

Human Skull Network Model

Esteve Altava, B. ¹, Marugán Lobón, J. ², Botella Sevilla, H. ^{1,3} y Rasskin Gutman, D. ¹

After biologists of all fields have finally recognized that their object of study are complex systems, the science of networks analysis have started to appear as an important methodological tool. Thus, we have witnessed quite recently an authentic boom in the use of network analysis in such disparate fields as biochemistry, molecular genetics, metabolism, structural biology, and ecology. However a seemingly natural arena to use this mathematical and statistical tool such as comparative anatomy has not been analyzed in terms of network structure.

Comparative anatomy offers suitable kinds of data that can be analyzed within a network framework. There is no doubt about the importance of connections between anatomical elements for the recognition of homologies. Thus, the fathers of comparative anatomy as George Cuvier, Geoffroy St. Hilaire and Adolf Remane used the connectivity concept for recognizing structural identities between related organisms, see Riedl (1978). Nevertheless, less efforts has been devoted to construct a comparative framework that will be able to use connectivity patterns as a morphological organization level fully operative, although several ideas had been developed in this direction in the past, see for example Woodger (1945), Rashvesky (1954), Riedl (1978), and more recently Rasskin-Gutman (2003).

Mathematically, a network is a set of vertices connected by edges. Each vertex represents one element of the system and while its edges are functional or structural relationships with other elements.

While several concepts in network theory have an intuitive anatomical interpretation, such as nodes as bones or links as junctions, many other concepts have mathematical expressions for which a direct anatomical interpretation is not possible. By themselves, these mathematical abstractions allow to characterize network models, but their anatomical interpretation is need to extract key morphological information and to understand the sutructure of the real system (tabla resumen conceptos).

Similarities in the network organization of different complex biological systems will indicate that them are governed by “generic organization principles and mechanisms” according to Wuchty *et al.* (2006). Several processes has been suggested as causes of each specific kind of network structure, such as preferential attachment rules for scale-free network, or rewiring for small-world, among other growing rules for more complex network structures, see Dorogovtsev & Mendes (2003).

Aim

We present a new way to study the structure of the human skull using network theory. A framework easily extended to other vertebrate. The physical articulation and junctions among skeletal parts in vertebrate offer a unique anatomical database to dwell into structural relationships and ask macroevolutionary, morphological and developmental questions about them. We present a new way to study the structure of the human skull using network theory. A framework easily extended to other vertebrate.

How do we proceed to construct a network model?

In the process of abstraction followed in the generation of a morphological network framework, each bone correspond to a node and the physical junctions between bones (sutures

in the skull) are represented as links that connected nodes. As a result we have a complete substructural abstraction representing the connections among nodes, which represents direct physical contact among bones.

Human cranial network model has 20 nodes corresponding to the following bones: Ethmoid, frontal, sphenoid, right maxilla, left maxilla, nasal concha, occipital, right palatine, left palatine, vomer, right lacrimal, left lacrimal, right parietal, left parietal, right temporal, left temporal, right zygomatic, left zygomatic, right nasal, left nasal. Data were codified in an adjacency matrix, the binary matrix of presence/absence of bone junctions, where the node degree for each bone is the sum of its connections.

Our null model for comparative purposes is a random network model $G(n, p)$, Gilbert (1959), generated with the same number of nodes (n) and average degree in links per node (p) than the human cranial network, Watts & Strogatz (1999).

There are many available software to simulate network models and analyze their properties. We use the free software Network Workbench Tool, free available online.

Results and discussion

We find human skull is a scale-free structure characterized by a power-law degree distribution with an exponential factor $\gamma = 2.12$. System properties are mainly determined by the most connected elements, which are called hubs. Frontal, ethmoid and sphenoid are the most connected bones. Scale-free networks exhibits high robustness to random perturbation but are vulnerable to specific perturbation on their hubs, Albert *et al.* (2000). From a biological point of view, it implies that skull has a structural robustness against random changes affecting its integrity. Robustness is we expect in a substructure which protect the brain and sensory organs.

The main growing mechanism accounting for scale-free organization in large networks is the preferential attachment, where new nodes are attached to highly connected previous ones, Barabási & Albert (1999). The study of skull development in terms of network growing-rules will bring out key information about the specific mechanism leading its final scale-free structure.

The topological connectivity of cranial bones is neither regular nor random, but small-world. Information inside human skull system flows faster than in regular and random equivalent systems. So, skull evolves in an integrative way, and co-evolution of both cranial bones and modules is facilitated. That allows to integrate developmental and evolutionary information, such as constraints and natural selection pressures.

Finally, applying a dynamic algorithm to partition the skull network we have obtained the following structural units, in dorso-ventral order: (1) Palatal, (2) Ethmoidal, (3) Orbito-nasal, (4) Frontal, and (5) Cranial.

The Palatal unit is formed by the palatines and the vomer. These elements are always linked, defining the choana (the opening or pathway communicating the nasal opening to the pharynx). The Ethmoidal unit is formed by the maxillae, the ethmoid, and the nasal concha. This unit forms the roof of the mouth and the floor of the sinuses. The Orbito-nasal unit is formed by the lacrimals, nasals, and zygomatic arches. This structural unit delimits most of the orbits except for the roof, delimited by the independent Frontal unit, which is formed only by the frontal bone, being the roof of the orbits and the roof of the braincase. Finally, the Cranial unit is formed by the parietals, temporals, occipital and sphenoid. It forms the floor and the walls of the braincase.

By compactness analysis between structural units, we have found that, even the human skull is composed of five structural units, only three of them can be considered modules: Palatal, Ethmoidal and Cranial. The remain two, Frontal and Orbito-nasal, cannot be

considered modules because they lack enough internal compactedness, even though they show similar connectivity patterns as a part of a structural unit.

Concluding remarks

Network theory offers a new quantitative framework to study structural homologies and anatomical organization. In this work, we develop network methodology for anatomical systems, applying it to human skull structure, expanding previous work in vertebrate skulls structure analysis by Rasskin-Gutman (2003). The quantitative characterization of skull by means of network theory will bring out important features of its structural organization.

References

- Albert, R., Jeong, H. and Barabási, A.L. 2000. Diameter of the World Wide Web. *Nature* **401**, 130-131.
- Barabási A.L. and Albert, R. 1999. Emergence of scaling in random networks. *Science* **286**, 509.
- Gilbert, E.N. 1959. Random Graphs. *Annals of Mathematical Statistics* **30**, 1141-1144.
- Riedl, R. 1978. Order in Living Systems: A Systems Analysis of Evolution. Wiley, New York.
- Rashevsky, N. 1954. Topology and life. *Bulletin of Mathematical Biophysics* **16**, 317-348.
- Rasskin-Gutman, D. 2003. Boundary constraints for the emergence of form. In: *Origination of Organisma Form* (Eds. G. Muller and S. Newman). MIT Press, Cambridge, 305-322.
- Watts, D.J. and Strogatz, S.H. 1998. Collective dynamics of 'small-world' networks. *Nature* **393**, 440-442.
- Woodger, J.H. 1945. On biological transformations. In: *Essays on Growth and Form presented to D'A. W. Thompson*, (Eds. Le Gros, W.E. and P.B. Medawar). Oxford University Press, Oxford.
- Wuchty, S. Ravasz, E. and Barabási A.L. 2006. The architecture of biological networks. In: *Complex Systems Science in Biomedicine* (Eds. T.S. Deisboeck and J.T. Kresh). Springer, Berlin, 165-181.
- Dorogovtsev, S.N and Mendes, J.F.F. 2003. Evolution of Networks: From Biological Nets to the Internet and WWW. Oxford University Press, New York.