Real-time Alignment for Connectomics

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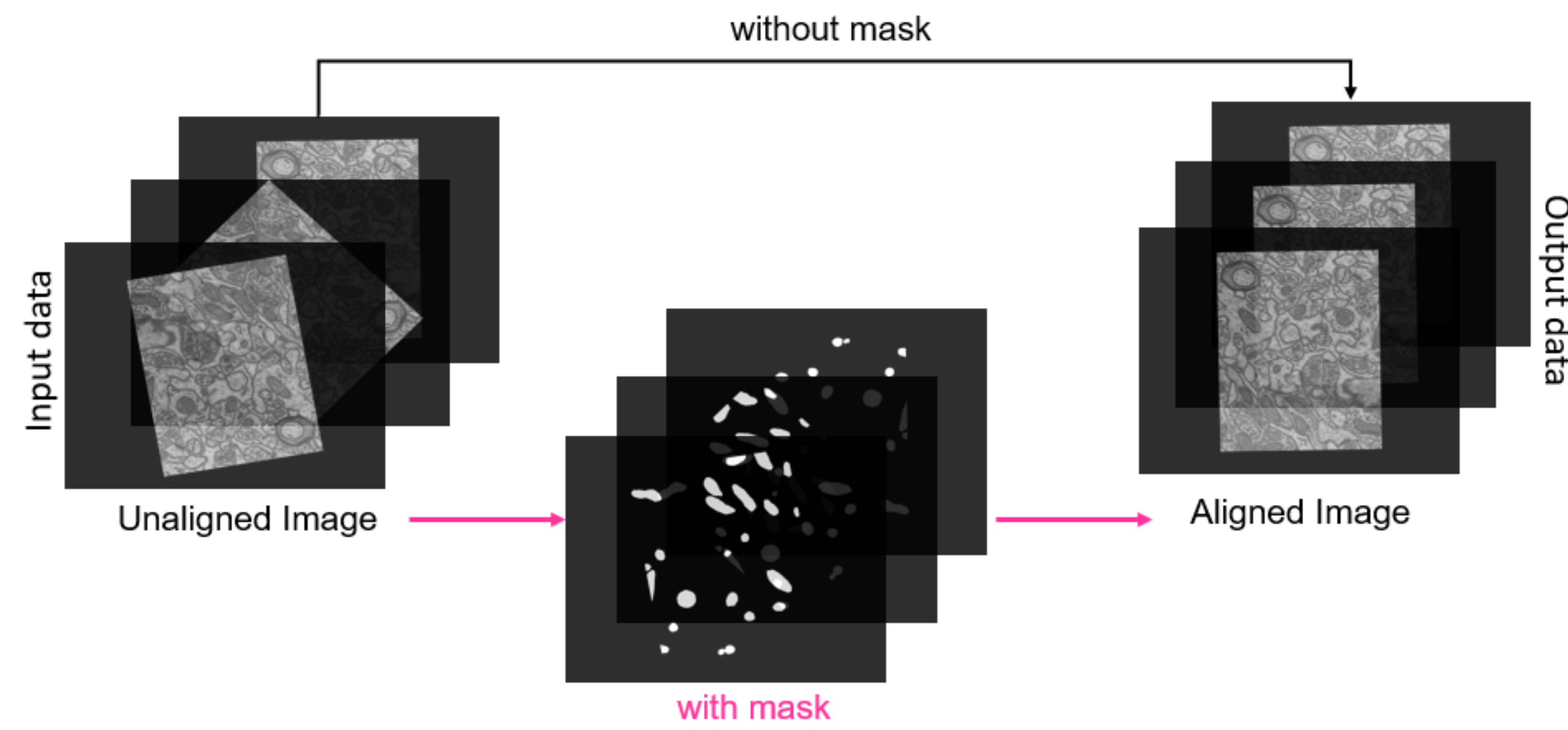[1]University of Massachusetts-Boston

Abstract

Figure 1. **Flow Diagram.** The unaligned input images were mapped in real-time using two approaches, with and without adding the biological features(mask data) to get the output aligned images with help of state-of-art feature matching algorithms.

In Connectomics, researchers are creating the wiring diagram of the brain at nanoscale. For this, 2D electron microscopy (EM) images need to be aligned to 3D volumes. To investigate if adding biological features can improve existing alignment methods, we use mitochondria masks data to guide the registration procedure in real-time. To align source and target image pairs using feature matching methods, features were detected with and without the help of labeled masks. Automatic registration was performed on randomly rotated unaligned EM images using a custom-build interactive program that runs conventional feature matching methods and calculates alignment score, execution time and throughput for the entire aligned image set. Two stacks of registered images with and without mitochondria mask are generated for comparisons. A new feature detection method, MITO, is proposed that uses biological features to detect the landmark points. A bounding box for each mitochondria mask is measured which then calculates the list of (x_i, y_i) coordinated points to draw an approximated polygon for each mitochondria mask. This list of points is considered as feature points to align the source and target images. The overall execution time to align images with and without the labeled mask data has decreased by 27%. With our proposed method, the aligned images are obtained in real time with a throughput greater than 33 MP/sec and with dice score greater than 0.89 for the entire image set in less than 12 seconds. Adding biological features for aligning images can yield faster alignment. We present detailed analysis for the following feature generators ORB, BRISK, FAST, FREAK, MITO(ours). All our research is openly available here.

Pattern Recognition

Image registration is a prerequisite when required to estimate similarities between images acquired at different times or across different subjects by different sensors. It involves aligning one dataset to another in the same coordinate space such that the mapped points in two datasets correspond to the same anatomic features. To align these similarities between source and target images, the model follows four significant steps: **Feature Detection**, **Feature Description**, **Feature Matching** and **Transformation Matrix**.
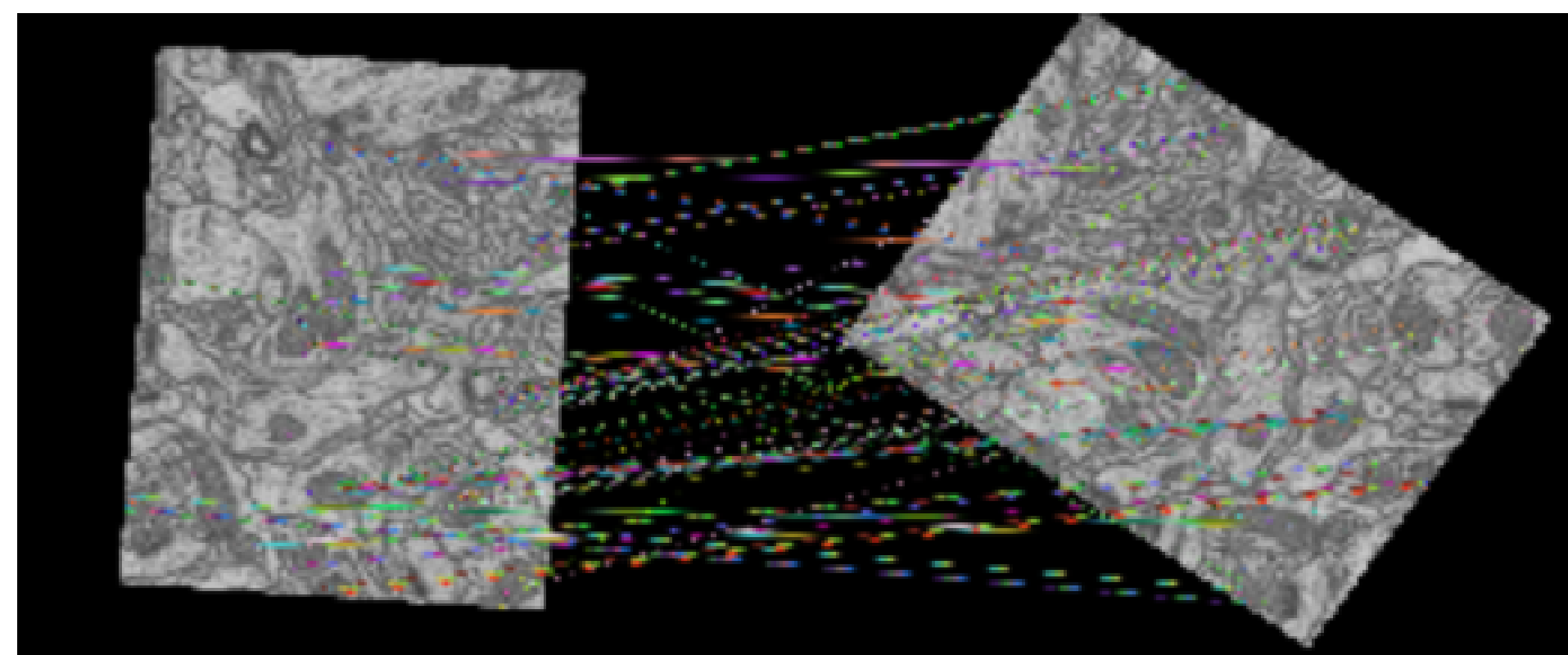

Figure 2. **Features Matched.** This figure shows the best matched keypoints between source image and target image

MITO

This is our proposed method for feature detection. The keypoints are detected using mask data. We used mitochondria as region of interest (ROI) to create the bounding boxes and relocate those on image data. For each bounding box, we calculated an approximate polynomial that contains a list of (x, y) coordinates points.
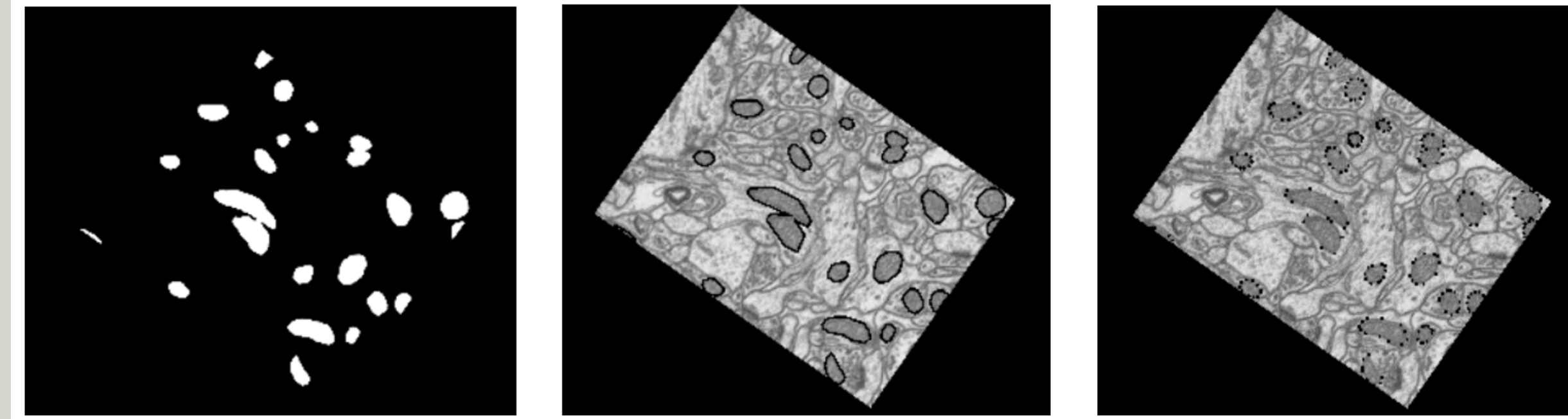

Figure 3. **Feature Detection with MITO.** With the help of ROIs in the mask image (left), MITO had located these ROIs on the EM image(center). List of (x, y) coordinate points for each ROI detected are considered as feature keypoints to map the source image to target image(right).

With the help of these coordinate points, we locate ROIs on the EM image tile. This list of points is the potential keypoint vector list which we have used to match the features. We have used the best matched keypoints to compute the transformation matrix that maps the source image to the target image. This matrix is applied to the source image and source label mask to yield the aligned image and mask image.

Real-time Alignment Results

Table 1. We show the performance of feature detector on Lucchi ++ datasets. Dice score, execution time (sec), throughput (MP/sec) calculation for image alignment with feature algorithm using BF and FLANN matcher.

| 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)**

Results
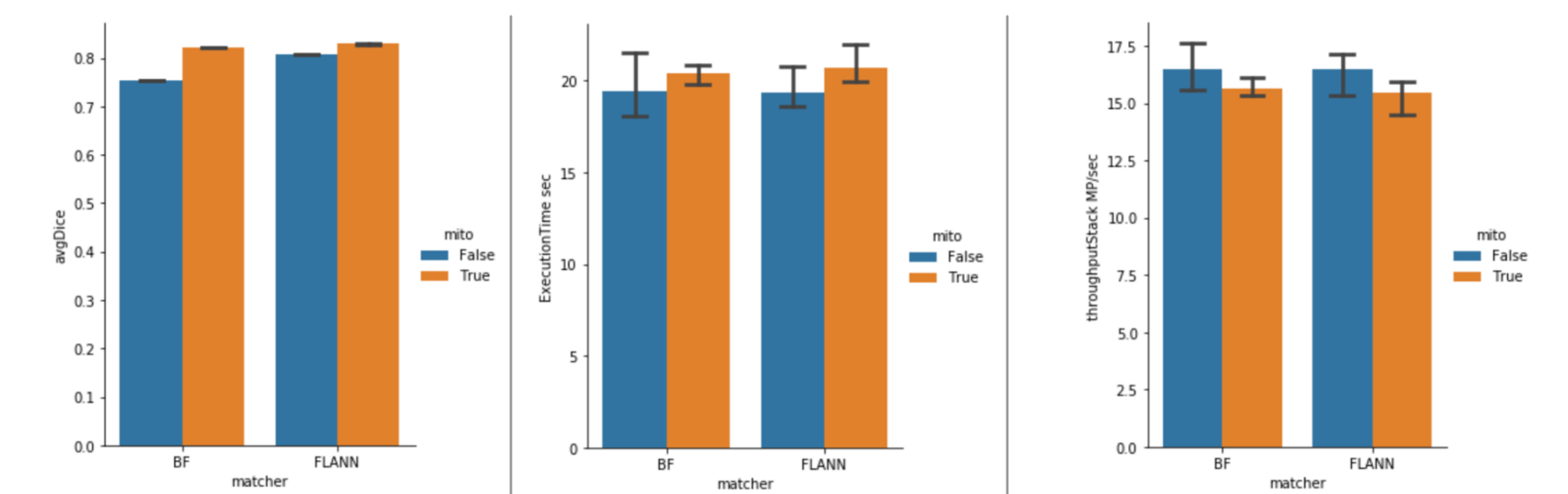
Figure 4. **Alignment performance using ORB algorithm** (left to right) We observe that the alignment score is higher when mito mask is true. Real-time alignment for the whole stack was completed in less than 22 seconds and a throughput higher than 11 MP/sec.
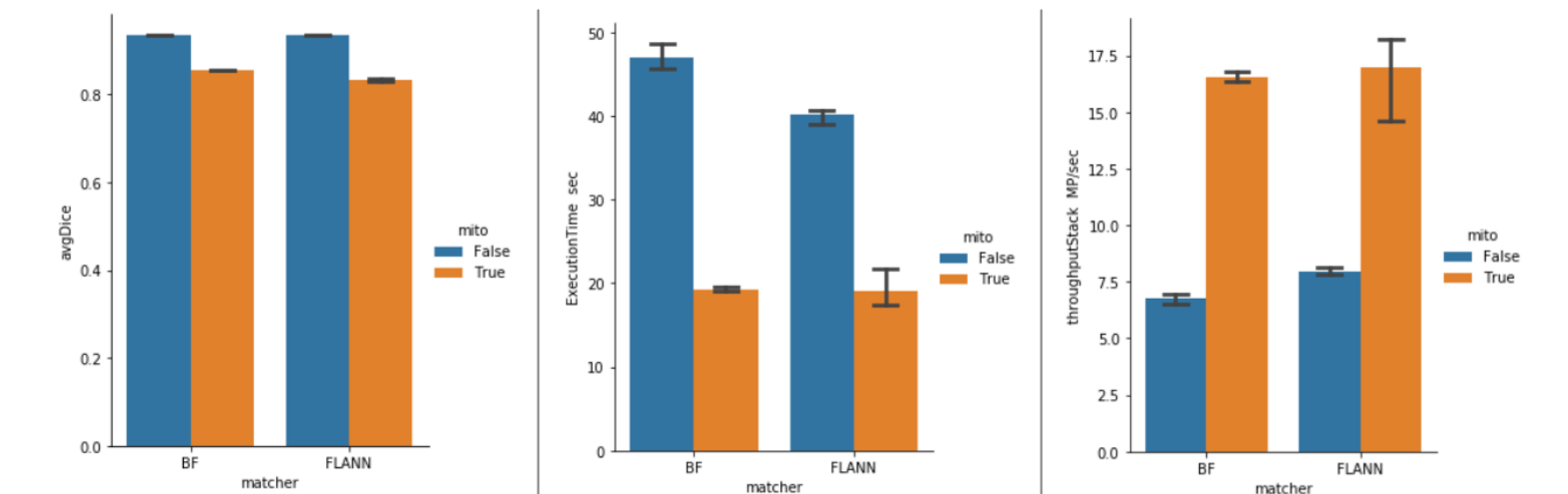

Figure 5. **Alignment performance using BRISK algorithm** (left to right) We observed that the dice score is higher than 0.8. The execution time measured for the real-time is less than 20 seconds, with a throughput higher than 11 MP/sec in the persence of mito mask.
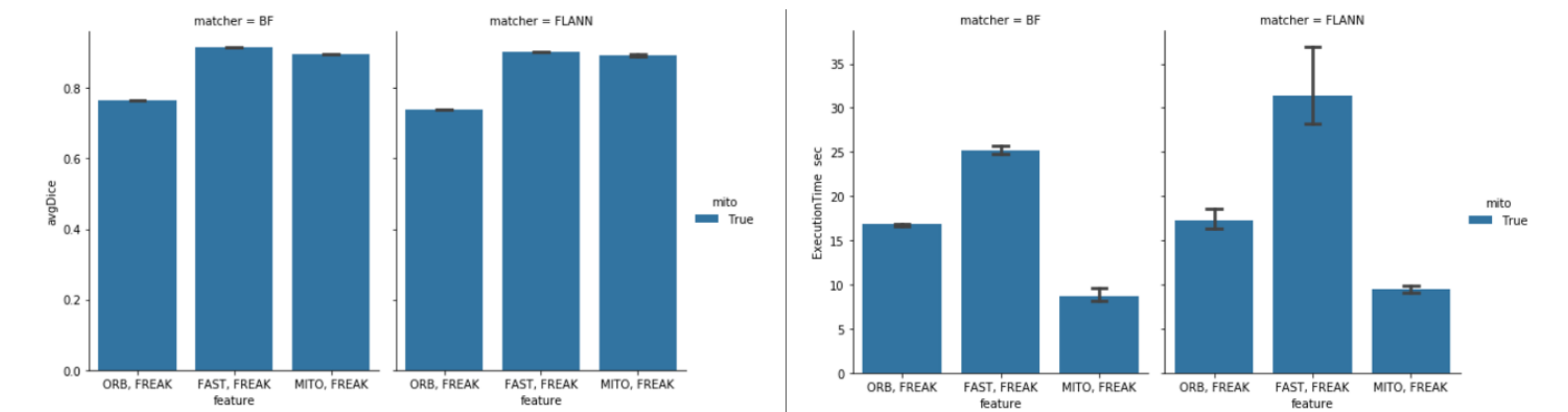

Figure 6. **Performance of image alignment across ORB, FAST and MITO with BRISK descriptors** The alignment performance is best with MITO detector and BRISK descriptor where the dice score is higher than 0.90 and real-time execution is less than 12 seconds.
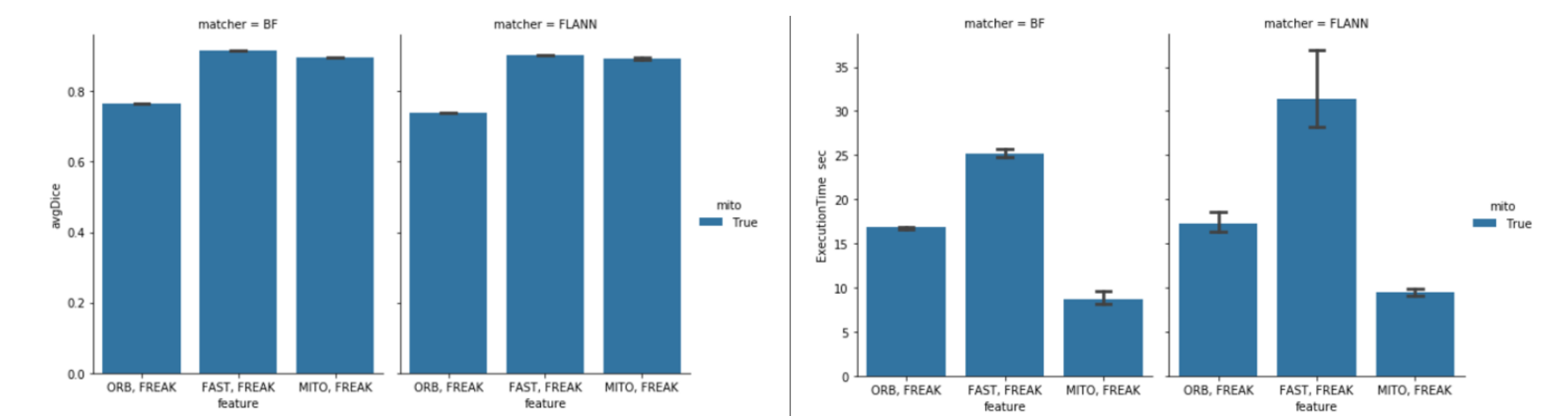

Figure 7. **Performance of image alignment across ORB, FAST and MITO with FREAK descriptors** When compared, it is observed that execution of alignment process is fastest with MITO detector with dice score higher than 0.85.

Conclusion

Fast registration is crucial as the datasets consist of unaligned EM images that are computationally expensive to map and create 3D volumetric datasets. Adding biological features to register these images resulted in faster alignment in real-time.