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Paper under double-blind review

ABSTRACT

Analyzing the intricate geometry of the cerebral cortex is fundamental to understanding the neuroanatomical basis of individual traits. However, the fundamental conflict between powerful, grid-dependent architectures like Transformers and the irregular cortical mesh has forced a compromise: the distortive practice of spherical projection. This act of simplification discards the geometric subtleties we aim to study. To resolve this foundational data-architecture mismatch, we propose the Native Cortical Surface Representation Learning Model (NCS-RL), an end-to-end framework that reshapes the data to fit the model, not the other way around. Its first component, the Canonical Surface Generator, creates a shared, regular topological grid across all subjects. Onto this grid, it precisely maps each individual's unique geometric details via diffeomorphic deformation. This single process achieves three critical goals simultaneously: it establishes a principled tokenization for Transformers, resolves inter-subject correspondence, and yields a spectrum of anatomically faithful variations for data augmentation. With the cortical surface now represented as a structured and geometrically rich sequence of tokens, the second component, the Cortical Transformer, is designed to interpret it. Its dual-pathway architecture is built to leverage this new data structure: one pathway uses our novel Adjacency Self-Attention to learn fine-grained local geometric patterns directly from the native surface priors, while the other captures global context. A gated mechanism then fuses these pathways, forging a holistic representation that understands not just what a cortical region is, but precisely how it is shaped. Moreover, to ensure geometric fidelity, our model was pre-trained on over 5,000 subjects from the ABCD, HCP, and ABIDE datasets. Our method demonstrates state-of-the-art performance in experiments and ablation studies, including phenotype prediction and functional map regression. Our implementation is available in the supplementary material and will be released.

1 INTRODUCTION

The geometric form of the cerebral cortex, characterized by its intricate folding patterns, serves as a ‘morphological fingerprint’ linking neuro-anatomy to individual traits (e.g. behavioral characteristics, cognitive abilities, or functional MRI signal variations) Dale et al. (1999). However, deciphering this link is complex, hindered by the challenge of analyzing high-dimensional, noisy, and topologically irregular cortical surface meshes. This irregularity complicates the establishment of meaningful correspondence across subjects, and crucially poses a major challenge to the application of powerful deep learning architectures like Transformers Han et al. (2022), which thrive on structured, grid-like data. Developing a framework that can operate directly on cortical surfaces while resolving this irregularity is paramount for unlocking the information implicit in brain anatomy.

A major line of research prioritizes geometric fidelity by operating directly on native cortical meshes. While existing methods in this vein, such as Yang et al. (2024) convolutions, successfully extract local geometric features, their local receptive fields prevent them from capturing the holistic patterns of the cortex. However, deploying powerful global architectures, the natural solution, needs a universal topological blueprint that yields tokens comparable both within and across subjects. And the sheer diversity of cortical geometry makes tokenization on raw surface impossible Fawaz et al. (2021). For instance, the fundamentally incompatible structures of different anatomical regions within the same brain—like the elongated precentral gyrus and the complexly folded calcarine sulcus, cannot

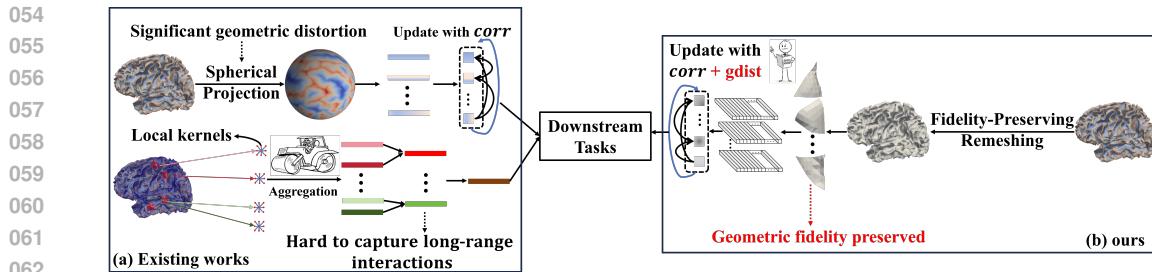


Figure 1: An illustration of the deep-learning based cortical analysis method workflow.

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be reconciled into a uniform patch topology Lohmann et al. (2008). This reveals the limitation of existing native-space methods: while anatomically precise, their nature as local feature aggregators precludes the extraction of higher-level semantic information. Overcoming this is our motivation.

To circumvent these tokenization and correspondence challenges, sphere-based methods became the dominant paradigm Zhao et al. (2023); Dahan et al. (2022b;a). By mapping cortices onto a common spherical domain, they establish a standardized topology that allows cortical data to be processed by architectures originally designed for images and grids, such as Vision Transformers. However, this solution is a critical compromise. The projection introduces non-linear geometric distortions, forcing models to learn from a surrogate, rather than the true, anatomy Bazinet et al. (2025). Crucially, this process decouples morphological features from their native geometric context. Critical measures like sulcal depth is preserved as a scalar value, but it loses its meaning as a descriptor of a real three-dimensional shape. Therefore, this work is dedicated to creating a Transformer that operates on the native cortical surface, free from the distortions of spherical projections.

To resolve this compromise between geometric fidelity and architectural power, we propose the **Native Cortical Surface Representation Learning Model** (NCS-RL). Our model operates directly on the native cortical surface, aiming to achieve high geometric fidelity and cross-subject comparability through a novel two-stage process, as illustrated in Fig. 1(b). The cornerstone of our model is the **Canonical Surface Generator**, a module designed to resolve the tokenization challenge. Adopting a template-first, personalization-second strategy, it first establishes a canonical topological foundation. Next, it precisely maps the fine-grained geometric details of each subject onto this regularized mesh. This process achieves two critical goals: it ensures high geometric fidelity while simultaneously yielding anatomically plausible samples for data augmentation. With the cortical surface now represented as a geometrically-rich sequence of tokens, the challenge is to interpret this data. Standard Transformer is geometry-agnostic. To overcome this, our **Cortical Transformer** employs a dual-pathway architecture. It runs our proposed Adjacency Self-Attention in parallel with standard self-attention to capture local geometric patterns and global semantic relationships, respectively. To ensure these pathways remain complementary, a mechanism for feature disentanglement and a subsequent gated fusion adaptively merge them to specialize the representation for the downstream task. Ultimately, this architecture learns not just what a cortical region is, but how it is intricately shaped.

In summary, our main contributions are as follows:

- We propose the Native Cortical Surface Representation Learning Model, an end-to-end framework that overcomes the core challenges of inter-subject comparability and geometric fidelity, paving the way for a new paradigm of large-scale, hypothesis-free discovery on cortical surfaces.
- We propose the Canonical Surface Generator, which decouples topological standardization from geometric personalization to simultaneously achieve robust inter-subject comparability and provide a principled source of anatomically plausible augmentation.
- We introduce the Cortical Transformer, whose expert-guided, dual-pathway architecture simultaneously learns geometric and semantic features to forge a link between neuroanatomy and cognitive or behavioral traits.
- Our method demonstrates state-of-the-art performance in experiments across phenotype prediction and functional activation map regression tasks.

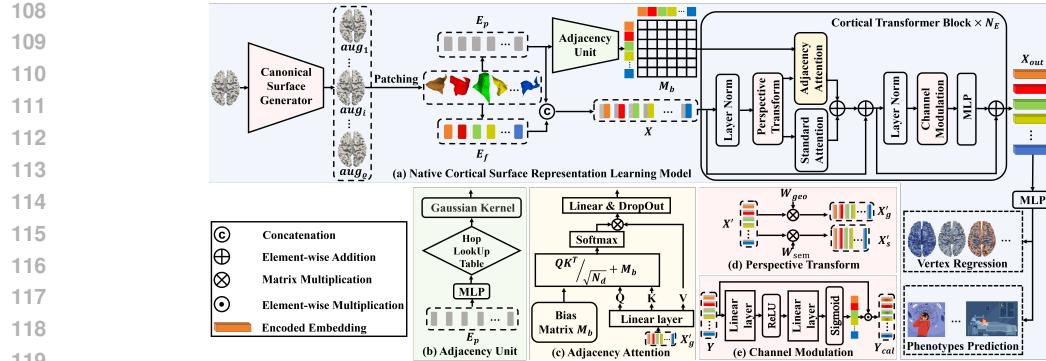


Figure 2: An overview of our framework.

2 METHOD

2.1 PRELIMINARIES AND OVERVIEW

Our NCS-RL employs a Masked Auto-Encoder (MAE) framework for brain mesh analysis (Fig. 2). Its Canonical Surface Generator (CSG) first normalizes each input mesh into a canonical form and creates augmentations. During pre-training, our Transformer learns to reconstruct the canonical mesh from masked patches, leveraging these augmentations for feature learning. For downstream tasks, we discard the decoder and use the pre-trained encoder to extract features from the canonical mesh for a final MLP predictor.

2.2 CANONICAL SURFACE GENERATOR

As illustrated in Fig. 3, our Canonical Surface Generator generates training samples through a three-stage pipeline that enforces a common topology while preserving subject-specific geometry.

2.2.1 SIMPLIFICATION

We begin by simplifying a group-average surface to create a base mesh with a standardized topology. This base mesh acts as the uniform topological foundation for all subjects.

The process starts with a cohort of white matter surfaces, $C = \{I_i = (P_i, F)\}$, which are registered by Glasser et al. (2013), defined by the common face set F and the vertex coordinate set P_i . From this cohort, we compute a group-average template, $I_T = \{P_T, F\}$, by averaging P_i . To preserve the points with significant anatomical features de Vareilles et al. (2023), we employ Fernández-Pena et al. (2023) to extract its cortical skeleton. This skeleton is represented by a vertex set, P_{able} , which corresponds to the sulcal fundi and gyral crowns. Based on these anatomical landmarks, we then construct a continuous field that quantifies the anatomical importance across the mesh surface.

To guide the simplification process, we introduce an adaptive cost function, $Cost(v)$, which balances geometric stability and anatomical importance of a vertex v :

$$Cost(v) = 0.5 \cdot C'_{geom}(v) + 0.5 \cdot C'_{anat}(v) \quad (1)$$

where C'_{geom} and C'_{anat} are the geometric and anatomical cost components, respectively. Each cost term is normalized with percentile ranking. The anatomical cost, $C_{anat}(v)$, is defined based on the geodesic distance of v to the cortical skeleton P_{able} . We invert the ranking so that vertices closer to the skeleton receive a higher cost:

$$C_{anat}(v) = 1 - \text{PercentileRank}(\text{dist}_{geo}(v, P_{able})) \quad (2)$$

Here, $\text{dist}_{geo}(v, P_{able})$ is the shortest geodesic distance from v to any vertex in the skeleton.

The geometric cost, $C_{geom}(v)$, ensures topological stability by penalizing distortion Lee et al. (1998). It is the ratio of the 1-ring neighborhood area after and before the removal of vertex v :

$$C_{geom}(v) = \frac{A_{new}(v)}{A_{old}(v)} \quad (3)$$

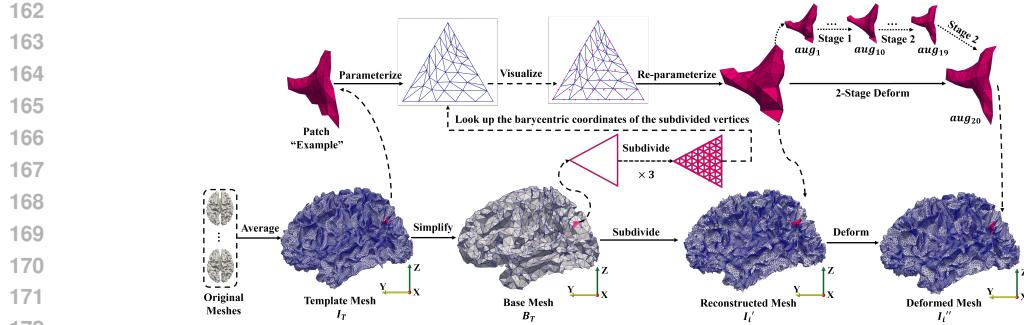


Figure 3: Illustration of Canonical Surface Generator.

To combine these two, before their summation, the raw C_{anat} and C_{geom} values are independently converted to their percentile ranks (C'_{anat} and C'_{geom}), mapping them to a uniform $[0, 1]$ interval.

With the cost function, we employ an iterative simplification algorithm described in Lee et al. (1998). Each iteration removes a vertex with the minimum cost. To re-triangulate the resulting hole, the vertex's neighborhood is projected onto a 2-D plane using a conformal map, and the new faces are generated with a constrained Delaunay triangulation. Concurrently, the global parameterization map Π is updated by storing the barycentric coordinates of the removed vertex relative to these new faces, thus preserving a continuous mapping to the base mesh. The iterative algorithm is repeated until a target of $N_p = 1024$ faces is reached, which is chosen to balance geometric fidelity with the computational demands of model training. After that, we can get the base mesh B_T .

2.2.2 SUBDIVISION

Next, for each subject, we reconstruct a high-resolution surface $I'_i = (P'_i, F')$ that shares a common topology derived from the base mesh B_T while preserving the subject's unique geometry.

To ensure the reconstructed topology is capable to represent the geometric details of I_T , we determine the subdivision level d as the smallest integer satisfying $|P_{\text{sub}}(d)| \geq |P_T|$. Here, $|P_{\text{sub}}(d)|$ is the vertex count resulting from d iterations of 1-to-4 Loop subdivision on the base mesh topology, and $|P_T|$ is the vertex count of the template I_T . With the subdivision level d established, we generate a common high-resolution connectivity graph F' . This is achieved by applying d iterations of a 1-to-4 Loop subdivision scheme to the connectivity of B_T . This operation is topological, refining the graph without computing new 3-D vertex positions. The result is a uniform face set F' that is shared by all reconstructed surfaces, guaranteeing their topological equivalence.

For recovering each subject i 's detail, we individualize the base mesh, $B_i = (P_{B,i}, F_T)$, where the vertex set $P_{B,i}$ is populated by extracting the corresponding vertices from the subject's original surface I_i via $I_{B,i} = \{v_k \in P_i \mid k \in \mathcal{K}_{base}\}$, with \mathcal{K}_{base} being the vertex indices from the original template preserved in B_T . This individualized base mesh B_i establishes the direct correspondence between the 2-D parameter domain and the vertex indices of the subject's original mesh I_i . Following Lee et al. (1998), we determine the spatial coordinates of the interpolated vertices in F' . Specifically, for each interpolated vertex, we first compute its 2-D coordinate, q_s , as the midpoint of its parents' coordinates. We then locate its enclosing triangle within the 2-D parameterization established by Π , which allows us to identify the corresponding three vertices, $\{v_{j,i}, v_{k,i}, v_{l,i}\} \subset V_i$, on the subject's original mesh. Next, we calculate the barycentric weights (α, β, γ) of q_s with respect to this triangle's vertices. These weights are then used to interpolate the 3-D position:

$$v'_{s,i} = \alpha v_{j,i} + \beta v_{k,i} + \gamma v_{l,i} \quad (4)$$

The resulting collection of vertices forms the subject-specific vertex set P'_i . Finally, we assemble the reconstructed mesh $I'_i = (P'_i, F')$ by combining P'_i with the common face set F' .

2.2.3 DEFORMATION

The subdivision, while establishing topological consistency, yields a surface I'_i that filters the high-frequency geometric details of I_i . To address this, We model the deformation from I'_i to I_i as a

216 geodesic flow within Ceritoglu et al. (2013), implemented using Bône et al. (2018). This deformation
 217 is driven by optimizing a time-varying velocity field that minimizes the energy functional:
 218

$$219 \quad O[v] = \int_0^1 \|v(t)\|_L^2 dt + \frac{1}{\sigma_d^2} \text{Dist}(\phi_v(1, I'_i), I_i) \quad (5)$$

221 To capture complex cortical features, we employ the Varifold distance for the data attachment term,
 222 $\text{Dist}(\cdot, \cdot)$. Unlike point-based metrics, the Varifold distance is sensitive to both face position and
 223 orientation, which is critical for aligning the sharp crests of gyri and the deep fundi of sulci.
 224

225 To ensure convergence, we implemented a two-stage optimization strategy. Specifically, the process
 226 begins with a small deformation kernel, $\sigma_{v,1} = L_{avg}(I'_i)$, where $L_{avg}(I'_i)$ is the average mesh
 227 edge length, and then transitions to a larger kernel ($\sigma_{v,2} = 10 \times L_{avg}(I'_i)$) for local refinement. A
 228 constant data fidelity was used throughout both stages, with the noise standard deviation term in the
 229 energy functional set to $\sigma_d = 0.001$. The optimization is performed using L-BFGS and terminates
 230 on energy convergence ($\epsilon = 10^{-4}$) or after 200 iterations. The output for each subject is I''_i that
 231 serves as a high-fidelity approximation of the original I_i . We sample $\varrho = 20$ time-points along the
 232 deformation path to generate a sequence of topologically-identical surfaces $\{aug_i\}$. This sequence,
 233 capturing a plausible anatomical evolution, constitutes our augmented dataset for pre-training.
 234

235 2.3 CORTICAL TRANSFORMER

236 2.3.1 SURFACE EMBEDDING

237 Constrained by GPU memory and the computational complexity of the self-attention mechanism,
 238 we use the base faces of the template surface B_T (from Section 2.2.1) to form our encoding units,
 239 which we refer to as patches. This design ensures that each patch consistently contains a fixed set
 240 of $N_v = 45$ vertices and $N_f = 64$ faces. Each patch is then encoded via two components: a feature
 241 embedding and a positional embedding. For the feature embedding, to enrich the representation and
 242 enhance its resolution, we define features at the face level. Specifically, for each face within the
 243 j -th patch, we compute a 10-dimensional feature vector, $z_{j,i}$ (face area, face normal vector, three
 244 internal angles, and three inner products between the face normal and the normals of its vertices).
 245 For the positional embedding, we use the centroid of the patch, c_j , to uniquely identify its spatial lo-
 246 cation. Finally, the feature and positional embeddings for the j -th patch are generated by multilayer
 247 perceptrons (MLP), formulated as $E_f = \text{MLP}(\{z_{j,i}\}_{i=1}^{N_f})$ and $E_p = \text{MLP}(c_j)$.
 248

249 2.3.2 ADJACENCY UNIT

250 The Adjacency Unit is designed to generate a hop bias matrix, denoted as $M_b \in \mathbb{R}^{N_p \times N_p}$, from the
 251 spatial coordinates of visible patches. This process begins with a given batch of center centroids
 252 $\{c_j\}_{j=1}^{N_p}$ for visible patches, where a pre-trained and frozen Locator layer is first used to determine
 253 an ID for each patch. This can be understood as the locator mapping each patch to a predefined
 254 standard location. Following this, the pairwise hop counts between the input patches are retrieved
 255 from a hop look-up table, which stores the hop counts between any two standard locations. Finally,
 256 a parameterized Gaussian function, $a \cdot \exp(-x^2/(2\delta^2)) + b$, is used to map these hop counts (x) to
 257 their final values, which constitute the attention bias matrix M_b . The amplitude a , standard deviation
 258 δ , and offset b are learnable parameters. For cases with a hop count of -1 , this value is replaced by
 259 a large number, causing the resulting bias to approach b and thus applying a strong negative bias.
 260

261 2.3.3 CORTICAL TRANSFORMER BLOCK

262 We introduce the Cortical Transformer Block to collaboratively process both global semantic corre-
 263 lations and local geometric structures. Its architecture (Fig. 2(a)) integrates standard and Adjacency
 264 Self-Attention, a Perspective Transform Layer, a Channel Modulation Layer, and an MLP.
 265

266 Let the input embedding be $X \in \mathbb{R}^{N_p \times N_d}$, representing a set of N_p tokens. Initially, the input X
 267 undergoes a first Layer Normalization, yielding X' . This normalized feature is then fed into the
 268 Perspective Transform Layer, which decouples the representation into two specialized perspectives
 269 using two learnable weight matrices: $X'_s = X'W_{sem}^T$ and $X'_g = X'W_{geo}^T$ (Fig. 2(d)). Here, X'_s
 is the semantic perspective, optimized for capturing high-level content, while X'_g is the geometric

270 perspective, optimized for perceiving spatial structures. Subsequently, X'_s and X'_g are channeled
 271 into their respective customized attention pathways. The standard self-attention takes X'_s as input to
 272 compute global, content-based dependencies among all tokens, producing X''_s .
 273

274 The Adjacency Self-Attention receives X'_g and incorporates the bias matrix M_b to compute attention
 275 with a geometric prior. As shown in Fig. 2(c), X'_g is linearly transformed into Query, Key, and
 276 Value matrices, which are then reshaped to form h attention heads: $\{Q_i\}_{i=1}^h, \{K_i\}_{i=1}^h, \{V_i\}_{i=1}^h$.
 277 Incorporating M_b , the attention output for the i -th head is calculated as:

$$278 \quad \text{Attention}_i = \text{softmax} \left(\frac{Q_i K_i^T}{\sqrt{d_k}} + B \right) V_i \quad (6)$$

280 The outputs from all heads are concatenated and passed through a linear projection layer to yield
 281 the final output, X''_g . For the outputs of the two pathways, X''_s and X''_g , we employ a learnable gate
 282 parameter, w_{gate} , to dynamically compute their fusion weights: $w_{geo} = \varsigma \cdot \text{Sigmoid}(w_{gate})$, $w_{std} =$
 283 $1 - w_{geo}$ where ς is a hyperparameter controlling the maximum influence of the geometric pathway.
 284 The fused feature representation is then $X_{mix} = w_{std}X''_s + w_{geo}X''_g$. Notably, this fusion is applied
 285 to patch tokens; the cls token’s output is derived solely from X''_s to preserve the purity of its global
 286 perspective. The fused attention result, X_{mix} , is added to the block’s input X via a first residual
 287 connection, followed by a second Layer Normalization, resulting in $Y = \text{LayerNorm}(X + X_{mix})$.
 288

289 The tensor Y is fed into Channel Modulation layer for feature recalibration. As illustrated in
 290 Fig. 2(e), each token passes through a two-layer MLP with a bottleneck structure and a Sigmoid
 291 function to generate the modulation weights W_{mod} . The calibrated output Y_{cal} is computed via
 292 element-wise multiplication as: $Y_{\text{cal}} = Y \odot W_{\text{mod}}$. To dynamically transform each token, the refined
 293 tensor Y_{cal} is passed through an MLP. Finally, the output of the MLP is added to the sub-layer’s initial
 294 input, Y , via a residual connection to produce the block’s final output, $X_{out} = Y + \text{MLP}(Y_{\text{cal}})$.
 295

296 3 EXPERIMENTS

297 3.1 EXPERIMENTAL SETUP

299 3.1.1 DATASETS AND METRICS.

301 **Adolescent Brain Cognitive Development (ABCD)** consists of MRI scans from over 11,500 chil-
 302 dren aged 9-10 years across the USA. From this dataset, we utilized 4,000 subjects for pre-training.

303 **Human Connectome Project (HCP)** contains brain MRI scans from 1,200 healthy young adults,
 304 preprocessed using the Glasser et al. (2013). On this dataset, we organized two experiments:
 305 phenotype prediction and functional activation map prediction. For **phenotype prediction**, we
 306 selected four phenotypes: VSPLIT_TC (VTC), PercStress_Unadj (PS), AngAggr_Unadj (AA),
 307 Strength_Unadj (STR) from 805 subjects, randomly split into training ($n = 643$) and testing
 308 ($n = 162$) sets; following He et al. (2024), predictions were evaluated using the Pearson Corre-
 309 lation Coefficient (PCC) and Root Mean Square Error (RMSE). For **functional activation map**
 310 **regression**, we targeted the Work Memory (WM) task, averaged the fMRI signal across time to
 311 create a 3D activation map, and projected it onto the surface; following Ellis & Aizenberg (2022),
 312 we evaluated spatial similarity using PCC and prediction error using Mean Absolute Error (MAE).
 313

314 **Autism Brain Imaging Data Exchange (ABIDE)** is a dataset of 1,112 individuals, from which
 315 we selected subjects with available Autism Diagnostic Observation Schedule (ADOS) scores. Our
 316 preprocessing involved feature extraction and feature harmonization to mitigate batch effects. The
 317 dataset was partitioned into training and validation sets by acquisition site. Following Moradi et al.
 318 (2017), we evaluated model performance via Leave-One-Site-Out, using the PCC, MAE, and Q^2 .
 319

320 3.1.2 IMPLEMENTATION DETAILS.

321 In both pre-training and downstream tasks, we employ the AdamW optimizer with a weight decay
 322 of 0.05 and a batch size of 20. We utilized a cosine learning rate schedule with a 10-epoch warmup
 323 period. The implementation is available in supplement, and we will release the codebase on GitHub.
 While hemispheres were analyzed independently for most tasks, their features were concatenated
 for ADOS prediction to capture the integrated neurological signatures of Autism. In our effort to

324 Table 1: Phenotype prediction results. Best and Second best results are highlighted and underlined.
 325 B, L, and R denote predict with the bilateral, left, and right cortical surfaces, respectively.
 326

METHOD	Side	VTC	PS	AA	STR
RMSE					
Dahan et al. (2022a)	B	0.169 \pm 0.028	0.157 \pm 0.025	0.232 \pm 0.016	0.116 \pm 0.015
Li et al. (2021)	B	0.201 \pm 0.360	0.195 \pm 0.028	0.309 \pm 0.034	0.133 \pm 0.026
Chen et al. (2022)	B	0.204 \pm 0.290	0.197 \pm 0.034	0.303 \pm 0.025	0.129 \pm 0.021
Ooi et al. (2022)	B	0.187 \pm 0.031	0.208 \pm 0.039	0.311 \pm 0.027	0.125 \pm 0.025
He et al. (2022)	B	0.195 \pm 0.033	0.193 \pm 0.031	0.291 \pm 0.038	0.136 \pm 0.029
He et al. (2024)	B	0.183 \pm 0.025	0.171 \pm 0.029	0.228 \pm 0.021	0.117 \pm 0.017
Yang et al. (2024)	R	0.184 \pm 0.032	0.195 \pm 0.051	0.255 \pm 0.048	0.115 \pm 0.029
	L	0.197 \pm 0.040	0.183 \pm 0.038	0.289 \pm 0.044	0.106 \pm 0.037
Liang et al. (2022)	R	0.176 \pm 0.051	0.165 \pm 0.029	0.259 \pm 0.055	0.110 \pm 0.018
	L	<u>0.163 \pm 0.047</u>	0.159 \pm 0.030	0.240 \pm 0.027	0.113 \pm 0.021
ours	R	<u>0.166\pm0.023</u>	0.147\pm0.036	<u>0.225 \pm 0.019</u>	0.094\pm0.021
	L	0.159\pm0.014	0.150 \pm 0.031	0.218\pm0.018	0.101 \pm 0.017
PCC					
Dahan et al. (2022a)	B	0.091 \pm 0.206	0.067 \pm 0.128	0.101 \pm 0.122	0.130 \pm 0.162
Li et al. (2021)	B	0.102 \pm 0.241	0.056 \pm 0.307	0.071 \pm 0.255	0.113 \pm 0.227
Chen et al. (2022)	B	0.098 \pm 0.315	0.061 \pm 0.324	0.088 \pm 0.262	0.131 \pm 0.274
Ooi et al. (2022)	B	0.111 \pm 0.372	0.053 \pm 0.333	0.086 \pm 0.349	0.122 \pm 0.305
He et al. (2022)	B	0.096 \pm 0.262	0.068 \pm 0.250	0.092 \pm 0.242	0.109 \pm 0.259
He et al. (2024)	B	0.122 \pm 0.227	0.073 \pm 0.291	0.105 \pm 0.273	0.133 \pm 0.264
Yang et al. (2024)	R	0.009 \pm 0.329	0.071 \pm 0.325	0.103 \pm 0.325	0.070 \pm 0.328
	L	0.011 \pm 0.320	<u>0.081\pm0.320</u>	0.054 \pm 0.328	0.082 \pm 0.327
Liang et al. (2022)	R	0.172\pm0.320	0.068 \pm 0.327	-0.079 \pm 0.326	0.098 \pm 0.182
	L	0.118 \pm 0.324	-0.238 \pm 0.312	0.108\pm0.325	0.088 \pm 0.328
ours	R	<u>0.125\pm0.122</u>	0.076 \pm 0.171	<u>0.105\pm0.126</u>	0.119 \pm 0.209
	L	0.113 \pm 0.209	0.081\pm0.207	0.101 \pm 0.152	0.135\pm0.197

354
 355 establish a fair comparison, we faced a challenge: a scarcity of methods from the last three years that
 356 are open-source, relevant to our task, and verifiable with available data. Therefore, we feature only
 357 three comparable methods in our experiments on surface fMRI regression and ADOS prediction.
 358

3.2 PHENOTYPE PREDICTION

361 For phenotype prediction, our method was benchmarked against state-of-the-art approaches (Table
 362 1 Upper for RMSE, Lower for PCC). In terms of RMSE, our model achieves top-tier performance,
 363 ranking first or second in 7 of 8 hemisphere-based predictions. For instance, on the Strength (STR)
 364 task, our model achieves an RMSE of 0.094 (R), outperforming the Liang et al. (2022) baseline
 365 (0.110). Regarding PCC, our model’s primary advantage is its robustness. Unlike Liang et al.
 366 (2022), which exhibits high volatility and learns erroneous negative correlations on certain tasks
 367 (e.g., PS, AA), our model consistently maintains positive correlations across all phenotypes. This
 368 avoidance of directionally incorrect predictions underscores its stability and reliability. We attribute
 369 this enhanced performance to two core architectural advantages. First, by outperforming Dahan et al.
 370 (2022a), our model confirms the importance of operating on the native cortical mesh, which avoids
 371 the geometric distortions of spherical projections. Second, its superiority over Liang et al. (2022)
 372 demonstrates that our bi-path attention design, by integrating multi-scale geometric information, is
 373 crucial for preventing overfitting to spurious correlations and thus enhancing prediction stability.
 374

3.3 FMRI ACTIVATION REGRESSION

375 As shown in Table 2, our method achieves the highest spatial similarity, with a PCC of 0.562 (R).
 376 Furthermore, our method yields the lowest prediction error, with an MAE of 0.075 (R). To visualize
 377 the result, we randomly select a subject and display their ground truth and predicted fMRI signal

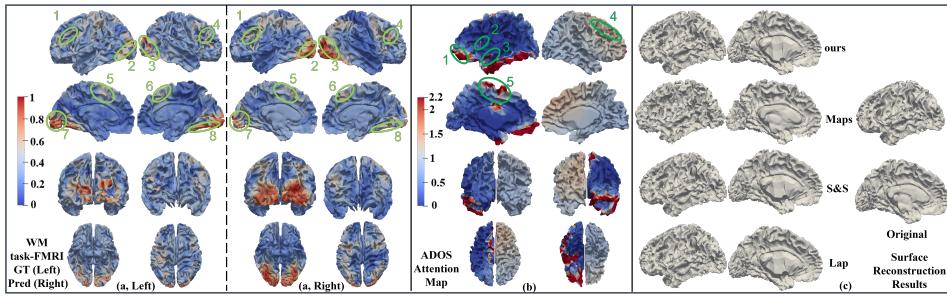


Figure 4: Visualizations of (a) FMRI activation map regression, (b) ADOS prediction model’s attention map, and (c) the surface reconstruction results.

Table 2: Results of FMRI activation map regression. Best results are highlighted. B, L, and R denote predictions made using the bilateral, left, and right cortical surfaces, respectively.

Method	Side	PCC	MAE
Ellis & Aizenberg (2022)	B	0.550	-
Yang et al. (2024)	R	0.533 ± 0.009	0.078 ± 0.04
	L	0.527 ± 0.007	0.079 ± 0.03
Liang et al. (2022)	R	0.523 ± 0.012	0.079 ± 0.06
	L	0.514 ± 0.013	0.081 ± 0.04
ours	R	0.562 ± 0.007	0.075 ± 0.003
	L	0.537 ± 0.005	0.078 ± 0.001

intensities in Fig. 4(a) (left and right, respectively). We also point eight regions with notably similar signal intensity distributions using light green circles: 1-the left middle frontal gyrus, 2-the left superior and lateral occipital gyri, 3-the right superior and lateral occipital gyri, 4-the right middle frontal gyrus, 5-the left paracentral lobule, 6-the right paracentral lobule, 7-the left lingual gyrus, and 8-the right lateral occipitotemporal gyrus. And these regions are components of the networks responsible for working memoryYee et al. (2010).

3.4 ADOS PREDICTION

As shown in Table. 3, our proposed method achieves a superior performance on ADOS prediction task, yielding PCC scores of 0.59 on the PITT site and 0.42 on the NYU site. A key comparison is with the linear model of Moradi et al. (2017), which reveals a classic bias-variance trade-off. While their method achieves a lower MAE by using smoothed, low-dimensional features, our end-to-end model attains a significantly higher PCC by leveraging rich, high-dimensional geometric features directly from the cortical surface to capture more complex biological patterns. The positive Q^2 scores (0.18 and 0.26) decisively show the superiority of our low-bias strategy, indicating that the model has genuine predictive power, unlike other baselines which fail to generalize ($Q^2 < 0$). This confirms that the significant gains in capturing the correct biological trend outweigh the moderately higher prediction variance. To investigate the neurobiological basis of these predictions, we visualized the attention map from the final layer of the fine-tuned model (shown in Fig. 4(b)). We also point out five important regions (colored in red, 1-left orbital gyrus, 2-left inferior frontal gyrus, 3-left superior temporal gyrus, 4-Right superior frontal gyrus, 5-Central anterior gyrus) with dark green circle, which are consistent with well-established Autism Spectrum Disorder-related biomarkersJacobson et al. (1988); Bauman (1991); Barnea-Goraly et al. (2004).

3.5 VALIDATE THE ANATOMICAL VALIDITY OF CSG.

Results in Table 4 highlight the trade-offs between accuracy and detail fidelity among methods. Our simplification&subdivision pipeline, *S&S*, significantly improves upon the baseline Lee et al. (1998), reducing Average Surface Distance (ASD) from 1.520 to 0.773 and increasing Curvature Correlation (CC) over fourfold from 0.159 to 0.652. Other methods show limitations. While Sorkine et al. (2004) achieves the lowest ASD (0.766), its high Hausdorff Distance (HD) (10.128) indicates

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434 Table 3: Results of ADOS prediction. Best results are highlighted.
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Method	Site	PCC	MAE	Q^2
Moradi et al. (2017)	NYU	0.22	1.57	-0.04
	PITT	0.56	1.08	0.22
Yang et al. (2024)	NYU	0.06	3.62	-0.38
	PITT	0.12	3.25	-0.25
Liang et al. (2022)	NYU	0.18	3.45	-0.15
	PITT	0.29	2.89	-0.05
ours	NYU	0.42	2.81	0.18
	PITT	0.59	2.05	0.26

444 large local errors, a flaw our method mitigates (HD: 8.190). Conversely, while Lee et al. (1998)
 445 attains the best HD (7.791), it fails to capture geometric detail (CC: 0.159). In contrast, our method
 446 achieves the highest CC (0.676) while maintaining competitive HD and ASD values. This demon-
 447 strates an balance between local detail and overall accuracy, as visualized in Fig. 4(c).

448
449 Table 4: Results of surface reconstruction. The best results are highlighted.
450

Method	HD	ASD	CC
Lee et al. (1998)	7.791 ± 0.052	1.520 ± 0.011	0.159 ± 0.003
<i>S&S</i>	10.207 ± 0.061	0.773 ± 0.005	0.652 ± 0.002
Sorkine et al. (2004)	10.128 ± 0.068	0.766 ± 0.004	0.658 ± 0.003
<i>ours</i>	8.190 ± 0.049	0.813 ± 0.005	0.676 ± 0.001

456
457 3.6 DECONSTRUCTION OF THE CORTICAL TRANSFORMER.
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459 To validate our design, we conducted an ablation study for the left hemisphere WM-task prediction,
 460 with results presented in the right sub-table of Table 5. The results show a incremental benefit for
 461 each added component. Starting from the Liang et al. (2022) baseline (PCC: 0.514), adding the
 462 BA module boosts performance to 0.526, which is further improved to 0.532 with the PT module.
 463 Our model integrates these components to achieve the highest PCC of 0.537 and the lowest variance
 464 (± 0.005), confirming that each part of our architecture is essential to its superior performance.

465
466 4 CONCLUSION
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468 We propose the NCS-RL, a framework for cortical analysis. Its Canonical Surface Generator es-
 469 tablishes cross-subject correspondence and augment surface, while its Cortical Transformer uses a
 470 dual-pathway attention to fuse local geometric details with global context. Experiments validate our
 471 approach, demonstrating superior performance across multiple tasks. However, a limitation emerged
 472 in our ADOS prediction experiment: the right hemisphere’s attention map lacked the clear hotspots
 473 seen on the left (Fig. 4(b)). We attribute this to the lack of an inter-hemispheric communication
 474 mechanism in our model. Future work will therefore prioritize developing a cross-hemispheric at-
 475 tention to capture the complex signatures of neuro-developmental disorders.

476
477 Table 5: Results of deconstruction of Cortical Transformer. Best results are highlighted. MM is
478 baseline Liang et al. (2022). BA is the Bi-Path Attention. PT is the Persppective Transform Layer.
479 CM is the Channel Modulation Layer.

Method	PCC
MM	0.514 ± 0.013
MM+BA	0.526 ± 0.008
MM+BA+PT	0.532 ± 0.005
MM+BA+CM	0.527 ± 0.007
ours	0.537 ± 0.005

486 5 THE USE OF LARGE LANGUAGE MODELS STATEMENT
487488 We use it on 2 ways: correct the code, polish the writing.
489490 6 ETHICS STATEMENT
491492 This work utilizes publicly available, de-identified data from the ABCD, HCP, and ABIDE datasets.
493 Data collection for these original studies was conducted with appropriate institutional review board
494 (IRB) approval and informed consent from all participants. Our research is foundational and in-
495 tended for methodological advancement, not for clinical diagnosis.
496497 7 REPRODICIABLITY STATEMENT
498500 Our code is provided in the supplementary material and will be made publicly available on GitHub
501 upon publication. The data used are publicly available from the ABCD, HCP, and ABIDE por-
502 tals. All hyperparameters and training details required to reproduce our main results are detailed in
503 Method section and the Experimental Setup subsection.
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