

Semi-automatic Cell Correspondence Analysis using Iterative Point Cloud Registration

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Introduction

In the field of biophysics, it is important to understand the response of tissue to a mechanism on the cellular level. However, automated cell correspondence analysis before and after deformation is an ongoing obstacle on the cellular level. We propose a novel approach to find the cellular correspondences.

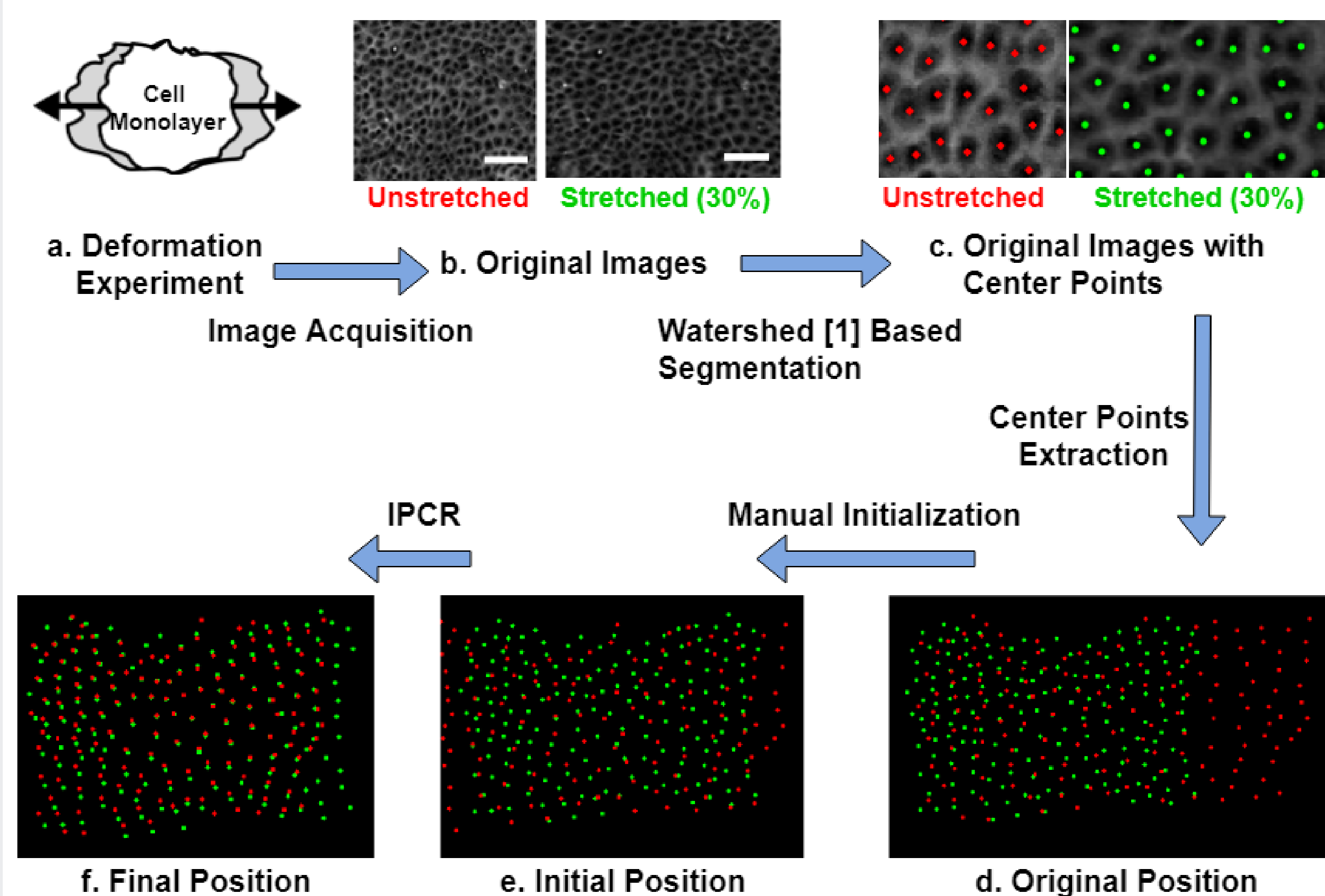
Aim:

Cellular correspondence analysis based on:

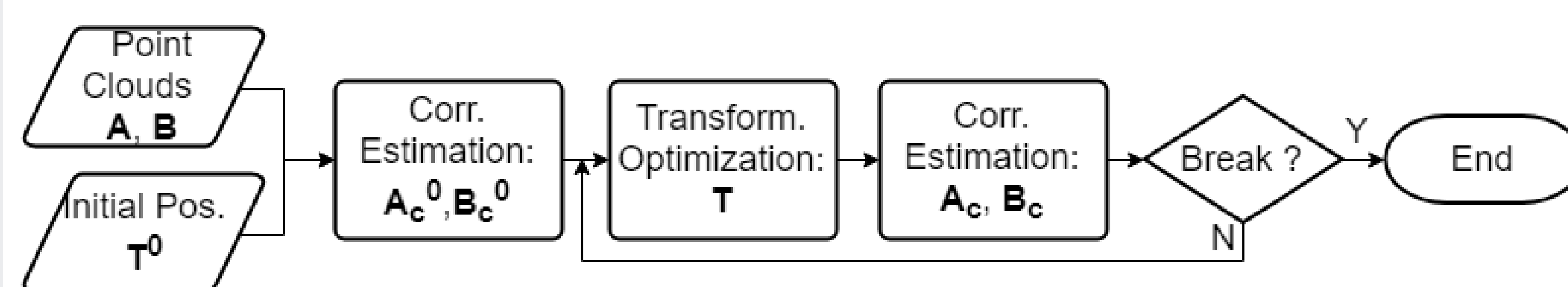
- (1) Watershed based segmentation
- (2) Iterative point cloud registration (IPCR)

Material and Methods

Workflow:



Iterative point cloud registration:



1. 2D point clouds $A = \{a_1, \dots, a_M\}$, $B = \{b_1, \dots, b_N\}$, initial position T_0
2. Calculate initial point matching A_c^0 and B_c^0 using T_0 based on k-d tree nearest neighbor search [2], $A_c \subseteq A$, $B_c \subseteq B$
3. Calculate T to achieve the optimal alignment of the two reciprocal point clouds A_c and B_c
4. Update point matching A_c and B_c using the new T
5. Repeat Step 3 and Step 4 until the termination criterion

$$f = \frac{M \cdot N}{K^3} \sum_{k=1}^K \|T \cdot a_{c,k} - b_{c,k}\|$$

is fulfilled

K : amount of the reciprocal pairs, $K \leq M$ and $K \leq N$

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Results and Discussion

- 3 data sets with different sizes and deformation scales
- Compared with the coherent point drift (CPD) [3]

	CPD [3]							Proposed				
	N_U/N_S	Deform.	N_O	$N_{eval.}$	N_C	F.	Acc.	N_O	$N_{eval.}$	N_C	F.	Acc.
#1	160/156	30%	142	142	137	0.91	0.88	142	142	140	0.91	0.90
#2	170/158	20.3%	136	136	52	0.86	0.33	146	146	145	0.92	0.92
#3	1264/900	20.3%	794	301	69	0.88	0.20	796	289	267	0.88	0.82

- N_U, N_S : cells of the unstretched (U) and stretched (S) images
- N_O : obtained pairs
- $N_{eval.}$: expert evaluated pairs
- N_C : correctly identified pairs

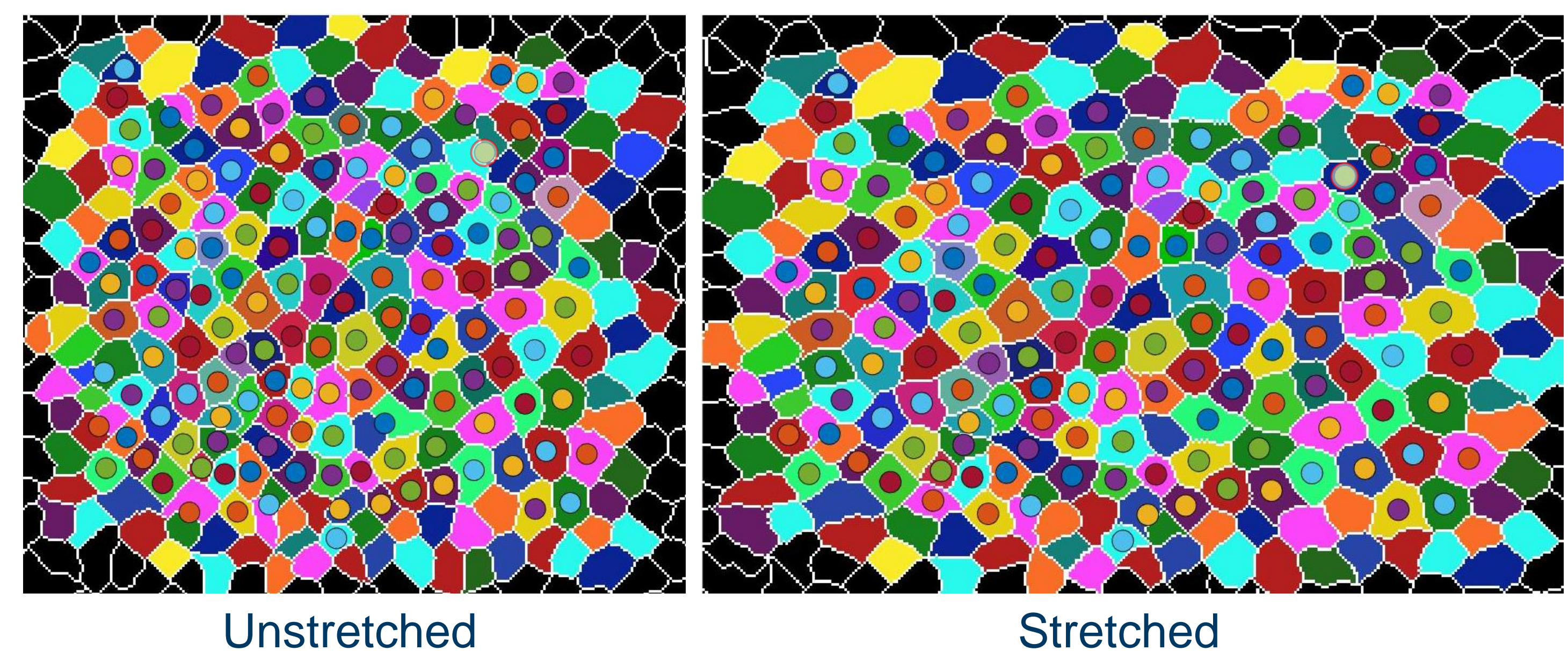
– Found (F.):

$$found = \frac{N_{obtained\ pairs}}{N_{max.\ possible\ pairs}} = \frac{N_O}{\min(N_U, N_S)}$$

– Accuracy (Acc.):

$$Acc. = found \times \frac{N_{correct\ pairs}}{N_{evaluated\ pairs}} = found \times \frac{N_C}{N_{eval.}}$$

- Example of obtained pairs on the ground truth



Conclusion

Contribution:

- A novel approach to identify the cellular correspondences using point cloud registration

Reliability:

- Obtained more pairs and higher accuracy than CPD
- Robust for datasets with different sizes and deformation scales

Expandability:

- The provided baseline can be further improved with other termination criterions or automatic initialization methods

References

- [1] Meyer F. Signal Processing. 1994
- [2] Muja M et al. VISAPP. 2009
- [3] Myronenko A et al. IEEE TPAM. 2010

