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Resting functional connectivity of the left inferior frontal gyrus with the dorsomedial prefrontal cortex and temporoparietal junction reflects the social network size for active interactions

Kazuma Mori[1,2] | Masahiko Haruno[1,3]

[1]Center for Information and Neural Networks, National Institute of Information and Communications Technology (NICT), Suita, Osaka, Japan

[2]Graduate School of Information Science and Technology, Osaka University, Suita, Osaka, Japan

[3]Graduate School of Frontier Biosciences, Osaka University, Suita, Osaka, Japan

Correspondence
Masahiko Haruno, Center for Information and Neural Networks (CiNet), National Institute of Information and Communications Technology (NICT), 1-4 Yamadaoka, Suita, 565-0871, Osaka, Japan.
Email: mharuno@nict.go.jp

Abstract

The size of an individual active social network is a key parameter of human social behavior and is correlated with subjective well-being. However, it remains unknown how the social network size of active interactions is represented in the brain. Here, we examined whether resting-state functional magnetic resonance imaging (fMRI) connectivity is associated with the social network size of active interactions using behavioral data of a large sample ($N = 222$) on Twitter. Region of interest (ROI)-to-ROI analysis, graph theory analysis, seed-based analysis, and decoding analysis together provided compelling evidence that people who have a large social network size of active interactions, as measured by "reply," show higher fMRI connectivity of the left inferior frontal gyrus with the dorsomedial prefrontal cortex and temporoparietal junction, which represents the core of the theory of mind network. These results demonstrated that people who have a large social network size of active interactions maintain activity of the identified functional connectivity in daily life, possibly providing a mechanism for efficient information transmission between the brain networks related to language and theory-of-mind.

KEYWORDS
active interactions, inferior frontal gyrus, language, resting-state fMRI, social media, social network size, theory of mind

1 | INTRODUCTION

Social networking services (SNS) such as Twitter, Facebook, and Instagram have become ubiquitous tools for the daily lives of many people and allow us to communicate socially on the web. Among SNS, Twitter is a blogging service with which users can broadcast short messages. The message is called a tweet, which appears on a user's profile and is visible to other users who are connected to him/her, that is, followers. These other users have the option of responding to the tweet on their own profile, that is, reply. These functions enable researchers to quantify several types of social communications, including the number of followed and followers, and the frequency of replies and tweets: the former and the latter represents the static social network size of acquaintances and the social network size of active interactions, respectively.

The size of an individual's active social network is a key parameter of their social behavior and is correlated with subjective well-being (Demir, 2015; Gable & Reis, 2010). Previous research reported that brain volume size is linked with the number of Facebook friends (Kanai, Bahrami, Roylance, & Rees, 2012; Von der Heide, Vyas, &

Olson, 2014) as well as real-world social network size (Bickart, Wright, Dautoff, Dickerson, & Barrett, 2011; Kwak, Joo, Youm, & Chey, 2018; Lewis, Rezaie, Brown, Roberts, & Dunbar, 2011; Noonan, Mars, Sallet, Dunbar, & Fellows, 2018; Powell, Lewis, Roberts, García-Fiñana, & Dunbar, 2012), indicating that the size of social networks has a neural basis. More specifically, consistent with the social-brain hypothesis (Dunbar, 2014; Dunbar & Shultz, 2007), individual differences in social network size were correlated with individual brain volumes in the regions mediating social cognition, such as the amygdala, medial prefrontal cortex (mPFC), and anterior temporal lobe (see review, Lin et al., 2020).

A separate body of research using resting-state functional magnetic resonance imaging (rs-fMRI) has shown that patterns of functional brain connectivity capture individual differences in a wide range of social, cognitive, and behavioral tendencies and capacities (Cui et al., 2020; Finn et al., 2015; Mira-Dominguez et al., 2014; Rosenberg et al., 2016; Tavor et al., 2016). Therefore, interindividual variability in functional connectomes may also reflect the size of the social network. Indeed, a recent study suggested that functional measures of MRI rather than structure measures may be more suitable for studying associations with social network size (Lin et al., 2020). Although previous studies using rs-fMRI indicated a correlation between amygdala-based functional connectivity and social network size (Bickart, Hollenbeck, Barrett, & Dickerson, 2012; Zou et al., 2016), the connectome of whole social brain systems (Alcalá-López et al., 2018) (see, Figure 1) may provide a deeper understanding of human social networks.

Several studies have investigated neural correlates of the static social network size, that is, the association between the number of SNS friends and brain activity (Kanai et al., 2012; Von der Heide et al., 2014). However, users may be interacting actively with a moderate number of SNS accounts while having a limited static SNS network size. Thus, it remains unaddressed how the social network size of active interactions is represented in the brain. Past studies showed that close friends have similar neural responses and functional connectivity (Hyon et al., 2020; Parkinson, Kleinbaum, & Wheatley, 2017, 2018). When close friends often communicate, it is possible that the social network of active interactions has specific neural correlates other than the ones for the static social network size. Elucidating neural correlates of the active social network size may also help understand a biological background of human subjective well-being.

Researchers have also investigated social connections using self-report measures (Kwak et al., 2018; Parkinson et al., 2018). However, survey results based on participants' retrospective thoughts are known to be noisy (Ernala, Burke, Leavitt, & Ellison, 2020; Scharkow, 2016). An advantage of using SNS data is that it can measure the size of active interactions and static networks objectively, since SNS behaviors are available as digital data. In Twitter networks, the social network size of active interactions can be defined as the total number of active contact members in a single (target) account, which can be measured by the number of accounts that replied to the target account (i.e., Reply network). On the other hand, the size of a static social network can be defined as the total number of Twitter members associated with the account, which is measurable by the number of follower/following (i.e., Follow network). To our knowledge, no previous study has examined the association between rs-fMRI and the social network size of active interactions in a social media network.

Therefore, in the present study, we investigated whether patterns of resting functional connectomes of the social brain are associated with the size of the social network using a large sample size ($n = 222$). Using social network information from subjects' Twitter accounts, we investigated the Reply network as a measure of the social network size of active interactions and the Follow network as a measure of the size of the static social network (see Section 2). We first conducted a region of interest (ROI)-to-ROI analysis to capture the relationship between the resting brain network of the whole social brain and social media network size. We next applied graph theoretical analysis to find the central (hub) brain region associated with the social media network size. To examine the generalizability of the identified brain network, we decoded the social media network size.
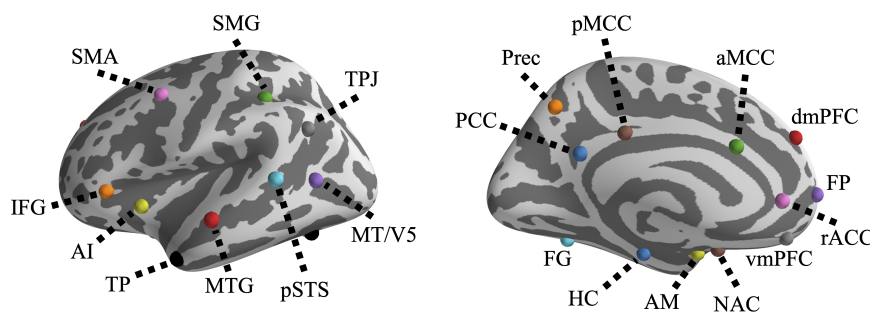

FIGURE 1 Social brain connectome. 6-mm ROIs from Alcalá-López et al. (2018). The left brain is a lateral surface of the left hemisphere, and the right brain is a medial surface of the left hemisphere. Colors are for readability. (left) IFG, inferior frontal gyrus; AI, anterior insula; TP, temporal pole; MTG, middle temporal gyrus; pSTS, posterior superior temporal sulcus; MT/V5, middle temporal V5 area; SMA, supplementary motor area; SMG, supramarginal gyrus; and TPJ, temporoparietal junction; (right) PCC, posterior cingulate cortex; Prec, precuneus; pMCC, posterior mid-cingulate cortex; aMCC, anterior mid-cingulate cortex; dmPFC, dorsomedial prefrontal cortex; FP, frontal pole; rACC, rostral anterior cingulate cortex; FG, fusiform gyrus; HC, hippocampus; AM, amygdala; NAC, nucleus accumbens; vmPFC, ventromedial prefrontal cortex

Given evidence from network neuroscience (Finn et al., 2015; Rosenberg et al., 2016; Tavor et al., 2016), we hypothesized that greater strength in an individual's social functional connectome is associated with a greater social network size. More specifically, because social interactions performed in language with various people should involve the theory of mind (ToM), which is the ability to understand how other people think (Frith & Frith, 2006; Van Overwalle & Baetens, 2009), we hypothesized that the Reply network is more strongly associated with functional connectivity between the ToM network, which includes the temporoparietal junction (TPJ), the superior temporal sulcus, and mPFC, and the inferior frontal gyrus (IFG), which plays an important role in language processing, than the Follow network (Molenberghs, Johnson, Henry, & Mattingley, 2016; Schurz, Radua, Aichhorn, Richlan, & Perner, 2014; see also Figure 1). In addition, we tested whether the identified relationship persists after controlling personality traits to capture some aspects of individual differences in the social network size (Hyon et al., 2020; Kardos, Leidner, Pléh, Soltész, & Unoka, 2017; Lin et al., 2020).

2 | METHODS

2.1 | Participants

Participants provided written consent to join the study and to the anonymous use of their Twitter log and questionnaire data for research purposes. The NICT ethics committee approved all study procedures. All 222 participants (149 males and 73 females; mean age 22.3 years old, $SD = 3.34$) completed the structural and resting-state MRI scans and personality traits questionnaires in the experimental room. We checked whether participants posted more than 100 tweets before participating to make the analysis reliable (Schulz et al., 2019). From the posted content, we manually confirmed that no Twitter accounts were bot accounts. Since most of the participants were undergraduate students, they rarely interacted with bot accounts for advertisement purposes. We conducted the measurements over 2 consecutive years (2016: $N = 133$, 2017: $N = 89$), and the participants received a reward (JP¥3,000) for their participation. We are taking an inclusive approach of all persons without limitations by (a) sex or gender, (b) race or ethnicity, or (c) age other than as scientifically justified and as specified in enrollment inclusion and exclusion criteria.

2.2 | Social media network indexes

We used Twitter's application programming interface (API) to retrieve demographic information of the accounts and past tweets posted by the target accounts for all the participants. This method assesses the observable social network properties instead of relying on subjective reports by the participants. The API can return up to a maximum of the 3,200 most recent tweets per account at the time of collection (Tweet number extracted by API: $M = 2,226$, $SD = 1,128$).

We transformed the data into two social media network indices. More specifically, we considered the Reply network (the total number of active contact members of a Twitter account) as the social network size of active interactions and the Follow network (the total number of social network members on a Twitter account) as the network size of the static social network (see Section 1). Briefly, in the Reply network, a Reply was defined as exchanging messages with friends and others on Twitter. We indexed the Reply network by how many other accounts an account interacted with in the collected tweets. The Reply network was normalized by dividing by the total tweet number, because this number varied among participants. Regarding the Follow network, in Twitter, following and followers represent the number of people who the account follows and the number of people who are following the account, respectively. The numbers of following and followers showed a very strong positive correlation in the current samples ($r = .92$), which is why we merged them into the Follow network. Both networks were log-scaled to reduce outliers and increase the normality due to the positively skewed distribution. There was mild correlation between the Reply and Follow networks ($r = .37$, $p < .001$).

Notably, we found that the Reply network is not significantly correlated with gender ($r = -.10$, $p < .144$), although several resting-fMRI studies have found gender differences in functional connectivity (Ingalhalikar et al., 2014; Ritchie et al., 2018; Satterthwaite et al., 2015). A potential reason for this discrepancy is that the number of male participants was more than twice as many as the number of female participants in our study.

2.3 | Personality traits and demographic information

Participants were asked to answer the questionnaire using a web browser on a computer. The psychological questionnaire included Big 5, empathy (IRI; interpersonal reflective index), and happiness (SHS; Subjective Happiness Scale). Big 5 represents the most prominent human personality traits (McCrae, John, & Costa, 1992). On the other hand, research has shown that empathy is related to real-life social network size (Kardos et al., 2017) and that social networks are important for happiness (Gable & Reis, 2010) and people who have higher subjective happiness have a larger social network size (Y. K. Chan & Lee, 2006). In addition, since smoking and alcohol use and education level can be associated with resting patterns in the brain (M. Y. Chan et al., 2018; Cheng et al., 2019), participants were also asked for their smoking habit using Fagerstrom Test for Nicotine Dependence (FTND) (Heatherton, Kozolowski, Frecker, & Fagerstrom, 1991), alcohol usage using Alcohol Use Disorders Identification Test (AUDIT) (Martin & Glynn, 2015), and education history using Socio Economic Status (SES) (Krieger, Williams, & Moss, 1997).

The experimenter instructed the participants that the study was about human personality and everyday thinking. An in-house system based on the Lime Survey program (LimeSurvey GmbH, Germany) was used to present the questionnaires on the web browsers. The presentation order of items within a questionnaire was randomized.

Each questionnaire was scored in line with its guidelines after correcting for inverse meaning items (see Table S1).

2.4 | MRI data acquisition

MRI measurements were performed on a 3 T Prisma scanner (Siemens Medical Systems) with a 64-channel head coil installed at our institute. T2-weighted functional images were obtained using an EPI sequence (repetition time [TR] = 1 s, echo time [TE] = 30 ms, flip angle [α] = 60°, 2.0 × 2.0 × 2.0 mm resolution, matrix size = 100 × 100 mm; 72 interleaved transverse slices with no gap; field of view [FOV] = 200 × 200 mm, slice thickness = 1.6 mm, multiband factor = 6). Each participant underwent a single rs-MRI session. For the 10-min rs-MRI measurement, 600 volumes were acquired. During the rs-fMRI scans, participants were instructed as follows: "Please relax. Don't sleep. Fixate on the central crosshair mark and do not think about specific things." High-resolution T1-weighted structural images were also acquired (TR = 1.9 s; TE = 3.37 ms; flip angle = 9°; voxel size = 1.0 × 1.0 × 1.0 mm; matrix size = 256 × 256 mm; 208 interleaved transverse slices with no gap; FOV = 256 × 256 mm).

2.5 | Rs-MRI preprocessing

Rs-fMRI data were preprocessed using the CONN toolbox (https://www.nitrc.org/projects/conn) on Matlab 2018b (MathWorks, USA). Spatial preprocessing of the CONN toolbox included fieldmap correction, realign and unwarp, slice-timing correction, denoising, normalization (onto the standard MNI space), and smoothing (6-mm FWHM Gaussian filter) using the default parameter settings of SPM12. Anatomical volumes were segmented into gray matter, white matter, and cerebrospinal fluid (CSF) areas, and the resulting masks were eroded to minimize partial volume effects. The temporal time series characterizing the estimated subject motion (three-rotation, three-translation parameters, plus another six parameters representing their first-order temporal derivatives, and scrubbing parameters containing the offending scans) as well as the BOLD time series within the subject-specific white matter mask and the CSF mask (five PCA parameters, CompCor; Behzadi, Restom, Liau, & Liu, 2007) were used as temporal covariates and removed from the BOLD functional data by linear regression.

Afterward, the linear trends of the time courses were removed, and band-pass filtering (0.008–0.09 Hz) was applied to the time series of each voxel to reduce the effect of low-frequency drifts and high-frequency physiological noise (Biswal, Yetkin, Haughton, & Hyde, 1995). Finally, functional connectivity (correlation matrix) was computed for each pair of ROI. The ROI-to-ROI correlation was normalized and transformed into z scores. To extract the brain regions involved in social cognition, we used the social brain connectome atlas including 36 cortical and subcortical areas (Alcalá-López et al., 2018) (Figure 1). This atlas is based on a meta-analysis of neural activity related to social-cognitive processing. All 36 ROIs were used to construct the social brain functional connectivity, resulting in 630 network elements.

2.6 | ROI-to-ROI analysis

In order to determine how the social media network size is associated with resting-state functional connectivity, each participant's two social media network size indices extracted from their Twitter data were regressed in a general linear model analysis using each of the 630 network elements. Demographic information (age, gender [male or female], recorded year [2016 or 2017], AUDIT, FTND, and SES) was also included in the regression model as control variables. The cluster maps, displayed at $p < .05$, were corrected for familywise error rate (FWE) multiple comparisons using a spatial pairwise clustering estimator derived from cluster-permutation simulations (1,000 iterations) with a combination of an uncorrected $p < .05$ height threshold (Zalesky, Cocchi, Fornito, Murray, & Bullmore, 2012) as implemented in the CONN toolbox.

2.7 | Graph theoretical analysis

The ROI-to-ROI connectivity analysis consistently associated several brain regions with the social media network size. To understand the relationship among these regions further, we computed several centrality measures of the functional connectivity using graph theory analysis (Bullmore & Sporns, 2009). We utilized the CONN toolbox and brain connectivity toolbox (Rubinov & Sporns, 2010) for this purpose. We examined three different centrality measures: degree, subgraph, and eigenvector. These measures were categorized into local, mesoscale, and global centralities, respectively (Zuo et al., 2012).

First, the ROI-to-ROI connectivity obtained for all participants was binarized with a thresholding cost of 0.04, because the thresholding method was reported to reduce false positives (Drakesmith et al., 2015). The resulting binarized graph of connectivity matrices for each subject was used in the subsequent analyses. Degree centrality is the sum of all edges for a given node. We summed each node's edges for each of the 36 ROIs to estimate the overall connectivity. Subgraph centrality was computed by the spectra of the adjacency matrix of the network and reflected by the number of closed edges originating at the node, where longer edges are exponentially down weighted. Finally, the eigenvector centrality counts both the number and the quality of connections, so that a node with few connections to other high-ranking nodes can outrank one with a larger number of mediocre contacts. A detailed account of the three graph theory measures can be found in other literature (Estrada & Rodríguez-Velázquez, 2005; Lohmann et al., 2010).

We conducted a general linear model analysis for the two social media network size indices based on one of the centrality metrics (degree, subgraph, and eigenvector) for each of the 36 ROIs and control variables (age, gender, year, AUDIT, FTND, and SES). This procedure was repeated 36 times for each of the centrality metrics

(Termenon, Jaillard, Delon-Martin, & Achard, 2016). The values of *p* were corrected with FWE multiple comparisons for each of the centrality metrics (*p* < .05).

2.8 | Seed-based analysis

From the ROI-to-ROI functional connectivity and graph theory analysis, the left IFG was selected as the seed to further explore the association between functional connectivity and social media network size. Spherical seeds were defined with the left IFG ROI (see Figure 1) in the social brain connectome (Alcalá-López et al., 2018). A voxel-based general linear model was applied to quantify the relationship between the seeds and other brain regions. As a result, a whole-brain correlation map was produced for the seed. Multiple regression analysis (age, gender, year, AUDIT, FTND, and SES as control variables) was used to investigate whether the social media network size is represented by seed-based functional connectivity. We used a significance threshold of *p* < .001 for second-level tests, uncorrected for multiple comparisons. To ensure a type 1 error at the individual voxel level, a threshold of *p* = .05 was corrected for FWE multiple comparisons at the cluster level based on Gaussian random field theory (Nieto-Castanon, 2020).

2.9 | Decoding analysis

Finally, we tested whether it was possible to predict the social media network size based on the seed-based connectivity. If so, it should be possible to build a predictive model of the social media network size by training an algorithm to recognize patterns of seed-to-voxel functional connectivity. Significant seed-based resting-state functional connectivity was used as the input feature-space (685 features per participant) to predict the social network size on Twitter. These features satisfied the above cluster-level significance threshold.

We conducted a machine-learning analysis using scikit-learn (Pedregosa et al., 2011). After feature scaling, linear ridge regression analysis was performed. Ridge regression uses an L2 penalty during the model fitting. This technique shrinks the regression coefficients, resulting in better generalizability for predicting unseen samples. The L2-based regression model is also effective for high-dimensional imaging data (Cui et al., 2020). Hyperparameters were optimized with a grid-search procedure. Values for λ (regularization parameter) ranged from 0.001 to 1,000 with increments of log 10 and included [0.001, 0.01, 0.1, 1, 10, 100, 1,000].

We also conducted a twofold cross-validation procedure, in which the data were randomly split into training (50%) and testing (50%) sets. Specifically, all participants were randomly assigned to two subsamples of 111 participants each. The optimal hyperparameter was computed based on the multivariate pattern of the 111 participants (training set) with the twofold cross validation and evaluated by the excluded 111 participants (test set). This procedure was repeated two times, with each subsample being the testing set. To avoid a potential bias of training-test splits, the cross-validation procedure was repeated 100 times by producing different splits in each repetition, and the resultant prediction performance was averaged to evaluate the generalization (Cui et al., 2020; Zhou et al., 2021).

Using the trained model, we conducted out-of-sample predictions for the test (i.e., holdout data). We calculated the predictive accuracy using Pearson's *r* value between the actual and predicted social media network sizes. We also calculated the mean absolute error to evaluate the model performance. The average *r* value across 100 predictions was then tested against a null distribution of *r* values generated by permutation testing. Functional connectivity data were randomly shuffled across participants 10,000 times while holding the social media network size in the dataset the same. In each permuted dataset, the machine learning analysis procedure was repeated to generate a null distribution of 10,000 *r* values. The values of *p* were determined by calculating the frequency with which the true model's *r* value exceeded the *r* values in the null distribution.

3 | RESULTS

3.1 | Basic statistics of social media network size

The descriptive statistics for each of the social media indices are depicted in Table 1. The participants show large individual differences in SNS profiles. Since the maximum value of the number of replies for each account was not large and most of the total replies did not come from a single or few accounts, the size of the Reply and Follow networks was regarded as a valid network index.

3.2 | ROI-to-ROI functional connectivity and social media network size

We evaluated whether the functional connectivity between 36 social-brain ROIs is associated with social media network size. The results revealed that the connectivity between several cortical regions is positively associated with the Reply network (Mass = 173.93, *p* = .010, FWE-corrected; the significant cluster in Figure 2a) but not with the

TABLE 1 Descriptive statistics of the social media network-related indices

Variables	Mean	Median	*SD*	Max	Min
Reply indexes					
Reply network	85	79	60	317	0
Reply number	884	816	641	2,614	0
Reply per account	11	10	9	107	0
Follower indexes					
Follow network	558	424	498	3,261	25
Following	284	229	254	1,869	14
Follower	273	197	259	1,916	10

Note: The scores in the table were calculated using raw scores, but the analysis was performed using log-transformed scores.
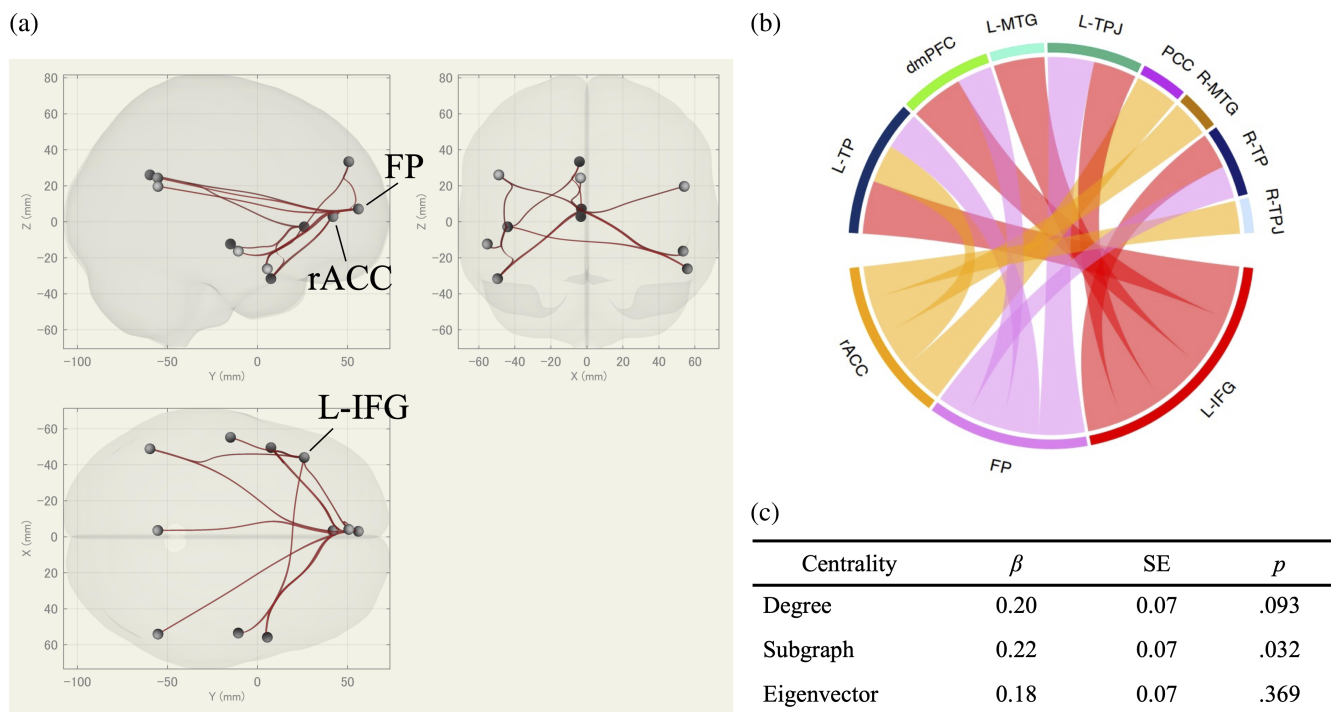
FIGURE 2 Neural correlates of the Reply network. (a) Significant associations between the ROI-to-ROI connectivity and Reply network. (b) Diagram of the significant associations. (c) Results of the regression analysis based on the centrality measures of the left IFG. L, left; R right; IFG, inferior frontal gyrus; FP, frontal pole; rACC, rostral anterior cingulate cortex; TP, temporal pole; dmPFC, dorsomedial prefrontal cortex; MTG, middle temporal gyrus; TPJ, temporoparietal junction; PCC, posterior cingulate cortex

Follow network size. Even if we examined Following and Follower separately, no ROI-to-ROI connectivity is associated with either of the measures. In addition, neither control variable (age and gender) nor the interaction between the Reply network and gender produced a significant result.

In the significant cluster, three key brain regions were observed: left IFG, frontal pole (FP), and rostral anterior cingulate cortex (rACC). As shown in Figure 2a,b, positive connections were found between the left IFG and the dmPFC, bilateral temporal pole, left TPJ, and left middle temporal gyrus (MTG); the FP and the left TPJ, bilateral temporal pole, and dmPFC; and the rACC and posterior cingulate cortex (PCC), left temporal pole, right TPJ, and right MTG.

To further examine whether the three regions constitute a hub for the network, we performed a graph theory analysis. The results showed that the subgraph centrality in the left IFG is positively associated with the Reply network (Figure 2c), but no other ROIs showed a significant result. In addition, even when the regression models included personality traits (Big 5, Empathic traits, and Subjective happiness), consistent results for both the ROI-to-ROI connectivity analysis and graph theory analysis were obtained (see Figure 1).

3.3 | Seed-to-voxel functional connectivity and network size in social media

Based on the results of the ROI-to-ROI analysis and the graph theory analysis, the left IFG was selected as the seed in our seed-to-voxel

analyses. As shown in Figure 3a, general linear modeling from the functional connectivity to the Reply network size found significant positive associations between the left IFG and dmPFC ($k = 232$, peak coordinates: $x = -2$, $y = 42$, $z = 28$), the left IFG and left TPJ ($k = 257$, peak coordinates: $x = -52$, $y = -54$, $z = 20$), and the left IFG and right TPJ ($k = 196$, peak coordinates: $x = 58$, $y = -50$, $z = 20$) (FWE-corrected at the cluster level, $p < .05$), indicating that people who have a large Reply network show strong connectivity between the left IFG and the dmPFC and bilateral TPJ at rest. No significant results were found for the Follow network size.

To further validate the functional connectivity basis for the social network size, we predicted the Reply network size from the significant seed-to-voxel connectivities by ridge regression (see Section 2). We found that the Reply network size predicted by the model was significantly correlated with the actual Reply network size ($r = .24$, mean absolute error = 0.78) (Figure 3b). We conducted a permutation test to estimate the significance of the correlation between the actual and predicted Reply network sizes. The estimated r value was found to be significantly greater than almost all of the 10,000 permuted r values ($p = .002$) (Figure 3c).

4 | DISCUSSION

This study investigated the relationship between the whole social brain functional connectome and active interactions in a social media network. From the ROI-to-ROI analysis, we found that the Reply
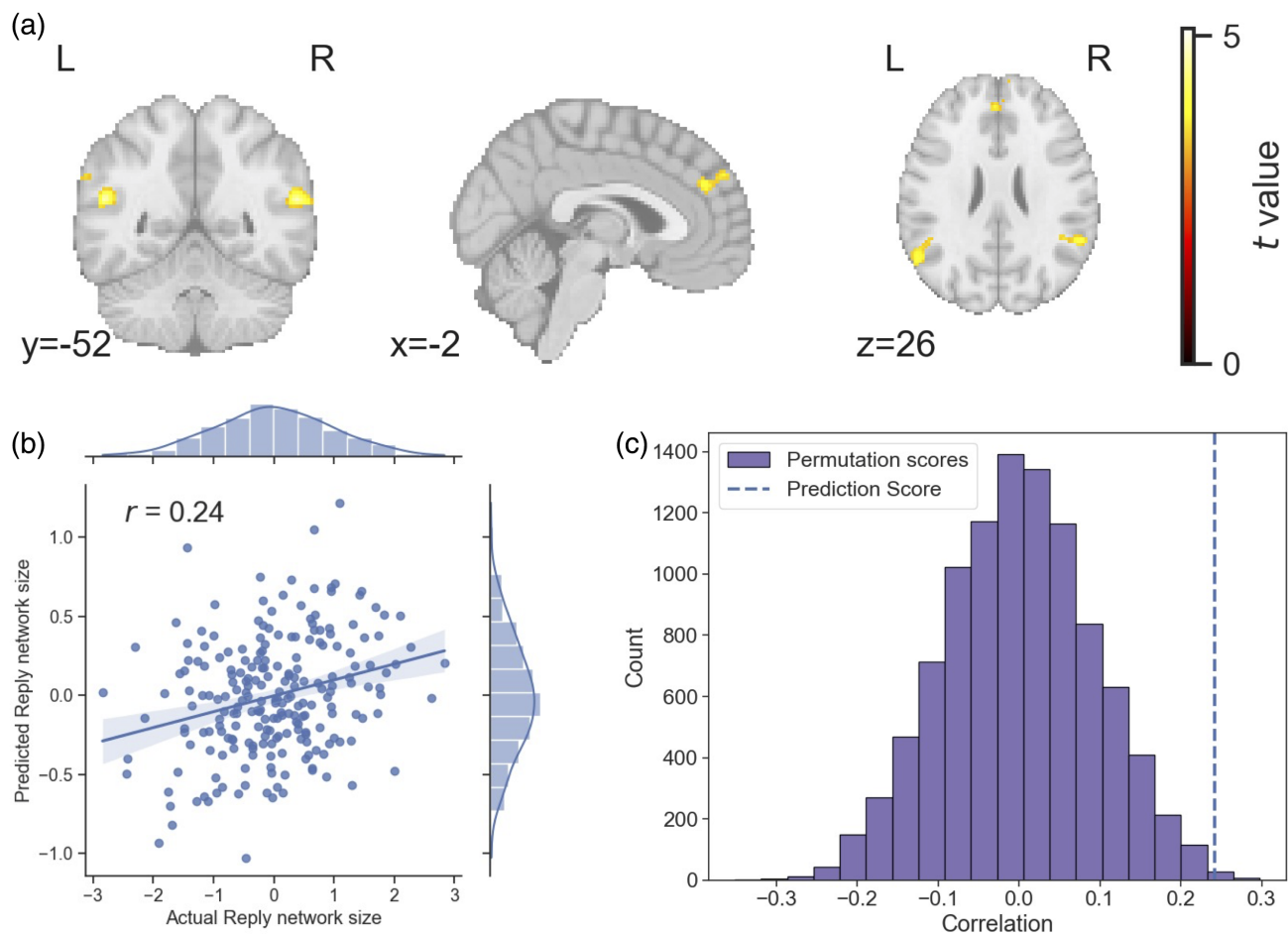
FIGURE 3 Reply network correlates of the functional connectivity between the left IFG and whole-brain voxels. (a) The significant association between the seed-to-voxel connectivity and Reply network. (b) Averaged machine learning (twofold cross validation with 100 times repetition) prediction from significant seed-to-voxel connectivity to the Reply network. (c) Permutation test for the machine learning prediction

network (social network size of active interactions) is correlated with the resting-state functional connectivity of three frontal brain regions (left IFG, FP, and rACC), but no association existed between the Follow network (social network size of static network) and resting functional connectivity. Analysis based on graph centrality indices suggested that the left IFG is a key brain structure for the Reply network. Importantly, these findings were validated even after controlling for personality trait scores and demographic information. Furthermore, our seed-based analysis and machine learning analysis demonstrated that connection of the left IFG with the dmPFC and TPJ can predict the Reply network size. Since the ToM network includes these three brain regions (Molenberghs et al., 2016; Schurz et al., 2014), the results partly support our hypothesis: the Reply network shows stronger functional connectivity between the language and ToM networks. Overall, the current study provides compelling empirical evidence that functional connectivity of the left IFG with the dmPFC and TPJ plays a key role in people who have a larger interaction size in social media networks.

We identified higher ROI-to-ROI functional connectivity patterns in social brain regions for people who have a large interaction size in a social network (i.e., Reply network), which included the three brain

regions: left IFG, FP, and rACC. Especially, the network centrality of the left IFG was positively associated with the social media interaction size. These findings indicate that the left IFG constitutes the most important hub for the social network size. As shown in Figure 1, the anterior part of the IFG (MNI coordinates: $x = -45$, $y = 27$, $z = -3$, BA45) identified in the current study has long been postulated as the region supporting language and semantic processes (Fedorenko & Blank, 2020; Friederici & Gierhan, 2013). Since a recent meta-analysis study also suggested that the anterior part of the left IFG plays a role in social cognition (Adolfi et al., 2017), more active left IFG functional connectivity for people with a larger Reply network may suggest that language and social cognition systems are coactivated even at rest.

The larger social network size of active interactions is related to higher functional connectivity of the left IFG with the dmPFC, TPJ, temporal pole (TP), and MTG. Moreover, a seed-to-voxel analysis supports the association between the left IFG with the dmPFC and TPJ. The dmPFC and TPJ are a core structure for ToM (Schurz et al., 2014; Van Overwalle & Baetens, 2009), which represents the ability to track the intentions, knowledge, and beliefs of others (Frith & Frith, 2006). The dmPFC is also known to be involved in processing socially or emotionally relevant information about others (Jamali et al., 2021;

Krol, Meyer, Lieberman, & Bartz, 2018; Saxe & Powell, 2006). A social function of the TPJ is perspective taking (Schurz et al., 2014; Weisz & Cikara, 2021). These functions seem to contribute to form ToM ability. Past studies reported co-activation of the left IFG and the ToM system in a language-based ToM task (Enrici, Adenzato, Cappa, Bara, & Tettamanti, 2011). Although we must be careful to avoid a reverse inference, it is possible that information about others' intentions is gradually processed from the left IFG gateways to the mPFC and TPJ regions (Tettamanti et al., 2017; van Ackeren, Smaragdi, & Rueschemeyer, 2016). In addition, the anterior temporal lobe, including the TP and MTG, is important for social semantic cognition (Binney & Ramsey, 2020; Ralph, Jefferies, Patterson, & Rogers, 2016) and anatomically connected with the IFG (Catani & Bambini, 2014). All these observations are consistent with the idea that people who have a large social media interaction size may always keep the functional brain network active for use in social interactions with language. This view might be related to a recently proposed similarity between the social brain and the default-mode brain networks (Meyer, 2019).

Unlike the ROI-to-ROI connectivity analysis, the centrality index of the left IFG was related to the Reply network, whereas the centrality index of the FP and rACC did not associate with the Reply network. These results indicated that the functional hub strength of the left IFG in the social brain connectome is especially important for the large social network size of active interactions. Specifically, only the subgraph centrality showed a significant relationship with the Reply network. The centrality index represents mesoscale centrality (Zuo et al., 2012) and emphasizes the weight of the closed edges originating at the node. Therefore, direct connection more than indirect connection between the left IFG and other social brain regions may reflect the Reply network well. Further study is needed to clarify the characteristics of the left IFG and social media interaction size.

Our functional connectivity results for social media interaction size were strengthened by machine learning prediction of the interaction size from the seed-to-voxel functional connectivity. We repeated a twofold cross validation process (50% of data for training and the other 50% for testing) 100 times. Previous studies reported that an individual's brain resting-state functional connectome can predict the social, affective, and behavioral characteristics of the individual (Cui et al., 2020; Finn et al., 2015; Tavor et al., 2016). A recent study also suggested that the similarity of resting-state connectivity between personscan predict the structure of a real social network (Hyon et al., 2020). We extended these previous studies by showing that resting-state functional connectivity can also predict cyber-space activity and physical-space activity. However, to confirm the generalizability of the predictive model, a larger independent dataset, like that used for connectome-based predictive models is preferred (Rosenberg et al., 2020; Spisak et al., 2020). Future studies should examine the generalizability of the current model by collecting new resting-state fMRI and Twitter behavior datasets. The brain mask of the seed-based functional connectivity available in the GitHub repository will allow others to test our analysis method.

The FP and rACC also showed higher functional connectivity in people who have a large social network size of active interactions.

The connection of the FP (which is part of the mPFC) with the dmPFC, TPJ, TP, and MTG may suggest that the FP works within the ToM network (Schurz et al., 2014). On the other hand, the rACC is an important neural system for social behavior across species (Lockwood, Apps, & Chang, 2020). Specifically, the rACC exhibits specialization for learning and computation about the motivation of others (Apps, Rushworth, & Chang, 2016; Behrens, Hunt, Woolrich, & Rushworth, 2008). In the current study, for people who have a large interaction size, the rACC was strongly connected with ToM (TPJ and PCC; Schurz et al., 2014) and social cognition (TP and MTG) regions at rest. These results are also consistent with our view that people who have a large interaction size activate the functional connectivity for social cognition and communication even at rest.

Considering accumulating evidences that the size of an individual's active social network is correlated with subjective well-being (Demir, 2015; Gable & Reis, 2010), the result of the present study may also poses a possibility that the interaction among the identified social brain regions connects with subjective well-being.

Our study leaves several open questions. First, although our results suggest that people with large social media interaction size show higher functional connectivity even at rest, we cannot dissociate the cause and effect of the networks size due to this study's correlational nature. Thus, future studies should examine whether resting-state functional connectivity predicts subsequent social media interaction size or if the change in resting functional connectivity follows the social media interaction size by conducting multiple time measurements.

Second, the range of social connections included in the present study was not the same as in social network indices of previous studies (Lin et al., 2020). Specifically, we measured the size of the social network by the number of reply and follow/followers on Twitter, which includes both real-world friends and non-friends (unlike Facebook friends; see Kanai et al., 2012). Although the participants (mainly university students) may use Twitter for friendship, people in different social layers use Twitter differently. Further investigation of the different social layers may provide a more conclusive understanding of how social media network sizes are associated with functional brain connectivity.

Third, although previous research suggested that the amygdala is the key node for social network size (Bickart et al., 2011, 2012; Zou et al., 2016), our study did not reveal amygdala-related connectivity. This may be because different social network size definitions are associated with different brain links (Kanai et al., 2012). Our definition of network size was based on an active social network size, while previous studies relied on a static network size. Moreover, the different scanning methods may have produced different results. That is, several recent studies have indicated that multiband scanning, which we used, does not detect well activity in the sub-cortical region (Seitzman et al., 2020; Srirangarajan, Mortazavi, Bortolini, Moll, & Knutson, 2021). In contrast, studies that reported an association between functional connectivity of the amygdala and social network size used conventional single band scanning methods (Bickart et al., 2012; Zou et al., 2016).

Last, when resting-state brain activity was measured in an MRI scanner, the participants may have let their minds wander freely although instructed to do otherwise. If so, their thoughts and imaginations may have differed from subject to subject (Javier, Julia, Colin, & Peter, 2021) in a way correlated with the social network size. Future studies need to ask subjects to report a summary of their retrospective experience immediately after the scanning session (Alexander Diaz et al., 2013). This information would make any identified relationship between resting-state functional connectivity and social network size more reliable.

Taken together, the present study demonstrated that people who actively interact with many others on social media have higher functional connectivity of the left IFG with other ToM-related brain regions even at rest. This finding suggests the possibility that people with a large social network size of active interactions are always prepared for communications between language and ToM brain networks. In addition, our results showed that left IFG-centered functional connectivity in combination with a core structure for the ToM network (dmPFC and TPJ) can predict the social media interaction size. Overall, social brain connectomes could serve not only as a neural signature to identify individuals who are likely to form large social networks but also as a powerful tool for understanding brain functions for both real- and digital-world communications.

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DATA AVAILABILITY STATEMENT

Preprocessed MRI data and reply frequency data that support the findings of this study are available from the corresponding author upon request. The analysis code is available online from the first authors' GitHub repository at https://github.com/mokazuma/replyerbrain

ORCID

Masahiko Haruno https://orcid.org/0000-0002-0817-0720

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