Microvascular structure variability explains variance in fMRI functional connectivity

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Abstract

The influence of regional brain vasculature on resting-state fMRI BOLD signals is well documented. However, the role of brain vasculature is often overlooked in functional connectivity research. In the present report, utilizing publicly available whole-brain vasculature data in the mouse, we investigate the relationship between functional connectivity and brain vasculature. This is done by assessing interregional variations in vasculature through a novel metric termed vascular similarity based on the Euclidean distance. First, we identify features to describe the regional vasculature. Then, we employ multiple linear regression models to predict functional connectivity, incorporating vascular similarity alongside metrics from structural connectivity and spatial topology. Our findings reveal a significant correlation between functional connectivity strength and regional vasculature similarity. We also show that multiple linear regression models of functional connectivity using standard predictors are improved by including vascular similarity. We perform this analysis at the cerebrum and whole-brain levels using data from both male and female mice. Our findings regarding the relation between functional connectivity and the underlying vascular anatomy may enhance our understanding of functional connectivity based on fMRI and provide insights into its disruption in neurological disorders.

1 Introduction

Understanding how behavior emerges from the underlying anatomy is one of the main goals of neuroscience. A starting point in this quest is to explore how brain function is related to its underlying anatomy. In recent years, this has been done by extensively studying the relationship between functional connectivity (FC) and structural connectivity (SC). FC is

the statistical relationship between specific neurophysiological signals in time across different regions of the brain and SC represents the anatomical connections between those regions.

In humans, studying this relationship at the whole-brain scale has been facilitated by advancements in magnetic resonance imaging (MRI) technology. The assessment of FC at this scale was enabled through the development of functional MRI (fMRI) [1–4] while diffusion-weighted MRI allowed the visualization of nerve tracts [5, 6] for SC. The combination of these imaging techniques permitted the comparison and prediction of resting-state FC with tract-tracing data [7–10]. In fixed mouse brains, SC can be studied through injections of viral vectors to trace individual axonal projections between regions. This method led to the mesoscale structural connectome [11] in the mouse, which has become a standard for comparing SC and FC [12–14].

Nevertheless, in mammals, the most common technique to measure large-scale FC is still fMRI which isn't a direct measurement of neuronal activity but rather a vascular correlate. Indeed, neuronal activity leads to an increase in oxygen consumption and cerebral blood flow which results in a net positive fMRI signal: the blood-oxygen-level-dependent (BOLD) signal [15–17]. However, it is well known that this signal depends upon the underlying brain vasculature [18–21]. Considering this, should models using SC alone be sufficient to describe fMRI-based FC?

To address this question, we leveraged whole-brain vasculature datasets recently made available [22–26]. Specifically, the data from Ji et al. (2021) [25] is utilized to quantify the relationship between regional vascular variability and FC. We accomplished this by using a new metric called vascular similarity (VS) in multivariable linear regression models, which have been used extensively in the study of FC and SC [27–29]. This kind of model allows us to quantify the impact of regional vascular variability in a functional connectivity model using other common predictors derived from spatial topology and SC.

2 Materials and methods

2.1 Functional connectivity data

2.1.1 fMRI data

In this article, two openly available resting-state fMRI datasets are used : the dataset of N = 14 male C57BL/6J adult mice from Gutierrez-Barragan et al. (2022) [30] and a dataset of N = 10 female C57BL/6J adult mice[1]. We obtained the raw data which we processed and used for computing functional connectivity. Both datasets were acquired in anesthetized mice, using a combination of medetomidine and isoflurane anesthesia (0.05 mg/kg bolus and 0.1 mg/kg/h IV infusion, plus 0.5% isoflurane) and artificial ventilation at a rate of 90 BPM. The male dataset resting-state fMRI scans were acquired using a single-shot echo planar imaging (EPI) sequence on a 7.0 Tesla animal scanner with the

[1] https://openneuro.org/datasets/ds001653/versions/1.0.2

following parameters: TR/TE=1000/15 ms, flip angle=60°, matrix=100×100, 18 coronal slices (voxel size $0.23 \times 0.23 \times 0.60$ mm^3) and 1920 time points. The female dataset scans were acquired on an 11.7 Tesla Bruker animal scanner using gradient echo EPI with the following parameters: TR/TE=1200/15 ms, flip angle=60°, matrix=90×60, 28 coronal slices (voxel size $0.18 \times 0.15 \times 0.40$ mm^3) and 180 time points. Female mice underwent three scans per session across two sessions, resulting in a total of six scans per mouse and an aggregate of 60 scans. Also, this dataset contained T2-weighted structural images of each mouse at both imaging sessions which were used as anatomical templates.

2.1.2 Preprocessing and confound correction

We preprocessed both datasets using the open-source RABIES software[2] [31]. Briefly, for each subject, a mean volumetric EPI image was derived using a trimmed mean across all frames after an initial motion realignment. This mean EPI image allows the estimation of head motion by registering each EPI frame to it using rigid transformations. For the female dataset, the structural T2-weighted images were initially corrected for inhomogeneities [32] and then used to generate an unbiased structural template using a re-implementation of the ANTs template construction pipeline[3] [33]. This newly generated unbiased template was then itself registered, using a nonlinear registration, to the DSURQE ex-vivo T2 MRI template [34–37] which had been registered to the Allen Institute for Brain Science (AIBS) Common Coordinate Framework space version 3[4]. After this, each EPI image was also corrected for inhomogeneities and slice timing (slice timing correction was made using AFNI's 3dTshift) [38] and registered to the same session anatomical scan. Then all the transformations required for these corrections were concatenated to allow the resampling of each EPI frame to generate EPI time series in the reference atlas space. For the male dataset, the same steps were followed with the exception that the EPI scans were used to generate the unbiased template which was registered to the DSURQE atlas instead of (unavailable) structural scans.

For consistency, the confound correction applied to the EPI time series was the same for the male and female datasets. First, frames with prominent corruption were censored as in Power et al. (2012) [39]. Framewise displacement was measured across time and each frame surpassing 0.05 mm of motion, together with 1 backward and 2 forward frames, were removed. Voxelwise detrending was applied to remove first-order drifts. Using ordinary least squares, the 6 rigid motion parameters and the mean signal from the white matter and cerebrospinal fluid masks were modeled at each voxel and regressed from the data. To normalize variance, each image was separately scaled according to its total variance. Finally, a spatial Gaussian smoothing filter was applied at 0.3 mm full-width at half maximum (FWHM).

2.1.3 FC computation

Following the confound correction for each subject, the mean fMRI timecourse of each region was extracted. The correlation between the timecourses of each pair of regions was calculated,

[2] https://github.com/CoBrALab/RABIES
[3] https://github.com/CoBrALab/optimized_antsMultivariateTemplateConstruction
[4] http://www.brain-map.org/

yielding a functional connectivity matrix for each mouse. The subject-specific matrices were then Fisher z-transformed before being averaged between each subject to obtain a group FC matrix. The final matrix results from averaging the FC matrices of both hemispheres. The brains were parcelled according to a mid-ontology level of the AIBS Common Coordinate Framework version 3 (CCFv3). The anatomical regions that were considered are the 213 anatomical regions of [11]. The two missing regions are due to the removal of the subdivision of the subiculum into its dorsal and ventral part from the Common Coordinate Framework version 2 (CCFv2) to the CCFv3 as well as the distinction between the subiculum and the prosubiculum [40]. FC matrices of two different subsets of the 211 regions of interest (ROIs) were analyzed. The first subset was an FC matrix of size 78×78 composed of the same subset of regions as in Mills et al. (2018) [41] minus the subdivision of the subiculum: the 78 regions in this subset are all part of the cerebrum. The other subset was composed of the 200 ROIs that were present in all subjects after registration in the two datasets. This led to an FC matrix of size 200×200 (to obtain the full list of 200 regions see supplementary material). We will differentiate the use of the FC matrix of 78 and 200 regions by referring to them as the cerebrum and whole-brain FC respectively.

2.2 Structural connectivity data

For structural connectivity data, the matrix from Knox et al. (2018) [42] was used. It was generated using a mathematical model at the level of 100 μm voxels using 428 of the 491 anterograde tracing experiments in wild-type C57BL/6J mice, mapping fluorescently labeled neuronal projections brain-wide from the AIBS connectivity atlas[5] [11]. This model of SC was chosen because it offers improved predictions at the regional level over the model from Oh et al. (2014) [11]. The weights of the SC matrix are the normalized connection strengths [42]. This matrix is directed as opposed to the FC, hence to compare the two the SC matrix must be undirected. This was accomplished by averaging the directed SC matrix with its transpose. Moreover, the structural connectivity matrix wasn't directly used in the linear model: instead, the communicability of the undirected SC was used. This was done to better explain the observed patterns of FC, as it is known that low SC strength doesn't imply low FC strength [10]. Communicability is a metric that describes the efficiency with which information can be transmitted across a network using direct and indirect pathways. The definition of communicability used is given by Crofts et al. (2009) [43]. We began by normalizing each connection weight of the network. We divided them by the product $\sqrt{d_i d_j}$, where d_i is the generalized degree of the node i to obtain a new matrix A'. The communicability is then given by the matrix exponential

$$\mathbf{CO} = \sum_{k=0}^{\infty} \frac{(A')^k}{k!} = e^{A'}. \tag{1}$$

The matrix exponential computes the weighted sum of walks of all lengths between pairs of nodes while penalizing longer walks by the $1/k!$ coefficients. Ultimately, pairs of nodes with stronger and more direct connections should have higher communicability weight. The steps to obtain the structural connectivity matrices are illustrated in figure 2B.

[5] https://connectivity.brain-map.org/

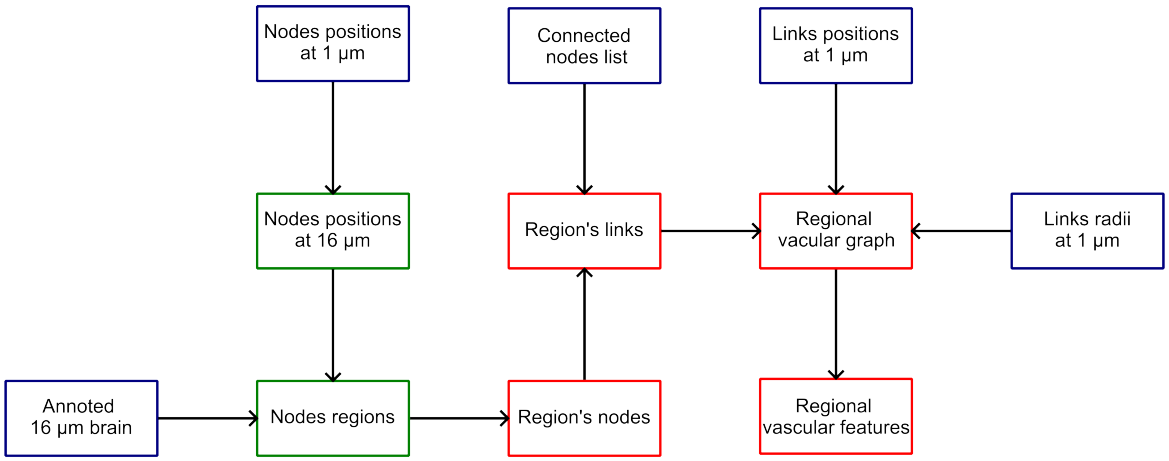

Figure 1: Numerical processing of the whole-brain vasculature graphs from Ji et al. (2021) [25]. Each box represents an object and the arrows signify a function that transforms the source object into the destination object. The blue boxes denote the objects constituting the comprehensive brain graph, the green boxes correspond to transformed objects at the whole-brain level, and the red boxes represent objects specific to distinct brain regions.

2.3 Brain vasculature data

To compare functional connectivity with regional vascular anatomy, vascular graphs of three adult male mice from Ji et al. (2021) [25] were used. In their paper, whole-brain microvasculature was imaged in fixed brains to the level of capillaries with serial fluorescence two-photon microscopy and modeled into a vascular graph. In this representation, edges represent vessels and nodes represent branching points. The available data was the position of centerline voxels composing edges, the voxels composing nodes, and the list of nodes connecting individual edges. Each brain was also registered to the Allen Brain Atlas template, making it possible to label each voxel to a brain region. Using the nodes composing a region of interest, we built a regional graph of the vasculature from which the regional features were extracted. This process was repeated for all ROIs in each brain. The procedure to retrieve each regional graph's features is illustrated in figure 1.

The regional features were then averaged over the two hemispheres and the three subjects. The vascular features that were tested are the following: the average tortuosity of the vessels, average capillary length, average capillary radius, the proportion of length covered by non-capillary vessels, the length, branching points and vessel density. Capillaries were defined as vessels with a median radius of their skeleton voxel radii lower than 3.5 μm as in Ji et al. (2021) [25]. Using the regional features a VS matrix is built using equation 2

$$\mathrm{VS}_{ij} = \frac{1}{1 + ||\mathbf{f}_i - \mathbf{f}_j||}. \tag{2}$$

where $\mathbf{f}_i$ is the feature vector of the region i (as illustrated in figure 2A) and $||\mathbf{f}_i - \mathbf{f}_j||$ is the

Euclidean distance between the feature vectors. To ensure equivalent scaling, each feature was z-scored across all regions before computing the values for VS.

Several of these characteristics may not significantly contribute to the explained variance of functional connectivity (as expressed by the coefficient of determination). To explore which vasculature features are the most relevant to describe FC, VS matrices were made using only one feature. Then, simple linear models of FC were built using only the single-feature VS as an independent variable. The features that were ultimately used for building the VS of the full multiple linear regression model were the four features that had on average the highest coefficient of determination (R^2) in the single-feature simple linear regression FC models.

As a means to determine the statistical significance of the correlation between functional connectivity and vascular similarity, two null models are used. The first one is called the random model and consists of making a new VS matrix by randomly shuffling the vector of features of each region before calculating VS. The second is labeled the spatial autocorrelation preserving model. As the name implies, this null model keeps the original spatial autocorrelation of each feature before calculating the VS. This process was accomplished through the application of BrainSMASH [44], a method that resamples the values of each vascular feature while maintaining the original spatial autocorrelation by leveraging the regional distance matrix. For both of these models, 1000 different VS matrices are computed. Subsequently, Pearson correlation coefficients between the FC matrices and the null VS matrices values for each region pair are computed.

2.4 Multiple linear regression models

To better understand the global association between functional and vascular similarity, several multiple linear models were built using combinations of the following independent variables: vascular similarity, communicability, inverse of the Euclidean distance between the geometric center of the regions, and spatial adjacency. The latter is a binary metric with a value of 1 if two regions are adjacent in space and 0 if they aren't. When these four predictors were used in a model we call it the full functional connectivity model. These predictors are illustrated in figure 2D. FC matrices and independent variables were z-scored before calculating the model parameters and only values below the diagonal of the matrices of the matrices were used for the linear models. The coefficients of the linear models were found using ordinary least squares. In the linear models employed in this study, intercept terms were computed. However, for the purposes of this analysis, these values were excluded from detailed discussion, as they were found to be negligible.

We compared the results from our FC models using the 78×78 matrices to those built in Mills et al. (2018) [41] which we will call the Mills models. In the Mills models, the 80×80 FC matrix was constructed using resting-state fMRI data from male subjects under isoflurane anesthesia, and was parcelled in accordance with CCFv2. The SC matrix is the inter-region connectivity model from Oh et al. (2014) [11]. The predictors derived from the structural connectivity were the communicability and the matching index. The model also

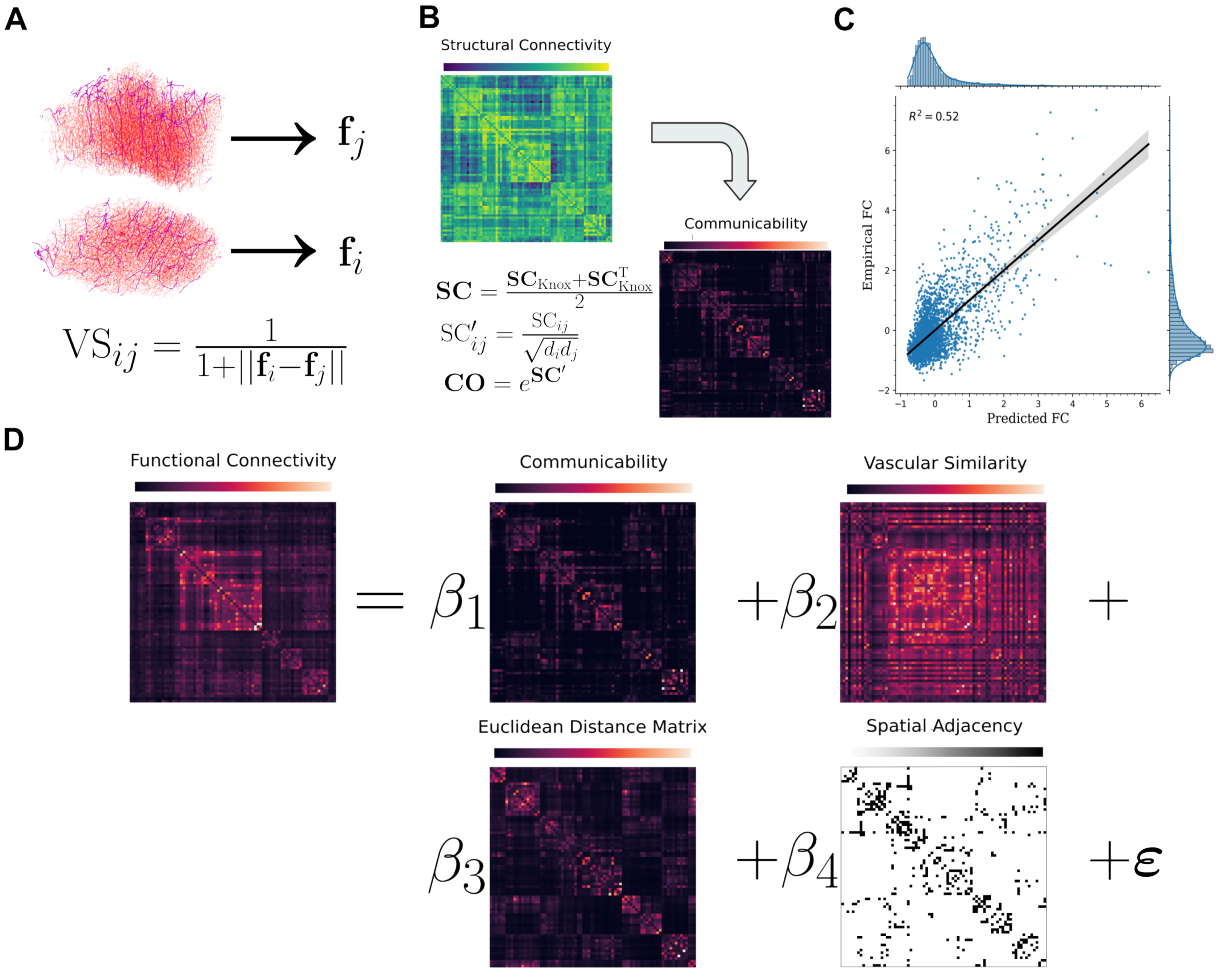

Figure 2: The full functional connectivity model. A) Representation of the vascular similarity strength between two vascular regional graphs i and j. B) Procedure for deriving the communicability predictor from the SC matrix. C) The full FC model of the female dataset using the subset of 78 ROIs. Empirical and predicted FC represent z-scored functional connectivity strength between regions. D) Illustration of the model, β parameters are estimated using ordinary least squares. For visualization purposes, the regions are ordered by FC communities calculated using the Louvain method for community detection.

Feature used	Cerebrum model		Whole-brain model	
	$R^2_{females}$	R^2_{males}	$R^2_{females}$	R^2_{males}
Average capillary length	0.075	0.043	0.024	0.014
Average tortuosity	0.057	0.059	0.020	0.022
Branching point density	0.052	0.043	0.025	0.021
Average capillary radius	0.043	0.044	0.027	0.029
Vessel density	0.045	0.042	0.020	0.018
Length density	0.035	0.037	0.025	0.020
Non-capillary length proportion	0.014	0.009	0.009	0.005
Proportion of volume filled by vessels	0.012	0.002	0.004	0.002

Table 1: Explained variance of functional connectivity by the different single-feature vascular similarity as the sole predictor in the linear model across both female and male datasets using the sets of regions of the cerebrum and the whole brain.

makes use of gene expression measured with in situ hybridization from AIBS as described in Lein et al. (2007) [45]. A subset of regional gene expression energies was then z-scored across all regions and Pearson's correlations were computed between region pairs and Fisher z-transformed, which is called the correlated gene expression (CGE) in the Mills model. To facilitate comparative analysis, we also computed CGE as described in Mills et al. (2018) [41] and included it in our model.

Finally, the multivariable linear regression models using the 200×200 FC matrices were calculated to examine the relationship between VS and FC at the whole-brain scale. Subsequently, to investigate the overlap between the vascular similarity and functional connectivity, binary FC and VS matrices were made by thresholding and binarizing the group female FC matrix and the VS matrix from 30% to 10% of connection density with 1% interval as in Mills et al. (2018) [41]. Then the intersection between the binary VS and FC matrices of the same density was calculated. This resulted in 21 overlap matrices, the edges that were present in more than half of these matrices were kept to produce an average binary overlap matrix.

3 Results

3.1 Relationship between functional connectivity and single-feature vascular similarity

The values of the coefficient of determination for simple linear regression models between FC and single-feature VS are presented in table 1. The explained variance by single-feature VS is higher for all features with the 78 regions models compared to the 200 regions ones. The explained variance difference between males and females was less than 1% for most features except for the average capillary length. The correlation between the male and female datasets group functional connectivity was computed, revealing significant correlations of

(r=0.816) for cerebrum FC and (r=0.668) for whole-brain FC. For both gender and region sets, the worst coefficients of determination are the proportion of the vessel length covered by non-capillary vessels and the proportion of the regional volume filled by vessels. The four features that explain the most variance on average are the branching point density (BPD), the average capillary length, tortuosity, and radius. They also correspond to the combination of features that explain the most variance in all the simple linear regression FC-VS models. These features are mostly driven by the capillary network of the region.

We computed the correlation between each pair of vascular features. Among the above four, the highest pairwise correlation values for the cerebrum are the BPD and the average capillary length (r=0.593). For the whole brain, it's the BPD and tortuosity pair (r=0.515). Across all features, the highest correlation values are between the BPD and the vessel density for cerebrum and whole-brain models (r=0.988 in females, r=0.959 in males). This is expected because most vessels split or recombine into two. High correlation values were also found for BPD and the length density (r=0.927 in females, r=0.830 in males).

3.2 Comparison with the linear model of Mills

Functional connectivity models of the cerebrum were built using the four-feature vascular similarity and compared to the values of Mills FC models. These results are presented in table 2. At this scale, vascular similarity alone explains about 15.9% and 15.1% of the variance in female and male FC. This is significant because these values are much higher than the average determination coefficient obtained using the spatial autocorrelation preserving null models $\langle R^2 \rangle = 0.01$ (SD=0.04) and $\langle R^2 \rangle = 0.002$ (SD=0.003) for female and male datasets (see supp. figure 2 for the correlation values distribution of the null models for the cerebrum). It can also be observed that VS increases the explained variance of FC when added to the communicability, Euclidean distance and spatial adjacency model. Furthermore, in the full model, the VS has the second highest standardized β coefficient after communicability despite explaining less variance than spatial adjacency and Euclidean distance using simple linear regression. In the cerebrum, VS is also less correlated to the inverse of the Euclidean distance than to all the other predictors as can be seen in supp. figure 1. For the full list of standardized parameters of the cerebrum model of this study see supp. table 1.

As for the comparison between the models in this study and the Mills models, the communicability alone explained significantly more variance in our models than in the Mills models. This can be attributed to the use of the Knox model of SC. In fact, when using the SC matrix from Oh et al. (2014) [11], as in Mills's article, to derive the communicability matrix, an important decrease in the explained variance is observed in both females and males (17.5% and 15.9%). Besides the communicability model of FC, the R^2 values of Mills were higher in all models. Moreover, spatial models of FC based on the Euclidean distance and spatial adjacency explain significantly less variance than the Mills model. One other considerable difference between the models of this study and the one from Mills [41] is how the Euclidean distance is used. In the model of Mills, the Euclidean distance is log-transformed before being used. In our cerebrum spatial models, if the log-transformed Euclidean distance is utilized, a decrease in explained variance is observed in the female and male (R^2=0.347 and R^2=0.369).

Linear model	$R^2_{females}$	R^2_{males}	R^2_{Mills}
$\hat{\mathbf{FC}} = \beta_1\mathbf{CO}$	0.416	0.411	0.227
$\hat{\mathbf{FC}} = \beta_1\mathbf{VS}$	0.159	0.151	-
$\hat{\mathbf{FC}} = \beta_1\mathbf{CGE}$	0.310	0.308	0.412
$\hat{\mathbf{FC}} = \beta_1\mathbf{ED}$	0.265	0.290	-
$\hat{\mathbf{FC}} = \beta_1\mathbf{SA}$	0.302	0.330	-
$\hat{\mathbf{FC}} = \beta_1\mathbf{ED} + \beta_2\mathbf{SA}$	0.355	0.388	0.549
$\hat{\mathbf{FC}} = \beta_1\mathbf{CO} + \beta_2\mathbf{VS}$	0.479	0.470	-
$\hat{\mathbf{FC}} = \beta_1\mathbf{CO} + \beta_2\mathbf{ED} + \beta_3\mathbf{SA}(+\beta_4\mathbf{MI})$	0.464	0.478	0.584
$\hat{\mathbf{FC}} = \beta_1\mathbf{CO} + \beta_2\mathbf{VS} + \beta_3\mathbf{ED} + \beta_4\mathbf{SA}$	0.520	0.529	-
$\hat{\mathbf{FC}} = \beta_1\mathbf{CO} + \beta_2\mathbf{CGE} + \beta_3\mathbf{ED} + \beta_4\mathbf{SA}(+\beta_5\mathbf{MI})$	0.493	0.502	0.615

Table 2: Comparison between the FC models of Mills and the cerebrum FC models of this study. The R^2 values for some of the Mills models included are calculated using the matching index as an additional predictor. These models are denoted by the addition of an extra term (**MI**). The β_i are the standardized coefficients of each parameter. $\hat{\mathbf{FC}}$ is the predicted FC connection weights. **CO** is the communicability connection weights. **CGE** is the correlation of selected genes expressions between each pair of ROIs. **VS** is the Euclidean distance similarity measure between the vascular feature vectors of each pair of ROIs. In our models, **ED** represents the inverse of one plus the Euclidean distance between the ROIs centroids. In the Mills models, these Euclidean distances are log-transformed instead. **SA** is the spatial adjacency between each pair of ROIs, if two regions are adjacent the value of the pair is 1, 0 otherwise.

Finally, when considering the four predictors models, the model of female and male FC with the highest explained variance is the one that includes the VS rather than the CGE. These models still explain lower variance than the four predictors models of Mills (R^2=0.520 and R^2=0.529 vs R^2=0.615). Another notable difference is that the standardized β coefficient of the Euclidean distance has the lowest values in our female and male models, while in the Mills model, it has the highest.

3.3 Whole-brain model of functional connectivity

The functional connectivity models using the 200 whole-brain ROIs and the different combinations of predictors tested are presented in table 3. Across all models, a decrease in explained variance is observed compared to the models using the 78 cerebrum ROIs. At this scale, the VS explains 10.8% and 9.8% of the variance of the FC of female and male models. These values are still significantly higher than the average Pearson correlation coefficient from the spatial autocorrelation preserving null model $\langle R^2 \rangle = 0.03$, SD=0.02 and $\langle R^2 \rangle = 0.02$, SD=0.02 for female and male datasets (see supp. figure 3 for the correlation values distribution of the null models). Furthermore, the addition of vascular similarity to the model still increases the explained variance, albeit its contribution in the full model decreases as reflected by the values of the standardized coefficients.

To investigate the decrease of the coefficient of variation in the simple linear regression model of FC using VS in the whole-brain model, an average overlap binary matrix between these two was made using thresholded matrices from 30% to 10% of connection density with 1% interval. The resulting overlap matrix is presented in figure 3. The strongest edges in the VS matrix are mostly the ones connecting two regions in the same major division of the brain. In fact, 32.7% of the top 10% edges with the strongest values are in the same major division. The same phenomenon is observed in functional connectivity where 41.2% of the top 10% strongest edges are in the same major divisions. Partly due to this, 47.9% of the overlap between the functional connectivity and vascular similarity occurs between regions in the same major division despite them constituting only 10.5% of all possible edges. Also, two major divisions that have more than 60% of their edges overlap are the isocortex (65.9%) and the cortical subplate (76.9%) which are all located in the cerebrum.

4 Discussion

In this work, the linear relationship between resting-state functional connectivity and vascular similarity was studied in the mouse. VS is an Euclidean distance-based similarity measure of the vasculature across anatomically defined regions. VS was used in conjunction with commonly used predictors of FC utilizing multiple linear models. This analysis was conducted using FC models composed of two sets of ROIs on female and male resting-state fMRI datasets. Some of the results of this study were compared to those of Mills et al. (2018) [41] in which multiple linear models of FC in mice were also exploited. Finally, the overlap between functional connectivity and vascular similarity was studied.

	Female models			Male models		
Model predictors	β	R^2	AIC	β	R^2	AIC
CO	0.512	0.262	50423	0.480	0.231	51259
VS	0.328	0.108	54213	0.313	0.098	54430
ED	0.444	0.197	52110	0.490	0.240	51023
SA	0.475	0.225	51401	0.530	0.281	49919
ED, **SA**	0.264	0.274	50102	0.286	0.338	48259
	0.331			0.374		
CO, **VS**	0.461	0.308	49140	0.431	0.273	50125
	0.221			0.212		
CO, **ED**, **SA**	0.316	0.341	48174	0.219	0.371	47265
	0.162			0.216		
	0.226			0.301		
VS, **ED**, **SA**	0.228	0.324	48694	0.199	0.376	47088
	0.239			0.264		
	0.301			0.349		
CO, **VS**, **ED**, **SA**	0.284	0.377	47073	0.190	0.400	46318
	0.195			0.177		
	0.151			0.206		
	0.211			0.288		

Table 3: Standardized coefficients β, R^2, and Akaike information criterion (AIC) values for the whole-brain (200 regions) multiple linear models of FC using different predictors. The β of each model are in the same order as the model predictors. The AIC is an estimator of prediction error, with lower values indicating a better model.

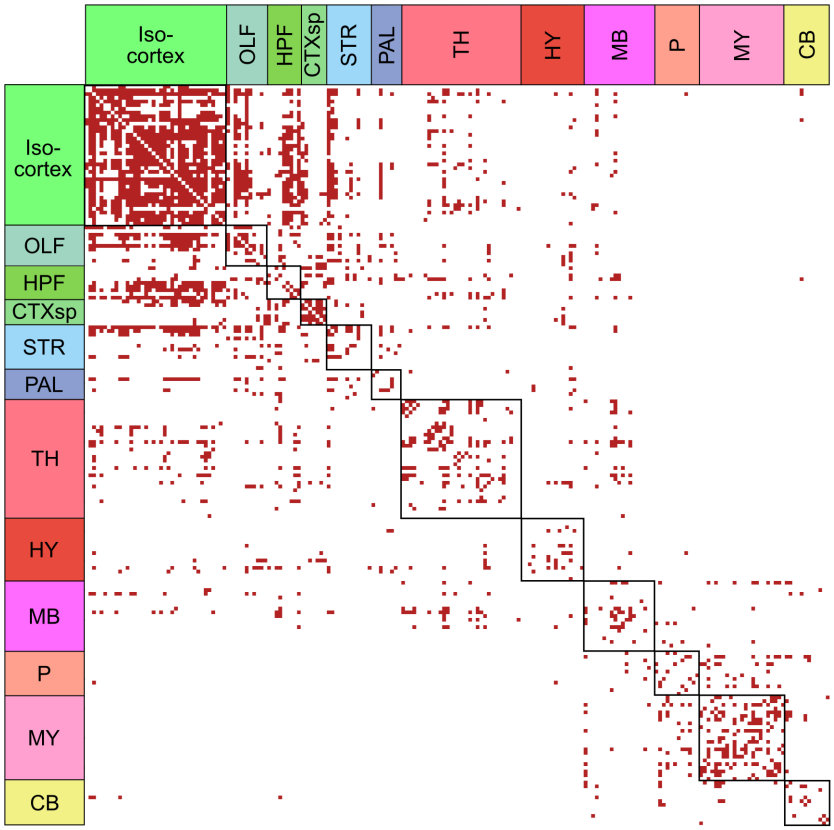

Figure 3: Average binary overlap adjacency matrix between vascular similarity and functional connectivity ordered by the mouse brain 12 major divisions: isocortex, olfactory areas, hippocampus, cortical subplate, striatum, pallidum, thalamus, hypothalamus, midbrain, pons, medulla, and cerebellum. The overlap matrix was made using 10 to 30% connection density. For visualization purposes, the regions in the same major division are outlined by black lines.

To begin, single-feature VS was studied. First, comparable R^2 values were found for both the female and male FC datasets despite the fact that the whole-brain vasculature dataset was only composed of male subjects. This was not necessarily expected because sex-related differences were found in the mouse brain vasculature [22]. Nonetheless, the authors also found that for some regions the similarities and dissimilarities of the vascular profile between subregions were conserved across sexes. Because VS is dependent on the relative difference between the features, the VS matrix could be mostly consistent across sexes. This proximity could also be explained by the strong correlation between the male and female FC (r=0.816).

Upon the results of the single-feature VS models, the four features that would be used in the multiple linear models were the branching point density, the average tortuosity and the average capillary length and radius. The exclusion of vessel and length density from the VS, despite them explaining a similar amount of variance, is coherent because the length density is highly correlated to the BPD, and its use in conjunction with the average capillary length provides a good estimate of the length density. The selected features principally describe the capillary network of the region, including the average tortuosity and the BPD because the capillaries represent the majority of the vessels. In future work, other vascular features could be calculated using graph theory metrics as described in other relevant papers [22, 25, 46, 47].

Using the 4-features VS in the cerebrum, a significant proportion of the FC variance can be explained in females (R^2=0.159) and males (R^2=0.151). The explained variance of VS alone is smaller than the one computed using simple linear regression with commonly used predictors (communicability, Euclidean distance, spatial adjacency and correlated gene expression). Yet, in the 4-variable models, the substitution of CGE with VS leads to higher explained variance. This is probably due to the collinearity of the variables, the spatial adjacency and the CGE being moderately correlated with the Euclidean distance (r>0.6). This makes the Euclidean distance predictor partially redundant in this model, as shown by its standardized coefficient value being at least one order of magnitude lower than other predictors.

When our models are compared to the results of Mills et al. (2018) [41], the variance explained is almost always lower. The only one of our models where explained variance is higher than in the Mills model is the simple linear model using communicability. This difference could be explained by the use of the SC model from Knox et al. (2018) [42]. A distinction between their model and the one of Oh et al. (2014) [11] lies in its prediction of minimal yet non-zero connections, in contrast to the latter, which attributes zero weight to such edges. This discrepancy may significantly influence communicability, particularly due to the greater emphasis it places on more direct regional connections. Indeed, the communicability derived from the SC matrix of Oh et al. (2014) [11] explained considerably less variance. However, it should be noted that the ROIs used to build this matrix are defined using the CCFv2 [11, 40]. Now, in the Mills models, the predictor that contributes the most is the Euclidean distance. In fact, the multivariable model using the Euclidean distance and the spatial adjacency explained more variance than all of our models. Upon a thorough review of the existing literature, we were unable to locate other values of the correlation

between the regional Euclidean distance and FC which could allow us to judge the accuracy of these values. Nonetheless, the similar values of the coefficient of determination between the male and female independent datasets attest to the reproducibility of this analysis.

The addition of VS in the full multivariable linear model using the whole-brain set of 200 ROIs allows for a more accurate depiction of the FC as shown by the R^2 and AIC values. Nonetheless, we found a decrease in the explained variance of all FC models using this set of ROIs. This might be accounted for by the fact that almost half of the overlap between FC and VS (47.9%) is between regions in the same major division of the brain. In the subset of 78 regions 28.3% of the possible edges between regions are inside the same major division compared to 10.5% in the full set of 200 regions. Furthermore, the two major brain divisions where the overlap is the highest (the isocortex and the cortical subplate) are also present in the smaller subset. Additionally, the fact that higher vascular similarity values are observed between regions in the same major division should not come as a surprise. It has been shown that the probability distribution of many features such as vessel length density, branch point density and radius size vary considerably across major regions [24, 25].

Finally, multiple causes could explain the correlation between the functional connectivity and the vascular variability. Three hypotheses are that the regional vasculature could predict the amplitude of the BOLD signal directly, indirectly or both. In a direct relationship, it is meant that the topology of the local vasculature could influence the amplitude of the BOLD signal measured by fMRI [17, 48, 49]. Secondly, the vasculature might serve as an indicator of the types of cells present in a given region. This aspect is significant as neurovascular coupling, and consequently, the amplitude of the BOLD signal is dependent upon the variability of cell types within a region [20, 21, 50]. For instance, length density is correlated with pericyte density and inversely correlated with the neuronal nitric oxide synthase-positive neurons (nNOS) density [26]. Both cell types are important in neurovascular coupling, as nNOS is known to impact blood flow through its vasodilatory effects [51–53] and it also has been shown that pericytes have a role in the regulation of blood flow [54, 55]. Here, the amplitude of the BOLD signal is related to the measured FC as it influences the Signal-to-Noise Ratio (SNR) and a reduced SNR can diminish the correlation between two time series, potentially leading to lower predictions of FC [56–58].

One approach to ascertain whether vasculature variability is intricately linked to neuronal FC or if it primarily affects the magnitude of the BOLD signal, subsequently impacting measured FC, is to explore the correlation between non-BOLD FC and VS. This kind of functional connectivity can be measured using genetically encoded calcium indicators (such as GCaMP) [59–61] in combination with fluorescence imaging techniques such as wide-field imaging as summarized in Guilbert et al. (2022) [58]. The combination of these techniques has been used in the mouse to image cortical functional connectivity [62, 63] and even simultaneously with BOLD FC [64].

5 Conclusion

Vascular similarity seems to explain a significant portion of the variance of resting-state fMRI-based functional connectivity. More specifically, regions with a similar capillary bed tend to have similar functional connectivity. Also, the use of VS in multivariable linear models leads to more accurate predictions of FC. This can be attributed partially to the fact that VS is less correlated with Euclidean distance than other commonly used predictors. Finally, the correlation of FC and VS seems to depend on the volume of the regions studied with more voluminous regions leading to higher correlation values.

Lastly, in this research, the data utilized was derived from average measurements across multiple subjects. Future studies might benefit from investigating the impact of regional vascular variability on functional connectivity at the individual level. Such an analysis could be facilitated through the acquisition of resting-state fMRI from individual subjects, followed by the application of methodologies described in recent literature to reconstruct the vasculature of the brain [22–26]. This approach could prove valuable in researching neurovascular disorders to study the influence of variables such as sex, age, and disease on an individual's vascular structure [22, 47, 65] and how it's reflected in whole-brain functional connectivity.

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Competing Interests

The authors have no conflict of interest to report.

Author Contributions

All authors contributed to the study conception and design. Data analysis was performed by François Gaudreault. The first draft of the manuscript was written by François Gaudreault and all authors commented on previous versions of the manuscript. All authors read and approved the final manuscript.

Data Availability

All the raw datasets used in this study are openly available or can be accessed upon request to the authors. The processed data in this study are available from the corresponding author on reasonable request.

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