Reconstruction of 3-D Histology Images by Simultaneous **Deformable Registration**

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Motivation

Creation of geometrically coherent 3-D histological volumes from serial 2-D sections is difficult due to sectioning process introducing artifacts and distortions (holes, folding, tears)

Current approaches:

- Registration between consecutive sections [e.g. Cifor et al, 2009] Problem: Drifts in stack direction
- Registration of sections to external reference (e.g. block-face) images [e.g. Bardinet et al, 2002] Problem: Smaller resolution, structural homogeneity between consecutive sections not guaranteed

Our approach: Registration of histological sections simultaneously to their corresponding reference images and to their neighboring sections

Problem Formulation

Given a set of histology images $\mathcal{I} = \{\mathcal{I}_1, \dots, \mathcal{I}_n\}$ and their corresponding block-face images $\mathcal{J} = \{\mathcal{J}_1, \dots, \mathcal{J}_n\}$, we seek a set of sufficiently smooth transformations $\mathbf{T} = \{T_1, \dots, T_n\}$, which align each \mathcal{I}_i to \mathcal{J}_i and to its adjacent neighbors $\mathcal{I}_{i-1}, \mathcal{I}_{i+1}$:

$$\mathbf{T}^* = \arg\min_{\mathbf{T}} \mathbf{E}_R(\mathcal{I}, \mathcal{J}, \mathbf{T}) + \mathbf{E}_C(\mathcal{I}, \mathbf{T}) + \mathbf{E}_S(\mathbf{T})$$

 $\mathbf{E}_R(\mathcal{I}, \mathcal{J}, \mathbf{T})$: energy between histology images and block-face images

 $\mathbf{E}_C(\mathcal{I},\mathbf{T})$: energy between consecutive histology slices

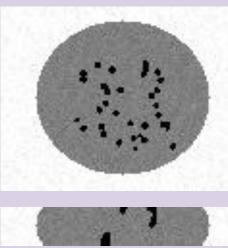
 $\mathbf{E}_{S}(\mathbf{T})$: independent *in-plane* regularizer

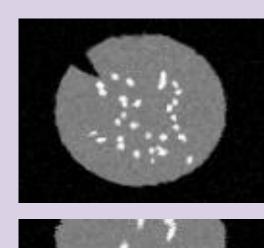
Evaluation

Synthetic data:

- Including tubular structures, tearing, random FFDs, staining, intensity variability, Gaussian noise
- Quantitative evaluation









reference

endpoint error

Real data:

- Rat kidney, HE staining
- 580 sections of 9 μm thickness

AE: relative angular error EE: absolute endpoint error IE: interpolation error NE: normalized IE

Markov Random Fields for Simultaneous Registration

in-plane grid nodes/

FFD control points p; q

consecutive link

labels l_r , displacements \mathbf{d}^l

- Uniform 2-D free-form deformation (FFD) grid for each T_i
- MRF [Glocker et al, 2008]: Assignment of a node to each control point of an FFD grid \mathcal{G}^{\imath}
- Creation of links between neighboring in-plane control points and neighbors in consecutive FFD grids
- Minimization of MRF energy ${f E}$ for labeling l

$$\begin{split} \mathbf{E}(\mathbf{l}) &= \sum_{i=1}^{n} \sum_{\mathbf{p} \in \mathcal{G}^{i}} \Theta_{R}^{i}(l_{\mathbf{p}}) + \\ \gamma \sum_{i=1}^{n-1} \sum_{\mathbf{p} \in \mathcal{G}^{i}, \\ \mathbf{p} \in \mathcal{G}^{i+1}} \Theta_{C}^{i,i+1}(l_{\mathbf{p}}, l_{\mathbf{q}}) + \lambda \sum_{i=1}^{n} \sum_{\mathbf{p} \in \mathcal{G}^{i}} \sum_{\mathbf{r} \in \mathcal{N}(\mathbf{p})} \Theta_{S}^{i}(l_{\mathbf{p}}, l_{\mathbf{r}}) \end{split}$$

with weighting factors γ, λ , the set of in-plane neighbors \mathcal{N} of control point **P**, and costs $\Theta_R^i(l_{\mathbf{p}}) = \int_{\Omega_i} \eta(\mathbf{x}, \mathbf{p}) D_1(\mathcal{I}_i(\mathbf{x} + \mathbf{d}_{l_{\mathbf{p}}})), \mathcal{J}_i(\mathbf{x})) d\mathbf{x}$

$$\Theta_C^{i,i+1}(l_{\mathbf{p}}, l_{\mathbf{q}}) = \int_{\Omega_i} \eta(\mathbf{x}, \mathbf{p}) \eta(\mathbf{x}, \mathbf{q}) D_2(\mathcal{I}_i(\mathbf{x} + \mathbf{d}_{l_{\mathbf{p}}}), \mathcal{I}_{i+1}(\mathbf{x} + \mathbf{d}_{l_{\mathbf{q}}})) d\mathbf{x}
\Theta_S^i(l_{\mathbf{p}}, l_{\mathbf{r}}) = \int_{\Omega_i} R(\mathbf{d}_{l_{\mathbf{p}}}, \mathbf{d}_{l_{\mathbf{r}}}) d\mathbf{x}$$

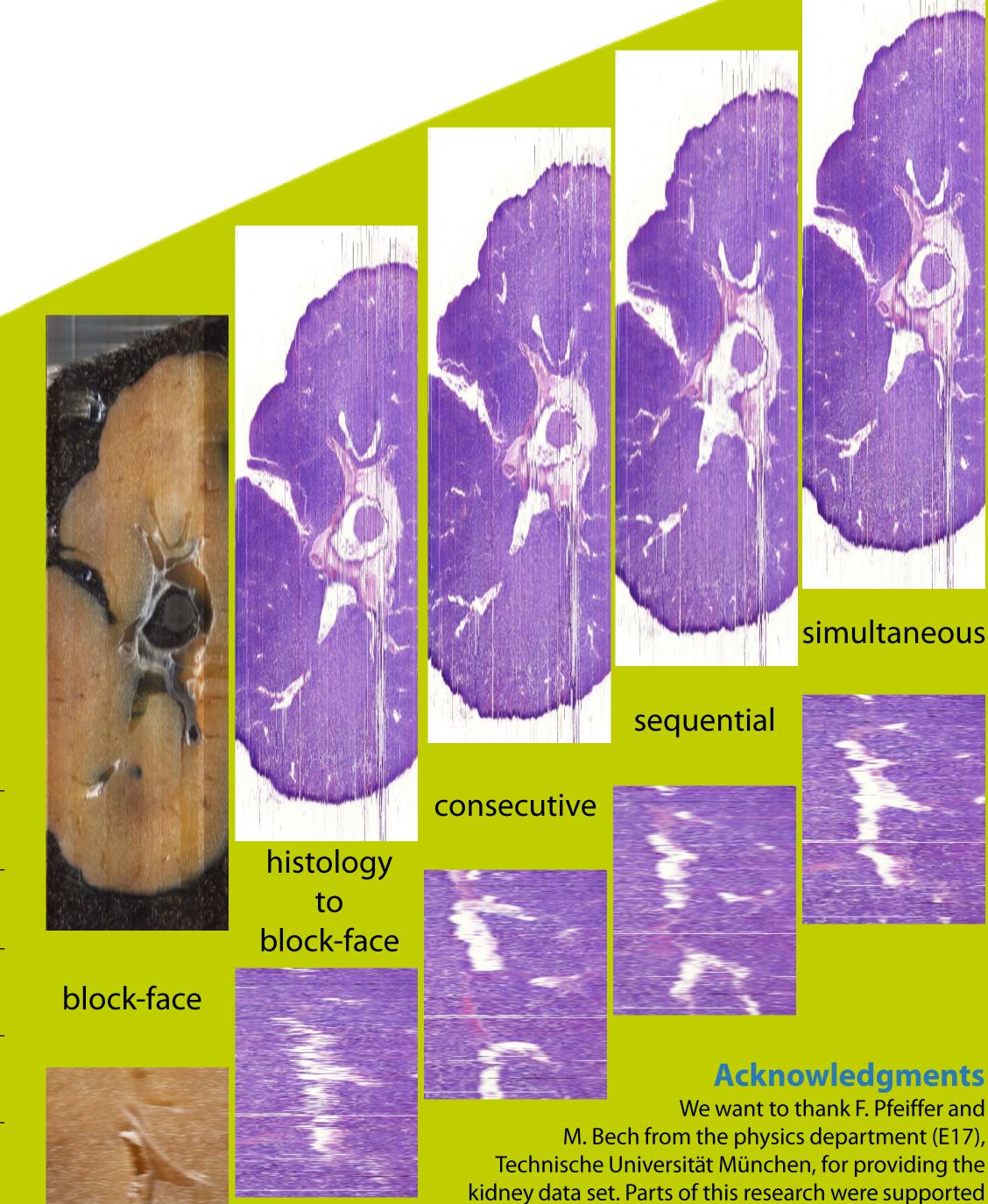
where D_1 and D_2 are dissimilarity measures using normalized mutual information and normalized crossed correlation, the regularizer $\,R\,$ uses the squared difference between displacement vectors, and η controls the influence of a control point to a pixel

Conclusion

- Fully automatic reconstruction of 3-D histology stacks
- Geometrical coherence by simultaneous registration approach
- Increased accuracy and robustness against artifacts

Results

	error measure			
method	AE	EE	IE	NE
initial alignment	50.84	1.57	26.06	13.28
histology-to-block- face registration	36.26 (+28.68%)	1.22 (+22.29%)	17.70 (+32.08%)	9.13 (+31.25%)
consecutive registration	57.41 (-12.92%)	1.91 (-21.66%)	25.76 (+1.15%)	12.35 (+7.00%)
sequential approach	36.56 (+28.09%)	1.23 (+21.66%)	24.97 (+4.18%)	11.72 (+11.75%)
simultaneous approach	34.30 (+32.53%)	1.17 (+25.48%)	16.69 (+35.96%)	8.66 (+34.79%)



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