Fast registration of segmented images by normal sampling

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Abstract

It is known that image registration is mostly driven by image edges. We have taken this idea to the extreme. In segmented images, we ignore the interior of the components and focus on their boundaries only. Furthermore, by assuming spatial compactness of the components, the similarity criterion can be approximated by sampling only a small number of points on the normals passing through a sparse set of keypoints. This leads to an order-of-magnitude speed advantage in comparison with classical registration algorithms. Surprisingly, despite the crude approximation, the accuracy is comparable. By virtue of the segmentation and by using a suitable similarity criterion such as mutual information on labels, the method can handle large appearance differences and large variability in the segmentations. The segmentation does not need not be perfectly coherent between images and over-segmentation is acceptable.

We demonstrate the performance of the method on a range of different datasets, including histological slices and Drosophila imaginal discs, using rigid transformations.

Overview

Goal

- Fast approximative image registration

To make it fast only consider

- **class** — use **segmented images**
- neighborhood of **class boundaries**
- **motion normal** to boundaries

Problem definition

Find a transformation

$$T^* = \arg\min_{T\in\mathscr{T}} J(T)$$

$$\text{with} \quad J(T) = \int_{x\in\Omega} \varrho\Big(f(\boldsymbol{x}), g\big(T(\boldsymbol{x})\big)\Big)\,\mathrm{d}\boldsymbol{x}$$

for segmented images f, g.

Mutual information on labels (MIL) similarity criterion

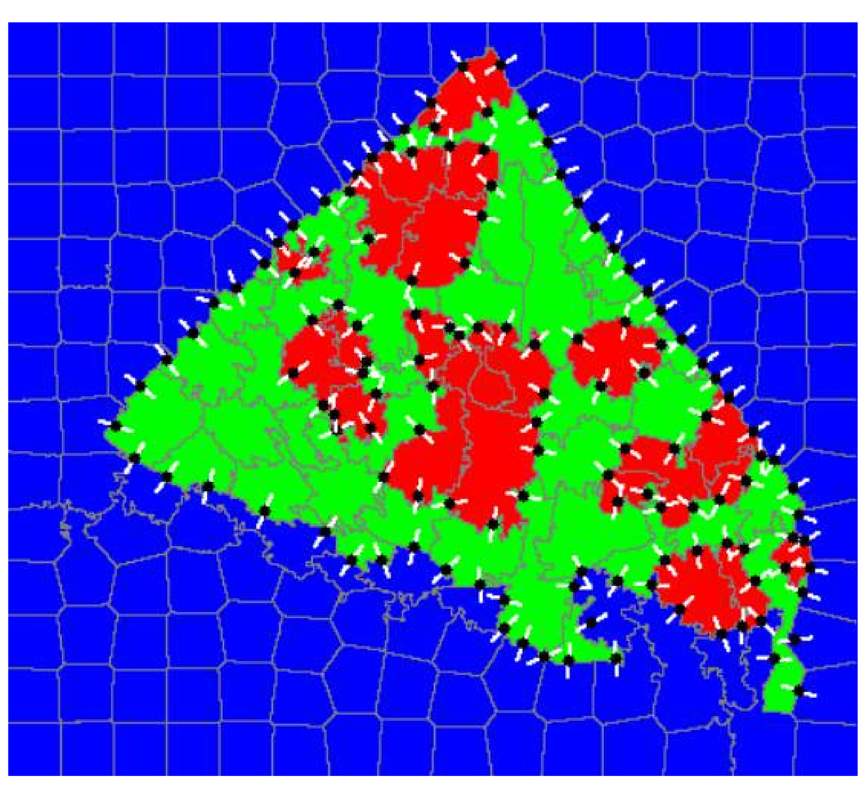
$$\varrho(l_f, l_g) = -\log \frac{P_{l_f l_g}}{P_{l_f} P_{l_g}}$$

$$\text{with} \quad P_{l_f l_g} = \frac{1}{\|\Omega\|} \big\|\{\boldsymbol{x}\in\Omega;\ f(\boldsymbol{x}) = l_f \wedge g(\boldsymbol{x}) = l_g\}\big\|$$

$$P_{l_f} = \sum_{l_g} P_{l_f l_g}, \quad P_{l_g} = \sum_{l_f} P_{l_f, l_g}$$

Image segmentation

- Supervised/manual segmentation
- Unsupervised segmentation
  1. Find SLIC superpixels [1]
  2. Calculate descriptors for each superpixels (color, texture,...)
  3. Cluster the descriptor vectors by the k-means algorithm to find $3 \sim 5$ classes.
- Joint segmentation and registration
  - Alternate between segmentation and registration [5]
  - Both maximize MIL criterion



Segmented image with keypoints (black), edge normals (white), and superpixels (gray).

Speed and accuracy

Comparison with the state of the art methods. Landmark error e [px]

Method	Time	$\mu(e)$	median(e)
ASSAR (Affine) [5]	45.78	37.04	13.45
bUnwarpJ (Fiji) [2]	572.98	51.44	10.19
ASSAR (B-splines) [5]	92.87	44.08	7.62
elastix (Affine) [4]	332.89	45.39	5.23
elastix (B-splines) [4]	555.64	52.17	4.80
RVSS (Fiji) [2]	91.26	83.86	4.89
SURF [3]+ASSAR	120.02	26.38	4.49
NEW	**11.92**	27.39	6.74

What takes time is mostly the preprocessing

Superpixels	k-means	Precompute	Registration	Total
6.38	3.94	0.94	**0.66**	11.92

References

[1] R. Achanta, A. Shaji, K. Smith, A. Lucchi, P. Fua, and S. Süsstrunk. SLIC superpixels compared to state-of-the-art superpixel methods. *IEEE Transactions on Pattern Analysis and Machine Intelligence,*, 34(11):2274–2282, Nov. 2012.

[2] I. Arganda-Carreras, C. Sorzano, R. Marabini, M. José Carazo, C. Ortiz-de Solorzano, and J. Kybic. Consistent and elastic registration of histological sections using vector-spline regularization. In *Computer Vision Approaches to Medical Image Analysis*, volume 4241, pages 85—95, 2006.

[3] H. Bay, T. Tuytelaars, and L. V. Gool. SURF: Speeded up robust features. *Computer Vision*, 3951:404–17, 2006.

[4] S. Klein, M. Staring, and K. Murphy. Elastix: a toolbox for intensity-based medical image registration. *Medical Imaging, IEEE*, 29(1), 2010.

[5] J. Kybic and J. Borovec. Automatic simultaneous segmentation and fast registration of histological images. In *International Symposium on Biomedical Imaging (ISBI)*, pages 774–777. IEEE, April–May 2014.

Criterion approximation

Normal approximation

- Integrate along boundaries

$$J_3(T) = \int_{z\in\partial\Omega f} \int_{-\gamma}^{\gamma} \varrho\Big(f(\boldsymbol{x}), g\big(T(\boldsymbol{x})\big)\Big)\,\mathrm{d}h\,\mathrm{d}\boldsymbol{z}$$

$$\text{with} \quad \boldsymbol{x} = \boldsymbol{z} + \boldsymbol{n}(\boldsymbol{z})h$$

- Class only depends on the normal shift ξ (approximately)

$$g\big(T(\boldsymbol{x})\big) = \tilde{g}\big(\boldsymbol{u}, \xi(\boldsymbol{z}) + h\big) / \|\boldsymbol{m}\|^2$$

$$\text{where} \quad \boldsymbol{m} = \big(\nabla T_0(\boldsymbol{z})\big)\boldsymbol{n}(\boldsymbol{z}) \quad \text{and} \quad \xi(\boldsymbol{z}) = \langle T(\boldsymbol{z}) - T_0(\boldsymbol{z}), \hat{\boldsymbol{m}}\rangle$$

- Criterion contributions D can be precomputed

$$J_4(T) = \int_{\boldsymbol{z}\in\partial\Omega f} D(\boldsymbol{z}, \xi(\boldsymbol{z}))\,\mathrm{d}\boldsymbol{z}$$

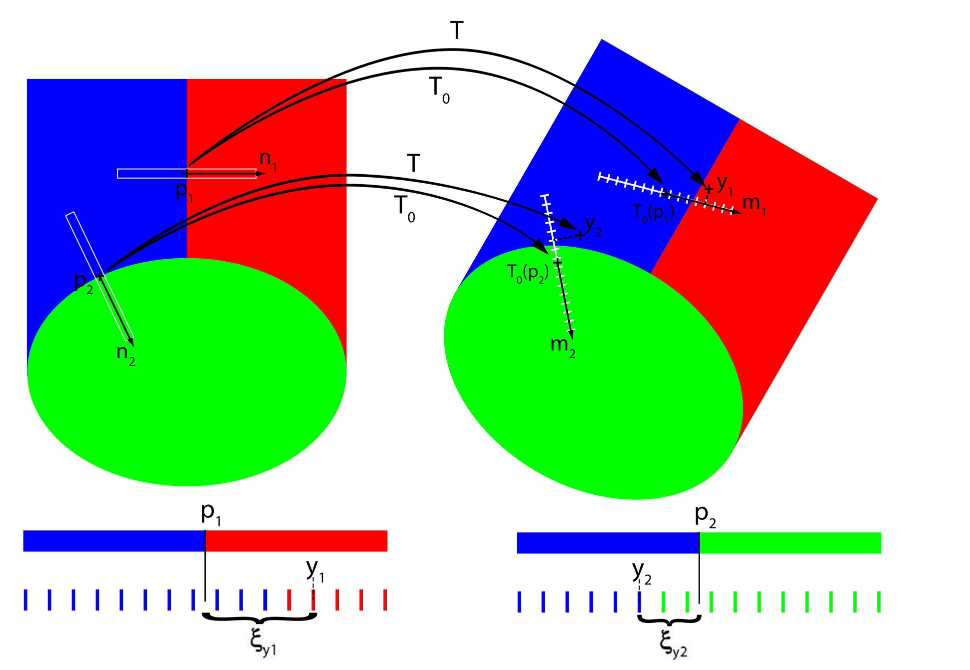
$$D(\boldsymbol{z}, \xi(\boldsymbol{z})) = \int_{-\gamma}^{0} \varrho\Big(l^-, \tilde{g}\big(\boldsymbol{u}, \xi(\boldsymbol{z}) + h\big)\Big)\mathrm{d}h + \int_0^{\gamma} \varrho\Big(l^+, \tilde{g}\big(\boldsymbol{u}, \xi(\boldsymbol{z}) + h\big)\Big)\mathrm{d}h$$

Discretization

- Find sparse keypoints $\boldsymbol{p}_i$ on boundaries
- Sample along normals $\tilde{g}_i(h) = \tilde{g}(\boldsymbol{p}_i, h) = g(T_0(\boldsymbol{p}_i) + \boldsymbol{m}_i h)$
- Discretized criterion

$$J_5(T) = \sum_{i=1}^{|P|} |S_i|\, D_i(\xi_i)$$

where D_i can be precalculated in time $O(\gamma)$



Iterative improvement

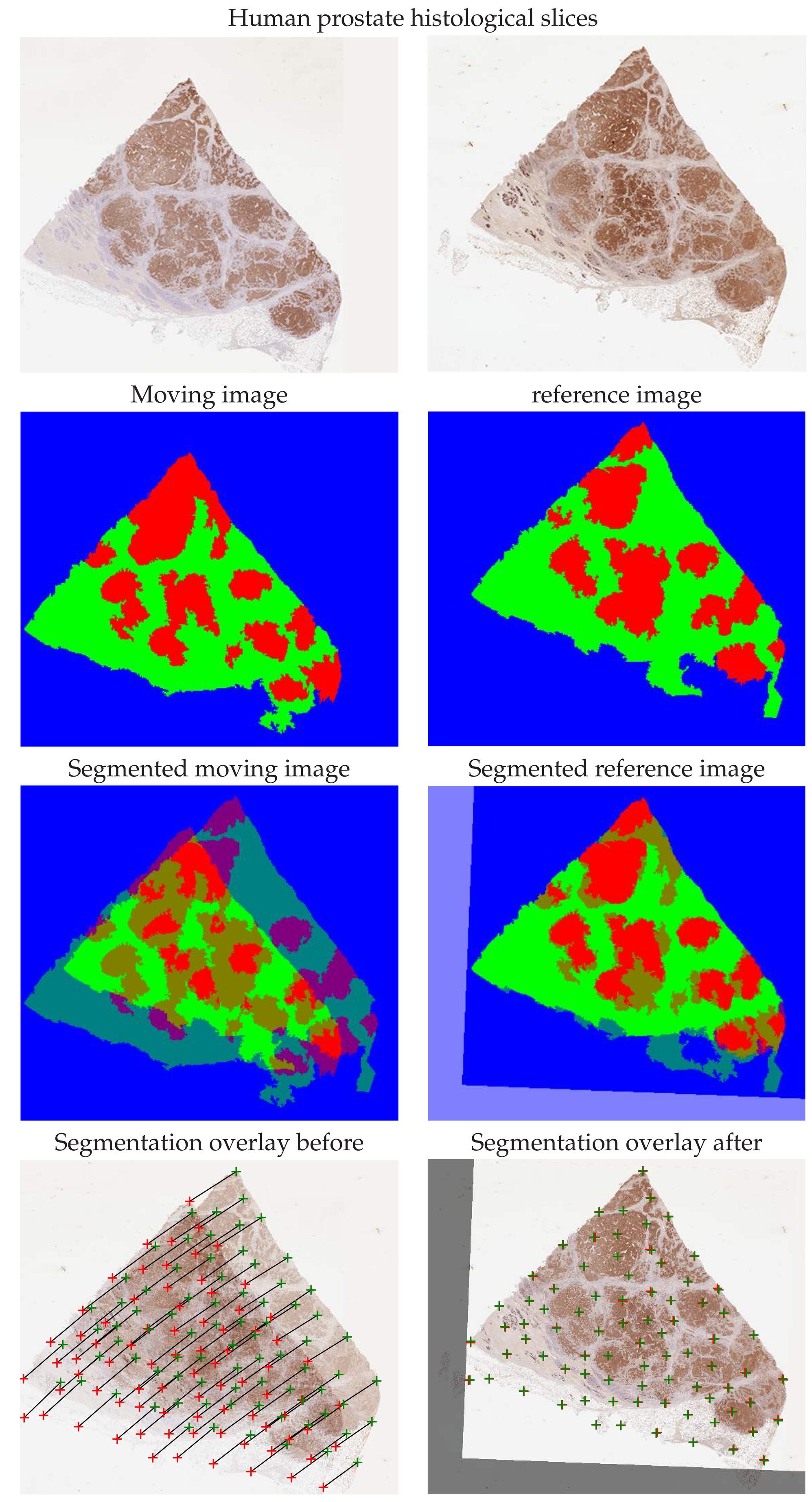
1. Given T_0, sample classes $\tilde{g}_i(\xi)$ along normals
2. Precalculate $P_{l_f l_g}$ and $D_i(\xi)$
3. Find T^* minimizing J_5
4. If the difference $T^* - T_0$ is big, repeat.

Multiresolution

- Downsampling by majority voting
- Subsample keypoints
- Maximum displacement larger at coarser scales

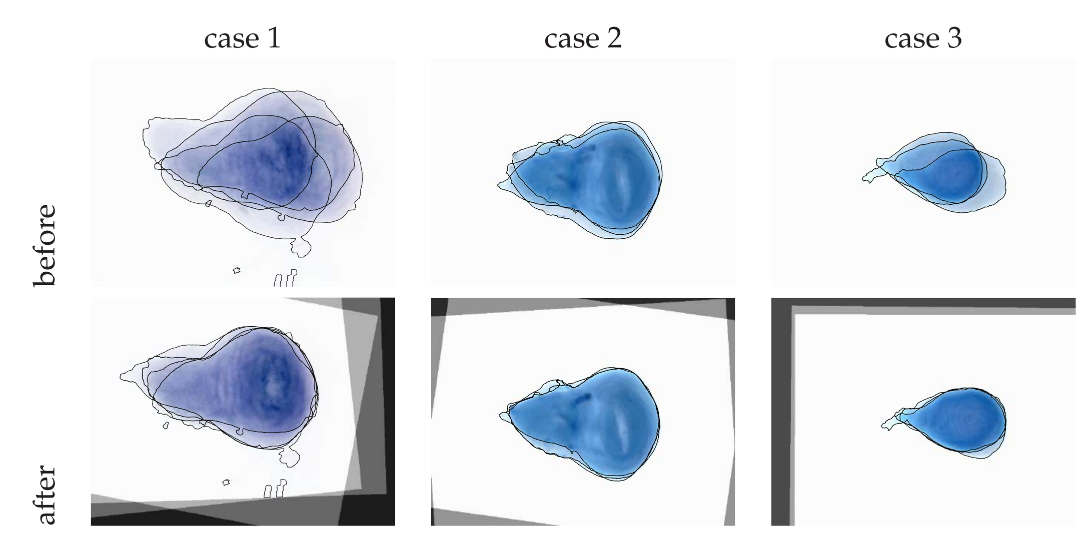
Registration example

Human prostate histological slices



Example gene expression images

Registering Drosophila imaginal disks, segmentation contours shown.



Example histology images

Validation using manually determined landmarks