Real-time Alignment for Connectomics

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Abstract. In Connectomics, researchers are creating the brain's wiring diagram at nanometer resolution. As part of this processing workflow, 2D electron microscopy (EM) images must be aligned to 3D volumes. However, existing alignment methods are computationally expensive and can take a long time. We hypothesize that adding biological features improve and accelerate the alignment procedure. Since especially mitochondria can be detected accurately and fast, we propose a new alignment method, MITO, that uses these structures as landmark points. With MITO, we can decrease the alignment time by 27%, and our experiments indicate a throughput of 33 Megapixels/sec, which is faster than the acquisition speed of current microscopes. We can align an image volume of $1268 \times 1524 \times 160$ voxels in less than 12 seconds. We compare our method to the following feature generators: ORB, BRISK, FAST, and FREAK.

Keywords: image alignment · registration · feature matching.

1 Introduction

Connectomics studies the functional and structural connections of a brain to understand the correlation between the physiology of the brain and its behavior. This correlation will help better treatment solutions, design new drugs for mental pathologies, construct custom neural prostheses, etc. Therefore, a registration process is required to map every synaptic connection to build a computer-generated brain wiring diagram. When needed, the image registration process is necessary to map the similarities between images acquired at different times or across other subjects by various sensors. Moreover, image registration is a crucial processing step in various other bio-medical image applications. In this study, we used diamond-knife-sliced electron microscopy (EM) images that provide high resolution such that individual synaptic connections between neurons are visible. We hypothesize to align these images by adding biological features can improve state-of-the-art registration methods. We have used a feature extraction model that follows four steps: feature detection, feature extraction, feature matching, and estimating the transformation matrix. Using the biological features, we get faster real-time alignment performance.

2 Methods

We used unaligned two-dimensional EM images with nanometer resolution, and the corresponding mitochondria mask data as labeled data. The original dataset

is called Lucchi++ and was the result of the study 'Fast Mitochondria Detection for Connectomics [1].' This dataset included two stacks: image and mask of 160 tiles, each having 768×1024 px. We created the unaligned dataset from the original by rotating each image tile and its corresponding mask tile at an arbitrary angle between $(-\pi, +\pi)$ and added a pad size of 250 px on all the sides to prevent information loss at the time of rotation. The new unaligned dataset has two stacks: image and mask, with 160 tiles and dimensions 1268×1524 px.

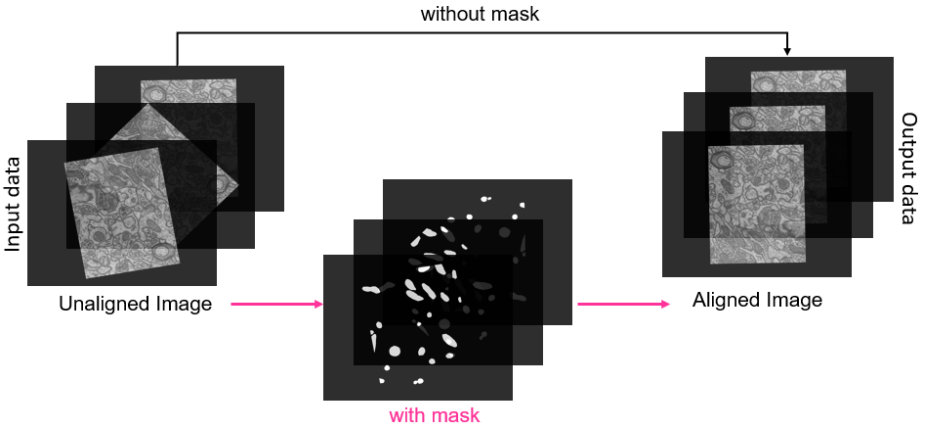

Fig. 1. Mapping of input images with and without adding the biological features. The unaligned input EM images (left) were mapped in real-time with and without adding the biological features (mask data). We generated a stack of aligned images (right) as output in both the cases to draw comparisons.

We performed an automatic registration on the unaligned EM images using a custom-build interactive program that runs the feature extraction model and calculates alignment score, execution time, and throughput for the entire dataset. This model used existing computer vision algorithms such as FAST[6], ORB[2], BRISK[3] to learn the features or patterns from the input dataset. We propose a new feature detector mechanism called **MITO** that detects the keypoints in EM images using mitochondria from mask images as a region of interest (ROI). In this feature detection step, we introduced mask images as additional biological features to improve the alignment performance. In the feature description step, the model uses ORB, BRISK, and FREAK[4] algorithms to create descriptors that are unique and could be referred to as a keypoint's numerical fingerprint. In the next step, we used feature matching algorithms such as BF[8] and FLANN[9] matcher to map (x_i, y_i) of the source image to $(x_i^{'}, y_i^{'})$ of the target image. Finally, with the help of the homography matrix, the model transforms the source image and outputs the aligned image. We generated two stacks of registered images with and without the help of mitochondria masks for comparisons (see Fig.1).

3 Results

We perform experiments on the unaligned Lucchi++ dataset to measure timing and alignment accuracy. When we combine biological features using the MITO method with the BF and FLANN matchers, we observe a maximum execution time of 9.49 (+-0.37) seconds for the whole stack. When comparing the accuracy, we measure a dice score of over 0.89 for both BF and FLANN, indicating quality alignment. The average throughput with MITO is at least 33 Megapixels/s which is faster than the acquisition speed of modern electron microscopes (11 Megapixels/s). Our findings indicate that MITO can be used to align connectomics image data in real-time during image acquisition. Table 1 shows the full evaluation.

Table 1. Alignment Results on Lucchi++. We compare the BF and FLANN matchers with a variety of feature descriptors. When using the MITO detector, we measure the throughput of at least 33 Megapixels/s, indicating real-time performance.

Matcher	Detector + Descriptor	Mask	Dice Score	Execution Time (sec.)	Stack Throughput (MP/sec)
BF	BRISK		0.9354	47.0052(±1.5173)	6.7879(±0.2170)
		✓	0.8569	**19.3020(±0.2625)**	**16.5210(±0.2256)**
	ORB		0.7529	19.4427(±1.8462)	16.4941(±1.4953)
		✓	0.8226	20.4218(±0.5493)	15.6208(±0.4259)
	FAST + BRISK		0.9184	2419.9270(±99.9857)	0.1319(±0.0053)
		✓	0.8762	**28.4635(±1.2776)**	**11.2167(±0.4908)**
	ORB + BRISK		0.6291	16.3020(±1.4923)	19.6693(±1.8124)
		✓	0.7935	16.9687(±1.6858)	18.9180(±1.9290)
	FAST + FREAK		0.9405	2391.9479(±137.7484)	0.1335(±0.0074)
		✓	0.9140	**25.1302(±0.5)**	**12.6912(±0.2498)**
	ORB + FREAK		0.8320	16.6458(±1.8088)	19.2979(±1.9733)
		✓	0.7637	16.8072(±0.1365)	18.9718(±0.1545)
	MITO(ours) + BRISK	✓	**0.9142**	**7.7708(±0.0888)**	**41.035(±0.4713)**
	MITO(ours) + FREAK	✓	**0.8963**	**8.3697(±0.0888)**	**38.0983(±0.4027)**
FLANN	BRISK		0.9344	40.1145(±0.9393)	7.9514(±0.1887)
		✓	0.8338	**19(±2.4111)**	**16.9513(±2.0058)**
	ORB		0.8069	19.3802(±1.2145)	16.4941(±0.9979)
		✓	0.8280	20.6875(±1.1149)	15.4417(±0.8082)
	FAST + BRISK		0.9338	3082.2343(±130.2627)	0.1035(±0.0043)
		✓	0.8784	**29.6041(±0.2350)**	10.7709(±0.0856)
	ORB + BRISK		0.6297	16.9322(±1.7772)	18.9655(±1.9261)
		✓	0.7648	15.2031(±1.1735)	21.0579(±1.6571)
	FAST + FREAK		0.9450	2628.3229(±32.5343)	0.1213(±0.0015)
		✓	0.9091	**31.4166(±4.7502)**	**10.2940(±1.4380)**
	ORB + FREAK		0.8285	16.2812(±0.0563)	19.5841(±0.0676)
		✓	0.7402	17.2083(±1.2107)	18.5882(±1.2665)
	MITO(ours) + BRISK	✓	**0.9062**	**9.2239(±0.7265)**	**34.7050(±2.6154)**
	MITO(ours) + FREAK	✓	**0.8928**	**9.4843(±0.3694)**	**33.6528(±1.3213)**

4 Conclusion

Fast registration is crucial to creating 3D volumetric connectomics datasets from unaligned EM images. This process can be computationally expensive. Based on our studies, adding biological features to register these images results in faster alignment. Specifically, we include mitochondria masks as part of our MITO feature detector. With MITO, the overall dice score is higher than 0.80, and the throughput is faster than 11 Megapixels/s. These measurements indicate the possibility of real-time alignment during the image acquisition with modern electron microscopes.

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