

Registration of Cortical Surfaces Using Sulcal Landmarks for Group Analysis of MEG Data

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Abstract. We present a method to register individual cortical surfaces to a surface-based brain atlas or canonical template using labeled sulcal curves as landmark constraints. To map one cortex smoothly onto another, we minimize a thin-plate spline energy defined on the surface by solving the associated partial differential equations (PDEs). By using covariant derivatives in solving these PDEs, we compute the bending energy with respect to the intrinsic geometry of the 3D surface rather than evaluating it in the flattened metric of the 2D parameter space. This covariant approach greatly reduces the confounding effects of the surface parameterization on the resulting registration.

Keywords: Brain Registration; Covariant Bending Energy; Thin Plate Splines

1. Introduction

In order to study and compare cortically-constrained MEG-based maps of neural activation across multiple subjects, their cortical surfaces need to be registered. The convoluted nature and the inter-subject variability of the surfaces make registration of cortical structures a challenging problem. We present a landmark-based technique which generalizes the well known thin-plate splines to non-euclidean surfaces using a covariant PDE approach. This covariant approach generalizes the thin-plate splines to non-euclidean surfaces and greatly reduces the confounding effects of the surface parameterization on the resulting registration.

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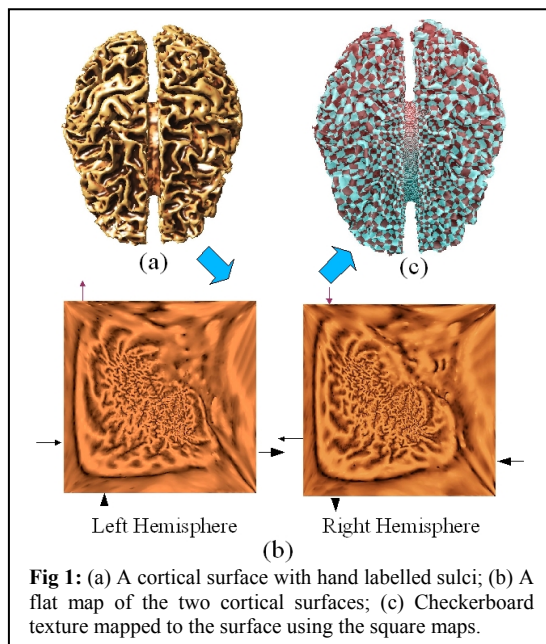
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2. Surface extraction and parameterization

We first extract a mask for the cortical surface from an MRI volume using the Brainsuite software (<http://brainsuite.usc.edu/>) [1]. The topology of the mask is corrected automatically using a graph-based approach and tessellated to produce a genus zero surface. We then use a p-harmonic functional minimization scheme [2] to map the each cortical hemisphere onto the unit square. The result is a bijective mapping between each hemisphere and the unit square in which a closed curve around corpus callosum is constrained to map to the boundary of the unit square. This allows us to calculate partial derivatives across the boundary and explicitly model continuity between the two cortical hemispheres.

We manually delineate 23 major sulci on each of the extracted cortical hemisphere meshes. Delineation is performed in accordance with a sulcal labelling protocol with established intra- and inter- rater variability [3]. We resample these sulci into 6 tag points which are spaced equidistantly according to geodesic length. These points serve as landmarks in our registration.

3. Thin-plate spline warping in the intrinsic geometry



Having parameterized the cortical surfaces of the subject and atlas, we align the coordinate systems between the subject and atlas such that a set of hand-labeled sulci are brought into register, i.e. we find a warping field which can be applied in the subject's surface parameter space to align the subject's sulcal features with those of the atlas or target brain. The alignment uses a set of interactively labeled sulci, sampled uniformly along their lengths, as a set of point constraints. To compute a smooth warping from one coordinate system to the other we use the thin-plate spline bending energy on the atlas surface as a regularizing function. Since the mapping onto the unit square will inevitably produce metric distortion relative

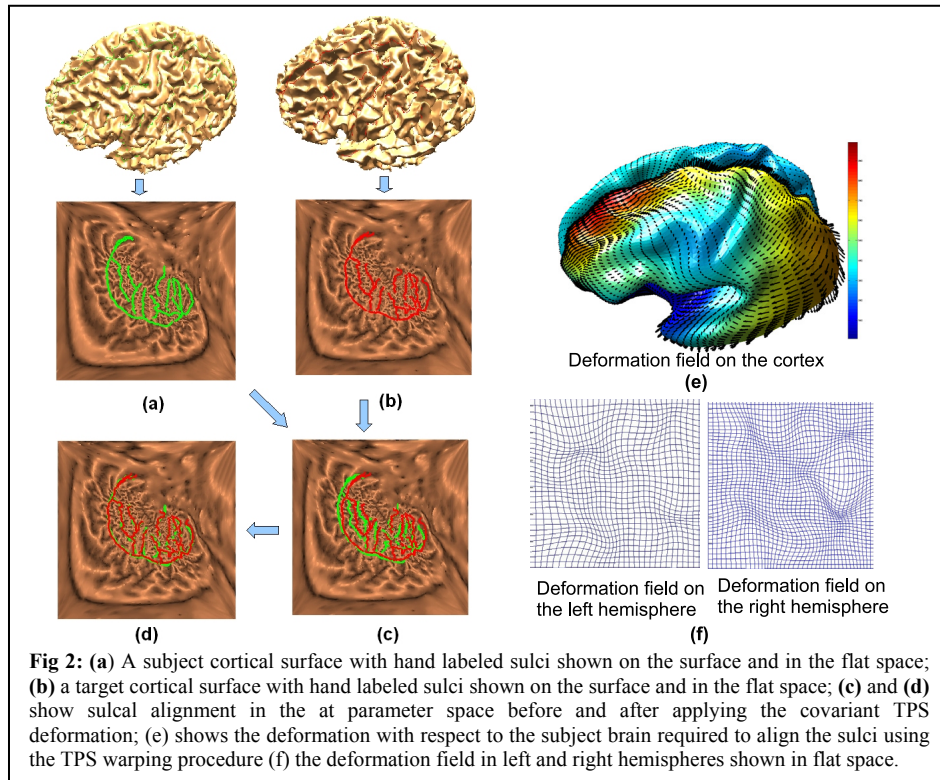
to the original surface, we use a covariant PDE approach [4] to compute the bending energy with respect to the intrinsic geometry of the 3D surface rather than the parameter space itself. To do this, we solve the biharmonic equation using covariant derivatives to obtain a thin-plate spline warp from subject to target coordinates.

The thin-plate bending energy in the Euclidean space is given by:

$$E_b = \int \left(\frac{\partial^2 \phi}{\partial x^2} \right)^2 + 2 \left(\frac{\partial^2 \phi}{\partial x \partial y} \right)^2 + \left(\frac{\partial^2 \phi}{\partial y^2} \right)^2 dx dy.$$

In the non-euclidean space, this generalizes to:

$$E_b = \int \left((\phi^j_{,11})^2 + (\sqrt{2} \phi^j_{,12})^2 + (\phi^j_{,22})^2 \right) g du dv. \quad (1.1)$$



Let \mathbf{x} denote the 3D position vector of a point on the cortical surface. Let u^1, u^2 denote the coordinates in the parameter space. The metric tensors $\{g_{ij}\}$ required in the computations of the covariant derivatives are given by

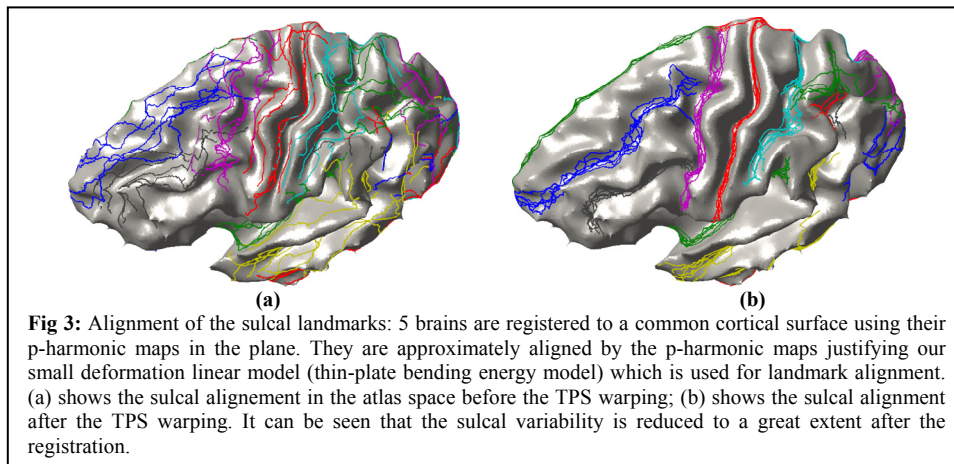
$$g_{11} = \left\| \frac{\partial \mathbf{x}}{\partial u} \right\|^2, g_{22} = \left\| \frac{\partial \mathbf{x}}{\partial v} \right\|^2, g_{12} = \left\langle \frac{\partial \mathbf{x}}{\partial u}, \frac{\partial \mathbf{x}}{\partial v} \right\rangle, g = g_{11}g_{22} - (g_{12})^2,$$

The covariant derivatives in (1.1) are then given by,

$$\phi^{\beta}_{, \sigma} = \frac{\partial \phi^{\beta}}{\partial u^{\sigma}} + \phi^{\kappa} \Gamma_{\kappa \sigma}^{\beta} \quad \text{where } \sigma, \beta, \kappa \in \{1, 2\}, \text{ and}$$

$$\phi_{,\beta\sigma}^{\zeta} = \frac{\partial \phi_{,\beta}^{\zeta}}{\partial u^{\sigma}} - \phi_{,\mu}^{\zeta} \Gamma_{\beta\sigma} + \phi_{\beta}^{\nu} \Gamma_{\nu\sigma}^{\zeta} \quad \text{where } \sigma, \beta, \zeta, \mu, \kappa \in \{1, 2\}.$$

For the purpose of discretization, the square maps for each hemisphere are resampled on a regular 256x256 grid. The spatial derivatives in $u-v$ parameters are then discretized in this space by finite differences. After discretization, the integral minimization problem reduces to a quadratic problem. We enforced the sulcal matching constraints by adding a quadratic penalty term. To illustrate the method we used one labeled brain as a target to which we registered 5 labeled surfaces using the TPS method. The results are shown in Fig. 3. Using this procedure we are then able to define a one to one correspondence between the cortical surfaces of subject and the target brain. With this correspondence we can then compute statistics across subjects from MEG activation maps to test for group effects. Standard parameteric or nonparametric tests to control for multiple hypothesis testing can then be used to control familywise error or false discovery rates [5].



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