A FAST METHOD FOR SHAPE TEMPLATE GENERATION

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ABSTRACT

Disease diagnosis often requires segmentation of structures from a given image followed by shape analysis. Shape analysis entails quantifying the variability in a shape by constructing a template for a given population. We propose an orientation-invariant representation using varifolds for the shape elements in a given shape population and present a novel diffeomorphic Log-demons based template creation pipeline. The proposed method generates a good quality template at a significantly less computation time compared to state of the art method.

Index Terms— Non-rigid Registration, Diffeomorphism, Varifold, Shape Template

1. INTRODUCTION

The shape of a biological structure extracted from medical images is very useful to diagnose structural abnormalities. For instance, the shape variation in hippocampus (from MRI) is a biomarker for Alzheimer's disease. Any such analysis requires a shape template. Creation of shape templates involves registration of a group of shapes. The large deformation diffeomorphic metric mapping (LDDMM) based approach is popular for the registration task but is computationally expensive [1] which becomes prohibitive in shape template creation. We address the computational bottleneck by proposing a complete pipeline for building a biological shape model using an approach based on diffeomorphic demons which has a lower computational complexity and a comparable performance to LDDMM. We employ varifolds which are a distribution of unoriented tangent spaces for this purpose. The advantages of using varifolds for shape representation are as follows. 1) They are orientation-invariant and suitable for both continuous and discrete shapes, 2) They have proven (using the field of geometric measure theory) efficiency [2] and 3) They enable comparison of two shapes without any point-point matching.

LDDMM based approaches have been used for shape registration [3] and template creation [4], [5], [6], [7] including the state of the art reported in [8]. The general strategy adopted is to move an initial template towards an optimal shape template via iterative registration. Since the initial template is usually a random element from a set of shapes, the algorithm has to perform N registrations in each iteration, where N is the number of shapes in the set. Improvement in the time complexity is possible with a better choice of the initial template [9]. This is done by choosing random pairs from the set and computing the midway elements first. These are then moved toward the population's centroid to derive a template which is a better choice for the initial template in shape template creation.

In the context of computational anatomy, it is reasonable to assume that large scale deformation will not be required for template creation since the structures being aligned are from the same class. Hence, we propose a method for template creation which is based on (i) an iterative midway deformation by leveraging the common geometric features that may be present among the shapes (ii) with the deformation based on varifolds and Log-demon's algorithm. This method, which is guaranteed to generate a unique template, is computationally lighter as it is based on demons based registration and requires fewer registration steps.

2. METHOD

We begin with some basics on diffeomorphic Log-demon's algorithm and varifolds.

2.1. Diffeomorphic Log-Demon's Registration

In a registration algorithm, the displacement field(s) between a Moving (M) and Fixed (F) image/shape is being captured. Initially Thirion proposed a diffusion model for registration which was later posed by other researchers as an optimization problem with iterative update field (u) calculation. In the symmetric, Log-demon's diffeomorphic framework [10], the deformation is constrained to be invertible which is achieved by defining an energy E based on a similarity metric (sim)

$$E(u) = c_1.(sim(F \circ -s \circ exp(-u), M)$$
$$+ sim(F, M \circ s \circ exp(u))) + c_2.dist(s, s \circ exp(u))^2 \quad (1)$$

In Eqn.1, u is the velocity update field and c_1, c_2 are weights. This formulation is widely used and many similarity metrics have been explored, with feature based ones being popular [11],[12]. We choose to use this framework for registration.

2.2. Varifold Representation

A varifold is a representation for any orientable/non-orientable manifold using un-oriented tangent spaces. Thus, given a Euclidean space of the shape population it can be represented using tangent planes [2] and any natural shape of dimension d can be represented in a manifold as a d-dimensional integral varifold [13].

Let S be a submanifold of $\mathbb{R}^n$ and $G_d S$ be the Grassmanian manifold of dimension d in S. A d dimensional varifold in S is defined as a non-negative Radon measure in $S \times G_d S$. At every point s in S, there exists a tangent space $T_s S$. For any smooth test function $\omega : \mathbb{R}^n \times G_d S \rightarrow \mathbb{R}^n$,

$$\mu_S(\omega) = \int \omega d\mu = \int_S \omega(s, T_s S) dH^d(s) \qquad (2)$$

where H^d is the Hausdorff measure and μ is the Radon measure. The varifold is nothing but radon measure on S.

Let us represent a discrete shape namely, a mesh as a varifold. Let $s_i \subset S \ \forall i = 1...N$ be the mesh cell centers; $T_{s_i} S \subset G_d S$ be the tangent space associated with the cell centers. In the case of a triangulated mesh, let the three associated vertices of an ith cell be $(\hat{s}_i^1, \hat{s}_i^2, \hat{s}_i^3)$ with cell centers $s_i = (\hat{s}_i^1 + \hat{s}_i^2 + \hat{s}_i^3)/3$. Now $T_{s_i} S \subset G_d S$ and therefore, the direction of the cell can be calculated as normalized version of the cross product of two edges, $T_{s_i} S = (\hat{s}_i^2 - \hat{s}_i^1) \wedge (\hat{s}_i^3 - \hat{s}_i^1)$. Assume $a_i \in \mathbb{R}_+$ as the d-volume (H^d : 1-volume is length, 2-volume is area and so on). For the ith cell $a_i = \left\| (\hat{s}_i^2 - \hat{s}_i^1) \wedge (\hat{s}_i^3 - \hat{s}_i^1) \right\|$. The Varifold associated with each face in the mesh can be approximated as

$$\mu_{s_i}(\omega) \approx a_i \omega(s_i, T_{s_i} S) = a_i \delta_{s_i, T_{s_i} S} \qquad (3)$$

Further, a discrete shape can be expressed as a dirac varifold sum [2] given by

$$\mu(S) = \sum_{i=1}^{N} \mu_{(s_i)}(\omega) = \sum_{i=1}^{N} a_i \delta_{s_i, T_{s_i} S} \qquad (4)$$

The distance between any two shapes can be determined from the varifold norm as

$$< \mu(F), \mu(M) >$$
$$= \sum_{i=1}^{N} \sum_{j=1}^{M} a_i^F a_j^M K_e(s_i^F, s_j^M) K_v(V_i^F, V_j^M) \qquad (5)$$

with two Guassian Kernels $K_e = K_v = 1$.

We propose a method for shape template generation with two key novelties: a varifold-based diffeomorphic Log-demons registration algorithm to align shapes and an iterative midway deformation technique to ensure an efficient and optimal solution.

2.3. Varifold based Symmetric Diffeomorphic Log-demons (V-SDLD) Shape Registration

The iterative steps we follow in the Diffeomorphic Symmetric Log-Demons are clearly explained in Algorithm 1 where K_F and K_D are a Guassian Convolution Kernels and we used $\sigma_F = 1$ and $\sigma_D = 0.5$.

Algorithm 1 V-SDLD Registration algorithm

Result: Deformation from M to F

Initialization $\mu(M), \mu(F)$

Repeat

- Compute update field (u) using Eqn.8

- $u \leftarrow K_F \star u$

- Update the stationary velocity field (v) $\leftarrow K_D \star (log(exp(v) \circ exp(u)))$

- Accept the updation if energy Eqn.6 is decreasing

Until convergence

The update field u is computed by minimizing the following energy term.

$$E(u, s) = c_1.(sim(\mu(F), \mu(M \circ s \circ exp(u)))$$
$$+ sim(\mu(F \circ -s \circ exp(-u)), \mu(M)) + c_2.dist(s, s \circ exp(u))^2 \qquad (6)$$

where $s = exp(v)$ is the current transformation in each iteration. In our experiments, $c_1 = c_2 = .5$ and the varifold distance(VD)/similarity metric in Eqn.6 is defined using the varifold norm in Eqn.5. We can approximate $dist$ in Eqn.6 as $dist(s, s(u)) = \|Id - exp(u)\| \approx \|u\|$

The similarity function is given as

$$Sim(\mu(F), \mu(M)) = \|\mu(F) - \mu(M)\|^2$$
$$= < \mu(F), \mu(F) > + < \mu(M), \mu(M) >$$
$$- 2 < \mu(F), \mu(M) > \qquad (7)$$

The update field is found via gradient descent optimization and the optimal value is given by

$$u^* = \frac{1}{2}\left(\frac{\partial \ sim(\mu(F), \mu(M'))}{\partial u} + \frac{\partial \ sim(\mu(F'), \mu(M))}{\partial u} \right) \qquad (8)$$

where, $M' = M \circ s$ and $F' = F \circ -s$. The first term in Eqn.8

67

is given by

$$\frac{\partial \, sim(\mu(F), \mu(M'))}{\partial u}$$

$$= 0 + \sum_{j=1}^{N} (a_j^{M'})^2 \frac{\partial K_e(s_i^{M'}, s_j^{M'}) K_v(V_i^{M'}, V_j^{M'})}{\partial u}$$

$$- 2 \sum_{j=1}^{N} a_j^F a_j^{M'} \frac{\partial K_e(s_j^F, s_j^{M'}) K_v(V_j^F, V_j^{M'})}{\partial u} \tag{9}$$

Similarly the second term can be computed in each iteration for the updations using Algorithm 1.

2.4. Iterative midway deformation based shape template

Our aim is to compute a template shape in an iterative way such that it is guaranteed to be the optimal representation of a given shape population let it be E. This is achieved by calculating the (nearest neighbour) closest shape in the population for all shapes and then deforming them sequentially. As only symmetric deformation is considered, the midway deformed shape $\hat{S}_i$ will be the same irrespective of the pair order. Once all $\hat{S}_i$ are calculated, the result is taken as the updated shape population and the process is repeated until only one element remains in the updated population. These steps are given in Algorithm 2

The key advantages in the above method are: (i) No initial template is assumed and hence no bias is introduced, (ii) The most common shape features are prioritised naturally as most common shape will repeatedly come in the first step, (iii) Ordering of the shapes does not matter and (iv) As iterations proceed, the number of registrations reduces and thereby reducing the overall computational complexity of the template derivation process.

Algorithm 2 Shape template creation

Result: Shape template
Initialization all $S \in E$
Repeat

- Calculate pairwise similarity $\forall S \in E$ w.r.t. each $S \in E$ using Eqn.6

- Take the closest pairs(S_i, S_j) and apply Algorithm 1 $\rightarrow \mathrm{v}_i$

- Compute the midway deformed shapes$\hat{S}_i$ as $S_i \circ exp(v_i/2)$

- Replace all elements in E with $\hat{S}_i \forall i$

Until convergence

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3. RESULTS

The proposed method was implemented on an Intel(R) Xeon(R) CPU E5-2630 v3 @ 2.40GHz processor using unoptimized codes in MATLAB. We report on the performance of the V-SDLD registration algorithm and present the shape template generation results. Comparison is done using 2 metrics to assess the global and local similarity between shapes: (i) Varifold distance (Eqn.7) VD with normalisation; this is computed with $K_e = K_v = 1$ and (ii) Hausdorff Distance (HD) metrics. The shapes referred to in the results were extracted from T1 MRI volumes using manual annotation by an expert followed by mesh creation.

3.1. Assessment of proposed registration method

Ten Hippocampus pairs were registered using the proposed V-SDLD algorithm and the average VD between the registered and reference shapes was computed. This was found to be $0.0679 \pm 7.89e^{-04}$ which indicates good alignment. Fig.1 shows the results of registration for Hippocampus and Amygdala pairs for visual comparison, while Fig.2 shows the registration results for a sample Amygdala pair at different time instances.
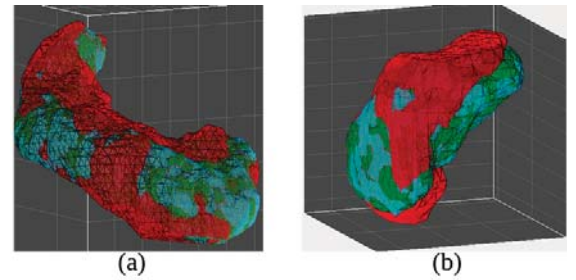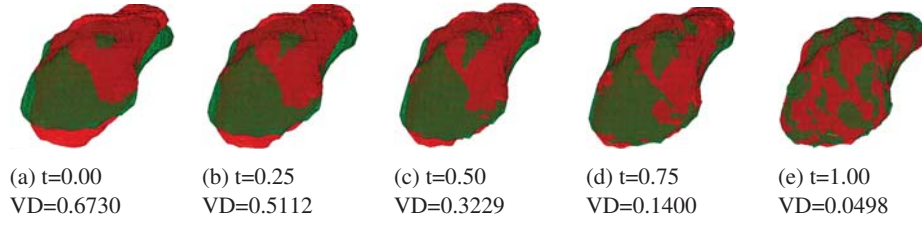

Fig. 1: Sample results for registration with V-SDLD (a)Hippocampus and (b)Amygdala (🟢 Reference , 🔴 Moving and 🔵 registered shapes)

Registered Shape Pair	LDDMM (hrs)	V-SDLD (hrs)
Hippocampus	5.70	0.05
Amygdala	0.98	0.01
Caudate	8.92	0.06
Puttamen	8.04	0.18
Thalamus	15.54	0.05

Table 1: Computational complexity for registration of pairs of brain structures

The computational complexity of V-SDLD was also compared with the shape varifold version of LDDMM-based state of the art method [8]. The time taken for registration (up-to a VD of 0.10 ± 0.01) is reported for 5 structures in Table 1.

68

(a) t=0.00	(b) t=0.25	(c) t=0.50	(d) t=0.75	(e) t=1.00
VD=0.6730	VD=0.5112	VD=0.3229	VD=0.1400	VD=0.0498

Fig. 2: The results of registration at different time instances and corresponding VD(mm) (● Reference and ● registered shapes)

These results indicate that registration with V-SDLD is consistently and significantly faster than LDDMM.

3.2. Assessment of shape template creation

Templates were created for the Left Hippocampus (T_H) and Amygdala (T_A) using 100 of these individual structure surfaces extracted from MRI images sourced from [14]. These were of subjects in 20-30 age group. These are shown in Fig.3.

The developed template was validated under the assumption that a good template is a good representation of the population it is developed from and it should help to differentiate elements from another population. Three validation sets of MRIs P1, P2 and P3 were considered. P1 is from the validation set of [14] that was used to generate T_A and T_H. So, P1 has MRIs of subjects from same population and same age group. P2 and P3 are from the OASIS project (http://www.oasis-brains.org/). MRIs in P2 belong to the same age group as P1 but are from a different population; MRIs in P3 belong to different age group and population. 10 Hippocampus and 10 Amygdala shapes were extracted from each set and these were compared against the templates. The computed values for VD and HD are given in Table2. The lowest(highest) distances are for P1(P3) which indicates that the templates are closest to the corresponding shapes from the same population in the same age group i.e. P1.

Next, we assessed if the shape template created by the proposed method is comparable to that created with the shape varifold version of [8](https://github.com/fshapes/fshapesTk). Two shape templates were created with [8] and V-SDLD using 5 hippocampus and 5 amygdala structures extracted from [14] dataset. Table 3 lists the average distances (VD, HD) between the templates and the 5 corresponding sample shapes used to construct the templates. Included here are the time taken for template construction. The distances are comparable for both methods (LDDMM and V-SDLD) which attests to the fidelity of the templates. This is remarkable given that the template construction is significantly (12 to 25 times) faster with V-SDLD for both structures. In Table 2 and Table 3, lowest HD value is obtained with V-SDLD indicating that it preserves the integrity of the structure better at local/fine level as well.
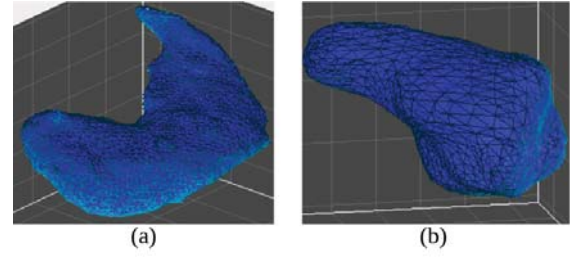
Fig. 3: Final templates for (a)Hippocampus and (b)Amygdala

	T_H		T_A	
	Average VD(mm)	Average HD(mm)	Average VD(mm)	Average HD(mm)
P1	0.89±0.13	3.23±0.54	0.82±0.22	2.10±0.56
P2	1.16±0.01	3.70±0.36	1.35±0.02	2.49±0.15
P3	1.18±0.02	3.82±0.65	1.37±0.02	2.62±0.25

Table 2: Average distance between T_A and T_H with corresponding structres in P1,P2 and P3

	Method	Average VD	Average HD	CPU time (hrs)
T_A	[8]	0.24±0.00	1.74±0.10	5.08
	V-SDLD	0.22±0.00	1.51±0.16	0.42
T_H	[8]	0.40±0.02	3.01±0.52	50.54
	V-SDLD	0.42±0.03	2.52±0.41	1.91

Table 3: Performance comparison between V-SDLD and shape varifold version of [8] for T_H and T_A

4. CONCLUSION

We have proposed a fast solution for shape template creation based on diffeomorphic Log-demons by using concepts from computational anatomy. The generated template is comparable in quality to the LDDMM-based state of the art method and can be used for clinical analysis of 3D shapes. There is sufficient scope to further reduce the computational time with code optimization or with GPU processing.

69

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