

Introduction

- Cardiac disease is often associated with remodeling.
 - Ventricular shape and function is influenced by this remodeling.
 - Assessing left ventricular shape and motion at the population level requires establishing anatomical correspondence using registration based techniques.
- Cardiac magnetic resonance imaging (MRI) provides detailed quantitative data about cardiac function and geometry.
- Cardiac MRI data are sparsely sampled that is not optimum for intensity-based registration methods.
- Methods that rely on fitting a smooth surface to the segmented contours may impose an artificial constraint to the registration process [1],[2].
- We propose:
 - to study the feasibility of matching sparsely sampled cardiac MR volumes using curve and surface matching in the context of large deformation diffeomorphic metric mapping [3],[4].

Preprocessing

- **Subjects:** Cardiac MR data from patients with familial cardiomyopathy (n = 5, 4 females, mean age of 50.4 ± 15.24 years). The in-plane resolution was approximately $\sim 1.4 \text{ mm} \times 1.4 \text{ mm}$ and thickness was of 8 mm with 2 mm gap.
- **Segmentation:** Epi and endocardial contours of left ventricle (LV) were isolated using *Segment* [5] software.
- **Breath Hold Correction:** A 2D Euclidean distance-based matching approach was used to correct for breath-hold related slice to slice motion using contour points from 3 different perpendicular planes: short axis (SA), horizontal long axis (HLA), and vertical long axis (VLA).
- **Rigid alignment:** Before performing nonrigid matching, we roughly aligned and scaled the objects (curves and surfaces).
- **Template surfaces:** The template surface is a triangulation of a binary volume, that was obtained using shape averaging in a previous study [6] using intensity CT images from 25 subjects.

Registration Methods

• Nonrigid Alignment between Segmentations

- Given two families of curves, $\Gamma^{(0)}$ and $\Gamma^{(1)}$ (with different number of points), we would like to find an optimal transformation, say ϕ , such that $\phi(\Gamma^{(0)}) \simeq \Gamma^{(1)}$ via minimizing the following objective function:

$$E(\Gamma, \alpha) = \int_0^1 F(\Gamma(t), \alpha(t)) dt + \frac{1}{\sigma^2} D(\Gamma(1), \Gamma^{(1)})^2. \quad (1)$$

The variables, Γ and α , are time dependent and the deformation cost function, F , is defined by:

$$F(\Gamma(t), \alpha(t)) = \sum_{k,l=1}^N \int \int \alpha_k(t, u)^T K(\gamma_k(t, u), \gamma_l(t, v)) \alpha_l(t, v) dudv. \quad (2)$$

The matching term, D , is a Hilbert space norm [3] measuring the discrepancy between the deformed template curves ($\Gamma(1)$ at time $t = 1$) and target ($\Gamma^{(1)}$).

$K(p, p')$ is a smoothing kernel function:

$$K(p, p') = \text{diag}(g(\|p - p'\|), g(\|p - p'\|), g(z - z'))$$

with $g(t) = \exp(-t^2/2a^2)$ for some parameter a (where z and z' are the long-axis coordinates of p and p'). This ensures a uniform motion in the LV long axis direction.

• Surface to curves registration

- Similarly in surface to curve registration we seek an optimal transformation that maps a closed surface $S^{(0)}$ to a collection of curves ($\Gamma^{(1)}$) via minimizing:

$$E(S, \alpha) = \int_0^1 F(S(t), \alpha(t)) dt + \frac{1}{\sigma^2} D(S(1), \Gamma^{(1)})^2. \quad (3)$$

The deformation cost is given by

$$F(S(t), \alpha(t)) = \int_{S^{(0)}} \int_{S^{(0)}} \alpha(t, p)^T K(S(t, p), S(t, q)) \alpha(t, q) ds(p) ds(q). \quad (4)$$

- The kernel K is now chosen isotropic, such that $K(p, p') = g(\|p - p'\|) \text{Id}_{\mathbb{R}^3}$ with g as above. The matching term, D , computes the sum of the integrals of the squared distances between each point in each curve in $\Gamma^{(1)}$ and the deformed surface $S(1)$.
- **Measure of robustness (Four experiments on 5 subjects)**
 - Matching high resolution template surface to complete target curve set.
 - Matching high resolution template surface to incomplete target curve set (removed one plane).
 - Matching complete curve set extracted from high resolution template data to complete target curve set (removed one plane).
 - Matching complete curve set extracted from high resolution template data to incomplete target curve set (removed one plane).

Results

• Nonrigid Alignment of segmentations

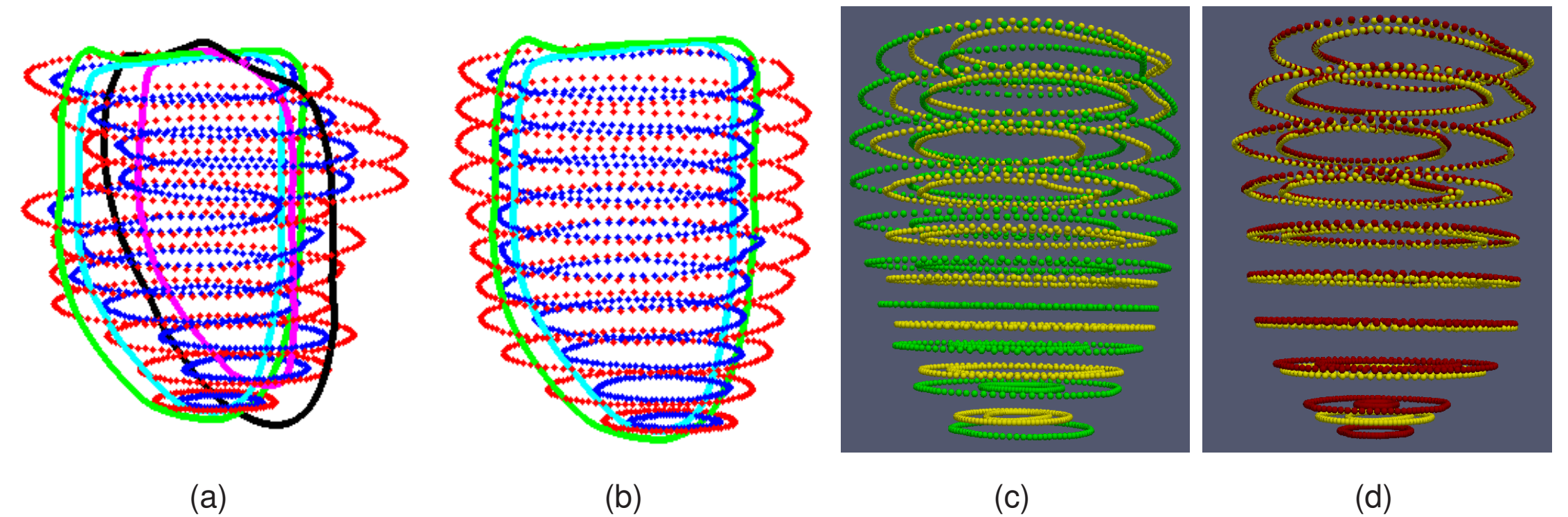


Figure: (a-b): Correction of slice-to-slice misalignment in SA view due to breath-holding motion. (a): Before correction. (b): After correction. (Blue and red : endo and epicardial surfaces from SA view, Cyan and green: endo and epicardial contours from vertical long axis view, Pink and black: endo and epicardial contours from horizontal long axis view. (c-d) Curve-to-curve matching using LDDMM. (c): LV contours before curve matching (green: template contours, yellow: target contours). (d): LV contours after deforming template subject contours (red) to match target subject (yellow).

• Nonrigid surface to curve registration

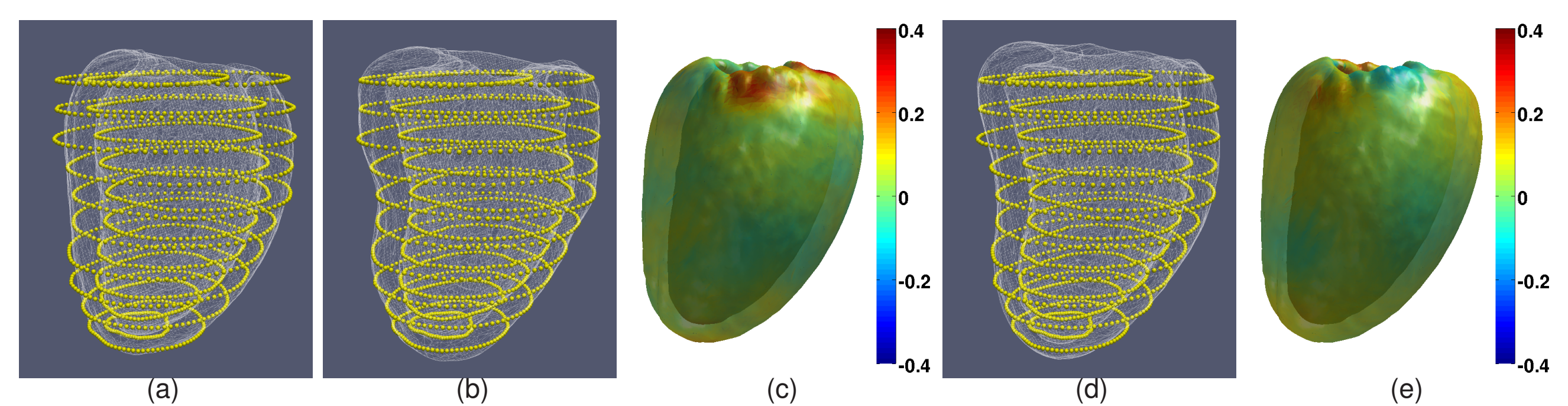


Figure: Surface-to-curve matching using distance-based LDDMM. (a): Surface template with target contours. (b): After registration. (c): Map of the surface area ratio of triangulated faces in deformed template relative to template superimposed on template mesh (scale is based on \log_{10}). (d): After registration using projection of gradients on the first 24 eigenvectors of smoothing kernel. (e): same as (c) but for the deformation estimated from (d). Grey wireframe represents high resolution triangulated mesh template. Yellow contours are representing LV epi and endocardial regions from the MRI cross-sections.

• Distance Error (mm)

- I) Matching high resolution surface to the complete curve set (distance between the removed cross-sectional curves to the deformed surface).
- II) Matching high resolution surface template to the incomplete curve set (distance between the removed cross-sectional curves to the deformed surface).
- III) Repeating case (I) with the curve to curve matching.
- IV) Repeating case (II) with the curve to curve matching.
- V) Pre-registration distance between the complete curve set and surface template.
- VI) Surface to curve matching error estimated by using the entire curve set as opposed to using curves from a single cross section (case I)
- VII) Curve to curve matching error estimated by the complete curve set

Experiments	I	II	III	IV	V	VI	VII
Mean(SD)	1.67(0.70)	2.79(0.80)	1.37(0.47)	4.31(1.71)	3.24(0.17)	1.75(0.29)	1.15(0.14)

Conclusions

- Surface to curve matching:
 - Does not rely on a predefined geometry.
 - Does not require same number of points for curves and surfaces.
 - Projection of gradient of objective function onto principal directions of smoothing kernel reduces the over-fitting problem.
- Curve to curve matching:
 - Does not require high resolution surface.
 - Sensitive to geometry coverage.
- Both approach are robust with respect to the missing data.

References

- [1] Frangi, A. et al. IEEE Transactions Medical Imaging 21(9), 2002.
- [2] Wang, V.Y. et al Medical Image Analysis 13(5), 2009.
- [3] Glaunes, J. et al. Int J Comput Vis 80, 2008.
- [4] Durrleman, S. et al. Medical Image Analysis 13(5), 2009.
- [5] Heiberg, E., et al. BMC Med Imaging 10(1), 2010.
- [6] Ardekani, S., et al. Ann Biomed Eng 37, 2009.

Acknowledgement

This research was supported by the Cardiovascular Research Grid Project R24HL085343.