CHAPTER

The human connectome from an evolutionary perspective

6

Dirk Jan Ardesch[a,*], Lianne H. Scholtens[a], Martijn P. van den Heuvel[a,b]

[a]*Connectome Lab, Department of Complex Trait Genetics, Center for Neurogenomics and Cognitive Research, Vrije Universiteit Amsterdam, Amsterdam Neuroscience, Amsterdam, The Netherlands*

[b]*Department of Clinical Genetics, Amsterdam UMC, Vrije Universiteit Amsterdam, Amsterdam Neuroscience, Amsterdam, The Netherlands*

**Corresponding author: Tel.: +31-20-59-82959, e-mail address: d.j.ardesch@vu.nl*

Abstract

The connectome describes the comprehensive set of neuronal connections of a species' central nervous system. Identifying the network characteristics of the human macroscale connectome and comparing these features with connectomes of other species provides insight into the evolution of human brain connectivity and its role in brain function. Several network properties of the human connectome are conserved across species, with emerging evidence also indicating potential human-specific adaptations of connectome topology. This review describes the human macroscale structural and functional connectome, focusing on common themes of brain wiring in the animal kingdom and network adaptations that may underlie human brain function. Evidence is drawn from comparative studies across a wide range of animal species, and from research comparing human brain wiring with that of non-human primates. Approaching the human connectome from a comparative perspective paves the way for network-level insights into the evolution of human brain structure and function.

Keywords

Connectome, Evolution, Comparative connectomics, Network, Graph theory, Human brain, Primate brain

1 Introduction

Human brain function is characterized by highly developed cognitive functions such as theory of mind and language (Berwick et al., 2013; Devaine et al., 2014). Understanding how this extended cognitive ability emerged during brain evolution is an important topic of research. Accelerated brain expansion, enlargement of cortical

Progress in Brain Research, Volume 250, ISSN 0079-6123, https://doi.org/10.1016/bs.pbr.2019.05.004

areas, and alterations at the cellular and genetic level have all been implicated as adaptations that define the human brain (e.g., Bird et al., 2007; Elston, 2011; Neubauer et al., 2018; Rilling, 2014; Zhu et al., 2018). Recently, adaptations have also been observed at the level of brain connectivity (Thiebaut de Schotten et al., 2018; van den Heuvel et al., 2016). The comprehensive set of neuronal connections in the brain forms a complex network known as the connectome. The connectome can be characterized using methods rooted in graph theory, a branch of mathematics that represents networks as collections of nodes and edges (Sporns et al., 2005). This approach has revealed network properties shared among connectomes, such as a capacity for efficient transfer of information between brain regions, but also subtle differences in brain network organization across species (Rubinov and Sporns, 2010; van den Heuvel et al., 2016).

The field of connectomics offers a new, network-based way to study brain evolution. It allows us to ask how brain function is shaped by the architecture of the brain's connections. Is the human connectome a scaled-up version of a general primate connectome blueprint, or does the exceptional size of the human brain require adaptations to the network to ensure efficient communication? Can we find specific network adaptations of the human connectome supporting the advanced cognitive repertoire of the human species, such as connectivity patterns adapted for high intelligence or complex language? And what are the limits imposed by the brain's biology on the structure and function of the human connectome? Finding answers to these questions will shed light on the evolution of human cognition and contributes insights to our fundamental understanding of the human brain.

The main aim of this chapter is to give an account of human macroscale brain connectivity from an evolutionary perspective. We argue that human brain wiring can be understood as a combination of (a) universal features of nervous systems that are widely shared across the animal kingdom and (b) species-specific features that represent adaptations to the specific environment in which the human brain evolved. To identify commonalities with other species, we outline the emerging network properties of the human connectome, followed by a discussion of the wiring principles proposed to guide connectome structure and function across species. We discuss evidence for potential specializations of the human connectome in relation to the evolution of advanced cognitive functions and possible implications of brain size and we conclude by pointing out challenges of the current methodology and directions for future investigation.

2 Mapping the human connectome

2.1 Connectome reconstruction

Magnetic resonance imaging (MRI) is among the most popular methods for reconstructing brain connectivity at the macroscale in humans, and has also been applied successfully to other species (Rilling, 2014; Thiebaut de Schotten et al., 2018). Diffusion-weighted MRI (DWI) is used extensively to map the structural

connectome in humans (Glasser et al., 2016; Sarwar et al., 2019), and methods such as resting-state functional MRI (rs-fMRI) are used to probe the functional connectome based on temporal correlations between brain regions (for review, see Smith et al., 2013) (Fig. 1A). Macroscale brain networks can be reconstructed by combining neuroimaging data with a regional parcellation of the brain. Parcellations can be based on a priori brain atlases (Desikan et al., 2006; Scholtens et al., 2018), gradients of connectivity fingerprints (Mars et al., 2018b), or randomly placed parcels of equal size (Hagmann et al., 2007)—each with their own strengths and limitations (Arslan et al., 2018; de Reus and van den Heuvel, 2013a).

2.2 Network neuroscience

Analysis of large, complex connectivity datasets derived from methods such as neuroimaging is the topic of the field of network neuroscience (Bassett and Sporns, 2017). Within this framework, the network properties of the human connectome can be analyzed using graph theoretical tools (Rubinov and Sporns, 2010), representing the brain network as a collection of nodes (e.g., brain regions) and edges (e.g., functional or structural connections) (Fig. 1B). The graph theoretical properties of a connectome vary depending on the topological layout of its nodes and edges. For example, a brain network with overall short path length is capable of efficient, global dispersion of information, while high clustering is associated with efficient local information flow and information segregation (Rubinov and Sporns, 2010; Watts and Strogatz, 1998) (Fig. 1B). Modular networks contain groups of nodes that are strongly connected within the group but show relatively weak connectivity between each other, resulting in

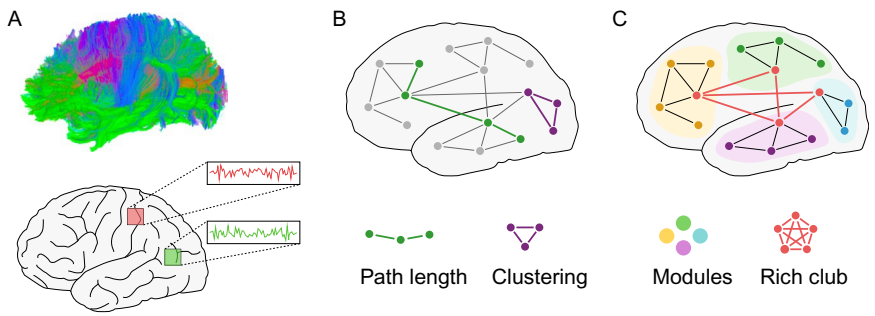

FIG. 1

Reconstruction and analysis of connectome data. (A) Structural brain networks can be reconstructed from diffusion-weighted imaging (top); functional brain networks can be reconstructed based on methods such as resting-state functional MRI, electroencephalography, or magnetoencephalography (bottom). (B) Connectome data are represented as nodes (e.g., brain areas) and edges (e.g., structural or functional connections between areas). Often-used metrics to characterize brain networks include characteristic path length (green) and clustering (purple). (C) Other network characteristics include the presence of modules or communities and rich clubs of dense connectivity between highly connected nodes.

segregated subnetworks (Girvan and Newman, 2002; Sporns and Betzel, 2016) (Fig. 1C). Networks that contain a set of highly connected nodes that are also disproportionately connected among each other are said to have rich-club connectivity, providing efficient integration of information from distant parts of the network (Colizza et al., 2006) (Fig. 1C). The application of graph metrics like those described above to the connectome can provide a parsimonious description of the topological properties of large-scale brain connectivity.

3 Conserved features of the human connectome

Brain network organization exhibits notable similarity across species, including humans. Conserved features of connectome organization are thought to constitute a shared blueprint of brain wiring (Goulas et al., 2019; Mars et al., 2018a; van den Heuvel et al., 2016). In the following section, we review evidence of human connectome properties that appear to be conserved across species, and outline potentially universal principles suggested to govern these commonalities.

3.1 Commonalities in connectome organization

Human brain connectivity consists largely of short links between neighboring cortical areas, while some connections span long spatial distances, effectively providing shortcuts between otherwise distant regions of the cortex (Alexander-Bloch et al., 2013; Bajada et al., 2019; Bullmore and Sporns, 2012). This spatial organization of the connectome resembles properties of a small-world network (for review see Bassett and Bullmore, 2017). Small-world networks combine high clustering of local (between-neighbors) connectivity with efficient global, network-wide communication through sparse connections with short topological path lengths (Fig. 1B) (Watts and Strogatz, 1998). Small-world organization appears to be a prominent topological feature of brain networks, consistently observed in the human structural and functional connectome (Achard, 2006; Salvador et al., 2005; Vaessen et al., 2010) and in the connectomes of a wide range of animal species including the nematode *Caenorhabditis elegans* and the mouse, cat and rhesus monkey (Hilgetag et al., 2000; Oh et al., 2014; Rubinov et al., 2015; Sporns and Zwi, 2004; Watts and Strogatz, 1998).

Another consistently reported feature of human brain connectivity is the presence of modules, characterized by cortical regions that are more densely connected with each other than with other sets of regions (Meunier et al., 2010; Sporns and Betzel, 2016) (Fig. 1C). Modules based on structural connectivity seem to be largely defined by their physical location in the brain (Hagmann et al., 2008). Studies of modules in functional connectivity data have revealed spatially distributed subnetworks that overlap with distinct cognitive functions (Bertolero et al., 2015; Meunier et al., 2009; Power et al., 2011; Yeo et al., 2011). Compartmentalization into modules seems to be a conserved feature of connectome organization across species and is found across spatial scales ranging from neuronal networks in *C. elegans* to region-to-region cortical networks in humans (Bassett et al., 2010; Bota et al.,

2015; de Reus and van den Heuvel, 2013b; Hagmann et al., 2008; Hilgetag et al., 2000; Shih et al., 2015).

The integrative core of the human connectome contains highly connected hub nodes that together form a rich club of connectivity (Colizza et al., 2006; van den Heuvel and Sporns, 2011) (Fig. 1C). Rich-club organization enables efficient transfer of locally processed information within the network, providing a backbone for the integration of multimodal information required for complex brain function. Rich-club hubs overlap with higher-order cortical regions and act as connectors between segregated modules (Hagmann et al., 2008; Sporns, 2013; van den Heuvel and Sporns, 2013a). Furthermore, regions that show high functional flexibility overlap with structural rich-club hubs (Bassett et al., 2013; de Pasquale et al., 2018; Zalesky et al., 2014). Like small-world and modular organization, rich-club architecture is found across a wide range of species and spatial scales and thus seems a conserved feature of connectome organization (for review, see Griffa and van den Heuvel, 2018).

3.2 Proposed principles of connectome wiring

If small-world topology, modular architecture, and rich-club organization represent universal features of connectome organization, might there be general selection pressures that have resulted in the evolution of these features across species and spatial scales? What are the benefits to the brain associated with these forms of wiring that have made them so pervasive in brain networks? Identifying the underlying principles that guide connectome wiring patterns across species informs our understanding of the organization and evolution of the human brain (Bassett and Bullmore, 2017; Clune et al., 2013; Griffa and van den Heuvel, 2018; van den Heuvel et al., 2016). The following section will review evidence that may provide a first step to answering these questions.

3.2.1 Economical wiring limits biological cost of brain networks

Evidence from the last few decades of connectome research suggests that the biological costs of building and maintaining a complex brain network represent a conserved principle of connectome organization (for review, see Bullmore and Sporns, 2012). The connectome's physical embedding in neurons and axons implies that every connection takes up physical space, with connections between remote areas being more expensive than those between neighboring areas (Chklovskii, 2004; Niven and Laughlin, 2008). On top of the costs of building a network, its maintenance is similarly expensive: even though most synaptic communication takes place in the gray matter, the housekeeping processes necessary to maintain the resting potential of axons in the white matter demand a considerable portion of the brain's energy budget (Yu et al., 2018).

It is thus hypothesized that nervous systems minimize their wiring costs in an effort to minimize expenditure of biological resources (Cherniak, 1994; Perez-Escudero and de Polavieja, 2007). Indeed, the connectomes of *C. elegans* and the rhesus macaque, among other species, were found to exhibit near-minimal physical wiring cost (Chen

et al., 2006; Cherniak, 2012; Ercsey-Ravasz et al., 2013). Furthermore, modeling studies demonstrated that in silico networks wired based on cost minimization rules resemble the modular topology of real brain networks (Chen et al., 2006; Ercsey-Ravasz et al., 2013). Modular networks are noted to naturally show small-world topology combining cost-efficient, segregated processing within modules with global intermodular communication (Meunier et al., 2010; Pan and Sinha, 2009). Next to the cost-effectiveness of modular organization, modules may also provide robustness to network perturbations and offer increased flexibility in response to changes in the animal's environment—additional benefits that might explain the pervasiveness of modules in brain networks (Sporns and Betzel, 2016).

It remains to be determined whether wiring minimization itself is the main factor driving the evolution of modular architecture in connectomes (Clune et al., 2013). A recently proposed process in which outgrowing axons simply have a higher chance of meeting nearby dendrites than distant ones was found to also result in economical wiring (Kaiser, 2017; Kaiser et al., 2009). With the inclusion of developmental time windows in neurogenesis, such a process could additionally explain the formation of modules (Chiang et al., 2011; Kaiser, 2017). Thus, it is possible that a simple tendency of connections to predominantly link neighboring areas could explain the apparent universality of brain networks to exhibit near-minimal wiring cost, modular organization, and small-world architecture. Nevertheless, biologically expensive topological features, such as hubs and rich-club organization, are not typically found in networks generated with wiring minimization or distance rules (Betzel et al., 2016; Nicosia et al., 2013; Rubinov et al., 2015; Vertes et al., 2012). Additional selection pressures for expensive circuitry appear to be necessary to more accurately capture the topology of empirical connectomes.

3.2.2 Costly network features support efficient brain function

Network hubs represent a costly feature of connectomes, not only due to their extensive connectivity but also because of their high metabolic activity (Collin et al., 2014; Shanahan, 2012; Vaishnavi et al., 2010; van den Heuvel and Sporns, 2011). Hub organization is thought to offset these costs by providing short topological paths in the network, which allows information to be efficiently exchanged between remote parts of the brain (van den Heuvel et al., 2012). Furthermore, hubs within the rich club may serve as integration centers that combine information from different modalities for higher-order cognitive processing (de Reus and van den Heuvel, 2014; Senden et al., 2014). Support for this theory comes from observations that hub regions overlap with multimodal association cortex and show convergence between different functional networks (Bassett et al., 2008; Crossley et al., 2013; Petersen and Sporns, 2015; van den Heuvel and Sporns, 2013b).

In addition to integrating information, biologically expensive connectivity provides other potential benefits to the network. A recent study reported that a region's long-range (i.e., biologically costly) connections link to distant regions with markedly different connectivity profiles than its short-range, neighboring regions (Betzel and Bassett, 2018). At the same time, connectivity profiles of long-range

connections are similar across regions, indicating degeneracy in the information pathways formed by long-distance connections. Thus, long-range connections may outweigh their costs by diversifying the inputs and outputs of brain areas which leads to enhanced and more robust complex network dynamics (Betzel and Bassett, 2018). Furthermore, evidence from functional connectome studies indicates that networks combining modular (Sporns and Betzel, 2016) and rich-club (Senden et al., 2014) topologies possess higher dynamic complexity, offering more flexible integration of functionally segregated subnetworks, than networks lacking these features (Zamora-López et al., 2016). Dynamic complexity allows the connectome to adaptively leverage cost-efficient, segregated brain states with metabolically expensive, integrative brain states (de Pasquale et al., 2018; Vaishnavi et al., 2010; Zalesky et al., 2014). Thus, costly connectome investments seem to support efficient integration of information and complex network dynamics.

3.2.3 A cost-efficiency tradeoff for connectome organization

Competing pressures for cost-effective and expensive connectivity patterns imply a tradeoff between wiring economy and complex brain function (Budd and Kisvárday, 2012; Bullmore and Sporns, 2012; Chen et al., 2013; Roberts et al., 2016; Rubinov et al., 2015). When such a tradeoff is incorporated into generative models of brain networks, many empirically observed properties including small-worldness, modular topology, and hub organization can be recovered (Bassett and Bullmore, 2017; Betzel et al., 2016; Chen et al., 2013; Rubinov, 2016; Samu et al., 2014; Vertes et al., 2012). It is therefore an interesting opportunity for future research to determine which network features represent direct targets of selection and which features may represent evolutionary byproducts or spandrels (Clune et al., 2013; Rubinov, 2016; Stiso and Bassett, 2018).

4 Human connectome adaptations

Although the tradeoff between economical wiring and efficient brain function appears to be a universal factor in connectome evolution, different environmental selection pressures are expected to yield different instances of functionally beneficial or adaptive brain organization across species. For example, the roundworm *P. pacificus* shows predatory behavior on other roundworms, while this behavior is not seen in the bacterial-feeding *C. elegans*. In accordance with this behavioral difference, the pharyngeal neurons in the predatory *P. pacificus* show increased synaptic connectivity and greater connectional complexity compared to *C. elegans* (Bumbarger et al., 2013). Bonobos, when compared with chimpanzees, display more white matter linking the amygdala with the anterior cingulate cortex, a pathway implicated in the control of aggression (Rilling et al., 2012). Such differential investments in connectivity provide a potential anatomical basis for behavioral differences between the two species, with bonobos showing lower levels of aggression than chimpanzees (Parish and de Waal, 2000).

Similarly, the human brain might be expected to show subtle but potentially important variations on the general theme of conserved connectome organization that evolved in the last 7–8 Mya since the divergence of the human lineage from the lineage leading to bonobos and chimpanzees (Langergraber et al., 2012). Human connectome adaptations may include changes that support the evolution of highly complex brain functions, as well as adaptations related to maintaining a cost-efficient network in an expanded brain.

4.1 Adaptations supporting complex brain function

4.1.1 Brain expansion and cortical plasticity

One of the most apparent features of human brain evolution is the three- to fourfold increase in size that took place during hominin evolution, resulting in a brain that exceeds allometric scaling predictions for a typical primate of the same body size (Holloway et al., 2009; Rilling, 2014, 2006; Schoenemann, 2013). However, the neocortex, credited with most of the highly evolved cognitive functions in humans, has recently been reported to fall within the expected size compared to the rest of the human brain (Finlay, 2019; Miller et al., 2019). If the advanced cognitive capacities of humans cannot be explained simply by a disproportionately sized neocortex, then which other adaptations underlie human brain function? Accumulating evidence suggests that evolutionary changes to specific brain components play a role beyond overall volume increases of the neocortex (Miller et al., 2019; Smaers and Soligo, 2013; Whiting and Barton, 2003).

One influential hypothesis postulates that, as the brain expanded, association areas became progressively untethered from the strong molecular gradients that constrain the development of primary areas, allowing for more plasticity of association areas (Buckner and Krienen, 2013) (Fig. 2, top). This idea is supported by observations of low heritability of cortical morphology, especially in association areas, yet high heritability of overall brain size in humans, while chimpanzees show high heritability of both (Gómez-Robles et al., 2015). Nonspecific selection for increased brain size in primates and specifically humans may thus have indirectly driven enhanced plasticity of association cortex (Stout and Hecht, 2017). It has been suggested that enhanced plasticity of association cortex facilitated the capacity for social or cultural learning in humans, which plays a role in the development of theory of mind—one of the abstract tasks supported by a subnetwork of association areas known as the default mode network (Heyes and Frith, 2014; Mars et al., 2012; Stout and Hecht, 2017).

4.1.2 Adaptations to particular fiber bundles

Adaptations to patterns of connectivity underneath the cortical gray matter represent another level for natural selection to act upon. An example of adaptations of specific connectivity patterns is the evolution of the mirror neuron system in primates. Compared with chimpanzees and macaques, the human mirror neuron system shows stronger connectivity along the inferior and superior longitudinal fasciculi linking

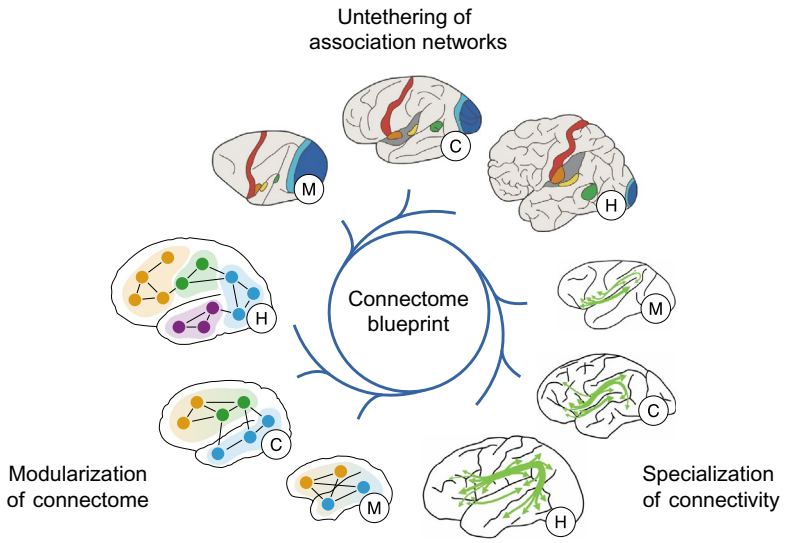

FIG. 2

The human connectome as a combination of a shared connectivity blueprint that is conserved across species (center) and specific connectome adaptations that may include processes such as untethering of association networks, specialization of connectivity in, for example, language networks, and an increase in modular organization of the network. M: macaque, C: chimpanzee, H: human.

Adapted with permission from Buckner, R.L., Krienen, F.M., 2013. The evolution of distributed association networks in the human brain. Trends Cogn. Sci. 17, 648–665. doi:https://doi.org/10.1016/j.tics.2013.09.017 (web archive link); Krubitzer, L.A., Kahn, D.M., 2003. Nature versus nurture revisited: an old idea with a new twist. Prog. Neurobiol. 70, 33–52. doi:https://doi.org/10.1016/S0301-0082(03)00088-1 (web archive link); Rilling, J.K., Glasser, M.F., Preuss, T.M., Ma, X., Zhao, T., Hu, X., Behrens, T.E.J., 2008. The evolution of the arcuate fasciculus revealed with comparative DTI. Nat. Neurosci. 11, 426–428. doi:https://doi.org/10.1038/nn2072 (web archive link).

parietal areas with temporal and frontal areas (Hecht et al., 2013a). This dorsal processing stream has been linked to the extraction of kinematic detail from observed actions, and its enhancement in humans may thus support an increased capacity for imitation and social learning (Hecht et al., 2013a,b). In addition, individual variation in lateralization of superior longitudinal fasciculus projections to the prefrontal cortex in chimpanzees predicts their performance on the mirror self-recognition test, such that chimpanzee with more (human-like) right-lateralization perform better on the task (Hecht et al., 2017).

The arcuate fasciculus, a well-studied pathway for its involvement in human language (Catani et al., 2005; Dick and Tremblay, 2012; Dick et al., 2014; Geschwind, 1970), extends into the superior temporal sulcus and middle temporal gyrus in humans but not in chimpanzees or macaques, and shows high left-lateralization in

humans (Eichert et al., 2018; Rilling et al., 2008) (Fig. 2, right). In humans, the additional regions connected by the arcuate fasciculus are involved in the semantic and lexical aspects of language processing (Dien et al., 2013; Visser et al., 2012; Wei et al., 2012). Another specialization relevant to human language involves the laryngeal motor cortex, which controls the movement of the vocal folds towards the larynx (Kumar et al., 2016). The laryngeal motor cortex shows much stronger structural connectivity to somatosensory and inferior parietal cortices in humans compared to macaques, and is left-lateralized in human functional networks (Kumar et al., 2016; Simonyan et al., 2009). Recent research has focused on identifying the possible evolutionary trajectories of this area (Belyk and Brown, 2017; Mars et al., 2018a; Simonyan, 2014).

4.1.3 Connectome-wide adaptations

Network studies comparing the human, chimpanzee, and macaque connectome have demonstrated a large overlap between structural and functional network organization across species (Goulas et al., 2014; Li et al., 2013; Mantini et al., 2013; Miranda-Dominguez et al., 2014; Neubert et al., 2014). Although the evidence is still limited, these studies also report some putative differences in the presence of structural hubs and functional networks (Li et al., 2013; Mantini et al., 2013). In addition, a comparative connectome study found higher network centrality of white matter connections linking multimodal association areas along with lower centrality of connections linking primary areas in humans compared to chimpanzees (Ardesch et al., 2019). These network adaptations may support the prominent expansion of cortical association areas, which has been reported in prefrontal, lateral temporal, and medial parietal cortex (Avants et al., 2006; Bruner et al., 2017; Donahue et al., 2018; Van Essen and Dierker, 2007). Whether expansion of the human neocortex, especially association areas, exceeds patterns of allometric scaling is still a matter of discussion (Barton and Montgomery, 2019; Barton and Venditti, 2013; Donahue et al., 2018; Finlay, 2019; Miller et al., 2019; Semendeferi et al., 2002). Nevertheless, differences observed in specific brain regions and their underlying connectivity together support the idea of human connectome specializations for complex cognitive functions.

4.2 Adaptations supporting brain expansion

In addition to adaptations that appear to be specifically selected for their associated benefits to brain function, human encephalization may have prompted connectome adaptations in response to the increased physical size of the brain network (Barrett, 2012; Hofman, 2012).

4.2.1 Limitations on the number of connections

In a network with a growing number of nodes, the number of connections needs to scale faster than the number of network nodes in order to keep constant connectivity (Fig. 3). Across species, white matter has indeed been found to scale faster than gray matter with increasing brain size, but not fast enough to maintain constant

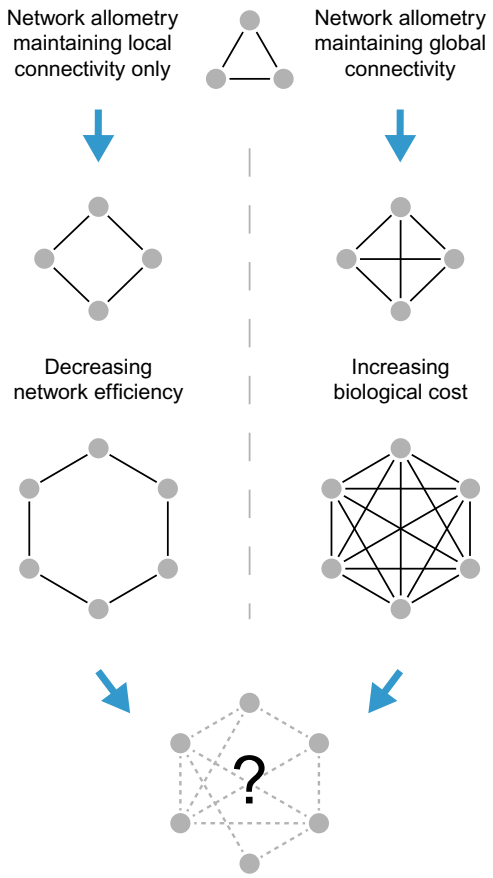

FIG. 3

Network allometry with increasing number of nodes. In a network maintaining local connectivity (left), the number of edges E scales linearly with the number of nodes N. In a network maintaining global connectivity (right), the number of edges scales much faster than the number of nodes. In a fully connected, undirected network as represented here, the number of edges is given by $E = N(N-1)/2$. Empirical brain networks with growing number of nodes are expected to show an intermediate topology between both extremes, trading off network efficiency and biological cost of the network.

Adapted with permission from Hofman, M.A., 2012. Design principles of the human brain. An evolutionary perspective. In: Progress in Brain Research. Elsevier, pp. 373–390. https://doi.org/10.1016/B978-0-444-53860-4.00018-0 (web archive link).

connectivity in larger brains (Herculano-Houzel et al., 2010; Ringo, 1991; Zhang and Sejnowski, 2000). Increases in size therefore imply decreases in interconnectedness of the brain (Hofman, 2012; Kaas, 2000). Evidence for this theory comes from observations of particular reductions in connectivity of pathways connecting the two

cerebral hemispheres, which span long physical distances (Ardesch et al., 2019; Rilling and Insel, 1999; van den Heuvel et al., 2016). The corpus callosum scales isometrically with brain size, implying that its cross-sectional area, which determines the total number of axons that can pass through it, increases at only two thirds of total brain volume (Rilling and Insel, 1999). Together with observations of lower axon density in the corpus callosum of larger primates (Phillips et al., 2015), this suggests that proportionally fewer axons are available to connect the two hemispheres in larger brains. Reduced interhemispheric connectivity has been argued to promote the lateralization of brain functions in humans (Rilling and Insel, 1999; Rilling and van den Heuvel, 2018).

4.2.2 Optimization of connection length

Larger brains may also be expected to show adaptations that minimize the white matter spent on connections that have been retained throughout evolution. For example, it has been hypothesized that the gyrification of large brains is a result of connection length minimization, with areas on either side of a gyrus being pulled together to reduce the amount of additional wiring necessary to connect the expanding cortical surface (Herculano-Houzel et al., 2010; Van Essen, 1997). Other large-brained species such as elephants and dolphins also show pronounced gyrification, suggesting a common solution to the wiring length problem in large brains (Zilles et al., 2013). Optimization of space taken up by white matter connectivity thus involves both reductions in connection number and reductions in connection length (Hofman, 2012).

A network solution towards economical wiring is the enhancement of modular network topology (see Section 1.3 and Fig. 2, left). The current evidence, while still limited, seems to support this process in human brain evolution (Ardesch et al., 2019; Rilling and Insel, 1999). Interestingly, enhanced modularity of the human connectome may have facilitated the evolution of specialized brain functions (Barrett, 2012). Corpus callosum size relative to the rest of the brain shows an inverse relationship with interhemispheric asymmetry and handedness across a range of primates (Hopkins et al., 2007; Hopkins and Rilling, 2000), suggesting that decreases in interhemispheric communication pave the way for functional lateralization in larger brains. More generally, the modular organization of human and chimpanzee brains is argued to promote mosaic evolution by allowing greater flexibility of independent brain structures to respond to particular selective pressures (Barton and Harvey, 2000; Gómez-Robles et al., 2014). This would in turn have facilitated the emergence of complex cognitive features in the human brain (Gotts et al., 2013). Thus, one interpretation is that the emergence of highly specialized brain functions in humans partly resulted from the constraints on network connectivity that accompanied brain expansion.

5 Summary and outlook

The human connectome describes the complex network architecture of the brain. This review has described the evolution of the human connectome as a combination of features shared with other animal species and specific adaptations that have

emerged in the human lineage. Conserved topological features of the human connectome include a small-world network organization combining economical local processing with efficient information integration, the existence of modules or communities, and an integrative core consisting of rich-club connectivity. This conserved network topology has been suggested to arise from a common tradeoff between wiring economy and network function, seen in many animal species across levels of complexity and spatial scales. Next to conserved network properties, the human connectome exhibits several adaptations that have been linked to the emergence of complex cognition, as well as adaptations that may be related to the pronounced encephalization that took place in human evolution.

There are important challenges for comparative connectomics. For example, it is still difficult to establish whether certain connectome features represent uniquely human adaptations, due to the limited availability of large, cross-species connectome data sets. Recent efforts are aiming to establish publicly available, large-scale primate connectivity databases, which will enable robust network comparisons that can take into account effects of allometry and phylogeny across a wide range of primate species (Markov et al., 2014; Milham et al., 2018; Miller et al., 2019; Sakai et al., 2018; Stephan et al., 2001). In addition, comparative connectomics requires reliable comparisons of brains that may differ greatly in size. As different brain sizes may require different imaging parameters and different numbers of brain regions that can be delineated, the resulting networks may have different numbers of nodes and edges. Comparisons of networks of different size and density calls for specialized analytical tools to accurately identify subtle cross-species variations in connectome organization (Thiebaut de Schotten et al., 2018; van Wijk et al., 2010).

Characterization of human connectome adaptations also offers exciting new directions for future research. Human-specific connectome features may inform the etiology of certain human-specific brain disorders involving disruptions in brain connectivity (Crossley et al., 2014; Fornito et al., 2015), and might provide novel, biology-based targets for therapy. Another promising direction is to further establish how the evolution of the human connectome at the macroscale relates to adaptations at the microscale of brain organization—including cellular characteristics, proteomics, and genetics (Elston, 2011; Fiddes et al., 2018; Scholtens et al., 2014; Zhu et al., 2018). Together, these different types of evidence will help provide an integrated view of human connectome evolution and its implications for brain function and dysfunction.

References

Achard, S., 2006. A resilient, low-frequency, small-world human brain functional network with highly connected association cortical hubs. J. Neurosci. 26, 63–72. https://doi.org/10.1523/JNEUROSCI.3874-05.2006.

Alexander-Bloch, A.F., Vértes, P.E., Stidd, R., Lalonde, F., Clasen, L., Rapoport, J., Giedd, J., Bullmore, E.T., Gogtay, N., 2013. The anatomical distance of functional connections predicts brain network topology in health and schizophrenia. Cereb. Cortex 23, 127–138. https://doi.org/10.1093/cercor/bhr388.

Ardesch, D.J., Scholtens, L.H., Li, L., Preuss, T.M., Rilling, J.K., van den Heuvel, M.P., 2019. Evolutionary expansion of connectivity between multimodal association areas in the human brain compared with chimpanzees. Proc. Natl. Acad. Sci. U.S.A. 116, 7101–7106. https://doi.org/10.1073/pnas.1818512116.

Arslan, S., Ktena, S.I., Makropoulos, A., Robinson, E.C., Rueckert, D., Parisot, S., 2018. Human brain mapping: a systematic comparison of parcellation methods for the human cerebral cortex. Neuroimage 170, 5–30. https://doi.org/10.1016/j.neuroimage.2017.04.014.

Avants, B.B., Schoenemann, P.T., Gee, J.C., 2006. Lagrangian frame diffeomorphic image registration: morphometric comparison of human and chimpanzee cortex. Med. Image Anal. 10, 397–412. https://doi.org/10.1016/j.media.2005.03.005.

Bajada, C.J., Schreiber, J., Caspers, S., 2019. Fiber length profiling: a novel approach to structural brain organization. Neuroimage 186, 164–173. https://doi.org/10.1016/j.neuroimage.2018.10.070.

Barrett, H.C., 2012. A hierarchical model of the evolution of human brain specializations. Proc. Natl. Acad. Sci. U.S.A. 109, 10733–10740. https://doi.org/10.1073/pnas.1201898109.

Barton, R.A., Harvey, P.H., 2000. Mosaic evolution of brain structure in mammals. Nature 405, 1055–1058. https://doi.org/10.1038/35016580.

Barton, R.A., Montgomery, S.H., 2019. Proportional versus relative size as metrics in human brain evolution. Proc. Natl. Acad. Sci. U.S.A. 116, 3–4. https://doi.org/10.1073/pnas.1817200116.

Barton, R.A., Venditti, C., 2013. Human frontal lobes are not relatively large. Proc. Natl. Acad. Sci. U.S.A. 110, 9001–9006. https://doi.org/10.1073/pnas.1215723110.

Bassett, D.S., Bullmore, E.T., 2017. Small-world brain networks revisited. Neuroscience 23, 499–516. https://doi.org/10.1177/1073858416667720.

Bassett, D.S., Sporns, O., 2017. Network neuroscience. Nat. Neurosci. 20, 353–364. https://doi.org/10.1038/nn.4502.

Bassett, D.S., Bullmore, E., Verchinski, B.A., Mattay, V.S., Weinberger, D.R., Meyer-Lindenberg, A., 2008. Hierarchical organization of human cortical networks in health and schizophrenia. J. Neurosci. 28, 9239–9248. https://doi.org/10.1523/JNEUROSCI.1929-08.2008.

Bassett, D.S., Greenfield, D.L., Meyer-Lindenberg, A., Weinberger, D.R., Moore, S.W., Bullmore, E.T., 2010. Efficient physical embedding of topologically complex information processing networks in brains and computer circuits. PLoS Comput. Biol. 6, https://doi.org/10.1371/journal.pcbi.1000748.

Bassett, D.S., Wymbs, N.F., Rombach, M.P., Porter, M.A., Mucha, P.J., Grafton, S.T., 2013. Task-based core-periphery organization of human brain dynamics. PLoS Comput. Biol. 9, e1003171. https://doi.org/10.1371/journal.pcbi.1003171.

Belyk, M., Brown, S., 2017. The origins of the vocal brain in humans. Neurosci. Biobehav. Rev. 77, 177–193. https://doi.org/10.1016/j.neubiorev.2017.03.014.

Bertolero, M.A., Yeo, B.T.T., D'Esposito, M., 2015. The modular and integrative functional architecture of the human brain. Proc. Natl. Acad. Sci. U.S.A. 112, E6798–E6807. https://doi.org/10.1073/pnas.1510619112.

Berwick, R.C., Friederici, A.D., Chomsky, N., Bolhuis, J.J., 2013. Evolution, brain, and the nature of language. Trends Cogn. Sci. 17, 89–98. https://doi.org/10.1016/j.tics.2012.12.002.

Betzel, R.F., Bassett, D.S., 2018. Specificity and robustness of long-distance connections in weighted, interareal connectomes. Proc. Natl. Acad. Sci. U.S.A. 115, E4880–E4889. https://doi.org/10.1073/pnas.1720186115.

Betzel, R.F., Avena-Koenigsberger, A., Goñi, J., He, Y., de Reus, M.A., Griffa, A., Vértes, P.E., Mišic, B., Thiran, J.-P.P., Hagmann, P., van den Heuvel, M.P., Zuo, X.-N.N., Bullmore, E.T., Sporns, O., 2016. Generative models of the human connectome. Neuroimage 124, 1054–1064. https://doi.org/10.1016/j.neuroimage.2015.09.041.

Bird, C.P., Stranger, B.E., Liu, M., Thomas, D.J., Ingle, C.E., Beazley, C., Miller, W., Hurles, M.E., Dermitzakis, E.T., 2007. Fast-evolving noncoding sequences in the human genome. Genome Biol. 8, 1–12. https://doi.org/10.1186/gb-2007-8-6-r118.

Bota, M., Sporns, O., Swanson, L.W., 2015. Architecture of the cerebral cortical association connectome underlying cognition. Proc. Natl. Acad. Sci. U.S.A. 112, E2093–E2101. https://doi.org/10.1073/pnas.1504394112.

Bruner, E., Preuss, T.M., Chen, X., Rilling, J.K., 2017. Evidence for expansion of the precuneus in human evolution. Brain Struct. Funct. 222, 1053–1060. https://doi.org/10.1007/s00429-015-1172-y.

Buckner, R.L., Krienen, F.M., 2013. The evolution of distributed association networks in the human brain. Trends Cogn. Sci. 17, 648–665. https://doi.org/10.1016/j.tics.2013.09.017.

Budd, J.M.L., Kisvárday, Z.F., 2012. Communication and wiring in the cortical connectome. Front. Neuroanat. 6, 1–23, article id 42. https://doi.org/10.3389/fnana.2012.00042.

Bullmore, E.T., Sporns, O., 2012. The economy of brain network organization. Nat. Rev. Neurosci. 13, 336–349. https://doi.org/10.1038/nrn3214.

Bumbarger, D.J., Riebesell, M., Rödelsperger, C., Sommer, R.J., 2013. System-wide rewiring underlies behavioral differences in predatory and bacterial-feeding nematodes. Cell 152, 109–119. https://doi.org/10.1016/j.cell.2012.12.013.

Catani, M., Jones, D.K., Ffytche, D.H., 2005. Perisylvian language networks of the human brain. Ann. Neurol. 57, 8–16. https://doi.org/10.1002/ana.20319.

Chen, B.L., Hall, D.H., Chklovskii, D.B., 2006. Wiring optimization can relate neuronal structure and function. Proc. Natl. Acad. Sci. U.S.A. 103, 4723–4728. https://doi.org/10.1073/pnas.0506806103.

Chen, Y., Wang, S., Hilgetag, C.C., Zhou, C., 2013. Trade-off between multiple constraints enables simultaneous formation of modules and hubs in neural systems. PLoS Comput. Biol. 9, e1002937. https://doi.org/10.1371/journal.pcbi.1002937.

Cherniak, C., 1994. Component placement optimization in the brain. J. Neurosci. 14, 2418–2427. https://doi.org/10.1523/JNEUROSCI.14-04-02418.1994.

Cherniak, C., 2012. Neural wiring optimization. In: Hofman, M.A., Falk, D.B.T. (Eds.), Progress in Brain Research. Elsevier, pp. 361–371. https://doi.org/10.1016/B978-0-444-53860-4.00017-9.

Chiang, A.S., Lin, C.Y., Chuang, C.C., Chang, H.M., Hsieh, C.H., Yeh, C.W., Shih, C.T., Wu, J.J., Wang, G.T., Chen, Y.C., Wu, C.C., Chen, G.Y., Ching, Y.T., Lee, P.C., Lin, C.Y., Lin, H.H., Wu, C.C., Hsu, H.W., Huang, Y.A., Chen, J.Y., Chiang, H.J., Lu, C.F., Ni, R.F., Yeh, C.Y., Hwang, J.K., 2011. Three-dimensional reconstruction of brain-wide wiring networks in drosophila at single-cell resolution. Curr. Biol. 21, 1–11. https://doi.org/10.1016/j.cub.2010.11.056.

Chklovskii, D.B., 2004. Exact solution for the optimal neuronal layout problem. Neural Comput. 16, 2067–2078. https://doi.org/10.1162/0899766041732422.

Clune, J., Mouret, J.-B., Lipson, H., 2013. The evolutionary origins of modularity. Proc. R. Soc. B Biol. Sci. 280, 20122863. https://doi.org/10.1098/rspb.2012.2863.

Colizza, V., Flammini, A., Serrano, M.A., Vespignani, A., 2006. Detecting rich-club ordering in complex networks. Nat. Phys. 2, 110–115. https://doi.org/10.1038/nphys209.

Collin, G., Sporns, O., Mandl, R.C.W., van den Heuvel, M.P., 2014. Structural and functional aspects relating to cost and benefit of rich club organization in the human cerebral cortex. Cereb. Cortex 24, 2258–2267. https://doi.org/10.1093/cercor/bht064.

Crossley, N.A., Mechelli, A., Vertes, P.E., Winton-Brown, T.T., Patel, A.X., Ginestet, C.E., McGuire, P., Bullmore, E.T., 2013. Cognitive relevance of the community structure of the human brain functional coactivation network. Proc. Natl. Acad. Sci. 110, 11583–11588. https://doi.org/10.1073/pnas.1220826110.

Crossley, N.A., Mechelli, A., Scott, J., Carletti, F., Fox, P.T., Mcguire, P., Bullmore, E.T., 2014. The hubs of the human connectome are generally implicated in the anatomy of brain disorders. Brain 137, 2382–2395. https://doi.org/10.1093/brain/awu132.

de Pasquale, F., Corbetta, M., Betti, V., Della Penna, S., 2018. Cortical cores in network dynamics. Neuroimage 180, 370–382. https://doi.org/10.1016/j.neuroimage.2017.09.063.

de Reus, M.A., van den Heuvel, M.P., 2013a. The parcellation-based connectome: limitations and extensions. Neuroimage 80, 397–404. https://doi.org/10.1016/j.neuroimage.2013.03.053.

de Reus, M.A., van den Heuvel, M.P., 2013b. Rich club organization and intermodule communication in the cat connectome. J. Neurosci. 33, 12929–12939. https://doi.org/10.1523/jneurosci.1448-13.2013.

de Reus, M.A., van den Heuvel, M.P., 2014. Simulated rich club lesioning in brain networks: a scaffold for communication and integration? Front. Hum. Neurosci. 8, 1–5. https://doi.org/10.3389/fnhum.2014.00647.

Desikan, R.S., Ségonne, F., Fischl, B., Quinn, B.T., Dickerson, B.C., Blacker, D., Buckner, R.L., Dale, A.M., Maguire, R.P., Hyman, B.T., Albert, M.S., Killiany, R.J., 2006. An automated labeling system for subdividing the human cerebral cortex on MRI scans into gyral based regions of interest. Neuroimage 31, 968–980. https://doi.org/10.1016/j.neuroimage.2006.01.021.

Devaine, M., Hollard, G., Daunizeau, J., 2014. Theory of mind: did evolution fool us? PLoS One 9, e87619. https://doi.org/10.1371/journal.pone.0087619.

Dick, A.S., Tremblay, P., 2012. Beyond the arcuate fasciculus: consensus and controversy in the connectional anatomy of language. Brain 135, 3529–3550. https://doi.org/10.1093/brain/aws222.

Dick, A.S., Bernal, B., Tremblay, P., 2014. The language connectome: new pathways, new concepts. Neuroscientist 20, 453–467. https://doi.org/10.1177/1073858413513502.

Dien, J., Brian, E.S., Molfese, D.L., Gold, B.T., 2013. Combined ERP/fMRI evidence for early word recognition effects in the posterior inferior temporal gyrus. Cortex 49, 2307–2321. https://doi.org/10.1016/j.cortex.2013.03.008.

Donahue, C.J., Glasser, M.F., Preuss, T.M., Rilling, J.K., Van Essen, D.C., 2018. Quantitative assessment of prefrontal cortex in humans relative to nonhuman primates. Proc. Natl. Acad. Sci. U.S.A. 115, E5183–E5192. https://doi.org/10.1073/pnas.1721653115.

Eichert, N., Verhagen, L., Folloni, D., Jbabdi, S., Khrapitchev, A.A., Sibson, N.R., Mantini, D., Sallet, J., Mars, R.B., 2018. What is special about the human arcuate fasciculus? Lateralization, projections, and expansion. Cortex. in press https://doi.org/10.1016/j.cortex.2018.05.005.

Elston, G.N., 2011. Pyramidal cells in prefrontal cortex of primates: marked differences in neuronal structure among species. Front. Neuroanat. 5, 1–17. https://doi.org/10.3389/fnana.2011.00002.

Ercsey-Ravasz, M., Markov, N.T., Lamy, C., Van Essen, D.C., Knoblauch, K., Toroczkai, Z., Kennedy, H., 2013. A predictive network model of cerebral cortical connectivity based on a distance rule. Neuron 80, 184–197. https://doi.org/10.1016/j.neuron.2013.07.036.

Fiddes, I.T., Lodewijk, G.A., Mooring, M., Bosworth, C.M., Ewing, A.D., Mantalas, G.L., Novak, A.M., van den Bout, A., Bishara, A., Rosenkrantz, J.L., Lorig-Roach, R., Field, A.R., Haeussler, M., Russo, L., Bhaduri, A., Nowakowski, T.J., Pollen, A.A., Dougherty, M.L., Nuttle, X., Addor, M.-C.C., Zwolinski, S., Katzman, S., Kriegstein, A., Eichler, E.E., Salama, S.R., Jacobs, F.M.J., Haussler, D., 2018. Human-specific NOTCH2NL genes affect notch signaling and cortical neurogenesis. Cell 173, https://doi.org/10.1016/j.cell.2018.03.0511356–1369.e22.

Finlay, B.L., 2019. Human exceptionalism, our ordinary cortex and our research futures. Dev. Psychobiol. 61, 317–322. https://doi.org/10.1002/dev.21838.

Fornito, A., Zalesky, A., Breakspear, M., 2015. The connectomics of brain disorders. Nat. Rev. Neurosci. 16, 159–172. https://doi.org/10.1038/nrn3901.

Geschwind, N., 1970. The organization of language and the brain. Science 170, 940–944. https://doi.org/10.1093/acprof:oso/9780195177640.003.0026.

Girvan, M., Newman, M.E.J., 2002. Community structure in social and biological networks. Proc. Natl. Acad. Sci. U.S.A. 99, 7821–7826. https://doi.org/10.1073/pnas.122653799.

Glasser, M.F., Smith, S.M., Marcus, D.S., Andersson, J.L.R., Auerbach, E.J., Behrens, T.E.J., Coalson, T.S., Harms, M.P., Jenkinson, M., Moeller, S., Robinson, E.C., Sotiropoulos, S.N., Xu, J., Yacoub, E., Ugurbil, K., Van Essen, D.C., 2016. The human connectome project's neuroimaging approach. Nat. Neurosci. 19, 1175–1187. https://doi.org/10.1038/nn.4361.

Gómez-Robles, A., Hopkins, W.D., Sherwood, C.C., 2014. Modular structure facilitates mosaic evolution of the brain in chimpanzees and humans. Nat. Commun. 5, 4469. https://doi.org/10.1038/ncomms5469.

Gómez-Robles, A., Hopkins, W.D., Schapiro, S.J., Sherwood, C.C., 2015. Relaxed genetic control of cortical organization in human brains compared with chimpanzees. Proc. Natl. Acad. Sci. U.S.A. 112, 14799–14804. https://doi.org/10.1073/pnas.1512646112.

Gotts, S.J., Jo, H.J., Wallace, G.L., Saad, Z.S., Cox, R.W., Martin, A., 2013. Two distinct forms of functional lateralization in the human brain. Proc. Natl. Acad. Sci. U.S.A. 110, E3435–E3444. https://doi.org/10.1073/pnas.1302581110.

Goulas, A., Bastiani, M., Bezgin, G., Uylings, H.B.M., Roebroeck, A., Stiers, P., 2014. Comparative analysis of the macroscale structural connectivity in the macaque and human brain. PLoS Comput. Biol. 10, e1003529. https://doi.org/10.1371/journal.pcbi.1003529.

Goulas, A., Majka, P., Rosa, M.G.P., Hilgetag, C.C., 2019. A blueprint of mammalian cortical connectomes. PLoS Biol. 17, e2005346. https://doi.org/10.1371/journal.pbio.2005346.

Griffa, A., van den Heuvel, M.P., 2018. Rich-club neurocircuitry: function, evolution, and vulnerability. Dialogues Clin. Neurosci. 20, 121–131.

Hagmann, P., Kurant, M., Gigandet, X., Thiran, P., Wedeen, V.J., Meuli, R., Thiran, J.-P., 2007. Mapping human whole-brain structural networks with diffusion MRI. PLoS One 2, e597. https://doi.org/10.1371/journal.pone.0000597.

Hagmann, P., Cammoun, L., Gigandet, X., Meuli, R., Honey, C.J., Van Wedeen, J., Sporns, O., 2008. Mapping the structural core of human cerebral cortex. PLoS Biol. 6, 1479–1493. https://doi.org/10.1371/journal.pbio.0060159.

Hecht, E.E., Gutman, D.A., Preuss, T.M., Sanchez, M.M., Parr, L.A., Rilling, J.K., 2013a. Process versus product in social learning: comparative diffusion tensor imaging of neural systems for action execution–observation matching in macaques, chimpanzees, and humans. Cereb. Cortex 23, 1014–1024. https://doi.org/10.1093/cercor/bhs097.

Hecht, E.E., Murphy, L.E., Gutman, D.A., Votaw, J.R., Schuster, D.M., Preuss, T.M., Orban, G.A., Stout, D., Parr, L.A., 2013b. Differences in neural activation for object-directed grasping in chimpanzees and humans. J. Neurosci. 33, 14117–14134. https://doi.org/10.1523/JNEUROSCI.2172-13.2013.

Hecht, E.E., Mahovetz, L.M., Preuss, T.M., Hopkins, W.D., 2017. A neuroanatomical predictor of mirror self-recognition in chimpanzees. Soc. Cogn. Affect. Neurosci. 12, 37–48. https://doi.org/10.1093/scan/nsw159.

Herculano-Houzel, S., Mota, B., Wong, P., Kaas, J.H., 2010. Connectivity-driven white matter scaling and folding in primate cerebral cortex. Proc. Natl. Acad. Sci. U.S.A. 107, 19008–19013. https://doi.org/10.1073/pnas.1012590107.

Heyes, C.M., Frith, C.D., 2014. The cultural evolution of mind reading. Science 344, 1243091. https://doi.org/10.1126/science.1243091.

Hilgetag, C.C., Burns, G.A., O'Neill, M.A., Scannell, J.W., Young, M.P., 2000. Anatomical connectivity defines the organization of clusters of cortical areas in the macaque and the cat. Philos. Trans. R. Soc. B Biol. Sci. 355, 91–110. https://doi.org/10.1098/rstb.2000.0551.

Hofman, M.A., 2012. Design principles of the human brain. An evolutionary perspective. In: Progress in Brain Research. Elsevier, pp. 373–390. https://doi.org/10.1016/B978-0-444-53860-4.00018-0.

Holloway, R.L., Sherwood, C.C., Hof, P.R., Rilling, J.K., 2009. Evolution of the brain in humans—paleoneurology. In: Binder, M.D., Hirokawa, N., Windhorst, U. (Eds.), Encyclopedia of Neuroscience. Springer, Berlin, Heidelberg.

Hopkins, W.D., Rilling, J.K., 2000. A comparative MRI study of the relationship between neuroanatomical asymmetry and interhemispheric connectivity in primates: implication for the evolution of functional asymmetries. Behav. Neurosci. 114, 739–748. https://doi.org/10.1037/0735-7044.114.4.739.

Hopkins, W.D., Dunham, L., Cantalupo, C., Taglialatela, J., 2007. The association between handedness, brain asymmetries, and corpus callosum size in chimpanzees (Pan troglodytes). Cereb. Cortex 17, 1757–1765. https://doi.org/10.1093/cercor/bhl086.

Kaas, J.H., 2000. Why is brain size so important: design problems and solutions as neocortex gets bigger or smaller. Brain Mind 1, 7–23.

Kaiser, M., 2017. Mechanisms of connectome development. Trends Cogn. Sci. 21, 703–717. https://doi.org/10.1016/j.tics.2017.05.010.

Kaiser, M., Hilgetag, C.C., Van Ooyen, A., 2009. A simple rule for axon outgrowth and synaptic competition generates realistic connection lengths and filling fractions. Cereb. Cortex 19, 3001–3010. https://doi.org/10.1093/cercor/bhp071.

Kumar, V., Croxson, P.L., Simonyan, K., 2016. Structural organization of the laryngeal motor cortical network and its implication for evolution of speech production. J. Neurosci. 36, 4170–4181. https://doi.org/10.1523/JNEUROSCI.3914-15.2016.

Langergraber, K.E., Prufer, K., Rowney, C., Boesch, C., Crockford, C., Fawcett, K., Inoue, E., Inoue-Muruyama, M., Mitani, J.C., Muller, M.N., Robbins, M.M., Schubert, G., Stoinski, T.S., Viola, B., Watts, D., Wittig, R.M., Wrangham, R.W., Zuberbuhler, K., Paabo, S., Vigilant, L., 2012. Generation times in wild chimpanzees and gorillas suggest earlier divergence times in great ape and human evolution. Proc. Natl. Acad. Sci. U.S.A. 109, 15716–15721. https://doi.org/10.1073/pnas.1211740109.

Li, L., Hu, X., Preuss, T.M., Glasser, M.F., Damen, F.W., Qiu, Y., Rilling, J.K., 2013. Mapping putative hubs in human, chimpanzee and rhesus macaque connectomes via diffusion tractography. Neuroimage 80, 462–474. https://doi.org/10.1016/j.neuroimage.2013.04.024.

Mantini, D., Corbetta, M., Romani, G.L., Orban, G.A., Vanduffel, W., 2013. Evolutionarily novel functional networks in the human brain? J. Neurosci. 33, 3259–3275. https://doi.org/10.1523/JNEUROSCI.4392-12.2013.

Markov, N.T., Ercsey-Ravasz, M.M., Ribeiro Gomes, A.R., Lamy, C., Magrou, L., Vezoli, J., Misery, P., Falchier, A., Quilodran, R., Gariel, M.A., Sallet, J., Gamanut, R., Huissoud, C., Clavagnier, S., Giroud, P., Sappey-Marinier, D., Barone, P., Dehay, C., Toroczkai, Z., Knoblauch, K., Van Essen, D.C., Kennedy, H., 2014. A weighted and directed interareal connectivity matrix for macaque cerebral cortex. Cereb. Cortex 24, 17–36. https://doi.org/10.1093/cercor/bhs270.

Mars, R.B., Neubert, F.-X., Noonan, M.P., Sallet, J., Toni, I., Rushworth, M.F.S., 2012. On the relationship between the "default mode network" and the "social brain.". Front. Hum. Neurosci. 6, 1–9. https://doi.org/10.3389/fnhum.2012.00189.

Mars, R.B., Sotiropoulos, S.N., Passingham, R.E., Sallet, J., Verhagen, L., Khrapitchev, A.A., Sibson, N., Jbabdi, S., 2018a. Whole brain comparative anatomy using connectivity blueprints. Elife 7, 508–517. https://doi.org/10.7554/eLife.35237.

Mars, R.B., Passingham, R.E., Jbabdi, S., 2018b. Connectivity fingerprints: from areal descriptions to abstract spaces. Trends Cogn. Sci. 22, 1026–1037. https://doi.org/10.1016/j.tics.2018.08.009.

Mars, R.B., Eichert, N., Jbabdi, S., Verhagen, L., Rushworth, M.F.S., 2018c. Connectivity and the search for specializations in the language-capable brain. Curr. Opin. Behav. Sci. 21, 19–26. https://doi.org/10.1016/j.cobeha.2017.11.001.

Meunier, D., Lambiotte, R., Fornito, A., Ersche, K.D., Bullmore, E.T., 2009. Hierarchical modularity in human brain functional networks. Front. Neuroinform. 3, 1–12. https://doi.org/10.3389/neuro.11.037.2009.

Meunier, D., Lambiotte, R., Bullmore, E.T., 2010. Modular and hierarchically modular organization of brain networks. Front. Neurosci. 4, 1–11. https://doi.org/10.3389/fnins.2010.00200.

Milham, M.P., Ai, L., Koo, B., Xu, T., Amiez, C., Balezeau, F., Baxter, M.G., Blezer, E.L.A., Brochier, T., Chen, A., Croxson, P.L., Damatac, C.G., Dehaene, S., Everling, S., Fair, D.A., Fleysher, L., Freiwald, W., Froudist-Walsh, S., Griffiths, T.D., Guedj, C., Hadj-Bouziane, F., Ben Hamed, S., Harel, N., Hiba, B., Jarraya, B., Jung, B., Kastner, S., Klink, P.C., Kwok, S.C., Laland, K.N., Leopold, D.A., Lindenfors, P., Mars, R.B., Menon, R.S., Messinger, A., Meunier, M., Mok, K., Morrison, J.H., Nacef, J., Nagy, J., Rios, M.O., Petkov, C.I., Pinsk, M., Poirier, C., Procyk, E., Rajimehr, R., Reader, S.M., Roelfsema, P.R., Rudko, D.A., Rushworth, M.F.S., Russ, B.E., Sallet, J., Schmid, M.C., Schwiedrzik, C.M., Seidlitz, J., Sein, J., Shmuel, A., Sullivan, E.L., Ungerleider, L., Thiele, A., Todorov, O.S., Tsao, D., Wang, Z., Wilson, C.R.E., Yacoub, E., Ye, F.Q., Zarco, W., di Zhou, Y., Margulies, D.S., Schroeder, C.E., 2018. An open resource for non-human primate imaging. Neuron 100, 1–14. https://doi.org/10.1016/j.neuron.2018.08.039.

Miller, I.F., Barton, R.A., Nunn, C.L., 2019. Quantitative uniqueness of human brain evolution revealed through phylogenetic comparative analysis. Elife 8, 1–25. https://doi.org/10.7554/elife.41250.

Miranda-Dominguez, O., Mills, B.D., Grayson, D., Woodall, A., Grant, K.A., Kroenke, C.D., Fair, D.A., 2014. Bridging the gap between the human and macaque connectome: a quantitative comparison of global interspecies structure-function relationships and network topology. J. Neurosci. 34, 5552–5563. https://doi.org/10.1523/JNEUROSCI.4229-13.2014.

Neubauer, S., Hublin, J., Gunz, P., 2018. The evolution of modern human brain shape. Sci. Adv. 4, https://doi.org/10.1126/sciadv.aao5961eaao5961.

Neubert, F.-X., Mars, R.B., Thomas, A.G., Sallet, J., Rushworth, M.F.S., 2014. Comparison of human ventral frontal cortex areas for cognitive control and language with areas in monkey frontal cortex. Neuron 81, 700–713. https://doi.org/10.1016/j.neuron.2013.11.012.

Nicosia, V., Vertes, P.E., Schafer, W.R., Latora, V., Bullmore, E.T., 2013. Phase transition in the economically modeled growth of a cellular nervous system. Proc. Natl. Acad. Sci. U.S.A. 110, 7880–7885. https://doi.org/10.1073/pnas.1300753110.

Niven, J.E., Laughlin, S.B., 2008. Energy limitation as a selective pressure on the evolution of sensory systems. J. Exp. Biol. 211, 1792–1804. https://doi.org/10.1242/jeb.017574.

Oh, S.W., Harris, J.A., Ng, L., Winslow, B., Cain, N., Mihalas, S., Wang, Q., Lau, C., Kuan, L., Henry, A.M., Mortrud, M.T., Ouellette, B., Nguyen, T.N., Sorensen, S.A., Slaughterbeck, C.R., Wakeman, W., Li, Y., Feng, D., Ho, A., Nicholas, E., Hirokawa, K.E., Bohn, P., Joines, K.M., Peng, H., Hawrylycz, M.J., Phillips, J.W., Hohmann, J.G., Wohnoutka, P., Gerfen, C.R., Koch, C., Bernard, A., Dang, C., Jones, A.R., Zeng, H., 2014. A mesoscale connectome of the mouse brain. Nature 508, 207–214. https://doi.org/10.1038/nature13186.

Pan, R.K., Sinha, S., 2009. Modularity produces small-world networks with dynamical time-scale separation. Europhys. Lett. 85, 68006. https://doi.org/10.1209/0295-5075/85/68006.

Parish, A.R., de Waal, F.B.M., 2000. The other "closest living relative". How bonobos (Pan paniscus) challenge traditional assumptions about females, dominance, intra- and intersexual interactions, and hominid evolution. Ann. N. Y. Acad. Sci. 907, 97–113. https://doi.org/10.1111/j.1749-6632.2000.tb06618.x.

Perez-Escudero, A., de Polavieja, G.G., 2007. Optimally wired subnetwork determines neuroanatomy of Caenorhabditis elegans. Proc. Natl. Acad. Sci. U.S.A. 104, 17180–17185. https://doi.org/10.1073/pnas.0703183104.

Petersen, S.E., Sporns, O., 2015. Brain networks and cognitive architectures. Neuron 88, 207–219. https://doi.org/10.1016/j.neuron.2015.09.027.

Phillips, K.A., Stimpson, C.D., Smaers, J.B., Raghanti, M.A., Jacobs, B., Popratiloff, A., Hof, P.R., Sherwood, C.C., 2015. The corpus callosum in primates: processing speed of axons and the evolution of hemispheric asymmetry. Proc. R. Soc. B Biol. Sci. 282, 1–9, 20151535. https://doi.org/10.1098/rspb.2015.1535.

Power, J.D., Cohen, A.L., Nelson, S.M., Wig, G.S., Barnes, K.A., Church, J.A., Vogel, A.C., Laumann, T.O., Miezin, F.M., Schlaggar, B.L., Petersen, S.E., 2011. Functional network organization of the human brain. Neuron 72, 665–678. https://doi.org/10.1016/j.neuron.2011.09.006.

Rilling, J.K., 2006. Human and nonhuman primate brains: are they allometrically scaled versions of the same design? Evol. Anthropol. 15, 65–77. https://doi.org/10.1002/evan.20095.

Rilling, J.K., 2014. Comparative primate neuroimaging: insights into human brain evolution. Trends Cogn. Sci. 18, 46–55. https://doi.org/10.1016/j.tics.2013.09.013.

Rilling, J.K., Insel, T.R., 1999. Differential expansion of neural projection systems in primate brain evolution. Neuroreport 10, 1453–1459. https://doi.org/10.1097/00001756-199905140-00012.

Rilling, J.K., van den Heuvel, M.P., 2018. Comparative primate connectomics. Brain Behav. Evol. 91, 170–179. https://doi.org/10.1159/000488886.

Rilling, J.K., Glasser, M.F., Preuss, T.M., Ma, X., Zhao, T., Hu, X., Behrens, T.E.J., 2008. The evolution of the arcuate fasciculus revealed with comparative DTI. Nat. Neurosci. 11, 426–428. https://doi.org/10.1038/nn2072.

Rilling, J.K., Scholz, J., Preuss, T.M., Glasser, M.F., Errangi, B.K., Behrens, T.E., 2012. Differences between chimpanzees and bonobos in neural systems supporting social cognition. Soc. Cogn. Affect. Neurosci. 7, 369–379. https://doi.org/10.1093/scan/nsr017.

Ringo, J.L., 1991. Neuronal interconnection as a function of brain size. Brain Behav. Evol. 38, 1–6.

Roberts, J.A., Perry, A., Lord, A.R., Roberts, G., Mitchell, P.B., Smith, R.E., Calamante, F., Breakspear, M., 2016. The contribution of geometry to the human connectome. Neuroimage 124, 379–393. https://doi.org/10.1016/j.neuroimage.2015.09.009.

Rubinov, M., 2016. Constraints and spandrels of interareal connectomes. Nat. Commun. 7, 13812. https://doi.org/10.1038/ncomms13812.

Rubinov, M., Sporns, O., 2010. Complex network measures of brain connectivity: uses and interpretations. Neuroimage 52, 1059–1069. https://doi.org/10.1016/j.neuroimage.2009.10.003.

Rubinov, M., Ypma, R.J.F., Watson, C., Bullmore, E.T., 2015. Wiring cost and topological participation of the mouse brain connectome. Proc. Natl. Acad. Sci. U.S.A. 112, 10032–10037. https://doi.org/10.1073/pnas.1420315112.

Sakai, T., Hata, J., Ohta, H., Shintaku, Y., Kimura, N., Ogawa, Y., Sogabe, K., Mori, S., Okano, H.J., Hamada, Y., Shibata, S., Okano, H., Oishi, K., 2018. The japan monkey centre primates brain imaging repository for comparative neuroscience: an archive of digital records including records for endangered species. Primates 59, 553–570. https://doi.org/10.1007/s10329-018-0694-3.

Salvador, R., Suckling, J., Coleman, M.R., Pickard, J.D., Menon, D., Bullmore, E., 2005. Neurophysiological architecture of functional magnetic resonance images of human brain. Cereb. Cortex 15, 1332–1342. https://doi.org/10.1093/cercor/bhi016.

Samu, D., Seth, A.K., Nowotny, T., 2014. Influence of wiring cost on the large-scale architecture of human cortical connectivity. PLoS Comput. Biol. 10, e1003557. https://doi.org/10.1371/journal.pcbi.1003557.

Sarwar, T., Ramamohanarao, K., Zalesky, A., 2019. Mapping connectomes with diffusion MRI: deterministic or probabilistic tractography? Magn. Reson. Med. 81, 1368–1384. https://doi.org/10.1002/mrm.27471.

Schoenemann, P.T., 2013. Hominid Brain Evolution. In: Bailey, D.H., Geary, D.C. (Eds.), A Companion to Paleoanthropology. Blackwell Publishing Ltd, Oxford, pp. 136–164. https://doi.org/10.1002/9781118332344.ch8.

Scholtens, L.H., Schmidt, R., de Reus, M.A., van den Heuvel, M.P., 2014. Linking macroscale graph analytical organization to microscale neuroarchitectonics in the macaque connectome. J. Neurosci. 34, 12192–12205. https://doi.org/10.1523/JNEUROSCI.0752-14.2014.

Scholtens, L.H., de Reus, M.A., de Lange, S.C., Schmidt, R., van den Heuvel, M.P., 2018. An MRI Von Economo–Koskinas atlas. Neuroimage 170, 249–256. https://doi.org/10.1016/j.neuroimage.2016.12.069.

Semendeferi, K., Lu, A., Schenker, N., Damasio, H., 2002. Humans and great apes share a large frontal cortex. Nat. Neurosci. 5, 272–276. https://doi.org/10.1038/nn814.

Senden, M., Deco, G., De Reus, M.A., Goebel, R., Van Den Heuvel, M.P., 2014. Rich club organization supports a diverse set of functional network configurations. Neuroimage 96, 174–182. https://doi.org/10.1016/j.neuroimage.2014.03.066.

Shanahan, M., 2012. The brain's connective core and its role in animal cognition. Philos. Trans. R. Soc. B Biol. Sci. 367, 2704–2714. https://doi.org/10.1098/rstb.2012.0128.

Shih, C.-T., Sporns, O., Yuan, S.-L., Su, T.-S., Lin, Y.-J., Chuang, C.-C., Wang, T.-Y., Lo, C.-C., Greenspan, R.J., Chiang, A.-S., 2015. Connectomics-based analysis of information flow in the Drosophila brain. Curr. Biol. 25, 1249–1258. https://doi.org/10.1016/j.cub.2015.03.021.

Simonyan, K., 2014. The laryngeal motor cortex: its organization and connectivity. Curr. Opin. Neurobiol. 28, 15–21. https://doi.org/10.1016/j.conb.2014.05.006.

Simonyan, K., Ostuni, J., Ludlow, C.L., Horwitz, B., 2009. Functional but not structural networks of the human laryngeal motor cortex show left hemispheric lateralization during syllable but not breathing production. J. Neurosci. 29, 14912–14923. https://doi.org/10.1523/JNEUROSCI.4897-09.2009.

Smaers, J.B., Soligo, C., 2013. Brain reorganization, not relative brain size, primarily characterizes anthropoid brain evolution. Proc. R. Soc. B Biol. Sci. 280, https://doi.org/10.1098/rspb.2013.0269.

Smith, S.M., Vidaurre, D., Beckmann, C.F., Glasser, M.F., Jenkinson, M., Miller, K.L., Nichols, T.E., Robinson, E.C., Salimi-Khorshidi, G., Woolrich, M.W., Barch, D.M., Uğurbil, K., Van Essen, D.C., 2013. Functional connectomics from resting-state fMRI. Trends Cogn. Sci. 17, 666–682. https://doi.org/10.1016/j.tics.2013.09.016.

Sporns, O., 2013. Network attributes for segregation and integration in the human brain. Curr. Opin. Neurobiol. 23, 162–171. https://doi.org/10.1016/j.conb.2012.11.015.

Sporns, O., Betzel, R.F., 2016. Modular brain networks. Annu. Rev. Psychol. 67, 613–640. https://doi.org/10.1146/annurev-psych-122414-033634.

Sporns, O., Zwi, J.D., 2004. The small world of the cerebral cortex. Neuroinformatics 2, 145–162. https://doi.org/10.1385/NI:2:2:145.

Sporns, O., Tononi, G., Kötter, R., 2005. The human connectome: a structural description of the human brain. PLoS Comput. Biol. 1, 245–251. https://doi.org/10.1371/journal.pcbi.0010042.

Stephan, K.E., Kamper, L., Bozkurt, A., Burns, G.A.P.C., Young, M.P., Kötter, R., 2001. Advanced database methodology for the collation of connectivity data on the macaque brain (CoCoMac). Philos. Trans. R. Soc. B Biol. Sci. 356, 1159–1186. https://doi.org/10.1098/rstb.2001.0908.

Stiso, J., Bassett, D.S., 2018. Spatial embedding imposes constraints on neuronal network architectures. Trends Cogn. Sci. 22, 1127–1142. https://doi.org/10.1016/j.tics.2018.09.007.

Stout, D., Hecht, E.E., 2017. Evolutionary neuroscience of cumulative culture. Proc. Natl. Acad. Sci. U.S.A. 114, 7861–7868. https://doi.org/10.1073/pnas.1620738114.

Thiebaut de Schotten, M., Croxson, P.L., Mars, R.B., 2018. Large-scale comparative neuroimaging: where are we and what do we need? Cortex 1–15. https://doi.org/10.1016/j.cortex.2018.11.028.

Vaessen, M.J., Hofman, P.A., Tijssen, H.N., Aldenkamp, A.P., Jansen, J.F.A., Backes, W.H., 2010. The effect and reproducibility of different clinical DTI gradient sets on small world brain connectivity measures. Neuroimage 51, 1106–1116. https://doi.org/10.1016/j.neuroimage.2010.03.011.

Vaishnavi, S.N., Vlassenko, A.G., Rundle, M.M., Snyder, A.Z., Mintun, M.A., Raichle, M.E., 2010. Regional aerobic glycolysis in the human brain. Proc. Natl. Acad. Sci. U.S.A. 107, 17757–17762. https://doi.org/10.1073/pnas.1010459107.

van den Heuvel, M.P., Sporns, O., 2011. Rich-club organization of the human connectome. J. Neurosci. 31, 15775–15786. https://doi.org/10.1523/JNEUROSCI.3539-11.2011.

van den Heuvel, M.P., Sporns, O., 2013a. Network hubs in the human brain. Trends Cogn. Sci. 17, 683–696. https://doi.org/10.1016/j.tics.2013.09.012.

van den Heuvel, M.P., Sporns, O., 2013b. An anatomical substrate for integration among functional networks in human cortex. J. Neurosci. 33, 14489–14500. https://doi.org/10.1523/JNEUROSCI.2128-13.2013.

van den Heuvel, M.P., Kahn, R.S., Goni, J., Sporns, O., 2012. High-cost, high-capacity backbone for global brain communication. Proc. Natl. Acad. Sci. U.S.A. 109, 11372–11377. https://doi.org/10.1073/pnas.1203593109.

van den Heuvel, M.P., Bullmore, E.T., Sporns, O., 2016. Comparative Connectomics. Trends Cogn. Sci. 20, 345–361. https://doi.org/10.1016/j.tics.2016.03.001.

Van Essen, D.C., 1997. A tension-based theory of morphogenesis and compact wiring in the central nervous system. Nature https://doi.org/10.1038/385313a0.

Van Essen, D.C., Dierker, D.L., 2007. Surface-based and probabilistic atlases of primate cerebral cortex. Neuron 56, 209–225. https://doi.org/10.1016/j.neuron.2007.10.015.

van Wijk, B.C.M., Stam, C.J., Daffertshofer, A., 2010. Comparing brain networks of different size and connectivity density using graph theory. PLoS One 5, e13701. https://doi.org/10.1371/journal.pone.0013701.

Vertes, P.E., Alexander-Bloch, A.F., Gogtay, N., Giedd, J.N., Rapoport, J.L., Bullmore, E.T., 2012. Simple models of human brain functional networks. Proc. Natl. Acad. Sci. U.S.A. 109, 5868–5873. https://doi.org/10.1073/pnas.1111738109.

Visser, M., Jefferies, E., Embleton, K.V., Lambon Ralph, M.A., 2012. Both the middle temporal gyrus and the ventral anterior temporal area are crucial for multimodal semantic processing: distortion-corrected fMRI evidence for a double gradient of information convergence in the temporal lobes. J. Cogn. Neurosci. 24, 1766–1778. https://doi.org/10.1162/jocn_a_00244.

Watts, D.J., Strogatz, S.H., 1998. Collective dynamics of "small-world" networks. Nature 393, 440–442. https://doi.org/10.1038/30918.

Wei, T., Liang, X., He, Y., Zang, Y., Han, Z., Caramazza, A., Bi, Y., 2012. Predicting conceptual processing capacity from spontaneous neuronal activity of the left middle temporal gyrus. J. Neurosci. 32, 481–489. https://doi.org/10.1523/JNEUROSCI.1953-11.2012.

Whiting, B., Barton, R.A., 2003. The evolution of the cortico-cerebellar complex in primates: anatomical connections predict patterns of correlated evolution. J. Hum. Evol. 44, 3–10. https://doi.org/10.1016/S0047-2484(02)00162-8.

Yeo, B.T.T., Krienen, F.M., Sepulcre, J., Sabuncu, M.R., Lashkari, D., Hollinshead, M., Roffman, J.L., Smoller, J.W., Zöllei, L., Polimeni, J.R., Fischl, B., Liu, H., Buckner, R.L., 2011. The organization of the human cerebral cortex estimated by intrinsic functional connectivity. J. Neurophysiol. 106, 1125–1165. https://doi.org/10.1152/jn.00338.2011.

Yu, Y., Herman, P., Rothman, D.L., Agarwal, D., Hyder, F., 2018. Evaluating the gray and white matter energy budgets of human brain function. J. Cereb. Blood Flow Metab. 38, 1339–1353. https://doi.org/10.1177/0271678X17708691.

Zalesky, A., Fornito, A., Cocchi, L., Gollo, L.L., Breakspear, M., 2014. Time-resolved resting-state brain networks. Proc. Natl. Acad. Sci. U.S.A. 111, 10341–10346. https://doi.org/10.1073/pnas.1400181111.

Zamora-López, G., Chen, Y., Deco, G., Kringelbach, M.L., Zhou, C., 2016. Functional complexity emerging from anatomical constraints in the brain: the significance of network modularity and rich-clubs. Sci. Rep. 6, 1–18. https://doi.org/10.1038/srep38424.

Zhang, K., Sejnowski, T.J., 2000. A universal scaling law between gray matter and white matter of cerebral cortex. Proc. Natl. Acad. Sci. U.S.A. 97, 5621–5626. https://doi.org/10.1073/pnas.090504197.

Zhu, Y., Sousa, A.M.M., Gao, T., Skarica, M., Li, M., Santpere, G., Esteller-Cucala, P., Juan, D., Ferrández-Peral, L., Gulden, F.O., Yang, M., Miller, D.J., Marques-Bonet, T., Imamura Kawasawa, Y., Zhao, H., Sestan, N., 2018. Spatiotemporal transcriptomic divergence across human and macaque brain development. Science 362 (80). https://doi.org/10.1126/science.aat8077eaat8077.

Zilles, K., Palomero-Gallagher, N., Amunts, K., 2013. Development of cortical folding during evolution and ontogeny. Trends Neurosci. 36, 275–284. https://doi.org/10.1016/j.tins.2013.01.006.