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Multi-resolution radiograph alignment for motion correction in X-ray micro-tomography

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ABSTRACT

Achieving sub-micron resolution in lab-based micro-tomography is challenging due to the geometric instability of the imaging hardware (spot drift, stage precision, sample motion). These instabilities manifest themselves as a distortion or motion of the radiographs relative to the expected system geometry. When the hardware instabilities are small (several microns of absolute motion), the radiograph distortions are well approximated by shift and magnification of the image. In this paper we examine the use of *re-projection alignment* (RA) to estimate per-radiograph motions. Our simulation results evaluate how the convergence properties of RA vary with: motion-type (smooth versus random), trajectory (helical versus space-filling) and resolution. We demonstrate that RA convergence rate and accuracy, for the space-filling trajectory, is invariant with regard to the motion-type. In addition, for the space-filling trajectory, the per-projection motions can be estimated to less than 0.25 pixel mean absolute error by performing a single quarter-resolution RA iteration followed by a single half-resolution RA iteration. The direct impact is that, for the space-filling trajectory, we need only perform one RA iteration per resolution in our iterative multi-grid reconstruction (IMGR). We also give examples of the effectiveness of RA motion correction method applied to real double-helix and space-filling trajectory micro-CT data. For double-helix Katsevich filtered-back-projection reconstruction ($\approx 2500 \times 2500 \times 5000$ voxels), we use a multi-resolution RA method as a pre-processing step. For the space-filling iterative reconstruction ($\approx 2000 \times 2000 \times 5400$ voxels), RA is applied during the IMGR iterations.

Keywords: cone beam, re-projection alignment, iterative reconstruction, space-filling trajectory

1. INTRODUCTION

Achieving high-quality and high-resolution microscopic and ultra-microscopic X-ray tomographic images requires acquisition system components to be aligned with sub-micrometer precision throughout the duration of the radiograph acquisition. While highly stable X-ray sources (e.g. synchrotron radiation) and nanometre-precision sample manipulators/stages (e.g. air-bearing) exist, they remain expensive and the number of systems which use these precise components is small when compared to the number of standard laboratory micro-CT systems. For standard laboratory micro-CT systems, the acquired radiographs do not always adhere to the strict geometrical assumptions of the reconstruction algorithm. The consequence of this inconsistency is that the reconstructed tomogram contains artefacts. The nature of the artefacts depends on the acquisition trajectory and the magnitude of the geometrical inconsistency, but typically acquisition imperfections manifest themselves as blurring, streaking, double-edges and distortions in the reconstructed tomogram. Here, we present a *re-projection alignment* method which corrects for geometry variations which occur over the course of the radiograph acquisitions.

Determining the exact system geometry is difficult due to measurement uncertainties. Even more challenging is the fact that the geometry varies during the acquisition of radiographs due to a combination of sample-manipulator (rotation/translation stage) inaccuracies, sample movement, and thermally induced system component (particularly X-ray source) movements. To achieve a motion-artefact-free tomographic reconstruction, one

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must estimate the experimental geometry parameters per-radiograph and subsequently correct the radiographs to a consistent geometry.

Motion-errors which stabilise with time or repeatable-motion-errors (e.g. repeatable rotation/translation stage positional errors) can be directly measured and corrections can be applied to radiographs prior to reconstruction. For example, Ref. 1 use a *reference-frame* technique to “compensate mechanical inaccuracies caused by slow and coherent mechanical drifts” where a short reference scan is acquired after the experiment. This reference-frame technique has been extended to incorporate changes in radiograph image magnification² which is important for high-cone-angle cone-beam radiograph acquisition where source drift perpendicular to the detector plane can significantly distort the radiographs.

Correction of random or unpredictable motions is more challenging. This problem was first tackled in electron tomography where imaging is at nanometre scale resolution. The use of fiducial markers (e.g. gold nanoparticles³) was a common practice in order to correct for unpredictable stage motions. The fiducial markers act as a known phantom which can be tracked in the radiographs and motions can be subsequently estimated based on the known geometry (position) of the markers. The first marker free solution was proposed by Ref. 4 where multi-resolution re-projection alignment (RA) was used to converge to a consistent geometry. RA 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. New per-projection motion estimates are calculated in each iteration and iterations continue until a relevant convergence criterion is satisfied.

The RA method concept was first applied to X-ray micro-tomography on the X-ray ultra-microscope (XuM) in Ref. 5, where it was noted that RA was particularly suited to resolving mis-alignment due to *jitter* (random motion) type positioning error of the sample-manipulator. In their⁵ simulations, the RA method converged in seven iterations for random (jitter) motions, compared with 27 iterations for smooth motions. Ref. 1 also utilise RA for correcting micro-CT per-projection motion and similarly note that RA is more effective for correcting jitter, preferring their reference-frame technique for correcting smoothly varying motions. Both Ref. 5 and Ref. 1 used RA for correcting *circular* trajectory acquired radiographs. In our simulations of Section 2.3, we examine RA convergence for the low-pitch-helix (LPH) trajectory and observe (as Ref. 1,5 observe for the circular trajectory) that RA converges more slowly for smooth-motion LPH perturbed projections than the random-motion LPH perturbed projections.

The RA method, at full resolution, is a computationally costly procedure, where each iteration involves forward-projection and back-projection operations. Seven iterations of RA at full-scale takes 14 times longer than a single filtered-back-projection reconstruction. This is impractical for large data-sets which require hours/days to reconstruct. Here, we demonstrate that RA can be performed to an acceptable accuracy at half-resolution (which is 16 times faster than full-scale) and we demonstrate improved accuracy per-iteration using a multi-resolution RA scheme. For real micro-CT data, our multi-resolution scheme starts at quarter-resolution with a small number of iterations (less than 5) performed to give an initial estimate of the per-projection motion parameters. The subsequent (and final) half-resolution RA iterations give per-projection motion parameters which are up-scaled to full-resolution and used to correct the full-resolution measured radiographs. Motions which result in radiograph movement of less 0.5 pixels on the detector are imperceptible in the reconstructed tomogram (as per *optimal unit* analysis of Ref. 6). Thus, 0.5 pixel RA accuracy is sufficient to produce a motion-artefact-free reconstructed tomogram.

For a typical *single-shot* filtered-back-projection (FBP) reconstruction methods, the RA motion estimation is used to correct radiographs as a pre-processing step. In iterative reconstruction (IR) schemes, the geometry correction can be applied in-iteration.^{7,8} Simulated radiographs (or projections) are generated as part of IR schemes, so introducing RA is a simple matter of registering the existing IR simulated projections with the measured experimental projections (and performing the appropriate motion correction). In this paper, we incorporate the RA correction into our multi-grid IR (IMGR⁹) scheme for our space-filling¹⁰ (SF) trajectory. We employ only one RA iteration per-resolution to accurately perform the motion correction so that the only significant computational overhead is the per-projection registration of measured projections with simulated projections.

Before presenting the RA algorithms and results for real micro-CT data in Section 3, Section 2 presents simulation results, for synthetic data, which examine how the convergence properties of RA vary with motion-type, trajectory-type and resolution. The simulations illustrate that, for the SF trajectory, smooth-motion perturbed projections and random-motion perturbed projections *each* result in blur and noise artefacts in the reconstructed tomogram. This is in contrast to the more traditional continuous helical (low-pitch-helix) and circular trajectories where random-motions produce blur and noise artefacts but smooth-motions produce *distortion* and *double edge* artefacts in the tomogram. The simulations also demonstrate that highly accurate motion-estimation can be achieved for the SF trajectory by performing a single quarter-resolution RA iteration followed by a single half-resolution iteration. This result explains the success of the “single RA iteration per resolution” in the IMGR scheme.

Section 3.1 presents our pre-processing RA method, which is in common use at the ANU micro-CT facility, for double-helix¹¹ trajectory acquired cone-beam data. Section 3.1 also illustrates the effectiveness of the method on an example double-helix trajectory data-set. This is followed by Section 3.2 which details the use of RA inside our IMGR⁹ scheme and also shows the effectiveness of the correction for a SF trajectory acquired data-set. The discussion and conclusions follow in Section 4.

2. RE-PROJECTION ALIGNMENT SIMULATIONS

In this section we explore how the convergence properties of the RA method vary with respect to:

motion type: random (jitter) and smooth,

acquisition trajectory: low-pitch-helix (LPH) and space-filling (SF), and

resolution scheme: full-resolution iterations (FR), one quarter resolution RA iteration followed by one half-resolution RA iteration (1QR-1HR), and two quarter resolution RA iterations followed by two half-resolution RA iterations (2QR-2HR).

Smoothly varying perturbations represent motions such as X-ray source drift or motions related to thermal effects. Short time-scale random-jitter is usually due to stage positioning repeatability errors. We use the synthetic phantom of Figure 1(a) to generate a set of synthetic projections for each of the LPH and SF trajectories. Each synthetic projection set is subsequently perturbed by the known set of per-projection motions in Figures 1(b) and 1(c). The per-projection x and y shifts lie in the interval $[-10, 8]$ pixels. The two trajectories and two motion-types give a total of 4 synthetic measured projection sets: LPH smooth-motion perturbed, LPH random-motion perturbed, SF smooth-motion perturbed and SF random-motion perturbed. The RA alignment algorithm is then applied to the synthetic measured projections in an attempt to recover the associated set of

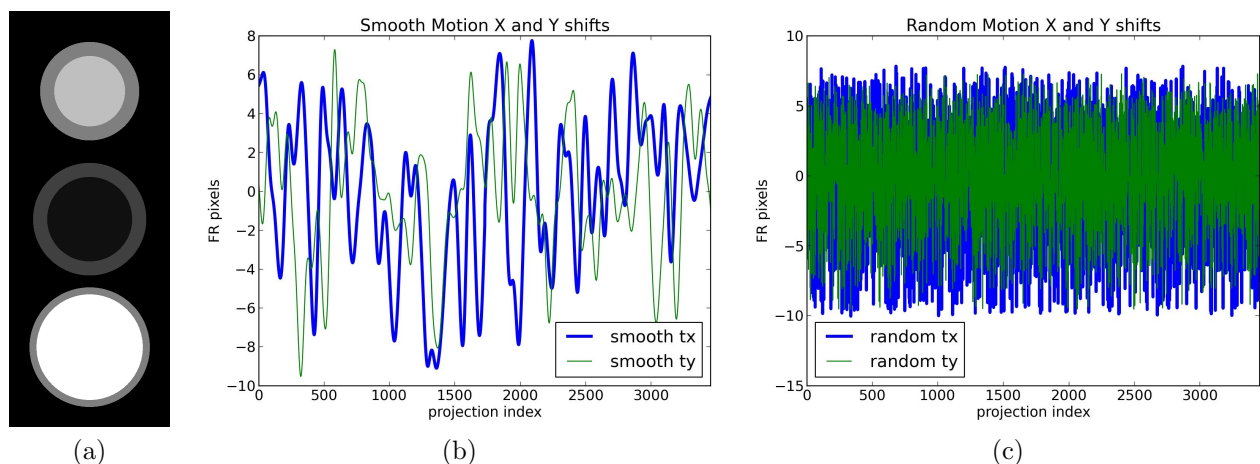


Figure 1. (a) Vertical (x - z) slice through 3D 3-sphere stack 480×480×1248 voxel phantom used in RA simulations, (b) Smooth per-projection motions, and (c) random per-projection motions.

known per-projection motions. The phantom is a $480 \times 480 \times 1248$ voxel image ($(0.004544 \text{ mm})^3$ voxel size) of a simple stack of three spheres, with each sphere differing in attenuation composition. There are two attenuation values for each sphere in a concentric arrangement. The synthetic acquisition geometry has camera-length of 436.27 mm and a sample-distance of 4.3627 mm with $(0.4544 \text{ mm})^2$ detector pixels. For the LPH trajectory, there are 3456 projections with angular spacing of 0.5° and vertical translation displacements of 0.001641 mm. The space-filling trajectory consists of the same number of projections (3456) and the same vertical translation displacements of 0.001641 mm, but with a larger angular spacing of $\approx 15.3^\circ$.

2.1 Algorithm

The RA method, in its simplest form, is described in Algorithm 1. Note that in Step 2, we employ ramp-filtered-back-projection to produce the tomogram which is subsequently used to generate the simulated projections in Step 3. For helical and space-filling trajectories, the Ramp-FBP tomogram has inaccurate intensity levels, however, the location of sample material boundaries (edges) are geometrically faithful. This produces simulated projections with geometrically faithful projection-edge-locations, which is sufficient for successful registration via phase-correlation. Algorithm 1 is simple, however, it is computationally expensive (at full resolution) and can be slow to converge when accurate registration (Step 4) of projections cannot be achieved (due to misalignment artefacts dominating simulated-projection-image features). Techniques for reducing computational cost are crucial for RA to be a practical solution for motion correction.

For the simulation results presented in Section 2.3, the registration step 4 is performed using a sub-pixel phase-correlation technique to obtain the x and y translations. Sub-pixel shifts are resolved by least-squares fitting a parabola to the phase-correlation peak pixel (and immediate neighbourhood pixels) and calculating the location of the maximum of this parabola. For real experiment data taken at large cone-angles and small source-sample distances (as used at the ANU micro-tomography facility¹¹) the registration step 4 needs to incorporate a magnification (i.e. scale) parameter,² in addition to the x - y translation, to compensate for source drift perpendicular to the detector plane.

Algorithm 1 Basic re-projection-alignment (RA).

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

2.2 Mis-alignment Reconstruction artefacts

Figures 2(a) and 2(b) show a horizontal slice through the middle sphere of FBP reconstructions generated from the perturbed projections for the LPH trajectory. The reconstruction from random motion (Figure 2(b))

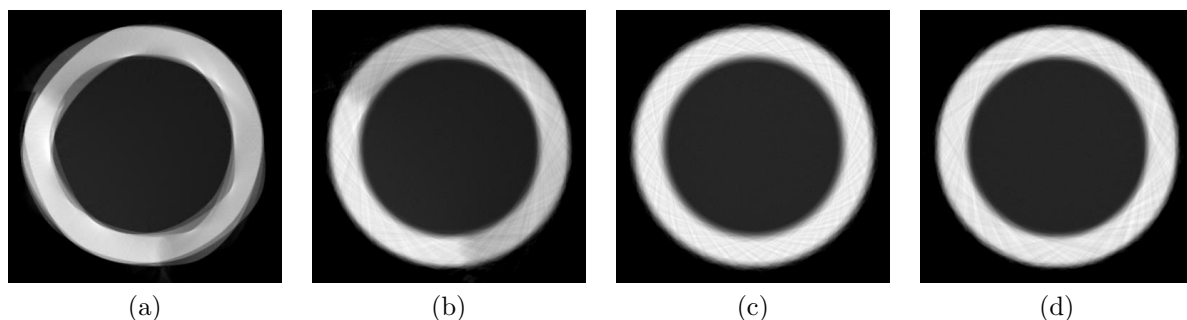


Figure 2. Perturbed projections FBP tomogram x - y slices from centre sphere: (a) LPH smooth motions, (b) LPH random motions, (c) SF smooth motions, and (d) SF random motions.

resembles a blurred version of true phantom slice, while the LPH FBP tomogram slice generated from the smooth motion perturbed projections shows greater distortion and *double edges*. As demonstrated in Section 2.3, distortion artefacts negatively impact the convergence rate of RA. Similarly, Figures 2(c) and 2(d) show the same slice through the middle sphere of FBP reconstructions generated from the perturbed projections for the SF trajectory. For the SF trajectory, the reconstruction motion artefacts for *both* smooth-motion and random-motion are structurally very similar to each other and very similar to the random-motion artefacts for the LPH trajectory, i.e. artefacts resemble blurring of the phantom image. The nature of the artefacts has consequences for the registration Step 4 of RA Algorithm 1. Artefacts which distort the morphology make the registration task more difficult and/or less accurate, whereas registering a blurred version of an image with itself is less challenging, provided the scale of the blurring is less than that of the dominant features.

2.3 Scale, Trajectory and Motion Type Influence on Convergence

Here, we present the convergence properties of the RA method by examining mean-absolute-error (MAE) of the estimated shifts for the 4 sets of synthetic measured projections. We re-iterate that achieving less than 0.5 pixel accuracy for the per-projection motion estimation is sufficient to produce a motion-artefact-free tomogram. Figure 3 plots MAE for the RA estimated x and y translation versus number of FR iterations, where 1 QR iteration is the computational equivalent of 1/16 FR iteration and, similarly, 1 HR iteration is the computational equivalent of 1/4 FR iteration. For the simulations, down-sampling is only performed on the projection images, no sub-sampling of the angle set is performed, so the RA estimates per-projection motion for the complete set of angles at all resolutions QR, HR and FR. Figure 3 provides a comparison of the RA results for varying trajectory-type (LPH and SF), motion-type (smooth and random perturbations) and multi-resolution strategy (FR, 1QR-1HR, and 2QR-2HR).

The plots of Figures 3(a) and 3(b) show MAE for the LPH trajectory. The most notable trend for both x and y components is that the LPH RA converges more rapidly for the random-motions than the smooth-motions. This due to the nature of LPH artefacts generated by the different motion-types. The random-motions produce blurred re-projections which can be more accurately registered with the perturbed measured projections. The LPH smooth-motions produce distorted re-projections and result in inaccurate registration (particularly for the early iterations). The smooth-motion LPH MAE plots also show the benefit of a multi-resolution approach. The 2QR-2HR scheme achieves the same MAE accuracy as 4 FR iterations with 6 times less computational cost. At QR, the smooth-motion LPH re-projection artefacts become more blurred (i.e artefacts become more like random-motion artefacts) resulting in an overall increase in registration accuracy. Even so, the 2QR-2HR scheme only achieves ≈ 0.65 pixel MAE accuracy for the y component (and takes a further 3 HR iterations, not shown in Figure 3, to reach 0.4 pixel MAE accuracy).

The random-motion LPH x component MAE plots also show improvements with the multi-resolution schemes. For the y component, there is significant MAE improvement for the 1QR-1HR scheme over the early FR iterations. Indeed the 1QR-1HR scheme for LPH random-motions yields MAE of less than 0.25 pixels, which is achieved after 3 FR iterations, i.e. the 1QR-1HR scheme achieves approximately the same accuracy as the 3 FR iterations with 9 times less computation.

The plots of Figures 3(c) and 3(d) show MAE for the SF trajectory. Remarkably, in these plots, there are only minor differences between MAE values for the smooth-motion perturbations and the random-motion perturbations. Indeed, the y translation component MAE for the smooth and random motions are almost identical, while the x translation component shows that the smooth-motions are corrected slightly more rapidly and slightly more accurately than the random-motions. Also of significance in SF MAE plots, is that 0.2 (or less) pixel MAE accuracy is achieved by the 1QR-1HR scheme for both smooth and random motion types.

Comparing the trajectories, we clearly see that the RA method for the smooth-motion perturbations converges more rapidly and equally accurately for the SF trajectory than the LPH trajectory. For random-motions, the SF trajectory shows a minor improvement in accuracy for the multi-resolution schemes over the LPH trajectory.

Because per-projection motion artefacts manifest themselves as blur and noise for the SF trajectory we observe similar (and rapid) RA MAE convergence for both the smooth motion and random motion perturbations. This is in stark contrast to the LPH results, where smooth-motion induces distortion artefacts (Figure 2(a)) which in-turn hinders accurate re-projection registration, resulting in a slowed RA MAE convergence rate.

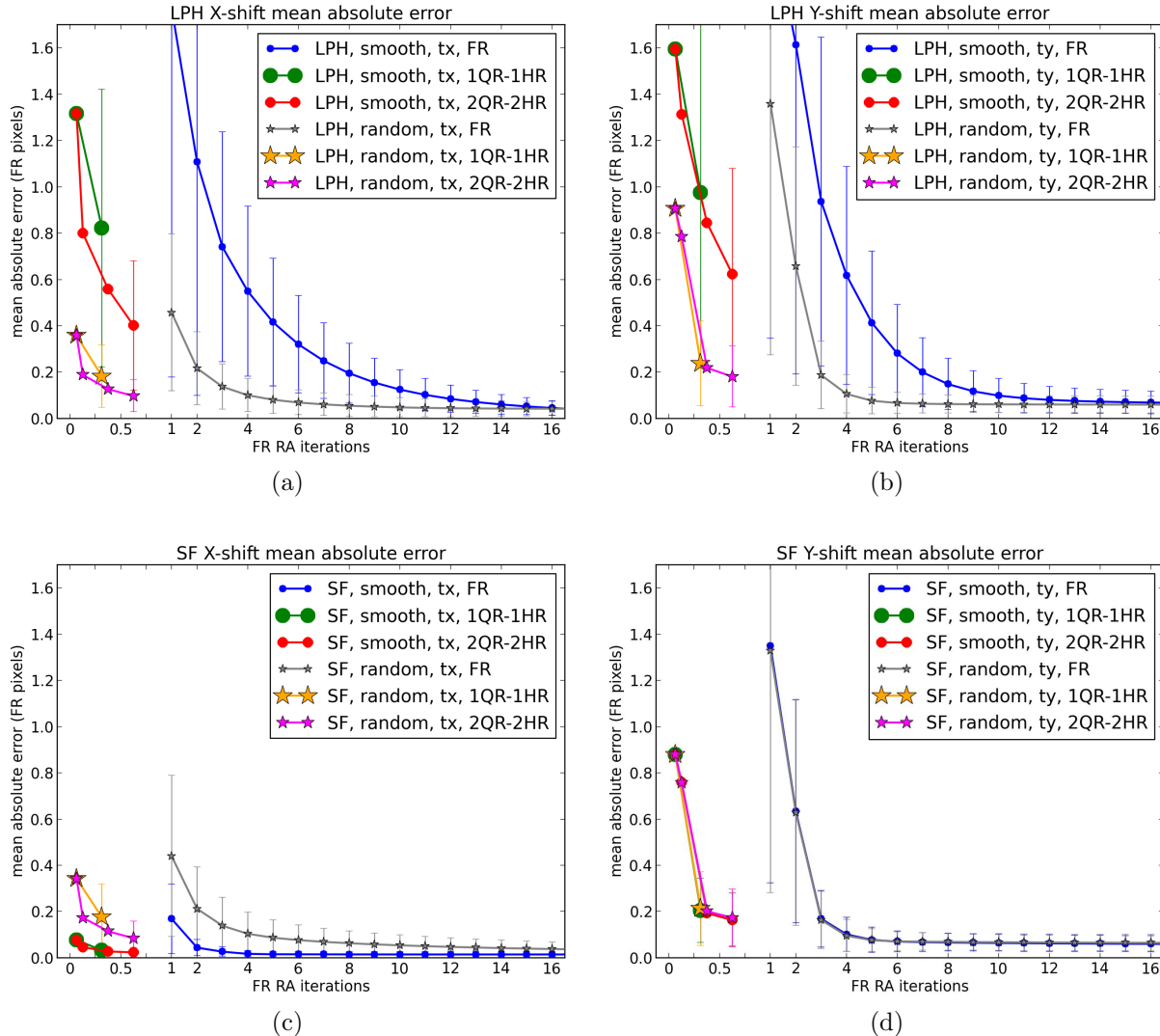


Figure 3. Mean Absolute Error of estimated motion versus number of FR RA iterations: (a) LPH x translation, (b) LPH y translation, (c) SF x translation, and (d) SF y translation. Error bars indicate one standard deviation from MAE. For 1QR-1HR and 2QR-2HR, the error bar is only shown on the final iteration MAE (to avoid clutter).

3. RE-PROJECTION ALIGNMENT ON EXPERIMENTAL DATA

In this section, we illustrate the effectiveness of RA for real high-cone-angle micro-CT data. Two examples are given: (1) as a pre-processing method performed prior to FBP reconstruction, and (2) as an in-iteration correction for IR methods. For the real experiment data the RA methods also estimate a magnification (i.e., scale) parameter, in addition to the translation, to compensate for source movement perpendicular to the detector plane. The registration step, of RA algorithms below, uses the method of Ref. 2 to estimate the per-projection shift and magnification parameters. Section 3.1 describes the multi-resolution pre-processing method which is being routinely applied to double-helix trajectory micro-CT data-sets at the ANU micro-CT facility. Section 3.2 details the inclusion of RA in the iterative multi-grid reconstruction method of Ref. 9.

3.1 Double-Helix Trajectory

For the case where reconstruction is performed using a single-shot FBP method, the RA correction is performed as a pre-processing step, where the measured projections are transformed (translated and scaled) to a consistent geometry prior to reconstruction. Section 3.1.1 presents a multi-scale RA pre-processing algorithm. The following

Section 3.1.2 gives an example where the multi-scale RA pre-processing method has been applied to a double-helix trajectory acquired data-set of a wood sample and Katsevich FBP is used to reconstruct the motion-corrected projections.

3.1.1 Pre-processing method

A multi-resolution RA approach is used to reduce the computational overhead associated with Ramp-FBP reconstruction and subsequent forward-projection to generated the simulated projections. Importantly, no iterations are performed at full resolution, the per-projection alignments generated at half-resolution are interpolated/up-scaled to full resolution. The steps involved are given in Algorithm 2. Typically QR convergence is achieved in fewer than 5 iterations, and HR convergence in fewer than three iterations.

Algorithm 2 Multi-resolution re-projection-alignment pre-processing.

- 1: Down-sample the full-resolution measured projection images to quarter resolution (QR)
 - 2: **repeat**
 - 3: Ramp-FBP reconstruct QR tomogram from *corrected* QR measured projections.
 - 4: Compute QR simulated projection images from the QR tomogram.
 - 5: Register QR measured projections with corresponding simulated projections to obtain per-projection shift and scale
 - 6: **until** converged
 - 7: Down-sample full-resolution measured projection images to half resolution (HR)
 - 8: Up-sample QR shifts and scale (from Steps 3-5) and apply to the HR measured projection images
 - 9: **repeat**
 - 10: Ramp-FBP reconstruct HR tomogram from *corrected* HR measured projection images.
 - 11: Compute HR simulated projection images from the HR tomogram.
 - 12: Register HR measured projection images with HR simulated projections to obtain per-projection shift and scale.
 - 13: **until** converged
 - 14: Up-sample HR shifts and scale (from Steps 10-12) to full resolution (FR) and apply them to the FR measured projection images.
 - 15: Correct FR measured projection images (prior to FR reconstruction).
-

3.1.2 Experimental Results

Figure 4 illustrates Katsevich FBP^{11,12} reconstructed tomograms using uncorrected (left) and RA corrected (right) radiographs. The sample was a 3 mm diameter core of wood (white beech), where 14136 projections were acquired (7068 projections per helix) using a 3040×3040 Varian Flat Panel detector ((0.139 mm)² pixels) with camera-length of 315.5 mm and specimen distance of 2.8823 mm (resulting fan-angle of 67.62°). The reconstructed tomogram was 2560×2560×5240 voxels with voxel size of (0.00131 mm)³. The left image in Figure 4 shows typical helical motion-related multi-edge artefacts which are eliminated (right image) by re-projection alignment pre-processing. Figure 5 plots the full-resolution per-projection shift (left) and per-projection magnification (right) corrections estimated during the re-projection-alignment pre-processing. Figure 5 shows estimated shifts of up to 4 pixels in the x (horizontal) direction and up to 3 pixels in the y (vertical) direction. Significant magnification estimates are also observed, where values outside the range [0.9993, 1.0007] are of a magnitude which results in scaling-motion artefacts. Shift motion estimates, for double-helix trajectory acquired data, typically show some degree of symmetry about the central projections (projection indices 7067 and 7068) suggesting that stage (sample manipulator) inaccuracy forms a significant contribution to the motion estimation, as the vertical travel of the stage during the second helix acquisitions is the reverse of the vertical travel of the first helix acquisitions.

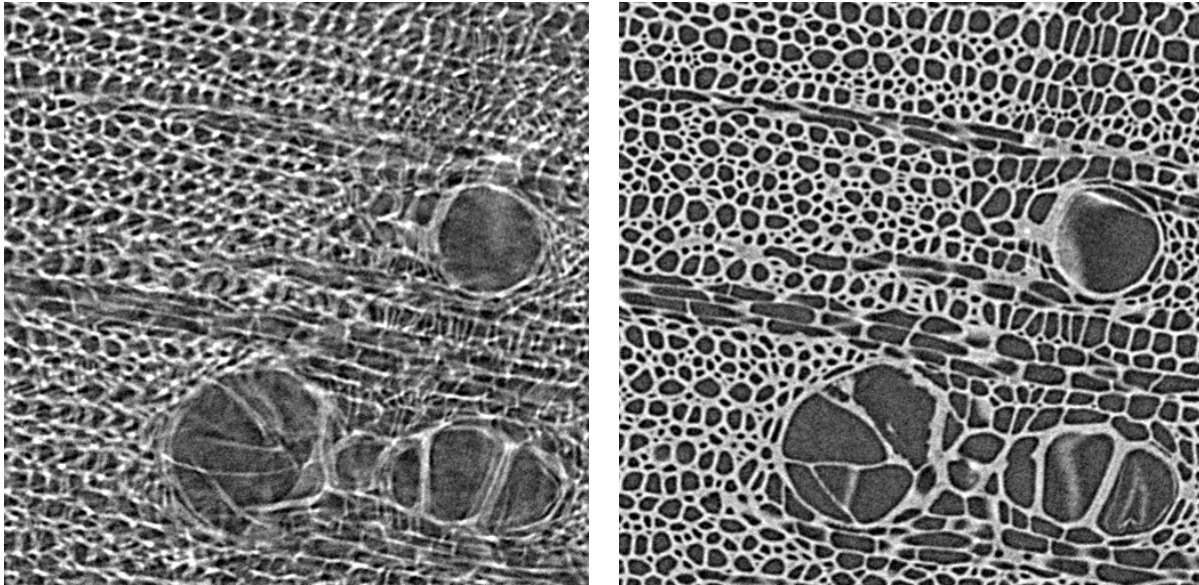


Figure 4. Left: cropped tomogram slice of wood sample, reconstructed from uncorrected double-helix radiographs, showing typical double-edge artefacts. Right: same tomogram slice reconstructed from re-projection-alignment corrected radiographs. Images show a $(0.67 \text{ mm})^2$ region, voxel size is $(0.00131 \text{ mm})^3$.

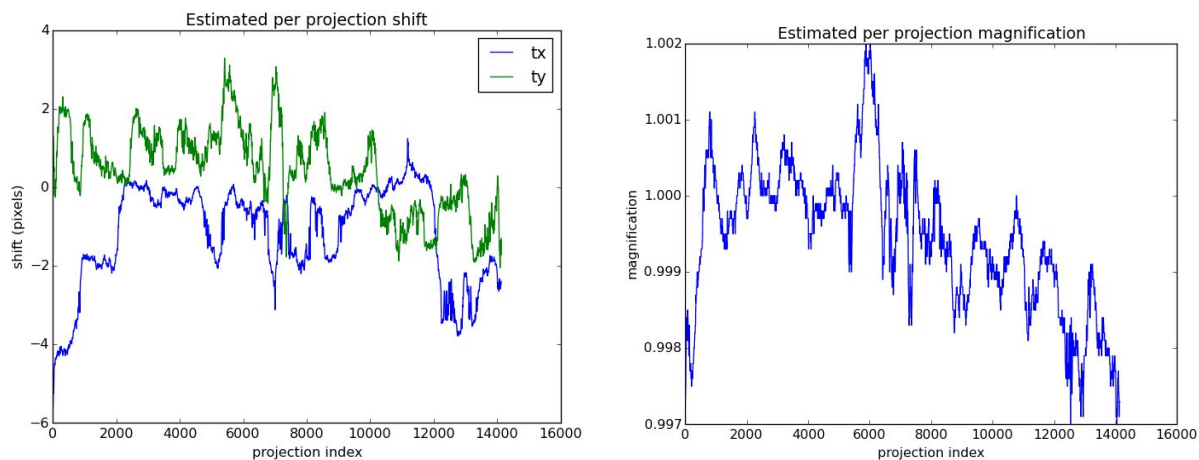


Figure 5. Re-projection alignment estimated per-projection shifts (left) and estimated per-projection magnifications (right) which were used to correct radiographs for the reconstruction of the wood sample in the right image of Figure 4.

3.2 Space-filling Multi-grid

The RA method (Algorithms 1 and 2) can be viewed as a form of IR (dedicated to reconstruction in the presence of per-projection motion/distortion), so it is natural to consider performing the RA in other IR schemes. Indeed, since IR already implies the calculation of simulated projections, it should be a simple matter to incorporate the registration and associated transformation into the existing iterations. In Section 3.2.1, we incorporate the RA into the IMGR method of Ref. 9. Section 3.2.2 presents IMGR reconstructions performed with and without RA for SF trajectory¹⁰ acquired micro-CT radiographs.

3.2.1 In-iteration method

Algorithm 3 lists a simplified (and abbreviated) version of the IMGR method presented by Ref. 9. Here, we set the lowest multi-grid resolution to be QR. Step 2 performs an initial Ramp-FBP reconstruction of a QR tomogram and this is used to estimate motions in the initial RA. Subsequent iterations of Step 5 use the down-sampled FR tomogram from Step 23 as the QR tomogram. The Ordered Subset Expectation Maximisation for Transmission

Tomography (OSEMTR) algorithm¹³ in Step 9 is used to reconstruct a QR tomogram. Multiple back-projection and forward-projection operations are performed as part of the OSEMTR iterations to generate the QR tomogram. Subsequent generation of the HR and FR tomograms involve just a single forward-projection and single back-projection to generate an update for the prolonged (up-sampled) tomogram from the previous resolution. Note that in Algorithm 3, there is only one “RA iteration” per resolution. The only computational overhead of introducing RA into the multi-grid iterative scheme is the registration (and associated re-sampling/shifting) of the measured projections with the simulated projections.

Algorithm 3 Multi-grid iterative reconstruction with in-iteration re-projection alignment. RA specific steps in red.

```

1: Down-sample the FR measured projection images to QR
2: Ramp-FBP reconstruct QR tomogram from QR measured projections.
3: repeat
4:   { /* QR RA */ }
5:   Compute QR simulated projection images from the QR tomogram.
6:   Register QR measured projections with corresponding QR simulated projections to obtain per-projection
   shift and scale
7:   Transform QR measured projections according to motion estimates from Step 6
8:   { /* QR IR */ }
9:   OSEMTR reconstruct QR tomogram (OSEMTRQR) from QR measured projections
10:  { /* HR IR */ }
11:  Prolongate OSEMTRQR tomogram to HR (PHR)
12:  Compute PHR simulated projections from PHR volume
13:  Register PHR simulated projections with HR measured projections
14:  Transform HR measured projections according to Step 13
15:  Calculate HR update, back-project and filter to obtain final HR tomogram
16:  { /* FR IR */ }
17:  Prolongate HR tomogram to FR (PFR)
18:  Compute PFR simulated projections from PFR volume
19:  Register PFR simulated projections with FR measured projections
20:  Transform FR measured projections according to motion estimates from Step 19
21:  Calculate FR update, back-project and filter to obtain final FR tomogram
22:  if not converged then
23:    Down-sample FR tomogram to QR tomogram.
24:  end if
25: until converged

```

3.2.2 Experimental results

Figure 6 illustrates IMGR^{9,14} reconstructed tomograms without RA (left) and with in-iteration RA (right). The sample was a 5 mm diameter core of sandstone and carbonate (two cylindrical samples glued end-to-end), where 4858 projections were acquired using a 2304×2304 pixel (3040×3040 masked) Varian Flat Panel detector ((0.139 mm)² pixels) in a space-filling trajectory. The camera-length was 335.6 mm and specimen distance was 7.068 mm (resulting fan-angle of 48.5°). The reconstructed tomogram was 2010×2010×5428 voxels with voxel size of (0.00293 mm)³. The left image in Figure 6 shows typical space-filling motion-related noise and blur artefacts which are eliminated (right image) by re-projection alignment performed during multi-grid iterative reconstruction. Figure 7 plots the full-resolution per-projection shift (left) and per-projection magnification (right) corrections estimated by the re-projection-alignment. Figure 7 shows estimated shifts of up to 2 pixels in the *x* (horizontal) direction and up to 1 pixel in the *y* (vertical) direction. For this experimental data, the magnification estimates are in the insignificant range [0.999, 1.001].

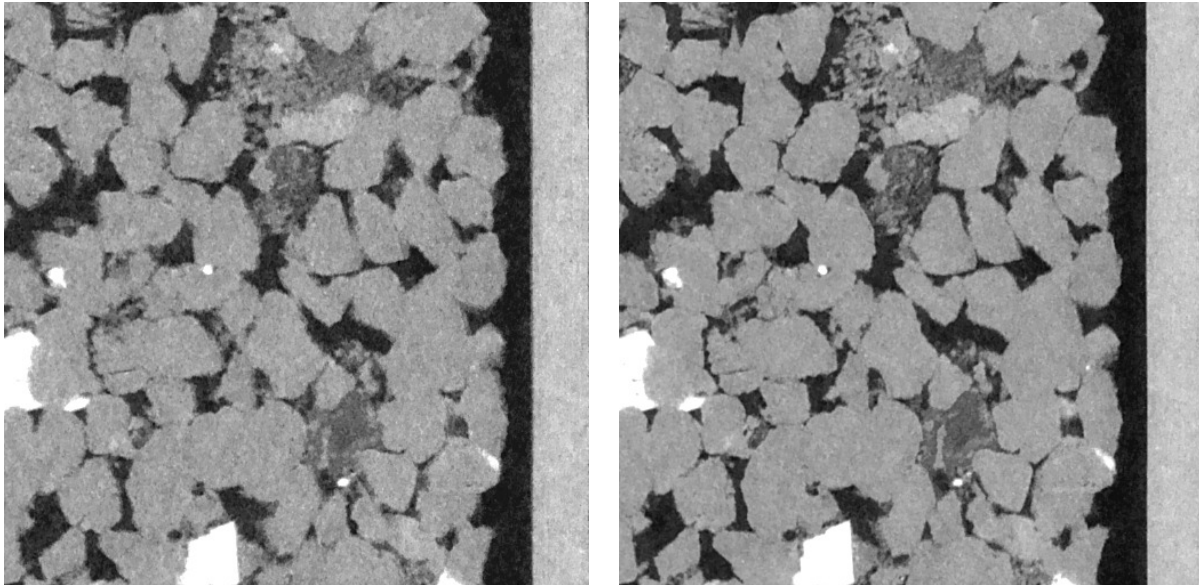


Figure 6. Left: tomogram slice of sandstone/carbonate (in aluminium container) from uncorrected iterative multi-grid reconstruction. Right: same tomogram slice reconstructed with in-iteration re-projection alignment. Images show a $(1.5 \text{ mm})^2$ region, voxel size is $(0.00293 \text{ mm})^3$.

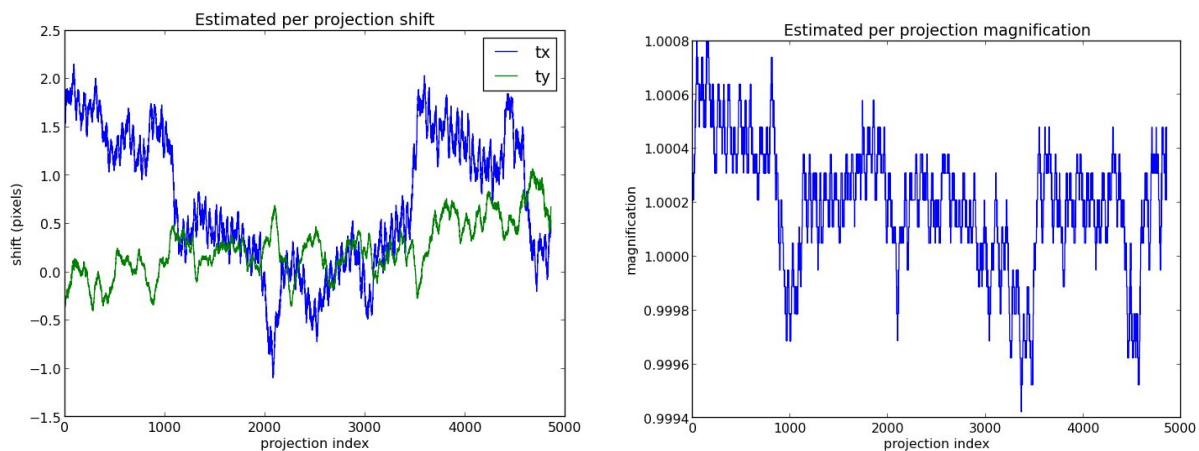


Figure 7. RA estimated per-projection shifts (left) and estimated per-projection magnifications (right) which were used to correct radiographs for the reconstruction of the sandstone/carbonate sample illustrated in the right image Figure 6.

4. DISCUSSION AND CONCLUSIONS

This paper has used simulation to examine how RA convergence varies with motion-type, trajectory-type and resolution-scheme. Our FR simulations for the LPH trajectory showed slow RA convergence for smooth-motions and rapid convergence for random-motions. FR simulations for the space-filling trajectory demonstrated rapid RA convergence for both smooth-motions and random-motions, with the convergence rate and accuracy almost identical (or better) compared to the LPH random-motion case. The difference in RA convergence for the smooth-motion LPH FR case and the smooth-motion SF FR case is attributed to the different nature of the artefacts induced by perturbation of the projections for the two trajectories. The LPH smooth-motion FBP tomogram contains distortion artefacts and double-edges (Figure 2(a)), while the LPH random-motion FBP tomogram, the SF smooth-motion FBP tomogram and the SF random-motion FBP tomogram resemble a noisy and blurred version of the phantom (Figures 2(b)-(d)). The noisy and blurred FBP tomograms produce similarly noisy and blurred re-projections which can be more accurately registered (via phase-correlation) with the corresponding measured projection. The distorted and double-edged tomogram produce similar artefacts in the re-projections

resulting in registration ambiguity, particularly for the phase-correlation technique. The registration accuracy then directly impacts the RA convergence rate.

In all simulation cases, the 1QR-1HR multi-resolution scheme produced lower MAE than two full-resolution iterations. More significantly, for the SF trajectory, the 1QR-1HR multi-resolution scheme produced a MAE of 0.2 pixels (or less) for both the smooth-motions and random-motions. Correcting per-projection motion to less than 0.5 pixel accuracy yields motion-artefact-free reconstructions.

For the double-helix trajectory experimental data in Section 3.1.2 we see the obvious improvement in the Katsevich FBP tomogram quality resulting from the multi-resolution RA pre-processing correction. By estimating the motion at HR, RA becomes a feasible method for improving helical reconstruction quality for large data-sets affected by radiograph motion.

Similarly, the SF trajectory experimental data of Section 3.2.2 also shows an obvious tomogram quality improvement when performing RA in our IMGR method. Only a minor overhead is incurred in IMGR, with the introduction of RA, as there is only need for a single “RA iteration” per resolution. The extra computation being the registration of the measured projections with the simulated projections.

The first fundamental pre-requisite for success of the RA method is that the acquisition motions can be approximated (and corrected) by shifting and scaling the measured radiographs. This places a constraint on the magnitude of the motions which can be estimated and corrected with this method. Non-rigid sample motions, where part of the sample moves relative to other parts of the sample, are generally outside capability of RA to correct precisely.

The second fundamental pre-requisite for successful RA correction is that it is possible to accurately register simulated projections with the measured projections. This means that features in the simulated projections must be able to be identified/aligned with features in the measured projections. Low contrast sample features which are at the size of imaging resolution are difficult to identify in the measured projections let alone motion corrupted simulated projections. Any significant motion tends to obliterate these features in the simulated projections of the initial RA iteration. For the multi-resolution approach presented here, the constraints on feature size are more severe, features need to survive at the greatest down-sampling of projections (both measured and simulated) for RA to produce accurate motion estimates.

RA does not enforce any constraints on the reconstructed tomogram image quality, it purely ensures that simulated projections are aligned with (the motion-corrected) measured projections. In the simulations, the authors have observed cases where the RA iterations converged to motion-estimates which differed from the motions which were used to perturb the projections. Whether these alternate RA solutions are of practical significance and their impact on the final tomogram image quality is yet to be investigated.

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