

Reprojection Alignment Local Minima when Correcting Helical Trajectory Perturbations

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Summary: We present simulations where the *reprojection alignment* method fails to accurately correct low-frequency radiograph motions. These failures highlight the need to employ *both* the *reference scan* and reprojection alignment radiograph corrections in order to accurately compensate for dynamic trajectory inaccuracies.

1. INTRODUCTION

For standard laboratory micro-CT systems, acquired radiographs do not always adhere to the strict geometrical assumptions of the reconstruction algorithm. The consequence of this geometrical inconsistency is that the reconstructed tomogram contains artefacts (blurring, streaking, double-edges) in the reconstructed tomogram. Typically, the geometry varies during the acquisition of radiographs due to a combination of sample-manipulator inaccuracies, sample movement, and thermally induced system component (particularly X-ray source) movements. To achieve a motion-artefact-free tomographic reconstruction, one must estimate the experimental geometry parameters per-radiograph. One can then either: correct the radiographs to be consistent with an assumed geometry, or utilise the estimated per-radiograph geometries directly in the reconstruction method.

The reprojection alignment (RA) method has been utilised to estimate experimental per-radiograph geometry parameters (hence referred to as per-radiograph *motions*). This method involves generating a set of simulated radiographs and using *image registration* to align each simulated radiograph with its corresponding measured (experiment) radiograph. Typically, this is an iterative procedure where a new set of simulated radiographs are generated using the estimated motion parameters calculated from the previous iteration. The RA motion correction method has been successfully applied for circular trajectories [3, 4], double-helix and space-filling trajectories [2] and even incorporated directly into iterative methods [1, 2]. A deficiency of the RA method is that it only guarantees that simulated projections align with the measured projections, there is no constraint on the quality/fidelity of the reconstructed tomogram. Here, we simulate cases of per-projection misalignments where the RA iterations converge to spurious solutions (*local-minima*). In particular, for helical-like trajectories, low-frequency shift perturbations in the direction of the sample translation axis are susceptible to these local minima.

2. EXPERIMENTAL METHOD

We use the synthetic phantom of Fig. 1(a) to generate a set of synthetic projections for the space-filling (SF) trajectory. The synthetic projection set is subsequently perturbed by the linear y -shift shown as the blue line (labeled “Known y ”) in Fig. 1(b). The RA method is then used to attempt to recover the (known) linear y shift. Alg. 1 describes the RA iteration.

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Algorithm 1 Basic reprojection-alignment (RA).

- 1: **repeat**
 - 2: Ramp-FBP reconstruct tomogram from *corrected* measured projections.
 - 3: Compute simulated projections from tomogram of Step 2.
 - 4: Register measured with corresponding simulated projections to estimate per-projection motion
 - 5: Transform measured projections according to values obtained from Step 4.
 - 6: **until** converged
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3. RESULTS

Fig. 1(b) plots the estimated y shift for RA iterations 1, 2, 3, 4 and 10. The iterations fail to converge to the “Known y ” linear shifts applied to the synthetic projections. The linear trend of the known y shift is resolved in two halves, with severe discontinuity occurring in the estimates of the middle projections. The known linear y -shift perturbation of the synthetic projections is equivalent to a change in pitch of the helix and the RA method of Alg. 1 fails to reconcile this inconsistency when the magnitude of the shifts (change in pitch) becomes large. Indeed, any linear trend in y -shift (with frequency of order of a projection *revolution/plenum*), of sufficient magnitude, can result in convergence to local minima. In practice, when the linear component of y shift is due to X-ray source drift, a *reference frame* technique [4] can be used to provide an initial estimate of the motion. The RA method can subsequently be applied to resolve the higher frequency components of the motion.

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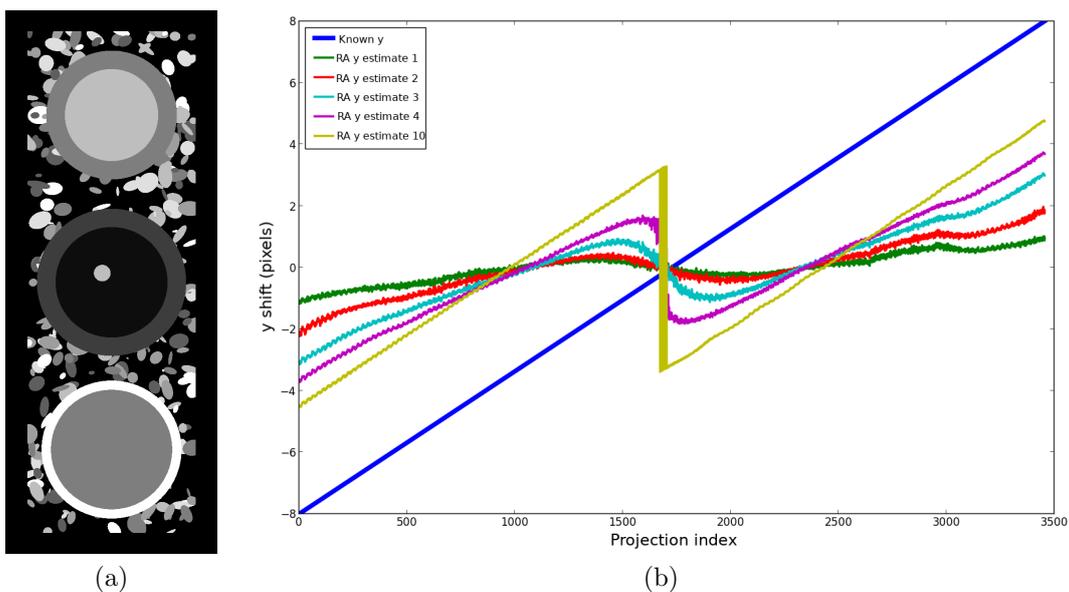


Figure 1: (a) Vertical (x - z) slice through 3D 3 -sphere stack $480 \times 480 \times 1248$ voxel phantom used in RA simulations, (b) Known y -shifts and RA-estimated y -shifts for iterations 1, 2, 3, 4 and 10.