

# THE MACROEVOLUTION OF PHENOTYPIC INTEGRATION

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## INTRODUCTION

Phenotypic integration is a central aspect of macroevolution. It is also an important concept in macroevolutionary theory. A number of empirical research questions and theoretical debates concerning evolution at and above the species level revolve around the issue of differential phenotypic integration through time. However, macroevolutionary studies in general and evolutionary paleobiology in particular have often conceptualized and documented phenotypic integration in ways that are not always comparable with standard, quantitative-genetic microevolutionary accounts. Thus, subjects such as evolutionary radiations, constraints, morphospace structure and occupation, disparity, allometry, heterochrony and heterotopy, the origin and proliferation of novelties, and clade dynamics, to name but a few, have been interpreted in terms of phenotypic integration (e.g., Valentine and Campbell 1975; Alberch et al. 1979 ; Maynard Smith et al. 1985; Gould 1989a,b ; Jablonski and Bottjer 1990 ; Erwin 1993 ; Zelditch and Fink 1996 ; Foote 1997 ; McGhee 1999), but with methodological protocols and theoretical motivations often distinct from those of microevolutionary research.

By extension, appreciating the status of phenotypic integration in macroevolution and its relationship with various genetic, developmental, and ecological approaches may help dissolve residual tensions between macroevolutionists and microevolutionists (notwithstanding the fact that some scholars may belong to both communities without apparent loss of sanity!). The essential tension has concerned the issue of reducibility. It is bound to disappear, though, upon recognition that macroevolution is not completely reducible

to microevolution because of differences in scale, in the hierarchical manifestation of evolutionary processes, in the extent and sources of contingency and constraint, and in the nature of the focal biological entities (Gould 1982, 2002; Eldredge 1989; Williams 1992; Erwin 2000; Jablonski 2000). None of these justifications for a relative autonomy of macroevolution are necessarily contentious nowadays, as macroevolutionary research has been rendered more rigorous conceptually, empirically, and theoretically, with operational definitions and methodologically sophisticated data collection, analysis, and modeling routinely guiding statistically testable inferences about large-scale evolutionary patterns and processes (Schopf 1972 ; Raup and Jablonski 1986 ; Gilinsky and Signor 1991; Erwin and Anstey 1995; Jablonski et al. 1996; Foote 1997; McKinney and Drake 1998 ; Eble 2000a, 2002a; Jablonski 2000; Jackson et al. 2001; Gould 2002). Macroevolution and microevolution are at times factually and theoretically distinct, but material irreducibility is only partial, and complete decouplement is logically impossible, because actual organisms must figure in both domains. There is no fundamental incompatibility between macroevolution and microevolution in a general evolutionary theory, if such theory incorporates biological hierarchies as matters of fact or at least as heuristic representations. Cross-hierarchical organization and dynamics are complex, but not intractable (Simon 1962 ; Lewontin 1970; Weiss 1971; Eldredge 1985; Vrba and Gould 1986 ; Vrba 1989 ; Eble 1999a; McShea 2001; Gould 2002), and the existence of biological hierarchies per se does not necessarily demand level-specific theories of process (e.g., Williams 1992; Maynard Smith and Szathmáry 1995).

At issue, then, is precisely which phenomena, explanations, and theoretical constructs associated with macroevolution are equivalent to those in the microevolutionary realm, which are only partially equivalent, and which – if any – are incommensurable. The study of phenotypic integration is of special relevance in this regard, since the phenotype figures in empirical and theoretical research in population biology, in systematics, in evolutionary developmental biology, and in paleobiology. Clarifying how phenotypic integration is manifested and studied in macroevolution, and understanding the nature of macroevolutionary phenotypic integration, may help in moving beyond the perhaps overly modular multidisciplinary of current integration studies and towards a more unifying interdisciplinarity (Zelditch 1996 ; Schlichting and Pigliucci 1998). This in turn may open the way for a more synthetic appreciation of the role of the phenotype in evolutionary theory at large.

In this contribution, I will examine this state of affairs and discuss macroevolutionary issues that have been or could be analyzed in the context of phenotypic integration, either explicitly or implicitly. In doing so, I will suggest that research protocols for studying the macroevolution of phenotypic integration are appropriate for certain questions but must be further refined to tackle a wider array of macroevolutionary problems and to allow new models to be advanced, and that certain conceptual and analytical approaches in macroevolution may prove useful, or at least illuminating, in microevolution as well. The intent, as unavoidable in a subject still in need of a synthesis, is not to be exhaustive or prescriptive, but to simply highlight the unique contexts of macroevolutionary phenotypic

integration, and the phenomenology of causes it implies. This can be viewed as a step towards developing a more solid account of the meaning of pattern and process in macroevolution, in a manner that is at the same time compatible with and enriching of microevolutionary theory.

## **PHENOTYPIC INTEGRATION IN MACROEVOLUTIONARY STUDIES**

### *From comparative anatomy to morphospaces*

A concern for phenotypic integration and its relationship with interspecific patterns of variation accompanied the history of comparative anatomy, and was particularly evident in the 19<sup>th</sup> century, with the establishment of such notions as the unity of type, functional correlation, structural correlation, the principle of connections, homology, and developmental laws (Russell 1916). Darwin and post-Darwinian morphologists recast all such notions in evolutionary terms while keeping their heuristic aspects intact. Yet with the new emphasis on phyletic transformation, the growing mechanicism of embryology, and the atomism of Mendelian genetics, organismal integration as a research theme soon faded into the background. In the search for the causes and consequences of variation, a genuine « disintegrative biology » rose to prominence, producing important knowledge but at the same time biasing knowledge production.

Integration thus stood as a secondary problem in evolutionary biology for most of the last century (Schlichting and Pigliucci 1998). In macroevolutionary biology, however, and in particular in paleobiology, the centrality of morphology as data and of taxa as the entities of

theoretical discourse ensured that organismal integration was not lost from sight. Simpson (1953), for example, while often emphasizing individual traits in his attempt to render paleontology fully compatible and explainable within the population-genetic framework of the Modern Synthesis, also asserted the importance of correlated phenotypic evolution and of character complexes. As Olson and Miller (1958) pointed out, Simpson's use of genera as the basic taxonomic units in his studies of evolutionary rate reflected his assessment that differences among genera were proportional to total morphological difference, and that taxa in general referred to whole organisms, even if by proxy.

Olson and Miller's 1958 landmark book attempted to establish the importance of morphological integration in evolutionary biology, and to devise rigorous methods for its study. Their work echoes that of Clausen and colleagues (Clausen et al. 1940 ; Clausen and Hiesey 1960), but while the latter directly addressed the genetic basis of phenotypic integration with crossing experiments in plants, Olson and Miller's focus was mostly paleobiological. They recognized, with genuine appreciation, the importance of genetic integration, but addressed causality in more exploratory fashion, in terms of trait associations reflecting known function or development, and also potentially referring to size, spatial location within the organism, or « some unifying biological factor ». More generally, part of the theoretical motivation was to show that many important questions in paleontology (trends, rates, speciation, hybridization, ontogenetic biases in evolution, and convergence) could and should be fruitfully addressed in terms of morphological integration.

Olson and Miller's work is symptomatic of a time of increasing quantitative sophistication in paleontology, and of more explicit interest in character correlation, allometry, and multivariate evolution (Kermack and Haldane 1950 ; Kermack 1954 ; Imbrie 1956 ; Raup 1956). The trend continued into the 1960's, when quantitative paleontology was relatively well established as an approach, and multivariate morphometrics routine in many studies of invertebrate groups. Morphological integration was often inferred statistically and interpreted in post hoc fashion, rather than tested against a priori predictions. But the premise that character correlation and organismal integration were important and needed to be causally understood was nearly universally agreed upon among students of organismal form.

In this context, the field of theoretical morphology (Raup 1966 ; Raup and Michelson 1965 ; McGhee 1999 ; Eble 2000b) arose in part as an attempt to distill a small number of constructional parameters in terms of which whole organisms could be graphically simulated with mathematical models of form generation. In theoretical morphology, morphospaces define the universe of possibilities, and clusters of taxa stand as evidence of phenotypic integration. Emphasis is placed on inter-object relationships within a clade treated as a statistical population, and integration is expressed as co-occurrence of taxa in certain regions of morphospace, regardless of whether the axes of the coordinate system are correlated or not. Theoretical morphology does not prescribe the nature of the biological entities (which can also be individuals within populations, rather than taxa within clades), but it seems clear that, with the explicit construction of morphospaces, a conceptual and analytical framework became available to view integration as a property of clades, to represent it in relation to the

geometry of evolutionary realizations, and to quantify it in terms of inter-object relationships.

The framework applies to empirical morphospace studies as well, although here a large number of variables is usually considered, inviting the use of multivariate ordination techniques (such as principal components analysis) to assess both inter-object and inter-variable relationships. The role of morphospaces in inferences about phenotypic evolution needs to be further refined (Foote 1997; Schlichting and Pigliucci 1998 ; Eble 1998, 2000b, 2002a), but morphospace thinking does constitute a distinct contribution of macroevolutionary studies to the topic of integration, by providing a cross-hierarchical platform for understanding constraints on and opportunities for the origin and maintenance of phenotypic variation and covariation.

### ***Phenotypic integration as cohesion and as a property***

However inferred and conceptualized, phenotypic integration in macroevolution relates to organismal cohesion, and as such refers as much to constrained variational patterns, the foci of morphometrics and quantitative genetics, as to organizational patterns, where structural, functional, and developmental stability or even invariance must be taken into account. Ultimately, the ontology of macroevolution presupposes phenotypic integration, even if character complexes and the strength of their integration may change in ontogeny and phylogeny (Arnold et al. 1989; Wagner and Misof 1993; Fink and Zelditch 1996; Shubin and Wake 1996; Chaline et al. 1998 ; Eble 2000 ; 2002a,b). Species and clades exist as units of evolution if at least some of their diagnostic traits are consistently integrated during their



evolutionary history, thus supporting statements of homology, relationship, identity, and stasis (Valentine 1990; Rieppel 1986, 1988; Nelson 1989; Jablonski and Bottjer 1990 ; Gould 2002). Taxa, whether conceived of as classes or individuals, are subject to a dynamics of differential representation, which is conditioned on sustained organismal cohesiveness and stability across generations. Different groups may exhibit different degrees of cohesiveness and stability across characters, different durations of stasis in individual traits or character complexes, and different rates of mosaic evolution, but strong integration of taxon-specific characters is an existence requirement until extinction or pseudoextinction marks the end of a lineage. Homology, in particular, is a key aspect of phenotypic integration in macroevolution, but it is hardly acknowledged in the formal structure of quantitative-genetic models of integration. These models as a rule focus on integration as manifested in correlated patterns of readily changeable quantitative traits, with lack of change and discrete traits that vary only on phylogenetic time scales standing as a non-issue.

In microevolutionary research the default loci of explanation are traits or groups of traits, and their quasi-independence is as much a target of study as their potential integration. Quasi-independence facilitates adaptation and response to selection. As the latter are assumed to have a preeminent role in population differentiation (notwithstanding the fact that established functional interdependencies may also promote evolution), one important goal of microevolutionary studies of phenotypic integration is to distill modular units of selection from the complex patterns of trait interactions constituting the organism -- in other words, to identify local phenotypic integration, and correlated responses to selection (e.g.; Lande and

Arnold 1983). In macroevolution, such question-oriented disintegration of the organism is invoked routinely in the study of individual lineages through time. Phenotypic disintegration is either accepted *faute de mieux*, when taphonomic bias forces the investigator to focus only on those characters with high preservation potential (e.g., molars in mammals), or because one may be concerned with characters of taxonomic importance or else presumed evolutionary importance (e.g., key innovations).

Yet for most large-scale studies of phenotypic integration, the focus is on integration as a whole-organism property of individuals and the clades they represent. Traits in isolation and trait interactions may be of less immediate interest because overall phenotypic integration is seen as a meaningful macroevolutionary phenomenon, expressed in summary statistics of evolutionary flexibility (e.g., various metrics of disparity) that are comparable across groups and time, regardless of trait identity and the details of trait interaction (Olson and Miller 1958; Hughes 1990; Wagner 1995 ; Eble 1998, 2000a). Such statistics codify, if not an emergent trait, at least the potential for emergent fitnesses at the species or clade level (much as with variability – Lloyd and Gould 1993). Far from assuming tight organismal integration by default and disregarding dissociability (for a critique of this position, see Gould 1977; Fink and Zelditch 1996), emphasis is placed on an operational « quasi-dependence » of traits in the context of clade definition (homology) and clade persistence (stasis) in geological time. More than adaptation, the interest is on adaptability and, more generally, evolvability (Kauffman 1993 ; Wagner and Altenberg 1996 ; Depew 1998). Recent studies of morphological disparity through time (e.g., Foote 1997) reflect this perspective; although, as will be seen

below, disparity relates to integration in some respects but not in others (see Cheverud et al. 1989 ; Eble in press). And, in macroevolutionary debates, phenotypic integration as a global trait or state is often invoked, and granted empirical reality by the very logic of tests of hypotheses usually proposed. This is the case for the dichotomy between developmental and ecological explanations of evolutionary radiations, both across body plans (Gould 1989a, 1993; Erwin 1993, 1999; McShea 1993; Ridley 1993 ; Valentine 1995 ; Eble 1998; Conway Morris 1998 ; Jablonski 2000), and within body plans (e.g., Wagner 1995 ; Foote 1999 ; Eble 2000a). There is of course much room for character-by-character analyses of correlations in the context of integration, despite limitations of sampling and temporal resolution. But in the practice of macroevolution, the dynamics of clades is the reference phenomenological domain and the main source of patterns to be explained. While mosaic evolution and dissociability are acknowledged and documented, phenotypic integration in macroevolution is more than a trait-by-trait business. It is also a macroevolutionary trait in its own right.

### ***Proxies for phenotypic integration in macroevolution***

Even though phenotypic integration has been quantified with morphometric data in a number of paleontological studies (e.g., Foote 1991, 1999 ; Wagner 1995 ; Eble 2000a), changing patterns of taxonomic diversity, origination, and extinction are often used as proxy evidence for differential clade-level phenotypic integration. The morphological disparity among phyla, for example, is still difficult to quantify because of extensive geometric incommensurability across body plans. Higher taxonomic status (phyla, classes, and orders)

thus has been used as a proxy for morphological distinctness, and asymmetries (e.g., decline) in the frequency of higher taxa through time have been hypothesized to reflect long-term changes in overall phenotypic integration (Valentine 1986, 1995; Erwin et al. 1987; Kauffman 1989, 1993 ; Jablonski and Bottjer 1990, 1991; Jacobs 1990 ; Valentine et al. 1991 ; Eble 1998, 1999b).

Further, at lower taxonomic levels, models of taxonomic diversification parameterized with (stochastically) constant per-taxon origination and extinction rates have been reasonably successful at describing macroevolutionary dynamics in a number of groups (e.g., Sepkoski 1978, 1979, 1984 ; Stanley 1979; Benton 1997). Constant rates of diversification, origination, and extinction in such models have been treated as intrinsic clade properties related to organismal construction and its correlates (e.g., Schopf et al. 1975 ; Vrba 1983; Eldredge 1989; Stanley 1990; Valentine et al. 1991a). High origination and extinction rates (e.g., trilobites) would suggest more labile, less integrated body plans, while low origination and extinction rates (e.g., bivalves) suggest resistance to change and more integrated phenotypes. In this context, differential per-taxon rates are hypotheses of differential phenotypic integration.

### ***Approaches to interspecific data***

Most neontological studies of phenotypic integration center on the quantification of intraspecific variation, which may then be compared among species (e.g. Olson and Miller 1958 ; Cheverud 1982, 1990; Bookstein et al. 1985 ; Cheverud et al. 1989). In a phylogenetic

context, interesting questions arise, such as whether cladogenesis tends to be associated with more substantial change in correlation structure than is population differentiation (Olson and Miller 1958), or whether niche breadth correlates with degree of integration. Issues of phenotypic integration and dissociability based on species-by-species comparisons have recently also been pursued in comparative neontological studies of ontogenetic variation (e.g., Alberch 1983 ; Shubin and Wake 1996; Smith 1996 ; Fink and Zelditch 1996), and in applications of phylogeny-based comparative methods (e.g., Harvey and Pagel 1991). The attempt to understand the macroevolution of phenotypic integration by comparing intraspecific patterns of variation across species may be most useful for closely related species, which would be expected to display smoothly gradational patterns of variation and covariation. However, if taxon sampling is sparse, species status or phylogenetic relationships poorly known, or if taxa are very distantly related, the assumption that intra- and interspecific patterns intergrade and are responsive to similar evolutionary processes becomes more difficult to assess, and biological interpretations accordingly become potentially less robust. Further, analysis of large numbers of species over long periods of time on the basis of intraspecific patterns of continuous variation and covariation is complicated by the need to take into account typical macroevolutionary phenomena such as innovations, character gains and losses, and character invariance. This complication is not merely analytical and representational. Aspects of phenotypic variation and integration in macroevolution may simply not be addressable (or modeled in canonical form) with sequential species-by-species comparisons of intraspecific variation, because of potential long-term changes in organismal

dimensionality during the history of clades and of potential inhomogeneity of variational properties among species, especially in large clades broadly distributed in time and space.

Whether and how temporal extension and geographic distribution may bias inferences about integration in particular groups is an open issue. At any rate, small, young clades are less likely to present such problems, and indeed most comparative analyses of intraspecific variation have appropriately focused on such « intermediate » scales of macroevolution.

Macroevolutionists are often more interested in patterns of integration at the level of more inclusive, species-rich clades, whose usually long histories allow for more robust quantification of patterns of disparity and morphospace occupation. Accordingly, phenotypic integration has been studied by directly considering species as individual data points (much as in evolutionary allometry studies). Thus, a variance-covariance or correlation matrix in the case of continuous data, or an association matrix in the case of discrete data, may capture how traits coevolve or co-occur across species in a clade. Species are observed or assumed to be relatively stable entities on the scale of the whole clade, and randomly selected specimens are treated as representative of each species' morphology. The presence of stasis, or alternatively of some consistent basis for species identity through time, justifies this approach. At least for morphospace studies, the interest is rather in the large-scale partitioning of morphological variation and in the evolutionary origins and consequences of phenotypic integration of a clade. Specimens are thus seen more as statistical samplers of morphospace regions than as typical members of evolutionary units (although they may figure as such in evolutionary interpretations of pattern).

An additional assumption, often defensible on geological time scales but not always tested, is that intraspecific variation rarely confounds interspecific patterns of variation, such that species (genera, families, etc.) would on average stand as relatively discrete clusters in (or samplers of) morphospace (Raup and Boyajian 1988; Sepkoski and Kendrick 1993). Operational issues aside, explicit quantification of interspecific variation and covariation patterns in whole clades, complements species-by-species comparisons of intraspecific integration. By identifying other scales and genealogical levels of phenotypic integration, the interspecific approach indicates that an empirical domain for a genuinely macroevolutionary notion of phenotypic integration exists. This naturally allows for hierarchical sorting and selection processes, homology, innovation, and changes in dimensionality to be considered rigorously as part of a broader explanatory framework for long-term patterns of phenotypic integration.

## **ON THE NATURE, REPRESENTATION, AND MEANING OF PHENOTYPIC INTEGRATION IN MACROEVOLUTION: BEYOND THE MATRIX?**

Movie plots are sometimes hard to understand or even meaningless, especially when multiple scales of time and space are considered simultaneously. In the movie "The Matrix ", our anti-hero "Neo" attempts to understand and eventually undermine the inner workings of the virtual reality matrix in which he is enslaved. By analogy with evolution, how much of our current understanding of phenotypic integration and of our confidence in the means to study it are not invariably tied to the formalism of the variance-covariance (or correlation)

matrix? What else can be learned, or is there anything else to learn, if one opts to study phenotypic integration with less conventional distillations of the data matrix, or even with other data representations?

The issue is important in light of the multiple kinds, sources, and contexts of integration (Olson and Miller 1958; Cheverud 1996; Roth 1996; Zelditch 1996 ; Schlichting and Pigliucci 1998; McShea 2001), and of potentially different manifestations of integration in microevolution and macroevolution. Should models for all these variations on the theme of phenotypic integration always refer to pairwise correlations or covariances, or can they also be framed *ab initio* in terms of global measures such as the total variance or total correlation (Van Valen 1974, 1978 ; Cheverud et al. 1989), which allow but do not demand an explicit matricial representation?

Assessments of phenotypic integration in macroevolution are distinct not only for their emphasis on taxa over variables and by a preference for global metrics, but also because data may be biased by smaller sample sizes and incomplete preservation. As a result, oftentimes the reference data matrix is one of nonparametric presence-absence data, inter-object distances, or coefficients of association. Modeling such data could benefit from generalizations of existing models of correlation and variance-covariance structure, but little work has been done in this area. In the absence of models, stochastic simulation (Foote 1996) and resampling methods (Cheverud et al. 1989) may help provide a set of null expectations.

Biological objects, and in particular parts or modular units (McShea and Venit 2001), can vary, covary, or not vary in a panoply of ways. Variation and covariation of discrete



characters on macroevolutionary time scales may mean no more than the discrete coming into and going out of existence and coexistence in the phylogenetic tree (Darden 1992 ; Eble in press). Organizational and variational properties of the phenotype may be expected to change in concert (Cheverud 1996 ; Wagner and Altenberg 1996), but patterns of historical constraint, stasis, and homology in macroevolution are often reflected in highly entrenched characters for which only discrete shifts in organization are possible.

The solution to the problem of representation and analysis of integration is not pluralism per se and an "everything goes" methodological attitude, but context-specific operationalism and heuristic methodological diversification. Granted, evolutionary biology is far from exhausting the analytical power of linear algebra, and granted that life in "the matrix" has only advanced our understanding of integration, one may look beyond the brackets and consider the possibility that certain kinds of integration, particularly in macroevolution, may invite different formalisms for its analysis and representation. For example, homology and homoplasy have at times been framed in terms of variation and covariation (e.g., Harvey and Pagel 1991; Grafen and Ridley 1996 ; Maddison 2000), but their representation and interpretation on phylogenies transcend the standard variational framework of variance-covariance matrices. Stasis, in turn, can be studied within lineages and its existence assessed in terms of the extent of variation and covariation of traits (Lande 1986), but many examples of stasis concern single discrete traits, a few taxon-specific traits whose covariation is of less interest than their persistence (i.e., relative invariance) through time, or homologies and their ontogenetic and phylogenetic entrenchment.

On macroevolutionary time scales, traits may be seen as highly integrated as much because of tight correlations with other traits as because of their internal resistance to change (see Wagner and Schwenk 2000) and their persistence through time (which may relate to various causes, both internal and external to the organism). In this sense, a distinction between a state of integration (in a proximal sense) and a dynamic of integration maintenance (in an evolutionary sense, by selection for example) becomes important. Further, while developmental constraints and constraints in general have been interpreted and formalized in terms of covariance structure (Maynard Smith et al. 1985; Lande 1986 ; Wagner 1988 ; Arnold 1992 ; Wagner and Altenberg 1996), many accounts of stasis as an outcome of developmental constraint involve organizational criteria cast in terms of either epigenetics or geometric structure in morphospace (Alberch 1982 ;Maynard Smith et al. 1985 ; Gould 1989b ; Eble 1998 ; Mueller and Newman 1999). While it is tempting to refer to these different styles of study and interpretation of phenotypic integration as the distinction between qualitative ("unrigorous") and quantitative ("rigorous") styles of biological research, qualitative statements convey data that can often be rendered rigorous, objective, testable, and precise.

What the diversity and complexity of macroevolutionary phenomena and the state of macroevolutionary theory suggest is that phenotypic integration, expressing multiple scales of time and space, multiple causes, and different levels in the organizational, genealogical, and ecological hierarchies, may well justify either modifications or alternatives to the "matrix-thinking" that stems from standard quantitative genetic approaches, on the one hand, and

morphometrics, on the other (see also Pigliucci, chapter 20 in this volume). Far from denying the centrality of heritability as a prerequisite for systematic sorting and selection processes, one may consider alternative formalisms that do not reduce to pairwise associations of characters or organisms. Additional sources of pattern are possible to the extent that some aspects of integration may not be contained in the representational structure of genetic or phenotypic variance-covariance matrices. For example, while the genotype-phenotype map can be explored by comparisons of genetic and phenotypic matrices, the mapping itself should ideally be represented in terms of developmental trajectories, patterns of gene expression, regulatory genetic and epigenetic networks, changing identities and roles of modules, and self-organization as a contributor to the emergence of form in ontogeny (Eble 2002a).

Novel biological insights on multiscale and multihierarchical organismal integration may invite more extensive use of representations such as graphs (including ontogenetic and phylogenetic trees and networks), contour diagrams, and non-Euclidean or nonmetric topological renditions of the state spaces in which characters and organisms are embedded (e.g., Olson and Miller 1958 ; Sneath and Sokal 1973 ; Schlichting and Pigliucci 1998; Newman 2000; Sporns et al. 2000; Magwene 2001 ; Stadler et al. 2001 ; Wagner and Stadler in press).

Further, even when matrices are retained as the default operational tool, the conclusions we standardly draw from current quantitative-genetic models for macroevolution are in need of revision. Rather than explanatorily reducing **P** matrices and vectors of putatively modular phenotypic units to arbitrarily invoked selection coefficients and a

monistic arena of **G** matrices, one might well consider **P** as a locus of constraint and explanation in its own right (Burger 1986 ; Wagner 1989, 1994, 1996 ; Mueller 1990; Goodwin 1994 ; Cheverud 1996 ; Mueller and Newman 1999 ; Erwin 2000 ; Jablonski 2000 ; Gould 2002 ; Eble 2002a, in press). Other sources of pattern not directly revealed in the structure of genetic variance-covariance matrices, and which may imply causal roles for the phenotype, are patterns of epigenetic covariation, ecophenotypic covariation, phylogenetic covariation, and temporal (stratigraphic) covariation.

In macroevolutionary theory, phenomenological generalization is justifiable because the goal is not to understand characters and their differential integration only, but characters and integration as they relate to a dynamics of taxon sorting that may often depend not only on function and development, but also on external factors (e.g., drastic environmental change, periodic forcing factors such as bolide impacts), on context (biogeographic phenomena, norms of reaction, innovation, morphospace), and on incidental causal consequences of the characters themselves when they lead to emergent fitnesses or organismal exaptation. If phenotypic integration is to be about population-genetic evolutionary processes, the current uniformitarian approach cast in terms of microevolution is appropriate. Yet in macroevolution uniformitarianism is hardly justifiable ; evolutionary processes conditioned on heritability must be generalized across levels and scales, and complemented by biological and non-biological factors which can change the course of evolution, reset or eliminate evolutionary trends, and modify evolvability and attainability even if they cannot count as "heritable". Can such additional factors be modeled? Perhaps not in detail, but their role is

an integral part of the orderliness (or lack thereof) of macroevolutionary phenotypic integration.

### **IS INTEGRATION THE CONVERSE OF MODULARITY?**

The simple answer is no, because the whole is more than the sum of the parts. But the answer might also be yes, depending on how one defines and quantifies integration and modularity. Theoretically (Wagner 1996 ; Wagner and Altenberg 1996), one might suppose that every hypothesis of the macroevolution of phenotypic integration could be expressed in terms of modularity, and vice-versa. All other things being equal, this appears reasonable. Indeed, the notions of parcellation (increase in modularity) and integration (decrease in modularity) figure together as opposites in conceptual discussions (Wagner and Altenberg 1996 ; Eble in press), in statistical operationalizations (Mezey et al. 2000 ; Magwene 2001), and in morphometric studies (Klingenberg et al. 2001). But is the opposition symmetric? Modularity and integration may actually not be strictly inversely proportional to each other because of factors such as the geometry of organisms, the topology of morphospace, and historical contingency.

#### ***The geometry of organisms***

Different modules may be differentially integrated and differentially cohesive, and this may depend to a large extent on organismal geometry. Character or part counts can serve as estimates of modularity (McShea and Venit 2001 ; Eble in press), but not of integration, for

example. The shape of parts itself affects the geometry of connectivity, but if they are homogeneous (e.g., serial homologs), modularity (measured as number of parts) may increase or decrease in evolution without a necessary change in the strength of interactions (within or between those parts), and hence no necessary change in the degree of integration.

### *The topology of morphospace*

Accessibility in morphospace may not be isotropic, because different regions may be accessible to different degrees, such that heterogeneities in the structure of morphospace may determine whether module creation, or increase in modularity, is reversible (see Stadler et al. 2001); if it is not reversible, or if it is but with a lower transition probability, then integration is not the converse of modularization. For example, a narrow route in morphospace may link a primitive taxon restricted in a small, homogeneous region of parameter space to a derived taxon in a broader, heterogeneous region. This configuration of morphospace would by itself promote exploration of the broader region by the derived taxon (assuming no change in intrinsic rates of origination and extinction, and stochastic diffusion in morphospace), with a possible increase in modularity; and it would bias against convergence back to the primitive restricted region because of the narrowness of the route connecting the regions. How to document and model inherent heterogeneities in morphospace, however, is an open issue.

### *Historical contingency*

How the geometry of organisms and the topology of morphospace affect modularity and integration may to some extent be a matter of chance, depending on which phenotypes happen to have evolved and where they are located in morphospace. Chance plays a role in determining which modules get entrenched or lost in evolution. Some modules, such as limbs, may be lost, and modularity arguably decreases, while the integration of remaining modules also decreases, as former connections with limbs are lost. Thus, a reduction in modularity need not correspond to an increase in integration.

### **TEMPORAL RESOLUTION AND SCALES OF INTEGRATION**

How coeval do organisms need to be for one to quantify integration? Integration is often considered to be an instantaneous property. But some relativization is necessary, because average integration is also biologically interpretable (as a tendency or potentiality, for instance), and temporal resolution is almost never equivalent in different taxa. For example, in an ant colony individuals at any one time are behaviorally integrated, and connectivity is realized by chemical signaling among individuals. At the same time, if one broadens the interval of time over which one observes and infers integration, some individuals that contribute to integration at time  $t$  may not have been born yet at time  $t-1$ . If one cannot, or does not want, to distinguish between  $t$  and  $t-1$ , one will assume time-averaged integration to be constant. If birth and death rates are stochastically constant, or if general statements about

average integration are useful in a particular theoretical context, then time averaging is acceptable and inconsequential.

In paleobiological studies time averaging is inescapable, and virtually all macroevolutionary research with fossils is pursued at a level of generality where time averaging does not compromise statistical inference or theoretical interpretation. Typically, samples of species are binned in intervals of time that may correspond to millions of years. In a morphometric study, a matrix of correlations might be computed, and morphological integration might be inferred as a property of the group of species on that scale. Characters  $a$  and  $b$  may be inferred to correlate in general across species even if late in the interval they did not. One may assume that species are randomly distributed over the interval, but if a disproportionately large number of species occurs early on and provide evidence for strong integration, and a smaller number of species occurs later on but provide no evidence for strong integration, a real change in degree of integration would not be identified.

Macroevolutionary inference necessarily proceeds by treating time-averaged integration estimates as average properties for the clade, and by comparing such averages across intervals. For long-ranging clades enough intervals may be included to render temporal patterns of time-averaged integration interpretable as average tendencies reflecting evolutionary potential and evolvability. Debates concerning changes in differential flexibility in macroevolutionary time, such as after the Cambrian explosion or during evolutionary radiations (e.g., Gould 1989a, 1991 ; Foote 1997 ; Valentine et al. 1991b ; Eble 1998, 1999b, 2000a), are addressed empirically with precisely such rationale, with degree of integration



standing as an average propensity across clades, exceptions notwithstanding (but see Hughes et al. 1999).

## **INTEGRATION BY CHANCE**

For some groups of organisms, a relatively small number of modules at a particular level of organization may compose the organism. In this case, drift may become important in coupling or uncoupling characters by chance, because of the small population of modules.

Null models of integration and parcellation need to be devised that take into account the number of modules in an organism. When modules are not numerous and their functionality is not obvious, drift may well be more important than selection or development in reinforcing integration. Further, in macroevolutionary studies a few broad modular regions may be more tractable and of more theoretical interest than the many sub-modules composing them (e.g., David and Mooi 1996 ; Mooi and David 1998 ; Eble 2000a).

It is encouraging that recent statistics of integration have been proposed which explicitly rely on appropriate null hypotheses (Mezey et al . 2000). Thus, from a range of possible boundary conditions and possible genotype-phenotype interactions, inferences about integration, or lack thereof, are conditioned on it being higher or lower than expected (the expectation potentially varying depending on the situation or the question of interest). While null hypotheses of integration for QTL data take into account gene number, gene effects, and pleiotropic interactions, in macroevolution purely phenotypic considerations are also reasonable. Null hypotheses then can be cast in terms of universes of possible trait

interactions at the organismal level, of probabilities of presence or absence of traits with high potential for entrenchment, and of expected trait variances and covariances. The range of possible patterns might also be simulated non-parametrically, with randomization procedures (Cheverud et al. 1989), or mechanistically, with theoretical morphology models.

### **IS DISPARITY A PROXY FOR PHENOTYPIC INTEGRATION?**

Disparity refers to the phenotypic distinctness of forms in morphospace. The quantification of disparity has proved an important approach to help resolve, in more focally morphological terms, debates about temporal asymmetries in clade histories, the nature of evolutionary radiations, and the relationship between evolvability and innovation (Gould 1991 ; Foote 1993, 1997 ; Wills et al. 1994 ; Wagner 1995 ; Conway Morris 1998 ;Eble 1998, 2000). It also holds promise in evolutionary developmental biology, as a means of assessing the geometry of global phenotypic variation in ontogenetic time and of addressing and testing in more rigorous terms ontogenetic regularities across taxa (Eble 2002a,b).

Disparity can be quantified in a number of ways (e.g. Foote 1991; Wills et al. 1994), most often as the total variance or the total range of  $n$  variables in a sample. As a general measure of variation in a clade, disparity can be expected to be promoted by variational modularity, because modularity allows opportunities for semi-independent variation; disparity might also itself be an operational proxy for modularity when common mechanistic sources (e.g., function, development) or causal roles (e.g., in evolvability, in clade selection and sorting, in character evolution) can be identified or hypothesized (Eble in press).

As discussed previously, modularity and integration need not be strictly proportional to each other, and thus disparity as a proxy for modularity may not be a proxy for integration in the same way. But on macroevolutionary scales and at the level of clades or body plans, change or maintenance of relative phenotypic integration is generally viewed as theoretically more important and empirically more tractable than quantification of absolute degrees of integration, or for that matter of modularity (Gould 1989a, 1991 ; Foote 1993, 1996, 1997 ; Wills et al. 1994). And indeed, documentation of disparity patterns through time is usually motivated by an interest in assessing whether integration has increased, decreased, or remained the same in the history of various clades. Integration is treated as a global, average property of clades in any given time interval, and tests of macroevolutionary hypotheses are devised accordingly, using disparity as a rough measure of integration.

Granted that disparity refers to variation and integration to covariation, being thus not formally equivalent (but see Van Valen 1974, 1978 ; Wagner 1984 ; Cheverud et al. 1989), the general logic of the evolutionary connection is the same as outlined above for modularity: strong phenotypic integration may constrain the production of novelties and hence disparity, and conversely loose integration may allow novelties to be generated and incorporated, with an associated increase in disparity. Functional and developmental constraints are expressed in patterns of integration, and disparity will reflect remaining possibilities for functional or developmental differentiation of integrated phenotypes. Furthermore, integration as well as disparity can influence evolvability, clade success, and character evolution.

Ultimately, disparity, modularity, and integration in macroevolutionary theory are thought to reflect the same concept: constraint. Constraint is a key subject in macroevolution and surfaces in theoretical and analytical morphology (Raup 1972), constructional morphology (Seilacher 1970), punctuated equilibrium (Eldredge and Gould 1972), heterochrony (Alberch et al. 1979), critiques of adaptationism (Gould and Lewontin 1979; Gould 1980), discussions about the role of chance in macroevolution (Eble 1999a; Gould 2002), and interpretations of evolutionary radiations and the origin of novelties (Valentine and Campbell 1975; Gould 1989a; Jablonski and Bottjer 1990; Erwin 1993; Valentine 1995; Conway Morris 1998; Eble 1998). Disparity appears to be appropriate as a rough measure of macroevolutionary phenotypic integration, but refining the conceptual and analytical intersections among constraint, integration, modularity, and disparity is much needed to determine the place of disparity in models of phenotypic integration.

## **CONCLUSIONS**

Phenotypic integration is almost universally modeled and interpreted in terms of genetic variance-covariance. Even when matches between phenotypic and genetic correlations hold, analysis and modeling of phenotypic integration proceeds as if it corresponded to genetic integration. Causality is forced to reside in genotypic space, and phenotypic integration stands as a passive object of explanation, devoid of theoretical role.

In macroevolution, the phenotype and phenotypic integration are both observational objects and causal subjects. Phenotypic integration can be modeled in its own terms, taking

into account a variety of evolutionary forces and scales of time. This constitutes a challenge for macroevolutionists. A way forward is to conceive of and to model relationships among characters not only in genetic terms, but also in terms of function (degree of functional correlation), epigenetics (degree of developmental correlation, say, by sharing of cell and tissue types or constructional elements), space (degree of contiguity in the whole organism), environment (plasticity integration), biomechanics (degree of shared structural stability, which need not imply shared function), fitness (degree of contribution to overall fitness, even if functions are not shared), and time (characters may be associated or correlated because of shared temporal origins, or else sequential origins, with one character conditioned on the appearance of another). No single model is likely to incorporate successfully all such sources of integration, but a diversity of models may actually be desirable to consider different domains, scales, and levels of integration. Domains, scales, and levels overlap and intersect, and so can models of phenotypic integration. Phenotypic organization, variation, and causal roles differ in microevolution and macroevolution, but are all manifested in the same biological hierarchies, which integrate different kinds of phenotypic integration.

In the vernacular, one meaning of "integration" is "to end segregation of and bring into equal membership in society or in an organization". This has been an aspiration of macroevolutionists for a long time. Phenotypic integration in macroevolution is sufficiently distinct and sufficiently important to justify a more effective incorporation of macroevolutionary data and theory into accounts of phenotypic integration in particular, and into evolutionary theory in general.

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