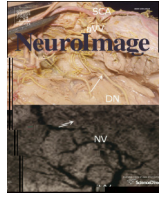




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ABSTRACT

Functional connectivity (FC) refers to the temporal correlation between spatially remote neurophysiological regions. FC is a key concept in network neuroscience and has been widely used to study brain organization and function. However, the interpretation of FC is often ambiguous because it can be influenced by various factors, including task-induced changes in brain activity and noise. In this paper, we propose a novel method to estimate FC that is robust to task-induced changes and noise. We use a task-based fMRI design to study FC in the human brain. The results show that our method can accurately estimate FC and is robust to task-induced changes and noise. This method may be useful for studying FC in other brain regions and tasks.

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Introduction

Functional connectivity (FC) refers to the temporal correlation between spatially remote neurophysiological regions. FC is a key concept in network neuroscience and has been widely used to study brain organization and function. However, the interpretation of FC is often ambiguous because it can be influenced by various factors, including task-induced changes in brain activity and noise. In this paper, we propose a novel method to estimate FC that is robust to task-induced changes and noise. We use a task-based fMRI design to study FC in the human brain. The results show that our method can accurately estimate FC and is robust to task-induced changes and noise. This method may be useful for studying FC in other brain regions and tasks.

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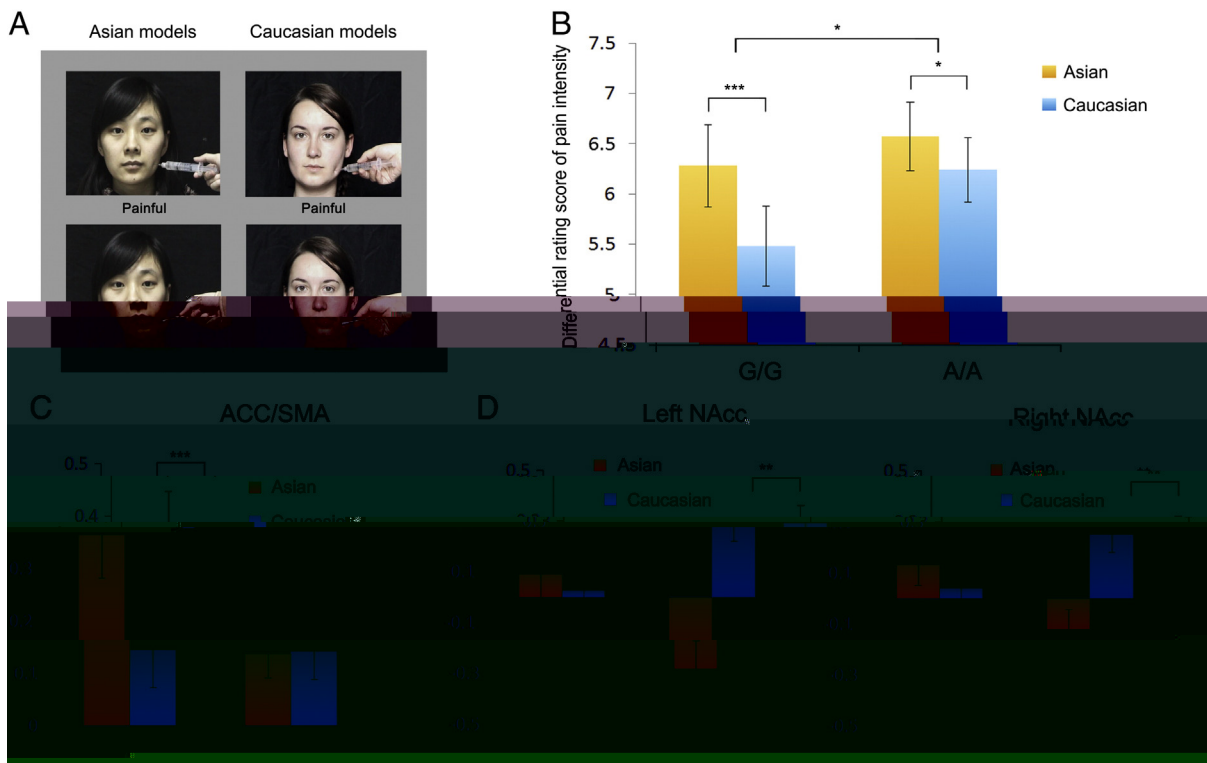


Fig. 1. (A) Asian and Caucasian models in painful states. (B) Differential rating score of pain intensity for Asian and Caucasian models. (C) Brain activation in ACC/SMA. (D) Brain activation in Left NAcc and Right NAcc. * p < 0.05; ** p < 0.01; *** p < 0.001.

$\mu = 2530$, $\sigma = 3.37$, $n = 1100$, $f = 0.07$.

fMRI data analysis

The analysis of fMRI data involves several steps, including data acquisition, preprocessing, and statistical analysis. The data is typically collected from participants using functional MRI technology. Preprocessing steps include motion correction, slice timing correction, and spatial normalization. Statistical analysis is then performed to identify areas of significant activation. This often involves using general linear models (GLMs) to model the blood oxygenation level dependent (BOLD) signal. The results are then interpreted in the context of the study's hypotheses. For example, significant activation in certain brain regions might indicate involvement in a specific cognitive or emotional process. The analysis is often done using software packages like SPM, FSL, or AFNI. The results are typically presented as statistical parametric maps, which are then overlaid on anatomical brain templates to show the location of significant activation. The significance is usually assessed using a permutation test or a similar non-parametric method to control for multiple comparisons. The results are then discussed in the context of the study's aims and compared with previous research in the field.

$$d_{RBE} = (M_{Asian} - M_{Caucasian}) / S_{Caucasian}$$

The calculation of d_{RBE} involves the mean difference between Asian and Caucasian groups, divided by the standard deviation of the Caucasian group. This metric is used to compare the results across different studies or conditions. The values for M_{Asian} and $M_{Caucasian}$ are typically obtained from the mean scores of the respective groups. The standard deviation $S_{Caucasian}$ is calculated from the variance of the Caucasian group. The resulting d_{RBE} value provides a standardized measure of the difference between the groups. For example, a positive value indicates that the Asian group has a higher mean score than the Caucasian group, while a negative value indicates the opposite. The magnitude of the value indicates the size of the difference in standard deviations. This metric is often used in meta-analyses to compare effect sizes across studies. The results are typically presented as forest plots, which show the mean difference and its confidence interval for each study. The overall mean difference and its confidence interval are also presented. The results are then interpreted in the context of the study's hypotheses and compared with previous research in the field.

$$d_{OXTR} = (M_{GG} - M_{AA}) / S_{Pooled} \sqrt{\frac{df_{GG}SS_{GG} + df_{AA}SS_{AA}}{df_{GG} + df_{AA}}}$$

The calculation of d_{OXTR} involves the mean difference between GG and AA genotypes, divided by the pooled standard deviation. This metric is used to compare the results across different studies or conditions. The values for M_{GG} and M_{AA} are typically obtained from the mean scores of the respective groups. The pooled standard deviation S_{Pooled} is calculated from the variance of both groups. The resulting d_{OXTR} value provides a standardized measure of the difference between the groups. For example, a positive value indicates that the GG group has a higher mean score than the AA group, while a negative value indicates the opposite. The magnitude of the value indicates the size of the difference in standard deviations. This metric is often used in meta-analyses to compare effect sizes across studies. The results are typically presented as forest plots, which show the mean difference and its confidence interval for each study. The overall mean difference and its confidence interval are also presented. The results are then interpreted in the context of the study's hypotheses and compared with previous research in the field.

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Results

Behavioral results

The behavioral results of the study are presented below. The first result is the mean difference between the Asian and Caucasian groups, which is $d_{RBE} = 6.84$, $p < 0.001$, $95\% CI: 5.88, 6.40$. This indicates a significant difference between the groups. The second result is the mean difference between the GG and AA genotypes, which is $d_{OXTR} = 0.70$, $p < 0.001$, $95\% CI: 0.48, 0.67$. This indicates a significant difference between the genotypes. The third result is the mean difference between the GG and AA genotypes, which is $d_{OXTR} = 0.70$, $p < 0.001$, $95\% CI: 0.48, 0.67$. This indicates a significant difference between the genotypes. The fourth result is the mean difference between the GG and AA genotypes, which is $d_{OXTR} = 0.70$, $p < 0.001$, $95\% CI: 0.48, 0.67$. This indicates a significant difference between the genotypes. The fifth result is the mean difference between the GG and AA genotypes, which is $d_{OXTR} = 0.70$, $p < 0.001$, $95\% CI: 0.48, 0.67$. This indicates a significant difference between the genotypes. The sixth result is the mean difference between the GG and AA genotypes, which is $d_{OXTR} = 0.70$, $p < 0.001$, $95\% CI: 0.48, 0.67$. This indicates a significant difference between the genotypes. The seventh result is the mean difference between the GG and AA genotypes, which is $d_{OXTR} = 0.70$, $p < 0.001$, $95\% CI: 0.48, 0.67$. This indicates a significant difference between the genotypes. The eighth result is the mean difference between the GG and AA genotypes, which is $d_{OXTR} = 0.70$, $p < 0.001$, $95\% CI: 0.48, 0.67$. This indicates a significant difference between the genotypes. The ninth result is the mean difference between the GG and AA genotypes, which is $d_{OXTR} = 0.70$, $p < 0.001$, $95\% CI: 0.48, 0.67$. This indicates a significant difference between the genotypes. The tenth result is the mean difference between the GG and AA genotypes, which is $d_{OXTR} = 0.70$, $p < 0.001$, $95\% CI: 0.48, 0.67$. This indicates a significant difference between the genotypes.

$\hat{\beta}_1 = \frac{0.36}{0.42} = 0.857$
 $\hat{\beta}_2 = \frac{-4}{-6} = 0.667$
 $t = \frac{0.857 - 0.7}{0.04} = 3.925$
 $t = \frac{0.667 - 0.5}{0.04} = 4.175$
 $t_{(59)} = 3.06$

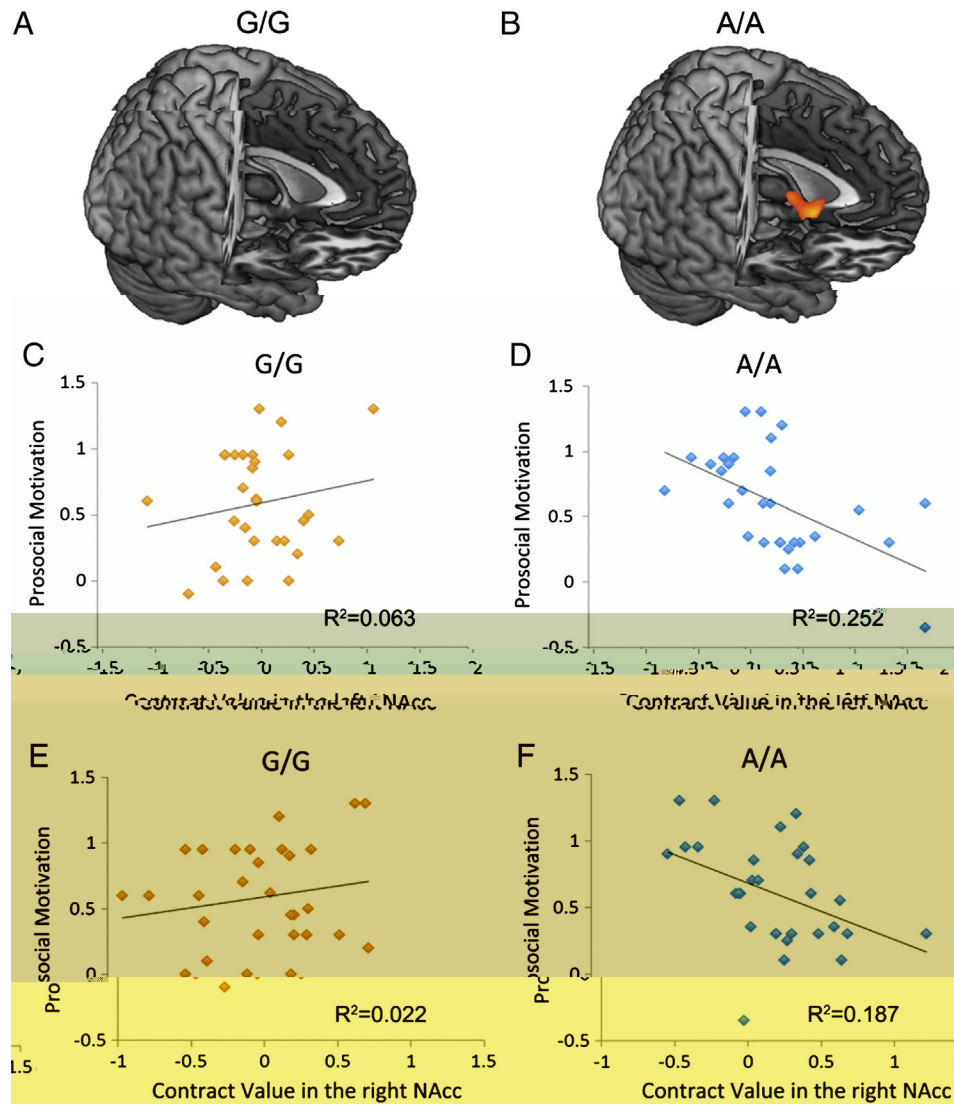


Fig. 4. The relationship between prosocial motivation and contract values in the Nucleus Accumbens (NAcc) for G/G and A/A genotypes. Panels A and B show brain slices with highlighted regions. Panels C and D show scatter plots for G/G and A/A genotypes in the left NAcc, with R-squared values of 0.063 and 0.252 respectively. Panels E and F show scatter plots for G/G and A/A genotypes in the right NAcc, with R-squared values of 0.022 and 0.187 respectively.

... (3). ... (59) = 2.35, $p < 0.05$ (58) = 0.20 & 0.47, $p > 0.6$ = -0.50, $p < 0.005$, ...

... = -0.43, $p < 0.05$, ... = 0.25, $p = 0.18$, ... = 0.15, $p = 0.43$, ... = 0.43, $p = 0.4$ 53576 ... (4) (5). ... (53576) ...

Discussion

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