

## Evaluation of feature based approaches for alignment of tilt-series without fiducial markers.

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Electron tomography is an important method in electron microscopy as it gives information about 3D structures of samples. Nevertheless, in order to get high resolution reconstruction, alignment of tilt series is mandatory. Most of the time, fiducial markers are added to samples in order to help achieving fine alignment. However, the use of fiducial markers has some drawbacks such as shadowing the structures of interest. The alignment methods using fiducial markers rely on detection of markers in the images. Alignment is then produced by creating a 3D model of the features. Other approaches propose replacing the fiducial markers by features existing on the original image. Those are points with special characteristics such as local minima [1] or corners [2]. Han R. et al. [3] proposes to use SIFT (Scale Invariant Feature Transform [4]), a recent feature detection and description algorithm used in image registration or object detection algorithms.

Our purpose is to evaluate the interest of new feature descriptors (SURF [5], ORB [6], BRISK [7], KAZE [8] and AKAZE [9]) compared to SIFT and to determine the robustness of these features for electron transmission microscopy on material science and biological samples. The evaluation is first done on 2D images in order to check the efficiency of each descriptor (figure 1) for electron microscopy acquired at different tilt angles. The analysis is then pursued on 3D reconstruction (figure 2), with the presentation of a workflow used to create chains of features seen on many images in the tilt series. The final alignment of tilt series is performed with a classical approach using the creation of 3D model of features. The whole process is integrated in the TomoJ software [10], thus offering the opportunity to mix the different methods of feature detection and description.

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[3] Han R. et al. A marker-free automatic alignment method based on scale-invariant feature. J Struct Biol, 186, 2014.

[4] Lowe D. Distinctive image features from scale-invariant keypoints. International Journal of Computer Vision, 2004

[5] Bay H., et al. Speed-Up Robust Features (SURF). Sciencedirect, 2007.

[6] Rublee E.. et al. ORB: An efficient alternative to SIFT of SURF. IEEE International Conference on Computer Vision, 2011.

[7] Leutenegger S. et al. BRISK : Binary Robust invariant scalable keypoints. IEEE International Conference on Computer Vision, 2011.

[8] Alcantarilla P. F. et al. KAZE features. European Conference on Computer Vision, 2012.

[9] Alcantarilla P. F. et al. Fast Explicit Diffusion for Accelerated Features in Nonlinear Scale Spaces. British Machine Vision Conference, 2013.

[10] TomoJ, an imageJ plugin. <http://www.cmib.fr/en/download/software/TomoJ.html>

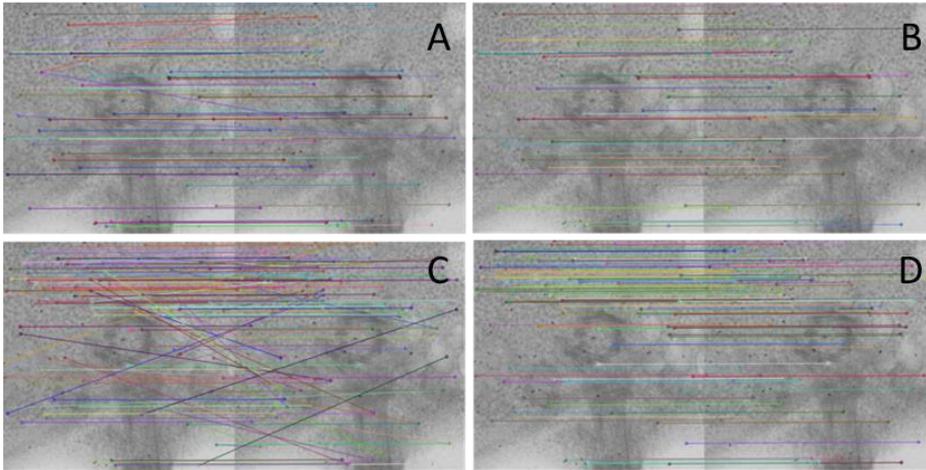


Figure 1: 2D comparison of matches found between 2 images (colored lines) from Imod tutorial data (images 24 and 25). First row corresponds to the use of KAZE as detector and descriptor A) after brute force matching and B) after selection based on homography determination. Second row corresponds to SIFT as detector and descriptor C) after brute force matching and D) after selection based on homography determination.

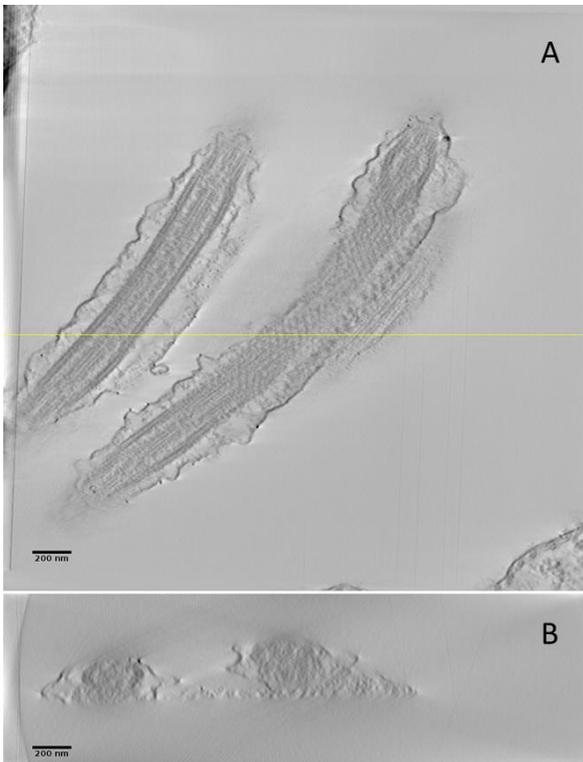


Figure 2: *Trypanosoma brucei* cilia reconstruction using the workflow presented in this study with AKAZE detector and descriptor: A) central XY plane of the reconstruction B) XZ plane number 576 of the reconstruction corresponding to the yellow line in XY plane.