

## RESEARCH ARTICLE

# Challenges in identifying and interpreting organizational modules in morphology

Borja Esteve-Altava<sup>1,2</sup> 

<sup>1</sup>Structure & Motion Laboratory, Department of Comparative Biomedical Sciences, Royal Veterinary College, United Kingdom

<sup>2</sup>Department of Anatomy, Howard University College of Medicine, United States of America

## Correspondence

Borja Esteve-Altava, Structure & Motion Laboratory, Department of Comparative Biomedical Sciences, The Royal Veterinary College, Hawkshead Lane, North Mymms, Hatfield, Hertfordshire, AL9 7TA, United Kingdom.

Email: boresal@gmail.com

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## Abstract

Form is a rich concept that agglutinates information about the proportions and topological arrangement of body parts. Modularity is readily measurable in both features, the variation of proportions (variational modules) and the organization of topology (organizational modules). The study of variational modularity and of organizational modularity faces similar challenges regarding the identification of meaningful modules and the validation of generative processes; however, most studies in morphology focus solely on variational modularity, while organizational modularity is much less understood. A possible cause for this bias is the successful development in the last twenty years of morphometrics, and specially geometric morphometrics, to study patterns of variation. This contrasts with the lack of a similar mathematical framework to deal with patterns of organization. Recently, a new mathematical framework has been proposed to study the organization of gross anatomy using tools from Network Theory, so-called Anatomical Network Analysis (AnNA). In this essay, I explore the potential use of this new framework—and the challenges it faces in identifying and validating biologically meaningful modules in morphological systems—by providing working examples of a complete analysis of modularity of the human skull and upper limb. Finally, I suggest further directions of research that may bridge the gap between variational and organizational modularity studies, and discuss how alternative modeling strategies of morphological systems using networks can benefit from each other.

## KEYWORDS

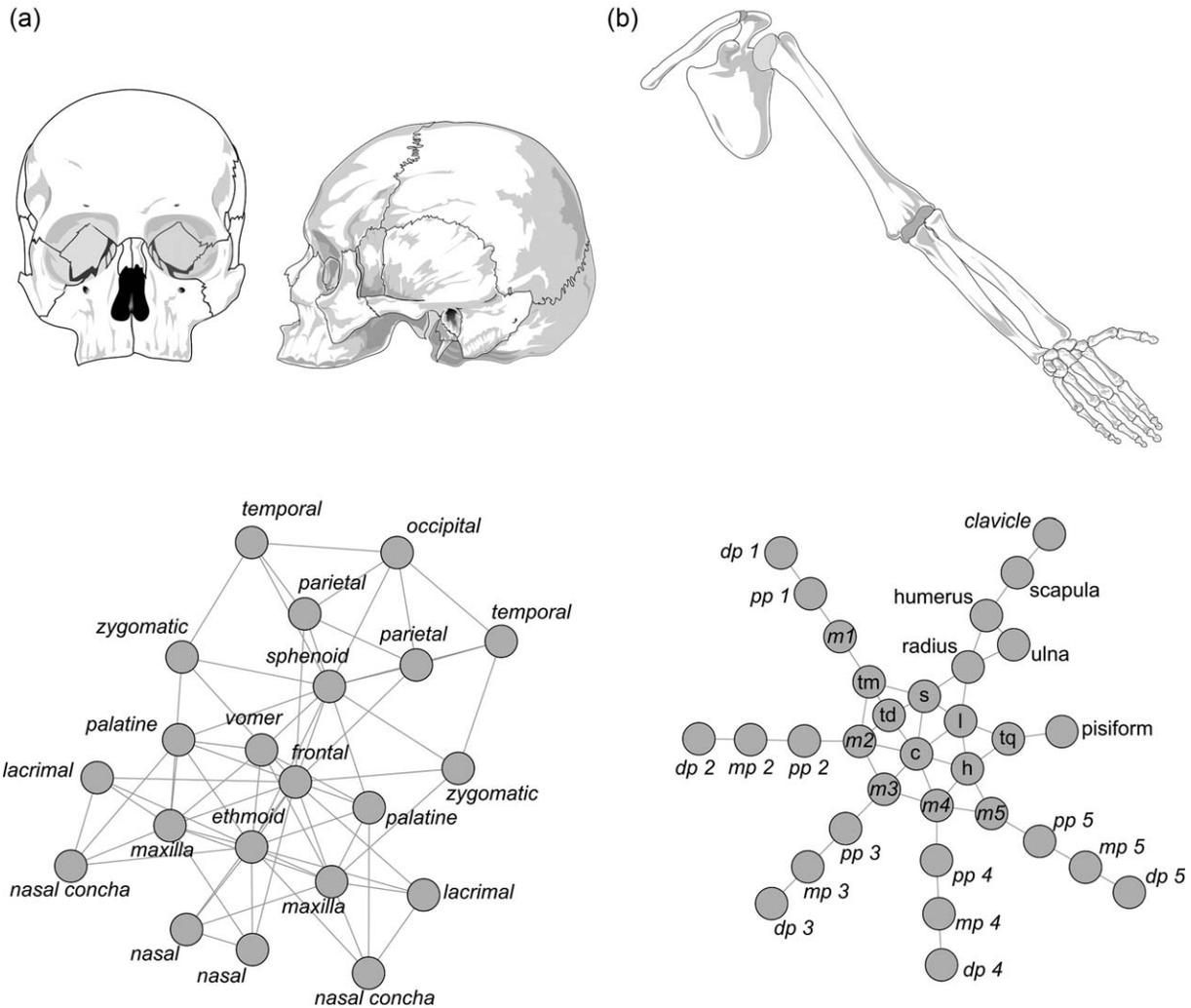
anatomical network analysis, community detection, human anatomy, theoretical morphology

## 1 | INTRODUCTION

Modularity is a widespread concept in modern science that emerged from the need to parcellate large, complex systems into smaller, hierarchically nested components (Simon, 1962). The study of modularity is commonplace in all biological disciplines because modularity affects the way complex biological systems, from genomes to ecosystems, originate, function, and evolve (Callebaut & Rasskin-Gutman, 2005; Schlosser & Wagner, 2004; Wagner, Pavlicev, & Cheverud, 2007). In morphology, the study of modularity focuses mostly on identifying regions of the body that covary in shape, by measuring traits covariation using distance-based morphometrics or landmark-based geometric morphometrics (reviewed in Esteve-Altava, 2016). The historical origin of this approach traces back to the influential book *Morphological Integration* by Everett Olson and Miller (1958) in the context of zoological studies, and to the seminal paper on *The ecological significance of correlation pleiades*

by Raissa Berg (1960) in botanical studies. Morphological modules identified on the basis of shape variation have been defined as variational modules (Eble, 2005; Wagner & Altenberg, 1996; Wagner et al., 2007). Variational modularity has been the focus of many scholarly reviews in recent years (e.g., Klingenberg, 2008, 2010, 2014; Melo, Porto, Cheverud, & Marroig, 2016). In short, a variational module is a group of traits that vary coordinately (i.e., they are morphologically integrated *sensu* Olson and Miller) and, to some extent, they vary independently of other groups of traits. Up to two thirds of research studies on morphological integration and modularity analyze shape variation (Esteve-Altava, 2016), using variational module (more or less explicitly) as a synonym of morphological module (Esteve-Altava, 2016). For this reason, in this essay I use the term variational modularity to refer to shape-variational modules as derived from morphometric analyses.

The intuitive notion of biological organization evokes a group of parts interacting to perform a function. Beyond its functional



**FIGURE 1** Network models of the skull (a) and of the upper limb (b). The first feature that catches the eye is the different organization of each network. On the one hand, the skull network shows a mesh-like organization, whereas the upper limb network shows a more star-like organization with serially connected nodes radiating from a central, small mesh. On the other hand, the skull network has a higher density of links ( $K_{\text{median}} = 5$ ,  $K_{\text{min}} = 4$ ,  $K_{\text{max}} = 13$ ) than the upper limb network ( $K_{\text{median}} = 2$ ,  $K_{\text{min}} = 1$ ,  $K_{\text{max}} = 7$ ). Networks are plotted using the Kamada-Kawai force-directed algorithm, which renders a natural layout for anatomical networks. Notice that the visual representation of a network model is trivial as long as the connections among nodes do not change

component, the idea of organization entails the presence of a structure of interactions between the parts of a system (Rashevsky, 1954, 1960). In this sense, morphological organization emerges from the interactions or relations among anatomical parts, which form distinguishable connectivity patterns that give the system its characteristic structure (Rasskin-Gutman, 2003; Rasskin-Gutman & Buscalioni, 2001). Thus, the modular organization of a morphological system is accessible on the basis of the relations among its constituent anatomical parts (Esteve-Altava, Marugán-Lobón, Botella, Bastir, & Rasskin-Gutman, 2013). This idea gave birth to a new conceptual framework that uses network models and community detection algorithms to identify modules in morphological systems, Anatomical Network Analysis (AnNA) (Esteve-Altava, Marugán-Lobón, Botella, & Rasskin-Gutman, 2011; Rasskin-Gutman & Esteve-Altava, 2014). Throughout this essay I will use AnNA to refer to the application of Network Theory to study gross-anatomy morphological systems (see Section 5 for a discussion

of neuronal or brain networks). A network is a mathematical object that comprises two sets of elements: a set of nodes that represent the constituent parts of the system, and a set of links that connect pairs of nodes and represent interactions or relations among these parts. Anatomical networks are abstract representations of an organism's topology (Figure 1): understanding topology as the way in which constituent parts are interrelated or arranged in the body (Rasskin-Gutman & Esteve-Altava, 2014). AnNA cover the suite of concepts and methods for the analysis of connectivity relations in morphological systems, which include, but are not limited to, the working examples used in this essay to illustrate this approach and the interpretation of its results. Although this quantitative approach is relatively new (but see Section 5), a more general use of topological relations in morphology dates back to the beginnings of comparative anatomy and to Geoffroy Saint-Hilaire's *principle of connections* (Geoffroy Saint-Hilaire, 1818). Ever since, connections among anatomical parts have been used in building

TABLE 1 Ontological and epistemological differences between variational and organizational modules

	Variational modules	Organizational modules
Natural object		Complex morphological systems
Level of study (what is form?)	Proportions ( <i>shape and size</i> )	Structure ( <i>topological arrangement</i> )
Component parts	Morphometric traits	Individualized anatomical parts
Relation among parts	Correlation or covariation	Topological boundaries
Mathematical object	Correlation matrix	Network model
Module definition	A group of traits that co-vary	A group of parts densely connected
Identification ( <i>exploration step #1</i> )	Cluster analysis	Community detection algorithm
Validation ( <i>exploration step #1</i> )	Statistical test	Optimization function Q Wilcoxon rank-sum test
Confirmation ( <i>a priori hypothesis test</i> )	RV, CR, PLS	Similarity
Comparison ( <i>with alternative partitions</i> )	EMMLi, z-score	Similarity

theoretical models of morphological organization (e.g., Woodger's *axiomatic method*, Rashevsky's *bio-topological mapping*, and Riedl's *diagrammatic morphotype*) and as a tool to establish homology between two body parts (reviewed in Rasskin-Gutman & Esteve-Altava, 2014; see Rasskin-Gutman & Esteve-Altava, 2014 for an historical review). Because anatomical networks focus on the explicit organization of relations among body parts within an organism, independently of their variation, modules identified using AnNA belong to the category of organizational modules (Eble, 2005). An organizational module is a group of elements that establish more and/or stronger interactions within the group than outside it. Thus, the emphasis is placed on interactions among component parts, as an important constructional or functional property of form, whether interactions are defined based on structure (as in the working examples), pleiotropy, development, or performance (see Eble, 2005). Notice that, independently of the definition of interaction (see Section 3.1), once the system is modeled as a network our focus is on the analysis of the topological organization of parts and interactions. Henceforth, I use organizational modularity to refer to topology-organizational modules as derived from Anatomical Network Analyses.

Even though variational and organizational modularity differ in their epistemological and ontological basis (Eble, 2005), both approaches face similar challenges: the identification of reliable modules, their validation, and their comparison to alternative or *a priori* hypotheses. These challenges have been reviewed recently in the context of variational modularity and shape analysis (e.g., Adams, 2016; Adams & Collyer, 2016; Garcia, de Oliveira, & Marroig, 2015; Goswami & Finarelli, 2016; Goswami, Smaers, Soligo, & Polly, 2014; Klingenberg, 2014; Melo et al., 2016) and I will not discuss them further. Here, I focus on these challenges in the context of organizational modularity and AnNA. First, I review the similarity of the challenges in studying variational and organizational modularity (Section 2). Second, I present two working examples (using the human

skull and upper limb) of how to identify, validate, and compare modules using AnNA (Section 3). Third, I discuss some challenges that this new framework for the study of form has to address in the near future. One is about how to integrate variational and organizational approaches (Section 4). Although, it is not well-known whether, and how, variation and organization work together in structuring and shaping the form of organisms (but see e.g., Esteve-Altava et al., 2013; Perez, de Aguiar, Guimarães, & dos Reis, 2009; Suzuki, 2013), the hope is that by bridging the gap between them we will have a better understanding of morphological modularity, and possibly help to tackle challenges on both sides. Another is the problem of having alternative approaches and different network realizations of the same morphological system, and how we can combine results from different studies (Section 5).

## 2 | VARIATIONAL VERSUS ORGANIZATIONAL MODULES

Studies on variational and organizational modules have ontological and epistemological differences, although both approaches seek to parcelate complex morphological systems into highly integrated regions (Table 1). The source of these differences are (1) that each approach uses its own definition of form, and consequently, (2) that they use different methods to analyze organismal forms. Form is a rich concept that agglutinates information about proportion (i.e., size and shape) and structure (i.e., topology and arrangement), as well as other information related to the relative orientation and functional articulation of parts (Rasskin-Gutman, 2003; Rasskin-Gutman & Buscalioni, 2001). In this context of multiple layers of morphological information, variational modules deal with form at the level of proportions, while organizational modules deal with form at the level of structure. As a consequence, each approach uses a different set of proxies and formalisms. The raw

data in morphometric-based variational modules are morphometric traits, such as linear distances and landmark coordinates, and the resulting mathematical objects analyzed are correlation or covariation matrices. In contrast, the raw data in network-based organizational modules are generally individual body parts and their topological relations (but see Section 3.1), and the resulting mathematical objects are network models.

Identifying morphological modules (variational and organizational) from the empirical data described above, without any previous hypothesis of what are the actual modules, requires to use specific mathematical tools. In morphometrics, we identify variational modules from the matrix of traits correlation using, for example, hierarchical clustering (Goswami, 2006) or graph modeling (Magwene, 2001). Note that in the latter method, graphs (or networks) are only used to summarize, or to help visualizing, statistical relationships among traits calculated from the correlation matrix; thus, the identification of modules does not rely on a network-based method as its name would suggest. However, it is possible to identify variational modules from correlation matrices using network-based methods of clustering (e.g., Perez et al., 2009; Suzuki, 2013; but see MacMahon & Garlaschelli, 2015 for methodological considerations). Moreover, correlation matrices can be constructed using a coordinate-based approach, treating each coordinate as a unit of variation (e.g., Klingenberg, 2008), or using a vector-based approach, treating each landmark (2D or 3D) as a unit of variation (e.g., Goswami & Finarelli, 2016; Goswami & Polly, 2010). Finally, we can validate the identified variational modules of the morphometric data using statistical tests (e.g., Fisher's *z*-transformation and Student's *t*-test, as in Goswami, 2006). Conversely, in network-based methods we identify organizational modules using community detection algorithms. Broadly speaking, a network module is a group of nodes with more interactions (i.e., links) within the group than outside it. The identification of modules in networks has grown in sophistication in parallel with the application of networks to telecommunications, sociology, and biology (e.g., Fortunato, 2010; Newman, 2006; Palla, Derényi, Farkas, & Vicsek, 2005); and within biology, most notably to ecology (e.g., Olesen, Bascompte, Dupont, & Jordano, 2007), neurobiology (e.g., Sporns, 2011), and molecular biology (e.g., Guimerà & Nunes Amaral, 2005). Community detection algorithms seek to delimit modules using the topological information represented in the network model. However, identifying modules is computationally costly because of the large number of alternative partitions in which we can group the nodes of a network. Even in relatively small networks, such as the 21-node network of the human skull (described in Esteve-Altava et al., 2013) there are about  $4.75 \times 10^{14}$  possible partitions. This is because the number of potential partitions of a network grows exponentially with the number of nodes, following the Bell's numbers progression (Bell, 1938). There are many different algorithms to identify modules in networks, which vary in their heuristic approach. For example, some algorithms search the space of possible partitions by optimizing a quality function, while others use sta-

tistical inference on generative models, dynamic diffusion or spin processes (reviewed in Fortunato, 2010). Common validation methods include (1) the quantification of a function that measures the overall quality of the partition (which is usually the same used in optimization methods, see Equation 1 below) according to the observed versus expected links within and between modules (Newman and Girvan, 2004), (2) evaluating every module individually to meet a mathematical definition of module (Fortunato & Barthelemy, 2007), or (3) calculating the significance of modules using statistical tests (e.g., a Wilcoxon rank-sum test on internal vs. external number of links) or bootstrapping. Unfortunately, identifying network modules and validating network partitions are still open problems without universal agreed solutions (Fortunato & Hric, 2016).

Processes taking place at genetic, developmental, and functional levels, and across ontogenetic and evolutionary scales, are causally related to the emergence of morphological modularity (review in Klingenberg, 2008, 2014; Melo et al., 2016). Thus, a fairly common experiment consists in testing whether an *a priori* hypothesis of modularity based on information from one or more of these levels matches the morphological modules observed empirically in ontogeny or evolution (Esteve-Altava, 2016). Testing the fit of variational modules (or more generally, of traits covariation) to genetic, developmental, and functional hypotheses has a long tradition in morphology (see e.g., Cheverud, 1982, 1989, 1996; Zelditch, 1988; Zelditch & Carmichael, 1989). There are various methods available to carry out such confirmatory tests, of which the most popular one in recent times is the Escoufier's RV coefficient (Klingenberg, 2009). However, some authors have some concerns about the reliability of RV coefficients and proposed alternative methods to validate *a priori* hypotheses of variational modularity. For example, Garcia et al. (2015) have proposed the modularity hypothesis index (MHI), which renders lower type I and II error rates than the RV; Adams (2016) has proposed to use the covariance ratio (CR), which (unlike RV) is not sensitive to the size of the sample and to the number of variables, thus, allowing to perform comparisons across different data sets; lastly, Goswami and Finarelli (2016) have proposed an approach based on maximum likelihood and the Akaike information index to select among alternative hypotheses of modularity (EMMLi). Note that this latter method would allow to compare competing partitions, such as those previously validated by one or more of the former methods. Conversely, under the network-based approach, testing the fit of organizational modules to *a priori* hypotheses of modularity rely on measuring the similarity between two alternative partitions. These methods include measures based on pair counting, cluster matching, and information theory (Fortunato, 2010; Fortunato & Hric, 2016), all of which estimate to what extent the partition identified on a topological basis resembles a previously known partition based on metadata (e.g., genetic, developmental, and/or functional modules) or another algorithm. For example, in the context of morphological organizational modules, the normalized mutual information index (NMI, Danon, Díaz-Guilera, Duch, & Arenas, 2005) has been used to measure the similarity

between the modules identified in the networks of the human limbs and various hypotheses based on the function and developmental origin of bones and muscles (Diogo, Esteve-Altava, Smith, Boughner, & Rasskin-Gutman, 2015).

### 3 | STUDYING ORGANIZATIONAL MODULES USING NETWORK ANALYSIS

This section summarizes the process of creating an anatomical network model, and of identifying, validating, and comparing organizational modules using community detection algorithms and related methods. As working examples, we use the anatomical networks of the skull and of the upper limb skeleton of humans. First, we introduce the concept of network model and how it formalizes the organization of morphological parts. Then, we present alternative approaches to evaluate the quality of partitions and of individual modules, which we apply afterward to validate the modules identified using a classic community detection algorithm based on the structural equivalence or topological overlap of nodes (GTOM) (Ravasz, Somera, Mongru, Oltvai, & Barabási, 2002). As we will see, the results of this approach will highlight most of the challenges we face when studying modularity in anatomical networks. To tackle these challenges, we also explored the use of a more sophisticated community detection algorithm based on local optimization of statistically significant communities (OSLOM) (Lancichinetti, Radicchi, Ramasco, & Fortunato, 2011). We close these working examples by quantifying the similarity between network partitions and alternative partitions based on biological criteria, using information theory measurements. For the most part of the analysis we have used the free software *R* 3.3.1 and the package *igraph* 1.0.1, unless otherwise stated; the source *R* code and the network models are freely available at Figshare (<https://doi.org/10.6084/m9.figshare.4543246.v1>). The software to run OSLOM is available from the author's page ([www.oslom.org](http://www.oslom.org)).

#### 3.1 | Anatomical network modeling

A graph is a mathematical object that comprises a set of elements (vertices) and a set of pairwise-relations among elements (edges). A network is a graph with a nontrivial topology (e.g., not regular or random), although most often the terms graph and network are used as synonyms. Likewise, nodes ( $N$ ) and links ( $K$ ) are used as synonyms of vertices and edges, respectively. The simplest type of network is undirected (i.e., links have no direction) and unweighted (i.e., links are either present or absent). This network is mathematically formalized as a symmetric binary adjacency matrix ( $A_{ij}$ ) of dimension  $N \times N$ , in which the presence of a link between nodes  $i$  and  $j$  is coded as 1 and the absence as 0. The following sections describe the methods to analyze undirected, unweighted networks, but they can be easily adapted to deal with more complex networks (see help documents in the referred software).

An anatomical network is a mathematical model that formalizes the way in which body parts interact, and, as such, it captures the organization of a morphological system. For the purpose of building a network model, we need an operative definition of part as an element that

can be identified as isolated from others by means of its boundaries (Weiss, 1971). For example, bones are the parts of the skull, isolated and identifiable of other bones and tissues by their boundaries (e.g., sutures, synchondroses, periosteum, or cartilaginous joints). Parts interact together to form a system, which produces a particular behavior or biological function as a consequence of the coordination or interaction of parts, not fully determined by the properties of each part in isolation (Weiss, 1971). Following the previous example, the skull is a system composed of bone with a collective behavior in development, growth, function, and evolution. The way we define interactions or relations among parts depends on what type of questions (e.g., developmental, functional, evolutionary, etc.) we are asking.

Therefore, the first step in the modeling of a morphological system—or, as a matter of fact, any system—as a network is to identify the parts of the system, and the interaction or relation that we are interested in (Butts, 2009). It is convenient that parts and interactions have unique and clear definitions that allow us to track them throughout our system and across our sample. For example, if we are interested in comparing the skulls of two species, one having only bony parts and another having a mix of bony and cartilaginous parts, we would need to define the parts of the skull in our network models in a way that encompasses the two types of elements in our sample of skulls, such as skeletal parts instead of bones. Likewise, if we aim modeling all the physical contacts of the skull we would define link as a physical articulation or joint, instead of, exclusively, as a suture or as a synchondrosis. Ultimately, our choice of what is a part and an interaction determines the features of the network model. As in any scientific inquiry using mathematical models (Gunawardena, 2014), the construction of our model has to be appropriate for the questions we ask to our sample of study. This means that there is no single, correct representation of a morphological system as a network, but an appropriate one for the problem at hand.

Figure 1 shows the two working examples we use in the following sections: the network models of the human skull (first published in Esteve-Altava et al., 2011) and of the human upper limb (first published in Diogo et al., 2015), in which nodes represent bones and links represent their physical joints (i.e., in the skull, craniofacial sutures and synchondroses; in the limb, mainly synovial joints). The interactions modeled in these networks are topological relations (i.e., physical articulation) among bones. Topological relations (connections) might also embody developmental and functional interactions that take place between two body parts (although this is not a formal requirement for a purely structural analysis of the topology, i.e., how parts are connected). In these examples, topological relations intrinsically bear well-known biological functions, which is why they were chosen as the definition of link in the first place (Esteve-Altava et al., 2011; Rasskin-Gutman & Esteve-Altava, 2014). Connections among skull bones are primary sites of bone growth and remodeling, while connections among limb bones are mobile articulations and fulcra. We will use these two networks as working examples to describe the process of identifying, validating, and comparing organizational modules in anatomical networks.

Anatomical network models can be enriched with additional information of the body parts and the interactions. For example, the skeletal networks of our example could be enriched with weighed links according to measures of the area of contact; thus, instead of all links having a binary value 0 (absence) or 1 (presence), they will have the value of the contact area measured (between 0 and 1 if we normalized them). Such models would require extra effort to build, but they have the potential to be more accurate in their predictions. We can also build a network of the same body parts using other biological interactions: topological, such as tendons or muscle masses connecting them; or nontopological, such as tissue types or common developmental factors. For the same morphological system, there might be many potential network realizations, depending on the type of interactions we are interested on. The choosing of one realization over others will vary with the morphological problem we aim to address. For example, a study on the growth patterns of the skull could use the same realization of the skull as in our example, while a study on the biomechanical performance of limbs would benefit from using a different network realization using shared muscles as connections rather than physical contact. Of course, the results of a network analysis, even using the same algorithms, are specific of the network realization we decide to use (i.e., our definition of what is a node and what is a link, see above). For this reason, we have to interpret the results of the analysis according to the information we used to create the network model (as in Section 3.5). For example, if we used interactions that capture growth information the outcome network modules will be growth modules, whereas if we used interactions that capture biomechanical information the outcome modules will be functional modules. The possibilities of AnNA are endless and will ultimately depend on the questions we are asking to the model and the type (and biological role) of the relations or interactions we consider. Additional network methods can also be used to attempt the reconstruction of incomplete networks (e.g., in fossils) using Bayesian inference tools (Guimerà & Sales-Pardo, 2009). The methods described in the following sections apply similarly to any realization of the network.

### 3.2 | Definition of module and validation partitions

A module (i.e., a community in network theory) is a subset of nodes more strongly connected with each other than with nodes outside the subset. To estimate how well a given partition of the network identifies the modules, Newman and Girvan (2004) defined the parameter *modularity* (commonly referred as  $Q$ ),

$$Q = \sum_{s=1}^m \left[ \frac{k_s}{K} - \left( \frac{d_s}{2K} \right)^2 \right], \quad (1)$$

where  $m$  is the number of modules of the partition,  $k_s$  is the number of links within module  $s$ ,  $d_s$  is the total number of links of nodes in  $s$  (both inside and outside  $s$ ), and  $K$  is the total number of links in the network.

The parameter  $Q$  quantifies how strongly connected are the modules identified compared to a randomization of the network.  $Q$  is 0 when the number of links within modules is no greater than expected in the randomization; higher values indicate a stronger modularity than expected, being  $Q = 1$  the theoretical maximum. In practice, Newman

and Girvan reported that strongly modular networks show values between 0.3 and 0.7. The expected error of  $Q$  can be calculated using a jackknife procedure where each link is considered as an independent observation. It is worth noticing that the value of  $Q$  is specific of each partition and network; thus, we can use it to compare among different partitions of a same network, but not to compare two different networks. In short, one network is not *more modular* than another because it has a higher value of  $Q$  for its best partition.

Equation 1 also includes the condition that one group of nodes has to fulfill to be a module, that is, having relatively more connections within the module than outside, which corresponds with the definition of module:

$$\frac{k_s}{K} - \left( \frac{d_s}{2K} \right)^2 > 0. \quad (2)$$

As a consequence, it is possible to have a partition of a network in which not all groups of nodes are modules according to Equation 2. In turn, individual modules fulfilling Equation 2 might have, in turn, sub-modules that also fulfill Equation 2, but where not identified by the community detection algorithm. This situation produces a resolution limit in those community algorithms that directly or indirectly seek to find the partition of the network that renders the maximum modularity (Fortunato & Barthelemy, 2007). The underlying reason of this resolution limit is precisely that most networks have a hierarchical grouping of nodes into nested submodules. Alternatively, we can also validate each module of a partition statistically, for example, using a Wilcoxon rank-sum test on internal ( $k_s$ ) versus external ( $d_s - k_s$ ) number of links. Here, we test the null hypothesis that there is no statistical difference between the number of internal and external links against the alternative hypothesis that the number of internal links is greater than the number of external links (i.e., the definition of a module). In our example, we used the Wilcoxon rank-sum on the modules identified by the first of the community detection algorithms used.

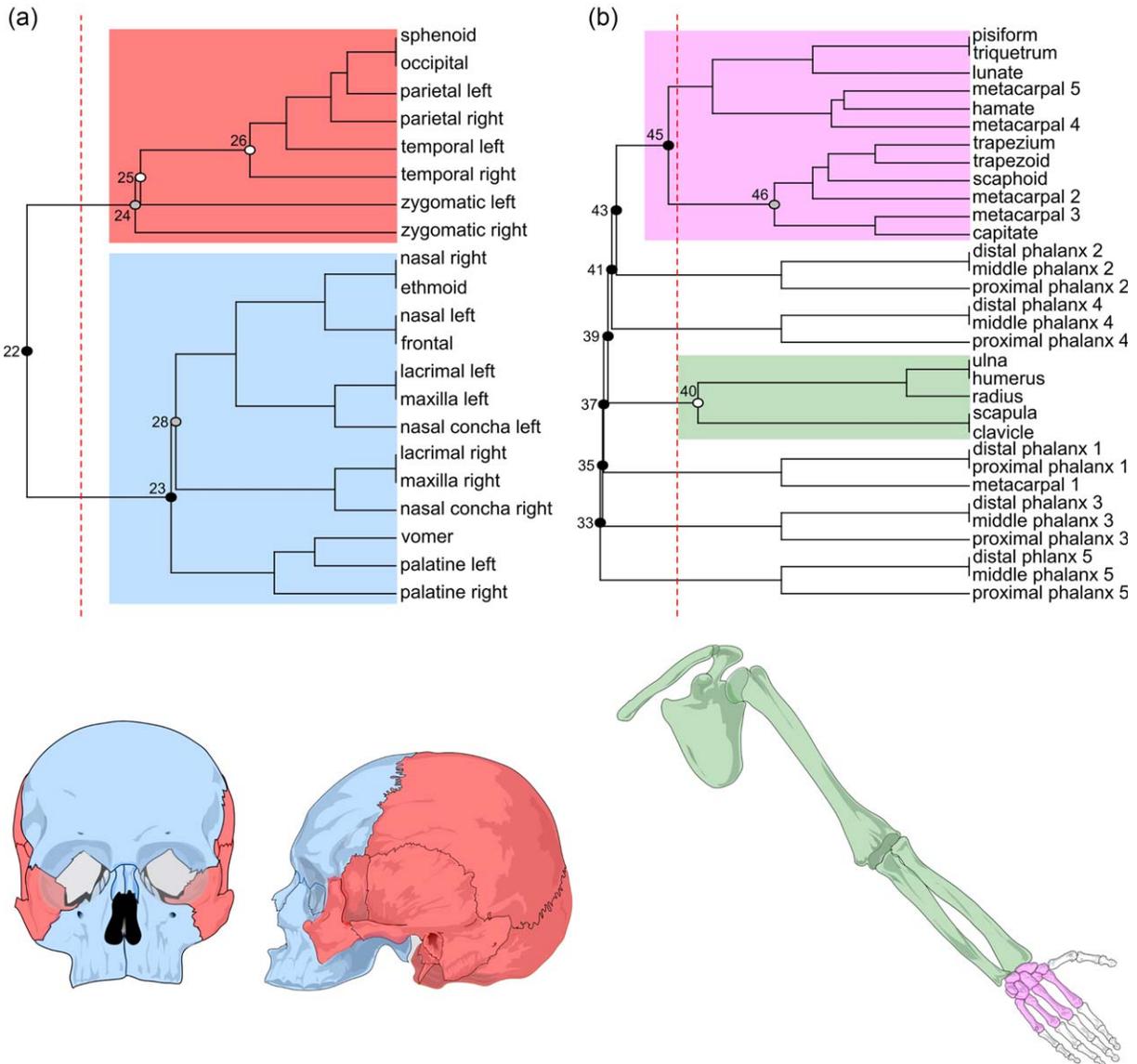
### 3.3 | Identifying modules with community detection algorithms

The first community detection algorithm shown is based on a hierarchical clustering of the generalized topological overlap similarity matrix among nodes (GTOM) (Ravasz et al., 2002), which is a classic method that uses a heuristic approach to identify modules. Heuristic methods are designed to overcome the otherwise computationally costly task of seeking and evaluating all the possible partitions of the network, by using an *a priori* reasoning of which nodes we would expect to group together. The heuristic of GTOM is that nodes that connect to the same other nodes (i.e., share neighbors) have a higher chance of belonging to the same module.

The topological overlap between two nodes is the number of common neighbors between two nodes, defined as

$$TO_{ij} = TO_{ji} = \frac{J(n_i, n_j)}{\min(k_i, k_j)}, \quad (3)$$

where  $J(n_i, n_j)$  is the number of neighbors in common between nodes  $i$  and  $j$ .  $TO$  is 1 when the two nodes share all their neighbors, that is,



**FIGURE 2** Modules identified with GTOM in the human skull (a) and upper limb networks (b). The dendrogram grouping the bones comes from the hierarchical cluster analysis of the TOM. The perpendicular dashed line in red indicates the partition of the dendrogram having the highest modularity (skull:  $Q_{max} = 0.27$ ,  $Q_{error} = .05$ ; upper limb:  $Q_{max} = 0.52$ ,  $Q_{error} = .08$ ). The circles on each bifurcation of the dendrogram indicate the statistical significance of that cluster in a Wilcoxon rank-sum test of internal versus external connections: *black*,  $p$  value  $< .001$ ; *gray*,  $p$  value  $< .01$ ; *white*,  $p$  value  $< 0.5$ ; bifurcations without a circle are nonsignificant

they connect to exactly the same other nodes. TO is 0 when the two nodes have no neighbor in common. By calculating the topological overlap over all pairs of nodes we get the GTOM, which is equivalent to a distance or dissimilarity matrix.

We can group nodes into clusters by using an agglomerative hierarchical cluster analysis on GTOM (in our example we used the average-linkage as in Esteve-Altava et al., 2013; Ravasz et al., 2002). The output is a hierarchical grouping of nodes, as in the two dendrograms shown in Figure 2. To identify the modules of the network we need then to decide at what level to cut the dendrogram. To make this decision we used (as it is customary in most hierarchical algorithms) the parameter Q explained before (Equation 1). Thus, we measured Q for each possible partition of the dendrogram to identify the best partition,

which is the one having the highest Q or  $Q_{max}$  (Figure 2; perpendicular dashed line in red). We can then calculate the statistical significance of each module or, as it is the case, of any cluster of the dendrogram, to evaluate the quality of each individual module identified by cutting the dendrogram at the level of  $Q_{max}$  (Figure 2; circles on the dendrogram clusters).

Using the GTOM algorithm the human skull network shows a relatively weak ( $Q_{max} < 0.3$ ) modular partition in two modules. One module groups mainly the bones of the neurocranium (cranial base and vault) and the other groups the bones of the face (Figure 2a, in red and blue, respectively). Both modules (Clusters 24 and 23 in the dendrogram) are statistically significant, and include some submodules that are also significant (Clusters 26 and 28) together with nonsignificant groups (e.g.,

vomer-palatines cluster) and singletons (e.g., the zygomatics). This pattern suggests that the human skull might have a partially hierarchical modularity, with some nodes having a lesser contribution. In contrast, the upper limb network shows a strong modular partition ( $Q_{\max} > 0.5$ ) in eight modules (Figure 2b). One module groups the bones of the pectoral girdle, stylopod, and zeugopod (in *green*); two modules group the bones of the wrist (in *purple*); and five modules group the phalanges of each of the five digits. However, only two of these modules are statistically significant (Clusters 40 and 46), which means that the GTOM algorithm returns weak (or potentially erroneous) modules as part of the best partition. Thus, we could ask whether it is possible to find higher in the hierarchy a significant module without nonsignificant sister modules, so that all modules identified are significant. For example, in Figure 2, the *purple* module corresponds to Cluster 45, which includes the significant Cluster 46 plus its sister cluster that is not significant. This shows that in a partition of the network using the  $Q_{\max}$  a significant module can split into two submodules, not all of which being significant. In fact, the only partition of the upper limb network where all its modules are significant is the one-module partition (Cluster 33), which would indicate that the whole network cannot be further divided into statistically significant modules (i.e., it is not modular, but fully integrated).

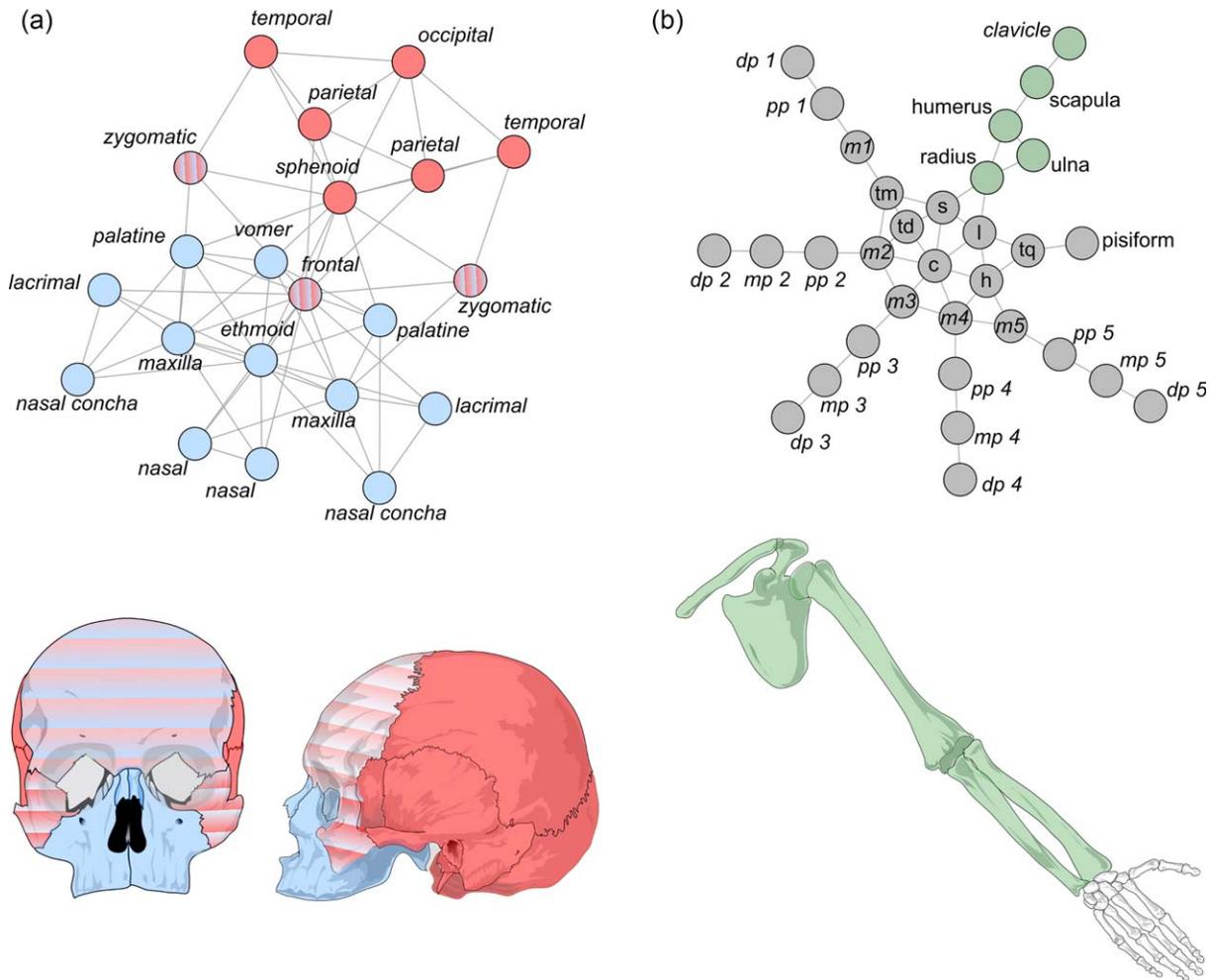
These examples illustrate two of the difficulties that the identification of modules in anatomical networks face: (1) the identification of weak partitions (as in the skull) and (2) of nonsignificant modules (as in the upper limb), which may be related to each other. The first difficulty is inherent to small size networks (e.g., tetrapod skull networks have between 20 and 60 nodes). The small size of networks hinders a correct statistical evaluation of their modules, in particular, when modules comprise only a few nodes (e.g., half of the modules of the upper limb had only three nodes); a small size also makes more difficult to discriminate between order and stochasticity in the connectivity patterns of the whole network. The second difficulty is imposed by the algorithm we choose. Many algorithms deal with the identification of rather simplistic modular organizations, placing aside (or underestimating) the presence of nested or overlapping modules, or even a partial or total lack of modularity. For example, it is possible that the anatomical networks of our examples are not truly hierarchical at this level, or that there is some degree of overlapping between their modules, or that these networks are not modular in part or in its wholeness after all.

To tackle these difficulties we used a second community detection algorithm based on the local optimization of statistically significant communities (OSLOM, Lancichinetti et al., 2011). OSLOM is specifically designed to identify significant modules locally, as well as the presence of hierarchical organization, overlapping modules (i.e., covers), partial modularity, and singletons (i.e., nodes not assigned to any module). Here, the module's significance is taken as a fitness function that measures the probability of that module in a network without modularity (i.e., a randomization of the empirical network that keeps the same degree distribution). This probability ( $bs$ ) is returned for every module identified as an estimation of the probability to find this module in the

randomized network. In short, the algorithm optimizes the module's significance by iteratively adding and deleting nodes, looking for the most significant configuration available. This process is then iterated at a higher level to look for hierarchical groups. Because OSLOM evaluates the significance of modules individually, it can recover overlapping modules. Moreover, because the algorithm focuses on how individual nodes rise or lower the local significance of modules, it can also identify nodes (or groups of nodes) that do not fit within any module (i.e., singletons).

In contrast to the first community detection algorithm presented, OSLOM is stochastic, which means that the output results may vary from one run to another. OSLOM returns the results of the majority consensus, that is, the result found in more than 50% of the runs. Finally, two parameters need to be specified explicitly: the *tolerance*, which controls the significance threshold of modules; and the *coverage*, which controls whether to merge or to split submodules; together they affect the number of modules identified and their size. The authors advise that if the network lacks of a well-defined modularity, the choice of parameters values might affect the results. Thus, for each anatomical network we ran 1000 iterations, setting the coverage to 0.5 (the default value of the program), and testing tolerances between 0.1 (default) and 0.5.

OSLOM returns two overlapping modules in the human skull network and one module plus a group of singletons in the upper limb network (Figure 3). For the skull network, OSLOM returns a slightly different arrangement of modules depending on the value of tolerance (Figure 4). For tolerance = 0.1, it returns no modules, which indicates that the network is highly integrated. For tolerance = 0.11, it identifies a *core-cranial module* that includes the occipital, sphenoid, parietal, and temporal bones ( $bs = 0.017$ ). For larger values of tolerance (between 0.12 and 0.2), it identifies two modules that are similar to the cranial and facial modules identified by the first algorithm. In all instances, the cranial and the facial modules overlap in the frontal and zygomatic bones, which are shared between the modules. Interestingly, in most cases only one of the two zygomatic bones (left or right) participates in the overlap, which one does it specifically varies from run to run, but since both have equally connected to both modules this difference is trivial. For this reason we consider both zygomatic bones as part of the overlap between the modules (Figure 3a). Sporadically, for tolerance = 0.2, a broader overlap occurs which also includes the sphenoid bone (Figure 4; *blue circle*). In general, the cranial module has a better estimated posterior significance than the facial module for all tolerance values, which means that a module like the cranial one is less likely to occur in a randomized network. In contrast, for the upper limb network, OSLOM returns only one module ( $bs = 0.153$ ) grouping together the bones of the girdle, the stylopod (humerus), and the zeugopod (radius and ulna); while all the bones of the autopod (wrist and fingers) are not assigned to any module (i.e., they are singletons, see above). The one module identified corresponds to the statistically significant module identified using the GTOM algorithm (Figure 2b; Cluster 40, in *green*); the other nonsignificant modules identified using GTOM are not returned by OSLOM, where these bones are singletons (Figure 3b, in *gray*).



**FIGURE 3** Modules identified with OSLOM in the human skull (a) and upper limb networks (b). For the skull, two modules were identified, one cranial (red) and one facial (blue), which overlap at the frontal and zygomatic bones (red–blue gradient pattern). For the upper limb, only one module was identified (green), while the rest of the bones do not form a module (gray)

### 3.4 | Comparing between two partitions (or how to test a $H_0$ )

We compared the partition of the skull and upper limb networks identified with the two algorithms to alternative partitions based on different developmental criteria. For the skull (Table 2), we compared the partitions by GTOM and OSLOM to a partition of bones by their ossification mechanism (dermal, endochondral, and mixed) and to a partition of bones based on their cellular origin (mesoderm, neural crest, and mixed). For the upper limb (Table 3), we compared the partitions by GTOM and OSLOM to two partitions of the limb based on its developmental patterning, the traditional one (girdle, stylopod, zeugopod, and autopod) and a variant that also includes the mesopod region (girdle, stylopod, zeugopod, mesopod, and autopod). For simplicity, we considered all the singletons of the upper limb (i.e., bones not assigned to any module) as forming one module of their own.

We compared partitions using an index based on information theory, the *normalized mutual information index* (NMI) (Danon et al., 2005). The normalized mutual information index measures the similar-

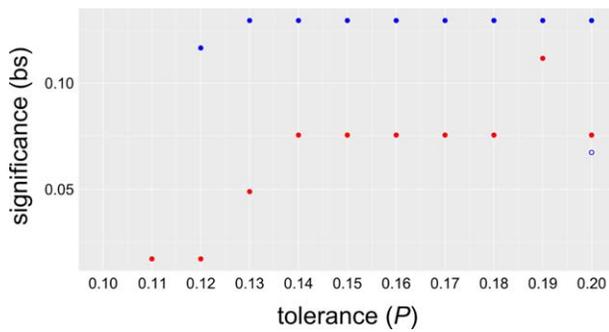
ity of two partitions based on the additional amount of information needed to infer one partition from the other (similar partitions would need less information) and normalizes it by dividing by the arithmetic mean of the entropy of both partitions as

$$I_{\text{norm}}(P_1, P_2) = \frac{2(H(P_1) - H(P_1|P_2))}{H(P_1) + H(P_2)}, \quad (4)$$

where  $H(P_1)$  is the Shannon entropy of the first partition and  $H(P_1|P_2)$  is the conditional entropy of the first partition given the second partition. NMI is 1 when the two partitions are identical, and it is 0 when they are totally different. For convenience we express the similarity between to partitions in percentages.

The partitions of the skull based on the ossification mechanism and on the cellular origin of bones are different, 46.8% similarity, which is almost half of the similarity between the results of GTOM and OSLOM, 70.8%.

This result is expected because the two latter partitions are both based on topology (GTOM vs. OSLOM), whereas the two developmental partitions are based on different criteria (ossification vs. cell origin).



**FIGURE 4** Significance of the cranial (red dots) and facial module (blue dots) identified with OSLOM for a range of tolerance values. The facial module is only identified for tolerances greater than 0.11 and always with a significance higher than the cranial module. The blue circle indicates the value of an alternative, less frequent facial module that includes also the sphenoid bone (see Main Text)

Partitions by GTOM and OSLOM are more similar to that based on cellular origin of bones, 52.6% and 68.3%, respectively, than to that based on ossification mechanism of bones, 24.7% and 30.8%, respectively.

In both comparisons, OSLOM outperforms GTOM in identifying a division of the human skull similar to those based on developmental criteria.

The partitions of the upper limb based on the alternative developmental patterning of the limb (with and without a mesopod) are similar, as we would expect, 70.8%, which is almost the double of the similarity between partitions of GTOM and OSLOM, 35.2%. It is surprising here the low similarity between both algorithms, which might be related with the number of modules identified by each algorithm, seven and one, respectively. The partition by GTOM is more similar to that of the developmental patterning with the mesopod, 45.1%, than without the mesopod, 33%; whereas the partition by OSLOM is more similar to that without the mesopod, 84%, than with the mesopod, 56.1%. In both cases, again, OSLOM outperforms GTOM in identifying a division of the human upper limb similar to those based on developmental patterning.

### 3.5 | Biological interpretation of network-based organizational modules

What does it mean for a group of bones to be in a same network module? The answer to that question depends on what are the actual biological functions of the topological interactions or relations that we formalized as the network links (see Section 3.1). This is best illustrated by our example of the human skull, which consistently shows a modular partition in two modules, one grouping the bones of the cranial vault and base (cranial module) and one grouping the bones of the face (facial module). We built the network model of the human skull by formalizing craniofacial sutures and synchondroses as the links of the networks. Among the most important functions of the sutures and synchondroses of the skull is to act as primary sites of bone growth and remodeling (Lieberman, 2011; Opperman, 2000; Rice, 2008). In other words, a link represents a shared (i.e., correlated) growth of the

two bones linked. Because a network module is a group of bones more densely connected among them than to other bones outside the module, bones that belong to the same module share more growth relations among them (on average) than with other bones. Thus, we interpret the facial and cranial modules as semi-independent units of growth (Esteve-Altava et al., 2013). Alternative interpretations of network modules are possible because connections among anatomical parts rarely carry one single biological function. For example, in addition to being growth sites, we know that connections among skull bones have an also an important biomechanical role, being key actors in processes of stress diffusion and tension release (Curtis, Jones, Evans, O'higgins, & Fagan, 2013; Moazen et al., 2009; Rafferty, Herring, & Marshall, 2003). In this context, we interpret the cranial and facial modules of the skull also as semi-independent biomechanical units.

Our example of the upper limb network is useful to illustrate the *a posteriori* interpretation of modules as evolutionary units or as constraints to evolvability. In the upper limb, both algorithms identify a well-defined module comprising the bones of the girdle, stylopod, and zeugopod; but algorithms differ in how to group the bones of the autopod. GTOM groups them in seven different modules, whereas OSLOM finds they are all singletons with not clear modular organization. The fact that most of the autopod modules identified by GTOM are not significant supports the result of OSLOM. In the upper limb network, links represent physical articulation, via cartilaginous joints, among bones. This pattern of articulation in the limb is highly conserved in evolution, and deviations of this connectivity pattern to accommodate functional adaptations of the upper limb (e.g., to run, burrow, flight, swim, etc.) take place mostly at the autopod level (Lewis, 1989). In fact, a similar pattern of connections between the girdle, stylopod, and zeugopod bones is already present in Devonian tetrapodomorphs, which lack of a well-defined autopod (Clack, 2009). Thus, we can interpret this module as a highly integrated evolutionary unit, which imposes a constraint to its evolvability. In contrast, the bones of the autopod do not group in a

**TABLE 2** Divisions of the human skull compared

Bone	Ossification	Cell origin	GTOM	OSLOM
<i>Occipital</i>	Mixed	Mesoderm	Cranial	Cranial
<i>Parietals</i>	Dermal	Mesoderm	Cranial	Cranial
<i>Temporals</i>	Mixed	Mixed	Cranial	Cranial
<i>Sphenoid</i>	Endochondral	Mixed	Cranial	Cranial
<i>Zygomatics</i>	Dermal	Neural crest	Cranial	Overlap
<i>Frontal</i>	Dermal	Neural crest	Facial	Overlap
<i>Ethmoidal</i>	Endochondral	Neural crest	Facial	Facial
<i>Nasals</i>	Dermal	Neural crest	Facial	Facial
<i>Maxillas</i>	Dermal	Neural crest	Facial	Facial
<i>Lacrimals</i>	Dermal	Neural crest	Facial	Facial
<i>Palatines</i>	Dermal	Neural crest	Facial	Facial
<i>Nasal conchae</i>	Dermal	Neural crest	Facial	Facial
<i>Vomer</i>	Dermal	Neural crest	Facial	Facial

TABLE 3 Divisions of the human upper limb compared

Bone	Dev. pattern I	Dev. pattern II	GTOM	OSLOM
Clavicle	Girdle	Girdle	Cluster 40	Module
Scapula	Girdle	Girdle	Cluster 40	Module
Humerus	Stylopod	Stylopod	Cluster 40	Module
Radius	Zeugopod	Zeugopod	Cluster 40	Module
Ulna	Zeugopod	Zeugopod	Cluster 40	Module
Trapezoid	Autopod	Mesopod	Cluster 46	Singleton
Trapezium	Autopod	Mesopod	Cluster 46	Singleton
Scaphoid	Autopod	Mesopod	Cluster 46	Singleton
Lunate	Autopod	Mesopod	Cluster 45 ( <i>ns</i> branch)	Singleton
Triquetrum	Autopod	Mesopod	Cluster 45 ( <i>ns</i> branch)	Singleton
Pisiform	Autopod	Mesopod	Cluster 45 ( <i>ns</i> branch)	Singleton
Hamate	Autopod	Mesopod	Cluster 45 ( <i>ns</i> branch)	Singleton
Capitate	Autopod	Mesopod	Cluster 46	Singleton
Metacarpal 1	Autopod	Autopod	Digit 1	Singleton
Metacarpal 2	Autopod	Autopod	Cluster 46	Singleton
Metacarpal 3	Autopod	Autopod	Cluster 46	Singleton
Metacarpal 4	Autopod	Autopod	Cluster 45 ( <i>ns</i> branch)	Singleton
Metacarpal 5	Autopod	Autopod	Cluster 45 ( <i>ns</i> branch)	Singleton
Proximal phalanx 1	Autopod	Autopod	digit 1	Singleton
Distal phalanx 1	Autopod	Autopod	digit 1	Singleton
Proximal phalanx 2	Autopod	Autopod	digit 2	Singleton
Middle phalanx 2	Autopod	Autopod	digit 2	Singleton
Distal phalanx 2	Autopod	Autopod	digit 2	Singleton
Proximal phalanx 3	Autopod	Autopod	digit 3	Singleton
Middle phalanx 3	Autopod	Autopod	digit 3	Singleton
Distal phalanx 3	Autopod	Autopod	digit 3	Singleton
Proximal phalanx 4	Autopod	Autopod	digit 4	Singleton
Middle phalanx 4	Autopod	Autopod	digit 4	Singleton
Distal phalanx 4	Autopod	Autopod	digit 4	Singleton
Proximal phalanx 5	Autopod	Autopod	digit 5	Singleton
Middle phalanx 5	Autopod	Autopod	digit 5	Singleton
Distal phalanx 5	Autopod	Autopod	digit 5	Singleton

*ns*, nonsignificant.

module, being more free to vary semi-independently of the proximal module and to accommodate functional needs without disrupting more proximal structures. This might suggest that the autopod can evolve semi-independently of the rest of the limb, which supports the idea of the autopod as an evolutionary novelty in tetrapods (albeit its developmental homologies with fin rays, e.g., see Nakamura, Gehrke, Lemberg, Szymaszek, & Shubin, 2016).

#### 4 | BRIDGING THE GAP BETWEEN VARIATIONAL AND ORGANIZATIONAL MODULARITY

Are shape-variational modules causally related to topology-organizational modules? The answer to that question depends on the existence of an actual relationship between shape and topology in the

generation of organismal forms. Some sort of relation exist between shape and topology due to the fact that landmarks covariation is constrained by the topological contiguity of the body parts on which landmarks are located (Chernoff & Magwene, 1999; Klingenberg, 2009; Magwene, 2001, 2008). This was first reported in a study on the factors determining individual bone shapes covariation in the human skull by Pearson and Woo (1935), who found that contiguity (i.e., adjacency or connection) between two bones correlates with a covariation of shape between them. This study showed that the adjacency of bones (i.e., a connection in a network model) is the most important factor, after symmetry, in explaining the co-variation in shape of two skull bones. Unfortunately, the correlation between topology and shape has not been the subject of further experimental studies since then. As a consequence, it is unknown whether this correlation comes from a one-way causation (from topology to shape or the other way around) or from a two-way causal relationship; furthermore, it is possible that this correlation is caused by a third factor acting on both features (e.g., growth), or even, it might be an artificial correlation due to flaws in the design of Pearson's experiment.

The simplest way to explore whether shape-variational modules match with topology-organizational modules is to use organizational modules as null hypothesis of shape variation, to be tested with morphometric methods—a task easier said than done. This hypothesis assumes that organizational modules, as derived from a network analysis of body parts, act as a map of correlations or co-variations imposing structural constraints on shape. Additionally, we might use an exploratory morphometric analysis to group bones according to their shape correlation and then use a similarity test, as the one shown in the previous section, to validate the match of both partitions. In any case, a well-rounded confirmatory analysis would use both validation approaches, ideally, using independent data sets.

Finally, information on shape variation might be directly included in the construction of the anatomical network model, so it is taken into account when we perform the community detection. For example, shape covariation of two bones might be used to weight their connection; thus, we would have a weighted anatomical network where each link represent a topological connection pondered by the actual shape covariation between the two bones. Since we only use the covariation of connected nodes, the resulting mathematical object would be different of a direct network of the matrix of correlations (as in Perez et al., 2009; Suzuki, 2013).

## 5 | ALTERNATIVE MODELING APPROACHES AND THE COMPARISON CHALLENGE

The way anatomical parts (cells, tissues, organs) are organized to form the body makes most morphological systems relatively easy to model as networks. An iconic anatomical network is precisely that of the brain. Not surprisingly, neuroanatomy was the first morphology-related field to apply network models and analyses, and has contributed deeply to the popularity and development of network sciences at large

(Sporns, 2011). In a brain network, nodes usually represent neurons or brain regions and links represent synaptic connections or co-activation patterns (e.g., from fMRIs). It was precisely in the context of neurosciences that the concept of anatomical networks first emerged highlighting the tight relationship between brain functions and physical connections of neurons or neuronal regions (see e.g., Jackson, Marrocco, & Posner, 1994; reviewed in Bullmore & Sporns, 2009). Similar ideas were later introduced in the context of vertebrate morphology to study the gross anatomy of the pelvis and skull of archosaurs (Rasskin-Gutman, 2003; Rasskin-Gutman & Buscalioni, 2001). In the last years, other morphological systems have been also studied using network models and tools. We have reviewed some examples of that in this essay, for example, in studying the organization of the vertebrate skeleton (Rasskin-Gutman & Esteve-Altava, 2014). As we already saw, in a skeletal network, nodes represent bones and links represent their physical articulation (but other interactions can be modeled as well, see Section 3.1 for discussion). Network models have also been applied to morphological comparative studies of invertebrates, such as echinoderms (Laffont et al., 2011; Saucède et al., 2015), in which nodes represented apical plates and links represented their physical arrangement. More recently, network models have been applied to study musculoskeletal systems in vertebrates for evolutionary and medical purposes (Diogo et al., 2015; Esteve-Altava, Diogo, Smith, Boughner, & Rasskin-Gutman, 2015; Murphy et al., 2016). In a musculoskeletal network, nodes represent muscles and/or bones and links can represent different type of relations among them (see below). As network tools grow in sophistication and the interests in anatomical networks diversify, new alternative approaches to the modeling of anatomical systems emerge to cope with new morphological problems.

The emergence of alternative approaches posits a challenge to the comparison of results from different studies, which might use not only different network tools but also model the same morphological system in different ways (e.g., using different criteria to define nodes and connections, see Section 3.1). For example, the limb skeleton as modeled in our example is only one of the possible realizations of the general organization of the limb. One in which the relation of bones is solely assessed by the way they are physically interacting at their articulation. This is useful when we do not have information about soft tissues, for example, when comparing extant and extinct taxa. However, an alternative realization of the skeletal network (using the same bones as nodes) would be obtained by modeling muscular attachments as links (i.e., two bones connect if a same muscle attach to them). Rather than seeing alternative realizations as an epistemological problem—which it is not (Butts, 2009)—they offer a unique opportunity to study different properties of the same system at different scales of organization and how they relate to each other. For instance, the skeletal network of bones connected by articulations might be more informative of some developmental processes, growth, and shape change, while the network of bones connected by muscles might embody more functional and biomechanical information. In addition, the same network realization can be fine-tuned by weighting the links among bones with a measure of their strength of interaction (e.g., area of contact, type of

articulation) rather than a binary present/absence coding, generating yet another network (discussed in Section 3.1). Inevitably, the same analyses run on different realizations of the network (or different network models of the same system) will yield different results, which we must interpret in the light of the type of relations modeled as links (as in Section 3.5). Moreover, because the morphological systems modeled are not static structures but develop continuously in ontogeny, we can create series of network models that capture the same morphological system through its development. Likewise ontogenetic trajectories in variational modules (Mitteroecker & Bookstein, 2009), network models of different developmental stages will also change at different stages. Such approach would open the door to studying organizational modularity as it develops.

The many ways in which the same morphological system can be modeled as a network do not diminish AnNA, but it opens the range of potential problems we can address with this method. Two recent publications (Diogo et al., 2015; Murphy et al., 2016) on the musculoskeletal organization of the human body show the synergy between different approaches within this framework, as well as the potential intertwine between musculoskeletal network and neuronal network approaches. Among other topics, these two studies deal with the division of the musculoskeletal system of the human body into morphological modules. The work by Diogo et al. compared the similarity of the modular organization of the upper and lower limbs between normal human morphology and pathological conditions derived from chromosome dosage disorders. To this end, Diogo et al. modeled human limbs as undirected, unweighted networks in which nodes represented bones and muscles, and links represented all forms of physical connections among them, such as articulations, attachments, and blending. The authors found key differences between upper and lower limbs in humans, but striking similarities in the way normal and pathological morphology are organized. Furthermore, the musculoskeletal modules identified in normal and pathological conditions resembled those predicted by developmental criteria. Conversely, Murphy et al. compared the modules identified in the muscular network to primary motor cortex somatotopic areas of the brain. Murphy et al. created the muscular network using a different formalism than the one used in Diogo et al. study. Here, the authors modeled the body as a hyper-network, in which nodes represented sites of muscles origin and insertion in the skeleton (e.g., external occipital protuberance, coracoid process of the scapula, iliac crest) rather than individual bones; while links represented muscular masses or muscular groups (e.g., lumbricals) connecting these sites. Since one muscle can attach to more than two sites (e.g., by having several heads) muscles in this network realization connect to multiple bones (hyper-links); hence the name of hyper-network. To obtain the muscular network, the hyper-network was transformed so that nodes represented muscles and links represented common attachment points. A modularity optimization algorithm (see Equation 1) was used to identify the modules of this muscular network. The authors found that muscular modules identified in the network model robustly resembled the organization of motor cortex control modules in the brain. These two studies depart from a very different approach to the

modeling of musculoskeletal networks, and yet they can be analyzed with similar tools and yield comparable, complementary results of a same general morphological problem: what factors determine the muscular organization of the human body. Together these studies suggest the possible presence of a conserved motor control of the limb muscles between normal and pathological conditions (even in functionally impaired limbs). This is an interesting observation with the potential to generate new research opportunities in the study of the human body, from a medical but also evolutionary perspective. How this the cortex-muscle modularity coupling emerged? Is it different in other species? What are the consequences for brain injuries and recovery by physical therapy? The possibilities of combining the results of AnNA using different network realizations of a same morphological system, or from to morphological systems (e.g., brain and muscles) is not a handicap of the method, but an opportunity worth taking.

## 6 | CONCLUDING REMARKS

Morphological systems have a multilevel modularity, which is not limited to the underlying modularity of their generative processes and their consequences on shape and function, but it is also manifested at a morphological level in the structural organization of body parts. Anatomical network models and their analysis using community detection algorithms offer a new, complementary set of tools to delimit morphological modules, and study how they change in development and evolution, how they function, and how they relate to modules at other levels of organization. We face the challenge now to further develop these tools in morphology, revealing the causal connections between growth, development, structure, shape, and function in the origin and evolution of organismal forms.

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