Fast registration by boundary sampling and linear programming

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Abstract

We address the problem of image registration when speed is more important than accuracy. We present a series of simplification and approximations applicable to almost any pixel-based image similarity criterion. We first sample the image at a set of sparse keypoints in a direction normal to image edges and then create a piecewise linear convex approximation of the individual contributions. We obtain a linear program for which a global optimum can be found very quickly by standard algorithms. The linear program formulation also allows for an easy addition of regularization and trust-region bounds. We have tested the approach for affine and B-spline transformation representation but any linear model can be used. Larger deformations can be handled by multiresolution. We show that our method is much faster than pixel-based registration, with only a small loss of accuracy. In comparison to standard keypoint based registration, our method is applicable even if individual keypoints cannot be reliably identified and matched.

Overview

Goal

- Fast approximative image registration

Key ideas

- Minimize image dissimilarity criterion
- Subsample boundaries
- Ignore tangential motion
- Piecewise linear and convex approximation → **NEW:** linear program
- Iterative improvement, multiresolution

Problem formulation

$$c^* = \arg\min_c \underbrace{J_c(f, g(T(x)))}_{\text{data part}} + \underbrace{R(c)}_{\text{regularization}}$$

Image dissimilarity and its discretization

$$J_c(f,g) = \int_{x\in\Omega} \varrho\big(f(x), g(x)\big)\,\mathrm{d}x \approx \sum_{i=1}^{M} D_i(\xi_i) + \text{const}$$

Geometric transformation and regularization

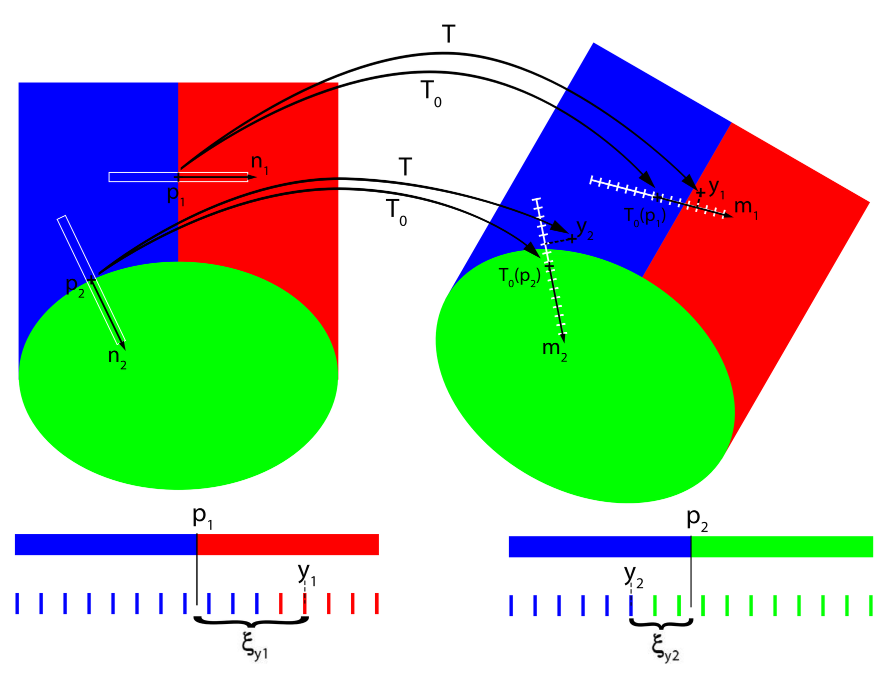
$$T(x) = \varphi_0(x) + \sum_{j=1}^{N} c_j \varphi_j(x)$$

$$R(c) = \gamma\,|\Delta c|_{\ell_1} + \lambda\,|c|_{\ell_1}$$

Normal approximation

$$T(p_i) \approx y_i + m_i \xi_i, \quad \text{where} \quad y_i = T_0(p_i), \quad m_i = \big(\nabla T_0(p_i)\big) n_i$$

$$\xi_i = \langle T(p_i) - y_i, \tilde m_i \rangle \quad \text{with} \quad \tilde m_i = m_i \,/\, \|m_i\|^2$$



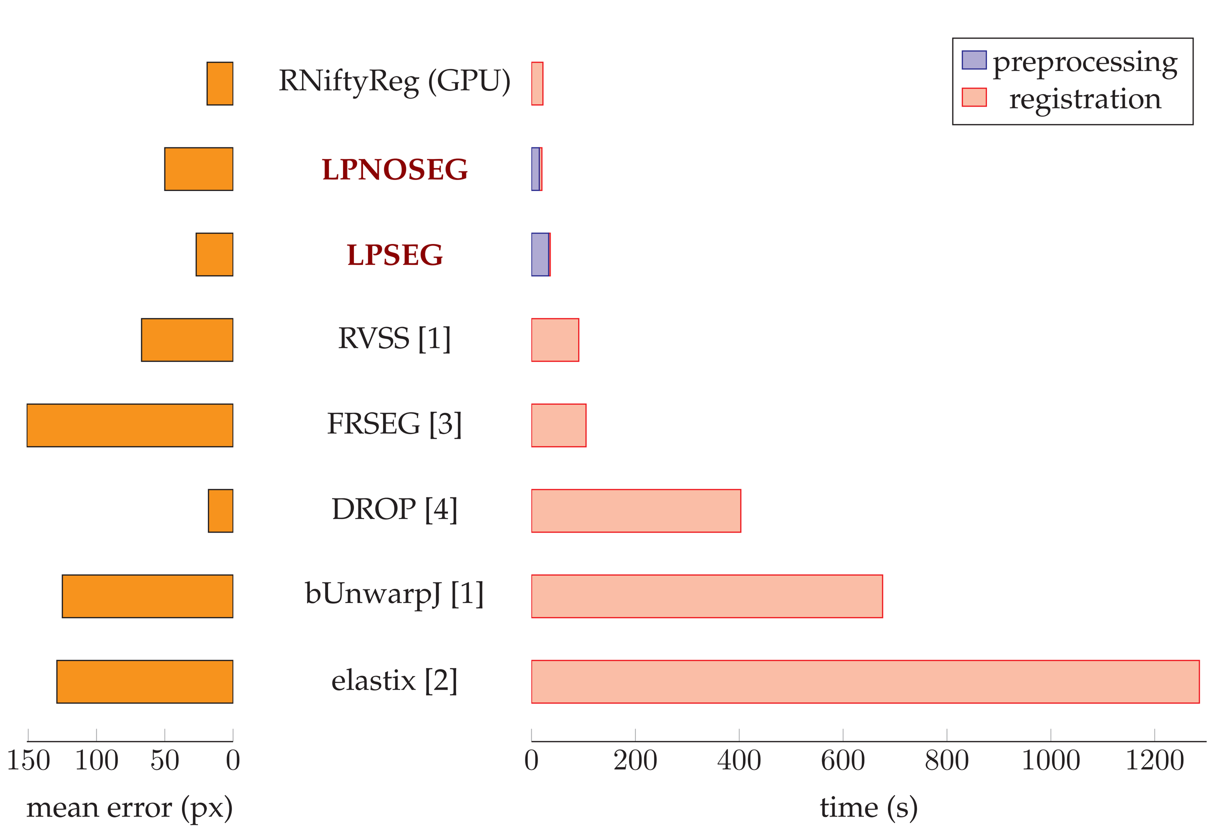
Iterative improvement

1. Given T_0, sample $\tilde f_i(h)$, $\tilde g_i(h)$ along normals
2. Precalculate $D_i(\xi)$, fit piecewise approximation
3. Find c^* by linear programming
4. If the difference $T^* - T_0$ is big (exceeds ξ_{max} or 60°) in > 10 % of points, repeat.

Multiresolution

- Downsample images
- Subsample keypoints
- Results at coarse scale → T_0 for the next finer scale
- First affine transformation, then B-splines with increasing N

Speed and accuracy



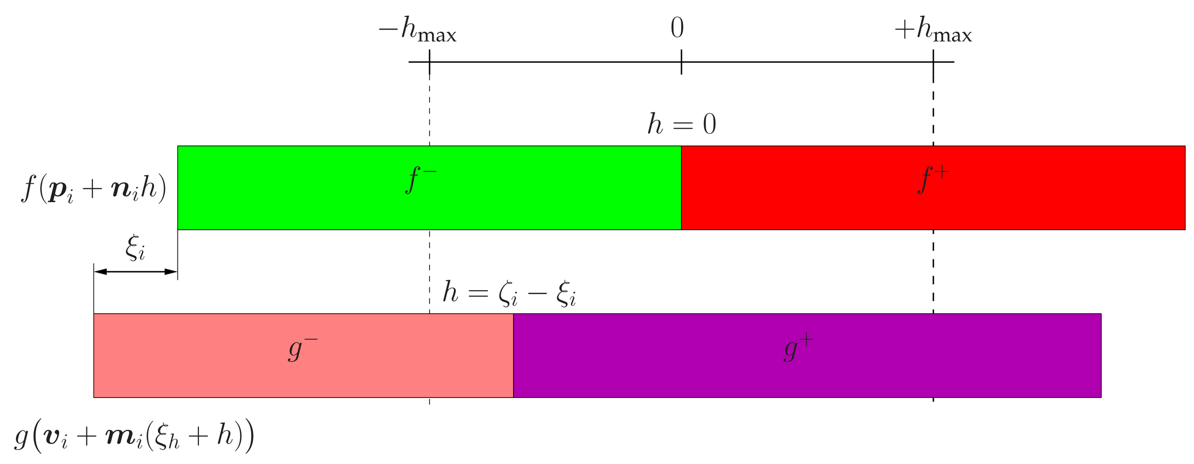
≈ 5000 × 3000 pixels
manually extracted landmark pairs
implementation in Julia, Intel Core i7, 2.1 GHz, 8GB RAM

Piecewise linear approximation

Contribution of a point p_i as a function of the shift ξ_i

$$D_i(\xi_i) = \sigma_i \int_{h=-h_{max}}^{h_{max}} \varrho\Big(\underbrace{f(p_i + n_i h)}_{\tilde f_i(h)}, \underbrace{g\big(v_i + m_i(\xi_i + h)\big)}_{\tilde g_i(h)}\Big)\,\mathrm{d}h \approx \sigma_i \sum_{h=-h_{max}}^{h_{max}} \varrho\big(\tilde f_i(h), \tilde g(h)_i\big)$$

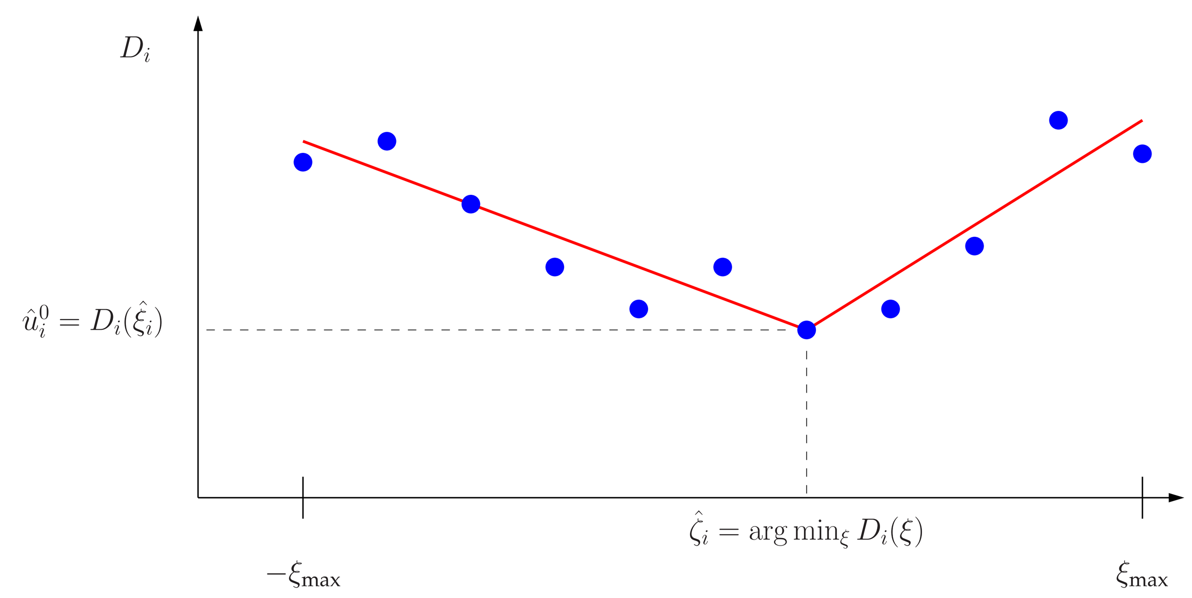
For homogeneous regions



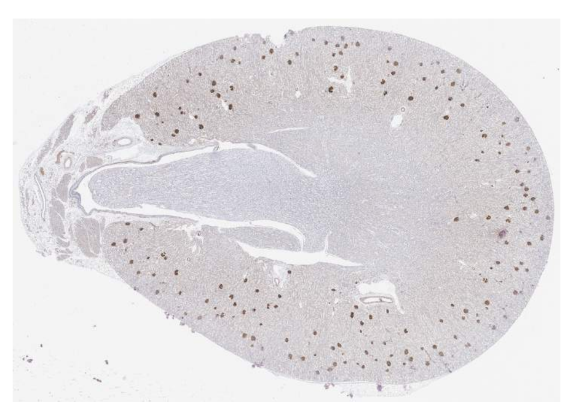
$$D_i(\xi_i) = \begin{cases} u_i^0 + h_{max} u_i^+ & \text{if } h_{max} \le t \\ u_i^0 + t u_i^+ & \text{if } 0 \le t \le h_{max} \\ u_i^0 + t u_i^- & \text{if } -h_{max} \le t \le 0 \\ u_i^0 - h_{max} u_i^- & \text{if } t \le -h_{max} \end{cases} \quad \text{with} \quad \begin{aligned} t &= \zeta_i - \xi_i, \\ u_i^0 &= h_{max}\big(\varrho(f^-,g^-) + \varrho(f^+,g^+)\big) \\ u_i^+ &= \varrho(f^+,g^-) - \varrho(f^+,g^+) \\ u_i^- &= \varrho(f^-,g^-) - \varrho(f^-,g^+) \end{aligned}$$

On real data use least-squares fitting to find $u_i^\pm$ from sampled $D_i(\xi_i)$ for $\xi_i \le \xi_{max}$.

Assume $|\zeta_i| \le \xi_{max}$.



Finding keypoints



Rat kidney, Podocin staining

LPSEG

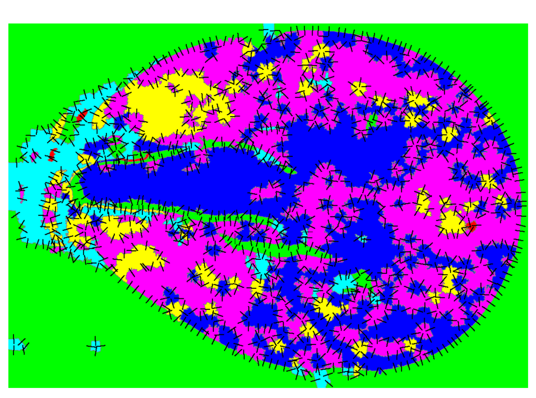
- Segmentation *(superpixels+k-means)*
- Finding class boundaries
- Greedy subsampling

Criteria: MIL, Hamming distance

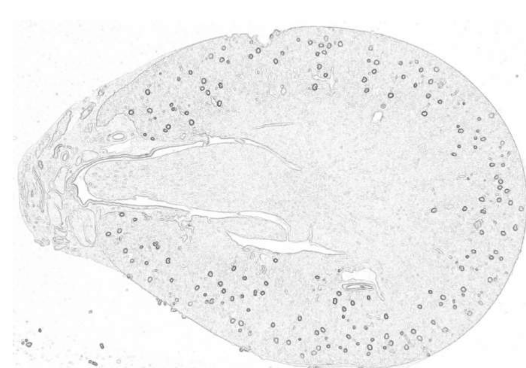
LPNOSEG

- Gaussian smoothing
- Gradient magnitude calculation
- Greedy subsampling

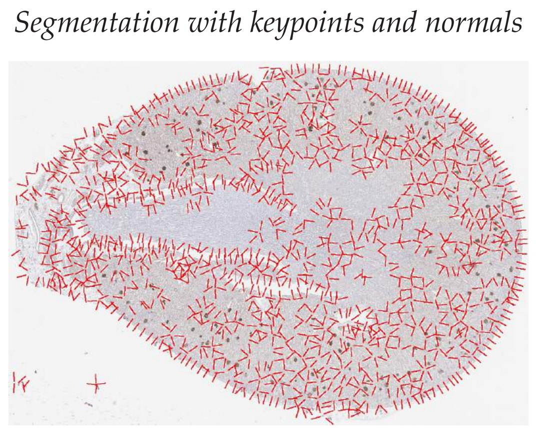
Criteria: SSD, correlation, MI…



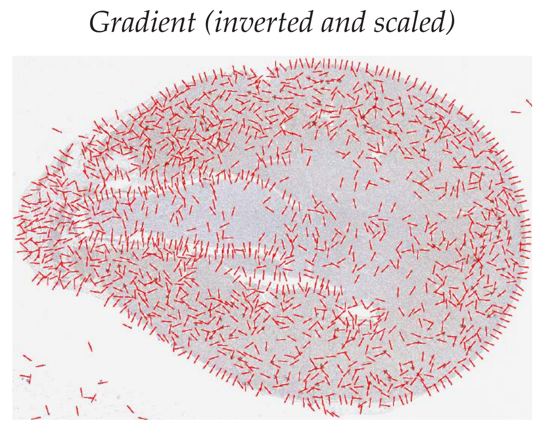
Segmentation with keypoints and normals



Gradient (inverted and scaled)



1463 LPSEG keypoints and normals



1463 LPNOSEG keypoints and normals

Linear program

Absolute values and piecewise approximations replaced by auxiliary variables

$$c^* = \arg\min_{c} \min_{r,s,D} \left[\sum_{i=1}^{M} D_i + \gamma \sum_{(j,k)\in N} r_{jk} + \lambda \sum_{j=1}^{N} s_j\right]$$

$$\xi_i = \langle \varphi_0(x_i) - v_i, \tilde m_i \rangle + \sum_{j=1}^{N} c_j \langle \varphi_j(x_i), \tilde m_i \rangle$$

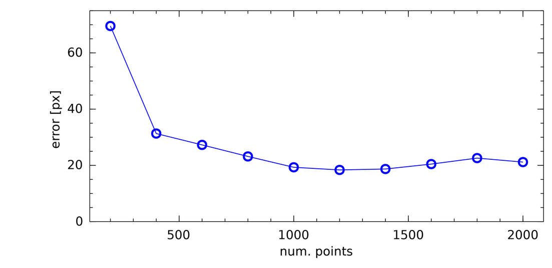
$$\begin{aligned} &c_j - c_k \le r_{jk}, && c_j \le s_j, && D_i \ge (\xi_i - \zeta_i) u_i^+, && \xi_i \le \xi_{max} \\ &c_j - c_k \le r_{jk}, && -c_j \le s_j, && D_i \ge (\xi_i - \zeta_i) u_i^-, && -\xi_i \le \xi_{max} \end{aligned}$$

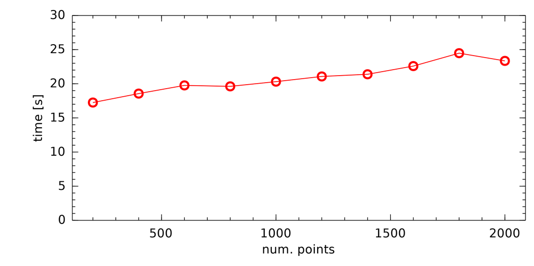
$O(N+M)$ unknowns, $O(N+M)$ constraints.

LP method	time
Gurobi simplex	54 ms
Gurobi interior point	79 ms
GLPK simplex	145 ms
GLPK interior point	failed

$M = 1200$ keypoints
$N = 128$ B-spline coefficients

Number of sampling points

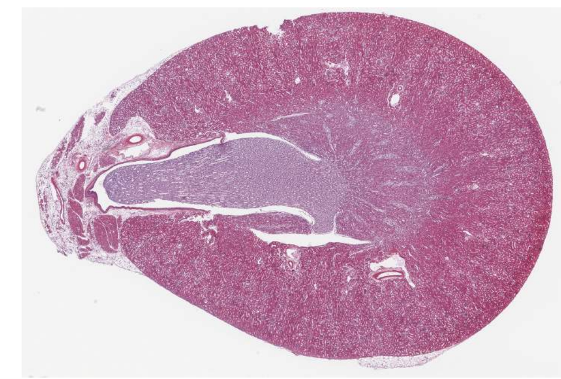




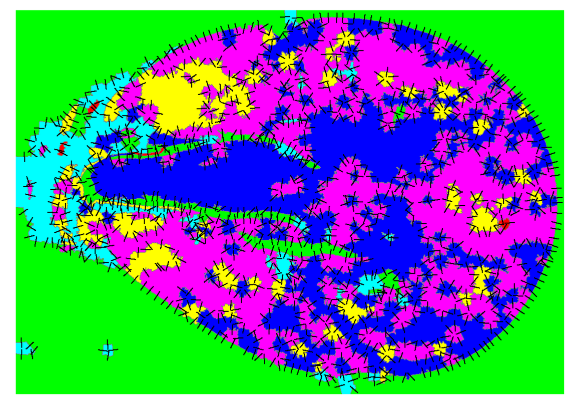
Example results

Rat kidney histology (≈ 1100 × 800 pixels)
LPSEG, MIL criterion, 1.8 s segmentation, 0.2 s registration

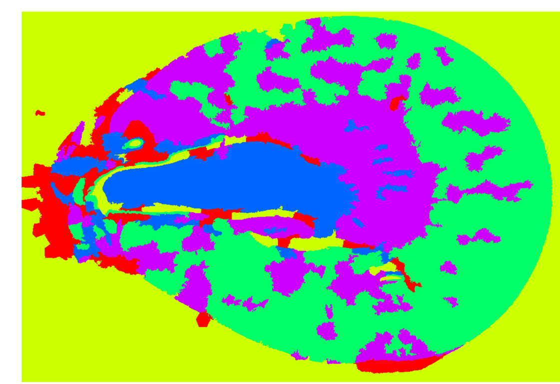
Reference image (Podocin staining)



Moving image (H & R staining)



Segmentation & keypoints

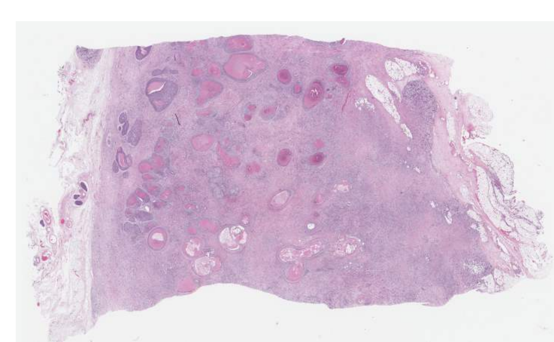


Segmentation

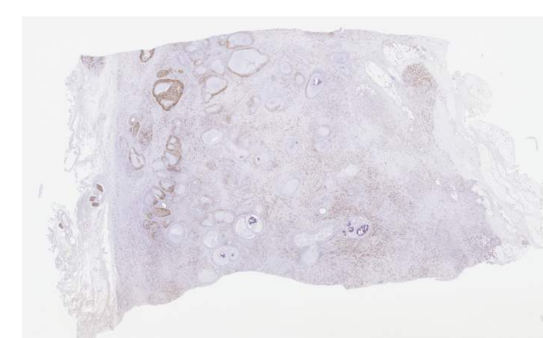
Image overlay before

Image overlay after

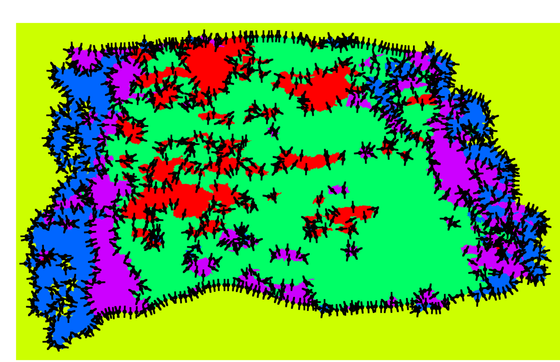
Human prostate histology (≈ 5000 × 3000 pixels)
LPSEG, MIL criterion, 33 s segmentation, 3 s registration



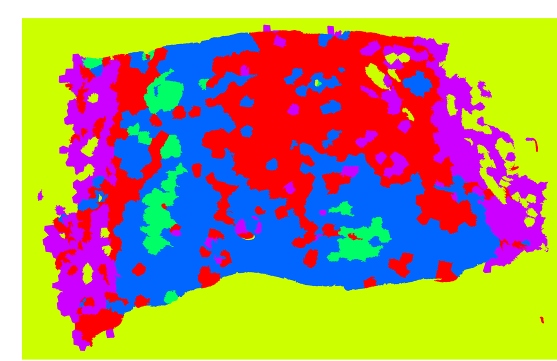
Reference image (H & E staining)



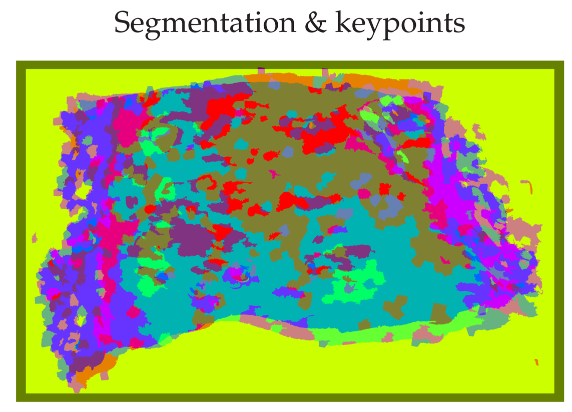
Moving image (PR staining)



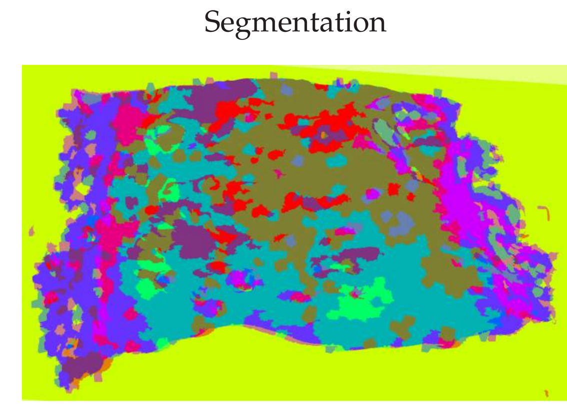
Segmentation & keypoints



Segmentation



Segmentation overlay before



Segmentation overlay after

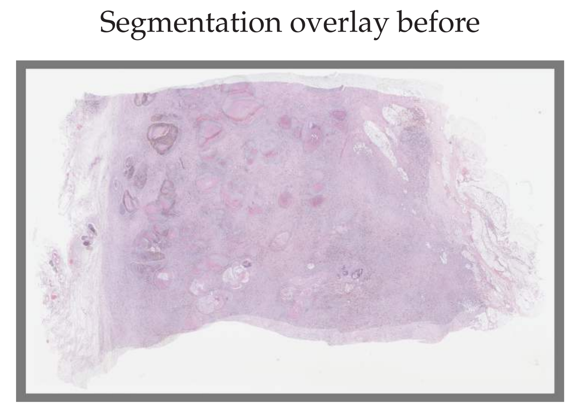


Image overlay before

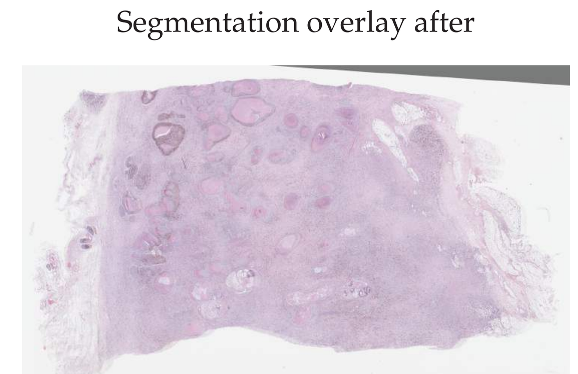
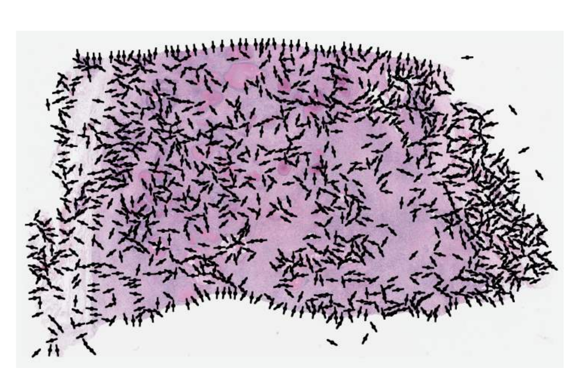


Image overlay after

LPNOSEG, gaussian MI criterion, 15 s finding keypoints, 5 s registration.



Gradient keypoints

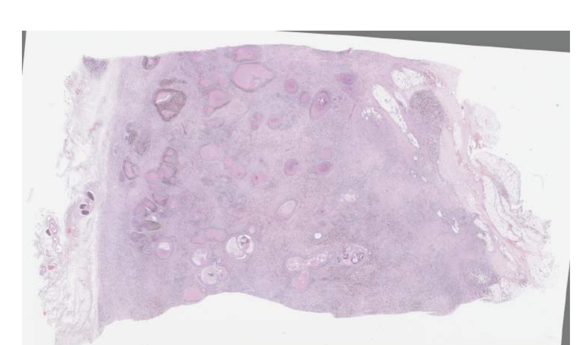


Image overlay after

References

[1] I. Arganda-Carreras *et al.*, "Consistent and elastic registration of histological sections," in *CVAMIA: Computer Vision Approaches to Medical Image Analysis*, May 2006, pp. 85–95.
[2] S. Klein, M. Staring, and K. Murphy, "Elastix: a toolbox for intensity-based medical image registration," *IEEE Trans. Medical Imaging*, vol. 29, no. 1, 2010.
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[4] B. Glocker *et al.*, "Dense image registration through MRFs and efficient linear programming," *Medical Image Analysis*, vol. 12, no. 6, pp. 731–741, 2008.