Using Scale Information to Improve SIFT-Based Electron Microscope Image Registration Method

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- Conclusion

Background:

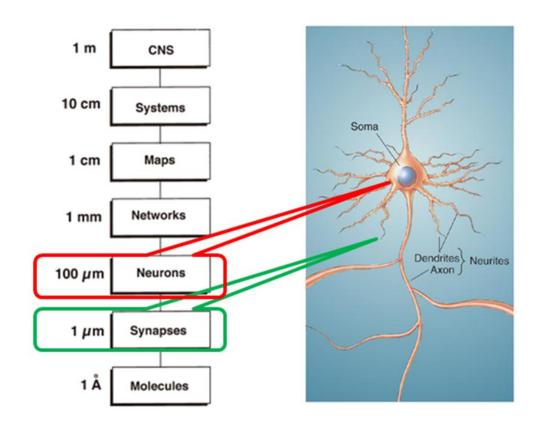
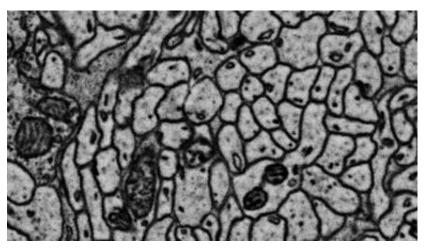
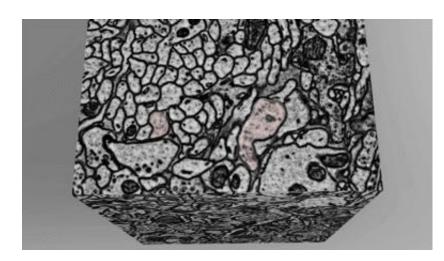


Diagram of a neuron, basic unit of neuronal circuit



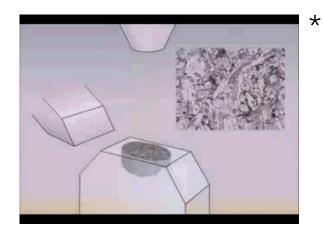
Imaging neuronal circuit at synaptic level



Reconstruction of neuronal circuit

Methodology:

Block-face with EM imaging



Advantage:

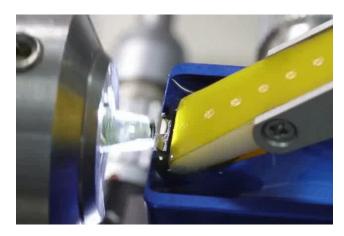
- + near isotropic resolution
- + simple alignment
- + less artifacts

Disadvantage:

- destructive
- non-parallel imaging

*animation from Yunfeng Hua

Serial section with EM imaging



Advantage:

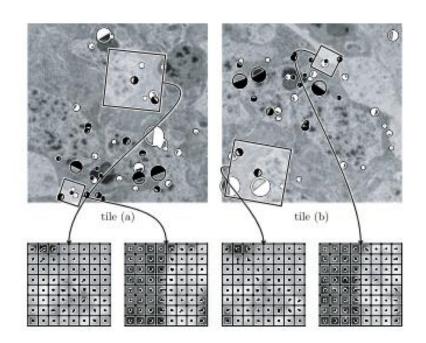
- + section retained
- + large reconstructed volume
- + parallel imaging

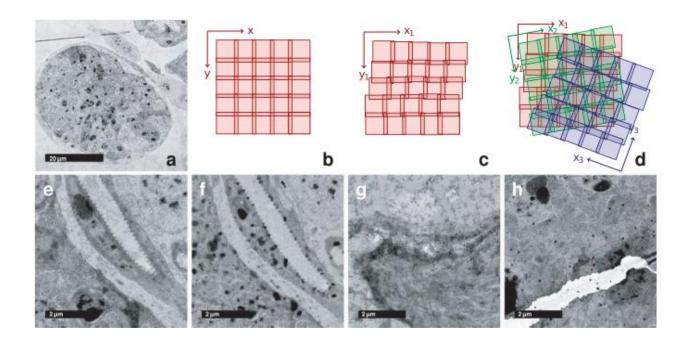
Disadvantage:

- anisotropic resolution
- complicated alignment

Previous method:

 Saalfeld, S., Cardona, A., Hartenstein, V., & Tomancak, P. "As-rigid-aspossible mosaicking and serial section registration of large ssTEM datasets," Bioinformatics, 26(12), 57-63, (2010).

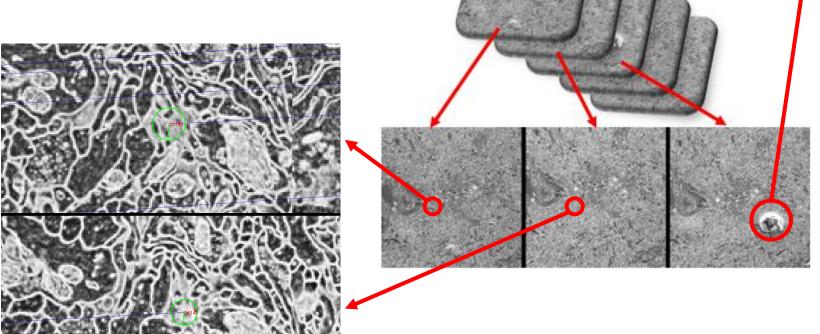


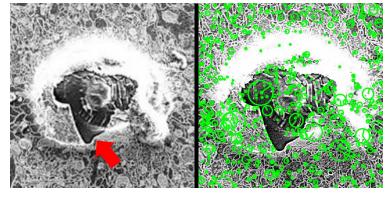


 advantage: use SIFT to identify corresponding landmarks within and across sections.

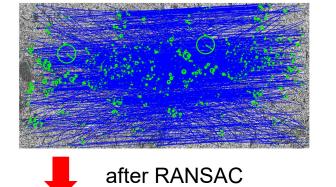
Difficulties:

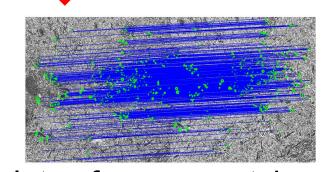
Serial Sections





damage and its keypoints

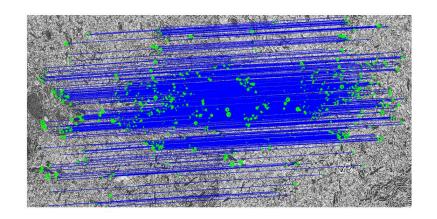


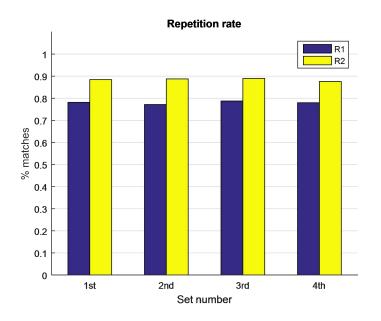


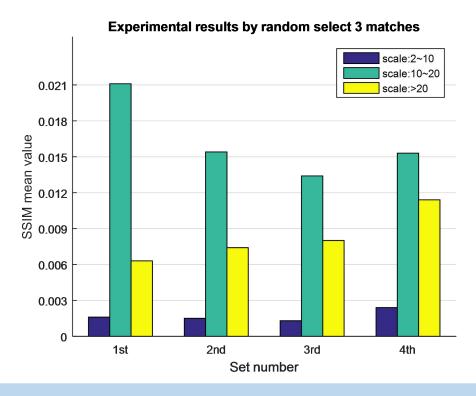
lots of wrong matches

adjacent parts have slightly change

Motivation:



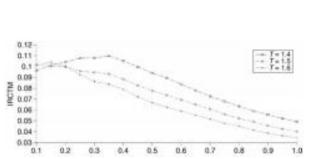


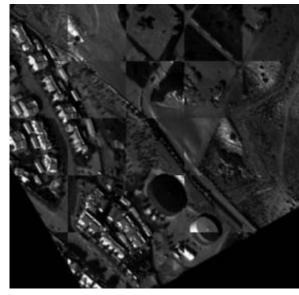


Use scale information of SIFT keypoints

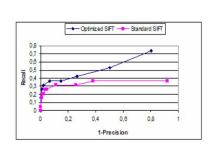
Related work:

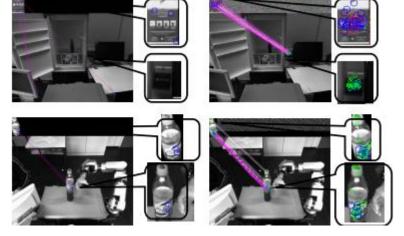
• Yi, Z., Zhiguo, C., & Yang, X. "Multispectral remote image registration based on SIFT," Electronics Letters, 44(2), 107-108, (2008).





 Alhwarin, F., Wang, C., Ristic-Durrant, D., & Graser, A., "Improved SIFT-Features Matching for Object Recognition," BCS International Academic Conference, 215-226, (2008).





Drawbacks:

not reduce time

Drawbacks:

only considered a part of keypoints

Our contribution:

- Use scale information in the feature matching process, reduce the matching time, eliminate the wrong matches.
- Use large-scale matches set in RANSAC firstly and eliminate false matches, make the transformation converge faster.

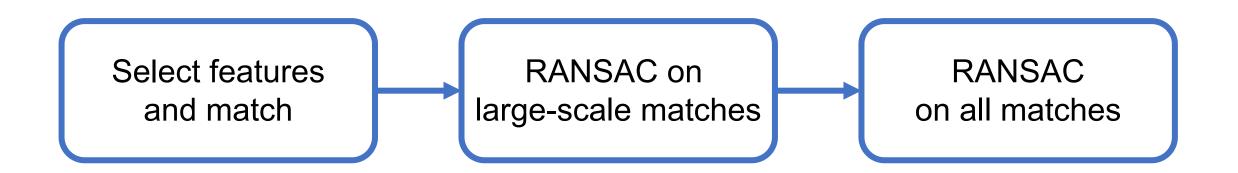
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Pipeline:

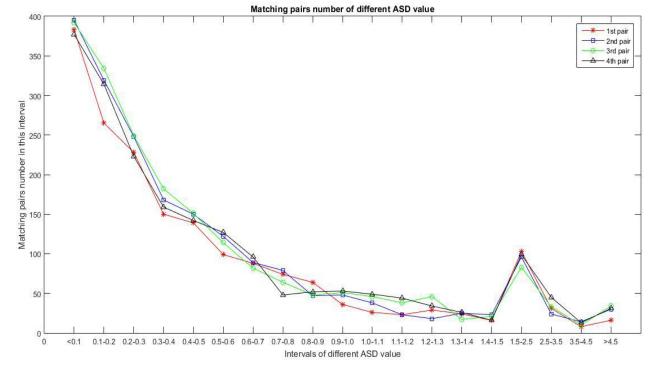


Select features:

• The definition of absolute value of the scale difference (ASD) of keypoint pair $P_1(x_1, y_1, \sigma_1, \theta_1)$ and $P_2(x_2, y_2, \sigma_2, \theta_2)$ is as follows:

$$ASD(P_1, P_2) = abs(\sigma_1 - \sigma_2)$$

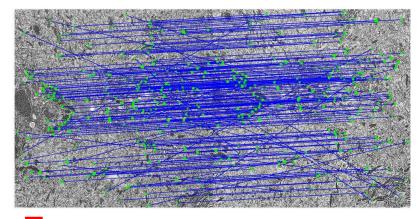
- We calculated the ASD values on the results obtained by matching process among different pair of EM images, and the average value of ASD is around 0.6.
- For every feature to be matched, we first pick all features that their ASD with this feature are less than 0.6, and then pick the most similar feature as the matching feature.

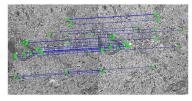


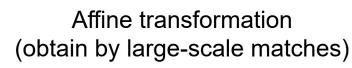
The number of matches for the distribution of ASD

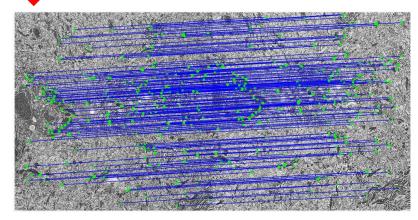
RANSAC:

- We first use large-scale matches and RANSAC process to obtain an affine transformation model to eliminate wrong matches in the small-scale matches set.
- Secondly, we combine small-scale matches
 with large-scale matches, then execute
 RANSAC over all matches to get correct
 transformation.









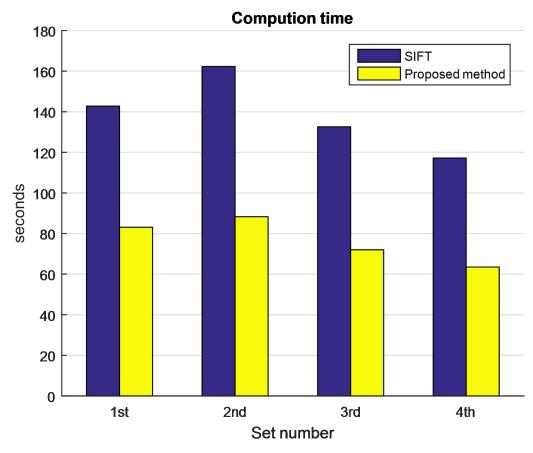
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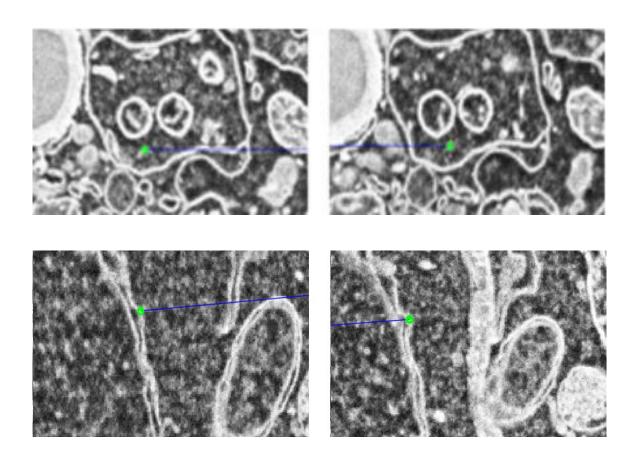
Results

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Results:



Our method saves up to 45.8% of the matching time compared to previous method.



New correct matching points that were not found by previous method.

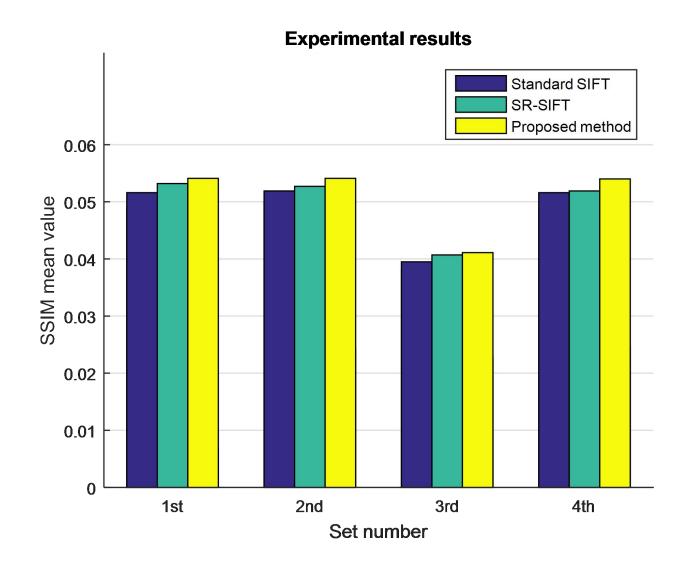
Results:

 Compute the structural similarity index (SSIM)* value for each pair of EM image in test set.

$$ext{SSIM}(x,y) = rac{(2\mu_x \mu_y + c_1)(2\sigma_{xy} + c_2)}{(\mu_x^2 + \mu_y^2 + c_1)(\sigma_x^2 + \sigma_y^2 + c_2)}$$

- μ_x the average of x;
- μ_y the average of y;
- σ_x^2 the variance of x;
- σ_y^2 the variance of y;
- σ_{xy} the covariance of x and y;
- c_1 = $(k_1L)^2$, c_2 = $(k_2L)^2$ two variables to stabilize the division with weak denominator;
- L the dynamic range of the pixel-values (typically this is 2#bits per pixel-1);
- $k_1 = 0.01$ and $k_2 = 0.03$ by default.

*Wang Z., et.al., IEEE Transactions on Image Processing, 2004



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Conclusion:

- In paper, we proposed an EM image registration method using scale information of SIFT points. The method saves up to 45.8% of the matching time compared to SIFT. The method also add stable matches to the matching set.
- After comparison, our method can improve the registration accuracy of EM images while reducing the matching time. It is suitable for automatic registration process of massive highresolution EM images.

Acknowledgments:







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Thanks!