Fast projection matching for X-ray tomography (Faproma)

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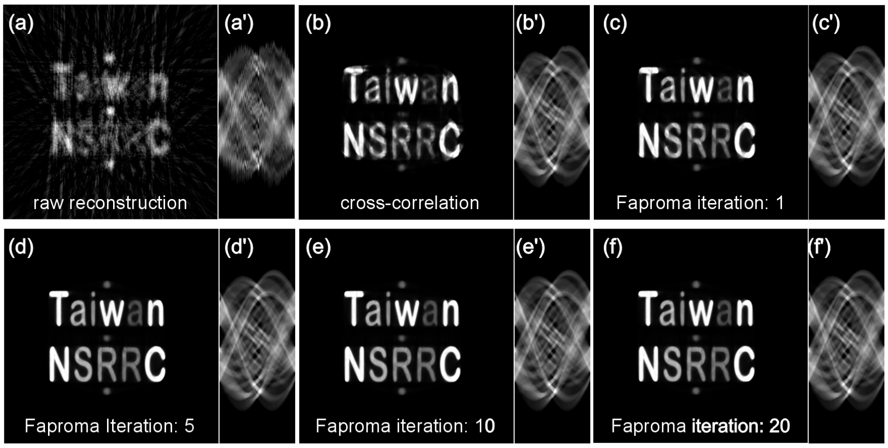
X-ray nano-tomography is one of crucial technique for investigating the fine internal structures of specimens on a nanometer scale [1]. However, precise registration of raw projections is key factor for the fidelity of tomographic reconstruction at nanometer spatial resolutions. When using X-ray micro-CT, near perfect sample positioning can be easily achieved using highly precise and stable rotational stages. However, with X-ray or electron nano-tomography, image registration precision is challenging due to the demanding structural details of specimens at nanometer level.

Here, we propose a new automatic registration algorithm that can gradually reduce the iterative computational complexity and increase the reliability of the optimized results by simplifying a traditional projection matching problem [2] into two one-dimensional matching problems. This Fast Projection-Matching (Faproma) algorithm [3] is comprised of two adjustment processes. The first process simultaneously corrects vertical shifts and rotational axis tilts based on common-line method; the second process corrects horizontal shifts of raw projections captured from different azimuth angles based on reduced projection matching method.

The most important advantage of the Faproma registration algorithm is that it dramatically reduces the hardware requirements for data processing compared to traditional three-dimensional projection matching methods. Alleviating the need for ultrahigh stable motion components in tomographic systems, precise tomography acquisition hardware requirements are reduced as well using the Faproma. It is worthy to note that the Faproma algorithm converged just within few iteration times (See figure, [3]), and the computational time is about two orders faster than traditional projection matching methods. The details of Faproma algorithm will be presented in the conference.



Demonstration of the Faproma performance using a computer-generated 3D phantom. (a–f) are layer reconstruction results of raw data, cross-correlation registration, and Faproma registration. (a'–f') are the corresponding sinograms of (a–f).

References

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[2] D. Y. Parkinson, C. Knoechel, C. Yang, et. al., *Journal of Structural Biology* **177**, 259-266 2012.

[3] C.-C. Wang, Cheng-Cheng Chiang, Biqing Liang, et. al., *Scientific Reports* **7**, 3691, 2017.