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Title: Deep learning models of cognitive processes constrained by human brain connectomes

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1 **Abstract**

2 Decoding cognitive processes from recordings of brain activity has been an active topic in
3 neuroscience research for decades. Traditional decoding studies focused on pattern classification in
4 specific regions of interest and averaging brain activity over many trials. Recently, brain decoding
5 with graph neural networks has been shown to scale at fine temporal resolution and on the full brain,
6 achieving state-of-the-art performance on the human connectome project benchmark. The reason
7 behind this success is likely the strong inductive connectome prior that enables the integration of
8 distributed patterns of brain activity. Yet, the nature of such inductive bias is still poorly understood.
9 In this work, we investigate the impact of the inclusion of multiple path lengths (through high-order
10 graph convolution), the homogeneity of brain parcels (graph nodes), and the type of interactions
11 (graph edges). We evaluate the decoding models on a large population of 1200 participants, under 21
12 different experimental conditions, acquired from the Human Connectome Project database. Our
13 findings reveal that the optimal choice for large-scale cognitive decoding is to propagate neural
14 dynamics within empirical functional connectomes and integrate brain dynamics using high-order
15 graph convolutions. In this setting, the model exhibits high decoding accuracy and robustness against
16 adversarial attacks on the graph architecture, including randomization in functional connectomes and
17 lesions in targeted brain regions and networks. The trained model relies on biologically meaningful
18 features for the prediction of cognitive states and generates task-specific graph representations
19 resembling task-evoked activation maps. These results demonstrate that a full-brain integrative model
20 is critical for the large-scale brain decoding. Our study establishes principles of how to effectively
21 leverage human connectome constraints in deep graph neural networks, providing new avenues to
22 study the neural substrates of human cognition at scale.

23

24 **Keywords:** fMRI, cognitive decoding, graph convolutional networks, human connectome

25 **1. Introduction**

26 Modern imaging techniques, such as functional magnetic resonance imaging (fMRI), provide an
27 opportunity to map the neural substrates of cognition in-vivo, and to decode cognitive processes non-
28 invasively. Brain decoding has been an active topic since Haxby and colleagues first proposed the
29 idea of using fMRI brain responses to predict the category of visual stimuli presented to a subject
30 (Haxby et al., 2001). Nowadays, a variety of computational models have been proposed in the field,
31 including multi-voxel pattern recognition (Haxby et al., 2014; Poldrack, 2011), linear regression
32 models (Huth et al., 2012; Nishimoto et al., 2011), as well as nonlinear models such as deep artificial
33 neural networks (Li and Fan, 2019; Wang et al., 2020). These decoding studies have been mainly
34 focused on distinguishing the spatial patterns of brain activation within a small region of interest
35 modulated by a few experimental tasks. Such brain decoders have gained many successes when
36 tackling unimodal cognitive processes, in particular vision (Schrimpf et al., 2020), and focusing on
37 specific brain regions, for example in the ventral visual stream network (Haan and Cowey, 2011). We
38 recently proposed a graph neural network (GNN) model to decode high-order cognitive functions
39 using distributed neural activity across large-scale brain networks (Zhang et al. 2021). This GNN
40 model relied on a fixed human connectome as a static graph, embedded task-evoked brain activity as
41 dynamic signals on the graph, and integrated within-network context of spatiotemporal dynamics
42 underlying cognitive processes through deep graph convolutions. We have shown that GNN can
43 successfully decode a variety of cognitive tasks in a large population of healthy subjects, achieving
44 high decoding performance on the Human Connectome Project (HCP) task benchmark (Zhang et al.,
45 2021). However, it remains unclear how the choices of connectome priors and the interactions at
46 different scales impact on large-scale cognition decoding.

47 Here, we investigate a form of graph convolution called ChebNet, which has the ability to propagate
48 information over a relatively larger neighborhood on the graph and integrate neural activity in a
49 multiscale manner, ranging from segregated brain activity from local areas ($K=0$), to information
50 integration within the same brain circuit/network ($K=1$) as well as between multiple networks ($K>1$),
51 and eventually towards the full brain. We propose a multi-domain decoding model using ChebNet

52 graph convolutions and investigate how to implement human connectome constraints in the decoding
53 pipeline, i.e. the implementation of multiscale functional integration and the construction of a proper
54 graph architecture. The connectome constraints start with a brain parcellation, which divides the
55 whole brain into hundreds of brain regions, and a brain graph that captures hierarchical and modular
56 structures in brain organization. A variety of parcellation schemes have been proposed in the literature,
57 see the review paper by (Eickhoff et al., 2018), which subdivide the entire cortex into non-
58 overlapping regions based on connectivity profiles derived from diffusion tractography (Fan et al.,
59 2016), functional organization (Yeo et al., 2011; Schaefer et al., 2018), or multimodal imaging
60 features (Glasser et al., 2016). As the abstract representation of human connectome, a brain graph
61 captures the network organization of the brain structure and function, by using anatomical and
62 functional connectivity, in both healthy and diseased populations (Bassett and Bullmore, 2009;
63 Bullmore and Sporns, 2009; Bullmore and Bassett, 2011). Brain atlas and connectivity are the two
64 key components to define the nature of interactions in GNN, with the scale of functional interactions
65 between areas specified by the path length of information propagation, i.e. K-order in ChebNet.
66 Studies have shown that the edge-sparsified graphs achieved superior performance on graph learning
67 benchmarks (Ye and Ji, 2021). Whether the edge-sparsified graphs outperform densely connected
68 human connectomes in the field of large-scale cognitive decoding remains unknown.

69 In the current study, we evaluate the ChebNet decoding model on a large population of 1200
70 participants, under 21 different experimental conditions, acquired from the task-fMRI database from
71 the Human Connectome Project (HCP). We explore the optimal choices of functional integration and
72 graph architectures on this decoding benchmark, including the resolution or homogeneity of brain
73 parcels (nodes), the type of interactions (edges), the inclusion of multiple path lengths on graphs
74 (graph convolutions), and the sparsity of brain graphs. Moreover, we assess the robustness of brain
75 decoding by introducing perturbations on the graph architecture, for instance network
76 misspecifications due to random rewiring and node attacks. Lastly, we visualize the contributing
77 salient neuroimaging features and the learned graph representations (i.e. activations of the last
78 ChebNet layer) of the decoding model and compare them to the findings in the neuroscience literature.

79 **2. Material and methods**

80 2.1. fMRI Datasets and Preprocessing

81 We used the block-design task-fMRI dataset from the Human Connectome Project S1200 release
82 (https://db.humanconnectome.org/data/projects/HCP_1200). The minimal preprocessed fMRI data in
83 both NIFTI and CIFTI formats were selected. The preprocessing pipelines includes two steps (Glasser
84 et al., 2013): 1) fMRIVolume pipeline generates “minimally preprocessed” 4D time-series (i.e.
85 “.nii.gz” file) that includes gradient unwarping, motion correction, fieldmap-based EPI distortion
86 correction, brain-boundary-based registration of EPI to structural T1-weighted scan, non-linear
87 (FNIRT) registration into MNI152 space, and grand-mean intensity normalization. 2) fMRISurface
88 pipeline projects fMRI data from the cortical gray matter ribbon onto the individual brain surface and
89 then onto template surface meshes (i.e. “dtseries.nii” file), followed by surface-based smoothing using
90 a geodesic Gaussian algorithm. Further details on fMRI data acquisition, task design and
91 preprocessing can be found in (Barch et al., 2013; Glasser et al., 2013). The task fMRI database
92 includes seven cognitive domains, which are emotion, gambling, language, motor, relational, social,
93 and working memory. In total, there are 23 different experimental conditions. Considering the short
94 event design nature of the gambling trials (1.5s for button press, 1s for feedback and 1s for ITI) which
95 constrain the temporal resolution of our brain decoding pipeline (i.e. using a 10s time window), in the
96 following experiments, we excluded the two gambling conditions and only reported results on the
97 remaining 21 cognitive states. The detailed description of the tasks used in this study can be found in
98 (Barch et al., 2013; Zhang et al., 2021) and is also listed in Table 1.

99 2.2. Decoding brain activity using graph convolution

100 As a representative model for brain organization, brain graph has been widely used in the
101 neuroscience literature by associating nodes with brain regions and defining edges via anatomical or
102 functional connections (Bullmore and Sporns, 2009). Graph Laplacian and graph convolution
103 provides a generalized framework to analyze data defined on irregular domains, for instance social
104 networks and brain networks. Thus, a non-linear embedding of brain activity can be learned to project

105 the brain graph onto a low-dimensional representational space (Ortega et al., 2018), for instance
106 mapping the gradients of brain organization (Margulies et al., 2016). We recently found that the
107 convolutions on brain graph encoded the within-network interactions of neural dynamics in cognitive
108 tasks (Zhang et al., 2021). In this study, we applied a generalized form of graph convolution by using
109 high-order Chebyshev polynomials and explored the impact of the following factors: 1) high-order
110 interactions to encode both within- and between-network interactions; 2) different graph architectures,
111 ranging from local regions (spatial graph), to neural circuits (anatomical graph) and to functional
112 networks (functional graph); 3) different brain atlases at various resolutions.

113 **Table 1. Scanning parameters and experimental designs of HCP task-fMRI dataset.**

114 The entire dataset includes in total 21 cognitive states and 14,895 functional runs across the six
115 cognitive domains. By using a 10s-time window (i.e. 15 functional volumes at TR=0.72s), we cut
116 long task trials into multiple data samples and resulted in 138,662 data samples of fMRI signals.
117 These data samples constituted the whole dataset for model training and evaluation. Each functional
118 run may contain multiple data samples of fMRI time-series depending on the number of task trials in
119 the fMRI paradigm as well as the duration of each experimental condition. For instance, using a 10s-
120 time window, we generated 10 data samples from one motor functional run (10 trials with one sample
121 per trial) and 16 data samples from one working-memory functional run (8 trials with two samples per
122 trial).

Task Domains	#Subjects	#Runs	#Volumes per run	#Effective Sample size	#Con d	Min duration per block (sec)
Motor	1083	2	284	21,670	5	12
Language	1051	2	316	36,164	2	10
Emotion	1047	2	176	10,470	2	18
Social cognition	1051	2	274	21,020	2	23
Working- memory	1085	2	405	34,736	8	25

Relational processing	1043	2	232	14,602	2	16
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123 2.2.1. Step 1: construction of brain graph

124 The decoding pipeline started with a weighted graph $\mathcal{G} = (\mathcal{V}, \mathcal{E}, W)$, where \mathcal{V} is a parcellation of
125 cerebral cortex into N regions, \mathcal{E} is a set of connections between each pair of brain regions, with its
126 weights defined as $W_{i,j}$. Many alternative approaches can be used to build such brain graph \mathcal{G} , for
127 instance using different brain parcellation schemes and constructing various types of brain
128 connectomes. Here, we investigated multiple choices in both aspects. First, different parcellation
129 schemes were used, including 1) functional subdivision of the cortical surface derived from resting-
130 state functional networks (Yeo et al., 2011); 2) anatomical parcellation of both cortical and subcortical
131 cortex derived from diffusion tractography (Fan et al., 2016); 3) a multimodal cortical parcellation
132 bounded by sharp changes in cortical architecture, function, connectivity, and topography (Glasser et
133 al., 2016); 4) a multi-scale atlas, consisting of brain parcels at different resolutions (Schaefer et al.,
134 2018). Here, we used Glasser’s atlas as the default parcellation scheme, which achieved the highest
135 performance on decoding 21 task states (see Results section). Second, we investigated various types
136 of brain connectivity, i.e. edges between brain parcels, including 1) resting-state functional
137 connectivity (RSFC); 2) anatomical connectivity (AC) derived from whole-brain tractography; 3)
138 structural covariance (SC) of cortical thickness; 4) spatially adjacency (SP) in brain topology. Among
139 which, the graph architecture derived from the anatomical and functional connectivity indicate
140 biological or connectome constraints, while the spatial and structural graphs represent topological and
141 morphological constraints respectively.

142 2.2.2. Step 2: mapping of brain activity onto the graph

143 After the construction of brain graph (i.e. defining brain parcels and edges), for each functional run
144 and each subject, we mapped the preprocessed task-fMRI data (e.g. “dtseries.nii” file for cortical
145 parcellation, and “.nii.gz” file for volume parcellation) onto the set of brain parcels, resulting in a 2-
146 dimensional time-series matrix. We created a task label with the same length as the fMRI time-series

147 based on the experimental designs, e.g. task onsets and durations. Then, we used these task labels to
148 extract a short series of fMRI responses from each functional run, by first splitting the entire run into
149 multiple task blocks and then cutting the blocks into the chosen window sizes (discarding shorter time
150 windows). To be noted that, each functional run usually contains multiple task blocks and each block
151 is split into multiple bins of short time windows. As a result, we generated various numbers of fMRI
152 time-series for each cognitive task, i.e. a short time-series with duration of T for each of N brain
153 parcels, $x \in \mathbb{R}^{N \times T}$, along with a unique task label for each time-series. In total, the entire dataset
154 includes 14,895 functional runs across the six cognitive domains and over 1000 subjects for each
155 domain, and results in 138,662 data samples of fMRI signals $x \in \mathbb{R}^{N \times T}$ when using a 10s time
156 window (i.e. 15 functional volumes at TR=0.72s), and 3,586,670 data samples when using a single-
157 volume prediction.

158 2.2.3. Step 3: spatiotemporal graph convolutions using ChebNet

159 Graph convolution relies on the graph Laplacian, which is a smooth operator characterizing the
160 magnitude of signal changes between adjacent nodes. The normalized graph Laplacian is defined as:

$$161 \quad L = I - D^{-1/2} W D^{-1/2} \quad (1)$$

162 where D is a diagonal matrix of node degrees, I is the identity matrix, and W is the weight matrix
163 which is specified by either multimodal brain connectivity (weighted graph) or the spatial adjacency
164 in brain topology (binary graph). The eigendecomposition of Laplacian matrix is defined as $L =$
165 $U \Delta U^T$, where $U = (u_0, u_1, \dots, u_{N-1})$ is the matrix of Laplacian eigenvectors and is also called graph
166 Fourier modes, and $\Delta = \text{diag}(\lambda_0, \lambda_1, \dots, \lambda_{N-1})$ is a diagonal matrix of the corresponding eigenvalues,
167 specifying the frequency of the graph modes. In other words, the eigenvalues quantify the smoothness
168 of signal changes on the graph, while the eigenvectors indicate the patterns of signal distribution on
169 the graph.

170 For a signal x defined on graph, i.e. assigning a feature vector to each brain region, the convolution
171 between the graph signal $x \in \mathbb{R}^{N \times T}$ and a graph filter $g_\theta \in \mathbb{R}^{N \times T}$ based on graph \mathcal{G} , is defined as
172 their element-wise Hadamard product in the spectral domain, i.e.:

$$173 \quad x * g_\theta = U(U^T g_\theta) \odot (U^T x) = U G_\theta U^T x \quad (2)$$

174 where $G_\theta = \text{diag}(U^T g_\theta)$ and θ indicate a parametric model for graph convolution g_θ , $U =$
175 $(u_0, u_1, \dots, u_{N-1})$ is the matrix of Laplacian eigenvectors and $U^T x$ is actually projecting the graph
176 signal onto the full spectrum of graph modes. Equation (2) provided an easy way of calculating the
177 graph convolution through a series of operations of matrix multiplication. To avoid calculating the
178 spectral decomposition of the graph Laplacian, ChebNet convolution (Defferrard et al., 2016) uses a
179 truncated expansion of the Chebychev polynomials, which are defined recursively by:

$$180 \quad T_k(x) = 2T_{k-1}(x) - T_{k-2}(x), \quad T_0(x) = 1, T_1(x) = x \quad (3)$$

181 Consequently, the graph convolution is defined as:

$$182 \quad x * g_\theta = \sum_{k=0}^K \theta_k T_k(\tilde{L})x \quad (4)$$

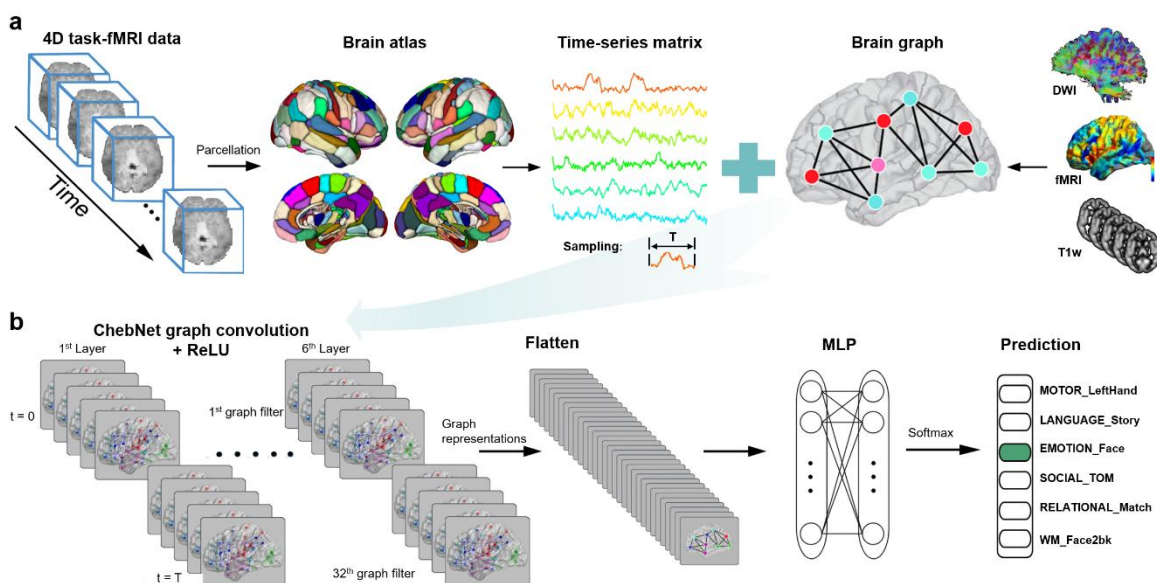
183 where $\tilde{L} = \frac{2L}{\lambda_{max}-1}$ is a normalized version of graph Laplacian with λ_{max} being the largest eigenvalue,
184 θ_k is the model parameter to be learned at each order of the Chebychev polynomials.

185 2.3. Brain-decoding pipeline

186 The proposed ChebNet decoding model (as shown in Figure 1) consists of 6 graph convolutional
187 layers with 32 graph filters at each layer, followed by a flatten layer and 2 fully connected layers (256,
188 64 units). The model takes in a short series of fMRI volumes as input, maps the fMRI data onto the
189 predefined brain graph and results in a 2-dimensional time-series matrix $X^1 \in \mathbb{R}^{N \times T}$, i.e. a short
190 time-series with duration of T for each of N brain parcels. The first ChebNet layer learns various
191 shapes of temporal convolution kernels by treating multiple time steps as input channels (t_0, \dots, t_T)
192 and propagates such temporal dynamics within ($K=1$) and between ($K>1$) brain networks. As a result,
193 a set of “brain activation” maps are generated and passed on to the second ChebNet layer for higher-
194 order information integration, and so on. The learned graph representations at the last ChebNet layer
195 (as shown in Fig. 9-S1c) are then imported into a 2-layer multilayer perceptron (MLP) for
196 classification.

197 The entire dataset includes in total 21 cognitive states and 14,895 functional runs across the six
198 cognitive domains. By using a 10s-time window (i.e. 15 functional volumes at TR=0.72s), we cut

199 long task trials into multiple data samples and resulted in 138,662 data samples of fMRI signals.
200 These data samples constituted the whole dataset for model training and evaluation. The dataset was
201 split into training (64%), validation (16%), test (20%) sets stratified by subject, which ensures that all
202 fMRI data from the same subject was assigned to one of the three sets. Approximately, the training set
203 includes fMRI data from 700 unique subjects (depending on data availability for different cognitive
204 tasks ranging from 1043 to 1085 subjects in total), with 174 subjects for validation set and 218
205 subjects for test set. Specifically, the training set was used to train/update model parameters at each
206 training epoch, the validation set was used to evaluate the model performance at the end of each
207 training epoch, and the best model with the highest prediction score on the validation set was saved
208 after 100 training epochs. The saved decoding model was then evaluated on the test set and reported
209 the final decoding performance. We used Adam as the optimizer with an initial learning rate of 0.0001
210 on all cognitive domains. Additional l2 regularization of 0.0005 on weights was used to control model
211 overfitting and the noise effect of fMRI signals. Dropout of 0.5 was additionally applied to the
212 neurons in the last two fully connected layers. The implementation of the ChebNet graph convolution
213 was based on PyTorch 1.1.0, and was made publicly available in the following repository:
214 https://github.com/zhangyu2ustc/gcn_tutorial_test.git.



215

216 **Figure 1. Pipeline of brain decoding using graph convolution network.**

217 We used a similar network architecture as proposed in our previous paper (Zhang et al., 2021) except
218 for a more sophisticated form of graph convolution, namely ChebNet graph convolution, along with
219 different brain graph architectures derived from various resolutions of brain atlas (nodes), and
220 different types of brain connectivity (edges). The decoding model consists of six ChebNet graph
221 convolutional layers with 32 graph filters at each layer, followed by a flatten layer and a two-layer
222 Multilayer Perceptron (MLP, consisting of 256-64 units). Specifically, for a short series of fMRI
223 volumes, the measured brain activity is first mapped onto a predefined brain atlas consisting of
224 hundreds of brain regions (e.g. 246 regions from Brainnetome atlas (Fan et al., 2016)) and resulted in
225 a 2D time-series matrix. Then, a brain graph indicating the edges between each pair of brain regions is
226 constructed via either tractography of fiber projections using diffusion-weighted images (DWI), or
227 functional correlation of low-frequency fluctuations in fMRI, or structural covariance of cortical
228 thickness or gray matter density across a large population. Next, both the time-series matrix and brain
229 graph are imported into the graph convolutional network (**b**). The model learns a new representation
230 of task-evoked neural activity by stacking multiple graph convolutional layers, which takes into
231 account both brain activity of each region (functional segregation) and the interactions within and
232 between brain networks (functional integration). Finally, the learned graph representations are passed
233 through a two-layer MLP and softmax function in order to predict the cognitive state associated with
234 each input time window. The implementation of the ChebNet graph convolution was based on
235 PyTorch 1.1.0, and was made publicly available in the following repository:
236 https://github.com/zhangyu2ustc/gen_tutorial_test.git.

237 2.4. Effects of K -order in ChebNet

238 As stated in equation (4), the graph convolution can be rewritten as follows at different K -orders:

$$239 \quad x *_{G} g_{\theta} = \{\theta_0 x \quad \theta_0 x + \theta_1 \tilde{L} x \quad \theta_0 x + \theta_1 \tilde{L} x + \theta_2 \tilde{L}^2 x \quad K = 0 \quad K = 1 \quad K = 2 \quad (5)$$

240 where \tilde{L} is a normalized version of graph Laplacian and $\{\theta_k\}_{k=1,2,\dots,K}$ are model parameters to be
241 learned. Specifically, ChebNet graph convolution with $K=0$ indicates a global scaling factor on the
242 input signal by treating each node independently; graph convolution with $K=1$ indicates information
243 integration between the direct neighbors on graphs, i.e. integrating neural activity within the same

244 brain network; graph convolution with $K=2$ indicates large-scale functional integration within a two-
245 step neighborhood on graphs, i.e. integrating the context of neural activity from local areas, within-
246 and between brain networks. Thus, the choice of K -order controls the scale of the information
247 integration on graphs. Generally speaking, when $K>1$, the graph convolution integrates information
248 flow within a K -step neighborhood by propagating graph signals not only within the same network but
249 also among inter-connected networks. A simulation experiment shown in Figure 2-S1 illustrates that
250 the propagation rate at all brain graphs converges to a similar level after $K>10$. For cognitive decoding,
251 we explored different choices of K -order in ChebNet spanning over the list of [0,1,2,5,10] and found a
252 significant boost in decoding performance by using high-order graph convolutions ($K>1$) instead of
253 integrating within the network ($K=1$) especially on high-order cognition.

254 2.5. Definition of edges: brain connectivity

255 Graph architecture is another factor that impacts the propagation of information flow in the brain. We
256 explored different types of edges (or brain connectivity) for brain decoding, including 1) local
257 architecture indicating spatially adjacency in the cortical surface (spatial-graph); 2) community
258 architecture representing neural circuits derived from whole-brain tractography (diffusion-graph); 3)
259 hierarchical network architecture indicating functional correlation of low-frequency fluctuations in
260 BOLD signals (functional-graph); 4) morphological networks derived from structural covariance of
261 cortical thickness across a large population of subjects. These brain graphs were all calculated based
262 on Glasser's multimodal parcellation (Glasser et al., 2016). Specifically, for each pair of brain parcels
263 in the atlas, the spatial-graph was evaluated by calculating the spatial adjacency matrix with each
264 element indicating whether two brain parcels shared one or more triangles in the cortical surface by
265 using the "wb_commond -cifti-label-adjacency" command from Connectome Workbench software.
266 The diffusion-graph was generated from the whole-cortex probabilistic diffusion tractography based
267 on HCP diffusion-weighted MRI data collected from 1065 subjects, with each element in the
268 connectivity matrix indicating the average proportion of fiber tracts (streamlines) between the seed
269 and target parcels (Rosen and Halgren, 2021). The functional-graph was calculated based on minimal
270 preprocessed resting-state fMRI data from 1080 HCP subjects, by using the 'tangent' method for

271 group-wise connectivity estimation with the ConnectivityMeasure method in nilearn (Varoquaux et al.,
272 2010), and then averaged the connectivity matrices across all subjects. The structural-graph was
273 generated by calculating structural covariance of cortical thickness based on the HCP structural MRI
274 database across 1096 subjects. To be noted that, for spatial and structural graphs, only one brain graph
275 was generated from the entire group. For the anatomical and functional graphs, we used the group
276 averaged connectivity matrix and fixed the graph architecture for all subjects. Moreover, considering
277 that the sparsification of graph is the key to superior performance on many graph learning benchmarks
278 (Ye and Ji, 2021), a k-nearest-neighbour (k-NN) graph was built for each brain connectome by only
279 connecting each brain region to its neighbours with the highest connectivity strength, resulting in an
280 edge-sparsified brain graph. We have also explored how the sparsity of brain graphs impact brain
281 decoding and compared them with the original densely-connected brain connectomes.

282 2.6. Definition of nodes: brain atlas

283 The parcellation scheme controls the scale of the graph. A variety of parcellation schemes have been
284 proposed in the literature by using different imaging modalities and features (see the review paper by
285 (Eickhoff et al., 2018)). We then investigated different parcellation schemes that have been widely
286 used in the literature, with variable resolutions and connectivity information (e.g. functional,
287 anatomical or multimodal connectivity information). For functional parcellation, considering the high
288 correspondence between resting-state functional networks and patterns of task-evoked brain responses
289 across multiple subjects, sessions, and cognitive tasks (Gordon et al., 2017; Gratton et al., 2018), we
290 evaluated functional networks, for instance Yeo's 7 and 17 resting-state networks consisting of 50 and
291 112 spatially continuous parcels in the cerebral cortex (Yeo et al., 2011), and functional parcellation at
292 multiple resolutions, for instance Schaefer's multiresolution brain parcellation, consisting of 100, 200,
293 400 and 1000 cortical parcels respectively (Schaefer et al., 2018). For anatomical parcellation, we
294 chose the Brainnetome atlas that delineates the differences in connectivity profiles derived from
295 diffusion tractography and consists of 246 brain regions in the cortical and subcortical areas (Fan et al.,
296 2016). For parcellation with multimodal information, we chose the Glasser's atlas that consists of 360
297 areas in the cerebral cortex, bounded by sharp changes in cortical architecture, function, connectivity,

298 and topography (Glasser et al., 2016). For each parcellation map, we evaluated the functional
299 homogeneity by calculating the averaged pairwise Pearson correlations within each brain parcel. We
300 further investigated the relationship between the parcel size and functional homogeneity as well as the
301 decoding performance among all parcellation maps.

302 2.7. Randomized brain graphs: edge rewiring

303 The robustness of the decoding model was investigated by introducing randomizations on both graph
304 architectures and brain parcels. In order to evaluate whether the decoding model was impact by small
305 fluctuations on the graph architecture, we generated a series of randomized null models that involves
306 rewiring of the functional-graph by swapping a proportion of connections such that local degree is
307 preserved while the global graph architecture is randomized (Sporns, 2018). These randomized null
308 models can preserve graph attributes from the original graph, including local node measures, spatial
309 locations, and wiring cost, and has been widely used as generative null models of the empirical data in
310 network neuroscience literature, for instance (Betzel and Bassett, 2017). We explored different ratios
311 of random swapping spanning over the list of [0, 0.1, 0.2, 0.5], where ratio=0.5 indicates that half of
312 edges in the functional-graph were rewired. The randomized graphs to some degree represent the
313 inherent mismatch between individuals or task-specific brain organization at a low ratio (e.g. 0.1), and
314 may simulate disconnections in brain networks due to brain disorders by using a high ratio (Hearne et
315 al., 2021; Sporns, 2011; Suárez et al., 2021). These randomized graphs were then compared with the
316 original functional-graph in terms of decoding accuracy at different K -orders.

317 2.8. Randomized brain graphs: node attack and network attack

318 In order to evaluate whether the decoding model was robust to random or targeted attacks, we
319 manually “silenced” a small portion of nodes (i.e. set their values to zero) and evaluated the reduction
320 in the prediction accuracy by using pre-trained models. This procedure has been commonly used to
321 simulate lesions due to brain injury or neurological disorders (Alstott et al., 2009; Honey and Sporns,
322 2008). For random node attack, we removed brain responses from randomly chosen nodes, ranging
323 from 10% to 80% of brain parcels and repeated the process for 100 times. The vulnerability of each

324 brain region was evaluated by associating the lesion state (i.e. lesion or normal) with the decays in
325 brain decoding. For targeted or network attacks, we removed nodes associated with one intrinsic
326 network at a time, identified by Yeo's 7 or 17 resting-state functional networks (Yeo et al., 2011).
327 Only brain regions with at least 30% areas affected were considered as lesions by silencing their
328 activities in the following analysis. The vulnerability of each brain network was measured by the
329 decay of decoding accuracy after applying network lesions as compared to the original decoding
330 model.

331 2.9. Saliency map of graph convolutions

332 The saliency map analysis aims to locate which discriminative features in the brain help to
333 differentiate between different cognitive tasks. There are several ways to visualize a deep neural
334 network, including visualizing layer activation (Springenberg et al., 2014) and heatmaps (Selvaraju et
335 al., 2020). Here, we chose the first method due to its easy implementation and generalization to graph
336 convolutions (Springenberg et al., 2014). The basic idea is that if the input from a brain parcel is
337 relevant to the prediction output, a little variation on the input signal will cause high changes in the
338 layer activation. This can be characterized by the gradient of the output given the input, with the
339 positive gradients indicating that a small change to the input signals increases the output value.
340 Specifically, for the graph signal X^l of layer l and its gradient R^l , the overwritten gradient $\nabla_{X^l} R^l$ can
341 be calculated as follows:

$$342 \quad \nabla_{X^l} R^l = (X^l > 0) \odot (\nabla_{X^{l+1}} R^{l+1} > 0) \odot \nabla_{X^{l+1}} R^{l+1} \quad (6)$$

343 In order to generate the saliency map, we started with a pre-trained model and used the above chain
344 rule to propagate the gradients from the output layer until reaching the input layer. This guided-
345 backpropagation approach can provide a high-resolution saliency map with the same dimension as the
346 input data. We further calculated a heatmap of saliency maps by taking the variance across the time
347 steps for each parcel, considering that the variance of the saliency curve provides a simplified way to
348 evaluate the contribution of task-evoked hemodynamic response. To make it comparable across
349 subjects, the saliency value was additionally normalized to the range $[0,1]$, with its highest value at 1
350 (a dominant effect for task prediction) and lowest at 0 (no contribution to task prediction).

351 **3. Results**

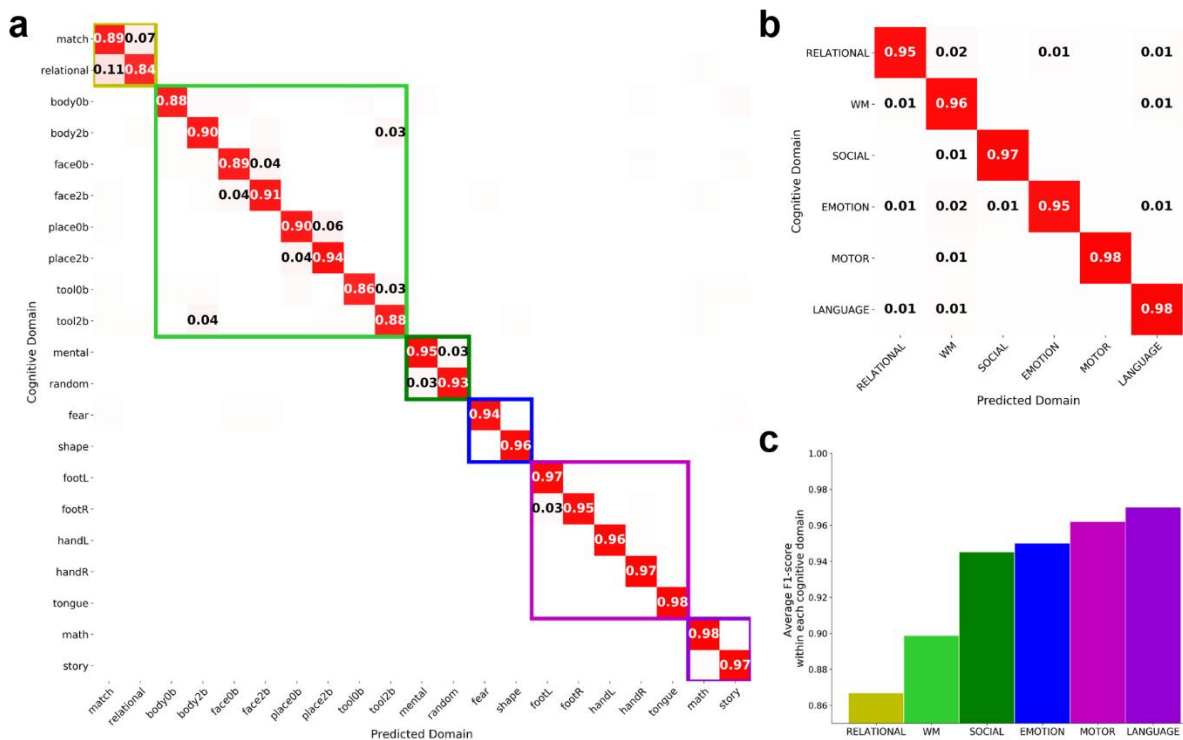
352 3.1. Decoding cognitive states with fine temporal resolution and high accuracy

353 We proposed a multi-domain decoding pipeline based on ChebNet graph convolution (Figure 1). The
354 ChebNet decoding model was evaluated using the cognitive battery of HCP task-fMRI dataset
355 acquired from 1200 healthy subjects. Using a 10-second window, the 21 cognitive states were
356 identified with an average test accuracy of 93% (mean=93.43%, STD=0.44% by using 10-fold cross-
357 validation with shuffle splits stratified by subject). The temporal resolution of the decoding model can
358 go down to a single fMRI volume (720 ms of duration), with a prediction accuracy well above chance
359 level (60%, chance level=4.8%). The accuracy of single-volume state annotation was highly improved
360 (reaching 76%) after taking into account the delay effect of hemodynamic response function in BOLD
361 signals, i.e. excluding fMRI volumes within 6s after the onset of each task trial from both training and
362 test sets. We have also evaluated other baseline approaches including multi-class support vector
363 machine classification (SVC) with linear and nonlinear kernels, random forest and a multilayer
364 perceptron (MLP, consisting of two fully connected layers) on the same dataset. The results with a 10-
365 second time window demonstrated that high-order ChebNet model outperformed all the other linear
366 and nonlinear decoding models by a wide margin (see Table 2). ChebNet also showed a significant
367 improvement over GCN which relies on first-order graph convolution.

368 3.2. Low misclassification rate within and between cognitive domains

369 In order to clarify the nature of errors made by the ChebNet brain decoder, we examined the
370 confusion matrix on the test set, which indicates the proportion of true and false predictions given a
371 cognitive task state or domain. When using a 10-second time window, the confusion matrix showed a
372 clear block diagonal architecture (see Figure 2a), where the majority of experimental tasks were
373 accurately identified for all task conditions (e.g. cross-domain misclassification rate<2%). Mistakes
374 were found in tasks with similar cognitive processes, for instance, between relational processing and
375 pattern matching conditions, as well as 0back vs 2back WM tasks. After summarizing the confusion
376 matrix according to the six cognitive domains (Figure 2b), each cognitive domain was identified with

377 an accuracy greater than 95%. Among the six cognitive domains, the language tasks (story vs math)
 378 and motor tasks (left/right hand, left/right foot and tongue) were the most easily recognizable
 379 conditions by showing the highest precision and recall scores (average F1-score = 98% and 97%,
 380 respectively for two language conditions and five motor conditions). Even higher scores were
 381 achieved when decoding a smaller number of experimental conditions restricted to a specific
 382 cognitive domain (Figure 2-S1), i.e. using task-fMRI data exclusively from a single cognitive domain
 383 during model training and evaluation. For instance, the model achieved near-perfect decoding on
 384 other high-order cognitive functions, including working-memory (94.51%, classifying 8 conditions
 385 using 25s) and social cognition (96.58%, classifying 2 conditions using 23s), as opposed to 92.6% and
 386 92.9% for the two domains when decoding on 30s of fMRI data (Li and Fan, 2019).



387

388 **Figure 2. Confusion matrices of decoding 21 cognitive states and 6 cognitive domains.**

389 We calculated the confusion matrix of cognitive decoding for the predicting cognitive states using
 390 every 10s of fMRI signals. We used the ChebNet-K5 model on a functional graph derived from
 391 Glasser's atlas in this analysis. The majority of misclassifications were found within the same
 392 cognitive domain rather than between domains. A clear block diagonal architecture of the confusion
 393 matrix, which indicates the majority of the cognitive tasks or domains were accurately identified, was

394 shown for both 21 task conditions (a) and 6 cognitive domains (b). For the visualization purpose, a
395 threshold of 0.02 was applied to the confusion matrix in (a), which indicates a low misclassification
396 rate between domains (<2%). The averaged F1-score for each domain was shown in (c), which was
397 calculated by averaging the scores within each cognitive domain based on the number of samples.
398 Among the six cognitive domains, the Language tasks (in dark violet) and Motor tasks (in magenta)
399 were the most easily recognizable conditions. Note: the six cognitive domains include relational
400 processing (RELATIONAL), working memory (WM), social cognition (SOCIAL), facial emotional
401 processing (EMOTION), body movements (MOTOR), and language comprehension (LANGUAGE).

402

403 **Table 2: Comparison of cognitive decoding by using linear and nonlinear models.**

404 We reported the best performance for the baseline models after a grid search of the hyperparameters.
405 For SVC approaches, we used the one-vs-rest ('ovr') decision function to handle multi-classes and
406 reported the highest accuracy after the grid search for the hyper-parameter ($C =$
407 $[0.0001, 0.001, 0.1, 1, 10, 100]$). For Random Forest, we reported the highest accuracy after evaluating
408 different settings of the classifier including depth of trees: $[4, 16, 64, 256, 1024]$ and number of trees:
409 $[100, 2000]$. For MLP (multilayer perceptron), GCN (using first-order graph convolution, (Zhang et al.,
410 2021)) and ChebNet (using 5-order graph convolution), we reported the mean and standard deviation
411 of the decoding accuracies among 10-fold cross-validation with shuffle splits stratified by subject.

Models	Train Accuracy	Validation Accuracy	Test Accuracy
SVC-linear	67.2%	63.3%	64.1%
SVC-rbf	99.7%	73.5%	73.8%
Random Forest	100%	48.0%	47.5%
MLP(256-64)	87.9%(+/-1.83%)	83.2%(+/-3.28%)	76.1%(+/-0.41%)
GCN	96.3%(+/-0.42%)	90.2%(+/-0.21%)	90.7%(+/-0.20%)
ChebNet	96.91%(+/-0.18%)	92.73(+/-0.12%)	93.43(+/-0.44%)

412 3.3. Order K in ChebNet controls the propagation rate on the graph

413 At each ChebNet graph convolutional layer, the context of brain activity is propagated within a K -step
414 neighborhood on the graph. As illustrated in Figure 2-S1, both the choices of K -order and graph
415 architectures significantly impact the propagation rate of information flow in the brain, estimated by
416 the expected first arrival time. We first investigated the impact of K -order on the decoding model by
417 spanning over the list of [0,1,2,5,10], where $K=0$ indicates a global scaling factor on the input
418 features by treating each node independently; $K=1$ indicates the integration of brain activity for each
419 node and its direct neighbors, while $K>1$ indicates the integration not limited to a region of interest or
420 within a specific brain network, but instead expanding among inter-connected brain networks.

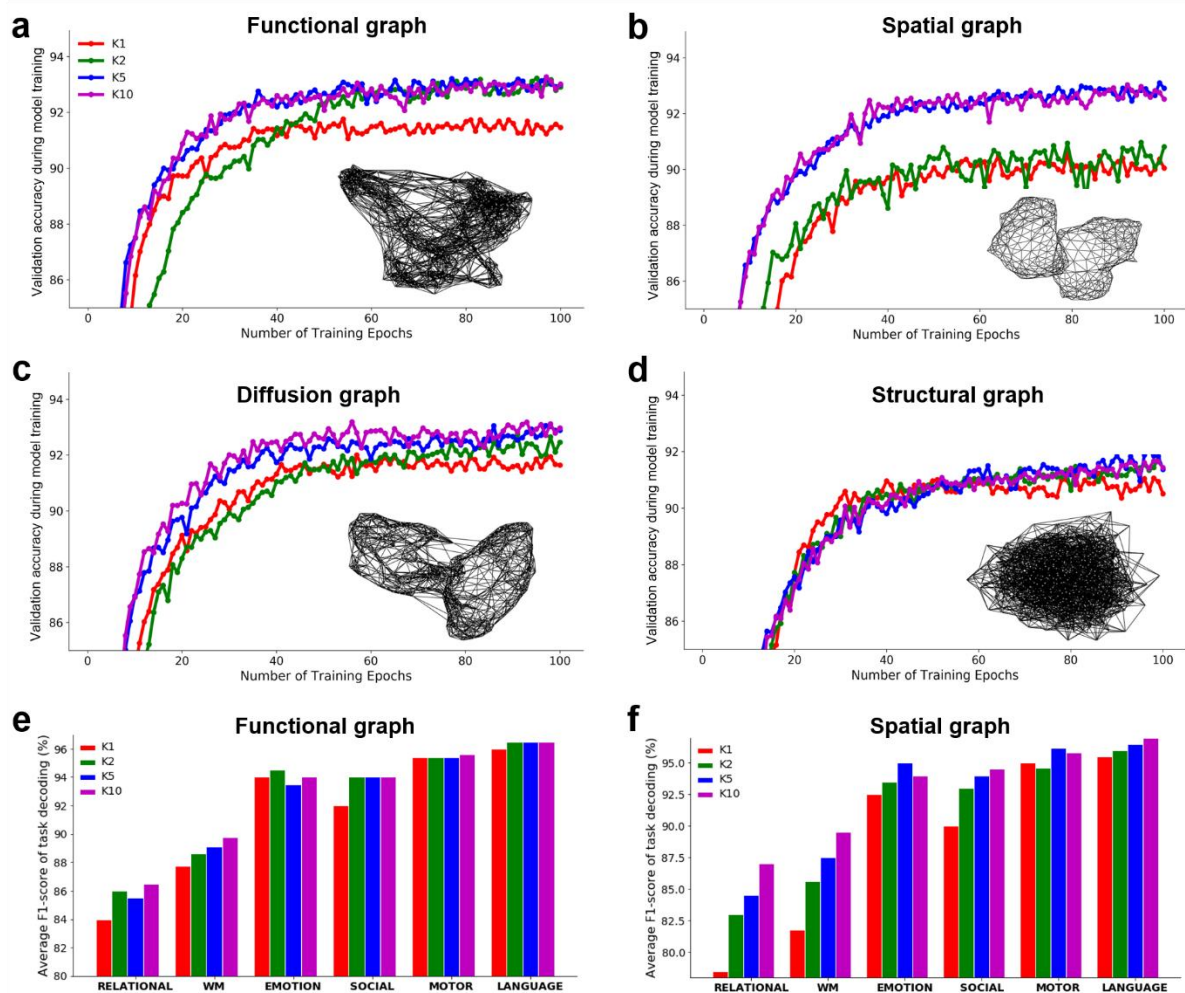
421 Our results (see Figure 3) showed that the decoding performance gradually improved by increasing
422 the K -order and reached a plateau when $K \geq 5$. For example, when using a functional graph (Figure
423 3a), the ChebNet- $K1$ model (i.e. ChebNet with $K = 1$) showed lower decoding accuracy than high-
424 order models (91.67% vs 93.22%, respectively for $K = 1$ and $K > 1$), but was substantially higher
425 than the $K = 0$ model (83.72%). When $K \geq 5$, the training curves (indicated by the validation
426 accuracy at the end of each training epoch) generally followed the same behaviors and the overall
427 prediction accuracy plateaued approximately at the same level. We evaluated the sensitivity to the K -
428 order for each cognitive domain, which demonstrated a strong domain-specific effect. For instance,
429 when using functional-graph (Figure 3e), the decoding on the Motor and Language tasks showed little
430 impact by the K -order, which indicates that decoding on the two tasks was driven by functional
431 interactions within the same functional network. On other hand, the decoding on the Working-
432 memory and Relational-processing tasks showed high sensitivity to the choice of K -order and were
433 continuously improved as increasing K , implying that the inter-network functional interactions might
434 play an important role in the high-order cognitive functions. Similar findings were observed using the
435 spatial-graph as well (Figure 3f), except that all cognitive tasks benefitted from high-order graph
436 convolutions including Language tasks, which involve spatially distributed brain networks for
437 language comprehension and numerical processing.

438 3.4. Communities and brain networks accelerate information propagation on brain graph

439 There are multiple ways of capturing the network organization of human brain, using either spatial
440 constraints (e.g. spatial adjacency in the geometry of brain surface (spatial-graph)), brain morphology
441 (structural covariance of cortical thickness across a population of subjects (structural-graph)), or
442 connectivity information (e.g. functional correlation of low-frequency fluctuations in BOLD signals
443 (functional-graph) and tractography of fiber projections using diffusion-weighted images (diffusion-
444 graph)), and others. Here, we mainly investigated these four types of brain graphs (Figure 4). Among
445 which, the spatial graph featured local geometric structures by connecting each parcel to its spatial
446 neighbors on the cortical surface mesh. By contrast, modular and community structures have been
447 widely demonstrated in the diffusion and functional brain graphs (Betzel and Bassett, 2017; Bullmore
448 and Sporns, 2009). The structural graph (i.e. structural covariance of cortical thickness) somewhat
449 resembles the functional graphs (Clos et al., 2014; Zielinski et al., 2010), but was contaminated by
450 random noise effects (as shown in Figure 4c).

451 The training curves on all brain graphs followed a similar trend as increasing the K -order (see Figure
452 **3 a-d**) and showed similar behaviors when using a high propagation rate (i.e. $K=5$, as shown in Figure
453 **4a**), except for the structural-graph which showed slightly lower performance than other graphs.
454 Besides, we observed a significant interaction between the K -order and choices of brain graphs, such
455 that the best decoding accuracy, evaluated on the test set after the entire training process, was
456 achieved on the functional graph with a high-order model (Figure 4b). When using spatial-graph (also
457 shown in Figure 3b), a gap in the decoding performance was detected between the low and high
458 propagation groups (90.36% vs 92.4% for $K \leq 2$ and $K > 2$, respectively) and reached a stable range
459 after $K > 5$ (93%). A much smaller impact of the K -order was shown in the functional-graph (Figure
460 **3a**), with a smaller gap in brain decoding appearing at $K=1$ (92.52% vs 93.22%, respectively for $K=1$
461 and $K > 1$). Diffusion-graph showed very similar behaviors as the functional-graph at all propagation
462 rates (92.19% vs 93.04%, respectively for $K=1$ and $K > 1$) and eventually converged to the same level
463 of decoding performance when using a sufficiently high propagation rate (Figure 3c). This is probably
464 because the spatial-graph is only composed of short-distance connections, which restricts the

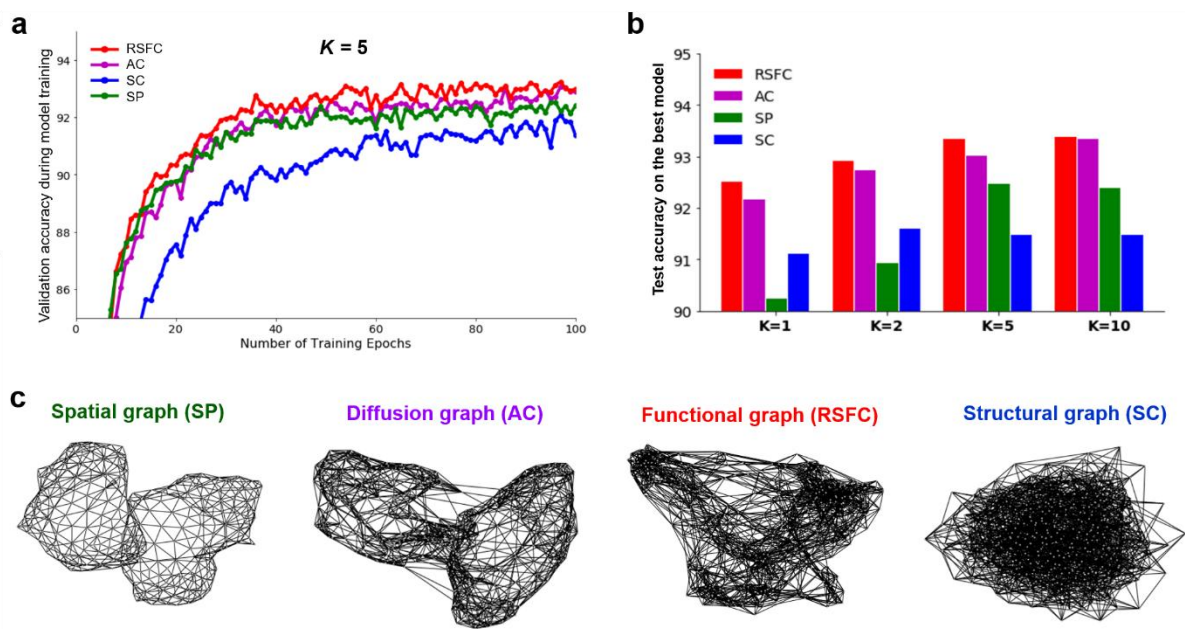
465 integration of brain activity to a small local area. In order to reach out for the spatially distributed
 466 functional networks and even multiple brain systems, the model requires a relatively high K -order or a
 467 high path length, i.e. taking multiple walks on the graph. However, even with a high-order model, the
 468 spatial-graph still showed lower decoding performance compared to the diffusion and functional
 469 graphs (Figure 4b). Our results indicated that the connectome-constrained graph architecture
 470 accelerates the propagation of information flow in the brain by integrating the neural dynamics
 471 through long-range connections. Moreover, considering that the sparsification of graph is the key to
 472 superior performance on graph learning benchmarks (Ye and Ji, 2021), we investigated functional
 473 graphs with different sparsity levels in brain decoding and found that, compared the original densely-
 474 connected brain connectomes, highly sparsified graphs performed much better at all K -orders (Fig.2-
 475 S2).



476

477 **Figure 3. Effect of the K -order in ChebNet on four brain graphs and six cognitive domains.**

478 We evaluated four different types of brain graphs in the construction of ChebNet, including
479 functional-graph computed using resting-state functional connectivity (**a**), spatial-graph representing
480 spatial adjacency in the cortical surface (**b**), diffusion-graph estimated from whole-brain diffusion
481 tractography (**c**), and structural-graph derived from structural covariance of cortical thickness across
482 subjects (**d**). We first evaluated the effect of K -order on each brain graph in terms of the training curve,
483 i.e. evaluating the model performance on the validation set at the end of each training epoch. We
484 found a significant boost in decoding performance by using high-order graph convolutions ($K>1$)
485 instead of integrating within the network ($K=1$) on all brain graphs. We also evaluated the impact of
486 K -order on each cognitive domain by calculating the averaged F1-score on the test set and compared
487 the effects across six cognitive domains and different brain graphs, e.g. the functional graph (**e**) and
488 spatial graph (**f**). These results indicate that the decoding of high-order cognitive functions relies more
489 on high-level interactions in the brain and this effect is more dramatic when using a graph architecture
490 purely based on the topological organization of human brain.



491

492 **Figure 4. ChebNet decoding at different K -orders and using different brain graphs.**

493 We evaluated four different types of brain graphs for the multi-domain brain decoder, with the
494 corresponding brain graph architecture shown in (**c**). We observed a strong interaction effect between
495 brain graphs and K -orders (**b**) such that the decoding performance gradually improved by increasing

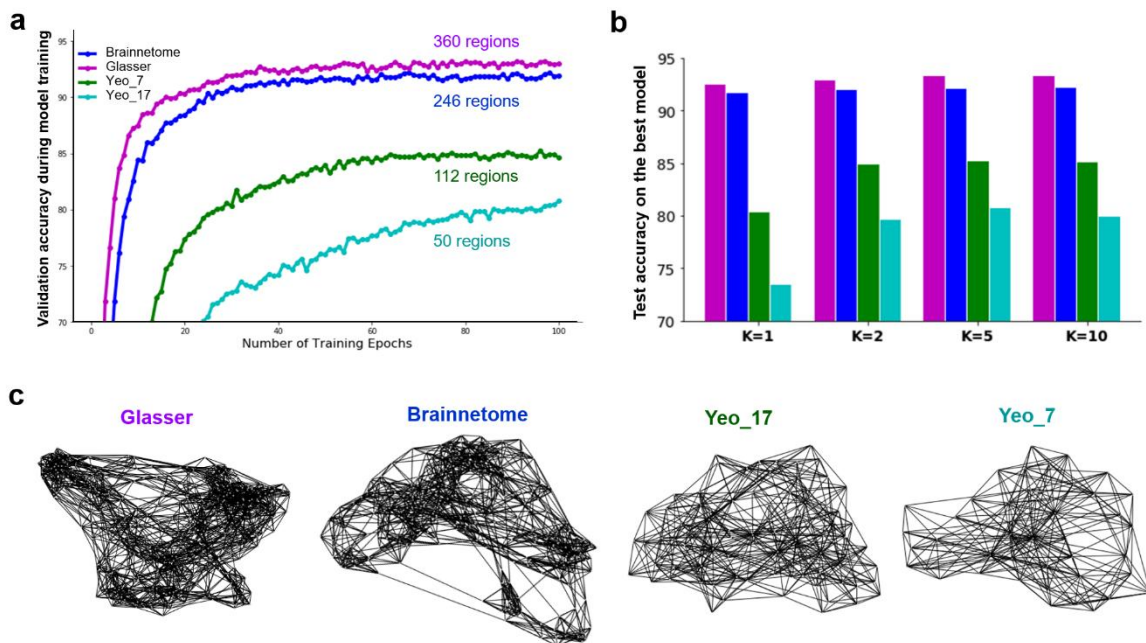
496 the K -order for all brain graphs, but the graph architecture also had a big impact on the decoding
497 performance. When fixing the K -order, for example using the ChebNet- $K5$ model (a), the functional
498 (RSFC, in red) and diffusion graphs (AC, in purple) showed similar performance during model
499 training, followed by the spatial graph (SP, in green) showing slightly lower decoding accuracy. The
500 structural graph (SC, in blue) showed the lowest performance during the entire training process.
501 Overall, the best decoding model was using ChebNet- $K5$ on the functional-graph (test
502 accuracy=93.43%). To be noted that the baseline $K=0$ model, which was invariant to the structure of
503 brain graphs by treating each node independently, achieved much lower decoding performance on the
504 same dataset (test accuracy=83.72%). Moreover, if we removed the graph convolutional layers from
505 the decoding model, i.e. using a two-layer multilayer perceptron (MLP) with 256 and 64 neurons
506 respectively, the decoding performance was further reduced (test accuracy=76.1%). These results
507 indicate that high-order functional integration as well as the proper graph architectures are critical
508 steps towards high-performing cognitive decoding.

509 3.5. Functional homogeneity and small parcel size promotes local information processing

510 Another factor that significantly impacts the decoding model is the scale of the graph, i.e. number of
511 brain parcels. Generally speaking, finer-scale atlases (smaller parcel size) will have higher internal
512 homogeneity (Figure 5-S2 d) and result in less information loss after data projecting and averaging.
513 Consequently, the decoding model using smaller parcels achieves better prediction of cognitive states
514 and eventually reaches the plateau with a balance of model complexity and local homogeneity (Figure
515 5-S1 and S2). In order to investigate this effect, we have tested four different brain atlases derived
516 from different modalities or human connectomes, including Yeo's 7 and 17 functional networks (Yeo
517 et al., 2011) (50 and 112 spatially continuous brain parcels), Brainnetome atlas (Fan et al., 2016)
518 derived from diffusion tractography (246 brain parcels), and Glasser's multi-model atlas (Glasser et
519 al., 2016) (360 brain parcels), as well as brain atlases at multiple resolutions, e.g. Schaefer's
520 multiresolution brain parcellation (consisting of 100, 200, 400 and 1000 parcels respectively)
521 (Schaefer et al., 2018). For each of the chosen atlases, we constructed the functional graph by
522 calculating the resting-state functional connectivity based on 1080 subjects from the HCP database

523 and evaluated the functional homogeneity of each brain parcel by calculating pairwise correlations of
524 the connectivity patterns between all vertex within a parcel (Schaefer et al., 2018; Urchs et al., 2019).
525 Coinciding with the literature that smaller parcels have higher functional homogeneity, we further
526 demonstrated that finer-scale atlas results in higher decoding performance across different parcellation
527 schemes (Figure 4-S2). Our results indicated that smaller parcel size resulted in higher functional
528 homogeneity and better decoding performance (Figure 5-S2). As shown in Figure 5a, the decoding
529 performance started with a relatively low accuracy, for instance, 80.78% when using 50 spatially
530 continuous regions derived from Yeo's 7 network, and quickly improved by simply increasing the
531 resolution of brain atlas, e.g. 85.23% when using 112 regions derived from the 17 network. Small
532 improvement was detected when using around 300 regions or more (92.16% vs 93.43%, respectively
533 for the Brainnetome atlas and Glasser's atlas). Moreover, we observed that, on all brain atlases, the
534 decoding performance gradually improved as increasing the K -order and reached the stable
535 performance at $K=5$ (Figure 5b).

536 We also evaluated Schaefer's multiresolution brain parcellation (Schaefer et al., 2018), consisting of
537 100, 200, 400 and 1000 parcels respectively. As shown in Figure 6, we found that higher resolution
538 (smaller parcel size) improved the decoding performance at all K -orders and more dramatic
539 improvement was detected at a small K -order than high-order models (e.g. $K=1$ vs $K=5$ in A and B,
540 respectively). For instance, when using the ChebNet-K5 model, the decoding performance plateaued
541 at 400 parcels with no further improvement by using higher resolutions, e.g. 1000 parcels. It's worth
542 noting that, compared to the Glasser's atlas, the Schaefer's atlas showed slightly lower performance at
543 all resolutions and K -orders (e.g. 91.35% vs 93.43%, respectively for Schaefer's (400 parcels) and
544 Glasser's atlas (360 parcels)). This is probably due to imperfect matching of cortical surface templates
545 between different populations and consequently having much lower functional homogeneity when
546 projecting Schaefer atlas onto the surface of HCP subjects (Figure 5-S1). The relationship of parcel
547 size, functional homogeneity, and decoding accuracy was systematically investigated in Figure 5-S1.
548 Our results indicate that the size and functional homogeneity of brain parcels significantly impact the
549 decoding model. By contrast, how the brain atlas was constructed, for instance, using different
550 imaging modalities or various types of connectome information, show little impact.



551

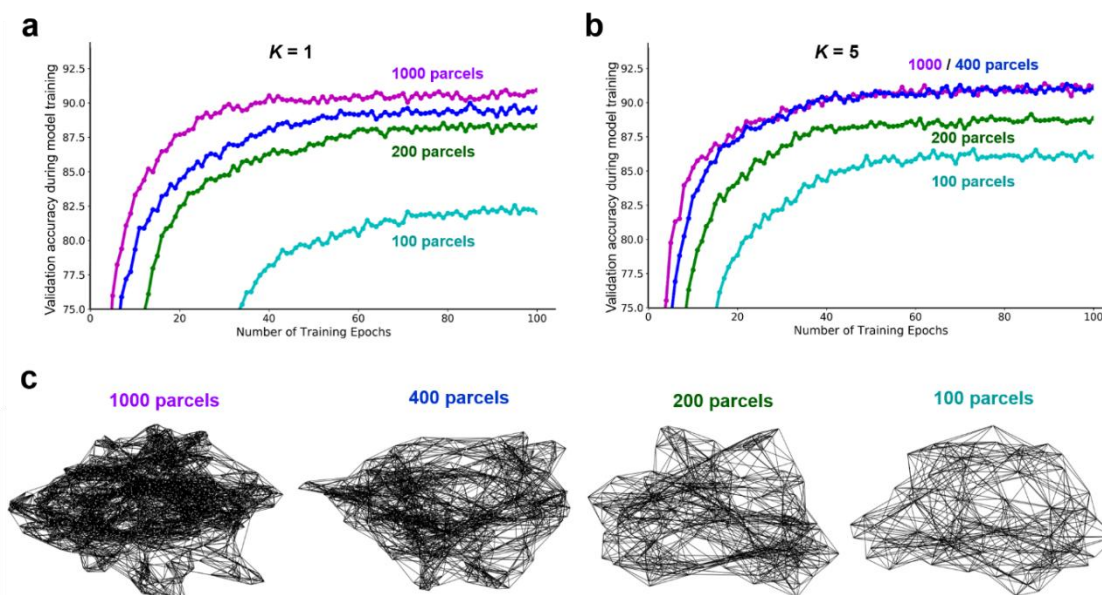
552 **Figure 5. ChebNet decoding at K -orders and using different brain atlases.**

553 We evaluated different brain atlases at various resolutions for the construction of brain graph,
554 including Yeo's 7 and 17 functional networks (50 and 112 spatially continuous brain parcels,
555 respectively), Brainnetome atlas derived from diffusion tractography (246 brain parcels), and
556 Glasser's multi-model atlas (360 brain parcels). For each brain atlas, we constructed the functional
557 graph by evaluating the region-wise functional connectivity based on resting-state fMRI data (c). We
558 trained separated decoding models at different K -orders and found that the Glasser's atlas achieved
559 the best decoding performance, followed by the Brainnetome atlas, and Yeo's 17 and 7 functional
560 atlases (b). When fixing the K -order, for example using the ChebNet- $K5$ model (a), we found
561 significant advantages in model training by using finer-scale brain atlases (i.e. more brain regions and
562 smaller parcel size) regardless of the information used for brain parcellation, e.g. functional, diffusion
563 or multi-modal human connectomes.

564 3.6.High-order ChebNet adapts to network misspecification

565 The robustness of the decoding model was first evaluated by using randomized brain graphs (as
566 shown in Figure 7c), which were generated by randomly swapping a proportion of edges in the
567 functional graph while keeping the node degrees unchanged. This procedure has been widely used as
568 null models in network neuroscience literature, for instance (Betzel and Bassett, 2017; Sporns, 2018).

569 Here we found that the network misspecifications only impact ChebNet decoding models with small
570 K s but barely influence the decoding performance when using high-order graph convolutions (Figure
571 7b). Specifically, when using a low random ratio (e.g. 0.1), the model achieved very similar decoding
572 performance as the original functional-graph when $K \geq 2$ (93.15% vs 93.22%, respectively for the
573 randomized and functional graphs). When using a relatively high random ratio (e.g. 0.5), the decoding
574 performance started with a low prediction accuracy and gradually improved by increasing the K -order
575 (86.95% vs 91.52%, respectively for $K < 2$ and $K \geq 2$), consistently lower than the original
576 functional-graph at all K -orders. Besides, during model training, the randomized graphs showed much
577 lower convergence speed than the original functional-graph and were prone to getting stuck in local
578 minima, especially when only a small set of subjects were available (as shown in Figure 7-S1).
579 Moreover, as stated before, structural-graph also exhibits some random effects (Figure 3d), which
580 resembles the behaviors of random graphs with the random ratio between 0.1 to 0.2 (91.13% vs
581 91.53%, respectively for $K < 2$ and $K \geq 2$).

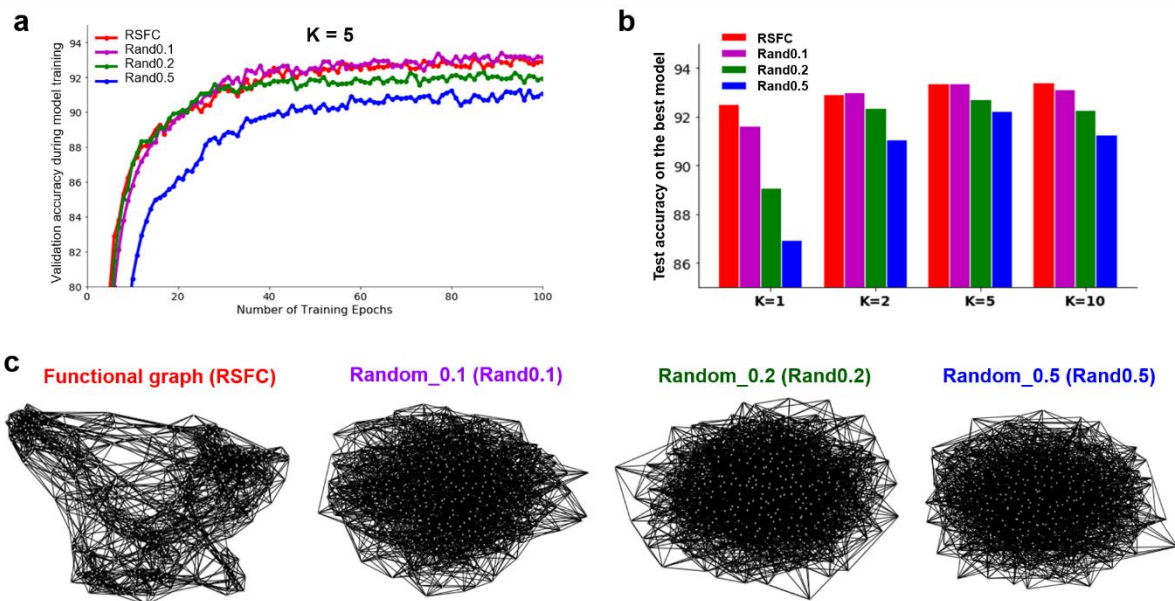


582

583 **Figure 6. Brain decoding using functional brain parcellation at multiple resolutions.**

584 We evaluated different brain atlases derived from Schaefer's multiresolution brain parcellation
585 (Schaefer et al., 2018), consisting of 100, 200, 400 and 1000 brain parcels respectively. For each
586 parcellation scheme, we constructed a functional graph by evaluating the region-wise functional
587 connectivity based on resting-state fMRI data (c). We found that brain parcellation at higher

588 resolutions (smaller parcel size or more regions) improved the performance of cognitive decoding,
589 especially at a small K -order (e.g. $K=1$ in a). By contrast, when using a high-order model (e.g. $K=5$ in
590 b), the model plateaued at 400 parcels with no further improvement on higher resolutions. However,
591 we still observed improvements at small resolutions. It's worth noting that, compared to the Glasser's
592 and Brainnetome atlases, both of which defined based on HCP subjects, the Schaefer's atlas (derived
593 from a different population) showed slightly lower performance (91.11% vs 92.16% vs 93.43%,
594 respectively for Schaefer's (400 parcels), Brainnetome (246 parcels) and Glasser's atlas (360 parcels)
595 when using the ChebNet- $K5$ model), probably due to imperfectly matching between surface templates
596 across populations which consequently impacts the functional homogeneity of brain parcels (see
597 Figure 5-S2).



598

599 **Figure 7. ChebNet decoding using random graphs derived from the functional graph.**

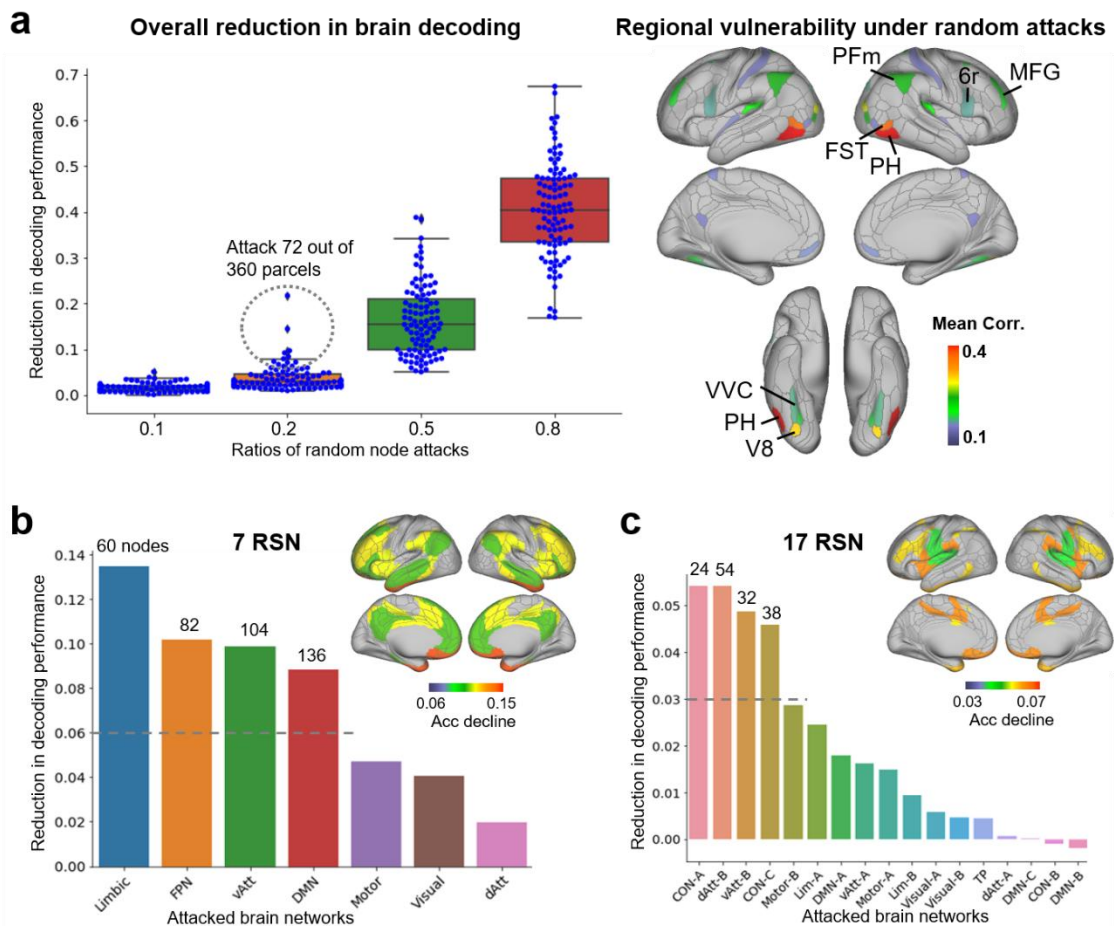
600 We generated three sets of randomized brain graphs by randomly swapping a portion of edges in the
601 functional graph while keeping the node degree unchanged. The graph structures at different random
602 ratios (e.g. 0.1, 0.2, 0.5) were shown in (c). When fixing the K -order, for example using the ChebNet-
603 $K5$ model (a), the functional graph (RSFC, in red) and its low randomness copy (Rand0.1, in purple)
604 showed very similar performance during model training, followed by the moderately (Rand0.2, in
605 green) and highly randomized graph (Rand0.5, in blue). We observed a strong interaction effect
606 between randomness ratios and the K -orders (b) such that the decoding performance on randomized

607 graphs started with a low prediction accuracy and gradually improved when increasing the K -orders,
608 consistently lower than the original functional-graph at all K -orders. The impact of graph
609 randomization was more dramatic at a small K -order (e.g. $K=1$) and smaller impact was detected
610 when using high-order models. The best performance was achieved by using a high-order model on
611 the functional graph or its low random copies.

612 3.7. Robustness to random attacks in brain regions and networks

613 The robustness of the decoding model was also evaluated under random attacks, by removing brain
614 responses from a small set of regions in the brain. This procedure has been commonly used to
615 simulate brain lesions due to brain injury or neurological disorders (Alstott et al., 2009; Honey and
616 Sporns, 2008). Here, we mainly focused on two types of attacks, either using randomly chosen
617 regions or targeted regions from a specific brain network. Our results demonstrated that the proposed
618 ChebNet graph convolution was resilient to random attacks on regions but not networks. Specifically,
619 lesions on a small set of randomly chosen brain regions, e.g. 40 parcels or less, did not affect the
620 decoding performance (median decay in the decoding accuracy: 1.2%). More severe decays were
621 detected as more regions were affected by lesions (median decay: 2.8%, 15.3% and 40.4%
622 respectively for 72, 180 and 288 affected regions). This pattern of performance decay was not related
623 to the betweenness or centrality of targeted regions ($r=0.091$, $p=0.08$), but rather associated with their
624 involvement in task-related brain activations. For instance, the decay in the decoding of WM tasks
625 was mostly driven by areas in the ventral visual stream, including PH, VVC and V8, as well as
626 frontoparietal network regions, including PFm, MFG and area 6r, as revealed by a correlation analysis
627 between the decay of decoding performance and the infection of each brain region (as shown in
628 Figure 8a). These regions have been reported to be engaged in the process of WM tasks (Christophel
629 et al., 2012; Harrison and Tong, 2009; Mayer et al., 2007) with a similar pattern revealed by the
630 saliency map analysis (as shown in Figure 9). On the other hand, much larger decays were observed
631 when switching to network attacks (around 10%), with most severe cases found in the limbic,
632 frontoparietal network (FPN) and attention networks (consisting of 60, 82, 104 affected parcels,
633 respectively). A similar pattern of decays was observed when using the 17-network parcellation, with

634 the largest decays found in the networks related to cognitive control and attention (as shown in Figure
 635 **8b** and **8c**). Interestingly, the distribution of performance decays in cognitive decoding was not related
 636 to the size of affected intrinsic networks ($r=0.097$, $p=0.332$). To conclude, the ChebNet decoding
 637 model was robust to random attacks but was more vulnerable to targeted attacks on task-related brain
 638 regions and networks. Moreover, compared to the low-order model (e.g. $K=1$), the high-order
 639 ChebNet model was more resilient to random or targeted attacks by showing smaller decays in
 640 cognitive decoding due to lesions on regions and networks (Figure 8-S1).



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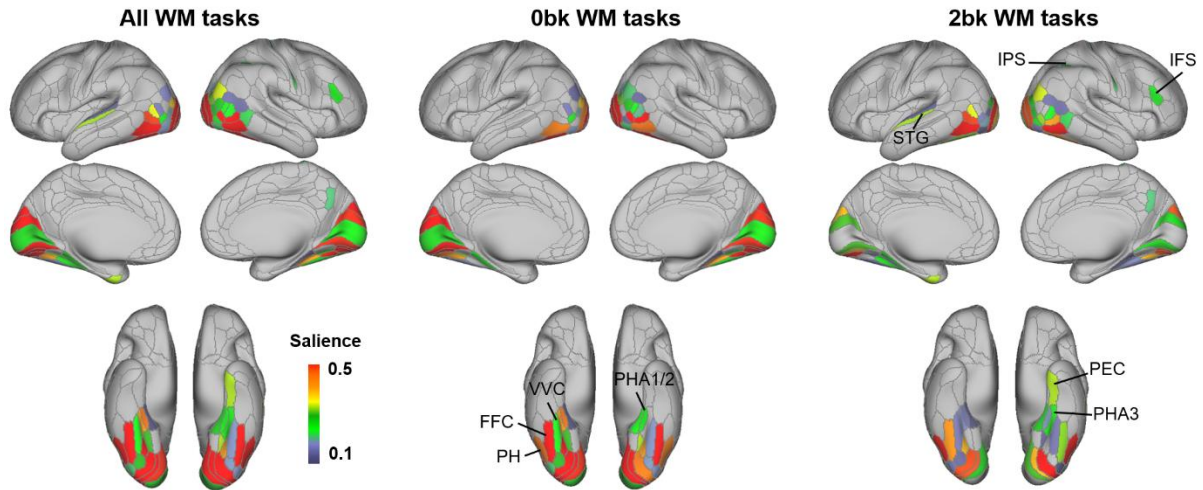
642 **Figure 8. Robustness of ChebNet decoding models to random attacks on nodes and networks.**

643 We simulated two types of brain lesions, either attacking randomly chosen regions or targeting for
 644 regions from a specific brain network. For random node attacks (**a**), we silenced brain responses from
 645 randomly chosen nodes, ranging from 10% to 80% of brain parcels, and repeated the process for 100
 646 times. We found that the decoding model was highly resilient to random node attacks by showing a
 647 small decay in the decoding accuracy ($<3\%$ when attacking around 80 regions). The most vulnerable

648 regions include areas in the ventral and dorsal visual streams (top right panel). For network attacks,
649 we removed one brain network at a time, identified by Yeo's 7 (**b**) and 17 (**c**) resting-state functional
650 networks, and silenced the associated brain parcels with at least 30% areas affected. We found severe
651 decays in the cognitive decoding when attacking specific brain networks (around 10% and 5% for 7-
652 and 17-network parcellation, respectively). Among which, the most vulnerable networks were those
653 related to cognitive control and attention, for instance the frontoparietal network (FPN) and ventral
654 attention networks (vAtt).

655 3.8. Node contributions revealed by saliency maps

656 In order to illustrate the biological basis of the decoding model, we generated the saliency maps on
657 the trained model by propagating the non-negative gradients backwards to the input layer
658 (Springenberg et al., 2014). An input feature is *salient* or *important* only if its little variation causes
659 big changes in the decoding output. As shown in Figure 9, category-specific salient features were
660 detected for all WM tasks and separately for 0back and 2back conditions. For 0back tasks, regions in
661 the visual cortex and ventral visual stream were identified, including V1-V3, PH, FFC and PHA,
662 coinciding with the literature that the ventral visual stream is involved in the recognition of visual
663 stimuli (Haan and Cowey, 2011; Haxby et al., 2014). By contrast, the frontoparietal network regions,
664 including IPS and MFG, and the temporal regions, e.g. superior temporal gyrus (STG) and Perirhinal
665 Cortex (PRC), were contributed to the decoding of 2back tasks. These regions have been shown to be
666 engaged in object recognition and visual working memory (Eriksson et al., 2015; Schon et al., 2016).
667 Our findings revealed that the ChebNet decoding model captured task-related brain regions and
668 category-specific patterns of brain activity, and consequently extracted biologically meaningful
669 features for the classification of different task conditions. This analysis also revealed high salience in
670 the primary sensorimotor cortices for Motor tasks (Fig.9-S1a) and in the perisylvian language-related
671 brain regions for Language tasks (Fig.9-S1b). Moreover, the learned graph representations, i.e.
672 activation maps in the last ChebNet layer, demonstrated distinct patterns of brain activity in the
673 perisylvian language-related regions among mathematics and story trials (Fig.9-S1c).



674

675 **Figure 9. Saliency maps for the decoding of WM tasks.**

676 We generated the salient features that showed high contributions to the classification of WM tasks by
677 using the guided backpropagation approach. The model detected biologically meaningful and
678 category-specific salient features on 0back and 2back WM tasks. For 0back tasks, the model
679 identified salient regions in the visual cortex and ventral visual stream, including V1-V3, PH, FFC
680 and PHA. For 2back tasks, the model detected salient features in the frontoparietal network regions,
681 including IPS and MFG, and the temporal regions, e.g. superior temporal gyrus (STG) and Perirhinal
682 Cortex (PRC). Note that only brain regions with a high saliency (saliency values > 0.1, full range of
683 saliency is (0,1)) and a significant 'task condition' effect ($p < 0.001$) were shown in the brain maps.

684 **4. Discussion**

685 We proposed a generalized framework for brain decoding based on ChebNet graph convolutions. The
686 model takes in a short window of fMRI time series and a brain graph (with nodes representing brain
687 parcels and edges representing brain connectivity), and integrates brain activity in a multiscale manner,
688 ranging from local regions, to brain circuits/networks, and across multiple brain systems. Using a 10s-
689 time window of fMRI signals, our model identified 21 different task conditions across multiple
690 cognitive domains with a test accuracy of 93% (chance level of 4.8%). We systematically investigated
691 the impacts of using high-order graph convolutions and connectome-constrained graph architectures
692 in the decoding model. Our findings revealed that 1) connectome constraints accelerate the
693 propagation and integration of brain activity by adding shortcuts through long-range connections; 2)
694 smaller parcel size or finer-scale atlas improves the internal homogeneity of brain parcels and boosts
695 the overall decoding performance; 3) high-order graph convolution encodes functional integration of
696 distributed brain activity at multiple scales and boots the decoding performance on all brain graphs.
697 These results support an important role of functional integration in cognitive decoding, which leads to
698 higher decoding accuracy as well as better adaptation to network misspecifications due to random
699 rewiring and node attacks.

700 4.1. Functional integration plays an important role in cognitive decoding

701 A variety of computational models have been proposed in the field of brain decoding in the last
702 decades, with the aim of learning a linear discriminative function on the spatial patterns of brain
703 activation under specific experimental conditions. For instance, researchers have successfully
704 attempted to use brain activity to reconstruct the frames of movies (Nishimoto et al., 2011), or to
705 decode the semantic context from words (Mitchell et al., 2008) and visual scenes (Huth et al., 2012)
706 by using linear regression models. Recently, with the fast development of deep learning, artificial
707 neural networks have been applied in the field of decoding human cognition from recorded brain
708 activity, for instance using classical convolutional (Wang et al., 2020) and recurrent neural networks
709 (Li and Fan, 2019), or a generalized form of convolutions in the graph domain (Zhang et al., 2021).

710 However, the majority of current brain decoding studies so far focused on segregating neural
711 substrates of different cognitive tasks by treating each brain area independently in the decoding model
712 (Haxby, 2012; Haxby et al., 2014; Poldrack, 2011; Varoquaux et al., 2018). The interactions between
713 different brain areas and networks have been largely ignored, but starts to play an important part in
714 the field. Cole and colleagues (Cole et al., 2016) demonstrated the possibility of predicting activations
715 of unseen brain regions or new subjects by transmitting information flow of brain activity within a
716 functional network. Using a similar idea, Li and Fan (Li and Fan, 2019) have successfully inferred
717 cognitive states from network-level neural activity by integrating signals from large-scale brain
718 networks. Accordingly, we recently proposed a GNN architecture that propagates brain activity
719 through functional connectomes and integrates the context of brain activity in both local and global
720 extent (Zhang et al., 2021). The model has achieved high decoding accuracy over a variety of
721 cognitive domains -90% in (Zhang et al., 2021)- outperforming other baseline approaches on the
722 benchmark, including non-integrative full-brain models, e.g. 64% in linear SVM and 76% in MLP.
723 In this study, we further extend the GNN framework by enlarging the scale of functional integration in
724 graph convolutions and exploring the impacts of different connectome priors in cognitive decoding.
725 Firstly, we implement high-level integration of task-evoked brain activity in the decoding model,
726 extending from a single brain network ($K=1$, similar to (Zhang et al., 2021)), to multiple brain
727 systems ($K>1$) and towards the full brain ($K>5$). Secondly, we explore different choices of graph
728 architectures that restrict the propagation of brain activity through the topology or connectome of the
729 human brain. Our results demonstrate a significant improvement in large-scale cognitive decoding by
730 implementing high-order interactions on functional connectomes (93% using the 5-order ChebNet
731 model). We observed this effect on all types of brain graphs (Figure 3). In addition, the high-order
732 integrative model resulted in a similar level of decoding performance when using different
733 connectome priors, for instance the diffusion-graph derived from whole-brain tractography of fiber
734 projections (Figure 4), but higher than topological and morphological priors.
735 The sensitivity to functional integration was not uniformly distributed among all cognitive domains
736 but rather depended on the cognitive demands of tasks (Figure 3e). For instance, WM and Relational-
737 processing required a high-order model to integrate brain activity across multiple brain systems, while

738 Language and Motor tasks already achieved the optimal performance by taking into account the
739 interactions within targeted brain networks. These findings may partially explain the excellent
740 decoding performance in previous decoding studies when tackling unimodal cognitive functions, for
741 instance, distinguishing body movements using patterns of brain activity from in the motor cortex
742 (Mottolese et al., 2013) or restricting the context of brain activity within a local area (Wang et al.,
743 2020), but showed poor decoding on high-order cognitive functions, for instance, classifying 0-back
744 and 2-back WM tasks (Wang et al., 2020). By contrast, when taking into account the integration
745 within the functional networks, the model achieved high accuracy on both unimodal and high-order
746 cognitive functions (Li and Fan, 2019; Zhang et al., 2021), and showed a further improvement by
747 implementing high-order interactions among brain networks (Figure 3e). Our results indicate that
748 high-performing cognitive decoding relies on the encoding of high-level functional integration in
749 brain activity, not limited to local brain activity or low-level interactions. In addition to higher
750 decoding accuracy, the integrative model also improved the robustness to perturbations on the graph
751 architecture, for instance, by using different types of interactions (Figure 4), network rewiring (Figure
752 7), as well as random attacks on brain regions and networks (Figure 8). These findings greatly expand
753 current main perspectives on brain decoding that aims to segregate neural substrates of different
754 cognitive tasks, and suggest an important role of functional integration during cognitive processes,
755 especially for high-order cognitive functions.

756 4.2. Connectome-constrained graph architectures accelerate information propagation and 757 functional integration

758 A series of studies in the literature have illustrated a great potential of using resting-state functional
759 connectivity in predicting cognitive functions, not only in behavior (Rosenberg et al., 2020;
760 Yamashita et al., 2018) but also in task-evoked brain activity (Cole et al., 2016; Tavor et al., 2016).
761 Recent decoding studies have shown that the connectivity patterns (Richiardi et al., 2011; Shirer et al.,
762 2012) as well as the activity flow on functional networks (Li and Fan, 2019; Zhang et al., 2021) are
763 also predictive of cognitive states. In the current study, we further demonstrated the potentials of
764 using other types of human connectomes beyond functional networks. As one of the basic graph

765 architectures, brain topology and its derived spatial constraints has been widely used in fMRI analysis,
766 for instance generating brain parcels on individual brains (Blumensath et al., 2013; Craddock et al.,
767 2012; Ma et al., 2021). When implementing GNN with such constraints, the model generalizes the
768 classical convolutional operations defined in the 3D volume space, e.g., (Wang et al., 2020), onto the
769 geometry of cortical surfaces. Interestingly, the topologically constrained decoding model achieved a
770 decent performance on unimodal cognitive functions, similar to previous studies (Wang et al., 2020),
771 but showed lower performance on high-order cognitions compared to functional connectomes (Figure
772 **3f**). The morphological brain networks, e.g. structural covariance of cortical thickness, on the other
773 hand, resembled randomized functional connectomes by showing slightly lower prediction accuracy
774 than the original graph in all cases (Figures **4** and **6**). Compared to them, the biologically constrained
775 graph convolutions using either functional or diffusion brain connectomes achieved the highest
776 decoding performance along with high robustness to network misspecifications due to random
777 rewiring and node attacks. Our results revealed a clear gradient in the contribution of graph
778 architectures for cognitive decoding, ranging from the lowest decoding performance by restricting
779 activity flow within local areas (spatial-graph), to moderate performance by integrating information
780 within neural circuits (diffusion-graph), and to the highest performance when using functional
781 networks (functional-graph). Moreover, this gradient was only dominant at a low propagation rate and
782 mostly diminished when using a high propagation rate, by converging to a similar level on all brain
783 graphs (Figure **4**). We observed a similar interaction effect on the randomized functional graphs as
784 well (Figure **7**). One possible explanation is that the spatial graph only consists of short-distance
785 connections, which restricts information integration to a small local area on the cortical surface. When
786 using a high-order propagation rate ($K>1$), the model expands the receptive field or neighborhood size
787 at each graph convolutional layer by taking multiple steps at once, and eventually reaches a large
788 neighborhood that includes distributed brain regions from a task-related functional network when K is
789 sufficiently high ($K>5$). On the other hand, by adding modular and community structures to the graph,
790 extracted from diffusion and functional connectomes, the model further accelerates the propagation of
791 brain activity in the brain by adding shortcuts through long-range connections. Numerous studies have
792 illustrated that the diffusion and functional brain networks, rather than regular spatial networks,

793 followed the small-world configuration with information segregation and integration at low wiring
794 and energy costs (Bullmore and Sporns, 2009; Bullmore and Bassett, 2011; Liao et al., 2017).
795 Our results revealed that, in addition to the K-order in ChebNet graph convolution, which controls the
796 propagation rate of information flow on the graph by taking multiple walks at once, the architecture of
797 brain graphs restricts the scale of the information flow at each step, ranging from local areas (spatial-
798 graph), to neural circuits (diffusion-graph), and to functional networks (functional-graph). Among
799 which, the biologically constrained graph structures derived from human brain connectomes highly
800 boost the decoding of cognitive processes.

801 4.3. Limitations and Future directions

802 In this study, we only investigated the choices of group-wise brain graphs in the decoding model, i.e.
803 all subjects taking the same definition of nodes and edges in the graph architecture. The benefit of
804 using such a brain graph is that the decoding model can easily generalize across large populations
805 (more than 1000 subjects in our case), transfer onto new populations and datasets, as well as better
806 adaptation to network misspecifications due to random rewiring and node attacks. However, our
807 findings did not rule out the possibility of using an optimal individual brain graph in cognitive
808 decoding, for instance constructing an individualized brain parcellation and subject-level graph
809 architecture. This might be beneficial when handling massive fMRI data from a single subject. Due to
810 the limited amount of functional imaging data from individual brains in the HCP database, this option
811 was not explored in the current study. In the next project, we plan to investigate how individual brain
812 parcellation schemes and individual graph architectures improve brain decoding of complex cognitive
813 processes on individual brains by using fMRI data from a local data collection (www.cneuromod.ca).

814 **5. Conclusions**

815 In summary, we propose a connectome-based graph neural network to encode the underlying
816 spatiotemporal organization of cognitive processes and explore the optimal connectome architectures
817 for large-scale cognitive decoding, including the path length, the homogeneity of brain parcels and the
818 type of interactions. The model propagates information flow of brain dynamics in a multiscale manner,
819 ranging from localized brain areas, to a specific brain network and towards the full brain. The scale of
820 functional integration is largely controlled by the path length, i.e. K-order of ChebNet, and is
821 restricted by the nature of interactions, i.e. brain connectomes. Compared to the topological and
822 morphological constraints, connectome-constrained graph convolutions achieved better decoding of
823 cognitive states. The edge-sparsified graph structures also contribute to superior performance of the
824 ChebNet decoding model. Together, our findings indicate that human connectome constraints and
825 multiscale functional integration are critical for large-scale cognitive decoding. Such decoding models
826 better adapt to small fluctuations on the graph architecture including disconnections and lesions in the
827 brain.

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834 **Author contributions**

835 Conceptualization: YZ, PB; Methodology: YZ, PB; Visualization: YZ, PB;
836 Investigation: YZ, NF, PB;
837 Writing—original draft: YZ, NF, PB
838 Writing—review & editing: YZ, NF, PB

839 **Competing interests**

840 The authors declare no competing financial interests.

841 **Data and materials availability**

842 We use the block-design task-fMRI dataset from the Human Connectome Project S1200 release,
843 downloaded from https://db.humanconnectome.org/data/projects/HCP_1200. In total, fMRI data from
844 1095 unique subjects under six different task domains and resting-state are used in this study. The
845 minimal preprocessed fMRI data are used, in both CIFTI and NIFTI formats, depending on the choice
846 of brain parcellation schemes. The proposed ChebNet decoding pipeline, as well as the optimized
847 decoding models and the construction of brain graphs, are made publicly available in the following
848 repository: https://github.com/zhangyu2ustc/gcn_tutorial_test.git.

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