

An Efficient Contrastive Deep Learning Model for Identifying Schizophrenia-Specific Neuroanatomical Variations

Lin Du^{1,2}, Yuqing Sun^{1,2}, Chaoyue Ding³, Xiaohan Tian^{1,2}, Biying Peng^{1,2}, Wenkun Lei^{1,2}, Junxing Xian^{1,2}, Jing Lou^{1,2}, Yingjie Peng⁴, Yuxuan Hong^{1,2}, RuoxinYang^{1,2}, Meng Wang^{1,2}, Xinghui Zhao^{1,2}, Xinyi Dong^{1,2}, Bing Liu^{1,2}

¹State Key Laboratory of Cognitive Neuroscience and Learning, Beijing normal university ²IDG/McGovern Institute for Brain Research, Beijing Normal University ³Brainnetome Center and National Laboratory of Pattern Recognition, Institute of Automation, Chinese Academy of Sciences, Beijing ⁴Institute of Biophysics, Chinese Academy of Sciences, Beijing

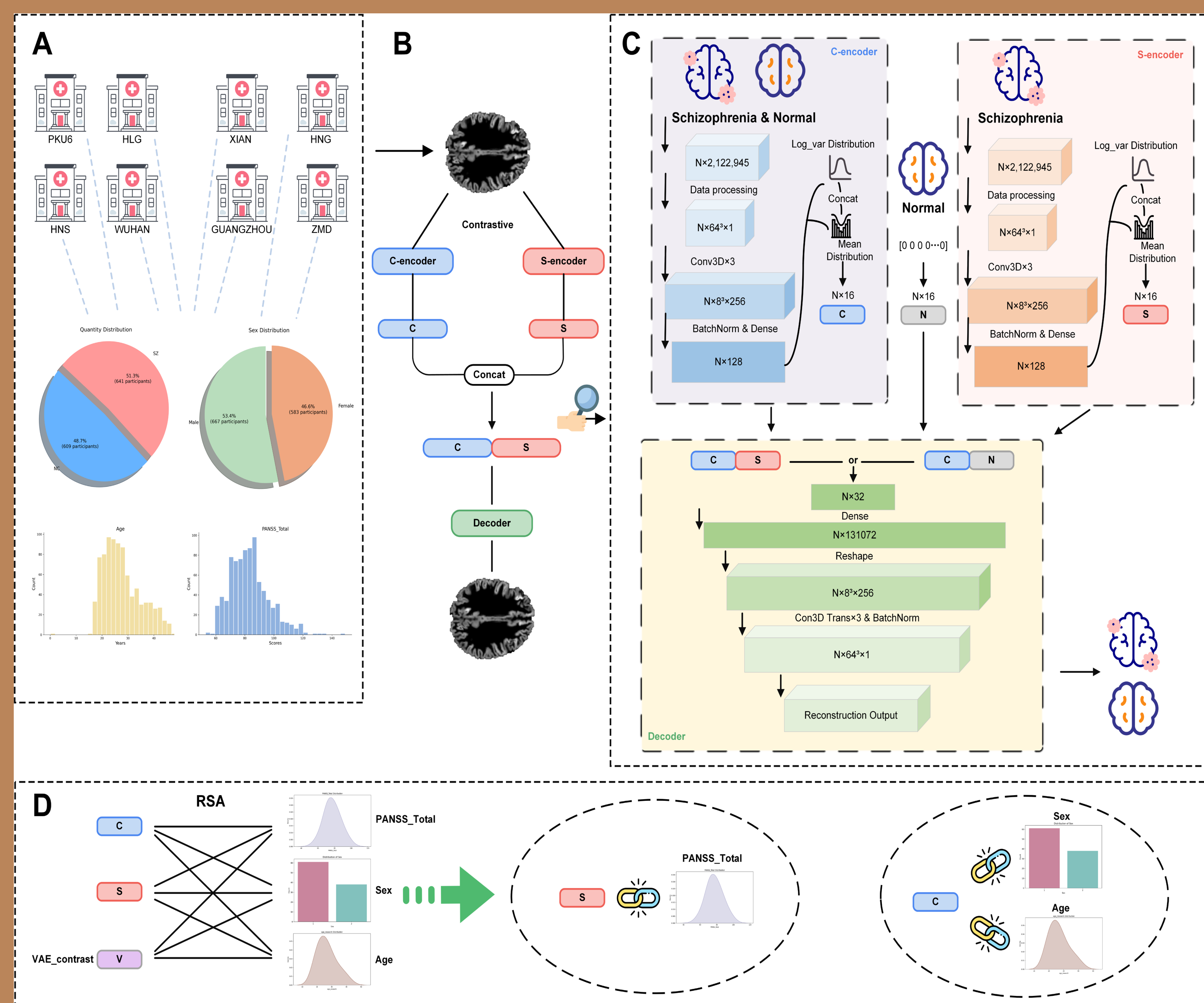
- Schizophrenia (SZ) is a debilitating mental disorder, affecting approximately 1% of the global population, with its etiology and underlying pathophysiological mechanisms still largely elusive.
- Clinically, individuals with schizophrenia typically exhibit positive and negative symptoms, along with generalized cognitive impairments, which severely disrupt social functioning and quality of life, while also imposing a heavy burden on families.
- For decades, extensive research has sought to identify brain abnormalities that could explain the clinical manifestations of schizophrenia. **However, a major challenge arises from the substantial heterogeneity among patients, as brain variations may be influenced by factors unrelated to schizophrenia itself, including sex, age, and other contributing variables.**

Data

- Whole-brain T1-weighted MRIs** : Incorporates data from **8** independent, multicenter hospital in China, encompassing a total of **1,250 participants**, including **641** individuals with schizophrenia and **609** healthy controls.
- MRI preprocessing** : Using the SPM Computational Anatomy Toolbox (CAT12), four key steps: skull stripping, non-linear correction, intensity normalization, and registration to standard MNI space using the DARTEL algorithm.
- Quality control** : Significant head motion (>3 mm), excessive noise, or large artifacts were excluded from the dataset to ensure high-quality data for analysis.

Methods

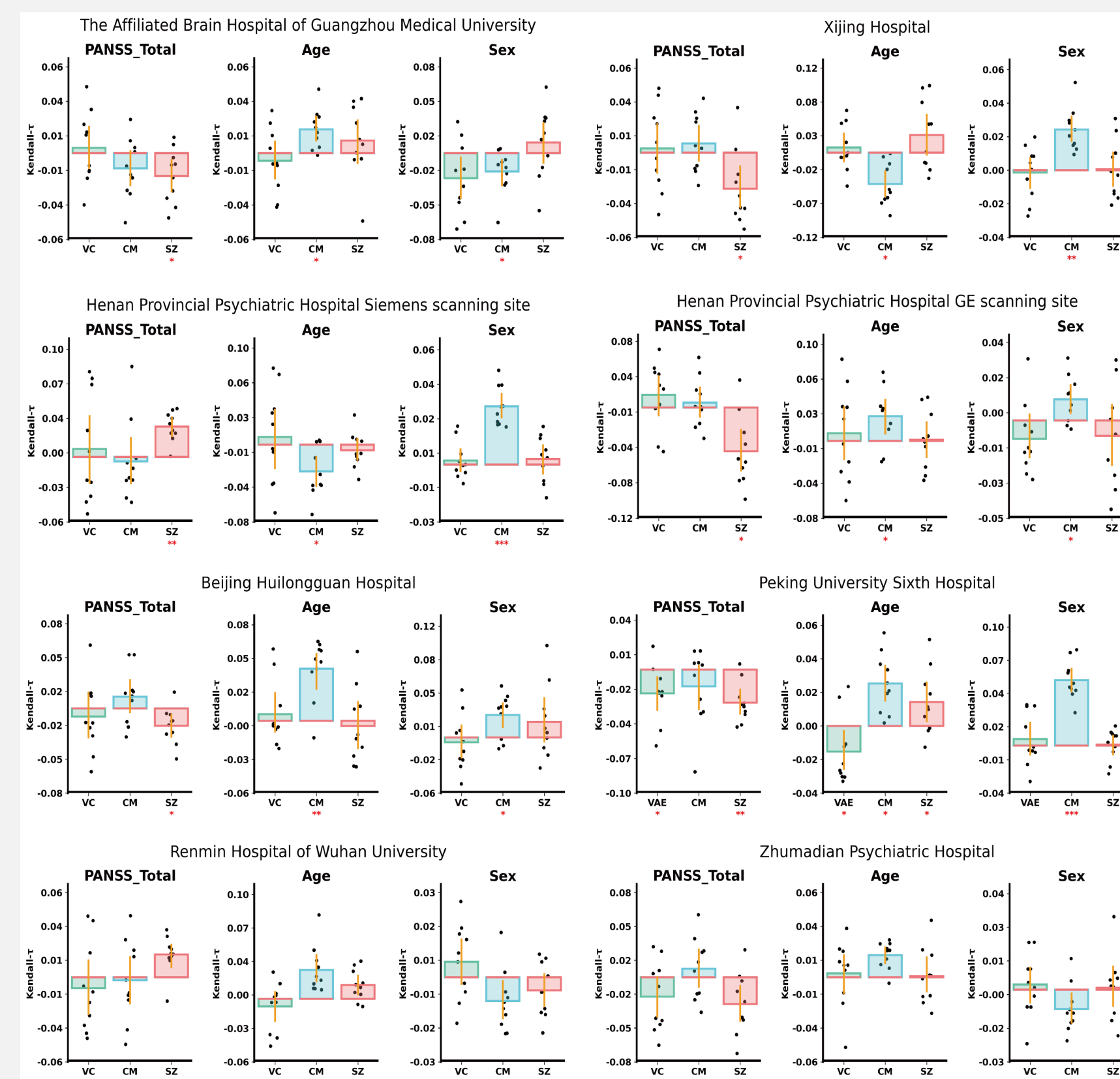
- DECODE-SZ** (Dual Encoder Contrastive Decoding for Schizophrenia) Model
- Combines contrastive learning, 3D convolutional neural network (3D CNN) architecture and variational autoencoder (VAE) structures to achieve exceptional generalizability while preserving individual specificity.



- Fig. 1.** Overview of the study workflow. (D) RSA analysis of the feature vectors S and C extracted by the DECODE-SZ, evaluating their associations with clinical PANSS_Total scores and demographic information (age, sex, education).

Results

Fig. 2. Representational Similarity Analysis (RSA) results.



- Validation across **8** independent sites was conducted through leave-one-site-out cross-validation strategy. Ensuring each site's evaluation served as a rigorous test of cross-site generalizability.

- DECODE-SZ model reduces total parameters by **73%** compared to the **previous best model**, while **improving performance**. It effectively distinguished schizophrenia-specific variations from common variations ($|\tau| > 0.025$, $p < 0.01$).

- Overlap heatmap of schizophrenia-specific neuroanatomical variation regions across 8 sites calculated by Jacobian determinant.

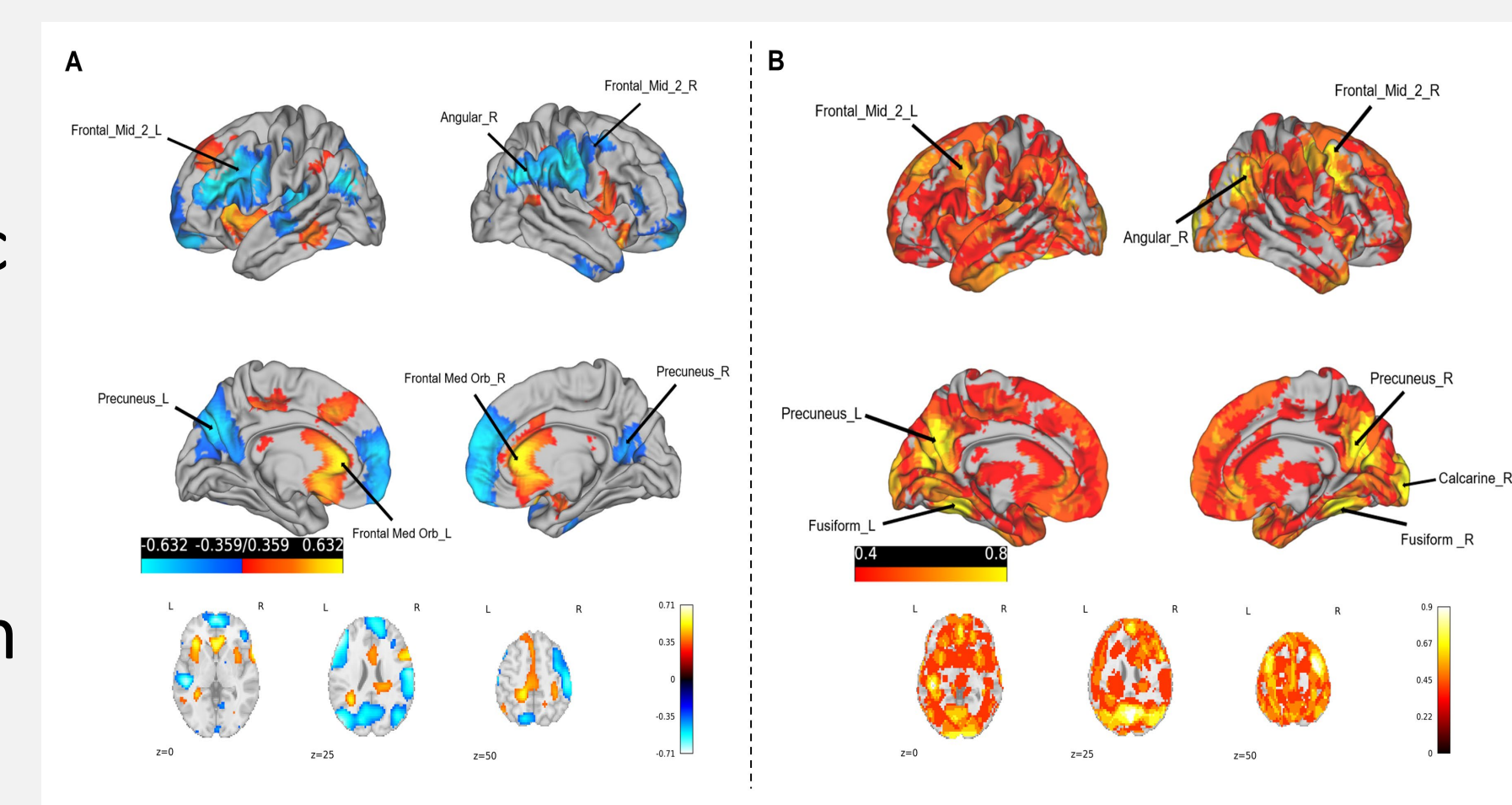


Fig. 3. Schizophrenia-specific neuroanatomical variation regions.

Conclusions

- This is the **first study** to explore schizophrenia-specific neuroanatomical variations using a contrastive learning strategy combined with a dual-encoder architecture within VAE framework.
- DECODE-SZ model separate schizophrenia-specific neuroanatomical variations, validated on **8** entirely independent sites, **yielding consistent results across all sites**.
- DECODE-SZ model reduces total parameters by **73%** compared to the **previous best model**, while **improving performance**.
- Finally, we explored schizophrenia-specific consistent variation regions across the 8 sites.

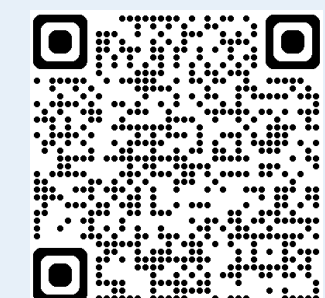
References

- Velligan DI, Rao S. The Epidemiology and Global Burden of Schizophrenia. *J Clin Psychiatry*. 2023;84(1):MS21078COM5.
- Marder SR, Cannon TD. Schizophrenia. *N Engl J Med*. 2019;381(18):1753-1761.
- Jauhar S, Johnstone M, McKenna PJ. Schizophrenia. *Lancet*. 2022;399(10323):473-486.
- Aglinskas A, Hartshorne JK, Anzellotti S. Contrastive machine learning reveals the structure of neuroanatomical variation within autism. *Science*. 2022;376(6597):1070-1074.
- Kingma DP, Welling M. Auto-encoding variational Bayes. In: *International Conference on Learning Representations*. 2014.
- Tenenbaum JB, de Silva V, Langford JC. A global geometric framework for nonlinear dimensionality reduction. *Science*. 2000;290(5500):2319-2323.

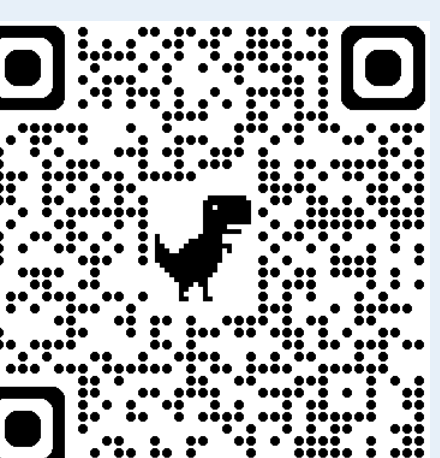
Acknowledgements

This work is funded by Natural Science Foundation of China; Beijing Municipal Science and Technology Commission, Administrative Commission of Zhongguancun Science Park >Beijing Nova Program

Poster



Author Info



Contact

dylan.lindu@gmail.com