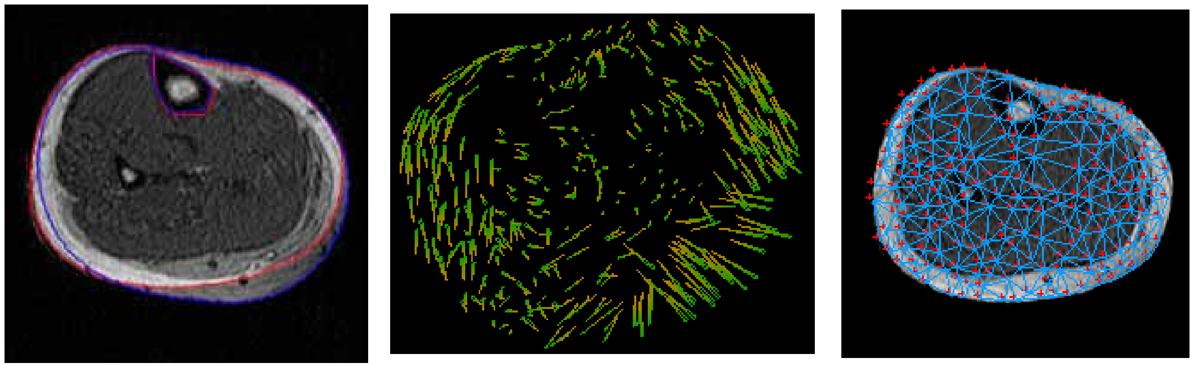
A Method for Non-rigid 3D Deformation Fields Measurement: Application to Human Calf MR Volumetric Images



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Outline

- Background
- Principle
- Feature extraction and matching
- Deformation fields measurement
- Experimental results and evaluation
- Conclusion

Background

Mechanical Modeling of Soft Biological Tissues

Image-navigated surgery
Surgery simulation
Diagnosis of disease

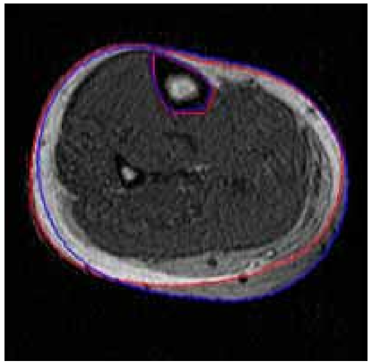
Modeling is OK but identification is not

Challenges

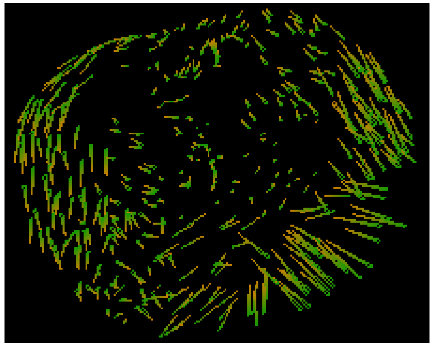
Non-uniform heterogeneous properties
(location dependent E and ν)

Principle

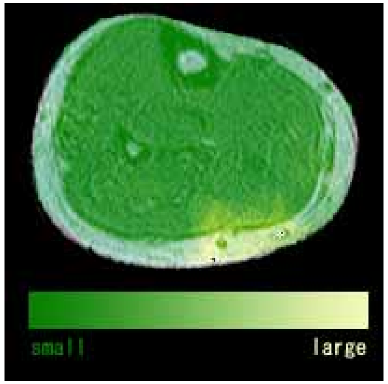
- **Measurement dense deformation fields using MR volumes before and after deformation.**
- **Non-uniform physical parameters are estimated using the deformation fields.**



MR images



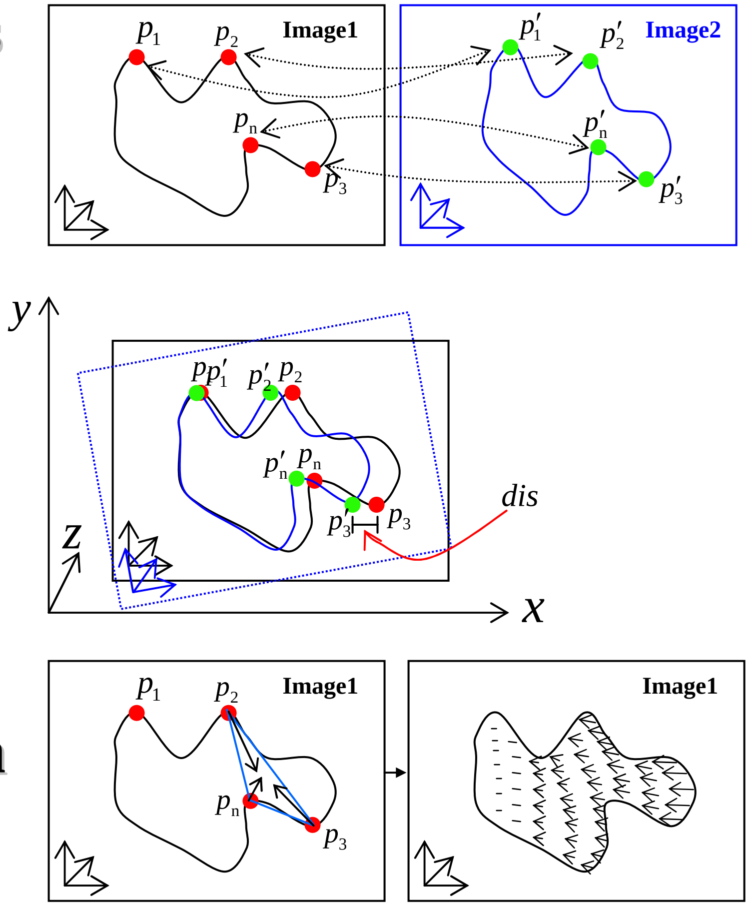
Deformation fields



Heterogeneous properties

Overview of the proposed method

1. **For extracted feature points in the initial MR volume, track their corresponding points in the deformed MR volume.**
2. **Obtain sparse deformation fields corresponding to feature point matches.**
3. **Interpolate the sparse into the inner dense deformation fields.**



Feature extraction and matching

--feature extraction

- **To extract feature points from MR volumes, we expanded 2D Harris operator to form a 3D feature point extraction operator. We have auto-correlation matrix**

$$M = \begin{pmatrix} I_x^2 & I_x I_y & I_x I_z \\ I_x I_y & I_y^2 & I_y I_z \\ I_x I_z & I_y I_z & I_z^2 \end{pmatrix}$$

where

I_x : image gradient along x orientation

I_y : image gradient along y orientation

I_z : image gradient along z orientation

- **With eigenvector**

$$\lambda = [\lambda_1, \lambda_2, \lambda_3]$$

- **To determine the feature points, we define a response function R_F**

$$R_F = \frac{det(M)}{trace(M)}.$$

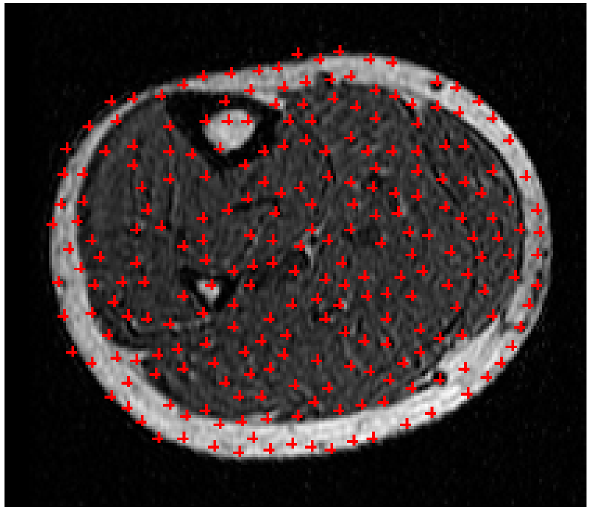
Note:

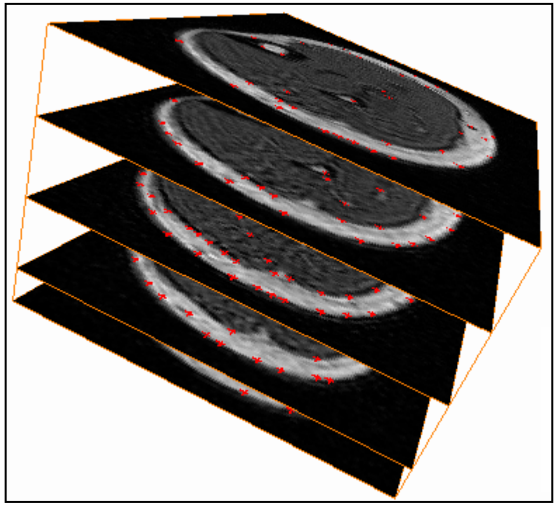
Those voxels whose R_F exceed a given threshold will be regarded as feature points

Feature extraction and matching

--feature extraction

3D Harris operator to extract feature points





Feature points in one slice.

Feature points distributed in different slices of the volume according to their z-coordinates.

+ Represents the location of feature point

Feature extraction and matching

--feature matching

- **Two steps for point matching (IEEE/CME2007)**
  - **First matching**
    - ***Correlation score***
  - **Relaxation**
    - ***Cost function***

$$\boxed{\varepsilon = \frac{1}{N}\sum_{i,j=1}^{N} SM(\mathbf{p_1}_i, \mathbf{p_2}_j)}$$

    - ***Strength of match (SM)***
      - SM is the key of cost function

SM Function In Relaxation

--first SM

- **SM function**

$$SM(\mathbf{p}_{1_i}, \mathbf{p}_{2_j}) = cs(\mathbf{p}_{1_i}, \mathbf{p}_{2_j}) + \alpha \sum_{k,l=1}^{s} \frac{cs(\mathbf{n}_{1_k}, \mathbf{n}_{2_l}) \cdot \eta(\mathbf{n}_{1_k}, \mathbf{n}_{2_l})}{1 + diff(\mathbf{p}_{1_i}, \mathbf{p}_{2_j}; \mathbf{n}_{1_k}, \mathbf{n}_{2_l})}$$

SM

$$diff(\mathbf{p}_{1_i}, \mathbf{p}_{2_j}; \mathbf{n}_{1_k}, \mathbf{n}_{2_l}) = \frac{d(\mathbf{p}_{1_i}, \mathbf{n}_{1_k}) - d(\mathbf{p}_{2_j}, \mathbf{n}_{2_l})}{dist(\mathbf{p}_{1_i}, \mathbf{p}_{2_j}; \mathbf{n}_{1_k}, \mathbf{n}_{2_l})}$$

Relative distance difference

$$\eta(\mathbf{n}_{1_k}, \mathbf{n}_{2_l}) = \frac{1}{\mathcal{Z}(\mathbf{n}_{1_k}, \mathbf{n}_{2_l})} \cdot \exp^{-\lambda \cdot \zeta(\mathbf{n}_{1_k}, \mathbf{n}_{2_l})}$$

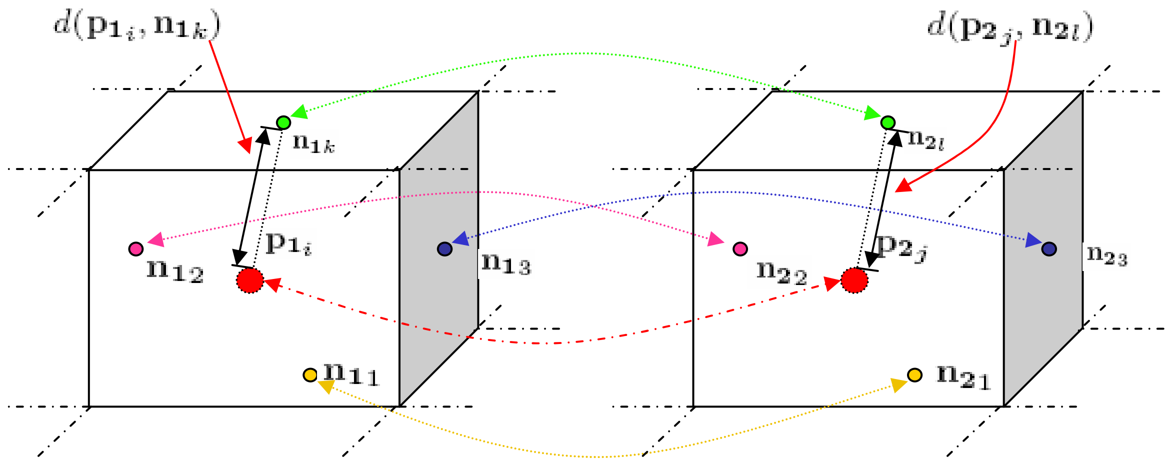
Gibbs distribution of residual

$$\mathcal{Z}(\mathbf{n}_{1_k}, \mathbf{n}_{2_l}) = \sum_{k,l=1}^{s} \exp^{-\lambda \cdot \zeta(\mathbf{n}_{1_k}, \mathbf{n}_{2_l})}$$

Normalizing constant

$\zeta(\mathbf{n}_{1_k}, \mathbf{n}_{2_l})$ Residual

λ is an attention constant. The principle of λ selecting is to ensure the η of those pairs with large residual quickly decrease as λ increasing.



SM Function In Relaxation

--improved SM

- **An improved SM is defined as:**

SM

$$SM(\mathrm{p}_i, \mathrm{p}'_j) = cs(\mathrm{p}_i, \mathrm{p}'_j) + \alpha \sum_{k=1}^{s} cs(\mathrm{n}_k, \mathrm{n}'_k) \cdot w_{(\mathrm{n}_k,\ \mathrm{n}'_k)}$$

Correlation Score

where weight of each potential match is given as:

$$w_{(\mathrm{n}_k,\ \mathrm{n}'_k)} = \exp(-\mathcal{J}_k), \quad k = 1,\ 2, \cdots, n$$

with notations

Relative distance difference

$$\mathcal{J}_k = \begin{cases} diff(\mathrm{p}_i, \mathrm{p}'_j; \mathrm{n}_k, \mathrm{n}'_k) & \text{if } \mathcal{O}(\mathrm{n}_k,\ \mathrm{n}'_k) = 0 \\ \mathcal{O}(\mathrm{n}_k,\ \mathrm{n}'_k) \cdot diff(\mathrm{p}_i, \mathrm{p}'_j; \mathrm{n}_k, \mathrm{n}'_k) & \text{otherwise} \end{cases}$$

$$\mathcal{O}(\mathrm{n},\ \mathrm{n}') = A^{\mathrm{n}\to\mathrm{n}'}_{\mathrm{p}\to\mathrm{p}'}/3.$$

Orientation constraint factors

SM Function In Relaxation

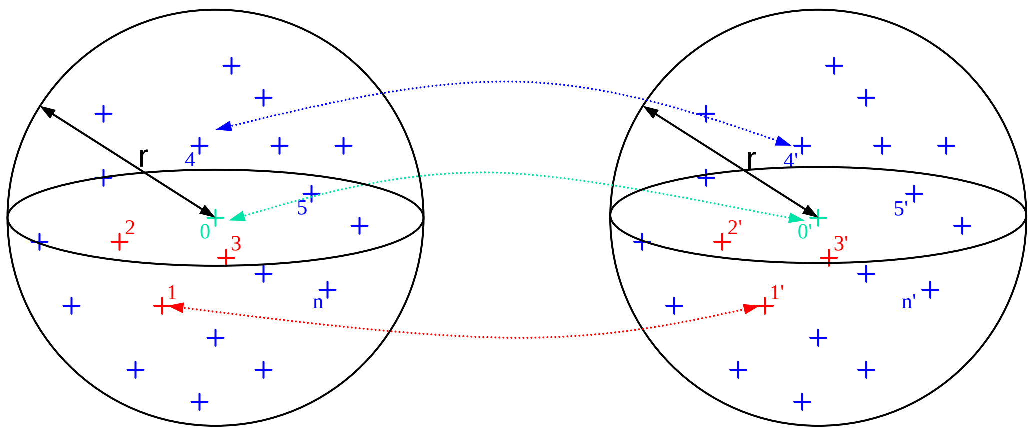
--improved SM

- **Why?**
  - **The deformation direction of different areas are different (non-uniform object)**
  - **The direction of deformation fields in a local area should be consistent (non-uniform object)**
  - **If a candidate match is a potential match (PM), we expect to see more PMs whose deformation direction consistent with currently candidate match, on the contrary, we expect to see few or even none.**
- **How ?**
  - **Using the angle between the candidate match and PMs in its neighborhood to determine the contribution ratio of each PMs in SM computation.**

SM Function In Relaxation

--improved SM

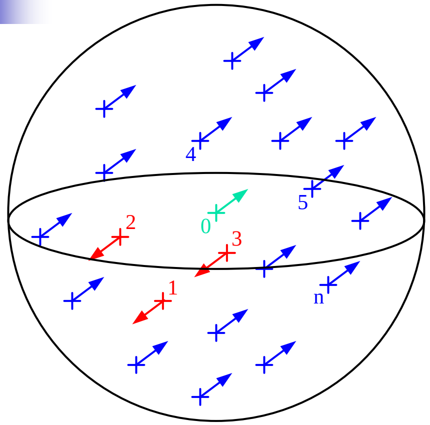
- **Concisely**



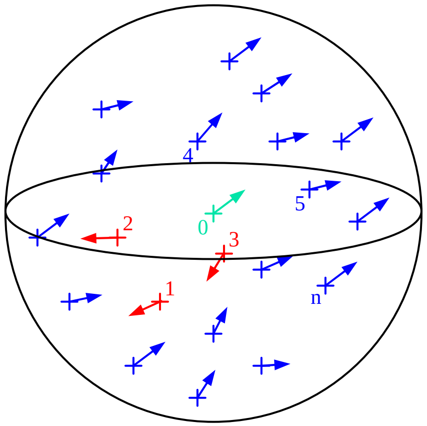
$$SM(0,0') = cs(0,0') + \alpha \sum_{n} cs(\mathbf{n},\mathbf{n}') \cdot \boxed{w_{(\mathbf{n},\ \mathbf{n}')}}$$

SM Function In Relaxation

--improved SM



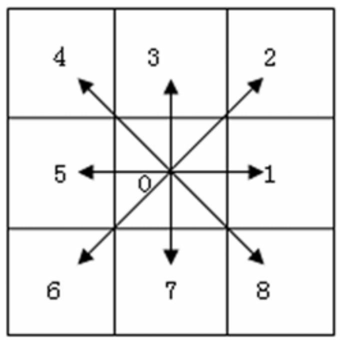
Ideally

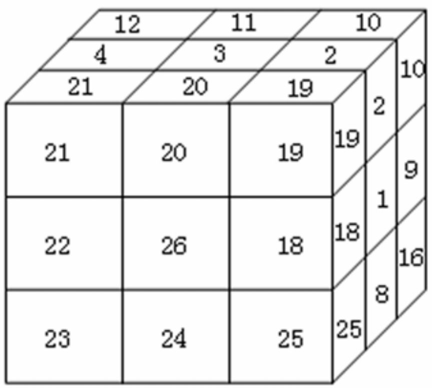


Actually

Note: the weight of red matches should take 0 in SM(.) computation of match 0, and the weight of blue matches should take 1 in ideally case, however, equal or less than 1 in actually case.

- **To determine the weight of each matches in the neighbor, we classify the direction of deformation fields to 8 types in 2D case and 26 types in 3D case.**





$\phi_{\mathbf{p}\rightarrow\mathbf{p}'} = \{\alpha \mid \alpha = 1,\ 2,\ 3\ ,\ldots,\ 8\}$ $\phi_{\mathbf{p}\rightarrow\mathbf{p}'} = \{\alpha \mid \alpha = 1,\ 2,\ 3\ ,\ldots,\ 26\}$

SM Function In Relaxation

--improved SM

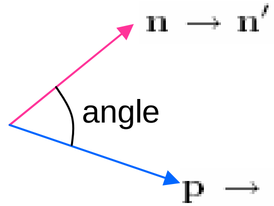
- **In this way, each deformation field will take an orientation value within [1, 8] in 2D case or [1, 26] in 3D case as it direction.**

$$\phi_{\mathbf{p}\to\mathbf{p}'} = \{\alpha \mid \alpha = 1,\ 2,\ 3\ ,\ldots,\ 8\}$$

$$\phi_{\mathbf{p}\to\mathbf{p}'} = \{\alpha \mid \alpha = 1,\ 2,\ 3\ ,\ldots,\ 26\}$$

- **The notation $A^{\mathbf{n}\to\mathbf{n}'}_{\mathbf{p}\to\mathbf{p}'}$ is determined by the angle between candidate match and PMs in its neighborhood:**

$$A^{\mathbf{n}\to\mathbf{n}'}_{\mathbf{p}\to\mathbf{p}'} = \begin{cases} 0 & \text{If angle = 0} \\ 1 & \text{If angle>0 and angle<90} \\ 2 & \text{If angle = 90} \\ 3 & \text{Otherwise} \end{cases}$$

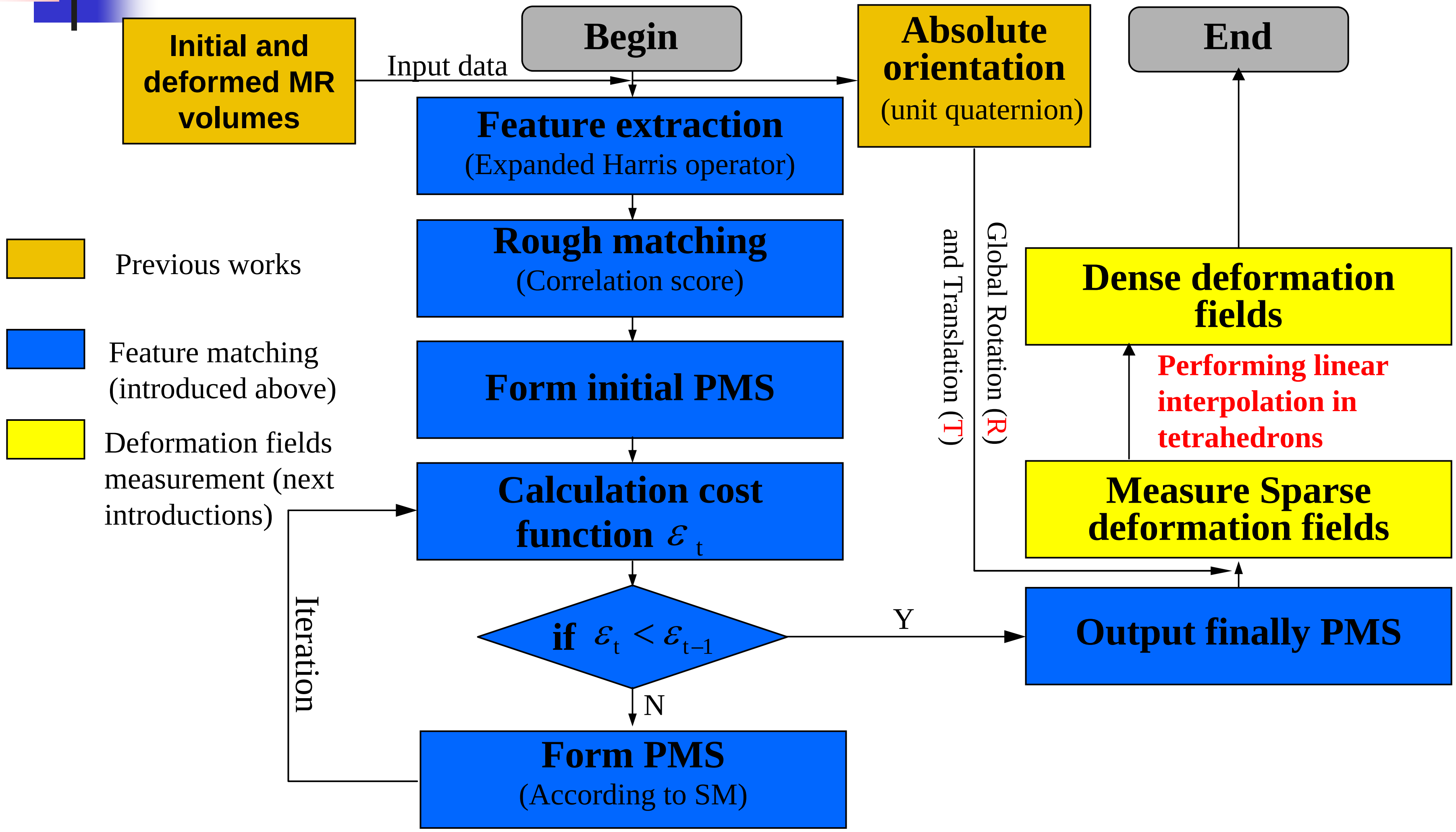


$$\mathcal{O}(\mathbf{n},\ \mathbf{n}') = A^{\mathbf{n}\to\mathbf{n}'}_{\mathbf{p}\to\mathbf{p}'}/3.$$

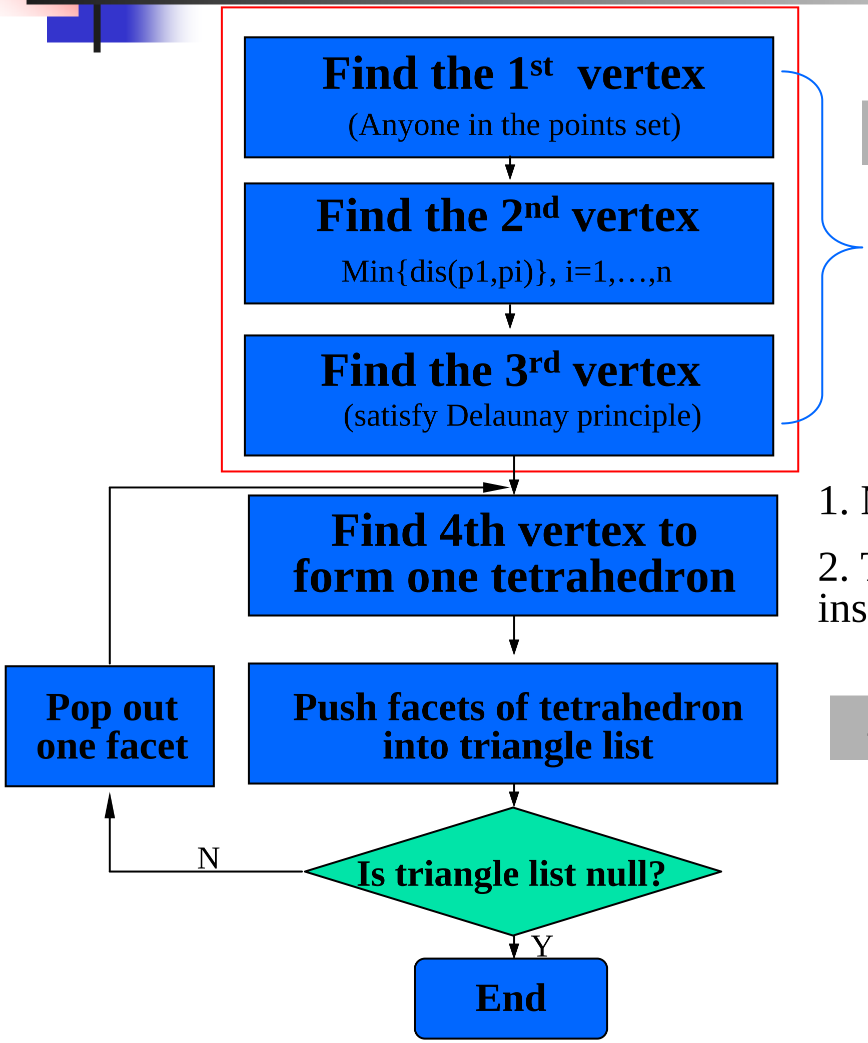
$$\mathcal{J}_k = \begin{cases} diff(\mathbf{p}_i, \mathbf{p}'_j; \mathbf{n}_k, \mathbf{n}'_k) & \text{if } \mathcal{O}(\mathbf{n}_k,\ \mathbf{n}'_k) = 0 \\ \mathcal{O}(\mathbf{n}_k,\ \mathbf{n}'_k) \cdot diff(\mathbf{p}_i, \mathbf{p}'_j; \mathbf{n}_k, \mathbf{n}'_k) & \text{otherwise} \end{cases}$$

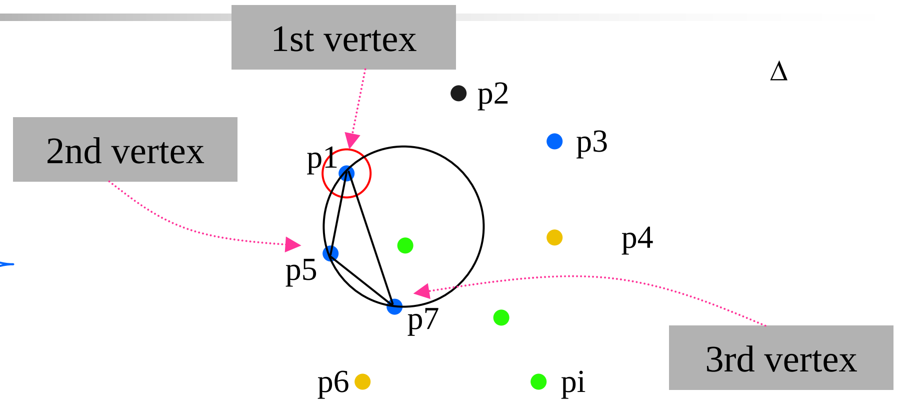
$$w_{(\mathbf{n}_k,\ \mathbf{n}'_k)} = \exp(-\mathcal{J}_k), \quad k = 1,\ 2, \cdots, n$$

Flow chart of implementation



Modeling algorithm

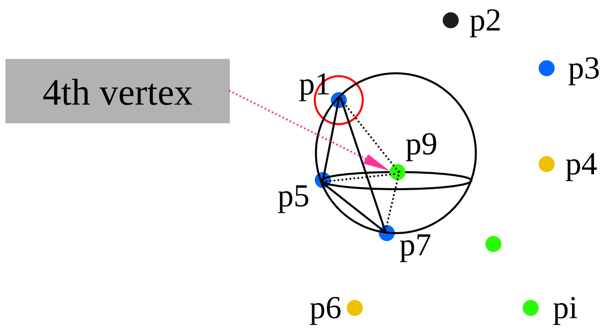




where:
c: is the center of circum-sphere
Δ: represents the plane of triangle

1. Min{dis(c,Δ)}

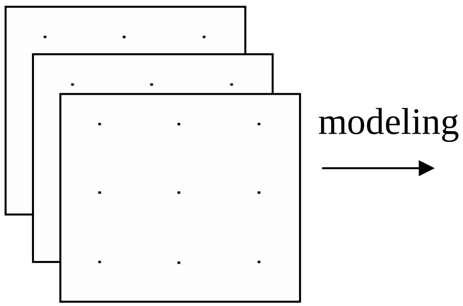
2. There is no other vertices inside the circum-sphere



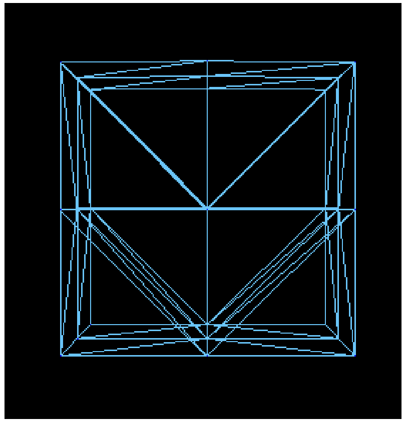
Note:

Different color of points represent the z coordinate are different.

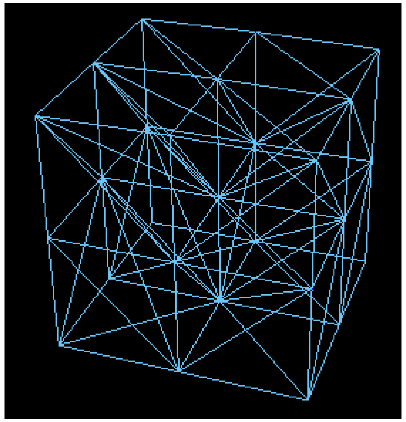
Modeling result



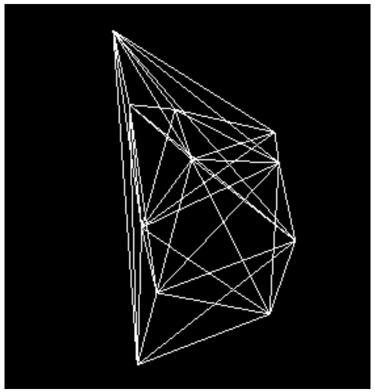
Regular dispersed simulation points (9*3=27 points)



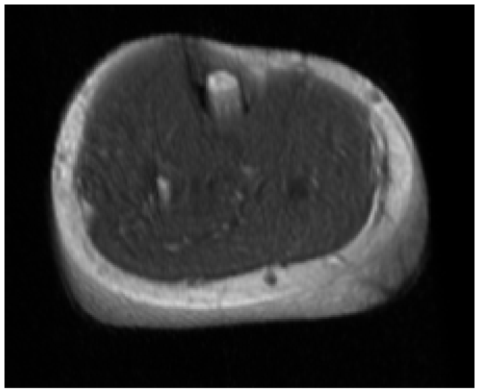
Face view (48 tetras)



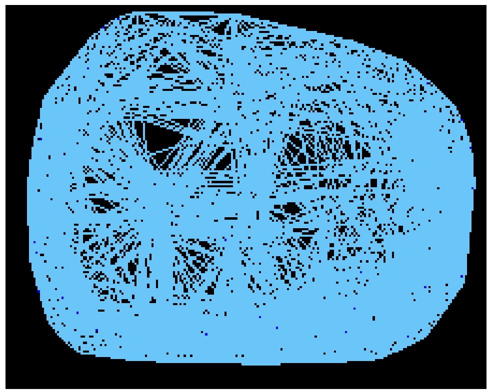
Side view



Irregular tetrahedra model of 12 random simulation points (20tets)



Actual volume from human calf



Modeled using 771 points (4344 tetras)

Deformation fields measurement

- **Sparse local deformation fields measurement**

$\mathcal{D} = \|\mathcal{R}(\mathbf{x}_1) - \mathbf{x}_2\|$ Local deformation corresponding to points in the PMS

$$\left.\begin{aligned} \mathbf{x}_1 &= (x_1,\ y_1,\ z_1) \\ \mathbf{x}_2 &= (x_2,\ y_2,\ z_2) \end{aligned}\right\}$$ Local coordinates of initial MR volume and deformed MR volume

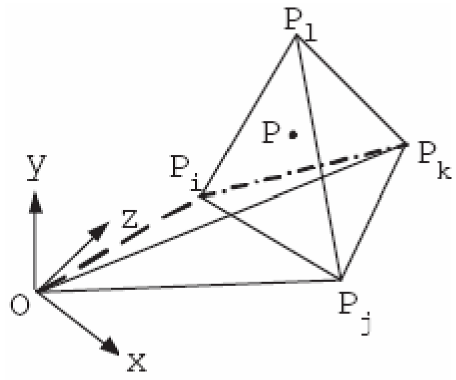
- **Interior dense deformation fields interpolation**

$$u(x, y, z) = u_i w_i + u_j w_j + u_k w_k + u_l w_l \quad (1)$$

$$\diamond P_i P_j P_k P_l = \diamond P P_j P_k P_l + \diamond P_i P P_k P_l + \diamond P_i P_j P P_l + \diamond P_i P_j P_k P \quad (2)$$

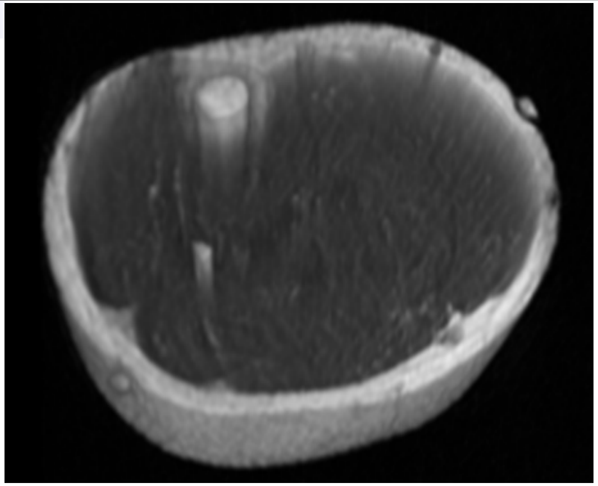
$$w_i = \frac{\diamond P P_j P_k P_l}{\diamond P_i P_j P_k P_l}, \quad w_j = \frac{\diamond P_i P P_k P_l}{\diamond P_i P_j P_k P_l}$$
$$w_k = \frac{\diamond P_i P_j P P_l}{\diamond P_i P_j P_k P_l}, \quad w_l = \frac{\diamond P_i P_j P_k P}{\diamond P_i P_j P_k P_l} \quad (3)$$

$$\diamond P_i P_j P_k P_l = \frac{1}{3!} \begin{vmatrix} x_i & y_i & z_i & 1 \\ x_j & y_j & z_j & 1 \\ x_k & y_k & z_k & 1 \\ x_l & y_l & z_l & 1 \end{vmatrix} \quad (4)$$

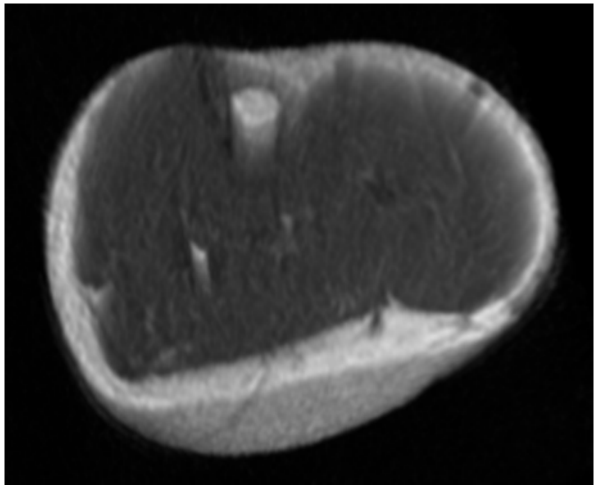


Experimental results

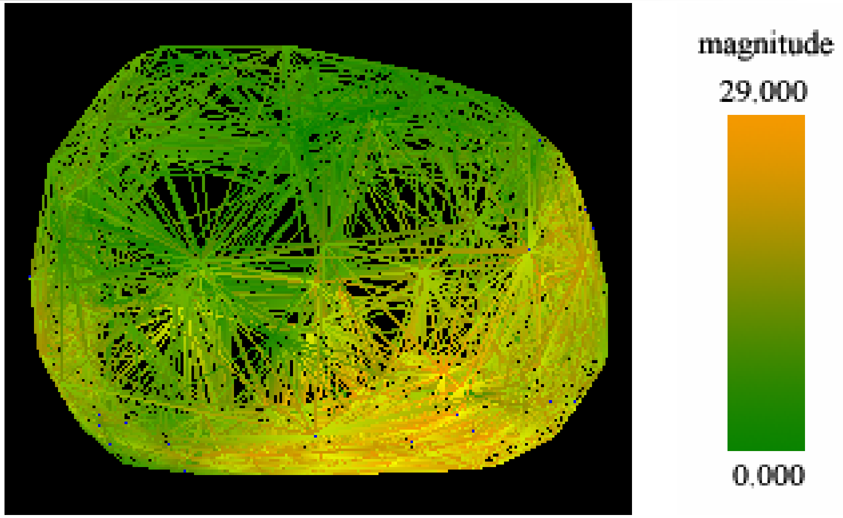
-sparse deformation fields



Initial volume of part human calf



deformed volume of corresponding area



Deformation magnitude on the node of FE model

Points in first volume:	1000
Points in final volume:	5000
Node numbers:	771
Tetrahedrons:	4344
Dark green:	non deformation
Orange:	deformation magnitude approximate to 29.00

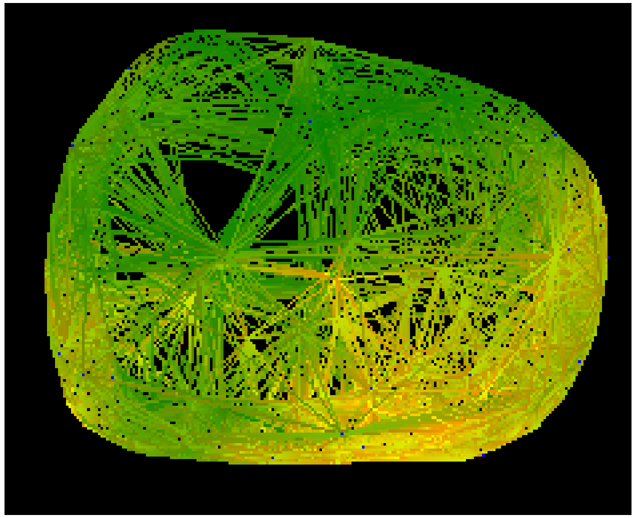
Evaluation

- **We compared our method with the robust feature matching algorithm proposed by George Q. Chen in 2001.**
  - ***First, re-sampling the initial volume using two sets of deformation fields. As the result, two computation volumes are obtained.***
  - ***Then, computation the root mean squared (RMS) of residual differences between computation volumes and actually deformed volume, respectively.***

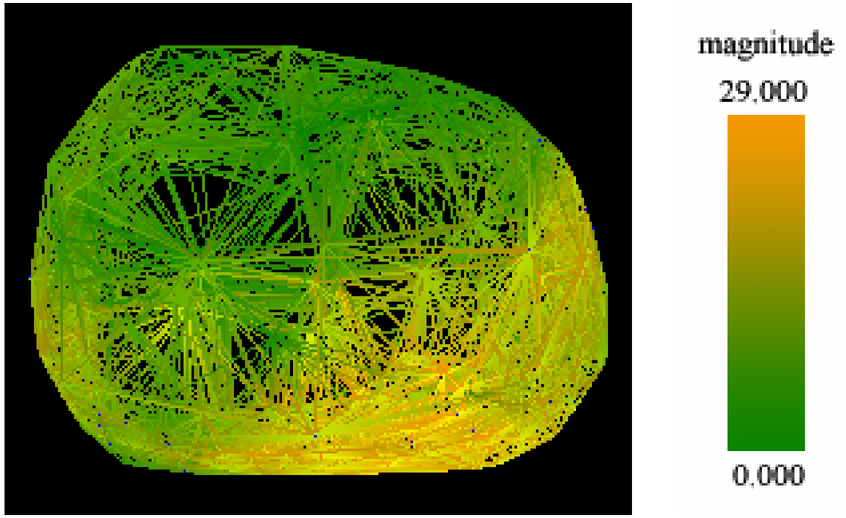
Approaches	Point Numbers in IV	Point Numbers in FV	Potential Matches	Tetrahedra	RMS
Our approach	1000	5000	771	4344	26.004284253441
George's approach	1000	5000	827	4798	26.3518732220353

(IV: Initial volume; FV: Deformed volume.)

Comparison



George's approach



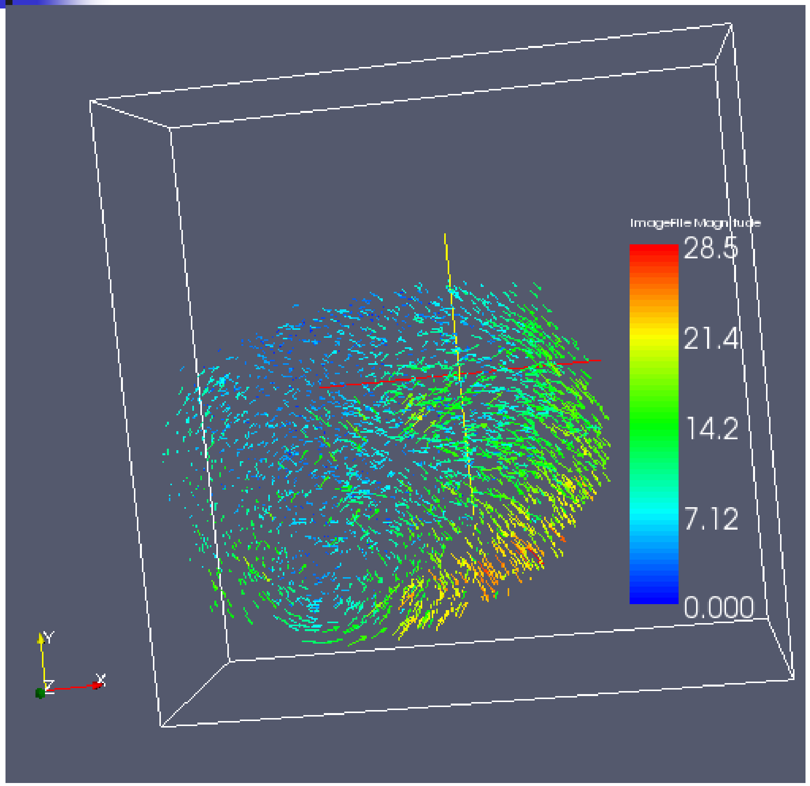
Our approach

Approaches	Point Numbers in IV	Point Numbers in FV	Potential Matches	Tetrahedra
Our approach	1000	5000	771	4344
George's approach	1000	5000	827	4798

(IV: Initial volume; FV: Deformed volume.)

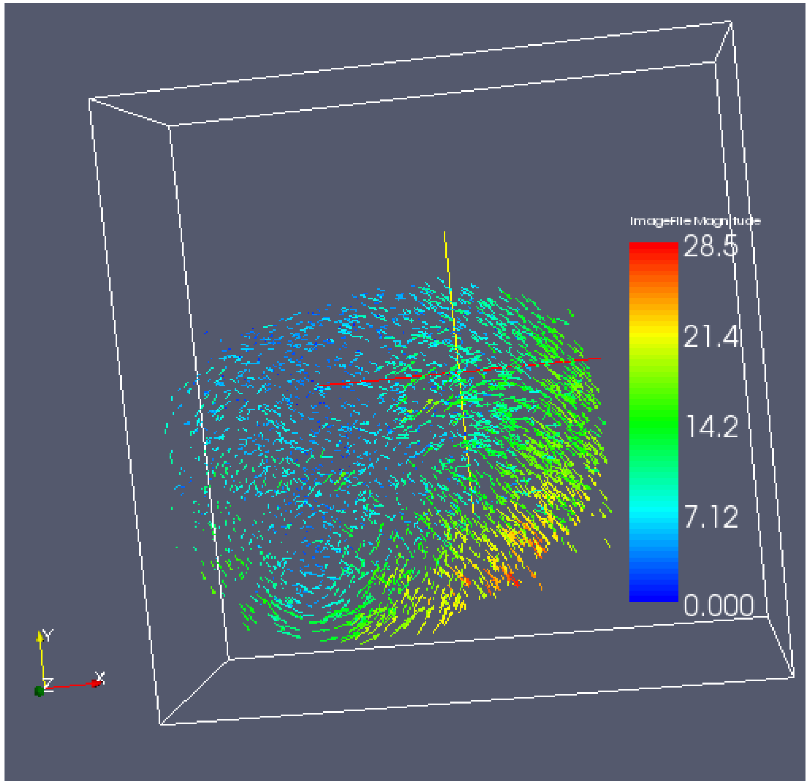
Note: The numeric data tell us that the matches obtained using George's approach are more than those obtained using the proposed approach. We will test cases where there are more inaccuracy matches.

Visualization of interior dense deformation fields



Deformation Field numbers: 10,000

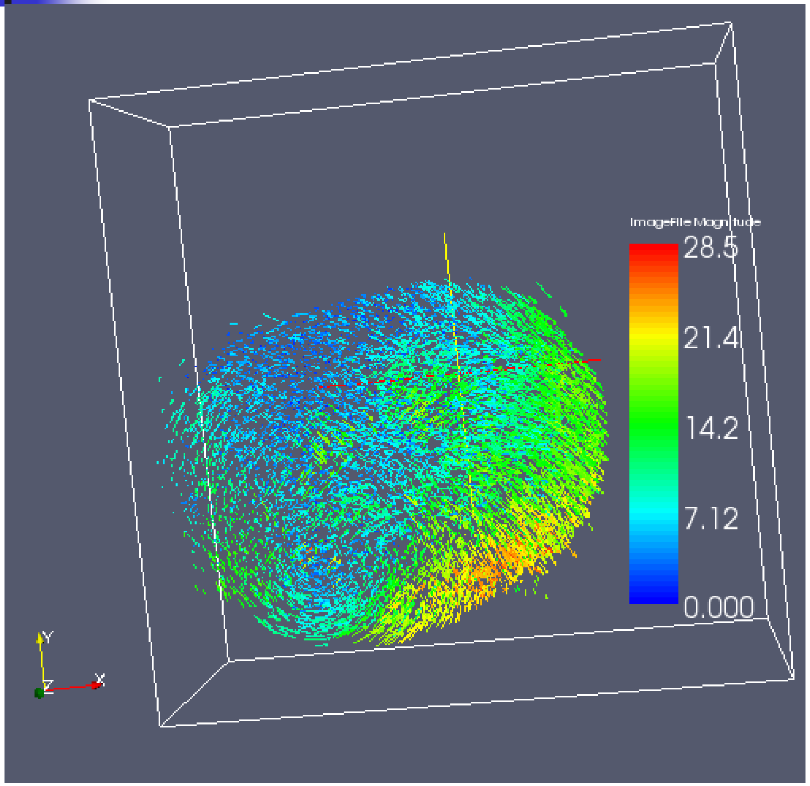
（George Q. Chen ）

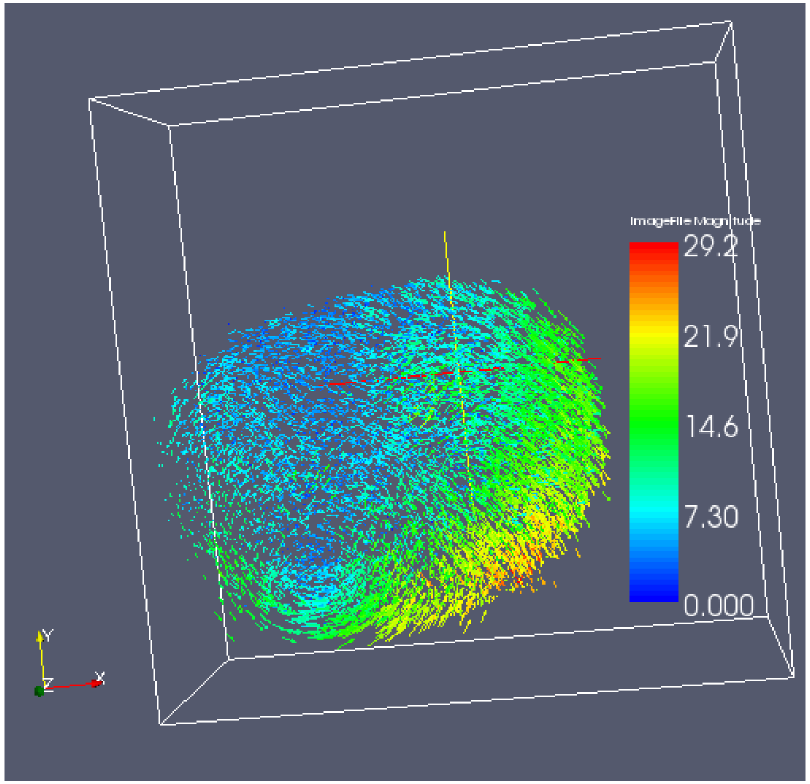


Deformation Field numbers: 10,000

（Our approach）

Visualization of interior dense deformation fields





Deformation Field numbers: 30,000

（George Q. Chen ）

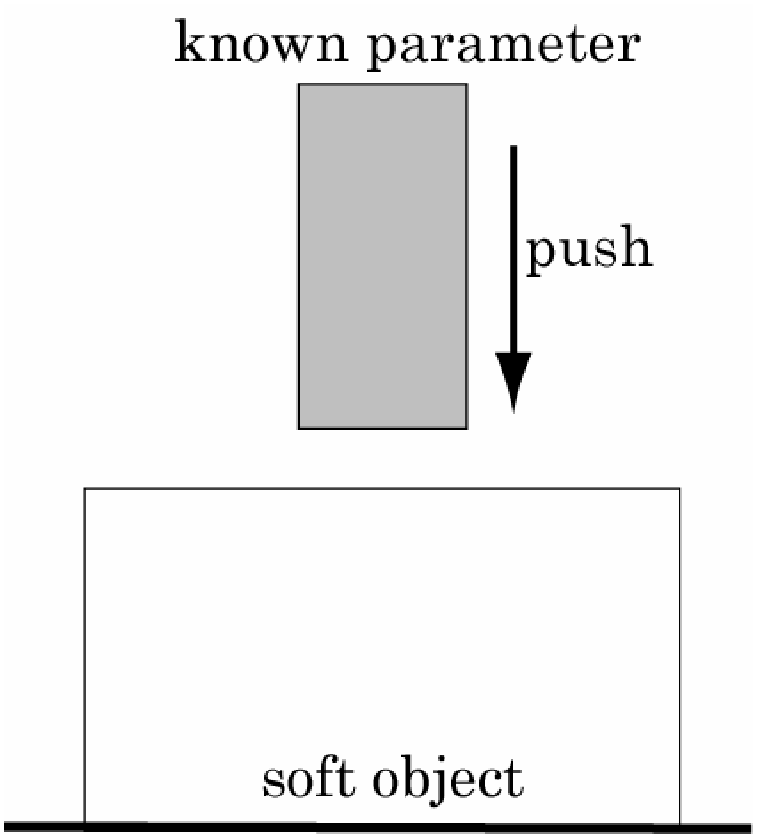
Deformation Field numbers: 30,000

（Our approach）

Evaluation

- Pros
  - Compared with a previous registration method, the proposed approach more suitable for interior deformation fields measurement.
  - The proposed approach fits for non-uniform objects.
  - The proposed approach need not initial contour or surface.
- Cons
  - The proposed approach need robust feature matching algorithm.
  - The feature numbers inside the object affects the accuracy of interior of deformation fields.

Identification of Deformation Parameters



1. Push a target soft object by another of which parameters are known.
2. Measure inner deformation of the both.
3. Identify parameters at the interface bet. the *known* and the *unknown*.

Identification without force/pressure sensing in MR

Conclusions

- Deformation fields based on feature point tracking.
- Experimental results suggest our approach works well.

Ongoing

- Evaluation using tissue phantoms
- Deformation property estimation without force/pressure sensing in MR