An edge-centric perspective on the human connectome: link communities in the brain

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Brain function depends on efficient processing and integration of information within a complex network of neural interactions, known as the connectome. An important aspect of connectome architecture is the existence of community structure, providing an anatomical basis for the occurrence of functional specialization. Typically, communities are defined as groups of densely connected network nodes, representing clusters of brain regions. Looking at the connectome from a different perspective, instead focusing on the interconnecting links or edges, we find that the white matter pathways between brain regions also exhibit community structure. Eleven link communities were identified: five spanning through the midline fissure, three through the left hemisphere and three through the right hemisphere. We show that these link communities are consistently identifiable and investigate the network characteristics of their underlying white matter pathways. Furthermore, examination of the relationship between link communities and brain regions revealed that the majority of brain regions participate in multiple link communities. In particular, the highly connected and central hub regions showed a rich level of community participation, supporting the notion that these hubs play a pivotal role as confluence zones in which neural information from different domains merges.

1. Introduction

The human brain is a complex network of neuronal interactions which facilitates efficient processing and integration of information. The macroscopic architecture of this intricate network, known as the human connectome [1], can be studied using graph theory, providing a formal network description in which brain regions are represented by nodes and their interconnecting white matter pathways by links or edges [2]. An architectural feature of particular interest, the subject of a large number of recent studies [3–7], is the connectome’s community structure, describing the existence of groups of nodes (i.e. brain regions) with high levels of connectivity between members of the same group and low connectivity between groups [8]. These ‘communities’ can be unveiled using specialized algorithms and typically reflect subsystems or building blocks of the network [9]. For neural systems, the presence of groups of densely interconnected nodes has been demonstrated in both human and animal brain networks [10–12]. The formation of neural communities has been suggested to be an important architectural attribute for functional specialization and segregation of information processing [10,13].

In addition to the traditional view on communities as groups of nodes, the community structure of complex networks may also be described from an edge-centric perspective, instead identifying groups of links or edges [14,15]. Such link communities have been reported for several empirical networks, including metabolic networks, mobile phone networks and social networks, and have been shown to highlight different subsystems than node-based communities [14–17]. Furthermore, link communities allow the examination of interaction between node and link properties in a network. This in particular includes the identification of...
‘community hot spots’ where links from multiple communities come together at a single node, reflecting the involvement of a node in multiple subsystems [14,15]. Reported overlap of resting-state functional brain networks [18,19] and overlap of communities in volumetric coupling networks [5] indicate that also brain network nodes are not always likely to belong to a single community, making an edge-centric perspective on community structure particularly suitable to provide further insight into the network organization of the brain.

In this study, we explore the link community structure of the brain’s white matter pathways using macroscopic connectome maps of the healthy adult brain derived from in vivo diffusion imaging measurements. We demonstrate that the connectome exhibits multiple link communities and we assess their robustness to variations in the underlying connectome data. To provide support for a possible first interpretation of the identified link communities, we extend our edge-centric perspective from communities to individual white matter pathways. By monitoring the effect of the hypothetical removal of individual edges, several network properties are estimated for each of the connectome’s connections, which are then compared across link communities. Furthermore, the relationship between link communities and network nodes is examined by assessing the overlap of link communities at brain regions. We report a pronounced role of a small collective of central hub regions [20,21] as ‘link community hot spots’ in the brain, establishing a connection between the edge-centric perspective adopted here and node-based findings.

2. Connectome reconstruction
The brain’s network of white matter pathways was represented by a group-averaged connectome map, including in vivo magnetic resonance imaging data of 50 healthy participants (see the electronic supplementary material). In short, for each participant, two diffusion weighted imaging sets with opposite k-space readouts were acquired at the University Medical Center Utrecht [21,22]. After correction for possible eddy-current [23] and susceptibility [24] distortions, the principal diffusion direction in each 2 × 2 × 2 mm voxel was determined using a robust tensor fitting method [25]. Fibre pathways were reconstructed by following these principal diffusion directions from voxel to voxel with the Fibre Assignment by Continuous Tracking algorithm [26]. In addition, a T1-weighted image was acquired to parcellate the cortical surface into 68 anatomically segregated cortical brain regions (34 in each hemisphere) using the FReeSurfer software suite (http://surfer.nmr.mgh.harvard.edu/).

The macroscopic anatomical brain network of each participant was reconstructed by combining the cortical parcellation with the estimated white matter fibre tracts. The 68 anatomically segregated cortical brain regions from the parcellation were defined to be the nodes of the network and, for each pair of regions i and j, an edge was placed between the corresponding nodes if a reconstructed fibre touched both regions i and j. The 50 resulting individual brain network reconstructions were put together to form a group-averaged connectome map by including only those edges that were found to be present in at least 60% (30) of the participants [27]. A detailed description of the outlined procedures and some basic statistics of the reconstructed brain networks are provided in the electronic supplementary material. An extensive analysis concerning the averaging procedure, based on the same sample of 50 healthy participants, was recently published as a separate article [27]. The group-averaged connectome map has been made available on the website of the Dutch Connectome Lab (http://www.dutchconnectomelab.nl).

3. Link communities
Link communities of the group-averaged connectome map were identified using the network’s associated line graph [14]. This line graph is formed by defining a ‘node’ for every link in the connectome map and a ‘connection’ between two of these nodes if the links that they represent have a common endpoint (figure 1a). Subsequently, communities...
within the line graph, the link communities, are identified by applying a traditional (node-based) community detection method to the line graph. Since nodes of the line graph correspond to links of the original connectome map, detected communities of densely interconnected line graph nodes map one-to-one to link communities of the connectome (figure 1b). For community detection on the line graph, we applied Rosvall and Bergstrom’s Infomap algorithm [28], identifying network partitions that minimize the description length of an infinite random walk on the network (see the electronic supplementary material).

Using this approach, the group-averaged connectome map revealed 11 link communities (figure 2). Five of the 11 identified communities spanned through the midline fissure, being (1) the precuneus/occipital (Pr/Oc) community, mostly spanning between brain regions from the occipital lobe, (2) the cingulate community, comprising anterior–posterior white matter connections that originate from the cingulum tract, (3) the medial frontal (medF) community of pathways between frontal and a few temporal regions, and (4,5) two homologous communities centred around the left and right paracentral (PC) lobule. The six other communities were found to be predominantly confined to a single hemisphere, forming three communities in the left hemisphere and three homologous communities in the right hemisphere. These link communities are: (6,7) the left and right middle frontal (midF) communities, comprising connections between frontal and insular regions, (8,9) the middle temporal (midT) communities, involving connections between temporal regions as well as connections between the temporal lobe and other lobes and (10,11) the parahippocampal/entorhinal (Ph/Er) communities, mainly involving projections from regions in the medial wall of the temporal lobe.

In §§4–6, we examine the consistency of these link communities and the individual white matter pathways that constitute them.
Figure 3. Consistency matrices. (a) The consistency of the identified link communities was verified by repeating community detection for 1000 bootstrap samples. The consistency matrix lists for every pair of links how often these links were clustered together (i.e. assigned to the same community) across bootstrap samples. As the rows and columns of the matrix are ordered according to the identified communities, the blocks on the diagonal reflect the consistency of a community, while off-diagonal stripes indicate exchange of connections between communities. (b) A similar matrix was formed by counting how often links were assigned to the same community when performing link community detection on individual brain network reconstructions. Although individual reconstructions are more susceptible to measurement errors and thus inevitably display more variability [27], the pattern of clustering scores was found to be highly similar to the observed clustering across bootstrap samples ($r = 0.87$, Pearson's correlation coefficient).

4. Consistency

To examine the level of robustness of link communities to variations in the underlying connectome data, from the total sample of 50 participants, individual brain network reconstructions of 15 participants were randomly selected and averaged using a 60% group threshold. This process was repeated a thousand times, generating group-averaged brain networks for 1000 bootstrap samples, all exhibiting their own link community pattern. Next, for each pair of links from the original group-averaged connectome, it was assessed in how many of the bootstrap samples in which these links were simultaneously present, they also appeared in the same community. Outcomes were scaled between 0 and 100%, with 100% reflecting that the pair of links was consistently clustered together across bootstrap samples.

The collected clustering scores (shown in figure 3a) were found to demonstrate a high consistency of the identified link communities. Across all 11 communities, connections that were assigned to the same link community in the group-averaged connectome (figure 2) also shared their community assignment in 91% of the bootstrap samples. The most consistent communities were the Pr/Oc, cingulate and both PC communities (all having an average score of 99%), reflected by the dark diagonal blocks in figure 3a. The least consistent communities were the left Ph/Er and left midT community, still displaying consistency percentages of 76% and 77%, respectively. The somewhat lower consistency of these link communities appears to be caused by relatively ‘fuzzy’ boundaries between bilaterally segregated communities in the same hemisphere. As reflected by the off-diagonal horizontal and vertical lines in figure 3a, connections from the Ph/Er communities were in some bootstrap samples instead assigned to the ipsilateral midT or midF communities. A similar exchange of connections was observed between the midT and midF communities.

An additional comparison of link communities identified on individual brain network reconstructions revealed a highly similar consistency pattern ($r = 0.87$, figure 3b), but with lower overall consistency values. Connections that were assigned to the same link community in the group-averaged connectome also shared their community assignment in 63% of the participants, the most consistent communities being the PC communities (left 90% and right 93%). For comparison, connections from different link communities in the group-averaged connectome shared their community assignment in only 7% of the participants. Together, these scores indicate that link communities observed in individual participants are quite similar to those identified on the group level. Clustering between connections from ipsilateral midT and midF communities was again observed to be elevated, underscoring that the boundary between these communities is relatively fuzzy.

5. Comparing communities by connection features

In order to obtain more insight into the identified link communities, it would be of interest to explore the network characteristics of the underlying white matter pathways. However, most network metrics capture properties of (single) nodes or the entire network, overlooking properties of individual connections. A notable exception is a metric known as ‘edge betweenness’, which assigns to each connection the fraction of shortest paths in which it participates [8]. Although a very useful and commonly applied measure, computing this betweenness metric still covers only a single aspect of the role of a connection in the network.

Inspired by ‘lesion’ models that assess the vulnerability of brain networks to simulated damage [21,29–32], we estimated several additional characteristics of the connectome’s connections by monitoring the effect of their hypothetical removal. To this end, traditional network metrics of the intact group-averaged connectome map were compared with those of slightly modified maps, missing only the single connection whose features were to be estimated. Measuring the percentage change caused by the absence of a connection in the modified maps, traditional (node oriented) metrics were effectively mapped to edge-centric ones, estimating the relevance of a connection for the network properties assessed by the metrics.
Figure 4 displays the results of four such ‘edge removal metrics’, measuring the relevance of the connections of the group-averaged connectome map for (i) the characteristic path length, (ii) the clustering coefficient, (iii) global communicability within the entire network and (iv) local communicability between the endpoints of a connection (details about the metrics are provided in the electronic supplementary material). Together with edge betweenness (also displayed in figure 4), a total of five different edge-centric measures were collected for each connection.

Aggregating the collected connection scores per link community (figure 5), edge-centric metrics were found to vary strongly within communities, suggesting that link communities comprise a heterogeneous mixture of connections with varying roles in the network. As shown in figure 5, the mean connection scores of link communities with respect to path length, clustering, local communicability and betweenness fluctuated only marginally, with none of the communities differing significantly from the global mean (i.e. the average over all connections). Interestingly, edge removal scores with respect to global communicability formed an exception, displaying significantly higher values than the global mean in the Pr/Oc and cingulate community, while significantly lower levels were observed in the left midT and the left/right midF and Ph/Er communities ($p < 0.05$, Bonferroni corrected, permutation tests). Also the connections of the left and right PC communities displayed a substantially (but not significantly) higher average impact on global communicability (exceeding the global mean by, respectively, 41% and 60%), implying that the Pr/Oc, cingulate and PC communities must comprise many connections with a pronounced relevance for communicability within the brain network.

6. Relationship with brain regions: community overlap

An important advantage of identifying communities of links instead of nodes is that community participation of brain regions is not limited to a single community. Instead, the white matter projections of a brain region may be divided over multiple link communities, indicating the involvement of this region in multiple subsystems [14,15]. Investigating how the presented edge-centric findings relate to the nodes of the network, we examined the number of communities coming together in each single node, providing a measure for the link diversity of brain regions. Figure 6 illustrates the distribution of these participation numbers over the brain regions. Approximately 56% of the brain regions (38 out of 68) were found to participate in multiple link communities, with their nodal participation numbers ranging from two to a maximum of eight communities per node. Such a relatively diverse link community participation of the nodes may be related to
recent observations showing that many brain regions participate in multiple functional domains and thus are, to some extent, involved in multimodal neural processes [19,33–35].

Triggered by the findings depicted in figure 6, showing that a selective number of brain regions even participated in as many as five, seven or eight of the 11 identified link communities, we specifically examined the community participation of previously reported ‘hub nodes’. Hub nodes are highly connected brain regions with a central position in the network [36] and have been noted to be involved in a variety of cognitive tasks and functions [7,37,38]. Together, the hubs of the brain form a densely connected ‘core’ or ‘rich club’ [21,39–41] which has been suggested to play a role in the integration of information between functional domains [19,42]. Considering these properties, we hypothesized a pronounced participation of rich club hubs in the identified link communities. In agreement with previous reports [21,43,44], rich club hubs were taken to include the left/right superior cingulate, right midF, left midT, left midF, right midT, left PC, right PC, left Ph/Er, right Ph/Er, Pr/Oc.

Figure 5. Connection scores per link community displayed as box plots. The outcomes of each edge-centric metric were first divided by the average over all connections, so that values above unity indicate a larger-than-average relevance and values below unity indicate a lower-than-average relevance.

Figure 6. Overlap of link communities at brain regions. (a) The colour of each brain region on the cortical surface indicates the number of link communities in which it was found to participate. The colours used on the cortical surface are identical to those in the histogram depicted in (b). The majority (56%) of the brain regions participated in multiple communities, their participation numbers ranging up to a maximum of eight of the 11 identified communities.
after performing a linear regression to compensate for the positive relationship between degree and community participation (more attached links generally giving access to more communities, figure 7b), indicating that the high community participation of rich club hubs is not only attributable to their high degree, but also to their specific wiring pattern in the overall brain network. Third, although some non-hub nodes also presented high community participation, reflecting a general heterogeneity of the nodes of the network [34,42], all hub regions scored among the top 14 nodes with a participation number of four or higher (figure 7b). Taken together, our findings support previous suggestions that brain hubs operate on the boundaries between communities [19,42] and therefore form ideal candidates to facilitate integration of information and intermodule communication [20,36,37].

7. Discussion

Our study shows that the brain’s white matter pathways display a rich and diverse community pattern. Examining the line graph of an anatomical brain network derived from diffusion imaging data, 11 link communities were observed, forming a Pr/Oc, cingulate and medF community and left and right PC, midF, midT and Ph/Er communities (figure 2). Moreover, the identified link communities were found to be highly consistent across bootstrap samples, indicating a good robustness to variations in the underlying connectome data (figure 3).

The biological meaning of link communities in the brain is not immediately clear and very much open to scientific debate. In network literature, community detection is generally applied to uncover a priori unknown subsystems or building blocks of the network [8,9,15,45]. This view on communities is also firmly anchored in the objective of community detection algorithms to find dense clusters of nodes or links that are relatively loosely attached to the rest of the network. Considering that functional brain networks are shaped by the underlying structural connections [46–48], one could therefore speculate that link communities form an anatomical substrate for functionally specialized subsystems in the brain, as is also often suggested for node communities [10,13]. In a first attempt to aid the interpretation of link communities using data-driven analyses, assessment of several network characteristics of individual white matter pathways showed that connection features vary strongly within link communities (figure 5). This observation may indicate that link communities do not form collections of similar pathways, but rather comprise a mixture of connections with varying roles in the network. Future studies are needed to investigate the potential biological relevance of such an arrangement of white matter connections and the biological meaning of link communities in general.

An interesting feature of link communities is that links from multiple communities may come together at a single brain region, allowing the identification of ‘community hot spots’. Among other regions, putative hub regions such as the insula, precuneus and superior frontal cortex were found to be involved in a variety of communities (figure 6). This diverse community participation of brain regions might reflect a multimodal internal organization emerging from different (functional) subparts. In favour of this hypothesis, the anterior part of the insula has been shown to project to the middle and inferior temporal cortex, to frontal regions and to the anterior
cingulate cortex, while the middle-posterior insula projects to premotor and sensorimotor regions and the posterior mid-cingulate cortex [49–51]. Similar functional specialization has been suggested for other regions with high community participation. For instance, examinations of the connectivity profile of the precuneus suggest the existence of structurally and functionally diverse anterior, posterior and central parts [37,52,53], confirming our observation of both the left and right precuneus to participate in a large number of link communities (figure 6). Also the superior frontal cortex, which showed the highest participation number, has been suggested to exhibit several functionally distinct subparts [54], underscoring a possible relationship between link community involvement and internal heterogeneity of brain regions. It may therefore be relevant for future studies to investigate whether link communities could be used to create finer parcelation templates and to examine how link communities are affected by the adoption of such templates [55].

The marked involvement of hub regions in a wide variety of link communities also supports the idea that brain hubs may play a pivotal role as confluence zones in which neural information from different domains merges [36]. All link communities were found to be directly attached to at least two different regions from a central hub collective [11,21] and participation levels of hub nodes significantly exceeded those of non-hubs. This distributed nature and diverse connectivity of hub regions with respect to link communities aligns with recent findings on the importance of hubs for the integration of functional subsystems in the cat and human brain [19,42] and the similarly pronounced participation of hub regions in node communities [4,20,34]. Moreover, a recent report by Crossley et al. [7] based on a meta-analysis of task-related activation studies showed that brain hubs were coactivated by a diverse range of experimental tasks, suggesting that hubs facilitate a large functional repertoire. It would be of interest for future studies to examine whether connections of a link community may correspond to coactivations of a specific set of behavioural domains, potentially providing a connection between this diverse coactivation of hubs and their link community participation.

Finally, it should be noted that the link communities presented in this article were obtained using unweighted brain networks, considering only the presence or the absence of white matter connections between brain regions without making inferences on the quality or strength of these connections. Although it is, in principle, possible to generalize the adopted link community detection approach to weighted networks [56], it is unclear whether a weighted approach is preferable and, if so, which choice of connection weights (fractional anisotropy, streamline count, streamline density, magnetization transfer ratio, etc.) would be most suitable. Instead, by keeping the results as general as possible, focusing on the topological structure of the network, the identified link communities can naturally serve as ‘link categories’ to illuminate contrasts with respect to any type of connection weight. Considering recently reported connectivity deficits in schizophrenia patients found using link categories [57,58] and the tendency of neurodegenerative diseases to target subsystems of the brain [59,60], link communities could prove to be a fruitful instrument for future case-control studies.

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