weakly integrated appendicular skeleton.

Discussion

The main aim of this review was twofold: (i) To ascertain the extent to which modules, identified on anatomical, developmental or functional criteria, are discernible in the primate skeleton. And subsequently (ii) to assess the extent to which any such modules are shared by all primate taxa. While the literature on patterns of integration and modularity of the cranium is extensive, relatively little comparative analyses have been performed on the postcranium, in the sense of incorporating both a broad range of taxa and multiple skeletal regions simultaneously. In terms of the cranium, it appears that some modular structure is detectable across all primates, particularly in patterns of covariation between the face and the rest of the neurocranium. In some cases, modular division between the basicranium and cranial vault was also detected, but patterns of cranial covariation seem highly conserved across primate lineages. Having said that, differences in relative magnitudes of cranial integration are also evident across different primate groups. Therefore, while the literature on primate cranial modularity appears exhaustive, further study using a broader range of strepsirrhine and haplorrhine taxa may be necessary to fully

understand the universality of primate cranial integration patterns. Surprisingly little is known about cranial and mandibular integration, outside of humans and other hominoids. The few studies that have been conducted point to relatively strong integration between the two units, particularly in humans. There is some evidence of modularity within the mandible related to the corpus and ramus, but the extent to which this pattern is mirrored across all primates remains to be tested.

In terms of the wider axial skeleton, there is some evidence for modularity within the vertebral column in line with expectations based on developmental regulatory gene expression patterns. In particular the first cervical vertebra tends to be tightly integrated with the cranial base, and the middle vertebrae of each section (i.e., mid-cervical, mid-thoracic and mid-lumbar) tend to be more tightly integrated than transitional vertebrae, perhaps reflecting the overlapping influence of different *Hox* genes in these regions. Moreover, some systematic differences appear to exist among primate lineages in terms of patterns of magnitudes of integration, with hominoids generally showing lower magnitudes of axial skeleton integration than cercopithecoids, and some evidence of convergence in modularity patterns between apes and more suspensory platyrrhines, indicative of the influence of shared locomotor behaviors. However, further analysis incorporating a broader range of locomotor repertoires and taxonomic diversity (including strepsirrhines) is needed to discern the extent to which axial skeletal modularity is driven by phylogenetic and/or functional factors.

A distinction between hominoids and other anthropoid taxa in terms of having overall lower magnitudes of integration is also evident in the appendicular skeleton, particularly in the limbs, and also, to some extent, in the pectoral and pelvic girdles. In the context of these taxonomic differences, some general modularity patterns are suggested; girdles are less strongly integrated than limbs, forelimbs appear to show different magnitudes of integrated than hindlimbs, and there is stronger integration between developmentally

homologous limb segments (e.g., between the humerus and femur) than between elements within limbs. However, robustly testing these general predictions across a wider range of primate taxa requires further analysis.

So where do we go from here? Obviously, there is a necessity for further empirical analyses of primate skeletal integration patterns, particularly for the postcranium and for a wider taxonomic sample, including strepsirrhines, tarsiers and anthropoids. There is also a dearth of analyses incorporating the cranium, mandible and postcranium, with only a handful of studies considering the potential covariation between the cranium and vertebral column (e.g., [Arlegi et al. 2022](#); [Jung and von Cramon-Taubadel 2022](#)) or between aspects of the cranium and the pectoral girdle (e.g., [Agosto and Auerbach 2021](#)). There is also a lot of variation among existing studies in terms of what skeletal elements are targeted, how they are quantified morphometrically, how data are treated prior to analyses, and which methods are used to quantify integration and modularity. As such, unless some agreed upon “gold standards” are employed consistently across studies, forming a cohesive framework for the comparison of integration and modularity across primates will remain elusive.

Table 1 proposes a general framework for how hypothetical modules might be constructed based on anatomical, developmental and functional criteria. The relative modularity of any proposed module can be assessed by comparing it against a null hypothesis of no modularity (i.e., combining traits from across the entire skeleton). Anatomically-defined modules comprise larger individual bones, while spinal column modules could be assessed as whole units (cervical, thoracic, lumbar, sacral) and/or as separate vertebrae. However, sub-division of any anatomical module is also possible. For example, each major bone in the cranium (*sensu* [von Cramon-Taubadel, 2009](#)) could potentially exhibit modularity when compared against the whole cranium. Similarly, the individual bones of the os coxa (pubis, ilium and ischium) could be tested separately. Developmental modules comprise

developmental limb and girdle homologs (see Conaway et al. 2018) or sub-units of the cranium differing in developmental mode of ossification (Lieberman 2011). Functionally-defined modules could comprise whole limb elements (forelimb etc.), portions of contiguous bones forming joints (Conaway et al. 2018), or sub-sections of the cranium related to specific functions such as mastication (see von Cramon-Taubadel 2011). If such a framework were to be widely adopted it may allow for a more faithful comparison of results across integration studies. Equally important, however, is also the consistency with which hypothetical modules are quantified morphometrically (Conaway and Adams 2022). Conaway et al. (2018) note that systematic differences in magnitudes of integration can arise simply as a side-effect of the shape of the bone in the context of integration statistics that are based on distributions of eigenvectors, such as the Integration Co-efficient of Variation (ICV; Shirai and Marroig 2010). High integration will result in more variance being constrained in the first few eigenvectors (principal components), while less tightly integrated structures will have variance spread out over more eigenvectors. For long bones, such as limb elements, the primary axis of morphological variation (length) will dominate an eigen-analysis relative to other smaller dimensions capturing shape variation of the proximal and distal ends. Additionally, some bones, due to their simpler structure require fewer measurements or landmarks to accurately depict patterns of shape variation, while more complex structures, such as the cranium, os coxa, and scapula, require a more detailed morphometric protocol. Alternatively, one way in which long bone curvature might be better captured is to include semilandmarks along the shafts, which automatically increases the number of landmarks. Hence, the need to vary the number of measurements to accurately capture the shape of different bones raises the problem of differing numbers of traits, since having more input traits automatically leads to higher integration values (Grabowski and Porto 2017). One approach to deal with this problem is to use a

resampling strategy to constrain the number of input traits such that different skeletal elements with differing numbers of traits/landmarks can be directly compared (e.g., Conaway et al. 2018). This method has the added advantage of resulting in distributions of integration values that can be compared statistically across skeletal elements as well as across taxa. However, because this method is based on resampling from among every possible set of interlandmark distances, it has the distinct disadvantage that certain dominant dimensions are likely to be oversampled (e.g., maximum length of a long bone), which would automatically lead to inflated integration values for simpler structures such as long bones. A potential solution to this problem is to carefully choose particular traits *a priori* to limit the effect of over-sampling, but then the ability to create an unbiased morphometric representation of bone form is also lost.

Another issue that plagues the study of integration is the need for robust sample sizes (e.g., Grabowski and Porto 2017), something which is often hampered by a lack of suitable specimens in museum collections. It has long been noted that sample sizes in the order of ~40+ specimens are required to generate stable estimates of variance-covariance matrices (e.g., Cheverud 1988; Ackermann 2009). Grabowski and Porto (2017) analyzed the relationship between sample sizes and accuracy of various evolvability and integration statistics, and suggest that sample sizes in the order of 100+ individuals are required when quantifying integration using the correlation co-efficient (r^2), when the average inter-trait correlation is 0.05. Jung et al. (2020) tested the effect of sample size, trait number, and inter-trait correlation on the stability of the ICV measure of integration, and found that for weakly correlated traits ($r^2 = 0.05$), sample sizes of 100 were required, but that for moderately to strongly correlated traits ($r^2 = 0.08$ -0.12) sample sizes of 40-60 were sufficient. As a point of reference, average r^2 -values for skeletal traits in *Macaca fascicularis* range from 0.22-0.51, while correlation co-efficients for the human cranium are in the order of 0.05, necessitating a larger sample size

($n \approx 100$). Therefore, minimum sample sizes of $n=40$ individuals are still necessary for the calculation of many integration statistics, and this may need to be increased for morphological structures with relatively weak inter-trait correlation (such as the human cranium).

Recently, Conaway and Adams (2022) proposed an alternative solution to the earlier noted problem of morphometric redundancy and its effects on integration. They compared the statistical properties of several eigenvalue dispersion indices for quantifying integration, and show that the relative eigenvalue variance (V_{rel} , Watanabe 2022) is stable regardless of sample size and number of variables. However, in order to be able to compare relative eigenvalue variances across morphological regions or across taxa, a Z-score transformation (e.g., Fisher 1921) is required to correct for variance and skewness that is related to the level of input trait covariance. Hence, this adjusted V_{rel} measure should allow for the direct statistical comparison of integration across skeletal regions and taxa, free from concerns about varying sample sizes, trait/landmark numbers and underlying inter-trait correlation/covariance structure.

Another issue that requires consideration when attempting to standardize methodological approaches to integration is how to deal with variation in size, both in terms of the relative sizes of traits within- and across modules, and accounting for large-scale differences in size between taxa and/or skeletal regions (e.g., Shirai and Marroig 2010; Grabowski et al. 2011; Porto et al. 2013; Conaway and von Cramon-Taubadel 2022). In standard morphometric comparisons of primate taxa, “size” (i.e., isometric scaling) is often removed in an attempt to compare relative shape differences (e.g., von Cramon-Taubadel 2018). However, in the context of comparing patterns of integration and modularity, it is unclear whether it is more appropriate to keep scaling information in (i.e., analyze collections of form variables) or whether scaling acts as a systematic confound to the uncovering of primate-wide modularity patterns (e.g., Klingenberg 2013, 2014;

Mitteroecker et al. 2005). For example, Shirai and Marroig (2010) demonstrated that size variation increases magnitudes of integration both within and between cranial modules (see also Porto et al. 2013; Conaway and Adams 2022). This makes sense given the direct relationship between variation and strength of correlation, such that traits with higher size variation will automatically show stronger degrees of correlation. Size is an emergent property of growth, and growth processes facilitate the integration of modules and the co-ordination of a modular structure (e.g., Magwene 2001; Porto et al. 2013), therefore, larger size variation will lead to greater covariance among modules as cohesion within the organism is maintained. Skeletally large species (and larger skeletal regions within species) will show more variability, as trait variances scale with trait means (Rolian 2020). Moreover, the first eigenvector of any morphological covariance matrix (P_{max} ; Marroig et al. 2009) will incorporate primarily scaling, and scaling-related shape variation and, therefore, the more variation the P_{max} accounts for, the greater the probability that a selection gradient will align with the P_{max} , as this becomes the “genetic line of least resistance” (*sensu* Schluter 1996). Taken together, this means that larger scaling variation leads to stronger magnitudes of integration, less distinct patterns of modularity, and more constraint on the potential response to selective pressures (Porto et al. 2009, 2013; Shirai and Marroig 2010; Rolian 2020). Hence, it is common practice to first standardize morphological traits either across sexes, across taxa and/or across skeletal modules of different scales, to ensure that the first eigenvector does not simply reflect size-related variation but instead represents the vector of greatest standardized variation (Grabowski et al. 2011). Nevertheless, we need a better understanding of the extent to which scaling variation is a problem due to the statistics we use to quantify integration being directly impacted by scaling variation, as opposed to scaling variation (be it due to sexual dimorphism, allometric factors, ontogeny or evolutionary history) being a confounding

Tab. 1 - Examples of suggested modules, based on anatomical, developmental and functional criteria, that can be tested across primates. A null hypothesis of no modularity can be generated by combining traits from across the entire skeleton, thus allowing for a baseline to be generated for each taxon.

NULL HYPOTHESIS OF NO MODULARITY: ALL TRAITS SAMPLED FROM THE WHOLE SKELETON (CRANIUM & POSTCRANIUM)		
ANATOMICAL	DEVELOPMENTAL	FUNCTIONAL
Whole cranium	Cranium: Chondrocranium (endochondral ossification)	Cranial Masticatory: Palatomaxilla & Zygotemporal
Mandible ^a	Cranium: Dermatocranium (intramembranous ossification)	Cranial Functional: Neurocranium, Basicranium & Face
Scapula	Girdles ^b : Scapula, clavicle, os coxa	Neck unit: Cranial base, cervical vertebrae, medial clavicle
Humerus	Axial elements: Chondrocranium, cervical vertebrae, thoracic vertebrae, lumbar vertebrae, sacrum	Entire forelimb: Including girdle, carpals, and autopods
Ulna	Stylopodia: Humerus & femur	Shoulder unit: Scapula, clavicle & proximal humerus
Radius	Zeugopodia: Tibia/radius & fibula/ulna	Elbow unit: Distal humerus, proximal radius/ulna
Os Coxa	Autopodia: metacarpals/metatarsals	Wrist/hand unit: Distal radius/ulna, carpals
Femur	Carpals/tarsals	Entire hindlimb: Including girdle, tarsals & autopods
Tibia		Hip unit: Sacrum, superior os coxa [ilium], proximal femur
Cervical spine		Knee unit: Distal femur, proximal tibia/ fibula
Thoracic spine		Ankle unit: Distal tibia/fibula, tarsals
Lumbar spine		Hands: Carpals/metacarpals
		Feet: Tarsals/metatarsals

^aMandible could also form a functional module related to mastication. ^bWhile girdles are functional homologues, it is not clear the extent to which they also share developmental or genetic homology (Sears et al. 2015).

factor in the assessment of primate skeletal modularity. As part of this, we need to also consider systematic differences among primate taxa in terms of their life histories, given that altricial mammalian species show systematically stronger magnitudes of cranial integration, with less clear modularity due to pervasive allometric scaling, and consequently more constraint in terms of morphological diversification. In contrast, more

precocial species show more homogeneously dispersed variation in morphospace, with evident modularity and more flexible potential evolutionary responses (Porto et al. 2013).

While *a priori* defined modules for the cranium, and to some extent the mandible, have been repeatedly suggested and tested, there has been relatively little attention given to the criteria by which we might delineate modules to

be tested in the postcranium (Conaway et al. 2018). Therefore, greater focus is also needed on the underlying embryology and developmental genetics of the postcranium, and the correlations in growth and development among different postcranial regions (Rolian 2014), in order to propose hypothetical units of selection for the postcranium that can be tested against empirical patterns of postcranial trait covariation. In this regard, it will also be important to keep asking ourselves, how modular does a module need to be (Zelditch and Goswami 2021)? In other words, what is the benchmark against which we measure whether covariances or correlations among traits demonstrate the existence of a probable module? This is particularly important given the above discussion of the influence of size variation on magnitudes of integration, given that traits will always covary across a sample of organisms of varying sizes. Correlation among traits is not, in and of itself, evidence of modularity; it must be assessed in the context of wider covariance patterns (Mitteroecker and Bookstein 2007; Hallgrímsson et al. 2009; Klingenberg 2014; Zelditch and Goswami 2021). One simple option is to ask whether the extent of covariation amongst a group of traits thought to comprise a module is stronger, weaker, or the same as the average covariation found throughout the whole skeleton (Conaway et al. 2018; Tab. 1). If the same sets of traits are consistently found to form a modular structure across primate taxa in a way that makes sense according to phylogenetic or functional criteria, and/or if they match modular structures found in mammals more generally, then we can be reasonably confident that they represent “real” patterns of morphological integration and modularity.

Finally, it will be necessary to cross-check our hypotheses of primate skeletal modularity with tests of how such modules would respond to hypothetical selection pressures (*sensu* Rolian 2020), and also to test the extent to which specific traits have been subject to direct selection in the past. For example, Savell et al. (2016) showed that some human postcranial trait variation, previously proposed to be the result of

adaptation to differing climates, was actually the result of correlated response to selection on other traits. They were able to identify those trait differences that match what is expected based on direct selection versus those that differ among populations but not due to direct selection. This cautions against using morphological differences among taxa as an indicator of past diversifying selection, without first considering how those traits covary across the entire skeleton (see also Savell 2020). A similar approach was applied to human pelvic morphology by Grabowski and Roseman (2015) to show that not all traits traditionally hypothesized to be the result of adaptation for bipedalism are actually the result of direct selection. Schroeder and von Cramon-Taubadel (2017) used Lande’s (1979) generalized genetic distance to examine patterns of cranial evolution across several hominoid lineages. While most lineages were characterized by pervasive stabilizing selection, they found evidence of diversifying selection in the lineage leading to modern humans since the last common ancestor with chimpanzees, and in the divergence of the small-bodied apes from the large-bodied apes. The cranial traits that had been subject to direct selection differed in both cases and did not always match up with the traits that actually show the greatest difference between these groups of taxa. While this analytical approach necessitates the reconstruction of ancestral states for individual traits, which comes with its own set of controversies (e.g., Griffin and Yapunchin 2015, 2016; Smaers et al. 2016; Smaers and Mongle 2017), it does allow for the parsing out of which aspects of morphology have been the target of past direct selection as opposed to having evolved as a correlated response due to integration with other traits. Therefore, combining approaches that examine morphological differences within a phylogenetically informed quantitative genetic framework (e.g., Grabowski and Roseman 2015; Schroeder and von Cramon-Taubadel 2017; Weaver and Gunz 2018; Baab 2018) with a better understanding of modularity will be key to unlocking the “mosaic” nature of primate skeletal evolution.

Acknowledgements

I am grateful to Giovanni Destro Bisol for the invitation to contribute to this special celebration of the history of the Journal of Anthropological Sciences. I thank Lauren Schroeder, Mark Conaway, Hyunwoo Jung, and Marianne Cooper for helpful conversations and constructive comments on this manuscript. The author is grateful for support from the National Science Foundation under grant number BCS-1830745.

References

- Ackermann RR (2002) Patterns of covariance in the hominoid craniofacial skeleton: implications for paleoanthropological models *J Hum Evol* 42:167-187. <https://doi.org/10.1006/jhev.2002.0569>
- Ackermann RR (2005) Ontogenetic integration of the hominoid face. *J Hum Evol* 48:175-197. <https://doi.org/10.1016/j.jhevol.2004.11.001>
- Ackermann RR (2009) Morphological integration and the interpretation of fossil hominin diversity. *Evol Biol* 36:149-156. <https://doi.org/10.1007/s11692-009-9050-2>
- Ackermann RR, Cheverud JM (2000) Phenotypic covariance structure in tamarins (genus *Saguinus*): A comparison of variation patterns using matrix correlations and common Principal Components Analysis. *Am J Phys Anthropol* 111:489-501. [https://doi.org/10.1002/\(sici\)1096-8644\(200004\)111:4](https://doi.org/10.1002/(sici)1096-8644(200004)111:4)
- Ackermann RR, Cheverud JM (2002) Discerning evolutionary processes in patterns of Tamarin (Genus *Saguinus*) craniofacial variation. *Am J Phys Anthropol* 117:260-271. <https://doi.org/10.1002/ajpa.10038>
- Agostini G, Holt BM, Relethford JH (2018) Bone functional adaptation does not erase neutral evolutionary information. *Am J Phys Anthropol* 166:708-729. <https://doi.org/10.1002/ajpa.23460>
- Agosto ER, Auerbach BM (2021) Evolvability and constraint in the primate basicranium, shoulder, and hip and the importance of multi-trait evolution. *Evol Biol* 48:221-232. <https://doi.org/10.1007/s11692-021-09532-2>
- Aiello LC (2015) *Homo floresiensis*. In: W Henke, I Tattersall (eds) *Handbook of paleoanthropology*, Springer, Berlin-Heidelberg, p. 2281-2297.
- Arlegi M, Gómez-Robles A, Gómez-Olivencia A (2018) Morphological integration in the gorilla, chimpanzee, and human neck. *Am J Phys Anthropol* 166:408-416. <https://doi.org/10.1002/ajpa.23441>
- Arlegi M, Pantoja-Pérez A, Veschambre-Couture C, et al (2022) Covariation between the cranium and the cervical vertebrae in hominids. *J Hum Evol* 162:103112. <https://doi.org/10.1016/j.jhevol.2021.103112>
- Arlegi M, Veschambre-Couture C, Gómez-Olivencia A, et al (2020) Evolutionary selection and morphological integration in the vertebral column of modern humans *Am J Phys Anthropol* 171:17-36. <https://doi.org/10.1002/ajpa.23950>
- Armbruster WS, Pélabon C, Bolstad GH, et al (2014) Integrated phenotypes: understanding trait covariation in plants and animals. *Philos Trans R Soc Lond B Biol Sci* 369:20130245. <https://doi.org/10.1098/rstb.2013.0245>
- Arnold P, Forterre F, Lang J, et al (2016) Morphological disparity, conservatism, and integration in the canine lower cervical spine: Insights into mammalian neck function and regionalization. *Mamm Biol* 81:153-162. <https://doi.org/10.1016/j.mambio.2015.09.004>
- Atchley WR, Hall BK (1991) A model for development and evolution of complex morphological structures. *Biol Rev* 66:101-157. <https://doi.org/10.1111/j.1469-185x.1991.tb01138.x>
- Baab K L (2018) Evolvability and craniofacial diversification in genus *Homo*. *Evolution* 72:2781-2791. <https://doi.org/10.1111/evo.13637>
- Barbeito-Andrés J, Ventrice F, Anzelmo M, et al (2015) Developmental covariation of human vault and base throughout postnatal ontogeny. *Ann Anat* 197:59-66. <https://doi.org/10.1016/j.aanat.2014.10.002>
- Bastir M (2008) A system-model for the morphological analysis of integration and modularity in human craniofacial evolution. *J Anthropol Sci* 86:37-58.

- Bastir M, Rosas A (2004) Facial heights: Evolutionary relevance of postnatal ontogeny for facial orientation and skull morphology in humans and chimpanzees. *J Hum Evol* 47:359-381. <https://doi.org/10.1016/j.jhevol.2004.08.009>
- Bastir M, Rosas A (2005) Hierarchical nature of morphological integration and modularity in the human posterior face. *Am J Phys Anthropol* 128:26-34. <https://doi.org/10.1002/ajpa.20191>
- Bastir M, Rosas A (2006) Correlated variation between the lateral basicranium and the face: a geometric morphometric study in different human groups. *Arch Oral Biol* 51:814-824. <https://doi.org/10.1016/j.archoralbio.2006.03.009>
- Bastir M, Rosas A (2009) Mosaic evolution of the basicranium in *Homo* and its relation to modular development. *Evol Biol* 36:57-70. <https://doi.org/10.1007/s11692-008-9037-4>
- Bastir M, Rosas A (2016) Cranial base topology and basic trends in the facial evolution of *Homo*. *J Hum Evol* 91:26-35. <https://doi.org/10.1016/j.jhevol.2015.11.001>
- Bastir M, Rosas A, Kurok K (2004) Petrosal orientation and mandibular ramus breadth: evidence for an integrated petroso-mandibular developmental unit. *Am J Phys Anthropol* 123:340-350. <https://doi.org/10.1002/ajpa.10313>
- Bastir M, Rosas A, O'Higgins P (2006) Craniofacial levels and the morphological maturation of the human skull. *J Anat* 209:637-654. <https://doi.org/10.1111/j.1469-7580.2006.00644.x>
- Bastir M, Rosas A, Stringer C, et al (2010) Effects of brain and facial size on basicranial form in human and primate evolution. *J Hum Evol* 58:424-431. <https://doi.org/10.1016/j.jhevol.2010.03.001>
- Berger LR (2013) The mosaic nature of *Australopithecus sediba*. *Science* 340:163. <https://doi.org/10.1126/science.340.6129.163>
- Berger LR, de Ruiter LR, Churchill SE, et al (2010) *Australopithecus sediba*: A new species of *Homo*-like australopithecine from South Africa. *Science* 328:195-204. <https://doi.org/10.1126/science.1184944>
- Berger LR, Hawks J, de Ruiter DJ, et al (2015) *Homo naledi*, a new species of the genus *Homo* from the Dinaledi chamber, South Africa. *eLife* 4:e09560. <https://doi.org/10.7554/eLife.09560>
- Biegert J (1963) The evaluation of characteristics of the skull, hands, and feet for primate taxonomy. In: S. L. Washburn (ed) *Classification and human evolution*, Taylor and Francis, pp. 116-145. <http://dx.doi.org/10.4324/9781315081083-6>
- Blue E (2018) Gene/QTL mapping. In: *The international encyclopedia of biological anthropology*, p. 1-3. <https://doi.org/10.1002/9781118584538.ieba0194>
- Bookstein FL, Gunz P, Mitteroecker P, et al (2003) Cranial integration in *Homo*: singular warps analysis of the midsagittal plane in ontogeny and evolution. *J Hum Evol* 44:167-187. [https://doi.org/10.1016/s0047-2484\(02\)00201-4](https://doi.org/10.1016/s0047-2484(02)00201-4)
- Chernoff B, Magwene PM (1999) Morphological integration: forty years later. In: EC Olson, RL Miller (eds) *Morphological integration*, Chicago University Press, Chicago, p. 319-353
- Cheverud JN (1982) Phenotypic, genetic, and environmental morphological integration in the cranium. *Evolution* 36:499-516. <https://doi.org/10.1111/j.1558-5646.1982.tb05070.x>
- Cheverud JN (1988) A comparison of genetic and phenotypic correlations. *Evolution* 42:958-968. <https://doi.org/10.1111/j.1558-5646.1988.tb02514.x>
- Cheverud JN (1989) A comparative analysis of morphological variation patterns in the papionins. *Evolution* 43:1737-1747. <https://doi.org/10.1111/j.1558-5646.1989.tb02623.x>
- Cheverud JN (1995) Morphological integration in the saddle-back tamarin (*Saguinus fuscicollis*). *Am Nat* 145:63-89. <https://doi.org/10.1086/285728>
- Cheverud JN (1996a) Developmental integration and the evolution of pleiotropy. *Am Zool* 36:44-50. <https://doi.org/10.1093/icb/36.1.44>
- Cheverud JN (1996b) Quantitative genetic analysis of cranial morphology in the cotton-top (*Saguinus oedipus*) and saddle-back (*S. fuscicollis*) tamarins. *J Evol Biol* 9:5-42. <https://doi.org/10.1046/j.1420-9101.1996.9010005.x>
- Conaway MA, Adams DC (2022) An effect size for comparing the strength of morphological

- integration across studies. *Evolution* 76:2244-2259. <https://doi.org/10.1111/evo.14595>
- Conaway MA, Schroeder L, von Cramon-Taubadel N (2018) Morphological integration of anatomical, developmental and functional postcranial modules in the crab-eating macaque (*Macaca fascicularis*). *Am J Phys Anthropol* 166:661-670. <https://doi.org/10.1093/icb/36.1.44>
- Conaway MA, von Cramon-Taubadel N (2022) Morphological integration of the hominoid postcranium. *J Hum Evol* 171:103239. <https://doi.org/10.1016/j.jhevol.2022.103239>
- Darwin C (1859) On the origin of species by means of natural selection, or the preservation of favoured races in the struggle for life, John Murray, London.
- de Oliveira FB, Porto A, Marroig G (2009) Covariance structure in the skull of Catarrhini: a case of pattern stasis and magnitude evolution. *J Hum Evol* 56:417-430. <https://doi.org/10.1016/j.jhevol.2009.01.010>
- Delezenne LK (2015) Modularity of the anthropoid dentition: Implications for the evolution of the hominin canine honing complex. *J Hum Evol* 86:1-12. <https://doi.org/10.1016/j.jhevol.2015.07.001>
- Diogo R, Molnar JL, Rolian C, et al (2018) First anatomical network analysis of fore- and hindlimb musculoskeletal modularity in bonobos, common chimpanzees, and humans. *Sci Rep* 8:5885. <https://doi.org/10.1038/s41598-018-25262-6>
- Dirks PM, Roberts EM, Hilbert-Wolf H, et al (2017) The age of *Homo naledi* and associated sediments in the Rising Star Cave, South Africa. *eLife* 6:e24231. <https://doi.org/10.7554/elife.24231>
- Enlow DH, Hans MG (1996) Essentials of facial growth, WB Saunders Company.
- Esteve-Altava B (2017) In search of morphological modules: a systematic review. *Biol Rev* 92:1332-1347. <https://doi.org/10.1111/brev.12284>
- Esteve-Altava B, Marugán Lobón J, Botella H, et al (2013) Grist to Riedl's Mill: A network model perspective on the integration and modularity of the human skull. *J Exp Zool B Mol Dev Evol* 320B:489-500. <https://doi.org/10.1002/jez.b.22524>
- Esteve-Altava B, Boughner JC, Diogo R, et al (2015) Anatomical network analysis shows decoupling of modular liability and complexity in the evolution of the primate skull. *PLoS One* 10:e0127653. <https://doi.org/10.1371/journal.pone.0127653>
- Falconer DS, Mackay TFC (1996) Introduction to quantitative genetics, Pearson Prentice Hall, London.
- Fisher RA (1918) The correlation between relatives on the supposition of Mendelian inheritance. *Philosophical Transactions of the Royal Society of Edinburgh* 52:399-433. <https://doi.org/10.1017/s0080456800012163>
- Fisher RA (1921) On the "probable error" of a coefficient of correlation deduced from a small sample. *Metron* 1:1-32.
- Foley R (2016) Mosaic evolution and the pattern of transitions in the hominin lineage. *Philos Trans R Soc Lond B Biol Sci* 371:20150244. <https://doi.org/10.1098/rstb.2015.0244>
- Gkantidis N, Halazonetis DJ (2011) Morphological integration between the cranial base and the face in children and adults. *J Anat* 218:426-438. <https://doi.org/10.1111/j.1469-7580.2011.01346.x>
- Gómez-Robles A, Polly PD (2012) Morphological integration in the hominin dentition: Evolutionary, developmental, and functional factors. *Evolution* 66:1024-1043. doi:<https://doi.org/10.1111/j.1558-5646.2011.01508.x>
- Goswami A, Polly PD (2010) The influence of modularity on cranial morphological disparity in Carnivora and Primates (*Mammalia*). *PLoS One* 5:e9517. <https://doi.org/10.1371/journal.pone.0009517>
- Goswami A, Smaers JB, Soligo C, et al (2014) The macroevolutionary consequences of phenotypic integration: from development to deep time. *Philos Trans R Soc Lond B Biol Sci* 369:20130254. <https://doi.org/10.1098/rstb.2013.0254>
- Grabowski MW (2013) Hominin obstetrics and the evolution of constraints. *Evol Biol* 40:57-75. <https://doi.org/10.1007/s11692-012-9174-7>

- Grabowski MW, Polk JD, Roseman CC (2011) Divergent patterns of integration and reduced constraint in the human hip and the origins of bipedalism. *Evolution* 65:1336-1356. <https://doi.org/10.1111/j.1558-5646.2011.01226.x>
- Grabowski MW, Porto A (2017) How many more? Sample size determination in studies of morphological integration and evolvability. *Methods Ecol Evol* 85:592-603. <https://doi.org/10.1111/2041-210x.12674>
- Grabowski MW, Roseman CC (2015) Complex and changing patterns of natural selection explain the evolution of the human hip. *J Hum Evol* 85:94-110. <https://doi.org/10.1016/j.jhevol.2015.05.008>
- Grieco TN, Rizk OT, Hlusko LJ (2013) A modular framework characterizes micro- and macroevolution of Old World monkey dentitions. *Evolution* 67:241-259. <https://doi.org/10.1111/j.1558-5646.2012.01757.x>
- Griffin RH, Yapuncich GS (2015) The Independent Evolution Method is not a viable phylogenetic comparative method. *PLoS One* 10:e0144147. <https://doi.org/10.1371/journal.pone.0144147>
- Griffin RH, Yapuncich GS (2016) Comment on Smaers et al (2016) A nonviable phylogenetic comparative method hampered by circularity, inaccuracy, and bias. *bioRxiv* 2016:058420. <http://dx.doi.org/10.1101/058420>
- Hallgrímsson B, Jamniczky H, Young NM, et al (2009) Deciphering the palimpsest: Studying the relationship between morphological integration and phenotypic covariation. *Evol Biol* 36:355-376. <https://doi.org/10.1007/s11692-009-9076-5>
- Hallgrímsson B, Lieberman DE, Liu W, et al (2007) Epigenetic interactions and the structure of phenotypic variation in the cranium. *Evol Dev* 9:76-91. <https://doi.org/10.1111/j.1525-142x.2006.00139.x>
- Hallgrímsson B, Willmore KE, Hall BK (2002) Canalization, developmental stability, and morphological integration in primate limbs. *Yearb Phys Anthropol* 45:131-158. <https://doi.org/10.1002/ajpa.10182>
- Hansen TF (2003) Is modularity necessary for evolvability? Remarks on the relationship between pleiotropy and evolvability. *BioSystems* 69:83-94. [https://doi.org/10.1016/s0303-2647\(02\)00132-6](https://doi.org/10.1016/s0303-2647(02)00132-6)
- Hansen TF, Houle D (2008) Measuring and comparing evolvability and constraint in multivariate characters. *J Evol Biol* 21:1201-1219. <https://doi.org/10.1111/j.1420-9101.2008.01573.x>
- Hlusko LJ, Mahaney MC (2009) Quantitative genetics, pleiotropy, and morphological integration in the dentition of *Papio hamadryas*. *Evol Biol* 36:5-18. <https://doi.org/10.1007/s11692-008-9048-1>
- Hlusko LJ, Sage RD, Mahaney MC (2011) Modularity in the mammalian dentition: mice and monkeys share a common dental genetic architecture. *Mol Dev Evol* 316B:21-49. <https://doi.org/10.1002/jez.b.21378>
- Hlusko LJ, Schmitt CA, Monson TA, et al (2016) The integration of quantitative genetics, paleontology, and neontology reveals genetic underpinnings of primate dental evolution. *Proc Natl Acad Sci USA* 113:9262-9267. <https://doi.org/10.1073/pnas.1605901113>
- Huxley J (1942) *Evolution: The modern synthesis*, George Allen and Unwin Ltd., London.
- Jung H, Conaway MA, von Cramon-Taubadel N (2020) Examination of sample size determination in integration studies based on the Integration Coefficient of Variation (ICV) *Evol Biol* 47:293-307. <https://doi.org/10.1007/s11692-020-09514-w>
- Jung H, Simons E, von Cramon-Taubadel N (2021a) Ontogenetic changes in magnitudes of integration in the macaque skulls. *Am J Phys Anthropol* 174:76-88. <https://doi.org/10.1002/ajpa.24119>
- Jung H, Simons E, von Cramon-Taubadel N (2021b) Examination of magnitudes of integration in the catarrhine vertebral column. *J Hum Evol* 156:102998. <https://doi.org/10.1016/j.jhevol.2021.102998>
- Jung H, von Cramon-Taubadel N (2022) Morphological modularity in the anthropoid axial skeleton. *J Hum Evol* 172:103256. <https://doi.org/10.1016/j.jhevol.2022.103256>
- Kenyon-Flatt B, Conaway MA, Lycett SJ, et al (2020) The relative efficacy of the cranium and

- os coxa for taxonomic assessment in macaques. *Am J Phys Anthropol* 173:350-367. <https://doi.org/10.1002/ajpa.24100>
- Klingenberg CP (2008) Morphological integration and developmental modularity. *Annu Rev Ecol Evol Syst* 39:115-132. <https://doi.org/10.1146/annurev.ecolsys.37.091305.110054>
- Klingenberg CP (2013) Cranial integration and modularity: insights into evolution and development from morphometric data. *Hystrix* 24:1-16. <https://doi.org/10.4404/hystrix-24.1-6367>
- Klingenberg CP (2014) Studying morphological integration and modularity at multiple levels: concepts and analysis. *Philos Trans R Soc Lond B Biol Sci* 369:20130249. <https://doi.org/10.1098/rstb.2013.0249>
- Komza K, Viola B, Netten T, et al (2022) Morphological integration in the hominid hindfoot. *J Hum Evol* 170:103231. <https://doi.org/10.1016/j.jhevol.2022.103231>
- Laird M F, Schroeder L, Garvin HM, et al (2017) The skull of *Homo naledi*. *J Hum Evol* 104:100-123. <https://doi.org/10.1016/j.jhevol.2016.09.009>
- Lande R (1979) Quantitative genetic analysis of multivariate evolution, applied to brain: body size allometry. *Evolution* 33:402-416. <https://doi.org/10.2307/2407630>
- Lande R (1980) The genetic covariance between characters maintained by pleiotropic mutations. *Genetics* 94:203-215. <https://doi.org/10.1093/genetics/94.1.203>
- Lande R (1984) The genetic correlation between characters maintained by selection, linkage and inbreeding. *Genet Res* 44:309-320. <https://doi.org/10.1017/s0016672300026549>
- Lawler RR (2008) Morphological integration and natural selection in the postcranium of wild Verreaux's Sifaka (*Propithecus verreauxi verreauxi*). *Am J Phys Anthropol* 136:204-213. <https://doi.org/10.1002/ajpa.20795>
- Lawrence J, Kimbel WH (2021) Morphological integration of the canine region within the hominine alveolar arch. *J Hum Evol* 154:102942. <https://doi.org/10.1016/j.jhevol.2020.102942>
- Leamy LJ, Routman EJ, Cheverud JM (1999) Quantitative trait loci for early- and late-developing skull characters in mice: A test of the genetic independence model of morphological integration. *Am Nat* 153:201-214. <https://doi.org/10.1086/303165>
- Lewontin R (1974) The genetic basis of evolutionary change, Columbia University Press, New York.
- Lewton KL (2012) Evolvability of the primate pelvic girdle. *Evol Biol* 39:126-139. <https://doi.org/10.1007/s11692-011-9143-6>
- Lieberman DE (2011) The evolution of the human head, Harvard University Press, Cambridge, MA. <https://doi.org/10.3378/027.084.0206>
- Lieberman DE, Hallgrímsson B, Liu W, et al (2008) Spatial packing, cranial base angulation, and craniofacial shape variation in the mammalian skull: testing a new model using mice. *J Anat* 212 720-735. <https://doi.org/10.1111/j.1469-7580.2008.00900.x>
- Lieberman DE, Pearson OM, Mowbray KM (2000) Basicranial influence on overall cranial shape. *J Hum Evol* 38:291-315. <https://doi.org/10.1006/jhev.1999.0335>
- Love A C, Grabowski M, Houle D, et al (2022) Evolvability in the fossil record. *Paleobiol* 48:186-209. <https://doi.org/10.1017/pab.2021.36>
- Lynch M, Walsh B (1998) Genetics and analysis of quantitative traits, Sinauer, Sunderland.
- Magwene PN (2001) New tools for studying integration and modularity. *Evolution* 55:1734-1745. http://nitro.biosci.arizona.edu/zbook/volume_2/vol2.html
- Makedonska J (2014) New insight into the phenotypic covariance structure of the anthropoid cranium. *J Anat* 225:534-658. <https://doi.org/10.1111/joa.12246>
- Mallard AN, Savell KRR, Auerbach BM (2017) Morphological integration of the human pelvis with respect to age and sex. *Anat Rec* 300:566-674. <https://doi.org/10.1002/ar.23547>
- Marroig G, Cheverud JM (2001) A comparison of phenotypic variation and covariance patterns and the role of phylogeny, ecology, and ontogeny during cranial evolution of new world monkeys. *Evolution* 55:2576-2600. <https://doi.org/10.1111/j.0014-3820.2001.tb00770.x>

- Marroig G, Cheverud JM (2004) Did natural selection or genetic drift produce the cranial diversification of neotropical monkeys? *Am Nat* 163:417-428. <https://doi.org/10.1086/381693>
- Marroig G, de Vivo M, Cheverud JM (2004) Cranial evolution in sakis (*Pithecia*, *Platyrrhini*) II: evolutionary processes and morphological integration. *J Evol Biol* 17:144-155. <https://doi.org/10.1046/j.1420-9101.2003.00653.x>
- Marroig G, Shirai L T, Porto A, et al (2009) The evolution of modularity in the mammalian skull II: Evolutionary consequences. *Evol Biol* 36:136-148. <https://doi.org/10.1007/s11692-009-9051-1>
- Martínez-Abadías N, Esparza M, Sjøvold T, et al (2012) Pervasive genetic integration directs the evolution of human skull shape. *Evolution* 66:1010-1023. <https://doi.org/10.1111/j.1558-5646.2011.01496.x>
- Martínez-Abadías N, Esparza M, Sjøvold T, et al (2015) Chondrocranial growth, developmental integration and evolvability in the human skull. In: JC Boughner, C Rolian (eds) *Developmental approaches to human evolution*, John Wiley and Sons, Inc., p. 46-68.
- Mitteroecker P, Bookstein FL (2007) The conceptual and statistical relationship between modularity and morphological integration. *Syst Biol* 56:818-836. <https://doi.org/10.1080/10635150701648029>
- Mitteroecker P, Bookstein FL (2008) The evolutionary role of modularity and integration in the hominoid cranium. *Evolution* 62:843-958. <https://doi.org/10.1111/j.1558-5646.2008.00321.x>
- Mitteroecker P, Gunz P, Bookstein FL (2005) Heterochrony and geometric morphometrics: a comparison of cranial growth in *Pan paniscus* versus *Pan troglodytes*. *Evol Dev* 7:244-258. <https://doi.org/10.1111/j.1525-142x.2005.05027.x>
- Moore W (1981) *The mammalian skull*, Cambridge University Press, Cambridge.
- Moss ML, Young RW (1960) A functional approach to craniology. *Am J Phys Anthropol* 18:281-291. <https://doi.org/10.1002/ajpa.1330180406>
- Neaux D (2017) Morphological integration of the cranium in *Homo*, *Pan*, and *Hylobates* and the evolution of hominoid facial structures. *Am J Phys Anthropol* 162:732-746. <https://doi.org/10.1002/ajpa.23163>
- Neaux D, Gilissen E, Coudyzer W, et al (2015) Integration between the face and the mandible of *Pongo* and the evolution of the craniofacial morphology of Orangutans. *Am J Phys Anthropol* 158:475-486. <https://doi.org/10.1002/ajpa.22807>
- Neaux D, Guy F, Gilissen E, et al (2013) Covariation between midline cranial base, lateral basicranium, and face in modern humans and chimpanzees: A 3D geometric morphometric analysis. *Anat Rec* 296:568-579. <https://doi.org/10.1002/ar.22654>
- Neaux D, Sansalone G, Ledogar JA, et al (2018) Basicranium and face: Assessing the impact of morphological integration on primate evolution. *J Hum Evol* 118:43-55. <https://doi.org/10.1016/j.jhevol.2018.02.007>
- Neaux D, Wroe S, Ledogar JA, et al (2019) Morphological integration affects the evolution of midline cranial base, lateral basicranium and face across primates. *Am J Phys Anthropol* 170:37-47. <https://doi.org/10.1002/ajpa.23899>
- Olson EC, Miller RL (1958) *Morphological integration*, University of Chicago Press, Chicago. <https://doi.org/10.1126/science.128.3316.138-a>
- Parravicini A, Pievani T (2019) Mosaic evolution in hominin phylogeny: meanings, implications, and explanations. *J Anthropol Sci* 97:1-24. <https://doi.org/10.4436/JASS.97001>
- Pilbeam D (1996) Genetic and morphological records of the hominoidea and hominid origins: A synthesis. *Mol Phylogenet Evol* 5:155-168. <https://doi.org/10.1006/mpev.1996.0010>
- Polanski JN (2011) Morphological integration of the modern human mandible during ontogeny. *Int J Evol Biol* 2011:1-11. <https://doi.org/10.4061/2011/545879>
- Polanski JN, Franciscus RG (2006) Patterns of craniofacial integration in extant *Homo*, *Pan*, and *Gorilla*. *Am J Phys Anthropol* 131:38-49. <https://doi.org/10.1002/ajpa.20421>
- Porto A, De Oliveira FB, Shirai LT, et al (2009) The evolution of modularity in the mammalian

- skull I: morphological integration patterns and magnitudes. *Evol Biol* 36:118-135. <https://doi.org/10.1007/s11692-008-9038-3>
- Porto A, Shirai LT, de Oliveira FB et al (2013) Size variation, growth strategies, and the evolution of modularity in the mammalian skull. *Evolution* 67:3305-3322. <https://doi.org/10.1111/evo.12177>
- Profico A, Piras P, Buzi C, et al (2017) The evolution of the cranial base and face in cerco-pithecoidea and hominoidea: modularity and morphological integration. *Am J Primatol* 79:e22721. <https://doi.org/10.1002/ajp.22721>
- Randau M, Goswami A (2017) Morphological modularity in the vertebral column of *Felidae* (Mammalia, Carnivora). *BMC Evol Biol* 17:133. <https://doi.org/10.1186/s12862-017-0975-2>
- Rogers J, Mahaney MC, Almas L, et al (1999) Quantitative trait linkage mapping in anthropology. *Yearb Phys Anthropol* 42:127-151. [https://doi.org/10.1002/\(sici\)1096-8644\(1999\)110:29](https://doi.org/10.1002/(sici)1096-8644(1999)110:29)
- Rolian C (2009) Integration and evolvability in primate hands and feet. *Evol Biol* 36:100-117. <https://doi.org/10.1007/s11692-009-9049-8>
- Rolian C (2014) Genes development, and evolvability in primate evolution. *Evol Anthropol* 23:83-104. <https://doi.org/10.1002/evan.21409>
- Rolian C (2020) Ecomorphological specialization leads to loss of evolvability in primate limbs. *Evolution* 74:702-715. <https://doi.org/10.1111/evo.13900>
- Rolian C, Lieberman DE, Hallgrímsson B (2010) The coevolution of human hands and feet. *Evolution* 64:1558-1568. <https://doi.org/10.1111/j.1558-5646.2009.00944.x>
- Ross C, Henneberg M (1995) Basicranial flexion, relative brain size, and facial kyphosis in *Homo sapiens* and some fossil hominids. *Am J Phys Anthropol* 98:575-593. <https://doi.org/10.1002/ajpa.1330980413>
- Ross CF, Ravosa MJ (1993) Basicranial flexion, relative brain size, and facial kyphosis in nonhuman primates. *Am J Phys Anthropol* 91:305-324. <https://doi.org/10.1002/ajpa.1330910306>
- Ruff CB, Holt B, Trinkaus E (2006) Who's afraid of the big bad Wolff? Wolff's Law and bone functional adaptation. *Am J Phys Anthropol* 129:484-498. <https://doi.org/10.1002/ajpa.20371>
- Ruvinsky I, Gibson-Brown JJ (2000) Genetic and developmental bases of serial homology in vertebrate limb evolution. *Development* 127:5233-5244. <https://doi.org/10.1242/dev.127.24.5233>
- Savell KRR (2020) Evolvability in human post-cranial traits across ecogeographic regions. *Am J Phys Anthropol* 172:110-122. <https://doi.org/10.1002/ajpa.24004>
- Savell KRR, Auerbach BM, Roseman CC (2016) Constraint, natural selection, and the evolution of human body form. *Proc Natl Acad Sci USA* 113:9492-9497. <https://doi.org/10.1073/pnas.1603632113>
- Schluter D (1996) Adaptive radiation along genetic lines of least resistance *Evolution* 50:1766-1774. <https://doi.org/10.1111/j.1558-5646.1996.tb03563.x>
- Schroeder L, Scott JE, Garvin HM, et al (2017) Skull diversity in the *Homo* lineage and the relative position of *Homo naledi*. *J Hum Evol* 104:124-135. <https://doi.org/10.1016/j.jhevol.2016.09.014>
- Schroeder L, von Cramon-Taubadel N (2017) The evolution of hominoid cranial diversity: A quantitative genetic approach. *Evolution* 71:2634-2649. <https://doi.org/10.1111/evo.13361>
- Schultz AH (1960) Vertebral column and thorax (Vol. 4), Karger Medical and Scientific Publishers.
- Sears KE, Bianchi C, Powers L, et al (2013) Integration of the mammalian shoulder girdle within populations and over evolutionary time. *J Evol Biol* 26:1536-1548. <https://doi.org/10.1111/jeb.12160>
- Sears KE, Capellini TD, Diogo R (2015) On the serial homology of the pectoral and pelvic girdles of tetrapods. *Evolution* 69:2543-2555. <https://doi.org/10.1111/evo.12773>
- Shirai LT, Marroig G (2010) Skull modularity in neotropical marsupials and monkeys: Size variation and evolutionary constraint and

- flexibility. *Mol Dev Evol* 314B:663-683. <https://doi.org/10.1002/jez.b.21367>
- Singh N, Harvati K, Hublin J-J, et al (2012) Morphological evolution through integration: A quantitative study of cranial integration in *Homo*, *Pan*, *Gorilla*, and *Pongo*. *J Hum Evol* 62:155-164. <https://doi.org/10.1016/j.jhevol.2011.11.006>
- Smaers J, Mongle CS, Kandler A (2016) A multiple variance Brownian motion framework for estimating variable rates and inferring ancestral states. *Biol J Linn Soc Lond* 118:78-94. <https://doi.org/10.1111/bij.12765>
- Smaers JB, Mongle CS (2017) On the accuracy and theoretical underpinnings of the multiple variance Brownian motion approach for estimating variable rates and inferring ancestral states. *Biol J Linn Soc Lond* 121:229-238. <https://doi.org/10.1093/biolinnean/blx003>
- Sodini SN, Kemper KE, Wray NR, et al (2018) Comparison of genotypic and phenotypic correlations: Cheverud's conjecture in humans. *Genetics* 209:841-948. <https://doi.org/10.1534/genetics.117.300630>
- Stearns FW (2010) One hundred years of pleiotropy: A retrospective. *Genetics* 186:767-773. <https://doi.org/10.1534/genetics.110.122549>
- Steppan SJ (1997) Phylogenetic analysis of phenotypic covariance structure. I. Contrasting results from matrix correlation and common principal component analysis. *Evolution* 51:571-586. <https://doi.org/10.2307/2411129>
- Steppan SJ, Phillips P C, Houle, D (2002) Comparative quantitative genetics: evolution of the G matrix. *Trends Ecol Evol* 17:320-327. [https://doi.org/10.1016/s0169-5347\(02\)02505-3](https://doi.org/10.1016/s0169-5347(02)02505-3)
- Szabo-Rogers HL, Smithers LE, Yakob W, et al (2010) New directions in craniofacial morphogenesis. *Dev Biol* 341:84-94. <https://doi.org/10.1016/j.ydbio.2009.11.021>
- Thompson D W (1917) *On Growth and Form*, Cambridge University Press, Cambridge.
- Torres-Tamayo N, García-Martínez D, Nalla S, et al (2018) The torso integration hypothesis revisited in *Homo sapiens*: Contributions to the understanding of hominin body shape evolution. *Am J Phys Anthropol* 167:777-790. <https://doi.org/10.1002/ajpa.23705>
- Torres-Tamayo N, Martelli S, Schlager S, et al (2020) Assessing thoraco-pelvic covariation in *Homo sapiens* and *Pan troglodytes*: A 3D geometric morphometric approach. *Am J Phys Anthropol* 173:514-534. <https://doi.org/10.1002/ajpa.24103>
- Villamil CI (2018) Phenotypic integration of the cervical vertebrae in the *Hominoidea* (Primates). *Evolution* 72:490-517. <https://doi.org/10.1111/evo.13433>
- Villamil CI (2021) The role of developmental rate, body size, and positional behavior in the evolution of covariation and evolvability in the cranium of strepsirrhines and catarrhines. *J Hum Evol* 151:102941. <https://doi.org/10.1016/j.jhevol.2020.102941>
- Villamil CI, Santiago-Nazario A (2022) Integration between the cranial boundaries of the nasopharynx and the upper cervical vertebrae in *Homo* and *Pan*. *Anat Rec* 305:1974-1990. <https://doi.org/10.1002/ar.24750>
- Villmoare B, Fish J, Jungers WL (2011) Selection, morphological integration, and Strepsirrhine locomotor adaptations. *Evol Biol* 38:88-99. <https://doi.org/10.1007/s11692-011-9108-9>
- von Cramon-Taubadel N (2009) Congruence of individual cranial bone morphology and neutral molecular affinity patterns in modern humans. *Am J Phys Anthropol* 140:205-215. <https://doi.org/10.1002/ajpa.21041>
- von Cramon-Taubadel N (2011) Global human mandibular variation reflects differences in agricultural and hunter-gatherer subsistence strategies. *Proc Natl Acad Sci USA* 108:19546-19551. <https://doi.org/10.1073/pnas.1113050108>
- von Cramon-Taubadel N (2018) Morphometrics, humans. In: W Trevathan (ed) *The International Encyclopedia of Biological Anthropology*, John Wiley and Sons, Inc.
- von Cramon-Taubadel N (2019) Multivariate morphometrics, quantitative genetics, and neutral theory: Developing a modern synthesis for primate evolutionary morphology. *Evol Anthropol* 28:21-33. <https://doi.org/10.1002/evan.21761>

- von Cramon-Taubadel N, Lycett SJ (2014) A comparison of catarrhine genetic distances with pelvic and cranial morphology: Implications for determining hominin phylogeny. *J Hum Evol* 77:179-186. <https://doi.org/10.1016/j.jhevol.2014.06.009>
- von Cramon-Taubadel N, Schroeder L (2018) Quantitative genetics. In: The international encyclopedia of biological anthropology, John Wiley and Sons, Inc. <https://doi.org/10.1002/9781118584538.ieba0006>
- von Cramon-Taubadel N, Weaver TD (2009) Insights from a quantitative genetic approach to human morphological evolution. *Evol Anthropol* 18:237-240. <https://doi.org/10.1002/evan.20233>
- Wagner GP (1996) Homologues, natural kinds and the evolution of modularity. *Am Zool* 36:36-43. <https://doi.org/10.1093/icb/36.1.36>
- Wagner GP, Altenberg L (1996) Complex adaptations and the evolution of evolvability. *Evolution* 50:967-976. <https://doi.org/10.1111/j.1558-5646.1996.tb02339.x>
- Wagner GP, Pavlicev M, Cheverud JM (2007) The road to modularity. *Nat Rev Genet* 8:921-931. <https://doi.org/10.1038/nrg2267>
- Wainschtein P, Jain D, Zheng Z, et al (2022) Assessing the contribution of rare variants to complex trait heritability from whole-genome sequence data. *Nat Genet* 54:263-273. <https://doi.org/10.1530/ey.19.5.17>
- Watanabe J (2022) Statistics of eigenvalue dispersion indices: quantifying the magnitude of phenotypic integration. *Evolution* 76:4-28. <https://doi.org/10.1111/evo.14382>
- Weaver TD, Gunz P (2018) Using geometric morphometric visualizations of directional selection gradients to investigate morphological differentiation. *Evolution* 72:838-850. <https://doi.org/10.1111/evo.13460>
- Welch JJ, Waxman D (2003) Modularity and the cost of complexity. *Evolution* 57:1723-1734. <https://doi.org/10.1111/j.0014-3820.2003.tb00581.x>
- Wellik DN (2007) Hox patterning of the vertebral axial skeleton. *Dev Dynam* 236:2454-2463. <https://doi.org/10.1002/dvdy.21286>
- Wijsman EN (2005) Mendel's laws In: Encyclopedia of biostatistics. <http://dx.doi.org/10.1002/0470011815.b2a05063>
- Williams SA (2010) Morphological integration and the evolution of knuckle-walking. *J Hum Evol* 58:432-440. <https://doi.org/10.1016/j.jhevol.2010.03.005>
- Wright S (1968) Evolution and the genetics of populations. Genetic and biometric foundations (Vol. 1). *J Biosol Sci* 2:301-304. <https://doi.org/10.1017/s0021932000007744>
- Young M, Selleri L, Capellini TD (2019) Genetics of scapula and pelvis development: An evolutionary perspective. *Curr Top Dev Biol* 132:311-349. <http://dx.doi.org/10.1016/bs.ctdb.2018.12.007>
- Young NN (2004) Modularity and integration in the hominoid scapula. *J Exp Zool* 302B:226-240. <https://doi.org/10.1002/jez.b.21003>
- Young NN (2005) Estimating hominoid phylogeny from morphological data: character choice, phylogenetic signal and postcranial data. In: D. E. Lieberman, R. J. Smith, J. Kelley (eds) *Interpreting the past: Essays on human, primate and mammal evolution in honor of David Pilbeam*, Brill Academic Publisher, Boston, p. 19-31. http://dx.doi.org/10.1163/9789047416616_007
- Young NN, Hallgrímsson B (2005) Serial homology and the evolution of mammalian limb covariation structure. *Evolution* 59:2691-2704. <https://doi.org/10.1111/j.0014-3820.2005.tb00980.x>
- Young NN, Wagner GP, Hallgrímsson B (2010) Development and the evolvability of human limbs. *Proc Natl Acad Sci USA* 107:3400-3405. <https://doi.org/10.1073/pnas.0911856107>
- Zelditch ML, Goswami A (2021) What does modularity mean? *Evol Dev* 23:377-403. <https://doi.org/10.1111/ede.12390>

