RESEARCH STATEMENT

Ronald Lok Ming Lui (malmlui@math.harvard.edu)

The main focus of my research has been on problems in computational conformal geometry and human brain mapping. The main goal is to develop mathematical models and algorithms to effectively study the human brain structure, using conformal geometry as a tool. In Human Brain Mapping, neuroscientists commonly aim to identify structural differences between healthy and unhealthy brains, in order to detect systematic patterns of alterations in brain diseases. The main obstacle is that the human brain is a very complicated manifold with difficult geometry. It is extremely difficult for neuroscientists to analyze diseases accurately and efficiently by directly looking at the brain. This motivated me to develop tools with computational differential geometry that help to detect and analyze diseases accurately and systematically.

My research mainly contributes to the following five aspects. Firstly, I am interested in computing the best global parameterization of the brain cortical surface which aligns landmarks consistently. The goal is to create an one to one correspondence between the brain surface and the simple parameter domain such as the unit sphere or the 2D rectangle. The geometric information on the brain should be well preserved under the map. It allows us to analyze brain diseases effectively on the simple domains, instead of working on the complicated brain surfaces. Secondly, I am interested in developing algorithms to solve variational problems and compute conformal structures on general manifolds. This lets us utilize conformal invariants to analyze the brain structure and develop variational models on the brain surface. Thirdly, I am interested in the problems of tracking important anatomical features on the brain surface automatically. Landmark features such as sulcal/gyri curves on the cortical surface are important information for doctors to analyze the brain. Manual labeling of these features is inefficient and inaccurate. It becomes utmost important to develop algorithms to delineate landmark features automatically. Finally, I am interested in the problem of detecting abnormal changes on the biological organs automatically. This is an important problem in shape analysis, especially in the medical research. For example, physicians commonly need to track changes or abnormalities in biological organs or tumors in order to evaluate the effectiveness of different treatments, or monitor disease progression. By determining the conformality distortion on the surface, we can effectively locate the abnormalities on the biological organs.

In the following sections, I am going to summarize my recent research, describe briefly my ongoing projects and conclude with my future goals.

A. Summary of selected recent research

I. Optimized conformal parameterizations of cortical surfaces

Rapid development of computer technology has accelerated the acquisition and databasing of brain data. An effective way to analyze and compare brain data from multiple subjects is to map them into a canonical space while retaining the original geometric information as far as possible. Surface-based approaches often map cortical surface data to a parameter domain such as a sphere, providing a common coordinate system for data integration [1, 2, 3]. One method to do this is to conformally map cortical surfaces to the sphere. It is well known that any genus zero Riemann surface can be mapped conformally to a sphere. Cortical surface is a genus zero surface. Therefore, conformal mapping offers a convenient method to parameterize cortical surfaces without angular distortion, generating an orthogonal grid on the cortex that locally preserves the metric. Although conformal mapping preserves the local geometry well, the important anatomical features, such as the sulci landmarks, are usually not aligned consistently. Problems arise when performing statistical analysis using the parameterization, such as taking the average shape of a sequence of brains. To compare cortical surfaces more effectively, it is advantageous to adjust the conformal parameterizations to match consistent anatomical features

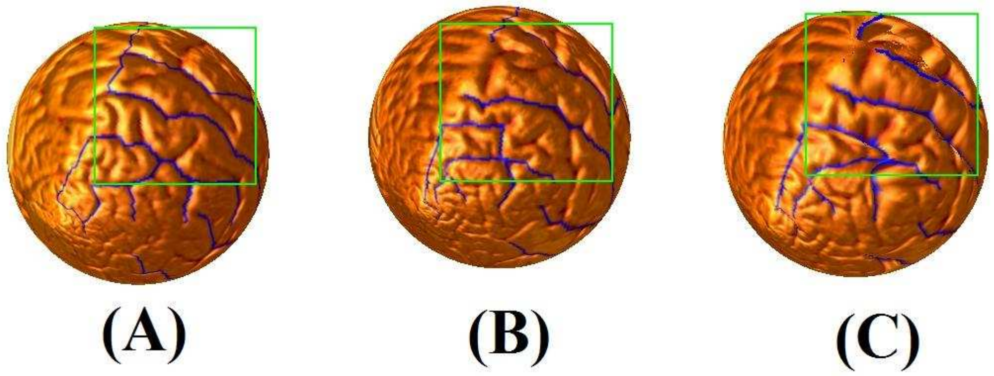

Figure 1: In (A), the cortical surface C_1 (the control) is mapped conformally ($\lambda = 0$) to the sphere. In (B), another cortical surface C_2 is mapped conformally to the sphere. Note that the sulcal landmarks appear very different from those in (A) (see landmarks in the green square). In (C), the cortical surface C_2 is mapped to the sphere using our algorithm (with $\lambda = 3$). Note that the landmarks now closely resemble those in (A) (see landmarks in the green square).

across subjects. Here we refer to these anatomical features as landmarks. This matching of cortical patterns improves the alignment of data across subjects, e.g., when integrating functional imaging data across subjects, measuring brain changes, or making statistical comparisons in cortical anatomy. In [4], we propose a variational approach to accomplish the task. It is based on optimizing the conformal parameterization of cortical surfaces by using landmarks, using a new energy functional. We propose to look for an optimized conformal map $f : \mathbb{S}^2 \to \mathbb{S}^2$ that minimizes the compound energy functional:

$$\begin{aligned} E_{new}(f) &= E_{harmonic}(f) + E_{landmark}(f) \\ &= \int_{\mathbb{S}^2} ||\nabla f||^2 d\mathbb{S}^2 + \frac{\lambda}{2}\int_0^1 ||f(p_i) - q_i||^2 dt \end{aligned}$$

Here, $p_i : [0,1] \to \mathbb{S}^2$ and $q_i : [0,1] \to \mathbb{S}^2$ are the corresponding landmark curves, represented on the parameter domain $\mathbb{S}^2$ with unit speed parametrization, for the two cortical surfaces. $E_{harmonic}$ is the harmonic energy of the parameterization. $E_{landmark}$ is the landmark mismatch energy, in which the norm represents the geodesic shortest distance on the sphere. By minimizing this energy functional, the distance between the corresponding landmarks on the sphere is minimized. λ is a weighting factor that balances the two penalty functionals. It controls how much landmark mismatch we want to tolerate. When $\lambda = 0$, the new energy functional is just the harmonic energy. When λ is large, the landmark mismatch energy can be greatly reduced. But more conformality will be lost. We prove theoretically that our proposed E_{new} is guaranteed to be decreasing using our algorithm and study the rate of changes of $E_{harmonic}$ and $E_{landmark}$. Experimental results on a dataset of 40 brain hemispheres showed that the landmark mismatch energy can be significantly reduced while effectively preserving conformality (See Figure 1). The key advantage of this optimized conformal parameterization approach is that any local adjustments of the mapping to match landmarks do not affect the conformality of the mapping significantly. It provides us with an attractive framework to help analyze anatomical shape, and to statistically combine or compare 3D anatomical models across subjects. We also apply this algorithm to build the average shapes (golden standard) of sets of real human cortical surfaces, using their optimized conformal parameterization. Experimental result shows that the average shapes preserve the important anatomical feature very well [5]. These average shapes are important for neuroscientists to analyze structural differences between healthy and unhealthy brain subjects.

	General parameterization:	**Conformal parameterization:**
Gradient:	$\nabla_M f = (g^{11}\partial_x f + g^{21}\partial_y f)\mathbf{i} + (g^{12}\partial_x f + g^{22}\partial_y f)\mathbf{j}$	$\nabla_M f = \frac{1}{\lambda}\partial_x f\mathbf{i} + \frac{1}{\lambda}\partial_y f\mathbf{j}$
Laplacian:	$\Delta_M f = \frac{1}{\sqrt{g_{11}g_{22}-g_{12}^2}}[\partial_x(\sqrt{g_{11}g_{22}-g_{12}^2}(g^{11}\partial_x f + g^{21}\partial_y f)) + \partial_y(\sqrt{g_{11}g_{22}-g_{12}^2}(g^{12}\partial_x f + g^{22}\partial_y f))]$	$\Delta_M f = \frac{1}{\lambda}(\frac{\partial^2 f}{\partial x^2} + \frac{\partial^2 f}{\partial y^2})$
Divergence:	$div_M(X\mathbf{i} + Y\mathbf{j}) = \frac{1}{\sqrt{g_{11}g_{22}-g_{12}^2}}[\partial_x(\sqrt{g_{11}g_{22}-g_{12}^2}X) + \partial_y(\sqrt{g_{11}g_{22}-g_{12}^2}Y)]$	$div_M(X\mathbf{i} + Y\mathbf{j}) = \frac{1}{\lambda}[\partial_x(\lambda X) + \partial_y(\lambda Y)]$

Figure 2: A comparison of the covariant formulae under the parameter domain using different parameterizations

II. Solving PDEs on general manifolds with global conformal parameterizations

Solving variational problem is an important topic in mathematics. A lot of daily life problems can be solved by formulating them as variational problems that minimize certain kind of energy functionals. Solving variational problems in the usual Euclidean domain has been studied extensively. Recently, researchers have been more and more interested in solving variational problems on general surfaces or manifolds. Applications exist in different areas of research, such as computer vision, computer graphics, image processing on the surface, geometry modeling, medical imaging as well as mathematical physics [6][7][8]. In medical imaging research, variational methods are often used for surface registration, feature extraction, surface parameterization and so on. Besides, a lot of 2D image processing techniques can be extended to the surface by variational methods on the manifolds, such as data denoising, surface inpainting, data segmentation, etc. Therefore, it is of great interest to develop a general and efficient method to solve variational problems on the surface.

In [9][10], we propose an explicit method to solve variational problems on general Riemann surfaces, using the conformal parameterization of the surface [11]. In general, variational problem is usually solved by computing its Euler-Lagrange equation, which is essentially a partial differential equation. Therefore, it is important to understand how to do calculus on general manifolds. On Riemann surfaces, differential operations are done through covariant derivatives. Essentially, they are a set of coordinate invariant operators for taking directional derivatives of the functions or vector fields defined on the surface. Covariant derivatives are defined locally through the local parameterization of the manifold. With arbitrary parameterization, the formulae for the covariant derivatives are generally very complicated. It results in computational difficulties and numerical inaccuracies. We propose to parameterize the surface conformally with the minimum number of coordinates patches. The Riemannian metric of the conformal parameterization is simple, which is just the scalar multiplication of the conformal factor, λ. The covariant derivatives on the surface can then be computed on the 2D domain with simple formula (See Figure 2). The corresponding formula for the covariant derivatives on $\mathbb{R}^2$ are similar to the usual Euclidean differential operators, except for a scaling factor λ. Therefore, with the conformal parameterization, the variational problems on general surfaces can be transformed to the 2D problems with much simpler equations. The problem can then be solved by using well known 2D numerical schemes.

With our developed method, a lot of 2D image processing techniques can be extended to general surfaces by solving the corresponding variational problems defined on the manifolds. We therefore propose to apply our algorithm to solve different image processing problems on surfaces, such as surface denoising, segmentation, surface inpainting on surfaces and so on (See Figure 3). These surface processing techniques have found important applications in Human Brain Mapping to process the human brain data.

Furthermore, the conformal parameterization is well known to be angle preserving. In other words, angles

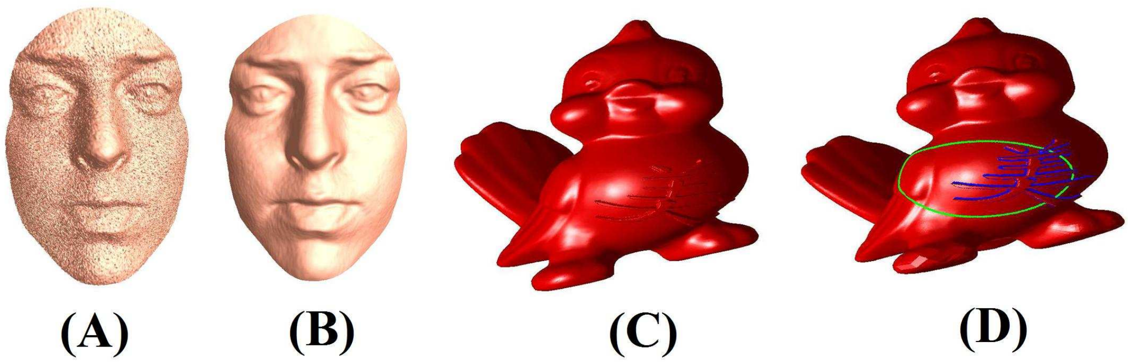

Figure 3: (A) and (B) illustrate the TV surface denoising on a human face. (A) shows a noisy surface. (B) shows the denoised surface. (C) and (D) illustrate texture extraction on the surface by extending the 2D Chan-Vese (CV) segmentation model onto 3D Riemann surfaces, using conformal parameterization.

between curves on the conformal parameter domain are mapped to curves with the same angle under the conformal parameterization. Therefore, the conformal parameterization of the surface inherits a natural orthogonal grid on the surface. This can be done by mapping the standard orthogonal grid structure onto the surface. With the regular structured grid on the surface, I am interested in developing faster numerical scheme for solving partial differential equations on surfaces, such as using the multi-grid method.

III. Automatic detection of anatomical features on cortical surfaces

One important problem in human brain mapping research is to locate the important anatomical features. Anatomical features on the cortical surface are usually represented by landmark curves, called sulci/gyri curves. These landmark curves are important information for neuroscientists to study brain disease and to match different cortical surfaces [12][13][14]. Manual labeling of these landmark curves is time-consuming, especially when large sets of data have to be analyzed. In [10], we present algorithms to automatically detect landmark curves on cortical surfaces. Firstly, we propose an algorithm to obtain a hypothesized landmark region/curves using the Chan-Vese segmentation method, which solves a Partial Differential Equation (PDE) on a manifold with global conformal parameterization. This is done by segmentating the high mean curvature region. It effectively extracts the sulcal regions on the cortical surface. An initial guess of the sulcal landmark can be obtained by computing a geodesic path within the sulcal region. Secondly, we propose a variational approach to trace the landmark curves on the cortical surface, based on the principal directions of the local Weingarten matrix. With the global conformal parametrization of the cortical surface, our method adjusts the landmark curves iteratively on the spherical or rectangular parameter domain of the cortical surface along one of the two principal directions, using umbilic points of the surface as anchors. Mathematically, the landmark curve $\vec{c} : [0,1] \to M$ should minimize the following energy function:

$$E_{principal}(\vec{c}) = \int_0^1 |\frac{\vec{c}'}{\sqrt{<\vec{c}',\vec{c}'>}} - \vec{V} \circ \vec{c}|_M^2 dt$$

Here, $\vec{V}$ is the principal direction field. By minimizing the energy $E_{principal}$, we iteratively minimize the difference between the tangent vector field along the curve and the principal direction field $\vec{V}$. The initial guess of the landmark curve is then evolved to a deeper sulci region. The landmark curves can then be mapped back onto the cortical surface. We test our algorithm on real human brain surfaces to label their major sulcal

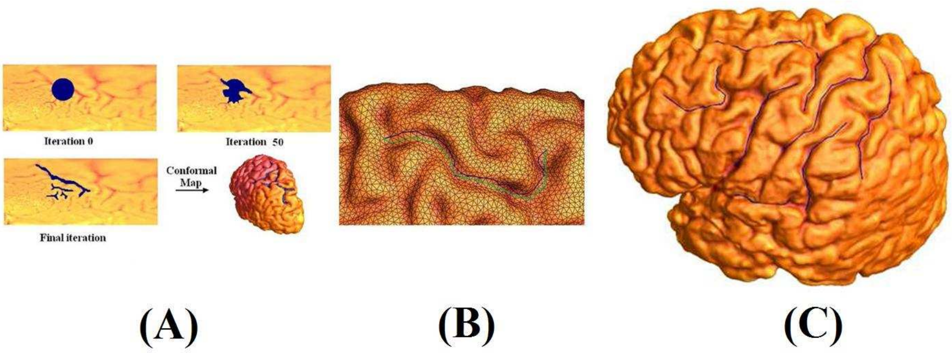

Figure 4: (A) shows the sulcal region extraction on the cortical surface by Chan-Vese segmentation.In (B), the initial landmark curve (blue curve) on the parameter domain is evolved to a deeper region (green curve) whose direction is closest to the principal direction field, using our variational approach. In (C), ten sulcal landmarks are automatically traced using our algorithm.

landmarks. Experimental results show that the landmark curves detected by our algorithm closely resemble these manually labeled curves (See Figure 4). Next, we applied these automatically labeled landmark curves to generate an optimized conformal parametrization of the cortical surface, in the sense that homologous features across subjects are caused to lie at the same parameter locations in a conformal grid. Experimental results show that our method can effectively help in automatically matching cortical surfaces across subjects [15][16].

IV. Surface Registration with Shape-based Landmark Correspondence

Surface registration, which transforms different sets of surface data into one common reference space, is an important process which allows us to compare or integrate the surface data effectively [17, 18, 21]. If a non-rigid transformation is required, surface registration is commonly done by parameterizing the surfaces onto a simple parameter domain, such as the unit square or sphere. For example, if two surfaces are parameterized using the same parameter domain, and the parameterizations are smooth bijective mappings, then a diffeomorphism can be constructed through their composition that associates pairs of corresponding points on the two surfaces. For the above diffeomorphisms to map data consistently across surfaces, parametrizations are required that preserve the original surface geometry as much as possible. Parameterizations should also be chosen so that the resulting diffeomorphisms between surfaces align important landmark features consistently. This kind of parameterization, with good feature alignment is particularly important for medical imaging research examining brain disorders such as Alzheimer's disease and schizophrenia, where systematic features of anatomy and function are identified by building an average brain shape from large numbers of subjects. This is advantageous as the surface average of many subjects would retain, and reinforce, features that consistently occur on sulci (the fissures in the brain surface), while spatially uniform parameterizations of the entire surface, which do not consider these embedded landmarks, may cause these features to cancel out.

In [22][23], we are interested in looking for *meaningful* registrations between surfaces through parameterizations, using prior features in the form of landmark curves on the surfaces. In particular, we generate optimized conformal surface diffeomorphisms which match landmark curves *exactly* with *shape-based* correspondences between them. We propose a variational method to minimize a compound energy functional that measures the harmonic energy of the parameterization *maps*, and the shape dissimilarity between mapped points on the landmark curves. The novelty is that the computed maps are guaranteed to align the landmark features consistently and give a *shape-based* diffeomorphism between the landmark curves. We achieve this by intrinsically model-

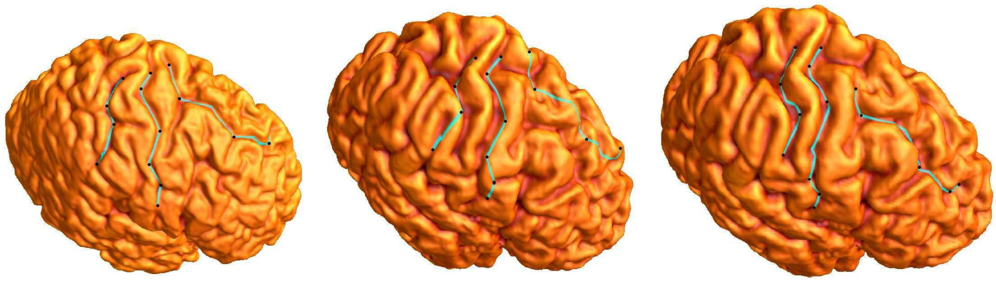

Figure 5: The figure illustrates the matching results for cortical surfaces with several sulcal landmarks labeled. (A) shows brain surface 1 with several landmarks labeled. It is mapped to brain surface 2 under the conformal parameterization as shown in (B). The sulcal landmarks on Brain 1 are not mapped exactly to the sulcal regions on Brain 2. (C) shows the matching result under the parameterization we proposed. The corresponding landmarks are mapped exactly to the sulcal region. Also, the correspondence between the landmark curves follows the shape information (corners to corners [See the black dot]).

ing our search space of maps as flows of smooth vector fields that do not flow across the landmark curves. By using the local surface geometry on the curves to define a shape measure, we compute registrations that ensure consistent correspondences between anatomical features.

Denote the conformal parameter domains of S_1 and S_2 by D_1 and D_2 respectively. We look for harmonic diffeomorphisms $\tilde{f}_1 : D_1 \to \Omega$ and $\tilde{f}_2 : D_2 \to \Omega$ that match landmark curves to the consistent location C. The composition map $\tilde{f}_2^{-1} \circ \tilde{f}_1$ is a landmark-matching harmonic diffeomorphism from D_1 to D_2. To start with, we compute any arbitrary maps $f_{01} : D_1 \to \Omega$ and $f_{02} : D_2 \to \Omega$. We then iteratively look for the smooth vector field $\vec{X}_i$ on Ω such that the composition map $\tilde{f}_i = \Phi^{\vec{X}_i} \circ f_{0i} : D_i \to \Omega$ is the landmark matching harmonic diffeomorphism ($i = 1, 2$). Here, $\Phi^{\vec{X}_i} : \Omega \to \Omega$ is the time-1 integral flow of the vector field $\vec{Y}_i = P_C \vec{X}_i$ satisfying the integral flow equation:

$$\frac{\partial \Phi}{\partial t}^{\vec{X}_i}(\mathbf{x}, t) = \vec{X}_i(\Phi^{\vec{X}_i}(\mathbf{x}, t)),$$
$$\Phi^{\vec{X}_i}(\mathbf{x}, 0) = \mathbf{x}.$$

$\vec{Y}$ is the projection of the vector field $\vec{X}_i$ such that it is tangential to C. This ensures the exact landmark matching property of $\tilde{f}_i$. The vector fields $\vec{X}_i = a_i \frac{\partial}{\partial x} + b_i \frac{\partial}{\partial y}$ minimizes the following energy functional:

$$\begin{aligned} J[a_i, b_i] = & \int_\Omega |\nabla \tilde{f}_1|^2 + |\nabla \tilde{f}_2|^2 \, dx \\ & + \beta \int_\Omega |\nabla \vec{X}_1|^2 + |\nabla \vec{X}_2|^2 \, dx \end{aligned}$$

The variational problem is then formulated to be defined over the space of C^1 smooth vector fields on Ω. The last integral in the energy is the smoothness term for the vector fields $\vec{X}_i$. The first two integrals are the harmonic terms which aim to preserve the harmonicity of the parameterization as much as possible.

We test our algorithm on synthetic surface data and on real brain cortical surfaces with anatomical (sulcal) landmarks delineated, which show that our computed maps give a shape-based alignment of the sulcal curves without significantly impairing conformality. This ensures correct averaging and comparison of data across subjects (See Figure 5).

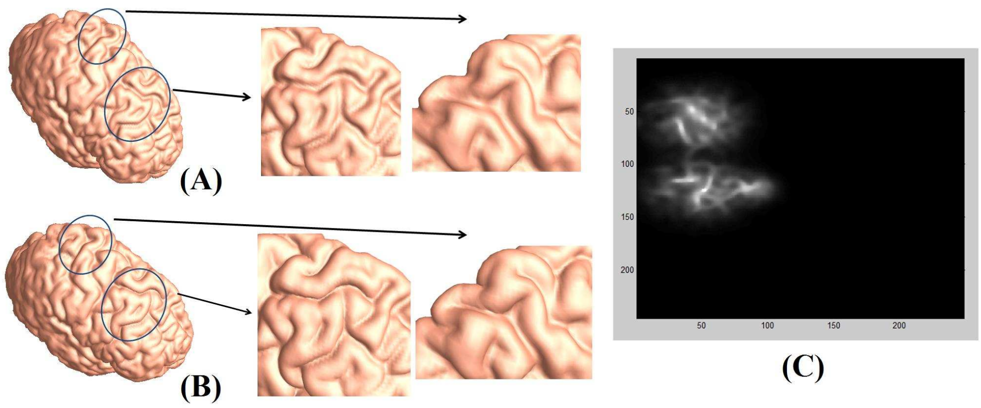

Figure 6: Example of detecting abnormalities on real brain surfaces. (A) shows the original brain surface. (B) shows the deformed brain surface with gyral thickening in the circled regions. (C) shows the distribution of $|\mu|$. The Beltrami coefficient μ clearly reflects the region of abnormal changes on the human brain cortical surface.

In future, we plan to apply this algorithm to cortical models from healthy and diseased subjects to build population shape averages. The enforcement of higher-order shape correspondences may allow subtle but systematic differences in cortical patterning to be detected, for instance in neurodevelopmental disorders such as Williams syndrome, where the scope of cortical folding anomalies is of great interest but currently unknown.

B. Ongoing and future projects

I. Detecting Abnormal Shape Deformations using Yamabe Flow and Beltrami Coefficents

Detecting abnormal changes in surfaces is a key problem in shape analysis, especially in medical research. For example, neuroscientists commonly aim to identify abnormal deformations of cortical and subcortical structures in the brain in order to detect systematic patterns of alterations in brain diseases. In cardiac imaging and oncology, physicians commonly need to track changes or abnormalities in biological organs or tumors in order to evaluate the effectiveness of different treatments, or monitor disease progression. Detecting and examining abnormalities by the human eye is inefficient and often inaccurate, especially on complicated surfaces such as the cerebral cortex of the brain. Therefore, it is of great importance to develop automatic methods to detect abnormalities and track abnormal geometric changes over time. In this work, we address the problem of detecting regions of abnormal changes on surfaces using quasi-conformal geometry.

We develop an effective algorithm to detect abnormal deformations by generating quasi-conformal maps between the original and deformed surfaces [24]. The original and deformed 3D surfaces are firstly flattened conformally onto 2D rectangles using the Yamabe flow method; a quasi-conformal map is then computed that matches features between the surfaces. By formulating abnormal changes as non-conformal deformations, we detect abnormalities by computing the Beltrami coefficient, which is uniquely associated with the quasi-conformal map. The Beltrami coefficient is a complex-valued function defined on the surface, which describes the conformality of the deformation at each point. By considering the norm of the Beltrami coefficient, we detect regions with abnormal changes, which are invariant under conformal deformation. Furthermore, by considering the argument of the Beltrami coefficient, we can capture abnormalities induced by local rotational changes. We tested the algorithm by detecting abnormalities on synthetic surfaces, 3D human face data and real MRI-derived brain surfaces. Experimental results show that our algorithm can effectively detect abnormalities and capture local rotational alterations (See Figure 6). In future, I am planning to apply this algorithm to study human brain diseases such as Williams syndrome, which results from genetically-mediated developmental abnormalities in cortical folding. I will also develop more efficient numerical schemes to speed up the computation.

II. Representation and Property Adjustments of Surface Diffeomorphisms

In this work, we propose a novel idea of representing surface diffeomorphisms using Beltrami coefficients, which are complex-valued functions defined on surfaces that describe local conformality distortions of surface maps. According to Quasiconformal Teichmuller theory, there is an one-to-one correspondence between genus zero surface diffeomorphisms and Beltrami coefficients with L_∞-norm strictly less than 1. For every such coefficient μ, we can reconstruct the diffeomorphism exactly using the so-called holomorphic Beltrami flow, which solves the Beltrami equation $f_{\overline{z}} = \mu f_z$. Mathematically, let $\{\mu(t)\}$ be a family of Beltrami coefficients depending on a real or complex parameter t. Suppose also that $\mu(t)$ is a differentiable at $t = 0$, that is, $\mu(t)$ can be written in the form

$$\mu(t)(z) = \mu(z) + t\nu(z) + t\epsilon(t)(z)$$

for $z \in C$, with suitable μ in the unit ball of $L^\infty(\mathbb{C})$, $\nu, \epsilon(t) \in L^\infty(\mathbb{C})$ such that $\| \ (\epsilon(t) \ \|_\infty \to 0$ as $t \to 0$. Then

$$f^{\mu(t)}(w) = f^\mu(w) + t\dot{f}^\mu(w)[\nu](w) + o(|t|)$$

locally uniformly on $\mathbb{C}$ as $t \to 0$, for $w \in \mathbb{C}$, and where

$$\dot{f}[\nu](w) = -\frac{1}{\pi}\int_{\mathbb{C}} \nu(z)\frac{f^\mu(w)(f^\mu(w)-1)((f^\mu)_z(z))^2}{f^\mu(z)(f^\mu(z)-1)(f^\mu(z)-f^\mu(w))}dx\,dy$$

With this equation, we can iteratively adjust the initial map to the diffeomorphism with desired Beltrami coefficient μ. The map obtained in each iteration is guaranteed to be a diffeomorphism. The use of Beltrami coefficients to represent surface diffeomorphisms is a powerful method because it captures the most essential features of the diffeomorphisms, including but are not limited to conformality distortions, rotational changes and dilations. Therefore, we can obtain diffeomorphisms with desired properties by simply adjusting the Beltrami coefficient. By changing the Beltrami coefficient at only a certain region while fixing the rest, we can obtain diffeomorphisms with desired properties at a specific region while retaining the properties of the original map outside that region. With this approach, we propose four main applications to properties adjustments of surface maps. These include: 1. accurate alignment of landmark curves; 2. reconstruction of surface diffeomorphisms; 3. local restoration of conformal maps; 4) construction of the Riemann map from any simply-connected open surface to the unit disk. We apply our algorithms on both synthetic data and human brain surfaces. Preliminary results show that the Beltrami coefficient can effectively assist us in fine adjustments of surface diffeomorphisms (See Figure 7).

III. Volumetric registration between human brains with diffusion tensor matching

Surface registration between brain cortical surfaces has been studied extensively and have found many important applications in disease analysis. However, the interior volume of the human brain also embeds many important information. Therefore, it is of great interest to develop algorithm for volumetric registration between human brains. In the interior volume of the human brain, there are lots of fiber tracts which are important information for doctors to examine brain structures. We propose to construct 3D harmonic maps between human brains that matches the correspondence fiber tracts as much as possible. The boundary condition is given by the landmark matching surface registration that we have developed earlier. The fiber tracts can be effectively represented by diffusion tensor imaging (DTI). At each voxel, a tensor can be computed from the diffusion tensor images. Let

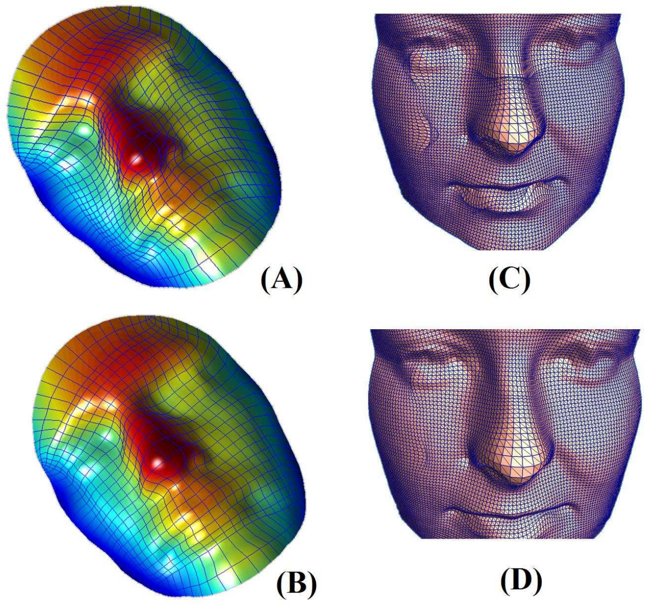

Figure 7: (A) and (B) shows how we can restore conformality by adjusting the Beltrami coefficient. (A) shows the surface map from an orthogonal grid on a unit disk to the surface, which is not conformal as it is not angle preserving. (B) shows the improved surface map from the orthogonal grid on the unit disk to the surface, which is conformal. (C) shows the surface map from an orthogonal grid on a 2D rectangle to the human face. Overlaps are observed which means the map is not diffeomorphic. (D) shows how we can restore the diffeomorphic property of the map by adjusting the Beltrami coefficient.

B_1 and B_2 are two human brains with tensor D_1 and D_2 respectively. We propose to compute the fiber matching harmonic map $f : B_1 \to B_2$ by minimizing the following energy functional:

$$E(f) = \int_{B_1} ||\nabla_{D_1} f||^2 + \int_{B_1} ||f^*(D_2) - (D_1)||^2 \tag{1}$$

where $f^*(D_2)$ is the pull-back of D_2 under the map f. The first term is the harmonic energy of f. The minimizing map will be an optimized tensor matching harmonic map which matches the corresponding fiber as much as possible. This volumetric registration between human brains is especially important for clinical applications such as defining the severity of diffuse traumatic brain injury and detecting brain tumor effectively.

IV. Analysis of William Syndrome disease using Teichmuller distance and hyperbolic Ricci flow

Analyzing the brain structure of unhealthy patients with Williams Syndrome disease is an important research topic in Neuroscience. The Williams Syndrome (WS) is an enigmatic disorder associated with a genetic deletion in the 7q11.23 chromosomal region, where the scope of cortical folding anomalies is of great interest but currently unknown. Over years, neuroscientists have observed some gyrification differences in WS. The fissuration pattern of the precentral, central, and postcentral sulci is typically very simple in healthy subjects but become more complex in WS. Also, gyri in the WS subject are usually thinner. Even so, it is still hard to characterize exactly what or where the differences are, as the brains are different in subtle ways and have complicated geometry. Therefore, it is of great importance to develop tools to systematically analyze the brain structure of WS brain subjects and identify their location of differences.

In this work, we propose to study the structural differences between WS subjects and healthy subjects, using the Teichmuller distance. Given a cortical surface, we firstly cut the surface open along its important sulcal landmarks. The surface will become an open surface with negative Euler characteristics. For surfaces with negative Euler characteristics, the canonical hyperbolic metric is conformal to the original metric and can be efficiently computed using hyperbolic Ricci flow. Hyperbolic Ricci flow induces diffeomorphisms between surfaces without singularity, and all the boundaries are intrinsically mapped to hyperbolic lines. The surface can then be canonically decomposed into disjoint regions where each regions are mapped to hyperbolic hexagons on the hyperbolic plane. More specifically, we can decompose the surface into regions whose boundaries are composed of adjacent sulci and geodesic curves joining the endpoints. Each region is mapped to a hyperbolic hexagon. Given a set of cortical surfaces, we apply this algorithm to decompose the surfaces into hyperbolic hexagons. Harmonic quasiconformal maps f_i between the corresponding hexagons of each cortical surfaces can be easily computed. Each quasiconformal map f_i is associated with a unique Beltrami coefficient ν_i. We can compute the Teichmuller distance D_{ij} between the quasiconformal maps f_i and f_j by:

$$D_{ij} = \frac{1}{2} \log K(f_i \circ f_j^{-1})$$

where $K(f_i) = \frac{1+k}{1-k}$ and $k = sup|v_i|$. With the Teimuller distance, we can determine the structural differences between healthy subjects and WS subjects statistically and locate their differences effectively.

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