High-resolution helical cone-beam micro-CT with theoretically-exact reconstruction from experimental data

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Abstract—In this paper we show that optimisation-based autofocus may be used to overcome the instabilities that have, until now, made high-resolution theoretically-exact tomographic reconstruction impractical. To our knowledge, this represents the first successful use of theoretically-exact reconstruction in helical micro-CT imaging. We show that autofocus-corrected, theoretically-exact helical CT is a viable option for high-resolution micro-CT imaging at high cone-angles (∼50°). The elevated cone-angle enables better utilisation of the available X-ray flux and therefore shorter image acquisition time than conventional micro-CT systems.

By using the theoretically-exact Katsevich 1PI inversion formula, we are not restricted to a low-cone-angle regime; we can in theory obtain artefact-free reconstructions from projection data acquired at arbitrary high cone-angles. However, this reconstruction method is sensitive to misalignments in the tomographic data, which result in geometric distortion and streaking artefacts. We use a parametric model to quantify the deviation between the actual acquisition trajectory and an ideal helix, and use an autofocus method to estimate the relevant parameters. We define optimal units for each parameter, and use these to ensure consistent alignment accuracy across different cone-angles and different magnification factors. The tomographic image is obtained from a set of virtual projections in which software correction for hardware misalignment has been applied.

We make significant modifications to the autofocus method that allow this method to be used in helical micro-CT reconstruction, and show that these developments enable theoretically-exact reconstruction from experimental data using the K1PI inversion formula. We further demonstrate how autofocus-corrected, theoretically-exact helical CT reduces the image acquisition time by an order of magnitude compared to conventional circular-scan micro-CT.

Autofocus-corrected, theoretically-exact cone-beam reconstruction is a viable option for reducing acquisition time in high-resolution micro-CT imaging. It also opens up the possibility of efficiently imaging long objects.

Keywords: micro-CT, helical micro-CT, tomography, exact reconstruction

I. INTRODUCTION

Non-destructive three-dimensional (3D) imaging through X-ray micro computed tomography (micro-CT) continues to find new applications in fields such as biology, materials science, and geology. Tomographic images, or tomograms, are not acquired directly, but are reconstructed from a set of projection images of the specimen, obtained from different viewing angles. The algorithm used to reconstruct a tomogram depends on the experimental geometry used for collecting the projections. A standard lab-based micro-CT system uses a fine-focus experimental configuration with a circular X-ray source trajectory. The tomograms are then typically reconstructed using the Felkamp-Davis-Kress (FDK) filtered backprojection (FBP) algorithm. Feldkamp et al. (1984)

Since the FDK reconstruction is an approximate algorithm, it should only be used for a limited range of cone-angles; Feldkamp et al. (1984) it is commonly recognised that the FDK algorithm produces reliable results as long as the cone-angle does not exceed ∼±5°. In order to ensure an artefact-free image, the distance between the X-ray source and the detector must therefore be large relative to the height of the detector (the extent of the detector perpendicular to the source-trajectory plane). This limits the solid angle of X-rays which can be utilised, and becomes problematic for high-resolution systems where the X-ray flux is low. Despite this obvious short-coming, the mechanical simplicity and accuracy of a single rotation stage, combined with some robustness to trajectory imperfections has kept circular trajectory and FDK reconstruction the method of choice for systems with micron-scale resolution.

Several systems exist that achieve (sub)micrometer resolution. Ultra-fine-focus systems utilise scanning electron microscopes (SEM) for X-ray generation. These can only produce X-rays up to about 30 keV, and are limited to sub-millimetre specimen diameter. Furthermore, since the specimen is placed in a vacuum chamber, they cannot easily accommodate experimental rigs. X-ray lens based systems use a condenser to increase X-ray flux from the source. These systems are also limited to low X-ray energies due to the high aspect ratios required in the Fresnel zone plates for hard X-rays. Good resolution is obtained by using very small detector elements, mandating a very thin scintillator. As a result, only a small fraction of the X-ray photons are detected, leading to long acquisition times despite the relatively high X-ray flux in these systems. As a third alternative, we have fine-focus systems. Like ultra-fine-focus systems they do not rely on X-ray optics, but offer much greater flexibility both in the range of X-ray energies which can be used – and as a consequence what objects can be imaged – since no vacuum chamber is needed. Furthermore, the propagation path between the X-ray source and the detector is completely open, making

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such systems ideally suited when auxiliary experimental rigs are required. A fourth configuration type is the *quasi-parallel* configuration, in which the sample is placed closer to the detector than the source, giving a geometric magnification close to 1. This geometry enables a much higher radiographic resolution for a given source spot size than the fine focus configuration, allowing the use of sources with a much higher flux. However, the large source-sample distance mandates the use of a small cone angle, meaning that in practice the flux incident on the sample is not improved dramatically. Secondly, at high resolution a thin scintillator must be used, resulting in a very low X-ray detection efficiency, typically less than 5%, compared to over 60% for modern large flat-panel detectors.

In the remainder of this paper we focus exclusively on the fine-focus system type.

A major obstacle when increasing the resolution of a fine-focus system is the relationship between radiographic resolution, (projected) X-ray source spot size, and projection data *signal-to-noise ratio* (SNR). Firstly, due to *penumbra* effects the radiographic resolution is limited by the size of the region from which the X-rays are generated; the X-ray source spot. Smaller spot size is therefore always better from a resolution point of view. Secondly, the amount of X-rays generated from the source is commensurate with the amount of heat deposited onto the target (the anode). Since there is an upper limit to how much energy the anode can dissipate per unit area, there is also a limit to the X-ray flux that can be generated for a given spot size. This relationship can to a certain degree be broken by introducing a rotating anode, thereby increasing the effective area over which the heat is deposited. However, for high-resolution systems, where a spot size on the order of a micron or less is required, sources with rotating anodes are not available. For such systems we therefore have as a rule of thumb that the maximum X-ray flux is proportional to the area of the source spot: to increase the resolution by a factor of two, one must decrease the source spot area, and consequently the X-ray flux, by a factor of four. Finally, the dominant contribution to image noise in a properly configured (*quantum limited*) detector is shot noise arising from finite photon numbers. Projection data SNR can be assumed to follow Poisson statistics and be equal to the square root of the amount of X-ray photons detected by each pixel. In order to preserve SNR while increasing the resolution of a given acquisition by a factor of 2, there is one quarter of the flux, resulting in four times longer acquisition time for the same SNR. This can lead to unacceptably long experiments, and places strain on stability requirements of the system.

In order to alleviate the diminishing SNR for the projection data acquired with a fine-focus system, we can increase the effective flux at the detector by capturing a larger solid angle of the X-ray beam; by moving the detector closer to the source. Fine-focus transmission sources produce a near-isotropic beam flux over a solid angle of almost \(2\pi\) steradians, and do therefore not impose additional restrictions or nonuniform noise statistics. In this regime, it is important to be able to operate at higher cone-angles than the \(\pm 5^\circ\) recommended for the FDK algorithm. A different trajectory/reconstruction technique is therefore required.

In contrast to a circular source trajectory, a helical source trajectory satisfies the Tuy data sufficiency condition.Tuy (1983) This allows the use of *theoretically-exact* inversion, often referred to as *exact reconstruction methods*. Exact reconstruction is of course impossible in a practical setting; noise, as well as finite sampling implies that exact reconstruction can only be realised under idealised conditions. The main point, however, is that these methods are not limited to small cone-angles.

Exact algorithms have been known for some time,Grangeat (1987); Defrise and Clack (1994); Axelsson and Danielsson (1994) Unfortunately, these methods require filtering in the direction parallel to the rotation axis. As a consequence, they can be used only when imaging objects with very limited vertical extent, where the projection data is not vertically truncated. The first exact inversion formula which does not require longitudinal filtering was the Katsevich 1PI (K1PI) inversion formula for a helical trajectory.Katsevich (2002,?)

An important ingredient in his work is the *Tam-Danielsson window*,Danielsson et al. (1997) which is used to avoid data redundancy. Also, as the K1PI inversion formula is of FBP type, this combination of data acquisition and reconstruction can be accomplished with minimal changes to a standard system: requiring only the addition of a translation stage and modification to the projection filtering step prior to backprojection. Other exact inversion formulas have since followed, both for helical trajectories Zou and Pan (2004,?) and for other trajectories.Katsevich et al. (2004); Ye and Wang (2005); Zhao et al. (2005) Implementation and optimisation strategies for reconstruction methods based on these have also been reported.Yan et al. (2009); Deng et al. (2006); Fontaine and Lee (2007); Yang et al. (2006) However, studies in the current literature are confined to simulations, and do not cover important aspects such as deviation from the desired trajectory.

While the K1PI inversion formula is theoretically-exact, it has also been shown to be very sensitive to imperfections.Yu and Wang (2004) In this paper we develop an autofocus method for K1PI reconstruction, and show that it can be used to compensate for imperfections in the acquisition trajectory. We show that autofocus-corrected K1PI reconstruction renders high-resolution micro-CT imaging at cone-angles approaching \(\pm 25^\circ\) (full cone-angle of 50°) a viable option. The elevated cone-angle leads to better utilisation of the available X-ray flux and shorter image acquisition time than a conventional circular micro-CT scan. Our development is an extension of the autofocus method presented by Kingston et al. for adaptive geometric alignment in the context of circular trajectories.Kingston et al. (2010) To our knowledge, autofocus-corrected K1PI reconstruction represents the first method based on the K1PI inversion formula in use for micro-CT imaging.

The paper is organised as follows: Section II presents the K1PI inversion formula and our implementation of it. In this section we also discuss associated pitch/scanning speed limitations. In Sec.III we describe how the autofocus method works and show how it needs to be modified in order to work reliably with K1PI reconstruction. Section IV contains images which demonstrate imaging capabilities and limitations using autofocus-corrected K1PI reconstruction. Finally, Sec. V gives
some concluding remarks.

II. KATSEVICH 1PI RECONSTRUCTION

In this section we briefly review the theoretically-exact Katsevich 1PI (K1PI) inversion formula. We then describe the algorithmic implementation of the reconstruction method for idealised projection data. Finally, we discuss pitch/scanning speed limitations.

A. Katsevich 1PI inversion formula

Take the cone-beam X-ray micro-CT acquisition geometry with helical trajectory depicted in Fig. 1. Assuming a perfectly aligned system with the origin placed on the rotation axis, the position of the source can be parameterised by the rotation angle \( \theta \)

\[
\Gamma(\theta) = [R \cos \theta, R \sin \theta, P \frac{\theta}{2\pi}]^T.
\]

Here \( R \) is the sample-distance, and \( P \) is the pitch, i.e., distance we move upwards along the rotation axis per revolution of the helix. For this geometry, Katsevich proposed an inversion formula which gives exact reconstruction of a function \( f(x) \) from its cone-beam transform, assuming \( f(x) \) is infinitely smooth and supported inside the helix. Katsevich (2002) This formula relies on the use of PI-segments of the helix, that were first introduced by Danielsson et al. Danielsson et al. (1997)

A PI-segment is a straight line with end points on the helix, separated by less than one revolution of the helix. It can be shown that every point inside the helix belongs to one and only one PI-segment. Danielsson et al. (1997) If the PI-segment containing \( x \) starts at \( \Gamma(\theta_a) \) and ends at \( \Gamma(\theta_b) \), we define the PI-interval

\[
I_{\Pi}(x) := [\theta_a, \theta_b].
\]

We now construct a parameterised family of planes \( \Pi(\theta, x) \): for given \( x \) and a source location \( \theta \in I_{\Pi}(x) \) we determine an alternate parameter \( \theta_0 \in I_{\Pi}(x) \) such that the plane containing \( x \), \( \Gamma(\theta) \) and \( \Gamma(\theta_0) \) also contains \( \Gamma(\theta_a) \). This plane is \( \Pi(\theta, x) \), and we denote its surface normal by \( u(\theta, x) \). Using this construction, we can now state the Katsevich inversion formula:

\[
f(x) = -\frac{1}{2\pi} \int_{\Gamma(\theta)} \left[ \frac{1}{|x - \Gamma(\theta)|} \right] \left. \frac{\partial}{\partial q} D_f(q, \Lambda(\theta, x, \gamma)) \right|_{q = \theta, \gamma = \sin \gamma} d\theta.
\]

Here \( D_f(\theta, \beta) \) is the cone-beam transform of the function \( f \), i.e., the (linearised) projection data:

\[
D_f(\theta, \beta) := \int_0^\infty f(\Gamma(\theta) + \beta t) dt,
\]

and \( \Lambda \) is

\[
\Lambda(\theta, x, \gamma) := \cos \gamma \beta(\theta, x) + \sin \gamma e(\theta, x),
\]

\[
e(\theta, x) := \beta(\theta, x) \times u(\theta, x).
\]

B. Filtering lines

In the construction of this inversion formula, we used a parameterised family of planes, \( \Pi(\theta, x) \), with surface normals \( u(\theta, x) \). The intersection between these planes and the detector surface defines a parameterised family of lines on the detector surface. The integral over \( \gamma \) in Eq. (3) is effectively a Hilbert transform of each projection data along these intersection lines.

C. Tam-Danielsson window

The integral over \( \theta \) in Eq. (3) is limited to the PI-interval of the helix. This ensures that for each point \( x \) at which the function is reconstructed, we get contributions only from projection data which lie within what is referred to as the Tam-Danielsson window: the region on the detector which is bounded by the projection of the trajectory segment \( \Gamma(\theta + q) \) for \( q \in [-2\pi, 2\pi] \). This way, the reconstruction at a point \( x \) never uses projection data which has been acquired more than one PI-interval apart.

It can be shown that for the helix of Eq. 1, the Tam-Danielsson window is bounded by the curves \((u, v_0(u))\) and \((u, v_1(u))\) on the detector

\[
v_0(u) = -\frac{P}{2\pi R} \left( \frac{u^2 + L^2}{L^2} \right) \left[ \pi/2 + \arctan(u/L) \right]
\]

\[
v_1(u) = \frac{P}{2\pi R} \left( \frac{u^2 + L^2}{L^2} \right) \left[ \pi/2 - \arctan(u/L) \right].
\]

D. Implementation of K1PI reconstruction

Like the FDK method, Katsevich’s inversion formula is of filtered backprojection type. In fact, implementations can utilise many of the same optimisation strategies which have been developed for FDK reconstruction. The difference lies in the filtering of the projection data, and in the carefully chosen subset of the projection data that is backprojected. Our implementation of the inversion formula in Eq. (3) is broken down into 6 computation steps, and follows the algorithmic description by Noo et al. Noo et al. (2003)

Consider a planar detector and let \((u, v)\) be a coordinate on the detector surface, and let the origin of this coordinate system coincide with closest point on the detector to the source. We denote the distance from the source to the detector by \( L \) (see Fig. 1). Let the projection dataset be \( g(u, v, \theta) \), where \( \theta \) is the parameter along the helix which denotes projection angle. The reconstructed tomogram is then obtained as follows:

1. Compute derivatives of the dataset:

\[
g_1(u, v, \theta) := \left( \frac{\partial g}{\partial \theta} + \frac{u^2 + L^2}{L} \frac{\partial g}{\partial u} + \frac{uv}{L} \frac{\partial g}{\partial v} \right)(u, v, \theta).
\]
2) Weighting of the dataset to account for incident angle of rays onto the detector:
\[ g_2(u, v, \theta) := \frac{L}{\sqrt{u^2 + v^2 + L^2}} g_1(u, v, \theta). \] (10)

3) Transform the data to a new coordinate system \((u, v, \theta) \rightarrow (u, \psi, \theta)\)
\[ g_3(u, \psi, \theta) := g_2(u, v(u, \psi), \theta) \]
\[ v(u, \psi) := \frac{P L}{2\pi R} \left( \psi + \frac{u}{\tan \psi} \right). \] (11a)

This transformation implies a re-sampling, and is therefore a potential source of blurring of the reconstruction.

4) Apply a Hilbert-transform along the \(u\)-direction:
\[ g_4(u, \psi, \theta) := P \sqrt{P} \frac{1}{\pi} \int_{-\infty}^{\infty} \frac{1}{u - \mu} g_3(\mu, \psi, \theta) d\mu. \] (12)

In these coordinates, the Hilbert transform is efficiently and accurately computed in the spatial frequency domain.

5) Transform back to \((u, v, \theta)\)-coordinates, i.e., invert the transform in step 3 to obtain \(g_5(u, v, \theta)\).
\[ g_5(u, v, \theta) := g_4(u, v(u, v, \theta), \theta). \] (13)

Again, re-sampling of the data is required.

6) Backproject the parts of \(g_5\) which lie inside the Tam-Danielsson window (see Sec. II-C) along straight lines intersecting the source location
\[ f(x, y, z) := \int w(x, y) g_5(u, v, \theta) \chi_{TD}(u, v) \, d\theta, \] (14)
where the weight function \(w(x, y)\) is
\[ w(x, y) := \left( \frac{L}{R} \right) \left( \frac{L}{L + \frac{R}{2\pi} (x \cos \theta + y \sin \theta)} \right), \] (15)

\((u, v)\) is the intersection of the line through the source location \(\Gamma(\theta)\) and \((x, y, z)\) with the detector plane:
\[ u(x, y, \theta) := w(x, y) \times [y \cos \theta - x \sin \theta], \]
\[ v(x, y, \theta) := w(x, y) \times \left[ z - \frac{P}{2\pi} \right], \] (16)
and \(\chi_{TD}(u, v)\) is an indicator function which is 1 inside the Tam-Danielsson window, and 0 outside. We use linear interpolation of each projection when computing the backprojected value.

It should be noted that the coordinate transform in step 5 could be combined with the backprojection in step 6 to effectively bypass one data re-sampling step. While this would reduce the amount of blurring introduced by the reconstruction process, it would also add complexity to the backprojection routine. The backprojection required for a tomographic cube with a side length of \(N\) voxels has computational complexity \(O(N^4)\), and is the singularly most expensive step in the reconstruction process. We have found it worth keeping the backprojection as simple as possible, and instead opted for having the additional re-sampling step. We perform all data re-sampling using cubic splines.

E. Maximum pitch (or scanning speed)

In order to reconstruct a tomogram using the K1PI method, the pitch of the helix must be such that the TD window fits inside the detector. This places an upper limit on the pitch.
For a fixed H and W, we can insert the extremities $u = \pm W/2$ and $v_i = \pm H/2$ into (8) to deduce that

$$|P| \leq \frac{\pi RLH}{((W/2)^2 + L^2)(\pi/2 + \tan(W/2L))}.$$  

(17)

If we now use the following notation for the fan-angle, $\alpha_f$, and the cone-angle, $\alpha_c$:

$$\alpha_f := \tan(W/2L),$$

(18)

$$\alpha_c := \tan(H/2L),$$

(19)

the pitch $P$ must satisfy

$$|P| \leq \frac{4r \sin \alpha_c \cos^2 \alpha_f}{\sin \alpha_f \cos \alpha_c(1 + 2\alpha_f / \pi)}.$$  

(20)

Here H and W is the detector height and width, respectively, and the object is supported inside a cylinder of radius $r := R \sin \alpha_f$. We refer to Appendix for further details.

Figure 2 shows the TD window given a configuration of $W = 400$ mm, $H = 300$ mm and $L = 332$ mm. For a sample-distance of 6 mm, corresponding to a field of view almost 6.2 mm wide, we can run at a maximal pitch of about 5.9 mm per revolution, moving upwards almost one full field of view per revolution. This corresponds to imaging with a cone-angle of approximately $\pm 25^\circ$; well outside the $\pm 5^\circ$ range acceptable for circular scanning.

III. AUTOFOCUS-CORRECTED K1PI RECONSTRUCTION

The K1PI reconstruction method, as presented in Sec. II, assumes that the data was collected using a perfect helical trajectory, with an aligned detector. In order to obtain high-quality tomograms, we need to make sure that the reconstruction method can handle deviations from this ideal acquisition geometry. As we increase the resolution, the absolute tolerance for error between presumed geometry and the actual acquisition geometry decreases. For high-resolution micro-CT the hardware alignment and stability becomes a major concern. Figure 3 shows examples of reconstruction artefacts resulting from applying the K1PI reconstruction method without knowing the acquisition geometry to sufficient precision.

To deal with the geometry uncertainty, we propose to solve the tomographic reconstruction as two related inverse problems where we recover not only the tomographic image, but also a parametric description of the acquisition geometry. Conceptually, this is performed as three separate steps:

1) determine a set of alignment parameters which describe the deviation of the actual acquisition geometry from the ideal helix;

2) apply a transform to each projection which maps them to a set of virtual projections acquired by a perfectly aligned virtual detector following an ideal helix trajectory;

3) reconstruct the tomogram from the virtual projections which do satisfy the alignment assumptions made by the K1PI reconstruction algorithm.

The same general approach has successfully been used for FDK reconstruction, where an autofocus method was developed to determine the best alignment parameters.Kingston et al. (2011) In the remainder of this section we will develop an autofocus method which is suited for use in concert with K1PI reconstruction. We refer to the extended reconstruction method as autofocus-corrected K1PI reconstruction.

A. A parametric alignment model

We distinguish between two types of deviations: those that vary on a time-scale which is sufficiently slow so that they may be assumed to be constant for the duration of the experiment (static misalignment), and those that change over the course of the experiment (temporal instabilities). In this
model we ignore stage errors, i.e., repeatable nonlinearities such as deviations from a circular motion of the rotation stage.

1) Temporal instabilities: The X-ray source experiences thermal expansion due to the intrinsic heat generation during operation. This expansion causes the physical location of the X-ray source spot to drift slowly over time. For large $R$, source movement in the direction of the detector becomes negligible. Provided the source drift corresponds to less than $\sim 1\mu\text{Rad}$ angle change, then to a first order approximation, it manifests itself as a rigid transformation of the projection data; it is sufficient to apply an appropriate horizontal and vertical shift to the projection data. For very short $R$, drift of the source in the direction of the detector is no longer negligible. The dominant effect of this is a relative magnification change between projections.

In order to characterise the time-dependent source drift we therefore need three parameters per projection. These parameters can be efficiently determined using an extended version of the reference scan approach.

The reference scan method was proposed by Sasov et al., and involves acquiring a sparse set of projections along the trajectory after the full dataset was obtained, and then determining shifts from the location of the maximum of the cross correlation with the corresponding projection in the full dataset. Sasov et al. (2008) The sparsely acquired projections can be obtained in a fraction of the total acquisition time. The geometry is therefore assumed to remain fixed during this process.

We have extended the reference scan method to include determination also of a magnification change; this is achieved by searching for the scaling factor which yields the overall highest correlation with the corresponding projection in the full dataset. The sparsely acquired projections can be efficiently determined using a Golden Section Search over this scaling parameter interval.

2) Static misalignment: The source drift correction results in a transformation from each projection to a stable, but unknown acquisition geometry. We now turn our attention to determining this geometry.

To characterise the deviation from a presumed helical trajectory, we use nine parameters:

- three translations of the detector; horizontal $D_W$, vertical $D_H$, and camera-length $L$
- two rotations of the detector; rotation about the detector normal $\phi$, rotation about the detector vertical axis $\theta$, and rotation about the detector horizontal axis $\psi$
- distance between source and sample; sample-distance $R$
- two rotations of the translation axis relative to the rotation axis

For simplicity, we will ignore the two rotations of the translation axis relative to the rotation axis. This is a reasonable assumption as long as the translation axis and rotation axis are reasonably parallel, and we consider projections which have not been taken too far apart. This simplification has the important consequence that the mapping of projections onto aligned virtual projections is the same for every projection, and leaves us with 7 parameters which needs to be determined. There is, however, no reason why our method could not be applied to the more general case. The process for determining the static alignment parameters is the topic of Sec. III-C.

B. Optimal units

We use optimal units to normalise the sensitivity to errors in the geometric alignment parameters. One optimal unit (1.0 ou) is defined separately for each parameter, and is the largest amount the parameter can be perturbed such that the deviation from the correct ray path through the tomogram is on the order of one voxel, and were derived for FDK reconstruction by Kingston et al. Kingston et al. (2011) Clearly, this is not a rigorously defined concept, but rather a guide for obtaining a consistent stopping criterion when searching for the optimal set of parameters. In this section, we derive the optimal unit for sample-distance $R$ in K1PI reconstruction, as this parameter plays a role in K1PI, but not for FDK.

We note that changing $R$ also changes the magnification factor $L/R$. However, if we reconstruct using the natural voxel size, i.e., a voxel size which is equal to the detector pixel size demagnified by this factor, then the resulting tomogram will remain the same size when measured in number of voxels. The ratio $L/R$ does therefore not affect the resulting image quality. However, backprojecting with an incorrect value for $R$ will introduce errors in the positioning of the TD window on the detector. Our starting point in the derivation of the optimal unit for $R$ is therefore Eq. (17), which describes the height of the TD window.

For a detector with $M$ elements vertically, we require 1.0 ou to result in less than one pixel change of the TD window on the detector. Therefore, the optimal unit must satisfy the following relation:

$$\frac{\pi RLH}{((W/2)^2 + L^2)(\pi/2 + \tan(W/2L))} = \pi (R + 1.0\text{ ou}) L \left( H - \frac{2W}{M} / \left( 1 + \frac{W}{\sqrt{L^2 + (W/2)^2}} \right) \right)
\quad \frac{((W/2)^2 + L^2)(\pi/2 + \tan(W/2L))}{},$$

or simplified

$$R = (R + 1.0\text{ ou}) \left( 1 + 1/M \right)$$

1.0 ou $= R \left( \frac{1}{M \left( \frac{1}{1 + \frac{W}{\sqrt{L^2 + (W/2)^2}}} - 1 \right)} \right)$. This leads to the following expression for the optimal unit

$$1.0\text{ ou} := \frac{R}{M} / \left( 1 + \frac{W}{\sqrt{L^2 + (W/2)^2}} \right)$$

We see that the optimal unit is proportional to the sample-distance.
We note that this derivation relies on the TD window, and is specific to FBP reconstruction methods that use this window. We also note that optimal units for the other parameters rely only on the backprojection part of the reconstruction and are therefore common for all cone-beam FBP reconstruction methods. In particular, they are also valid for FDK reconstruction. The optimal units for the other parameters are summarised in Table I, and derived in Appendix. We note that our expressions differ from those presented in Kingston et al. (2011) since we have aimed to make their cone-angle and fan-angle dependence explicit.

C. Autofocus parameter estimation

In Kingston et al., the inverse problem of determining the acquisition geometry was cast as an autofocus problem, i.e., the resulting tomogram was obtained using the parameter set which resulted in the sharpest tomogram: Kingston et al. (2010)

Formulation 1 (FDK autofocus): Let \( \gamma \) be a set of alignment parameters, and let \( f_\gamma \) be the tomographic reconstruction obtained from: first, re-mapping the projections \( p \) onto a set of aligned virtual projections according to the parameter set \( \gamma \); second, reconstructing a tomogram from the virtual projections assuming an ideal acquisition geometry. A parameterised representation of the actual acquisition geometry is obtained as the set of parameters which maximises the sharpness function

\[
\text{Sharpness}(\gamma; p) := \|\nabla f_\gamma\|^2 = \int |\nabla f_\gamma(x)|^2 \, dx.
\]  

(23)

It is natural to attempt the same also for K1PI reconstruction. Unfortunately, this proves to be a fruitless exercise. Figure 4 (top left) shows an example of how sharpness of the K1PI reconstruction fails to produce a global maximum at the correct value for the alignment parameters. We therefore have to find an alternative formulation of the autofocus problem in order to determine the alignment parameters in a robust and reliable manner.

There are of course many different metrics that have been used to characterise image quality, e.g., minimum support, minimum entropy, and maximum contrast. Subbarao et al. (1993); Kingston et al. (2011) In contrast to many of these measures, however, the sharpness measure as defined in (23) has the property that it favours well-defined edges explicitly. This intuitive quantification of image quality makes sharpness a compelling choice for an autofocus method across a wide range of images. Instead of abandoning it, we will therefore proceed to investigate the reasons why the autofocus formulation above works so well for FDK reconstruction, but fails miserably for K1PI reconstruction.

FDK uses projection data from a full 360° trajectory to reconstruct every point in the tomogram. This means that we have a significant amount of redundant information contributing to the reconstruction. As long as the object which is imaged does not have perfect cylindrical symmetry, a mismatch between acquisition geometry and backprojection geometry will mean that an image feature is backprojected to slightly different locations depending on the projection angle, resulting in a degraded reconstruction. Backprojecting diametrically opposed projection rays mean that the misalignment-induced shift of a feature will be in opposite directions, and therefore a blurring. The K1PI reconstruction method, on the other hand, limits the use of diametrically opposed projection rays;

<table>
<thead>
<tr>
<th>parameter</th>
<th>slices</th>
<th>optimal unit</th>
<th>num value</th>
</tr>
</thead>
<tbody>
<tr>
<td>( D_W )</td>
<td>three horizontal</td>
<td>( \frac{\pi}{(1 + \sin \alpha_f)} )</td>
<td>0.13 mm</td>
</tr>
<tr>
<td>( R )</td>
<td>two orthogonal vertical</td>
<td>( \frac{2 \pi}{(1 + \sin \alpha_f)} )</td>
<td>2.6 µm</td>
</tr>
<tr>
<td>( D_H )</td>
<td>two sets of three orthogonal</td>
<td>( \frac{\pi}{\tan \alpha_f} )</td>
<td>0.17 mm</td>
</tr>
<tr>
<td>( L )</td>
<td>two sets of three orthogonal</td>
<td>( \frac{2 \pi}{\tan \alpha_f} )</td>
<td>0.37 mm</td>
</tr>
<tr>
<td>( \phi )</td>
<td>two orthogonal vertical</td>
<td>( \text{asin} \left( \frac{2 \pi}{(1 + \sin \alpha_f)} \right) )</td>
<td>0.86 mRad</td>
</tr>
<tr>
<td>( \theta )</td>
<td>three horizontal</td>
<td>( \text{asin} \left( \frac{\pi}{2 \tan \alpha_f} \right) )</td>
<td>1.1 mRad</td>
</tr>
<tr>
<td>( \psi )</td>
<td>three horizontal</td>
<td>( \text{asin} \left( \frac{\pi}{3 \tan \alpha_f} \right) )</td>
<td>2.0 mRad</td>
</tr>
</tbody>
</table>

Table I

The magnitude of optimal units and 2D slices used to inspect each misalignment parameter. The detector has \( N \) elements horizontally and \( M \) elements vertically. Right-most column shows the numerical value for 1.0 in given \( L = 330 \) mm, \( W = 400 \) mm, \( H = 300 \) mm, \( M = 1536 \) and \( N = 2048 \).
a property of the PI-lines is that every point has only one PI-line going through it. Danielsson et al. (1997) The lack of opposing projection rays mean that features tend to be shifted rather than blurred.

![Fig. 5. Tomography slices from circular trajectory using FDK reconstruction (top row), and helical trajectory using K1PI reconstruction (bottom row). From left to right, we have an offset of 0.0°ou, 4.0°ou, 8.0°ou. Sharpness normalised to their peak values are (left to right) 1.00, 0.70, and 0.73 for the FDK reconstructions, and 1.00, 0.98 and 0.95 the K1PI reconstruction. This demonstrates how sharpness is significantly more robust for K1PI reconstruction. Grayscale is linear with X-ray attenuation from 0 to 255; 50 is mean value for air, and 200 is mean high-density value.]

In Figure 5 we see a comparison between a tomogram reconstructed from a circular scan using FDK reconstruction, and a tomogram reconstructed from a helical scan using K1PI reconstruction. In this comparison all alignment parameters except the horizontal translation of the detector are correct. While the sharpness value is highest for the correct horizontal offset in both cases, the sharpness decays more rapidly for the FDK reconstruction than for K1PI reconstruction. This suggests that adding data redundancy is the key to a robust autofocus method.

1) Fast Filtered Backprojection: The FDK algorithm has been generalised to provide approximate reconstruction for helical trajectories. Wang et al. (1993) To keep the distinction clear between FDK for circular trajectories and FDK for helical trajectories, we will refer to them as FDK and HFDK, respectively. Both HFDK and K1PI assume the same underlying acquisition geometry, and have the same alignment parameters. In fact, their respective backprojection routines differ only in the choice of which data are backprojected, and in the weighting factor which is applied to ensure that every voxel gets the same amount of data. In contrast to the K1PI method, however, HFDK reconstruction uses a significant amount of redundant data as it does not limit the backprojection to the TD window. This redundant data should ensure sufficient data conflict – with the associated blurring – whenever the geometric assumptions are not being met for HFDK reconstruction.

There are some drawbacks with using full-blown HFDK, however. Firstly, it is a low-cone-angle reconstruction method. We can therefore not expect good images at elevated cone-angles. Secondly, it uses the same amount of data redundancy at every image point. In order to cover every point in the tomogram with 360 degrees of data, we are forced to use a significantly reduced pitch. Even if partial-scan weighting is applied, the reduced pitch impacts on the maximum scanning speed at which our system can run.

As it turns out, the issue of low-quality images at elevated cone-angles is not a major concern since we are primarily interested in the position and relative sharpness of edges. Even if the backprojected edges are somewhat blurred due to incorrect filtering, data redundancy will ensure additional blurring when the backprojection geometry is incorrect. Our main problem with using HFDK is therefore the associated restrictions on the scanning pitch.

In order to avoid pitch restrictions, rather than trying to obtain a true reconstruction during autofocus, we instead consider the following basic algorithm which we will refer to as Fast Filtered Backprojection (FFBP):

1) filter the projections horizontally with a ramp filter, as is done for FDK reconstruction;
2) backproject the entire projection as if it was acquired using a circular trajectory, but adding a simple height offset relative to the tomogram according to the helix trajectory.

For zero pitch, and an integer number of revolutions, this is the FDK reconstruction.

Clearly, FFBP will in general not produce a good reconstruction. However, it has some useful properties. First of all, horizontal filtering is not affected by vertically truncated data. We can therefore use all the available projection data as a source of redundancy. Secondly, once we have filtered the projection data, we do not need to re-apply the filter, but can perform reconstructions assuming various alignment parameters by backprojection alone. Its computational cost is therefore low. Thirdly, even if the relative weighting between each voxel in the tomogram is incorrect, the weighting is very smooth. Smoothness of the weight function is important when we try to evaluate the sharpness function, since it ensures that

$$ \int \left| \nabla \left( f_\gamma \cdot w \cdot f \right) \right|^2 dx = \int \left| \nabla f_\gamma \right|^2 \left| w \right|^2 dx + \int \left( f(x) w(x) \right) \left( \nabla f_\gamma \cdot \nabla w \right) dx + \int \left| \nabla w \right|^2 dx \approx \int \left| \nabla f_\gamma \cdot (x) \right|^2 \left| w(x) \right|^2 dx. $$

A large sharpness value for $f_\gamma$, $w$ will therefore correspond to a large sharpness value also for $f_\gamma$.

Figure 6 shows reconstruction using FFBP for different horizontal detector offsets. We see the underlying haze resulting from the inappropriate filtering, and some streaks resulting from data truncation. However, we can clearly see that edges are preserved. When comparing it to Figure 5 (FDK vs K1PI), we see that the FFBP reconstruction leads to a significantly more blurred result than the K1PI reconstruction when incorrect horizontal detector offset is applied, and as a result the sharpness values decay much quicker.
2) Relative sharpness: The sharpness measure, as defined in Eq. (23), is a measure of the absolute edge content in a tomogram. The value of the sharpness function does therefore greatly depend on the size of the region over which the sharpness is computed.

When autofocus was developed for FDK reconstruction, great care was taken to ensure that the same image features were included in the region over which sharpness was evaluated for every choice of a given parameter. Kingston et al. (2011) This was accomplished through a combination of moving the region appropriately, and using the natural voxel size based on a demagnified detector pixel to keep the resulting object size fixed when measured in number of pixels (effectively keeping the magnification factor $L/R$ fixed).

It turns out that using the natural voxel size does a reasonable job of keeping the reconstructed object size fixed as long as the fan-angle is small. For large fan-angles, however, we notice a significant nonlinear relationship between camera-length and magnification. This is discussed further in Appendix D. The implication of this is that the change in object size may bias the sharpness value and lead to incorrect estimates.

Also other alignment parameters distort the shape of the reconstruction in such a way that the size changes: sample-distance stretches the tomogram along the rotation axis. Finally, if we use a set of 2D slices to compute the sharpness value of a tomogram (see Sec. III-D), at high cone-angles the issue of features coming in and out of the plane becomes more of a problem. Due to these complications, keeping the domain of integration consistent is difficult. Instead we consider relative edge content rather than absolute edge content, and use the following measure for relative sharpness of a function $f$:

$$\text{RelSharpness}(f) := \frac{||\nabla f||^2}{||f||^1} = \frac{\int |\nabla f(x)|^2 \, dx}{\int |f(x)| \, dx}.$$  (25)

As with sharpness, adapting the relative sharpness measure to more noisy data may include smoothing the projection data before reconstructing, and thresholding the gradient before integrating. Subbarao et al. (1993); Kingston et al. (2011)

Smoothing the data will of course result in a blurred reconstruction. However, it will also reduce the small fluctuations which are caused by noise. As a result, the sharpness value is predominantly influenced by large edge features – the edges which remain after smoothing are those which persist across multiple scales. Since misalignment produces additional blurring, identifying correct alignment through the reconstruction with the highest relative sharpness value is still a valid approach. In our present exposition we deal with data where the SNR is sufficiently high for noise not to be an issue.

3) Autofocus formulation: While not producing very convincing image quality the FFBP has the property we need: edges are blurred if the alignment parameters are incorrect. The required data redundancy stems from utilising the regions of the projections outside the TD window (see Fig. 2). This is data which under normal circumstances would be thrown away during K1PI reconstruction. In fact, all available data is used.

We can now re-formulate the inverse problem of determining the alignment parameters as follows:

**Formulation 2 (K1PI autofocus):** A parameterised representation of the acquisition geometry for a projection set $p$ is obtained as the set of parameters $\gamma_0$ which maximises the relative sharpness function

$$\gamma_0 := \arg\max_{\gamma} \text{RelSharpness}(f_\gamma)$$  (26)

over all parameters in a suitable neighbourhood of the assumed geometry, where RelSharpness is defined in Eq. (25), and $f_\gamma$ is the tomographic reconstruction obtained from: first, mapping the projections $p$ onto a set of aligned virtual projections according to the parameter set $\gamma$; second, reconstructing a tomogram from the virtual projections using FFBP assuming an ideal acquisition geometry.

Once the geometry has been determined, the autofocus-corrected K1PI reconstruction is obtained by mapping the projection data onto virtual projections using the parameter set $\gamma_0$, and reconstructing the tomogram using the K1PI method.

D. Implementation

A search for all 7 parameters simultaneously is not feasible if the full tomogram is to be reconstructed for each evaluation of the sharpness. Since the reconstruction of an $N^3$ tomogram requires $O(N)$ projections, resulting in a computational complexity of $O(N^4)$ for FBP reconstructions. We employ the same techniques as described in Kingston et al. (2010) to make the search more efficient, reducing the search to a carefully ordered sequence of 1D parameter searches, which require evaluation of the relative sharpness only on $k$ representative 2D slices of the tomogram. This reduces the computational complexity to $O(k N^3)$. Furthermore, the initial search is performed at a coarse scale, with sub-sampled projection data. This further reduces the cost of each sharpness evaluation to $O(q^{-1} N^3)$, where $q$ is the down-sampling factor. Finally, since $k$ and $q$ are much less than $N$, the overall complexity is $O(N^3)$ per evaluation of the relative sharpness function.
As for the circular case, there is a natural hierarchy of the alignment parameters, arising from the fact that for some parameters, the relative sharpness function attains its maximum at the correct value even if the other parameters are significantly off. Figure 4 shows a typical example of the sharpness function as a function of horizontal detector offset and sample-distance. We see that there is a ridge along the correct value for $D_W$. This means that we can obtain a good estimate for the detector offset using a 1D search even if the sample-distance is incorrect, and motivates performing the 1D search over $D_W$ before the 1D search over $R$.

The order we use is as follows:
1) Horizontal detector offset, $D_W$
2) Out-of-plane detector tilt, $\theta$; rotation about the detector vertical axis
3) Sample distance, $R$; modifying also $L$ to keep the magnification $L/R$ constant
4) In-plane detector rotation, $\phi$; rotation about detector surface normal
5) Vertical detector offset, $D_H$
6) Camera-length, $L$.
7) Out-of-plane detector tilt, $\psi$; rotation about the detector horizontal axis

The optimal value for each of the alignment parameters is determined in order by performing a linear search, sampling the sharpness function at intervals of one optimal unit at the coarsest scale, before continuing to the next scale. At the finer scales, only a very narrow search interval about the optimal value from the previous scale is necessary. We use parabolic interpolation of the sharpness function to determine the peak location to a precision which exceeds that of our search steps of 1.0 ou. Since the cost of each function evaluation is $O(N^3)$, and typically only a few hundred function evaluations are required, the overall cost of determining the geometry is less than that of a single reconstruction of the full tomogram.

IV. RESULTS: CAPABILITIES AND LIMITATIONS

The autofocus-corrected K1PI reconstruction presented in the previous section allows us to perform tomographic reconstruction from projection data acquired at very high cone-angles. In this section we present results which demonstrate this.

Figure 7 shows the system used to acquire all projection data used in this paper. The detector is a $400 \times 300 \text{ mm}$ amorphous-silicon flat panel with $2048 \times 1536$ pixels of size $194 \mu\text{m}$, and a detective quantum efficiency (DQE) in excess of 60%. X-rays are generated by a $160\text{kV}$ nano-focus X-ray transmission source capable of producing X-rays from a sub-micron spot. Both the sample stage and the detector are mounted on rails with optical encoders allowing independent adjustment of both sample-distance and camera-length. Precision translation and rotation stages, and material matching give sufficient mechanical accuracy and thermal stability for sub-micron control of the sample position. The instrument can image specimens ranging from less than 1 mm up to over 100 mm in diameter.

The images presented in this section were acquired using the acquisition geometry which was described previously: camera-length of $L = 332 \text{ mm}$, sample-distance of $R = 6 \text{ mm}$. Since the SNR measured in the resulting tomograms is we are using a detector with width and height dimensions of $W = 400 \text{ mm}$ and $H = 300 \text{ mm}$, respectively, this results in a fan-angle of about $30^\circ$, and a maximal cone-angle of about $\pm 25^\circ$. This therefore leads to a reconstruction with $1760$ voxels across the sample diameter; the resulting tomogram voxel size is about $3.5 \mu\text{m}$.

The object which was imaged is a $20 \text{ mm}$ tall and $5 \text{ mm}$ diameter carbonate rock sample which was imaged using $2880$ projections per revolution. Acquisition time for each projection was $18 \times 0.135 \text{ s}$, with X-ray source set to $80 \text{ kV}$ and $100 \mu\text{A}$.

A. Signal-to-noise/acquisition time

In Fig. 8 we compare tomographic slices using FDK reconstruction and K1PI reconstruction, obtained from $2880$ projections and $2880$ projections per revolution, respectively. In both cases the exposure time was $18 \times 0.135 \text{ s}$ per projection. The SNR measured in the resulting tomograms is...
1.36 times higher for FDK reconstruction than for the K1PI reconstruction. Since FDK uses a full revolution to reconstruct each voxel in the tomogram, and K1PI uses only half as much data per reconstructed voxel, we should expect that projection data with the same SNR should lead to a SNR difference in the tomograms of $\sqrt{2}$. The fact that we observe a difference slightly less than $\sqrt{2}$ is most likely due to the additional re-sampling, and associated blurring, involved in the K1PI reconstruction. We therefore see that in order to obtain truly comparable images at the same camera-length, we need to expose for twice as long per projection when doing K1PI reconstruction.

One of the benefits of using a helical micro-CT system is the ability to image very long objects. In Fig. 9 we show a vertical slice through a tomogram of a the full 20 mm high sample.

For this geometry, we recall that K1PI reconstruction can be run at a maximal pitch of 5.9 mm/revolution. This means that scanning 20 mm requires a minimum of 3.4 revolutions of data. To compare this with circular trajectory scanning, we consider two scenarios.

In the first, a standard setup is used, with a roughly square detector, so that a single revolution of data produces a near-cubic tomogram. In this case, one could not image such a long/tall sample; a minimum of 4 tomograms would typically be used to cover the full height of 20 mm. These 4 revolutions of data is slightly more than would be required to image the same height using a helical trajectory and our rectangular detector (it evens out when we take into account the over-scan which is discussed in the next section). In order to keep the cone-angle below $\pm 5^\circ$, a square detector with sides of 400 mm would need to be placed over 2000 mm away from the source. To keep the same SNR in the projection data with the longer camera-length, we would in turn need $(2000/330)^2 = 36$ times longer acquisition time per projection. Since we get comparable SNR in the tomograms by exposing for half as long per projection when doing FDK reconstruction as compared to K1PI reconstruction, our high-cone-angle approach would be about 15 times faster – an order of magnitude speed-up over a conventional circular micro-CT system.

The second scenario is a high-fan-angle FDK approach where we leave the camera-length at 330 mm also for the circular scan. In this case, the FDK reconstruction would only be able to reconstruct a height of about 1.2 mm when limited to $\pm 5^\circ$ cone-angle (about 300 voxels); it would require 17 revolutions of data to cover the full 20 mm height, while our high-cone-angle system can image the region in less than 4 revolutions, i.e., we to acquire more than four times more projections than with a helical setup. A comparable tomogram SNR using a high-fan-angle FDK solution (some times referred to as a series scan) therefore takes more than twice as long. Given that a system capable of this a high-precision series scan would require the same hardware, and is subject to the same precision requirements as a system performing high-cone-angle autofocus-corrected K1PI imaging, the K1PI is clearly the preferred.
In Fig. 10 we see how the object gradually fades into focus at the top, and then gradually fades out of focus again towards the bottom. The reason for this is that we do not have a complete set of projection data for the end regions. The helical trajectory is an open path, and can in principle be used to scan an object of arbitrary height. However, we need to scan a bit extra at the top and bottom in order to get full coverage. The amount we need extra is referred to as the \textit{overscan}. The size of the overscan region was discussed by Yan et al.\cite{yan2009}. We can show that the overscan, measured in radians as a rotation angle around the helix, is given by (see Appendix.0.g)

\[
\text{Overscan}(\alpha_f) := \max_{\alpha \in [-\alpha_f, \alpha_f]} \left( \frac{\pi}{2} + \alpha \right) \times \left( 1 + \sqrt{1 - \frac{\cos^2 \alpha_f}{\cos^2 \alpha}} \right).
\]

Since the overscan is a strictly convex function of the fan-angle, we immediately have a simple explicit upper and lower bounds for the overscan:

\[
\frac{\pi}{2} (1 + \alpha_f) \leq \text{Overscan}(\alpha_f) \leq \frac{\pi}{2} + 3\alpha_f. \tag{27}
\]

Figure 11 shows the overscan plotted as a function of fan-angle. The dash-dotted lines show closed-form bounds from Eq. (27) for the overscan region.

\begin{figure}[h]
\centering
\includegraphics[width=\textwidth]{overscan_plot}
\caption{Overscan as a function of fan-angle. The dash-dotted lines show closed-form bounds from Eq. (27) for the overscan region.}
\end{figure}

\section{Misalignment effects on KIP1 reconstruction}

In Fig. 12 we see that a moderate horizontal detector offset does not blur the image significantly. However, we see from the black/white edge patterns in the difference images of Fig. 12 that an incorrect $D_W$ introduces a geometric distortion in the form of a disjoining vertically-connected parts of the tomogram. This is also depicted as a disjoin in the left vertical edge in Fig. 3, and comes as a result of predominantly shifting in opposite directions two parts of the tomogram which are reconstructed using diametrically opposed projections. This misalignment will have the effect of closing off narrow vertical connections in the tomogram.

Similarly, in Fig. 13 the black/white edge pattern reveals that an incorrect $R$ results in compressing/stretching the reconstructed image along the vertical axis. An error in $R$ of 4.0\,\mu m (about 10\,\mu m) produces noticeable artefacts where we see fine structures disappear, and large voids partially invaded. Altering the sample-distance has the effect of altering the slope of the filtering lines along which the Hilbert transform is performed, as seen from Eq. (11b). Secondly, it shifts the boundary of the TD window (see Eq. (8)). Katsevich reconstruction has already been reported to be sensitive to the manner in which the boundary is discretised when working with simulated data.\cite{yu2004} The need for high accuracy in specimen distance, $R$, and by extension the location of the TD window boundary are therefore expected. This poses a practical problem, however: the X-rays are generated from a point inside the X-ray tube that cannot be measured to micrometer precision. The aforementioned source drift makes it even harder to obtain sufficient sample-distance accuracy. Auto-focusing enables us to determine $R$ to the required accuracy for each experiment.

We also note that the projected error resulting from inaccurate $R$ will increase with pitch. This can be seen by...
considering a ray incident at a height $v$ on the edge of the TD window. In this case the angle $\sigma$ to the detector normal is $\tan \sigma = P/2R = v/L$. A change in sample-distance will move the edge of the TD window such that $\tan \sigma' = P/2R' = v'/L$. The associated displacement on the detector is therefore $\delta v = \frac{v}{2R} \left(1 - \frac{1}{1 + \frac{R'}{R}}\right)$; the displacement is proportional to the pitch $P$. Therefore, we have less tolerance to errors in the sample-distance $R$ when we run at a high pitch $P$. There is a similar increase in sensitivity to errors in detector distance $L$, and to detector tilt, since both these errors are also longitudinal misalignments.

V. CONCLUDING REMARKS

We have presented autofocus-corrected K1PI reconstruction; a reconstruction method based on the Katsevich 1PI (K1PI) inversion formula. We have furthermore demonstrated reduced acquisition time for high-resolution tomograms, as well as the ability to efficiently scan long objects.

Our hybrid-reconstruction approach consists of solving two related inverse problems: first we recover the acquisition geometry, and second we perform the actual tomographic reconstruction. In order to determine the acquisition geometry we introduce Fast Filtered Backprojection (FFBP) – a naïve FDK-based reconstruction – which uses redundant data to ensure that an incorrect backprojection geometry results in a blurred tomogram. We also introduce relative sharpness as a robust measure for reconstruction quality. Once the geometry has been determined, we re-map the projection data onto virtual projections from which a high-quality reconstruction can be obtained using K1PI reconstruction.

Presumably other reconstruction methods that utilise redundant projection data will also introduce sufficient blurring to ensure a global maximum. Such methods include exact methods such as Katsevich’s 3PI method, or approximate fractional-PI methods. These methods have a higher filtering cost, and are therefore less favourable for an autofocus step, where the filtering overhead is significant. They also impose pitch restrictions for our system. It is beyond the scope of the current paper to investigate such alternatives.

In this work we have considered the case where the translation axis is parallel to the rotation axis. A situation where this does not hold may be thought of as a perturbed trajectory, and accounted for by using more general reconstruction methods. In fact, it has been shown that the reconstruction method holds also for perturbed trajectories, as long as they satisfy certain convexity criteria. Katsevich et al. (2004) Unfortunately, this means that the Tam-Danielsson
window will depend on the projection angle. Consequently the optimisation strategies, which largely rely on pre-computing the Tam-Danielsson window and filtering lines and re-using the result for all projections, are no longer applicable. As long as the perturbations are small, it is still reasonable to re-map the projections onto an ideal geometry, thereby attempting to remove the inconsistency in the projection dataset caused by the trajectory perturbation. The only difference is that for this case the mapping will depend on the location on the source location along the helix.

For very long objects, where the translation axis and rotation axis no longer can be assumed to be parallel, we can break the problem into segments. As long as we can make the assumption that they are parallel on sufficiently short segments, we can estimate alignment parameters on these segments separately. The overall correction is then obtained by smoothly interpolating the alignment parameters between each segment to form a continuously deforming distorted trajectory. In particular, this is a way to determine the full set of 9 alignment parameters.

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REFERENCES


**APPENDIX**

The extra data which is required from outside the TD window lies along straight filtering lines which also passes through data within the window. For a rectangular detector, the convex shape of the upper TD window boundary ensures that any data required along the filtering lines also will be contained inside the detector. Likewise for the concave shape of the lower TD window boundary. Therefore, ensuring the TD window fits inside the detector area is sufficient to guarantee that all the required projection data is available.

For a fixed $H$ and $W$, we insert the extremities $u = \pm W/2$ and $v = \pm H/2$ into (8) to deduce that

$$|P| \leq \frac{\pi RLH}{(W/2)^2 + L^2}(\pi/2 + \arctan(W/2L)).$$

(29)

Introducing the following notation for the fan-angle, $\alpha_f$, and the cone-angle, $\alpha_c$:

$$\alpha_f := \arctan(W/2L)$$

$$\alpha_c := \arctan(H/2L).$$

(30)

(31)

we can re-write Eq. (29) as follows:

$$|P| \leq \frac{2\pi R\tan\alpha_c}{(\tan^2\alpha_f + 1)(\pi/2 + \alpha_f)}.$$  

(32)

Therefore

$$|P| \leq \frac{4\pi R\tan\alpha_c}{(\tan^2\alpha_f + 1)(\pi/2 + \alpha_f)}$$

$$= \frac{4\pi \tan\alpha_f \cos^2\alpha_f}{\sin\alpha_f \cos\alpha_c(\sin^2\alpha_f + \cos^2\alpha_f)(1 + 2\alpha_f/\pi)}.$$  

(33)

(34)

Here we have used $r := R\sin\alpha_f$ as the radius of the cylinder inside which the object is supported. Finally, for a square detector we have $\alpha_f = \alpha_c$

$$|P| \leq \frac{4\pi \cos\alpha_c}{(1 + 2\alpha_c/\pi)}.$$  

(35)

For a square detector, the maximal height we can image per revolution is therefore limited to

$$h_{helix}(\alpha_c) := \frac{4\pi \cos\alpha_c}{(1 + 2\alpha_c/\pi)}.$$  

(36)

For conventional micro-CT the magnification factor, $M$, of a tomogram is defined as $M = L/R$ where $L$ is the distance...
between the source and the detector, and \( R \) is the distance between the source and the rotation stage (see Fig. 1). Since a detector pixel is de-magnified by the factor \( M \) when it is projected back to the rotation axis, using cubic voxels with side lengths equal to the sides of the de-magnified pixel yields a reasonable volumetric sampling relative to the spatial sampling of the projection data.

By keeping the ratio between the camera-length and the sample-distance constant, we can keep the magnification the same for experiments with different camera-lengths. However, there is a catch: if we again place the object close enough to fill the detector width, for an object of radius \( R \), if we use a sample-distance of \( R = r / \sin \alpha_f \). If we furthermore express camera-length in terms of the fan-angle, \( \tan \alpha_f = W/2L \), we obtain

\[
M(\alpha_f, r) := \frac{W}{2r} \cos(\alpha_f).
\]  

For an object of a given size, the maximum magnification we can obtain becomes fan-angle dependent. Since we are working with a detector with a finite number of detector elements and thereby a finite spatial sampling rate across, this implies that we are sacrificing image resolution in order to obtain the increased number of X-ray photons captured at the detector. At a camera-length of 330 mm, the field of view corresponds to reconstructing a cylinder with about 1760 voxel diameter.

Here we derive the optimal units, as defined in Sec. III-B, for each of the alignment parameters.

**a) Horizontal detector offset** \( D_H \): Backprojecting with an incorrect value for the horizontal detector offset will introduce the largest backprojection error at the opposite side of the reconstructed volume from the source. For a detector with \( N \) elements horizontally, we therefore require 1.0 ou to satisfy the following relation:

\[
\frac{1.0 \text{ ou}}{L} = \frac{W}{L + \frac{W}{2} \cos \alpha_f}.
\]  

Expressing \( \cos \alpha_f \) in terms of \( D_H \) and \( L \)

\[
1.0 \text{ ou} = \frac{W}{L + \frac{W}{2 \sqrt{L^2 + (D_H)^2}}} L.
\]

We therefore define the optimal unit for horizontal detector offset as

\[
1.0 \text{ ou} := \frac{W}{N} \left(1 + \frac{W/2}{\sqrt{L^2 + (W/2)^2}}\right) = \frac{W}{N} \left(1 + \sin \alpha_f \right).\]

For moderate fan-angles, the optimal unit is about the width of one detector pixel.

**b) Sample-distance** \( R \): For sample-distance, we can derive the optimal unit from Eq. (29). Note that changes in the ratio \( L/R \) only affects scaling of the reconstruction, and not image quality. We therefore only consider horizontal error

\[
\frac{\pi R L H}{(W/2)^2 + L^2} (\pi/2 + \tan(W/2L)) = \frac{\pi (R + 1.0 \text{ ou})}{L} \left(\frac{H - 2H}{M} \left(1 + \frac{W/2}{\sqrt{L^2 + (W/2)^2}}\right)\right) / ((W/2)^2 + L^2) (\pi/2 + \tan(W/2L)),
\]

or simplified

\[
R = (R + 1.0 \text{ ou}) (1 + 1/M)
\]

This leads to the following expression for the optimal unit

\[
1.0 \text{ ou} := \frac{R}{M} \left(\frac{1}{1 + \frac{W/2}{\sqrt{L^2 + (W/2)^2}}} - 1\right).
\]

**c) Vertical detector offset** \( D_V \): Vertical detector offset will predominantly lead to a vertical shift of the reconstruction. To capture the blurring, we look at how much a backprojected data is shifted at the far side of the tomogram relative to the shift at the tomogram side closest to the source.

For simplicity, we use the projection line through the top middle pixel of the detector. For this point we have

\[
\frac{H/2}{L} = \frac{h_{\text{close}}}{L - W/2} = \frac{h_{\text{far}}}{L + W/2}.
\]

Shifting by one optimal unit we get

\[
\frac{H/2 + 1.0 \text{ ou}}{L} = \frac{h_{\text{close}}}{L - W/2} = \frac{h_{\text{far}}}{L + W/2}.
\]

We now require the height difference to change by one pixel

\[
h_{\text{far}} - h_{\text{near}} = h_{\text{far}} - h_{\text{near}} + \frac{H}{M}.
\]

From Eqns. (47) and (48) we have

\[
\frac{h_{\text{far}} - h_{\text{near}}}{L} = \frac{(H/2)}{L}(L + W/2) = \frac{(H/2)(L - W/2)}{L}.
\]

\[
\frac{h_{\text{far}} - h_{\text{near}}}{L} = \frac{(H/2 + 1.0 \text{ ou}) (L + W/2)}{L} - \frac{(H/2 + 1.0 \text{ ou}) (L - W/2)}{L}.
\]

Combining this with Eq. (49) we therefore define the optimal unit as

\[
1.0 \text{ ou} := \frac{HL}{WM} = \frac{H}{2M} \tan \alpha_f.
\]

In the limit where the camera-length becomes infinitely long *i.e.*, we have parallel-beam illumination, the optimal unit also becomes infinitely long. This is consistent with the fact that vertical detector offsets will not blur the tomogram in the parallel-beam case, but only introduce a vertical shift of the reconstruction.
**d) Camera-length \( L \):** The effect of incorrect camera-length is similar to that of vertical detector offset. We therefore use the same argument for deriving the optimal unit. Starting from the relations

\[
\frac{H}{L} = \frac{h_{\text{close}}}{L - W/2} = \frac{h_{\text{far}}}{L + W/2}\,.
\]

we shift by one optimal unit to obtain

\[
\frac{H}{L + 1.0 \text{ ou}} = \frac{h_{\text{close}}}{L - W/2 + 1.0 \text{ ou}} = \frac{h_{\text{far}}}{L + W/2 + 1.0 \text{ ou}}.
\]

This can be rewritten as

\[
h_{\text{far}} - h_{\text{near}} = \frac{(H/2)(L + W/2)}{L} - \frac{(H/2)(L - W/2)}{L}
\]

\[
= \frac{(H/2)(L + W/2 + 1.0 \text{ ou})}{L + 1.0 \text{ ou}} - \frac{(H/2)(L - W/2 + 1.0 \text{ ou})}{L + 1.0 \text{ ou}}.
\]

If we now require

\[
h_{\text{far}} - h_{\text{near}} = h_{\text{far}} - h_{\text{near}} - \frac{H}{M},
\]

we arrive at

\[
\frac{H}{M} = \frac{W H/2}{L} - \frac{W H/2}{L - 1.0 \text{ ou}} = \frac{L W H/2 - L W H/2 + 1.0 \text{ ou} W H/2}{L^2 + 1.0 \text{ ou} L},
\]

which to first order is

\[
\frac{H}{M} = \frac{1.0 \text{ ou} W H/2}{L^2}.
\]

We therefore define the optimal unit as

\[
1.0 \text{ ou} = \frac{L}{M} \tan \alpha_f.
\]

**e) Detector rotation \( \phi \):** The simplest characterisation of the blurring introduced by this detector rotation is obtained by considering the horizontal shift which is introduced in the projection data along the top and bottom edges. Requiring rotation to introduce horizontal shift on par with a horizontal detector offset we get the relation

\[
\frac{H}{2} \sin(1.0 \text{ ou}) = D_W.
\]

The optimal unit is therefore defined as

\[
1.0 \text{ ou} := \sin \left( \frac{2D_W}{H} \right)\,.
\]

**f) Detector tilt \( \theta \):** Detector tilt \( \theta \) will predominantly introduce a horizontal compression of the projection data. It is therefore natural to start by using the cosine rule to obtain the following relation

\[
x^2 + (W/2 - D_W)^2 = 2x(W/2 - D_W) \cos(\alpha_f + \pi/2) = (W/2)^2 - 2xW(\cos(\alpha_f + \pi/2)) - x^2.
\]

For small angles, we approximate \( x^2 \approx 0 \) to get

\[
(W/2 - D_W)^2 - (W/2)^2 = -2xW(W/2 - D_W) \cos(\alpha_f + \pi/2)
\]

or

\[
x = D_W \frac{W - D_W}{(W - 2D_W) \sin(\alpha_f)}.
\]

This is simplified to

\[
x \approx D_W \sqrt{L^2 + (W/2)^2}.
\]

Now, from the sine-rule:

\[
\sin(1 \text{ ou}) = \frac{\sin(\alpha_f + \pi/2)}{W/2},
\]

we get

\[
\sin(1 \text{ ou}) = x \cos(\alpha_f) = \frac{4L}{N W} \left( \frac{1 + W/2}{\sqrt{L^2 + (W/2)^2}} \right)
\]

We therefore define the optimal unit as

\[
1 \text{ ou} := \sin \left( \frac{4L}{N W} \left( \frac{1 + \sin \alpha_f}{} \right) \right)\,.
\]

**g) Detector tilt \( \psi \):** The detector tilt \( \psi \) leads to a vertical compression of the projection data. Since the backprojection is performed using the pitch, without regard for this compression, the blurring effect is similar to that of the horizontal shift introduced by \( \theta \). Using the same argument as above, with obvious modifications, we arrive at the following definition of the optimal unit for \( \psi \):

\[
1 \text{ ou} := \sin \left( \frac{4L}{N H} \left( \frac{1 + \sin \alpha}{} \right) \right)\,.
\]

By symmetry, the overscan region is of the same length both at the top and bottom. Consider therefore without loss of generality the projection angle \( \theta = 0 \). In order to get an accurate expression for the overscan, we resort to cylinder coordinates rooted at \( a(0) \). A ray emanating from \( a(0) \), and hitting the boundary of the TD window will intersect the helix trajectory at a position described as \( (\rho_A, \theta, z_A) \):

\[
\alpha \in [-\alpha_f, \alpha_f]
\]

\[
\rho_A = 2R \cos \alpha
\]

\[
z_A = \frac{P}{2\pi} (\pi + 2\alpha).
\]

Similarly, using the relationship \( r = R \sin \alpha_f \), the rays which intersect the helix will describe a path along the perimeter of the cylindrical support of the object given in the same cylindrical coordinate system given by

\[
\theta \in [-\alpha_f, \alpha_f]
\]

\[
\rho_B = R \left( \cos \alpha \pm \sqrt{\cos^2 \alpha - \cos^2 \alpha_f} \right)
\]

\[
z_B = h(\alpha, \alpha_f),
\]
and the additional trigonometric constraint

\[
\frac{z_A}{\rho_A} = \frac{z_B}{\rho_B}. \quad (77)
\]

Therefore, the height function \( h(\alpha, \alpha_f) \) is

\[
h(\alpha, \alpha_f) = \left( \frac{P}{2\pi} \right) (\pi + 2\alpha) \times \frac{\cos \alpha \pm \sqrt{\cos^2 \alpha - \cos^2 \alpha_f}}{\cos \alpha}.
\quad (78)
\]

What this means is that a projection acquired using \( a(0) \) as a source position, will contribute to reconstruction of points all the way up to a height \( h(\alpha, \alpha_f) \). The maximum height of contribution is therefore

\[
h_{\text{max}}(\alpha_f) := \max_{\alpha \in [-\alpha_f, \alpha_f]} h(\alpha, \alpha_f) \quad (79)
\]

\[
= \max_{\alpha \in [-\alpha_f, \alpha_f]} \frac{P}{2\pi} \left( \frac{\pi}{2} + \alpha \right) \times \left( 1 + \sqrt{1 - \frac{\cos^2 \alpha_f}{\cos^2 \alpha}} \right).
\quad (80)
\]

Furthermore, the reconstruction at any point higher than \( h_{\text{max}}(\alpha_f) \) will only depend on projections acquired from source positions \( a(\theta) \) with \( \theta > 0 \). As such, the height \( h(\alpha_{\text{max}}) \) covers the extent of the initial overscan. The overscan, measured as a rotation angle around the helix, is now given by

\[
\text{Overlap}(\alpha_f) := \frac{2\pi}{P} \times h_{\text{max}}(\alpha_f) \quad (81)
\]

\[
= \max_{\alpha \in [-\alpha_f, \alpha_f]} \left( \frac{\pi}{2} + \alpha \right) \times \left( 1 + \sqrt{1 - \frac{\cos^2 \alpha_f}{\cos^2 \alpha}} \right).
\quad (82)
\]