Release the Krakencoder: A unified brain connectome translation and fusion tool

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ABSTRACT

Brain connectivity can be estimated in many ways, depending on modality and processing strategy. Here we present the Krakencoder, a joint connectome mapping tool that simultaneously, bidirectionally translates between structural (SC) and functional connectivity (FC), and across different atlases and processing choices via a common latent representation. These mappings demonstrate unprecedented accuracy and individual-level identifiability; the mapping between SC and FC has identifiability 42-54% higher than existing models. The Krakencoder combines all connectome flavors via a shared low-dimensional latent space. This "fusion" representation i) better reflects familial relatedness, ii) preserves age- and sex-relevant information and iii) enhances cognition-relevant information. The Krakencoder can be applied without retraining to new, out-of-age-distribution data while still preserving inter-individual differences in the connectome predictions and familial relationships in the latent representations. The Krakencoder is a significant leap forward in capturing the relationship between multi-modal brain connectomes in an individualized, behaviorally- and demographically-relevant way.

1 Introduction

The brain is a vastly complex, interconnected network of neurons (and other types of cells) whose proper function allows us to move, think, feel, and observe as well as interact with our environment. Studying how the brain's connections relate to behavior, so-called brain connectome-behavior mapping, is crucial not only for understanding how the brain works generally but also for identifying biomarkers of disease, predicting outcomes in neurological disorders, and designing personalized interventions. Brain connectivity can be probed through various structural and functional neuroimaging techniques. Structural connectivity (SC) can be captured with diffusion MRI (dMRI) measures of white matter, or the anatomical wiring, that connects different brain regions. Functional connectivity (FC), as measured with blood oxygen level dependent functional MRI (BOLD-fMRI), quantifies the temporal similarity between brain regions' dynamic neural activity patterns.The association between SC and FC is a subject of intense research, as it is believed that structural pathways provide the backbone over which functional activation flows. Despite this, correlations of SC and FC are moderate at best. Understanding the relationship between SC and FC is key to deciphering how the brain's physical structure supports its dynamic functions and may offer insights into the neural mechanisms underlying behavior, injury or disease, and recovery[1–4].

There are many approaches to modeling the relationship between SC and FC, most of which focus on using SC to predict FC. These methods include i) biophysical models, e.g. linked neural mass models[5–10], ii) graph theoretical models, e.g. communication strategies[11–15], iii) statistical models, i.e. that model SC and FC topological metrics[16–19], and iv) network control theory[20–23]. More recently, machine learning has been used to predict FC from SC[24–27], predict SC from FC[28], or to translate a connectivity estimate between parcellations[29,30]. Many of these studies have shown that metrics of SC-FC relationships vary with age, sex, and behavioral variables[16,27,31], or disease/injury and recovery[4,32,33].

Among the challenges and considerations in modeling this relationship, the assumption that estimated SC is an objective, fixed constraint on possible FC patterns is increasingly questioned. Evidence suggests that the brain's functional dynamics can be highly flexible and adaptive, and maybe driven by geometric factors not measured with SC[34]. Variability in SC estimation techniques, particularly in their sensitivity to detect faint or indirect connections, further complicates the interpretation of connectivity data. Moreover, the performance metrics and loss functions currently employed in connectivity studies often fail to adequately account for inter-subject variability, potentially skewing the results and interpretations.

Despite the utility of modeling the relationship between connectomes, there is strong methodological disagreement in the literature as to how to extract the connectomes themselves from brain images[35–37]. Studies have shown that biases inherent in different processing choices, referred to here as "flavors", can lead to different or even contradictory conclusions[38,39]. Each connectome flavor may differ in how the brain is parcellated into regions, how potential noise, artifacts, or confounds are removed, and how the connectivity between regions is quantified, among other methodological choices. Furthermore, connectome data from different studies are often shared only in certain flavors, making comparisons between datasets challenging.

In this work, our fundamental assumption is that each set of choices in the imaging and processing pipelines provides a different view of the same underlying system. Drawing inspiration from recent advances in multi-view learning[40], we develop and share a tool called "Krakencoder" that provides a way to combine these choices (i.e. connectome fusion), and thus create a more comprehensive representation of the brain's connectivity. Deriving a unified latent representation from within-modality and/or across modality connectome estimates may allow reconciliation of differing views of the same underlying network in order to overcome limitations and combine benefits from various processing choices. Krakencoder is a novel "universal" brain connectivity encoding architecture and is capable of transforming connectivity estimates between parcellations, estimation techniques, and modalities with unprecedented precision. Importantly, the Krakencoder is able to preserve inter-individual differences in a way that is behaviorally and demographically relevant. This element is crucial if we are to use the Krakencoder to improve our understanding of how brain structure and function and their interplay maps to behavior, impairment, or recovery after disease or injury.

2 Results

2.1 Krakencoder model architecture and training

The Krakencoder architecture comprises a set of encoders and decoders that allow transformation of each connectivity type into every other connectivity type via a common low-dimensional latent representation, see **Fig. 1** . The Krakencoder was trained to optimize for both reconstruction accuracy and preservation of individual differences. The latter was achieved by enforcing latent-space representations of different connectivity types from the same subject to be close to one another and far from other subjects' latent space connectome representations. The model was trained on resting-state FC and white-matter SC data from 683 healthy young adults (366 female, aged 28.6$\pm$3.8) from the Human Connectome Project, validated during training on 79 held-out subjects (43 female, aged 29.1$\pm$3.8), and finally tested on 196 subjects (107 female, aged 29.1$\pm$3.6). Care was taken to ensure that no siblings spanned the divisions, as this data leakage can lead to over-optimistic model performance. Connectivity flavors include 3 parcellations (with 86, 268, and 439 regions), 3 common FC estimates (Pearson correlation, Pearson correlation following global signal regression, and regularized partial correlation), and 2 SC estimates (volume-normalized streamline counts from deterministic and probabilistic tractography), for a total of 15.

We create a separate encoder and decoder for each of the 15 connectivity flavors and then train the model to predict each flavor from each other flavor. There are 225 total training paths, including 15 autoencoders that map between the same flavor (See **Fig. 1a**) and 210 transcoders that predict one flavor from another (See **Fig. 1b**). Each encoder is a single fully-connected linear layer, followed by L^2 normalization that constrains the latent representation to the surface of a 128-dimensional hypersphere. Each decoder is a single fully-connected linear layer. Dimensionality of the connectivity flavors varies between parcellations, which could lead to an imbalance in the training to favor higher dimension connectivity flavors. Thus, we balanced the contributions of each flavor by reducing each connectivity input to 256 dimensions using a precomputed PCA, derived using only training data to avoid leakage between train and test sets. Reconstruction loss for each training path includes both Pearson correlation and Euclidean distance. We include a contrastive component to the correlation and Euclidean loss functions, to explicitly preserve inter-subject variability of predicted connectomes. A contrastive loss term is applied to the latent representation as well to further promote inter-subject variability of the representations. Finally, we include an intra-subject latent space consistency loss to maximize the similarity of the latent representations from each connectome flavor for a given subject (See **Fig. 1c**). This combination of loss functions allowed us to fine-tune the tradeoff between reconstruction accuracy and inter-subject variability (See **Fig. S2b**), and to condition the latent space representation. See Methods for details on training procedure and loss functions.

During model inference, the Krakencoder predicts each of the 15 connectivity flavors from any other, transforming predictions that exist in the reduced 256-dimensional space to their higher native dimensions using the inverse of the precomputed PCA transforms. The model can also combine information from multiple connectomes by averaging their latent space representations to obtain a "fusion" representation; this fusion representation can then

be decoded to predict all 15 connectome flavors. The encoding and averaging step in the fusion process can include all available connectome flavors, or a subset of flavors to, for instance, predict FC flavors from the fusion latent representation of all SC flavors or vice versa ("fusionSC" or "fusionFC", **Fig. 1d**), or to predict one parcellation using inputs from the averaged latent representations of all other parcellations ("fusion-parc", **Fig. 1d**). The latter fusion version is particularly important if one is using the Krakencoder to translate connectome data to a desired atlas on which it had not been computed.

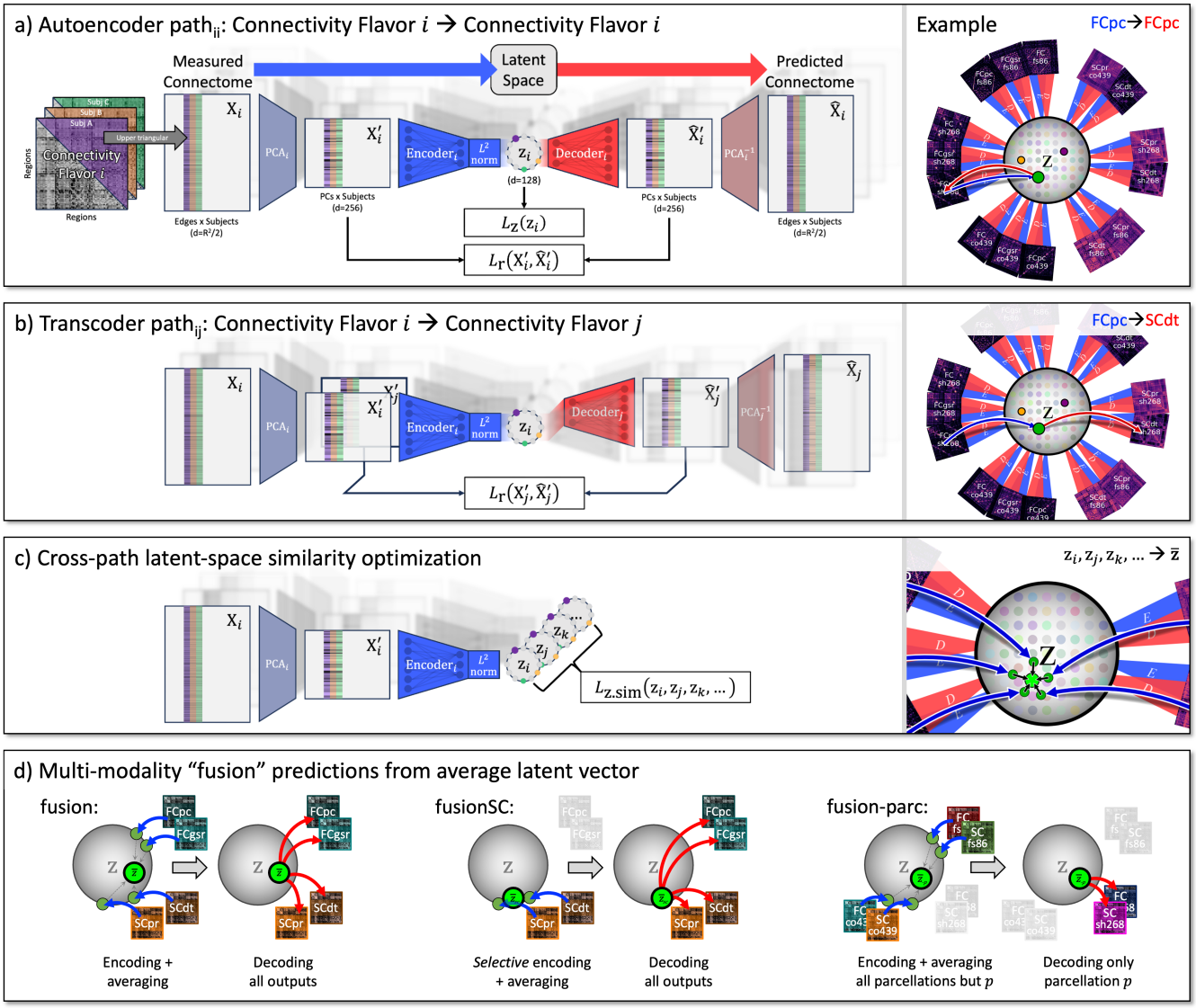

Figure 1. Key features of the Krakencoder architecture. a. Autoencoder for connectivity flavor i (i.e., $path_{ii}$) begins by stacking the upper triangular portion of each subject's connectivity matrix into input $X_i \in \mathbb{R}^{n_{edges} \times n_{subj}}$. A precomputed, fixed PCA transformation normalizes the data and reduces dimensionality to $X_i' \in \mathbb{R}^{256 \times n_{subj}}$, equalizing the size of disparate input flavors. A single fully-connected layer $Encoder_i$ followed by L^2 normalization transforms X_i' into a latent hypersphere surface $z_i \in \mathbb{R}^{128 \times n_{subj}}$. Batch-wise encoding loss $L_z(z_i)$ controls inter-subject separation in latent space. A single fully-connected layer $Decoder_i$ transforms z_i to $\hat{X}_i'$, and batch-wise reconstruction loss $L_r(X_i', \hat{X}_i')$ and $L_z(z_i)$ are backpropagated to optimize $Encoder_i$ and $Decoder_i$. **b.** Transcoder $path_{ij}$ converting input flavor i to output flavor j begins the same as $path_{ii}$, transforming $X_i \rightarrow X_i' \rightarrow z_i$, then $Decoder_j$ transforms $z_i \rightarrow \hat{X}_j'$, and reconstruction loss $L_r(X_j', \hat{X}_j')$ is backpropagated to optimize $Encoder_i$ and $Decoder_j$. **c.** Latent similarity loss $L_{z.sim}(z_i, z_j, z_k, \ldots)$ provides explicit control to ensure the latent representations of each subject are consistent across connectivity flavors. See **Table 2** for details about loss terms. **d.** Illustration of "fusion" predictions from averaged latent space vectors. For these predictions, we average the encoded latent vector from all input flavors (as in the "fusion" model), or a subset of input flavors (as in the "fusionSC" model which only averages latent vectors from SC inputs), and then decodes this average vector to all output flavors. The "fusion-parc" model demonstrates cross-parcellation prediction, by averaging only inputs from the *other* parcellations.

2.2 Measuring connectome prediction accuracy

A key consideration when assessing the performance of a connectome prediction model is the high degree of similarity of measured connectomes with the population mean. The Pearson correlation between connectomes of unrelated individuals can exceed 0.9, depending on the flavor, and a model that simply predicts the population mean for every subject can appear to have a very high prediction accuracy if it uses Pearson correlation as its metric (See **Fig. 2d** , "pop. mean" in bottom subpanel). One simple solution to this issue is to subtract the population mean calculated from training subjects before correlating measured and predicted connectomes; here we refer to this metric as $\mathrm{avgcorr}_{\mathrm{demean}}$. However, this metric still cannot distinguish whether predictions faithfully capture individual variation, particularly when there is clustering within the population (see **Fig. S1b**). Our goal here is to create individualized connectome predictions to understand the sources and consequences of across-subject variability. Thus, we also consider the identifiability of our predictions: whether our measured connectome for a subject is closer to the predicted connectome for that subject than the predicted connectome of any other subject. The "top-1 accuracy" is a winner-take-all measure that reflects the fraction of subjects for which this is true. For a more continuous measure of identifiability, more suitable to assessing imperfect predictions, we use an "average rank percentile" measure ($\mathrm{avgrank}$), which is the fractional rank of the similarity (Pearson correlation) of a subject's measured and predicted connectomes compared to all other predicted connectomes, averaged across subjects (**Eq. 4**). Taken together, prediction accuracy and identifiability, as measured by $\mathrm{avgcorr}_{\mathrm{demean}}$ and $\mathrm{avgrank}$, convey a more complete picture of how well a model explains individuals' connectomes.

In addition to these measures of prediction accuracy for the connectivity matrix values, we compute several common graph theoretical metrics to assess how faithfully the predicted connectomes capture the network properties of the measured connectomes. We use the Brain Connectivity Toolbox[41] to compute average node strength, average betweenness centrality, characteristic path length, and modularity (Louvain community detection) for each measured and predicted connectome, and compute the Spearman rank correlation between the predicted and measured values across all test subjects for each metric.

2.3 Connectome prediction performance

The accuracy of the Krakencoder's connectome predictions was assessed on 196 held-out test subjects via identifiability (top-1 accuracy and $\mathrm{avgrank}$) and (de-meaned) correlation ($\mathrm{avgcorr}_{\mathrm{demean}}$). The heatmaps in **Fig. 2a-c** illustrate the various metrics for every pair of the 15 connectome flavors, as well as "fusion" predictions decoded from the averaged latent vectors from groups of encoded connectome flavor inputs (See **Fig. 1d**). The "*average*" column and row show the average performance metric for each source and target flavor, respectively.

Top-1 identifiability (**Fig. 2a**) measures the fraction of subjects whose predicted connectome is more similar (higher Pearson correlation) to their measured connectome than any other subject's measured connectome (random chance $1/n_{subj}$ = 0.005). Average rank percentile (**Fig. 2b**) is the fractional rank of the similarity (Pearson correlation) of a subject's predicted and measured connectomes compared to all other measured connectomes, averaged across subjects (random chance 0.5). The $\mathrm{avgcorr}_{\mathrm{demean}}$ metric (**Fig. 2c**) is the average Pearson correlation between a subject's predicted and measured connectomes, after subtracting the population average of the measured connectome flavor from the predicted and measures connectomes. The average rank percentile for FCs predicted from FCs of different parcellations or connectivity estimations (FC $\rightarrow$ FC) shows near-perfect identifiability (**Fig. 2b** , upper section, upper left block mean=1.0). Similarly, SC $\rightarrow$ SC predictions have near-perfect identifiability (upper section, lower right block mean=0.99). Inter-modality predictions performed worse than within-modality, but still far exceeding chance, with the overall mean of SC $\rightarrow$ FC (lower left block) and FC $\rightarrow$ SC (upper right block) average rank identifiability of 0.82 and 0.85, respectively. In general, better $\mathrm{avgrank}$ prediction identifiability coincides with connectome sparsity, with higher dimensional parcellations (Coco439) and more sparse FC estimates ($\mathrm{FC}_{\mathrm{pcorr}}$) being more easily identifiable. The $\mathrm{avgcorr}_{\mathrm{demean}}$ metric (**Fig. 2c**) shows an average of 0.38 for FC $\rightarrow$ FC, and an average of 0.35 for SC $\rightarrow$ SC. Inter-modality predictions are again more difficult, with average FC $\rightarrow$ SC=0.16, and SC $\rightarrow$ FC=0.09. Lower dimensional parcellations generally had higher $\mathrm{avgcorr}_{\mathrm{demean}}$.

Predictions of regularized partial correlation FC ($\mathrm{FC}_{\mathrm{pcorr}}$) had the highest $\mathrm{avgrank}$, but the lowest $\mathrm{avgcorr}_{\mathrm{demean}}$ among FC flavors, which reflects the noise inherent in this estimate, even with regularization, but also an increased sparsity that drives identifiability. SC predicted from $\mathrm{FC}_{\mathrm{pcorr}}$ yielded consistently better performance than other FC inputs, likely due to the increased sparsity and removal of non-specific correlations. The best single FC input for predicting all SC flavors was the Shen268 $\mathrm{FC}_{\mathrm{pcorr}}$, which predicts Coco439 $\mathrm{SC}_{\mathrm{pr}}$ with an $\mathrm{avgrank}$ of 0.99 and $\mathrm{avgcorr}_{\mathrm{demean}}$ of 0.19. The best single SC input for predicting all FC flavors was the Coco439 $\mathrm{SC}_{\mathrm{pr}}$.

The bottom subpanel of **Fig. 2a-c** shows connectome predictions using the "fusion" latent space average from multiple input flavors. The "fusion-parc" predictions exclude inputs of the same parcellation from the averaged latent vectors, and their relatively high values demonstrate the level of shared information across flavors within the Krakencoder's unified latent space.

Finally, we show that the Krakencoder's fusion prediction also preserves the network properties of the measured connectomes. **Fig. S4** shows the Spearman correlation between the measured connectomes' network properties (mean node strength, mean betweenness centrality, characteristic path length and modularity) and the Krakencoder's predicted connectomes' network properties, across 196 held-out individuals in the test set. The three fusion representations are used as input and each of the 15 connectome flavors as output; correlations between measured network metrics from the various familial relatedness groups are shown as comparison. The Krakencoder's predicted connectomes generally preserve the network properties of the measured connectomes as well as or better than the correlation between network properties extracted from identical twins (MZ) or two scans of the same individual (self-retest).

2.4 Connectome similarity of related individuals

The "fusionSC-parc" and "fusionFC-parc" rows in **Fig. 2a-c** represent the accuracy of the Krakencoder when predicting an SC or FC connectome flavor from all other SC or FC flavors (excluding those from the predicted parcellation). If we compare this directly to **Fig. 2d** , we can see how the Krakencoder's predicted connectome accuracy compares to several baseline estimates: measured connectomes from age- and sex-matched individuals who are unrelated, family members (non-twin siblings, dizygotic [DZ] and monozygotic [MZ] twins), retest sessions from the same individual (self retest), or the population mean connectome. For instance, the "self retest" row in the **Fig. 2d** heatmaps can be considered a measurement reliability ceiling, while the "unrelated" row shows the performance that can be explained by age- and sex-matching alone. Within a modality, top-1 accuracies (ranging from 0.93-1 for "fusionFC-parc"$\rightarrow$FC and 0.83-0.97 for "fusionSC-parc"$\rightarrow$SC) and average rank percentiles (all equal to 1 for the "fusionFC/SC-parc") in **Fig. 2a** and **Fig. 2b** are similar to the self retest identifiability (when connectomes derived from imaging the same person twice are used to perform the identification) and better than the identifiability of individuals who are genetically identical (MZ twins). Similarly, the diagonal entries in **Fig. 2c**

, representing the autoencoder $\text{avgcorr}_{\text{demean}}$ for each flavor, range from 0.13-0.74, which is comparable to the "self retest" noise ceiling (0.15-0.81), and are larger than the "MZ twin" row (0.07-0.47, a 40-110% increase). This indicates that the autoencoders with a 128-dimensional bottleneck preserve more inter-subject connectome variability than can be explained by identical genetics, and about the same amount of variability as expected when measuring the connectome from the same individual twice. The "fusionSC" and "fusionFC" rows in **Fig. 2c** represent the $\text{avgcorr}_{\text{demean}}$ for the unified SC (or FC) $\rightarrow$FC (or SC) connectome predictions, with values ranging from 0.03 to 0.16 for SC$\rightarrow$FC and 0.16-0.26 depending on the flavor. These exceed the similarity observed in the "sibling" or "DZ twin" row from the $\text{avgcorr}_{\text{demean}}$ subpanel in **Fig. 2d** , indicating that predicting FC from our unified SC representation preserves more intersubject FC variability than can be explained by age, sex, and 50% genetic similarity.

2.5 Spatial variation in edge prediction accuracy

The primary performance metrics assess global connectome similarity. We further assessed the spatial variability of prediction accuracy to determine whether certain brain regions are more accurately predicted than others. For fusion-parc, fusionFC-parc, and fusionSC-parc (fusion predictions made without the parcellation being predicted), the prediction accuracy for each edge is the Pearson correlation between the predicted and measured values for the 196 held-out test subjects. To simplify visualization and enable comparison across varied size parcellations, each region is assigned to one of 7 cortical resting state networks[42] or subcortical and cerebellar networks. The edge-wise accuracies (region $\times$ region) are then grouped and averaged into a 9×9 network representation for each connectome flavor. In the top block of **Fig. 3a** , the network-averaged edge prediction accuracy is presented for each of the fusion types as input (rows) and each connectivity flavor as output (columns). The bottom block shows the baseline network-averaged edge similarity comparing measured connectomes of unrelated age- and sex-matched subjects and related individuals. The figure demonstrates that the Krakencoder's prediction accuracy is relatively uniform throughout the cortex and subcortex. Networks with lower Krakencoder predictability (e.g., the limbic network), also show low self-retest measurement reliability (bottom row). In **Fig. 3b** , each network $\times$ network heatmap in **Fig. 3a** is correlated with the corresponding self-retest measurement reliability (bottom row), to quantify the consistency of the spatial pattern of edge-wise accuracies with the reliability of the edge-wise measurements. We see that the spatial pattern of the edge-wise accuracy of the Krakencoder's fused intra- and inter-modality predictions is as similar to the spatial pattern of the edge-wise self-retest measurement reliability as the MZ twins' spatial patterns of edge-wise reliability. **Fig. S3** summarizes the edge-wise prediction accuracy at a region level for each connectivity flavor in its own parcellation, showing a similar agreement between prediction and measurement reliability.

2.6 Demographic and behavioral prediction from the Krakencoder's latent space representations

We next tested if the Krakencoder latent space preserves inter-subject variation related to family structure as well as demographic and behavioral features. **Fig. 4a** shows the inter-subject similarity of latent space representations for pairs of age- and sex-matched unrelated individuals, non-twin siblings, DZ and MZ twins, and self-retest, along with inter-subject similarity of observed connectomes. By comparing ROC separability of each pair of violin plots, we see that separation is greater for the Krakencoder latent space than for the observed connectomes, with statistical significance for unrelated vs sibling, DZ vs MZ twins, and MZ vs unrelated ($p_{perm} < .05$, 10000 permutations, FDR-corrected).

To demonstrate the preservation of demographically- and behaviorally-relevant features in the Krakencoder's latent space, we trained linear models to predict individuals' age, sex, and cognitive scores ("total", "fluid", "crystallized", and "early childhood" composite scores from the NIH toolbox) from the Krakencoder latent space, and compared them to the same predictions based on observed connectome data. Linear kernel ridge regression models for each variable were built from the mean latent vectors (fusionFC, fusionSC, fusionFCSC, each of which is $n_{subj} \times 128$) or from the average inter-subject cosine similarity of observed data (i.e. the average of 9 FC, 6 SC, or 15 SC+FC $n_{subj} \times n_{subj}$ matrices). **Fig. 4b** shows Krakencoder and observed connectome data predict sex with a similar balanced accuracy of $\geq$ 0.93. The Krakencoder's latent space predicts age with Pearson $r \geq 0.5$, (fusionFC r=0.50, MAE=2.35; fusionSC r=0.51, MAE=2.57; fusionFCSC r=0.58, MAE=2.33), similar to the predictions from observed data (observed FC r=0.57, MAE=2.31; observed SC r=0.49, MAE=2.58; observed FC+SC r=0.59, MAE=2.33). For the age predictions, fusionSC outperformed observed SC and observed FC outperformed fusionFC ($p_{perm} < 10^{-3}$, FDR-corrected), but the observed data and fusion SCFC models performed similarly. Interestingly, the Krakencoder's latent space predictions significantly outperformed the observed data model predictions for predicting all cognitive composite scores. See Methods for details on inter-subject similarity calculations and model fitting.

2.7 Krakencoder performance on on out-of-sample, out-of-distribution data

To assess generalizability of the Krakencoder to new datasets, we applied our frozen, pretrained Krakencoder model to data from the multi-site HCP Lifespan study[43–45], including both the Development cohort (HCP-D) and the Aging cohort (HCP-A). These two studies differ from the original HCP young adult study in both subject demographics (ages 8-21 for HCP-D and 36-100+ for HCP-A vs 22-37 for HCP-YA) and acquisition parameters, with voxel sizes and scan durations more similar to those used in typical neuroimaging studies (see Methods for more details). To account for domain shift, we linearly mapped the population mean of each connectome flavor to the population mean of the HCP-YA training subjects before applying the HCP-YA derived PCA dimensionality reduction and Krakencoder latent space projection. Despite the demographic and acquisition differences, the Krakencoder still predicts connectome flavors with high accuracy and precision. **Fig. 5a-d** shows $\mathrm{avgrank}$ and $\mathrm{avgcorr}_{\mathrm{demean}}$ for the HCP-D (age 8-21) and HCP-A (age 36-100+) cohorts. Within-modality connectome prediction identifiability remained high for both HCP-D and HCP-A ($\mathrm{avgrank} > 0.96$). Inter-modal prediction identifiability was reduced 6-12% compared to held-out HCP-YA subjects, though still well above chance ($\mathrm{avgrank} > 0.75$). Intra-modal $\mathrm{avgcorr}_{\mathrm{demean}}$ was reduced by 10-26%, while inter-modal $\mathrm{avgcorr}_{\mathrm{demean}}$ was 30-50% lower than held-out HCP-YA. Thus, despite significant differences in age and acquisition reducing prediction accuracy, the Krakencoder model still performs well above chance and preserves inter-individual differences when mapping between connectome flavors.

The HCP-D dataset contains 76 sibling pairs (50 same-sex, 26 opposite sex, Δage 0-9yr), so we performed a familial similarity analysis similar to that for HCP-YA. In **Fig. 5e** , we show that siblings were more separable from age- and sex-matched individuals in latent space than in the observed data for all three fusion types (fusionFC, fusionSC, fusionFCSC) ($p_{perm} < 10^{-3}$, FDR-corrected). Finally, we performed a regression analysis to predict age, sex, and cognition in the HCP-D and HCP-A datasets (See **Fig. S5**). New predictive models using the same approach as the HCP-YA predictions were fit and cross-validated for each of the two new datasets. As with HCP-YA, sex was predicted very accurately by both latent and observed data models (balanced held-out test accuracy = 0.86-0.95). Age was predicted with much higher accuracy than in HCP-YA (HCP-D r=0.84-0.95, MAE=1.45-1.72; HCP-A r=0.76-0.85, MAE=6.13-6.52 on held-out test data), likely due the much larger age-range and larger age-related changes during development and aging. Cognitive score prediction performance for the HCP-A data was similar to or better than HCP-YA, perhaps due to larger age-related cognitive effects, but performed considerably worse for the HCP-D dataset. This decrease in predictive ability was especially pronounced when predicting cognition from SC, where accuracy (Pearson's r) from latent and observed data models was not significantly greater than 0. For all other predictions, observed data models performed significantly better than those on the Krakencoder latent space ($p_{perm} < 10^{-3}$, FDR-corrected), though the Krakencoder predictions remained well above chance.

2.8 Comparison with existing techniques

While predicting FC from SC is not the only application of our model, this route of prediction is among the most commonly studied problems in brain connectivity mapping. To compare our current Krakencoder model with this previous literature, we gathered a few recent studies that used different approaches to predict FC from SC. The first is a deep neural network proposed by Sarwar et. al[24] ("deepnet") and the second is a graph neural network from Neudorf et. al[25] ("graphnet"). The Krakencoder model incorporates 2 flavors of SC per parcellation (6 total) and 3 flavors of FC per parcellation (9 total). These two previous SC-FC prediction frameworks are designed to predict a single flavor of FC from SC. Thus, we trained 12 separate models for each of the two frameworks for all combinations of $\mathrm{SC}_{\mathrm{dt}}$/$\mathrm{SC}_{\mathrm{pr}}$ and FC/$\mathrm{FC}_{\mathrm{pcorr}}$. $\mathrm{FC}_{\mathrm{gsr}}$ was excluded due to computational constraints and relative redundancy with FC.

By both $\mathrm{avgrank}$ and $\mathrm{avgcorr}_{\mathrm{demean}}$ metrics, the predictions from our model outperform both "deepnet" and "graphnet" models across all connectome flavors and parcellations (See **Fig. S6**). Specifically, the Krakencoder $\mathrm{avgrank}$ was 17-86% higher (average 42%) than "deepnet" or "graphnet" models for the same single SC inputs, and 18-90% higher (average 54%) using the fusionSC input to predict each FC flavor. Krakencoder $\mathrm{avgcorr}_{\mathrm{demean}}$ was 1-890% higher (average 335%) than either model using single SC inputs, and 25-980% higher (average 450%) using fusionSC. Similarly, the accuracy of network properties for FC predicted by Krakencoder exceeded that from either alternative SC to FC framework. These particular results highlight the special emphasis of the Krakencoder on preservation of individual differences when mapping from SC to FC.

A note on computational efficiency: training all 12 "deepnet" models required approximately 140 GPU hours on an Nvidia A100 (4x5 hours for FS86, 4x10 hours for Shen268, and 4x20 hours for Coco439), and all 12 "graphnet" models required 1200 GPU hours (4x50 hours for FS86, 4x100 hours for Shen268, 4x150 hours for Coco439). For comparison, the Krakencoder required only 30 GPU hours to train a model for all 15x15=225 prediction paths simultaneously.

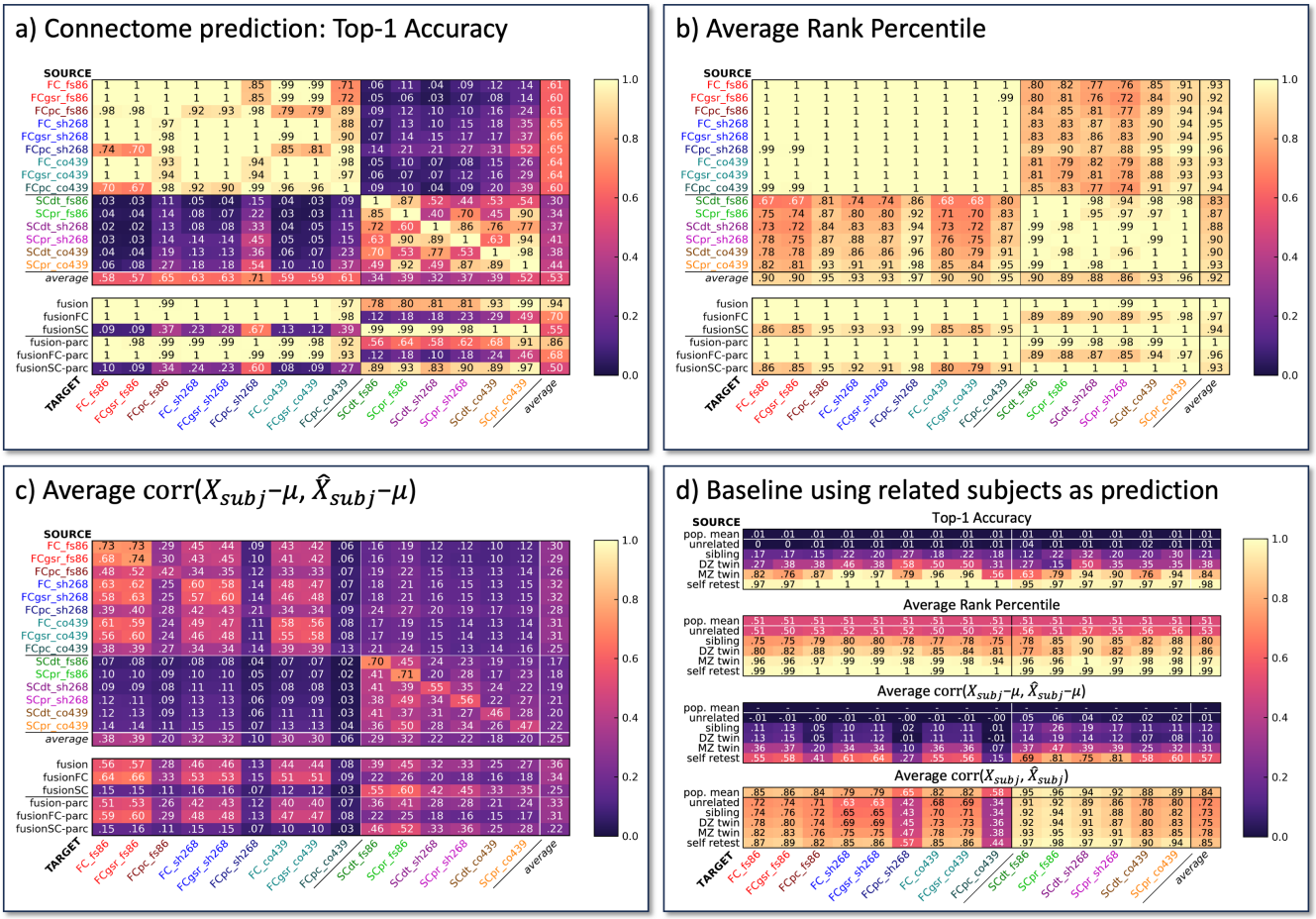

Figure 2. Connectome prediction performance for all input and output flavors on 196 held-out HCP-YA subjects. Heatmaps in **a**-**c** show connectome prediction performance from each *source* flavor (row) to each *target* flavor (column). Flavors include 3 parcellations (fs86, sh268, co439), 3 FC estimates (FC=Pearson, FCgsr=global signal regressed Pearson, and FCpc=regularized partial correlation), and 2 SC estimates (SCdt=deterministic tractography, SCpr=probabilistic tractography). The "*average*" row is the mean of performance metrics for all sources in the column above. The "fusion" row shows predictions from the average latent vector from all 15 connectome flavors (See panel **e**). "fusionFC" and "fusionFC" are predicted from the average of 9 FC or 6 SC latent vectors, respectively. "fusion-parc" predicts each parcellation from the average of all parcellations *except* itself. **a.** Top-1 accuracy measures the fraction of test subjects whose predicted connectome is closer to their own measured connectome than any other subject's measured connectome. Chance level is 1/196=0.005. **b.** Average rank percentile measures the fraction of *other* subjects' measured connectomes that are further from the target subject's predicted connectome than its own measured connectome. This rank percentile is then averaged across subjects. Chance level is 0.5. **c.** Average correlation of each subject's measured and predicted connectomes, after subtracting the population average ($\text{avgcorr}_{\text{demean}}$). **d.** For each subject s_a, we select an age- and sex-matched individual s_b of a given relatedness (unrelated, sibling, DZ/MZ twin, or self retest) and consider the measured connectome from s_b as the prediction for s_a. For each relatedness level, we compare the set of pseudo-predictions to measured connectomes using each performance metric, as though they were predictions from our model. Thus, we can observe the reliability and utility of each flavor and performance metric, and provide multiple baselines for evaluating model performance. We also show performance using the population average for each flavor ("pop. mean") as pseudo-prediction, which for the avgcorr metric (bottom) exceeds test-retest, but for all other metrics is zero or chance.

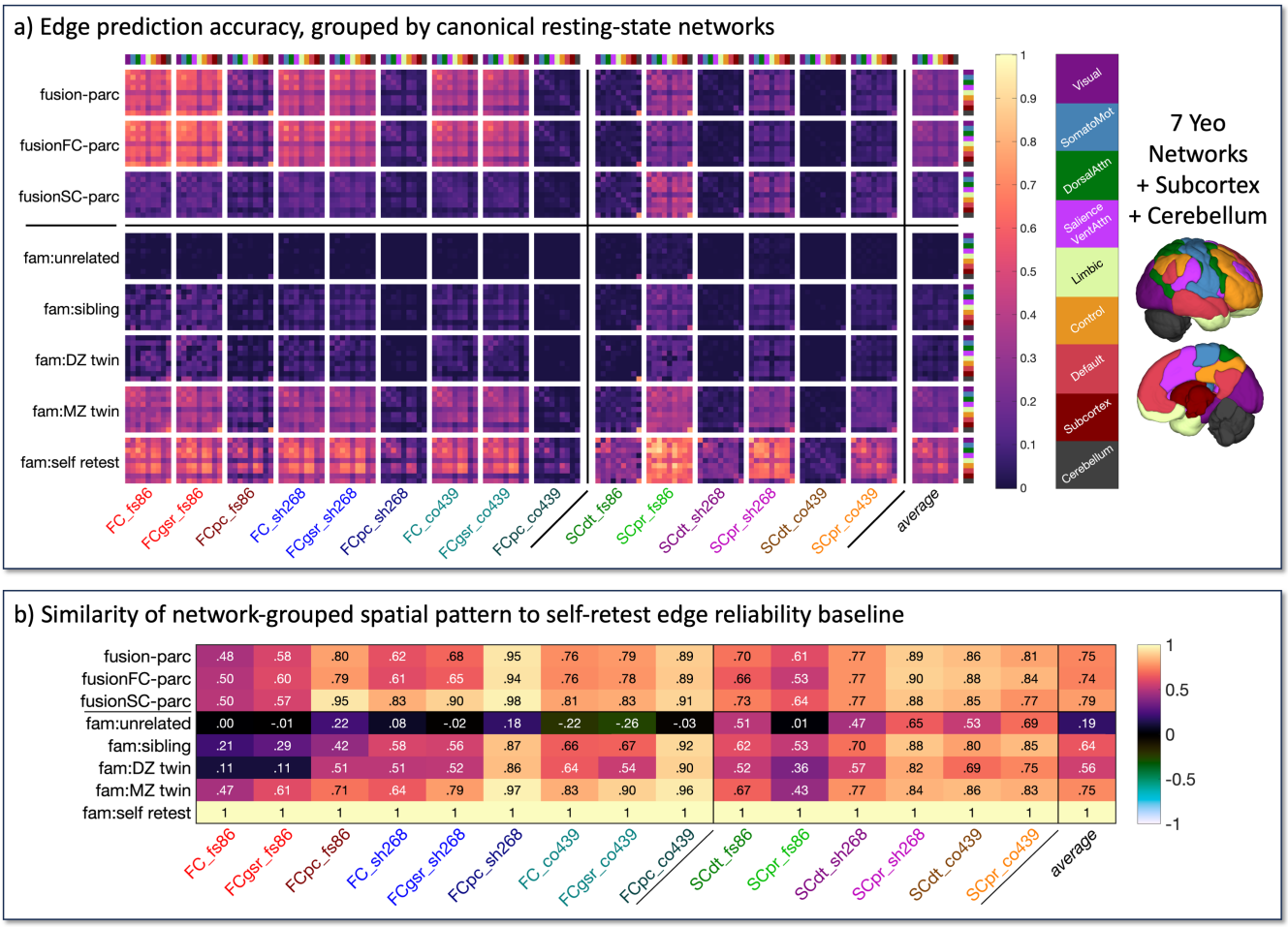

Figure 3. Spatial variation in edge prediction accuracy and baseline reliability. For the Krakencoder's fusion predictions made without the parcellation being predicted (fusion-parc, fusionFC-parc, and fusionSC-parc), the prediction accuracy for each edge is the Pearson correlation between the predicted and measured values for 196 held-out test subjects. To simplify visualization and compare across parcellations, each region is assigned to one of 7 cortical resting state networks[42] or separate subcortical and cerebellar networks, and the edge-wise accuracies (region $\times$ region) are then grouped and averaged into a 9×9 network representation. Age- and sex-matched individuals of given relatedness, as well as self-retest, are correlated and averaged in the same manner, in order to provide a baseline for comparing the spatial patterns of edge-wise accuracy. **a.** The spatial heatmaps show that prediction accuracy is relatively uniform throughout the cortex and subcortex. Networks with lower predictability (e.g., the limbic network), also show low reliability in self-retest measurement reliability (bottom row). **b.** Each network $\times$ network heatmap in **a** is correlated with the corresponding self-retest (bottom row), to show the consistency of the spatial pattern of edge-wise predictions.

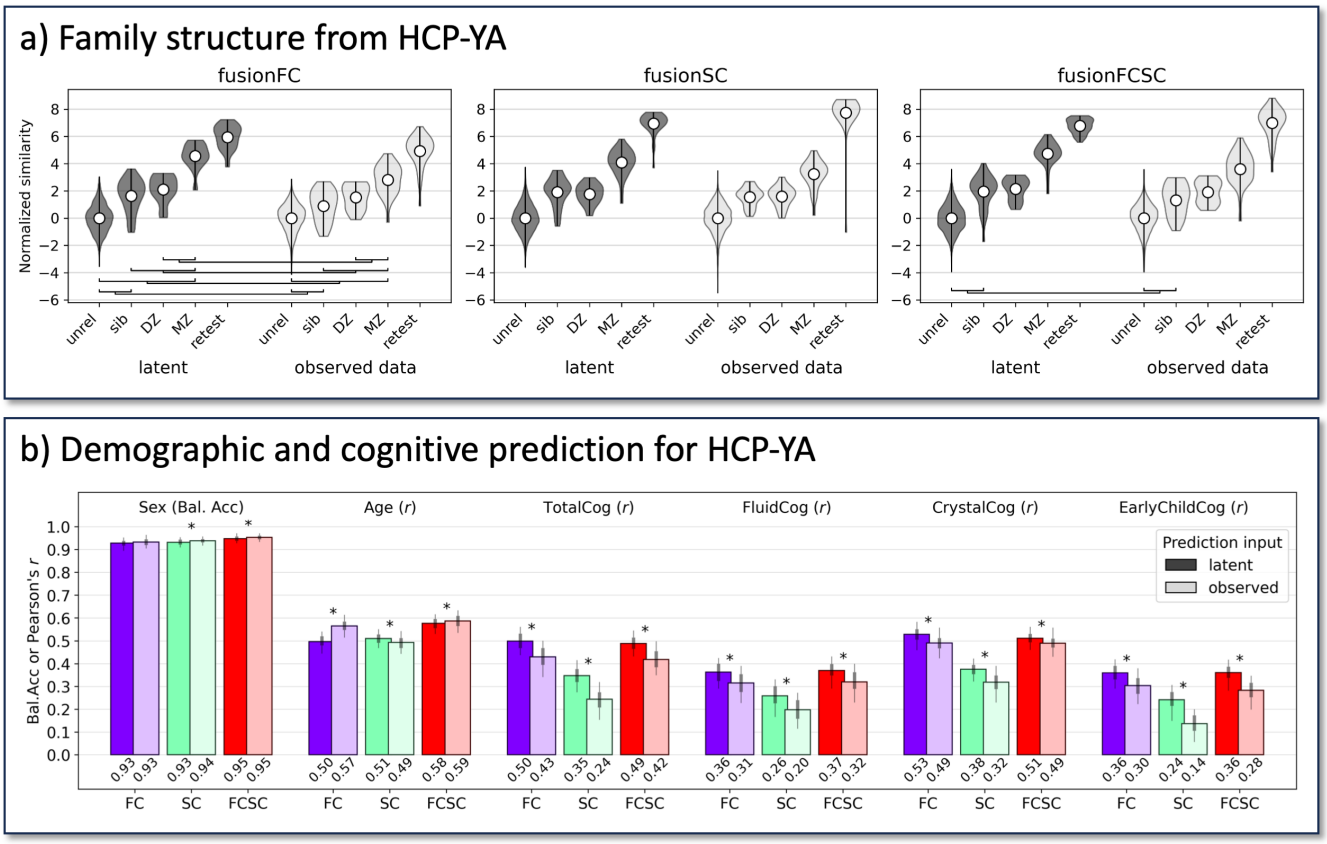

Figure 4. Familial connectome similarity and demographic prediction for held-out HCP-YA subjects. a. Inter-subject similarity of latent space representations and observed SC/FC data, stratified by family relationship. Each violin plot shows the distribution of inter-subject similarity for age- and sex-matched pairs for each familial relationship, as well as unrelated pairs and self-retest. Due to the high baseline similarity in observed data, latent and observed data similarity measures were independently z-scored by the mean and standard deviation of the similarity of unrelated subjects for visual comparison. Separability of each pair of violins within a modality was computed as the area under the receiver operating characteristic (ROC) curve. Separability estimates for a given relationship pair from the latent space and observed data were statistically compared using a permutation test, where bars show family-level pairs where latent space separability exceeds observed data separability ($p_{perm} < .05$, 10000 permutations, FDR-corrected). **b.** Prediction accuracy of demographic and cognitive metrics from different subsets of the Krakencoder's latent space and observed SC and FC data. Variability of prediction accuracy was assessed through bootstrap resampling (N=100). $*=$ significant difference between prediction accuracy from latent space and observed data. ($p_{perm} < 10^{-3}$, 10000 permutations, FDR-corrected).

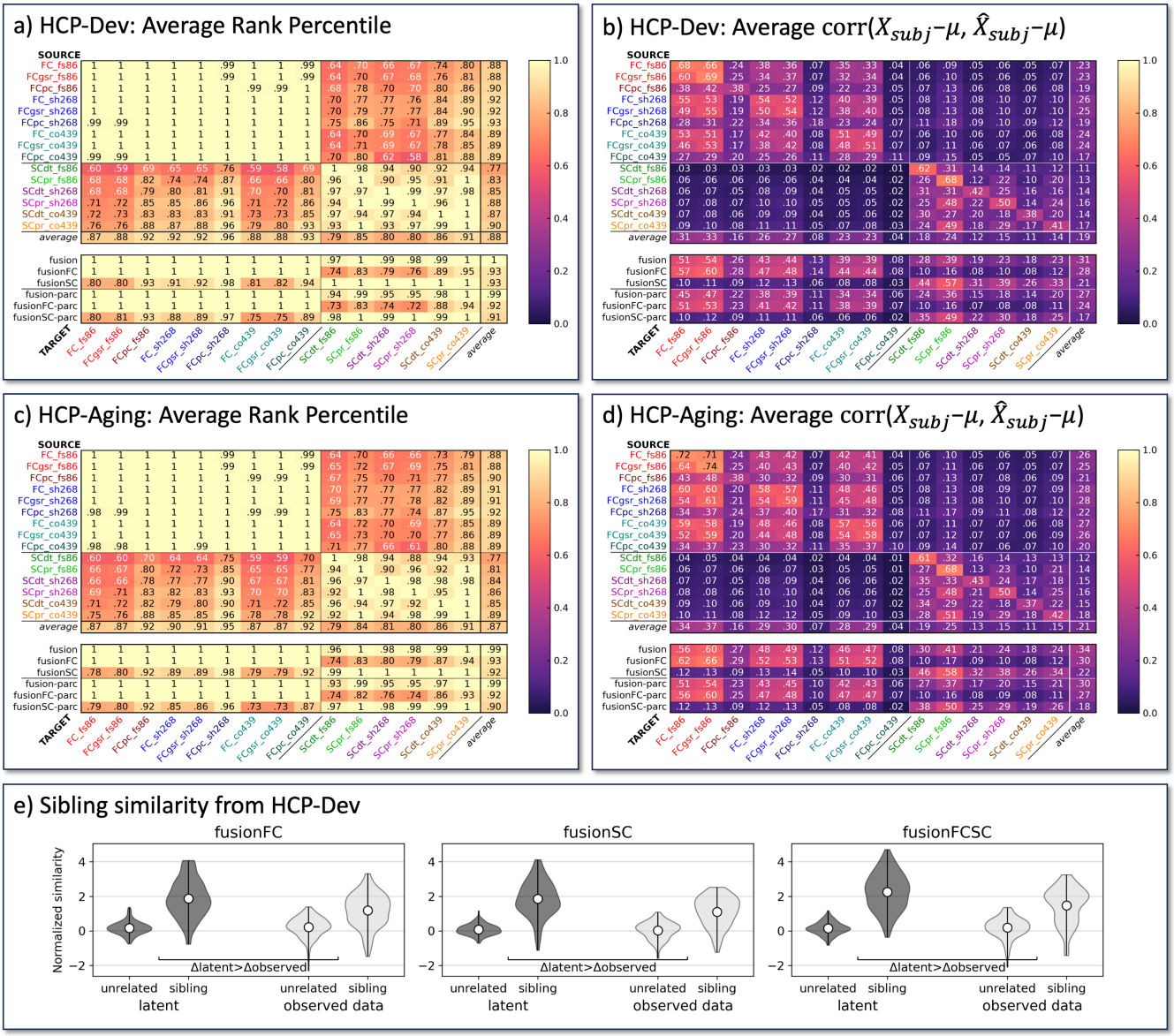

Figure 5. Out-of-sample performance of the Krakencoder on individuals from across the lifespan. Heatmaps in **a**-**b** show connectome prediction performance for subjects from the HCP-Development study (ages 8-21) and heatmaps in **c**-**d** show connectome prediction performance for subjects from the HCP-Aging study (ages 36-100). The Krakencoder model applied was trained on HCP-YA data (ages 22-37) and frozen; no re-training or fine-tuning was performed. **a,c.** Average rank percentile (**Fig. 2b**) is the fractional rank of the similarity (Pearson correlation) of a subject's predicted and measured connectomes compared to all other measured connectomes, averaged across subjects (random chance 0.5). **b,d.** Average correlation of each subject's measured and predicted connectomes, after subtracting the population average. **e.** Connectomes from sibling pairs in HCP-D are more similar than age- and sex-matched unrelated pairs, with latent space similarity significantly more separable than observed data. Each violin plot shows the distribution of inter-subject similarity for sibling pairs or pairs of unrelated individuals with matching age and sex disparity. As in **Fig. 4a** , latent and observed connectome similarity were independently normalized for visualization. Separability was measured by ROC analysis, and significance was assessed using permutation testing. For all three fusion types (fusionFC, fusionSC, fusionFCSC), siblings were more similar in the Krakencoder's latent space than in the observed data ($p_{perm} < 10^{-3}$).

3 Discussion

Here, we present the Krakencoder, a joint connectome encoder/decoder tool, capable of simultaneously, bidirectionally translating between structural and functional connectivity, and connectomes from different atlases and processing choices. The Krakencoder's predicted connectomes match measured connectomes with an unprecedented level of accuracy and individual-level identifiability, while also preserving their network properties. The Krakencoder's across modality mapping (from SC to FC and vice versa), which is arguably the most commonly performed mapping, had identifiability that was 42-54% higher than existing deep learning models. In addition to translating between connectome flavors, the Krakencoder can fuse connectome representations to create a single low-dimensional representation of all measured connectome flavors, each of which provide a different view of the true underlying connectome. The latent space of the Krakencoder appears to i) better reflect familial relatedness (compared to observed connectome data), ii) preserve age- and sex- relevant information and iii) enhance cognition-relevant information (again, compared to the observed connectome data). Finally, we demonstrated that the Krakencoder can be applied without any retraining to completely new, out-of-age-distribution lifespan data and still preserve inter-individual differences in the connectome predictions and familial relatedness in the fused latent space representations. Overall, we believe the Krakencoder has several novel aspects and applications, and is a significant leap forward in quantifying the relationship between multi-modal brain connectomes and how these relationships map to behavior.

Previous work in mapping between connectomes, mostly predicting FC from SC, has largely focused on optimizing accuracy in the model predictions by maximizing the correlation between predicted and measured FC. However, we argue here that over-emphasis on this metric can result in a model that predicts FC that is close to the population mean and/or does not preserve individual differences. The deepnet model did incorporate into its loss function a term that aimed to reduce inter-subject similarity of predicted FC, however it appears that this only pushed the individual FC predictions away from one another and not toward the particular individual's measured connectomes as its identifiability was just above chance[24]. The Krakencoder's connectome predictions, on the other hand, achieve perfect average rank identifiability within the same connectome modality, and consistently high average rank identifiability predicting FC from SC.

The Krakencoder has many novel aspects, including its ability to translate between connectome flavors without requiring raw data. This is useful when researchers only have access to a connectome from a particular pipeline or atlas and need it in another. One previously developed tool called CAROT does allows translation of a connectome from a different atlas into another without requiring the raw data[30]; however, this tool does not allow translating connectomes between different processing pipelines or mapping between SC and FC. There is not one FC or SC processing pipeline that has been agreed upon by the field; many researchers chose one pipeline and replicate on others. The ability of the Krakencoder to predict other flavors within the same modality suggests a common, latent connectomic backbone that gives rise to each FC or SC flavor when a given parcellation or connectome estimation strategy is employed. The Krakencoder's fusion functionality removes the burden of having to choose one pipeline or replicate findings on several different pipelines and attempt to make general conclusions. More than that, we believe the fusion of various snapshots of the underlying connectome increases the SNR of the connectome representations and perhaps becomes more than the sum of its parts. This latter statement is supported by the finding that models predicting cognition from the fused latent space representations outperformed models based on the observed connectome data; age and sex predictions were similar between the models but these are generally easier to predict compared to cognitive scores.

The Krakencoder is robust when applied to completely new, out-of-distribution data from individuals across the lifespan (8-100+). The frozen model (trained on young adult data) still retained a high level of identifiability and explained variance when mapping between connectomes from the HCP-D and HCP-A datasets. The Krakencoder appears somewhat impervious to the sweeping connectomic changes that occur throughout human development and aging[46,47]. The drop in demographic predictions of the latent space may mean there may be a benefit of the Krakencoder from further training (perhaps fine tuning) using lifespan data.

Future work will apply the Krakencoder to predict connectomes under clinical conditions, and further explore the relationship between the common latent representation and factors of neuroscientific or clinical significance. We will also create a fine-tuning procedure to further increase the robustness of the Krakencoder when applied to novel datasets in order to promote its wider applicability.

Dataset	N	Demographics		Acquisition
HCP-YA (training and testing)	958	Age 22-37 442 M (27.9±3.7) 516 F (29.5±3.6) 40 retest sessions 11 M (27.3±3.8) 29 F (31.8±1.9)	115 MZ twin pairs 43×2 M (27.8±3.5) 72×2 F (30.4±2.8) 64 DZ twin pairs 29×2 M (26.9±3.5) 35×2 F (30.7±3.1)	**Resting-state fMRI**: 2mm vox, TR 720ms, LR/RL phase-encoding, **1 hour total** **Diffusion MRI**: 1.25mm vox, b=1000,2000,3000, 90dir/shell, LR/RL phase-encoding, **1 hour total**
HCP-D (testing)	608	Age 8-21 282 M (14.8±3.8) 326 F (14.6±4.0)	76 sibling pairs (50 MM/FF, 26MF, Δage 0-9yr)	**Resting-state fMRI**: 2mm vox, TR 800ms, AP/AP phase-encoding, **25.5 min total** **Diffusion MRI**: 1.5mm vox, b=1500,3000, 90dir/shell, AP/PA phase-encoding, **22.5 min total**
HCP-A (testing)	716	Age 36-100+ 312 M (60.8±15.6) 404 F (60.1±15.7		

Table 1. Summary of datasets used in this study

4 Methods

4.1 Data description

The data for this study come from the original Human Connectome Project (HCP)[48] and the HCP Lifespan studies[43–45], which together includes high-resolution 3T MRI data for 2490 healthy participants aged 8-100+. Primary model training and testing was performed using data from 958 subjects from the original "young adult" HCP study (HCP-YA), aged 22-37, which includes monozygotic and dizygotic twin pairs as well as non-twin siblings. For benchmarking performance, we include a subset of 40 HCP-YA subjects who returned for a complete "retest" session 1-11 months after their initial session. The HCP-Development (HCP-D, 608 subjects, aged 8-21, including 76 pairs of non-twin siblings) and HCP-Aging (HCP-A, 716 subjects aged 36-100) cohorts from HCP Lifespan were used to evaluate our pre-trained model on out-of-sample, out-of-distribution data. HCP Lifespan data differs from HCP-YA in both age range and acquisition parameters, with Lifespan acquiring less than half as much fMRI and dMRI data as HCP-YA. HCP Lifespan studies were also collected across four different sites using standard MRI scanners while the HCP-YA data were all acquired on a custom MRI scanner at a single site. See **Table 1** for demographic and acquisition details. For all three datasets, we excluded subjects with incomplete resting-state fMRI or diffusion MRI, and subjects with known acquisition or QC issues.

4.2 Construction of Functional Connectomes

All resting-state fMRI timeseries were preprocessed by HCP using the Minimal Preprocessing Pipeline[49], which includes motion correction, susceptibility distortion correction, coregistration to anatomy and nonlinear template space (FSL MNI152 template, 6th generation), as well as automated denoising using ICA-FIX[50]. We used a custom post-processing pipeline to identify motion and global signal outlier timepoints (global signal>5σ, motion derivative >.9mm), regress out tissue-specific nuisance time series (5 eigenvectors each from eroded white matter and CSF masks[51]), temporally filter (high-pass >0.01 Hz for HCP-YA, >0.008 Hz for HCP-A/D, using DCT projection), and parcellate time series using each atlas. Outlier timepoints were excluded from nuisance regression and temporal filtering. Regional time series for each brain region were obtained by averaging voxels in the denoised time series data. Regional time series for each of the four (for HCP-YA) or two (for HCP-Lifespan) were variance-normalized and concatenated, and Pearson correlation between regional time series (excluding outlier timepoints) resulted in an region×region resting-state functional connectivity (FC) matrix for each subject. We also computed an FC matrix with global signal regression, FC_{gsr}, by regressing the mean gray matter time series and its temporal derivative from each regional time series before computing region×region Pearson correlation. Finally, we computed a Tikhonov-regularized partial correlation FC_{pcorr} (or FCpc) that minimizes the average distance between subject FC_{pcorr} and the unregularized population average partial correlation[36]; see **Supplemental Methods** for regularization details.

4.3 Construction of Structural Connectomes

Diffusion MRI were preprocessed by HCP using the Minimal Preprocessing Pipeline, which jointly corrected for motion, EPI distortion, and eddy current distortion using FSL's "topup" and "eddy" tools[52,53], before being linearly coregistered to the anatomical image. Preprocessed diffusion MRI were further processed using MRtrix3[54], including bias correction, constrained spherical deconvolution (multi-shell, multi-tissue FOD estimation, lmax=8[55]), and whole-brain tractography. We performed both deterministic (SD_STREAM[56], or SCdt) and probabilistic, anatomically-constrained tractography (iFOD2+ACT[57,58], or SCpr) using dynamic white-matter seeding[59] for both methods, resulting in 5 million total streamlines per subject for each tractography algorithm. Structural connectivity (SC) matrices were constructed for each atlas by counting the number of streamlines that ended in each pair of gray matter regions, normalized by the total volume of each region pair.

4.4 Parcellations

We used three different whole-brain atlases, covering a range in size and construction methodology. The 86-region FreeSurfer atlas (FS86) combines 68 cortical gyri from Desikan-Killiany and 18 subcortical gray matter regions (aparc+aseg[60,61]). The 268-region Shen atlas (Shen268 or sh268) is an MNI-space cortical and subcortical volumetric atlas based on resting-state fMRI clustering[62,63]. The 439-region CocoHCP439 atlas (Coco439 or co439) combines 358 cortical regions from the HCP multimodal parcellation[64], defined using anatomical and functional connectivity gradients, with 12 subcortical regions from FreeSurfer "aseg" (further modified by FSL FIRST[65]), 30 thalamic nuclei derived from FreeSurfer7[66] (50 original outputs included many small nuclei, which were merged into the final set of 30), 27 cerebellar regions from the SUIT atlas[67], and 12 additional subcortical nuclei from AAL3[68]. The FS86 and Coco439 atlases were defined based on each individual subject's FreeSurfer surface and subcortical parcellations, whereas the Shen268 atlas was applied directly to MNI-resampled data for each subject. The FS86, Shen268, and Coco439 parcellations result in 3655, 35778, and 96141 pairwise connectivity estimates, respectively.

4.5 Evaluating connectome predictions

As previously discussed, and as illustrated in **Fig. S1** , we consider several complementary assessments of how predicted connectomes (denoted $\hat{X}_s$ for subject s) reflect measured connectomes (denoted X_s). Based on these considerations, we use the following metrics for evaluating model performance:

$$\text{avgcorr} = \frac{1}{n_{subj}} \sum_{s=1}^{n_{subj}} \text{corr}(X_s, \hat{X}_s) \tag{1}$$

$$\text{avgcorr}_{\text{demean}} = \frac{1}{n_{subj}} \sum_{s=1}^{n_{subj}} \text{corr}(X_s - \mu_{\text{tr}}, \hat{X}_s - \mu_{\text{tr}}), \text{ where } \mu_{\text{tr}} = \left(\frac{1}{n_{subj}} \sum_{s=1}^{n_{subj}} X_s\right) \text{ for training subjects} \tag{2}$$

$$\text{top1acc} = \frac{1}{n_{subj}} \sum_{s=1}^{n_{subj}} [\text{argmax}_{a \in 1 \ldots n_{subj}}(\text{corr}(X_s, \hat{X}_a)) = s], \text{ where } [\cdot] \text{ represents an indicator function} \tag{3}$$

$$\text{avgrank} = \frac{1}{n_{subj}} \sum_{s=1}^{n_{subj}} \left(\frac{1}{n_{subj}} \sum_{a \neq s}^{n_{subj}} [\text{corr}(X_s, \hat{X}_a) < \text{corr}(X_s, \hat{X}_s)]\right) \tag{4}$$

4.6 Model training

Each model training epoch comprises two stages: 1) path-wise reconstruction and inter-subject dispersion and 2) latent space consistency. For a given path $i \rightarrow j$, we loop through batches of subjects ($n_{batch} = 41$), apply $Encoder_i$ to transform input flavor X_i' ($256 \times n_{batch}$) to latent representation z_i ($128 \times n_{batch}$), and $Decoder_j$ to transform z_i to predicted output flavor $\hat{X}_j'$ ($256 \times n_{batch}$). Path-wise reconstruction loss and inter-subject dispersion terms ($L_{r.corrI}$, $L_{r.mse}$, $L_{r.marg}$) are computed per batch from X_j' and $\hat{X}_j'$. These reconstruction losses collectively penalize reconstruction error in both absolute MSE and correlation terms, and promote inter-subject separation in the reconstruction space. Path-wise latent space dispersion loss ($L_{z.dist}$), computed from z_i, promotes inter-subject separation in the latent space. This forward pass and backpropagation is repeated for each batch of training subjects, before moving on to the next training path. The order in which paths are selected is randomly reshuffled

each epoch. The second stage of each training epoch, latent space consistency, enforces similarity of the latent space representations from each input flavor. We re-compute z_i for all input flavors from the encoders updated in the path-wise stage, and then compute $L_{z.sim}$ as the total MSE between the set of z_i matrices for all flavors. Explicit weights were applied to the reconstruction MSE loss term $L_{r.mse}$ ($w_{rm} = 1000$), the combined path-wise latent space dispersion loss L_z ($w_z = 10$), and the latent space intra-subject consistency loss $L_{z.sim}$ ($w_{zs} = 10000$). See **Algorithm 1** for pseudocode depiction of training procedure, and **Table 2** for details of loss function terms.

After each training epoch, we compute predicted connectomes for all paths on a held-out set of 80 validation subjects, and the inverse PCA transform (pre-computed on the training data only) is applied to compute $\hat{X}_j \in \mathbb{R}^{n_{edges}}$ from $\hat{X}'_j \in \mathbb{R}^{256}$. Reconstruction accuracy and identifiability are computed in this high-dimensional data space. Loss term weights were tuned empirically to balance the reconstruction ($\text{avgcorr}_{\text{demean}}$) and identifiability ($\text{avgrank}$) performance metrics in the validation dataset. **Fig. S2** illustrates this trade-off when tuning MSE reconstruction loss.

The model was implemented in PyTorch 1.10, using the AdamW optimizer with learning rate 10^{-4}. Model weights were regularized by weight decay 10^{-2}, as well as dropout in all encoders and decoders (dropout rate 0.5). The model was trained for 5000 epochs, which took approximately 36 hours on an Nvidia A100 GPU. Due to the regularization and the largely linear nature of the model, we did not observe significant overfitting. Validation performance plateaued after 500-1000 epochs, and we selected the 2000 epoch checkpoint for further evaluation.

Algorithm 1 Krakencoder model training procedure. (See **Table 2** for loss function details)

Initialization: $X'_i \leftarrow \text{PCA}(X_i)$ for all $i \in 1 \ldots n_{flav}$ # Transform inputs into $\mathbb{R}^{256 \times n_{subj}}$ PCA space

for *epoch* = 1, . . . , n_{epochs} **do**

  # Stage 1: Path-wise reconstruction loss
  for each $path_{ij} \in \text{shuffle}((i,j) \in 1 \ldots n_{flav})$ **do** # Loop through each path $i \rightarrow j$
    for each *subject_batch* **do**
      $z_i \leftarrow Encoder_i(X'_i)$
      $\hat{X}'_j \leftarrow Decoder_j(z_i)$
      $L_{path} \leftarrow L_r(X'_j, \hat{X}'_j) + w_z * L_z(z_i)$ # Latent space and reconstruction loss for $X'_i \rightarrow z_i \rightarrow \hat{X}'_j$
      backprop(L_{path}) # Update $Encoder_i$ and $Decoder_j$ for this *subject_batch*
    end for
  end for

  # Stage 2: Latent space consistency
  for each *subject_batch* **do**
    $z_i \leftarrow Encoder_i(X'_i)$ for all $i \in 1 \ldots n_{flav}$ # All input flavors $\rightarrow$ latent space using updated $Encoder_i$
    $L_{z.sim} \leftarrow \sum_{i,j \neq i} \|z_i - z_j\|_2^2$ # Similarity of latent space across flavors for each subject
    backprop($L_{z.sim}$) # Update all $Encoder_i$ for this *subject_batch*
  end for

  Evaluation: $\hat{X}_i \leftarrow \text{PCA}^{-1}(\hat{X}'_i)$ for all $i \in 1 \ldots n_{flav}$ # Predicted PCA outputs $\rightarrow$ high dimensional $\mathbb{R}^{n_{edges} \times n_{subj}}$
end for

4.7 Procedure for comparing family structure and predicting demographics

To examine how the connectomes (predicted and measured) reflect family structure, we first compute the averaged latent vector in the Krakencoder for each subject from either all 15 flavors ("fusion") or the 9 FC ("fusionFC") and 6 SC ("fusionSC") separately, and then compute a $n_{subj} \times n_{subj}$ inter-subject latent similarity matrix using Pearson correlation. These pairwise similarities are grouped according to the inter-subject relationship. For comparison, we also compute the inter-subject similarity for all 15 flavors of the high-dimensional measured connectome data, average these 9, 6, or 15 $n_{subj} \times n_{subj}$ similarity matrices, and group them according to relatedness. Due to the high baseline similarity in observed data, latent and observed data similarity measures were independently z-scored by the mean and standard deviation of the similarity of unrelated subjects for visual comparison. Differences of ROC separability of the distributions (e.g., separability of DZ and MZ distributions in latent space, compared to separability of DZ and MZ in observed data) was assessed through permutation testing (10000 matched permutations).

Loss category		Equation	Description
Path loss	Reconstruction accuracy and inter-subject dispersion	$L_{r.corrI}(X_i', \hat{X}_i') = \lVert \mathrm{corr}(X_i', \hat{X}_i') - I_{n_{subj} \times n_{subj}} \rVert_2$	$[n_{subj} \times n_{subj}]$ correlation matrix of measured→predicted should be high along the diagonal and low off-diagonal
		$L_{r.mse}(X_i', \hat{X}_i') = \lVert X_i' - \hat{X}_i' \rVert_2^2$	MSE between measured→predicted should be low
		$L_{r.marg}(X_i', \hat{X}_i') = -\min_{a,b \neq a}(\lVert X_i'(s_a) - \hat{X}_i'(s_b) \rVert_2)$	Predicted $\hat{X}'$ for subject s_a should be far from nearest measured X' for $s_{b \neq a}$
	Latent space inter-subject dispersion	$L_{z.corrI}(z_i) = \lVert \mathrm{corr}(z_i, z_i) - I_{n_{subj} \times n_{subj}} \rVert_2$	$[n_{subj} \times n_{subj}]$ correlation matrix of latent space vectors (for the same path) should be low off-diagonal
		$L_{z.dist}(z_i) = -\sum_{a,b \neq a}^{n_{subj}} \lVert z_i(s_a) - z_i(s_b) \rVert_2$	Mean inter-subject latent space distances should be high
	Combined path loss	$L_r(path_{ij}) = L_{r.corrI}(X_j', \hat{X}_j') + L_{r.marg}(X_j', \hat{X}_j') + w_{rm} * L_{r.mse}(X_j', \hat{X}_j')$ $(w_{rm} = 1000)$ $L_z(path_{ij}) = L_{z.corrI}(z_i) + L_{z.dist}(z_i)$ $L_{path} = L_r(path_{ij}) + w_z * L_z(path_{ij})$ $(w_z = 10)$	
	Latent space intra-subject consistency	$L_{z.sim}(z) = \sum_{a=1}^{n_{subj}} \left(\sum_{i,j \neq i}^{n_{flav}} \lVert z_i(s_a) - z_j(s_a) \rVert_2^2 \right)$	Total MSE between all latent vectors from all flavors for each subject should be low

Table 2. Loss function summary

For demographic predictions, we used a linear support vector classifier (SVC) to predict sex, and kernel ridge regression with linear kernel to predict age and cognition[69]. For the Krakencoder, models were fit using cross-validation on the average latent vectors for the 683 subjects used to train the Krakencoder model, and tested on the 196 held-out subjects. For the observed connectome data, we computed the inter-subject cosine similarity matrix of each connectome flavor, and used the averaged similarity matrices as input into the model, using the same training and testing splits as for the Krakencoder. Regression hyperparameters were selected by nested cross-validation grid search. Variability of prediction accuracy was assessed through bootstrap resampling (N=100), and significant differences between Krakencoder and observed data models was assessed using permutation testing of matched bootstrap samples (10000 permutations).

Data and code availability

Code is available at https://github.com/kjamison/krakencoder. Post-processing code for FC can be found here: https://github.com/kjamison/fmriclean. Additional data files are available at https://osf.io/dfp92.

Preprocessed data for this study are available for download from the Human Connectome Project (www.humanconnectome.org). Users must agree to data use terms for the HCP before being allowed access to the data and ConnectomeDB, details are provided at https://www.humanconnectome.org/study/hcp-young-adult/data-use-terms. Data from the HCP Aging and HCP Development studies can be downloaded as part of the HCP-Lifespan 2.0 release, distributed by the NIMH Data Archive (https://nda.nih.gov). See https://www.humanconnectome.org/study/hcp-lifespan-aging/data-releases and https://www.humanconnectome.org/study/hcp-lifespan-development/data-releases for more information about data use terms.

Post-processed connectomes and related input files can be made available upon reasonable request from corresponding author KJ, subject to HCP data use restrictions described above.

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Acknowledgements

This work was supported by the following grants: RF1 MH123232 (AK), Ann S Bowers Foundation (AK), R01 AG053949 (MS), NSF CAREER 1748377 (MS).

Data were provided by the Human Connectome Project, WU-Minn Consortium (Principal Investigators: David Van Essen and Kamil Ugurbil; 1U54MH091657) funded by the 16 NIH Institutes and Centers that support the NIH Blueprint for Neuroscience Research; and by the McDonnell Center for Systems Neuroscience at Washington University.

Research reported in this publication was supported by the National Institute Of Mental Health of the National Institutes of Health under Award Number U01MH109589, National Institute On Aging of the National Institutes of Health under Award Number U01AG052564. The HCP-Development 2.0 Release data used in this report came from DOI: 10.15154/1520708. The HCP-Aging 2.0 Release data used in this report came from DOI: 10.15154/1520707.

The authors would like to thank Fang-Chang Yeh for sharing pre-processed diffusion MRI data for HCP-Development and HCP-Aging subjects.

Author contributions statement

K.W.J. conceived the study and developed the software with help from Z.G.. K.W.J., A.K., and M.R.S. analyzed results, and Q.W. helped with validation. K.W.J., A.K., and M.R.S. wrote and edited the manuscript. All authors reviewed the manuscript.

Competing interests

The authors declare no competing interests.