

CT-Pro 2.0

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CT Pro User Manual

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Metris, Icknield Way, Tring,
Hertfordshire, HP23 4JX, UK

t: +44 (0)1442 828700
f: +44 (0)1442 828118
e: tring.support@metris.com
w: www.metris.com

CT Pro User Manual

by Metris

This user manual for the CT Pro application.

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CT Pro User Manual

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SECTION 1

Introduction

1 Introduction



Welcome to Metris CT Pro software application for Windows XP Professional 32 & 64 bit editions.

This application performs offline 3-D Computer Tomography Reconstruction for 32/64-bit processors.

Limitations of Liability

Whilst every effort has been made to ensure that all of the information supplied in this manual was correct at the time of generation, CT Agent is being continually developed by Metris. Metris cannot and do not accept any liability, whatsoever, for any damage or injuries caused to either persons, data or materials that may arise from the use or misuse of any information supplied in this manual regardless of the accuracy of said information.

Trademarks

All brands, company and product names are trademarks or registered trademarks of their respective holders and are hereby acknowledged.

Installation

There are 2 categories of software available

- 32-bit
- 64-bit

CT Software for 32 / 64-bit machines

Normally a 32-bit application under Windows XP can only access memory up to 3 GB, and this limits the size of the output volume to modest sizes. In practice only between 2 GB and 2.5 GB of memory can actually be used as other processes and the operating system itself reduce the available memory by a small amount. The CT software needs to maintain other buffers in memory too, reducing the free memory slightly more. For reconstruction on 32-bit computers you are recommended to have 3 GB of memory installed.

64-bit computers have a much higher memory limit of ~18 billion GB; otherwise termed *18 EB* (*exabytes*). There is therefore at this time no practical memory other than the amount of memory a particular brand of motherboard can support.

SECTION 2

Installation Trouble Shooter

2 Installation Trouble Shooter

The following problems may be experienced on installation.

2.1 Licence File

This software requires a **Licence File** in order to activate it and control its distribution and usage to licensed users.

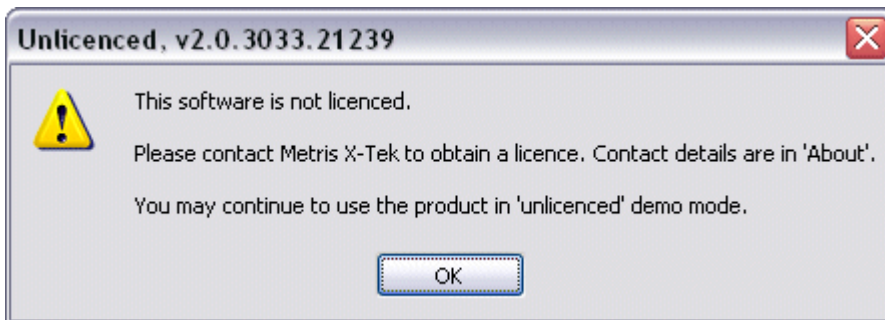
If you purchase a system with the CT software already pre-loaded you will not need to do anything further. However if you experience a problem in running the software, then you will need to contact Support.

If you wish to run additional CT software on other machines, you will need to contact Sales to purchase additional licences for each new hardware platform.

The licence file location is normally **C:\Windows\XTek.lic** If this file is missing or incorrect then you may not perform any reconstructions.

Demo mode

You may install the CT software on any computer, however if you are missing a licence file or it is invalid the software will enter its demo mode. In this mode all functionality is available, however no reconstructions may be started. This is indicated by the following message which appears on application startup.

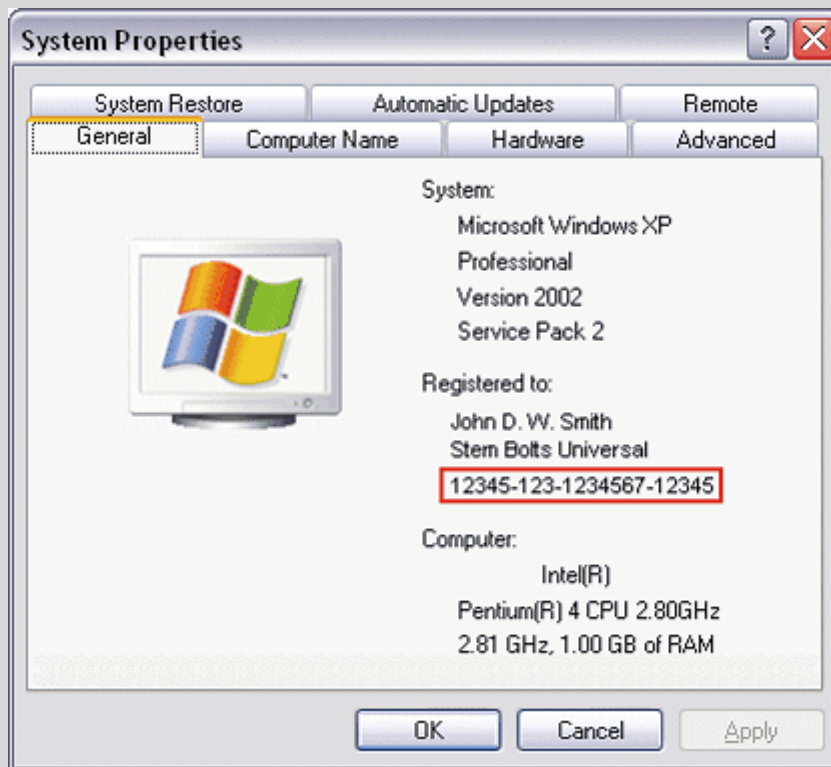


Purchasing additional licences

To purchase a licence you will need to supply us with the following information:

- 1) Your full name
i.e. "John D. W. Smith"
- 2) Your international telephone number.
- 3) The company name and shipping address,
i.e. "Stem Bolts Universal, 1 Bay Rd, San Francisco, CA USA 94132"
- 4) The serial number on the side of the inspection machine, ie "SN 0001".
On older machines this may be a works order number of format "W 0001".
If you bought CT Pro to run on your own computer then you will not have this information and you should mark it as "Sold separately"
- 5) The version and type of CT Pro you have installed,
ie "[#19] [2007.12.21] [64-bit] [v1.0.2911.19153]"

- 6) The windows product id of your version of Microsoft windows. This can be found in System Properties, General, Registered to:

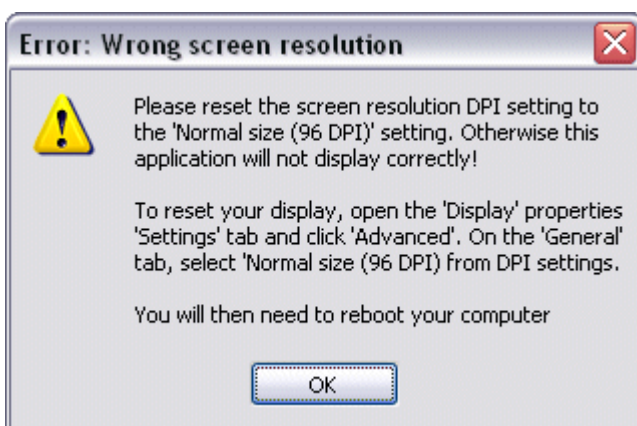


Then please contact service at tring.service@metris.com to obtain the licence.

The supplied licence should be put in the operating systems \Windows folder.

2.2 Wrong Screen Resolution

The font size displayed on the screen is normally 96 DPI. However occasionally a user may change this to display a bigger font for a given screen resolution. This however can break software applications which do not handle this. This product is only designed to run in standard 96 DPI mode. If another value is detected the following warning message will be displayed. The application will then terminate.



2.3 Memory Problems

The following problems may be encountered

32 bit PC 2 GB Memory Limit

If you have more than 2 GB of memory installed in the computer then to access this you will need to make the following modifications.

Edit the **boot.ini** file to include the following as shown in this example.

```
[boot loader]
timeout=30
default=multi(0)disk(0)rdisk(0)partition(2)\WINNT
[operating systems]
multi(0)disk(0)rdisk(0)partition(2)\WINNT="???" /3GB
```

You can find further info on this topic at the Microsoft website:

Memory Support and Windows Operating Systems

64 bit PC MIL Library Problem

There is no need to make the /3GB modification on these systems as they are inherently able to access all their memory.

Troubleshooting: If you install the MIL library on a 64 bit computer you will not be able to access above 2 GB of memory because this library (as of 2006) is 32-bits and modifies memory to enable it to run. If this occurs, check the boot.ini file for the /MAXMEM=2048 switch. If found then uninstall MIL (or whatever application placed it there) and reboot. The following example shows the problem and this switch needs to be removed.

```
[boot loader]
timeout=30
default=multi(0)disk(0)rdisk(0)partition(1)\WINDOWS
[operating systems]
multi(0)disk(0)rdisk(0)partition(1)\WINDOWS="Windows XP Professional x64 Edition" /MAXMEM=2048
/noexecute=optin /fastdetect
```

You can find further info on this topic at the Microsoft website:

Available Switch Options for Windows NT Boot.ini File

Setup: Video Memory

CT Pro uses video memory for some processing. It auto-senses the amount of video memory on the computer. If the video card is changed or some of the memory is shared, the program may try to use an inappropriate amount causing the reconstruction to abort or not be efficient. To correct this do:

- 1) Find out the quoted video size of your graphics card. This must be onboard video and NOT shared memory with the CPU.
- 2) Go to the installation directory. This can be found by opening your desktop icon properties page and examining the 'Target' field.
- 3) Start CT Pro and then immediately close it again.
- 4) You should now find a file called CTClientOptions.xml in the folder. This stores the applications options. Open this file with NOTEPAD or a similar simple editor which will not alter the content.
- 5) Find the following entry

```
<VideoMemorySizeMB>640</VideoMemorySizeMB>
```

Change the default 640 to be the video size (in MB) of your video card. Save the file.

You are now done. If you experience a problem, then amend the video size down by 10%. On some older video cards, problems occur when the whole of the video memory is consumed.

You are now done. If you experience a problem, then amend the video size down by 10%. On some older video cards, problems occur when the whole of the video memory is consumed.

SECTION 3

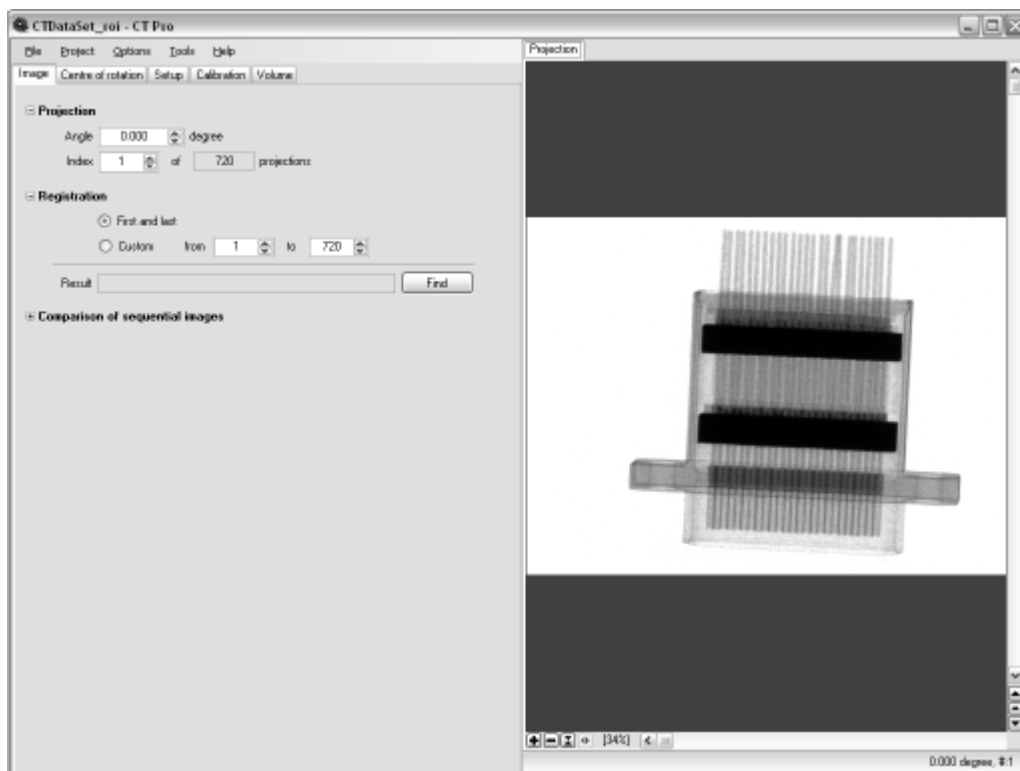
User Guide

3 User Guide

The interface is illustrated below.

This is separated into two functional areas. On the left are the selection and setup controls and on the right is an image display window.

Using File Open (Alt+F, O), the open file dialog is displayed. Browse to the \CTData folder and select an *.xtekt parameter file to open. If all validations are passed, the first projection in the projects dataset of projections will be shown on the Image Tab as shown below.



Processing Tabs



The processing tabs are ordered left to right to take you through the process of loading, setting up and then producing a volume in the correct order. This briefly explained is:

Image Examine loaded dataset. You may check that the sample did not move during the CT scan. This is usually due to insufficient support.

Centre of Rotation Correct the centre of rotation misalignment with the X-ray axis

Setup Choose Beam hardening, noise reduction and other quality factors

Calibration If you require to calibrate the reconstruction, ie for Hounsfield units, do so here.

Volume Produce 3D volume information for a given region of interest and resolution

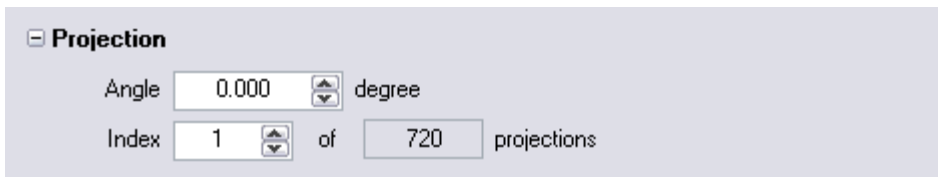
3.1 Image

The project consists of a dataset of collected radiograph images acquired from the X-ray machine. From these along with the parameter file a volume can be reconstructed.

The Image tab shown below allows you to examine the images forming the dataset and evaluate them for quality as follows:



Projection



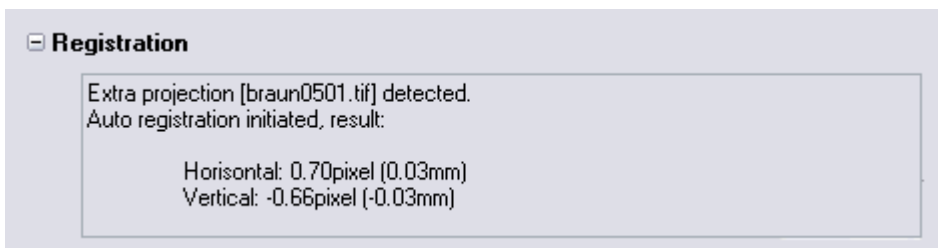
This control allows you to either type in an angle (usually negative) and display the projection which most closely matches the angle, or enter a index of the image directly, 1..N.

When you use the image control to scroll through the images, these controls update automatically to indicate the current projection shown.

Use this control to inspect the images if you suspect any of them may be damaged.

Registration

Image registration between the first and last image is important. If the object has moved during the scan, then the data will be useless. From August 2008, an extra image is captured which should be identical to the first image in the scan. A registration algorithm is applied and any lateral or vertical movement is reported automatically as shown below.



If the extra image is not available, you should compare the first and last image. These will not be exactly registered as their will be a small angle of rotation difference. However as this angle is small, it should be a good indicator. You may choose to compare any other two projections by selecting Custom.



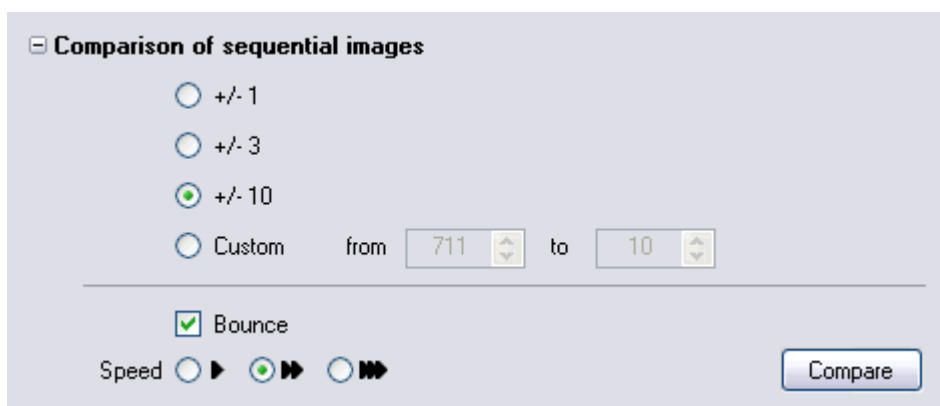
The image shows a software control panel titled "Registration". It has two radio button options: "First and last" (which is selected) and "Custom". The "Custom" option is followed by "from" and a spin box containing the number "1", then "to" and another spin box containing the number "720". Below these options is a "Result" text field and a "Find" button.

At most a mismatch of only one or two pixels should be tolerated.

Care should be taken to do a manual visual comparison on the first and last image to validate the above result.

Movement in the object is often due to poor support of the object, ie Blue-Tack. Another mechanism is thermal movement due to temperature changes. This is most noticeable at high magnification. If this is a problem, a temperature control module should be purchased.

Comparison of Sequential Images



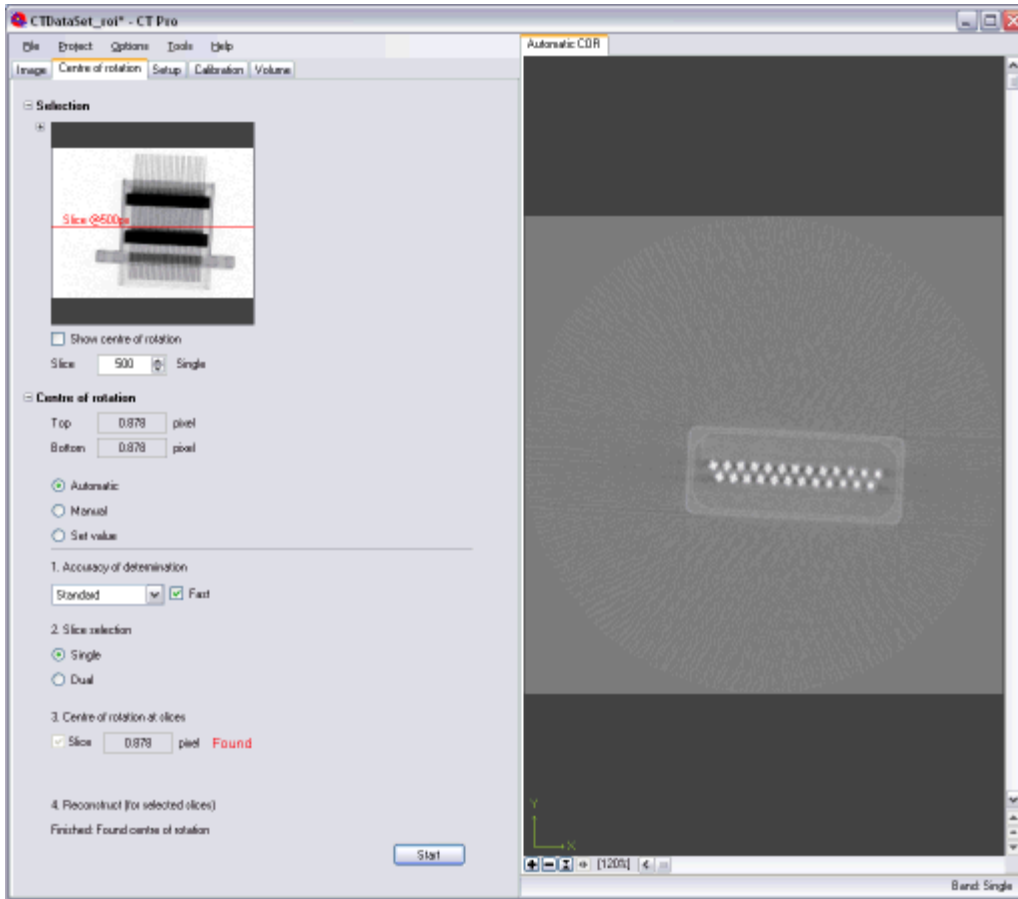
The image shows a software control panel titled "Comparison of sequential images". It has four radio button options: "+/- 1", "+/- 3", "+/- 10" (which is selected), and "Custom". The "Custom" option is followed by "from" and a spin box containing the number "711", then "to" and another spin box containing the number "10". Below these options is a checked checkbox labeled "Bounce". At the bottom left, there is a "Speed" section with three radio button options: a play button, a double play button (which is selected), and a fast play button. A "Compare" button is located at the bottom right.

This control is used for comparing the first and last image in the dataset. It works by taking a few images at the end of the run followed by the same number at the beginning and showing them in sequence as a short video. Your eye can then spot any irregularity such as the object sagging due to poor support. If you do find a problem, you should rescan the project.

3.2 Centre Of Rotation

The first task is always to correct the Centre-Of-Rotation (COR). This arises due to the centre of rotation of the object not being exactly on the X-ray source to detector midpoint axis.

The Centre of Rotation tab shown below enable you to quickly calculate this:



An detailed discussion and explanation of this is given in the following [COR Explanation](#) link.

Methods

Three methods are given for calculating the COR as follows:

Automatic: This is the normal choice and allows the user to quickly and automatically determine the centre of rotation with minimal input. This is explained further in [COR Automatic](#).

Manual: Occasionally due to low contrast or difficult data, the automatic method fails. In this case the user must gauge the sharpness of the reconstruction and choose the value to use. This is explained further in [COR Manual](#).

Set Value: This method is used for batches of identical components. The first sample in a batch has its COR determined normally and the values noted by the operator. It can then be reasonably assumed that a short batch of identical scans may use the same values. This is explained further in [COR Set Value](#).

Value

the typical value is about 1 pixel. However some values up to 100 can be seen if the operator forgets to centre the rotation stage. Values over 300 pixels cannot be reconstructed. Quality typically diminishes rapidly and the error increase and normally values over 10 pixels require the system to be recalibrated or the sample re-scanned following the correct procedure.

3.2.1 Explanation

Causes of Centre Of Rotation Errors

The Centre Of Rotation (COR) misalignment of the object rotation point with the X-ray centre axis is typically very small on a well maintained and regularly calibrated system, ie a few microns.

Misalignment is inevitable and no amount of engineering or money can eliminate this, only reduce the problem. Opting for more expensive manipulator, coolers etc reduces the error.

The error arises generally for the following reasons.

- 1) Thermal movement, which may necessitate a cooler unit being installed.
- 2) The weight of the sample depressing the arm
- 3) Placing the subject on the turntable
- 4) The turntable not being true vertical, for above reasons.
- 5) Poor maintenance and calibration

When a large magnification is used, any misalignment is magnified so very small deviations result in an error of up to one or two pixels misalignment on the detector.

Note: The smaller the correction needed, then the better the reconstruction will be as less error has to be corrected.

Explanation

The reconstruction algorithm expects the projection images to be perfectly vertical and centred on the rotation axis. As this is not physically possible, the projection images need to be shifted and sheared to correct for this displacement prior to reconstruction.

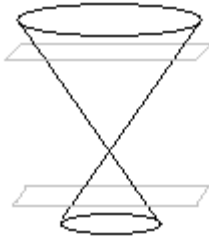
Note: This is *not* the same as if the object being placed off-centre on the rotation stage. All that happens then is that the volume of reconstruction selection is off-centre. If however the object were placed too far off centre, then as the object is rotated, if part of the object you wish to capture moves out of the capture region, then information is lost.

To determine the correction needed, a test slice is reconstructed and the sharpness of the data assessed. The projections are then shifted to one side by a pixel, the reconstruction done again and the sharpness reassessed. From this the required shift is estimated, and iterative movement and reconstruction done until the slice has reached the desired quality.

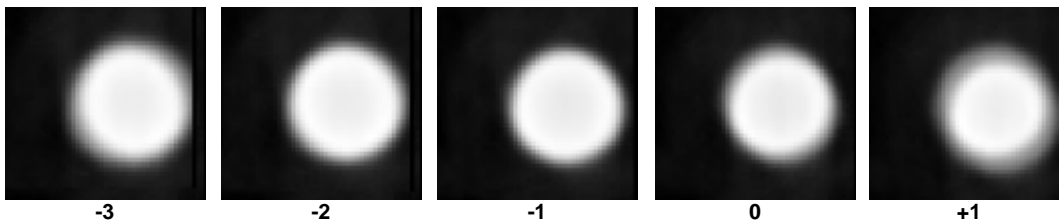
This is done for a slice near the top and bottom of the region of interest, and these two values indicate the misalignment at the top and bottom of the image, and thus the shift and shear needed to correct all of the projections.

Usually the correction at the top and bottom are very similar, so a single slice in the centre of the region of interest is sufficient. However for very high quality reconstruction, doing two slices, at the top and bottom of the region of interest yield a better result.

The concentricity error of a misaligned rotation stage is shown graphically below in this exaggerated example:.



For example, the following image series shows a small vertical wire and the reconstruction obtained when a parallel offset correction between -3 and +1 pixels is made. From this we deduce that a top/bottom correction of -1.5 pixels will give the sharpest image.



3.2.2 Automatic

This method is the default recommended method for determination of the Centre Of Rotation.

Note: Sometimes the automatic method is unable to calculate the centre of rotation offset for a slice. This may be due to poor contrast, or feature in the reconstruction which confuse the algorithm. By changing the slice height by a small amount and retrying, the algorithm will normally succeed. However if this fails you should try the Manual method.

Centre of rotation

Top pixel

Bottom pixel

Automatic

Manual

Set value

1. Accuracy of determination

Fast

2. Slice selection

Single

Dual

3. Centre of rotation at slices

Upper pixel

Lower pixel

4. Reconstruct (for selected slices)

Press 'Start' to find centre of rotation

Accuracy of Determination

This determines how accurate you desire the centre of rotation to be determined. For nearly all purposes the Standard accuracy is sufficient.

Standard: Provides high accuracy at a reasonable speed, suitable for most samples.

Fine: Choose this if you are inspecting detail. This is much slower than Standard.

Ultimate: Choose this if looking for very fine detail or cracks which are at the limit of the systems rates X-rayresolution. This will take a very long time to calculate.

Slice Selection

You may select either Single or Dual. Single assumes that the rotation stage is off centre but not tilted and a single slice in the middle of the region of interest will calibrate the top and bottom COR values. If Dual is chosen, then you suspect the rotation stage is also tilted, so choose test slices at the top and bottom of the region of interest to calculate the COR.

Centre of Rotation at Slices

This displays the Centre of Rotation offset found at the particular slice being reconstructed. For Dual slice selection, you may choose to optionally re-reconstruct only one of the slices if there is a problem obtaining a value for it.

Reconstruction

If you wish, you may reconstruct the chosen slice to validate its sharpness, but this is not normally done for batch's. You may also set the Resolution and Quality.

3.2.3 Manual

This method is **only** used if the Automatic method fails.

This is an advanced feature enabling the operator to visually appraise the sharpness of the image when the automatic method fails. This method works by reconstructing a series of slices with different centre of rotation offset values, and the user manually selecting the one which looks sharpest. Usually when a close match is found, the values should be noted, and the automatic method then used to finish the calculation.

Centre of rotation

Top pixel

Bottom pixel

Automatic
 Manual
 Set value

1. Slice selection

Single pixel
 Dual upper pixel
 Dual lower pixel

2. Slice 'guess' for middle value

pixel

3. Range search parameters

Coarse (+) Quality Fast Med Fine Max
 Coarse Steps
 Medium Increment pixel
 Fine Spread ±pixel
 Fine (+) Start pixel
 Custom End pixel

4. Reconstruct (range for selected slice)

Press 'Start' to find centre of rotation

5. Results, choose and apply

1	2	3	4	5	6	7
<input checked="" type="radio"/>	<input type="radio"/>	<input type="radio"/>	<input type="radio"/>	<input type="radio"/>	<input type="radio"/>	<input type="radio"/>
-15.00	-10.00	-5.00	0.00	5.00	10.00	15.00
<input type="checkbox"/>	<input type="checkbox"/>	<input type="checkbox"/>	<input type="checkbox"/>	<input type="checkbox"/>	<input type="checkbox"/>	<input type="checkbox"/>
<input type="text"/>	<input type="text"/>	<input type="text"/>	<input type="text"/>	<input type="text"/>	<input type="text"/>	<input type="text"/>

Value to use pixel

Slice Selection

In the manual mode only one slice can be processed at a time. thus you must decide if you wish to use a single slice to set both the top and bottom COR values if you think they have little or no shear, or either the top or bottom value if you thing the rotation stage is tilted.

Slice 'Guess' for Middle Value

For the slice chosen, this is the initial middle seed value for the COR value. When a range of reconstructions are made, this will be the middle value in the range, and is the one you consider to be the most correct value initially. The default is 0.0 if this has not been specified previously, or some other value if this was set up earlier or elsewhere.

Range Search Parameters

Select the range of values you feel suit the initial range of values you are expecting. Typically Coarse is chosen, which gives a very large spread of possible values. From this select the next finer value to zero in on the value required. If the error is unusually large or you wish to reconstruct a large range of value, choose Custom and set the values manually.

Reconstruction

If you wish, you may reconstruct the chosen slice to validate its sharpness, but this is not normally done for batch's. You may also set the Resolution and Quality.

Results, Choose and Apply

For each reconstructed result, the value used is shown and you may select the radio button to view this result. Use the left and right arrow keys to then select the other samples.

For each sample an automatic value calculation is also made, with a recommendation of the best result. You may choose to accept or reject the automatic recommendation.

When you select either a projection or recommendation, this value is displayed in the *Value to use* numeric control. You may also modify this value. You must then Apply this result to accept it.

3.2.4 Set Value

This method is used for batches of identical components.

The first sample in a batch has its COR determined normally and the values noted by the operator. It can then be reasonably assumed that a short batch of identical scans may use the same values, and the operator may enter these directly in "2. Value" as shown below.

Note: You should determine the maximum length of run that the COR value is stable over for the quality of results you desire. As a guide, this is about 4 hours, however for well maintained systems in a controlled environment, this may be a whole work shift.

Centre of rotation

Top pixel

Bottom pixel

Automatic

Manual

Set value

Reconstruction (of a slice)

Resolution Quality

Mode

You may select either Vertical or Tilted. Vertical assumes that the rotation stage is off centre but not tilted and a single slice in the middle of the region of interest will calibrate the top and bottom COR values. If tilted is chosen, then you suspect the rotation stage is also tilted, so choose test slices at the top and bottom of the region of interest to calculate the COR.

Value

Enter previously determined values for a batch run, (or manual values for direct user testing - but this is not recommended).

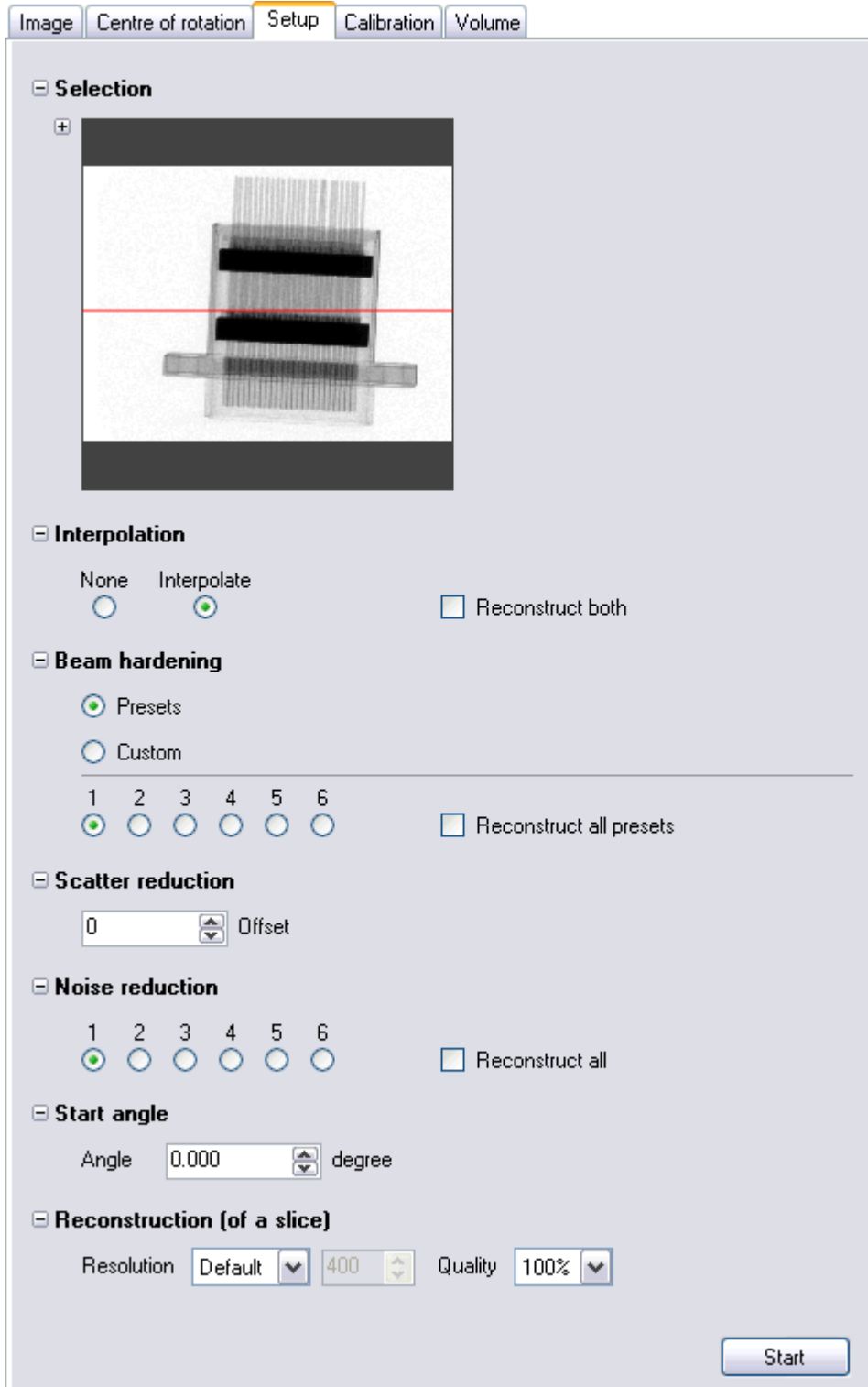
Reconstruction

If you wish, you may reconstruct the chosen slice to validate its sharpness, but this is not normally done for batch's. You may also set the Resolution and Quality.

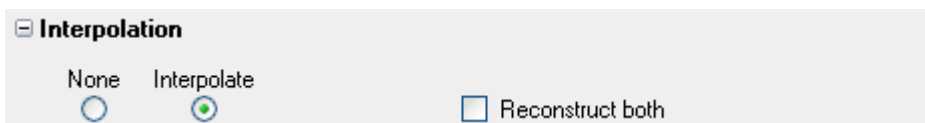
3.3 Setup

Once the Centre Of Rotation calculation has been performed, your data will be sharp.

You may now perform other setup corrections as shown below.



Interpolation



This chooses the value selection method when the back projected beam intersects the projection image to get the value from the projection.

None: The nearest pixel is chosen. This is marginally faster computationally but gives a lower quality result. This is **not** recommended.

Interpolate: The interpolated value is taken as the pro-rata proportions of the four pixel neighbourhood where the beam intersects the image

Reconstruct both: Reconstruct all the above options so you may compare these.

Beam Hardening

If you take a solid uniform rod and look at a CT slice image of it, you will see that the edge is slightly brighter than the middle due to Beam Hardening. Most of the lower energy X-rays are stopped by the first few millimetres of the sample, and the remaining X-ray spectrum is shifted to a more energetic, more penetrating level. As a result of this, the linear X-ray attenuation displayed in the CT slices appears lower. By analysing the drop-off in X-ray attenuation in a material as a function of thickness, for the X-ray conditions in use, you can compensate for this during reconstruction.

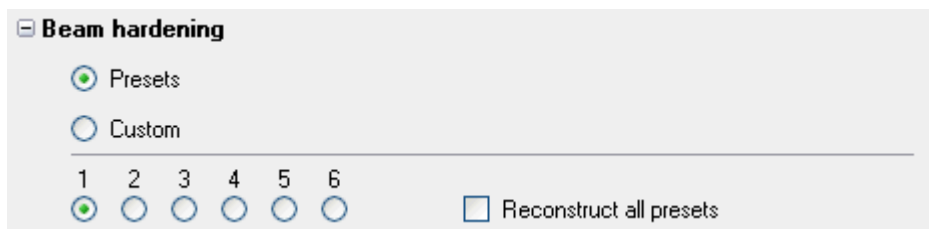
If the sample is made of only one material, then this effect can be compensated for in software. If the sample is made of more than one material, any result will be a compromise.

By default beam hardening correction is not performed. For hard materials such as steel of more than a few mm thickness, beam hardening is necessary.

For further information ask for article: "144TN178 Format of Data in CT Volumes.doc"

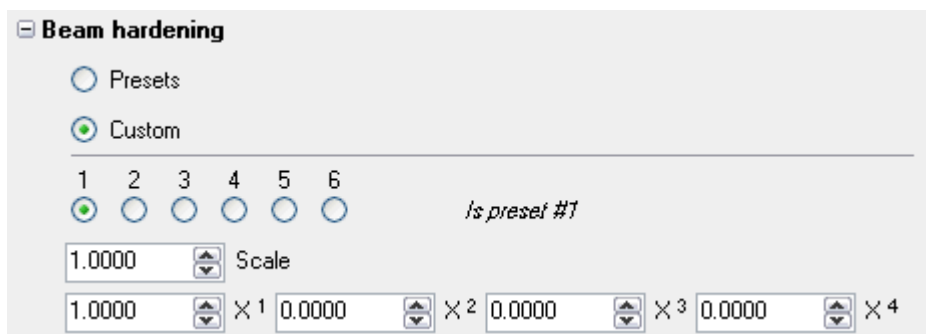
You have two types of Beam Hardening selection.

Presets: A selection of typical values to use for increasingly hard materials. Select "*Reconstruct all presets*" to reconstruct all these preset then choose the value which most closely eliminates the effect of Beam Hardening.

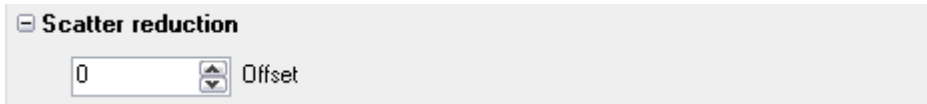


Custom: This is an advanced setting which requires the measurement of the flux density through different thicknesses of sample material to make corrections for beam hardening.

If you wish to use this mechanism and enter values directly, please contact Metris directly and ask for the documentation which describes 'Custom Beam Hardening Settings'.

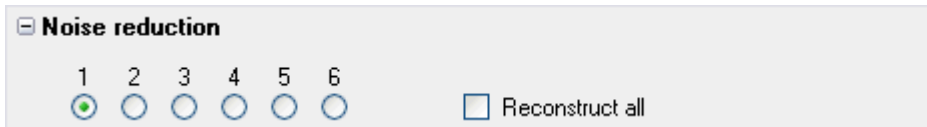


Scatter Reduction



This removes the excess intensity in the image which is caused by scattering. This is linear in nature. So a value which removes half the scattering can be doubled to remove all the scattering. The image will appear to dim a little as this value is subtracted from the data.

Noise Reduction



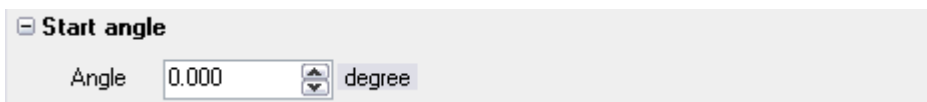
CT volumes are reconstructed using a filtered back-projection method. The ideal filter, in the absence of noise is a ramp filter. However, noise in the projection images may be enhanced by such a filter and other filters may be used as a compromise to reduce the resultant noise in the CT volumes.

A CT volume is formed by back-projecting a line from a pixel in a filtered projection image through the volume back to the source. As each projection is added the new line of information is summed into the volume. Where lines intersect, their values reinforce each other. Where they don't intersect, they don't reinforce each other, and without a filter would generate a high background noise level. The use of the correct filter causes this background noise to cancel out to almost zero. When all the projections have been added, the volume is normalised to the output range, and the noise is correspondingly reduced to a very low level. Taking more projections increases the ratio of signal to noise.

The noise can be removed in the slice view images by ignoring all values below a threshold and only scaling the data above this.

The filtering options provided give a sliding scale between preserving detail, but also noise, or removing noise, but reducing detail.

Start Angle



This allows the reconstruction to be rotated by the angle entered, so that the reconstruction is orientated in a particular way. Ie you may wish the front face of an object to lie on the horizontal. This can also reduce the volume size by making the object fit the region of selection better.

When you enter the angle, the preview will turn to display the radiograph which most closely matches this angle.

Note: The Volume tab Selection images will also update to show the views associated with the is angle. i.e. for an angle of 0 deg, the preview will show the 0 deg and 90 deg views. If the angle entered is not exactly the angle of a radiograph, allow a few extra pixels in your selection to take into account the fraction by which the reconstruction position will differ.

Reconstruction

If you wish, you may reconstruct the chosen slice to validate its sharpness, but this is not normally done for batch's. You may also set the Resolution and Quality

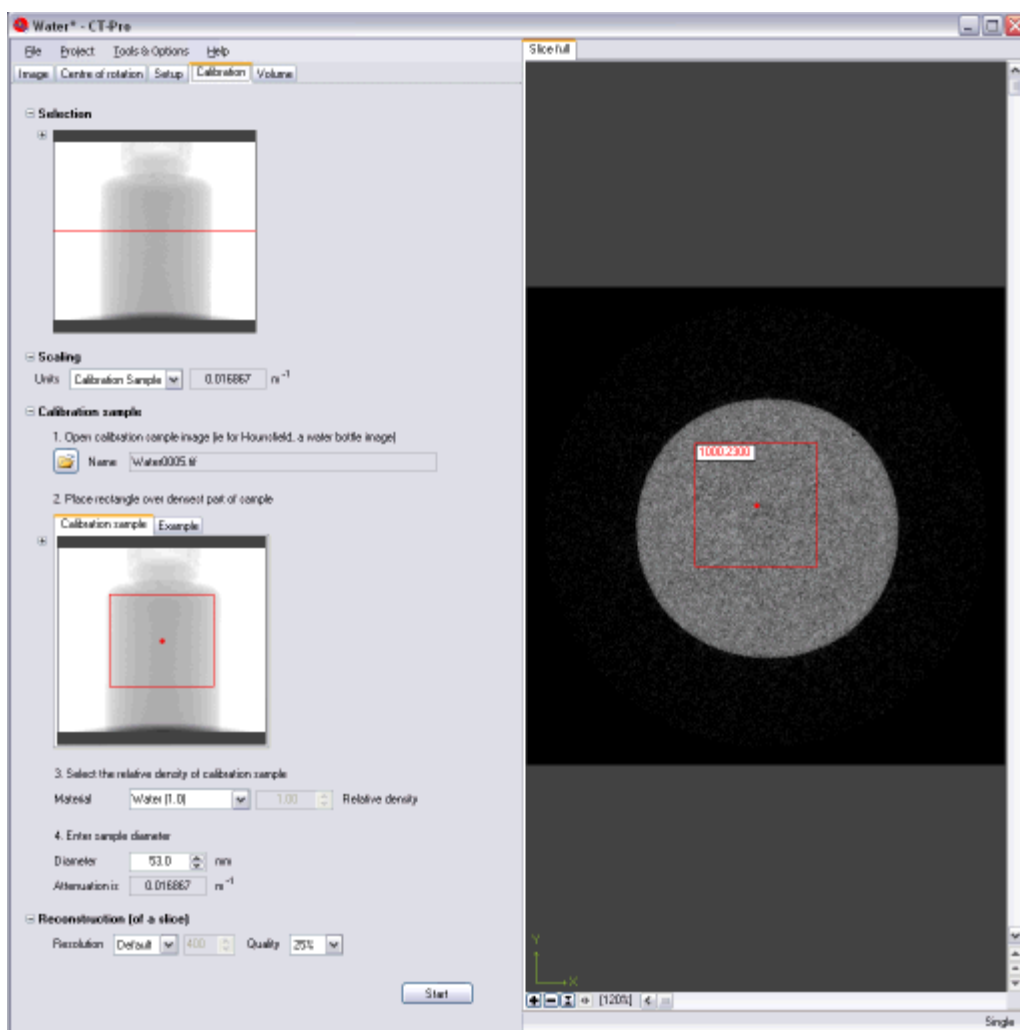
3.4 Calibration

Calibration is only used if you wish to scale the output volume data so that specific areas have a known output value. Otherwise this stage can be skipped.

Typically this is used in the Medical arena to scale medical samples of bone and tissue to the Hounsfield scale defined in topic Hounsfield Scale

Other material are often scaled in this manner when necessary. This requires a calibration sample of the material usually provided as a cylinder of single material with a known diameter. A radiograph of the sample material is taken with the same conditions as a CT scan of other samples containing the same material. Often a short CT scan of the calibration sample is also done so that settings for beam hardening and checking of the calibration output value for CT scans can be made.

Below is an example water bottle sample scan.

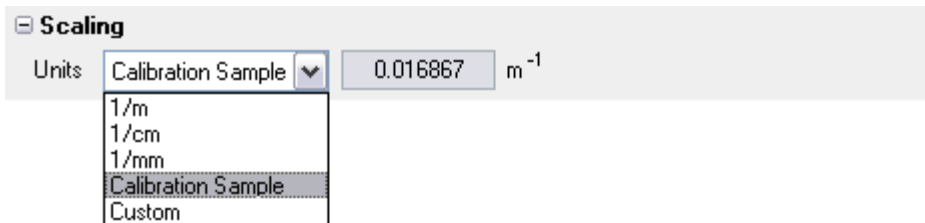


Selection



If you have also done a CT scan of your calibration sample (recommended) then select the middle of the sample at its thickest position. This would also hopefully be near the centre of the image.

Scaling



The normal scaling of a reconstruction is inverse meters (m^{-1}). However to accommodate other common values, inverse cm and mm are also offered.


The final two values of *Calibration Sample* and *Custom* are used with Calibration Sample scaling. Before you can select Calibration Sample, you must setup and evaluate the Calibration Sample parameters as follows:

Calibration Sample

The input control for calibration is shown below.

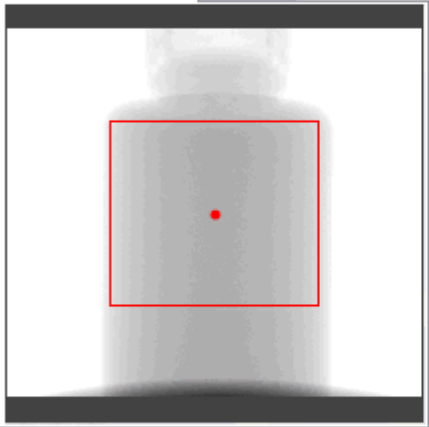
Calibration sample

1. Open calibration sample image (ie for Hounsfield, a water bottle image)

 Name

2. Place rectangle over densest part of sample

Calibration sample **Example**



3. Select the relative density of calibration sample

Material Relative density

4. Enter sample diameter

Diameter mm

Attenuation is m⁻¹

1) **Calibration File:** Browse to and open the radiograph taken of the calibration sample. If you did a CT scan of the sample then this corresponds to the first projection image of the dataset. If you do not supply a valid image, the remaining entry fields will not be accessible.

2) **Area selection:** Place the rectangle over the image so that the densest part is centred in the middle of the rectangle.

3) **Material:** Choose the relative density of the material from the drop down list, or Custom and enter the appropriate value.

3. Select the relative density of calibration sample

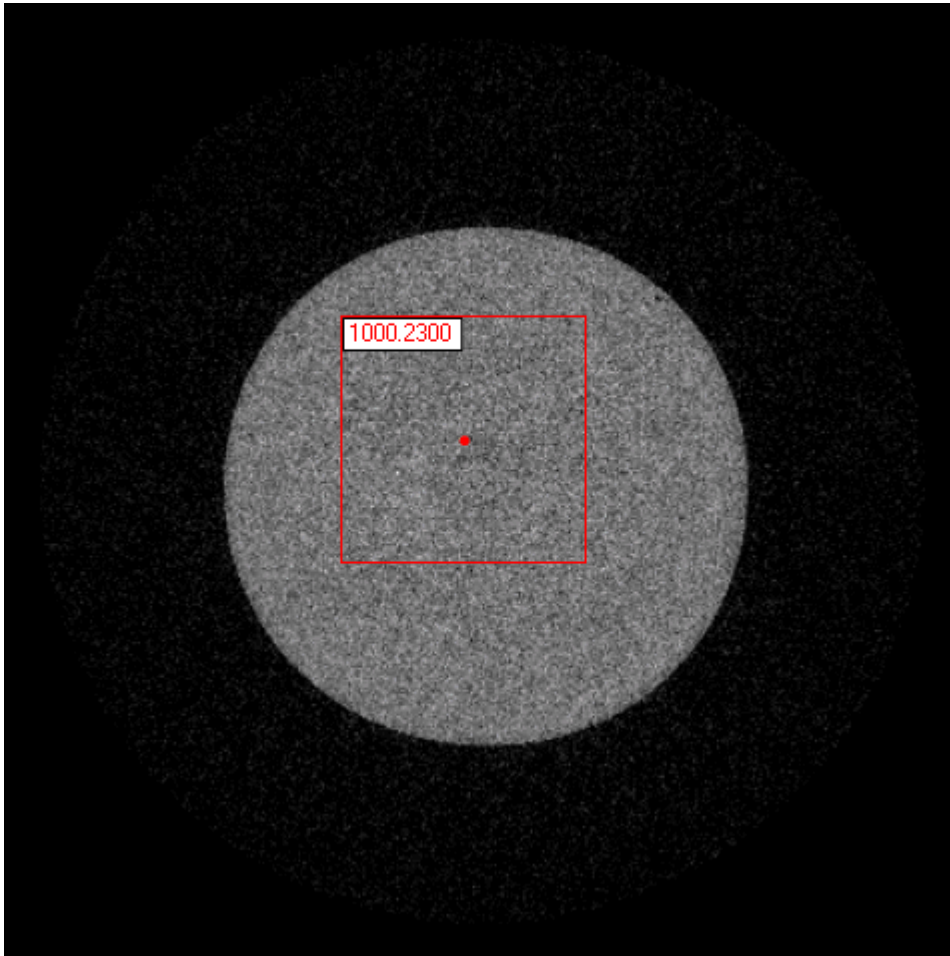
Material Relative density

4) **Sample diameter:** The diameter of the material. If this is a water bottle, this will be the inside diameter, however the bottle wall also contributes to the absorption of X-ray, so you may find that the outer diameter works better. This can be problematic. You should also be aware that temperature changes may cause problems changing the apparent density of the material. For this reason a CT scan of the material is recommended rather than a simple radiograph.

Reconstruction

If you wish, you may reconstruct the chosen slice to validate its sharpness, but this is not normally done for batch's. You may also set the Resolution and Quality

When complete, click on the reconstruction and pull the square drawn to cover the centre of the calibration sample. An average value will be displayed. In the example below of a water bottle we are expecting a value of 1000.000. The value returned is close enough to be a good result.



If however you have problems getting the correct scaling factor, you may wish to enter a custom attenuation in the Scaling selection box. Take the Attenuation found and multiply this by the percentage error to get a custom attenuation value and enter that. Ie

$$0.016867 * 1000.230 / 1000.0 = 0.016870$$

This will give a value closer to 1000.0, ie 1000.0360 in this particular case.

3.4.1 Hounsfield Scale

The Hounsfield scale is a quantitative scale for describing radiodensity.

Definition

The radiodensity of distilled water at standard pressure and temperature (STP) is defined as zero Hounsfield units (HU). The radiodensity of air at STP is defined as -1000 HU.

In industrial use (ie CT Pro), the Hounsfield scale is redefined as starting at zero such that air is 0 and water 1000

Rationale

The above standards were chosen as they are universally available references and suited to the key application for which computed axial tomography was developed: imaging the internal anatomy of

living creatures based on organized water structures and mostly living in air, e.g. humans.

The HU of common substances

Substance	HU (Medical)	HU (Industrial)
Air	-1000	0
Fat	-120	+880
Water	0	+1000
Muscle	+40	+1040
Bone	+1000	+2000

3.4.2 Godfrey Hounsfield



Sir Godfrey Newbold Hounsfield CBE 1919-2004 was an English electrical engineer who shared the 1979 Nobel Prize for Physiology or Medicine with Allan McLeod Cormack for his part in developing the diagnostic technique of X-ray computed axial tomography (CAT, or CT scans).

His name is immortalised in the Hounsfield scale, a quantitative measure of radiodensity used in evaluating CT scans. The scale is defined in Hounsfield units (symbol **HF**), running from air at -1000 HF, through water at 0 HF, and up to bone at +1000 HF.

CT machines were the first imaging devices for detailed visualization of the internal three-dimensional anatomy of living creatures, initially only as tomographic reconstructions of slice views or sections. Since the early 1990s, with advances in computer technology and scanners using spiral CT technology, internal three-dimensional anatomy is viewable by three-dimensional software reconstructions, from multiple perspectives, on computer monitors. By comparison, conventional X-ray images show only compressed two-dimensional images of complex anatomy, i.e. radiodensity shadows on acetate film.

3.4.3 Volume Scaling Issues

Notes: Calibrated Volumes

Volume values can be calibrated so that specific objects are reconstructed with a specific value. Hounsfield calibration is a specific example of this whereby specific substances such as water have a volume value of 1000.

Once a dataset has been acquired by Inspect-X, CTPro is used to analyse and calibrate the data prior to reconstruction by CAgent to produce a volume and VGI file. VGStudioMax then reads in these VOL and VGI files and displays the reconstructed volume to the user.

A problem arises with VGStudioMax whereby it has a bug involving how it represents imported data values. The following is a typical VGI file when opened in Notepad.

```
{volume1}
  [representation]
    size = 62 107 7
    mirror = 0 0 0 0
    resamplemode = not activated
    datatype = unsigned integer
    datarange = 0 65535
    bitsperelement = 16
  [file1]
    RegionOfInterestStart = 0 0 0
    RegionOfInterestEnd = 61 106 6
    FileFormat = raw
    Size = 62 107 7
    Name = MyScan1.vol
    datatype = float
    datarange = 0 1559.69
    bitsperelement = 32
```

....

This has two sections, the first `[representation]` section encodes how the volume data imported is scaled and represented in VGSM. The second `[file1]` represents the actual volume data. This is always float with a min and max range.

Thus given the above, volume values of range 0 to 1559.69, will be scaled to a range 0 to 65535 and made integer, thus changing the scale of the data and reducing the resolution of the data. A value of 1000=Water will now become $(\text{int})(1000 \cdot 65535 / 1559.69) = 42017$, ie not what is expected. The quantization of data happens at 0.024 volume values, so this is not so significant.

Solution

The usual solution is that most customers do a volume import of the raw VOL file, and specify float as the scaling units.

Otherwise, the user can modify the VGI file and replace the `[representation]` values for `datatype` and `datarange` with the values in the `[file1]` section.

If the range of volume values is in the range 0 to 65535, which it usually is, then the `datatype` can remain as unsigned integer.

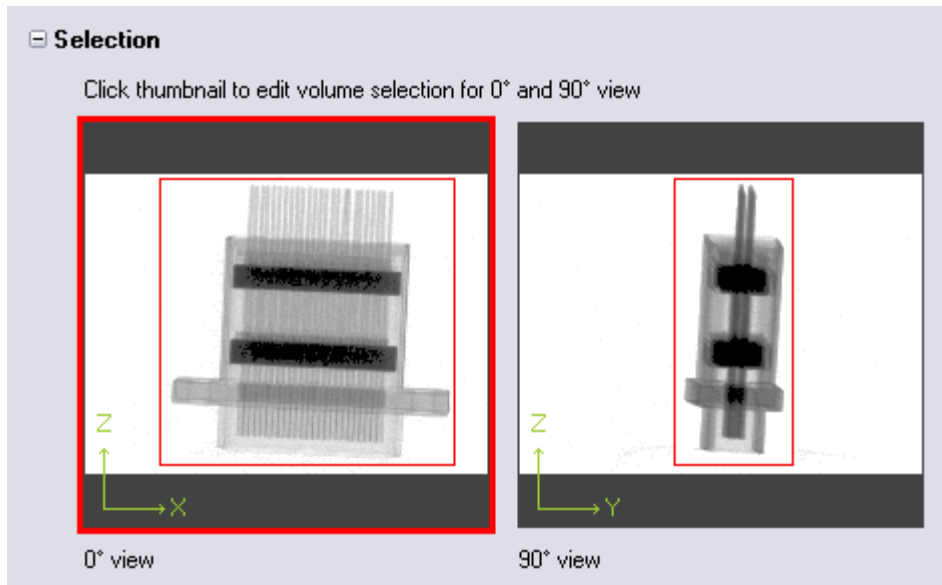
3.5 Volume

Here we define the region of interest to be reconstructed as the output volume.



The controls on this tab are explained as follows:

Selection

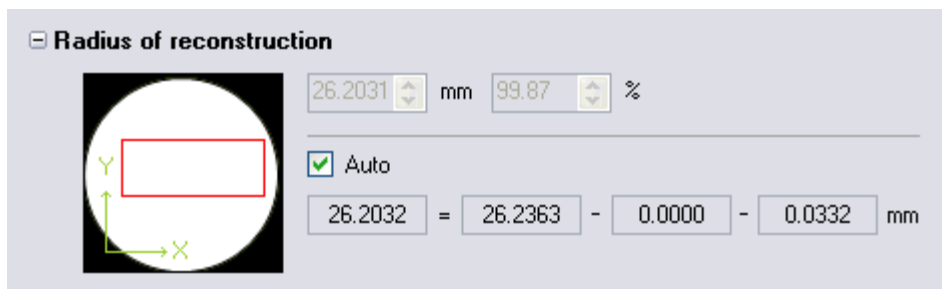


The above show two projections at 90 degrees to each other. By outlining the region of interest in both, this will ensure that all parts contained within the region will be reconstructed.

Click on the thumbnail image to display it in the large image window, where the selection rectangle may be manipulated.

Note: Do not define the selection too closely. Due to parallax, so items depending upon their distance into the object may appear less large than they actually are, so the above is an indication of the typical margin that should be given to compensate for this effect.

Radius of Reconstruction



This shows a top down view from above, ie an X-Y axial view. As the selection region changes in Selection above, a rectangle in the third dimension is drawn.

Because of the nature of this type of reconstruction, a cylinder is created, from which we select a cuboid volume. If we move the volume to near the cylinder edge, then some of the volume will be empty.

The radius of reconstruction corresponds to the width of the projection image as back projected to the object location. However certain factors can reduce this width.

Centre of Rotation: The shift reduces the apparent width.

Shuttling: Used in stop-start CT to reduce ring artefacts, approximately 10% of the projection width is lost.

These combine to reduce the real radius of reconstruction, and if the Auto checkbox is selected, this reduction is calculated for you.

You may however choose to manually enter a value less than this. Alternatively you can enter a value of 100% when this exceeds the automatic value. When you do this, data near the edge of the volume will be reconstructed from incomplete data, and hence contain meaningless data.

Resources

Resources

Volume file size (VGI & VOL)

Size Free space

Minimum volume viewer requirements

PC type Estimated memory

This indicates the output size of the volume, the type of computer you will need to view the result on and the memory capacity required.

Resolution

Resolution

Quality *Nearest ~~x~~ approximating resolution*

Resolution xyz μm

Link resolution in x, y & z

This control allows you to specify the resolution of the voxels generated in the volume. You should normally choose 100%.

You may however choose values between 10% and 1000%, however results at these extrema are usually meaningless. Typical values selected are 50% and 75%. Values greater than 100% are not recommended except in special cases.

You should always keep the x, y and z axis resolutions linked. This should only be unlinked if a detector with non-square pixels has been used. There are currently no non-square detectors used in any systems shipped to retail customers.

A display of the size of the volume in whole voxels is also shown. You may change this if you desire.

Volume

Volume

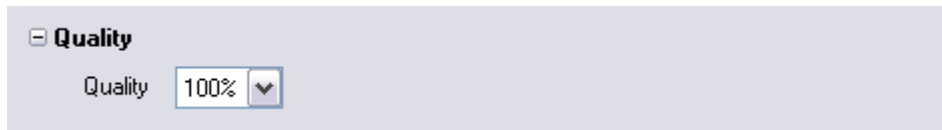
Size xyz Voxels

Size xyz mm

Offset xyz mm

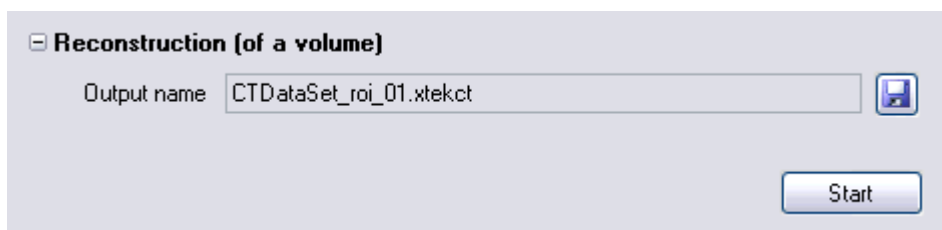
This is the numeric representation of the selection cuboid volume selected. If you wish, you may enter these values, and thus compare a number of scans of identical samples.

Quality



This is the percentage of projections used to reconstruct the data. This should always be 100%. the only reason to reduce this value is to get a quick low resolution look at the volume to check region selection. The time of reconstruction scales linearly with percentage of projections used.

Reconstruction



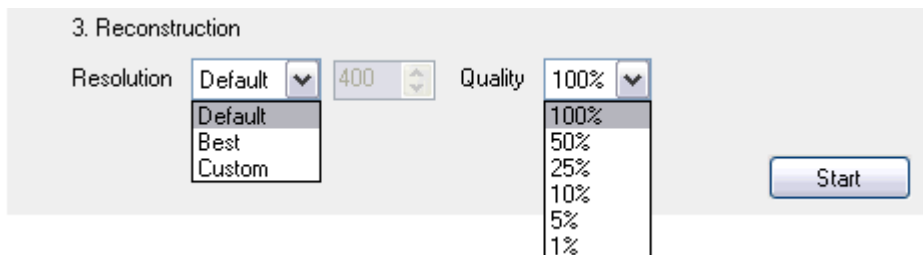
You may chose the output volume name or accept the default volume name generated for you.

Press the "Start" button to start the reconstruction.

Progress and status messages will be displayed as appropriate.

3.6 Reconstruction Resolution & Quality

Reconstruction of slices is normally done at a default resolution and quality as shown below as these are generally the fastest settings which give good results. You may however choose different settings:



Resolution

This is the resolution size of the reconstructed voxels. Best results are normally given when 1 voxel matches a pixel on the detector. However for slice analysis, a lower resolution is typically acceptable. Three choices are thus presented.

Default: This reconstructs an X-Y slice 400 voxels square. This is typically a much lower resolution than the best resolution and typically is 25% to 50% of this.

Best: You get more voxels reconstructed (a little slower), at 100% resolution. However normally not very much extra information is gained by doing this.

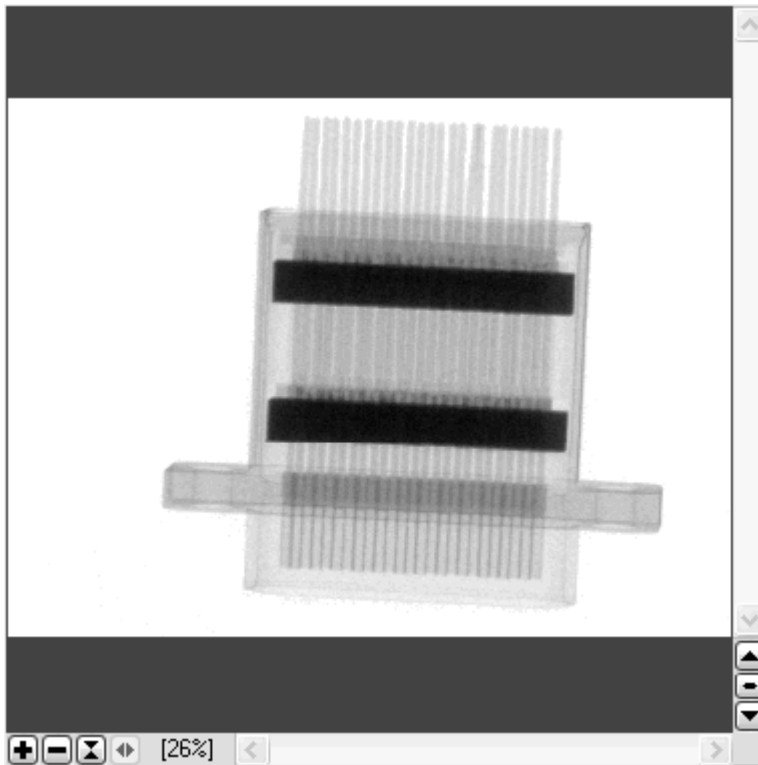
Custom: You may choose a specific number of square voxels between Default and Best. You may typically do this if you wish to compare results of different samples (of similar size and reconstruction geometry).

Quality

This may be changed to directly affect the speed of reconstruction. 100% means that all the projections are used to reconstruct the slice. 50% uses every other slice, etc. This linearly scales the speed of reconstruction, so 50% will be twice as fast as 100%, but with half the image quality.

This is used when initially gauging the approximate value for other reconstruction parameters such as beam hardening etc, where speed rather than image quality is required.

3.7 Image Control



The image control above is a common control used throughout the application for displaying image and reconstruction slice data as an image.

The scroll bars along the bottom and right edge of the control can be used to reposition the image.

Note: For Image tab image display, when the image is zoomed. double clicking on a part of the zoomed image will re-centre that location to the centre of the control.

In detail the edge controls are as follows:

Zoom





The image may be zoomed in or out, scaled as a real size or made to fit the size of the control. The current zoom scale is indicated at the right hand end.

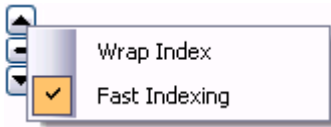
Hovering the mouse over the control pops up an indicator showing the level of zoom.

Select

This is used in two situations only. On the Image tab, to select from any of the projections available in the radiograph dataset, or secondly when a number of slice reconstructions are generated and you need to select between them.



This allows you to scroll through the entire set of radiographs. Clicking the up arrow  (or down arrow ), increments to the next image. Holding the mouse button down causes the images to be displayed in sequence automatically until the mouse button is released.




From the right click context menu, you can choose two behaviours.

Wrap Index: When the end of the set of radiographs is reached, either stop, or wrap to the start of the images and keep going

Fast Indexing: When the mouse button is continually held down, after a few seconds, start indexing through the images faster.

Clicking the mouse wheel button will cause the advancement of images by 45 degrees.

The middle selector  is a drag control. Select and hold it with the mouse button, then move the selector up and down. This will now scroll through the images depending on how far you move the mouse vertically. As before, depending if the Wrap Index is selected or not, you will either warp or stop when the end of the radiograph set is reached.

Clicking the mouse wheel button will cause the reset of the control to the first radiograph.

Hovering the mouse over the control pops up an indicator showing the radiograph index of the displayed image.

Right Click Context Menu

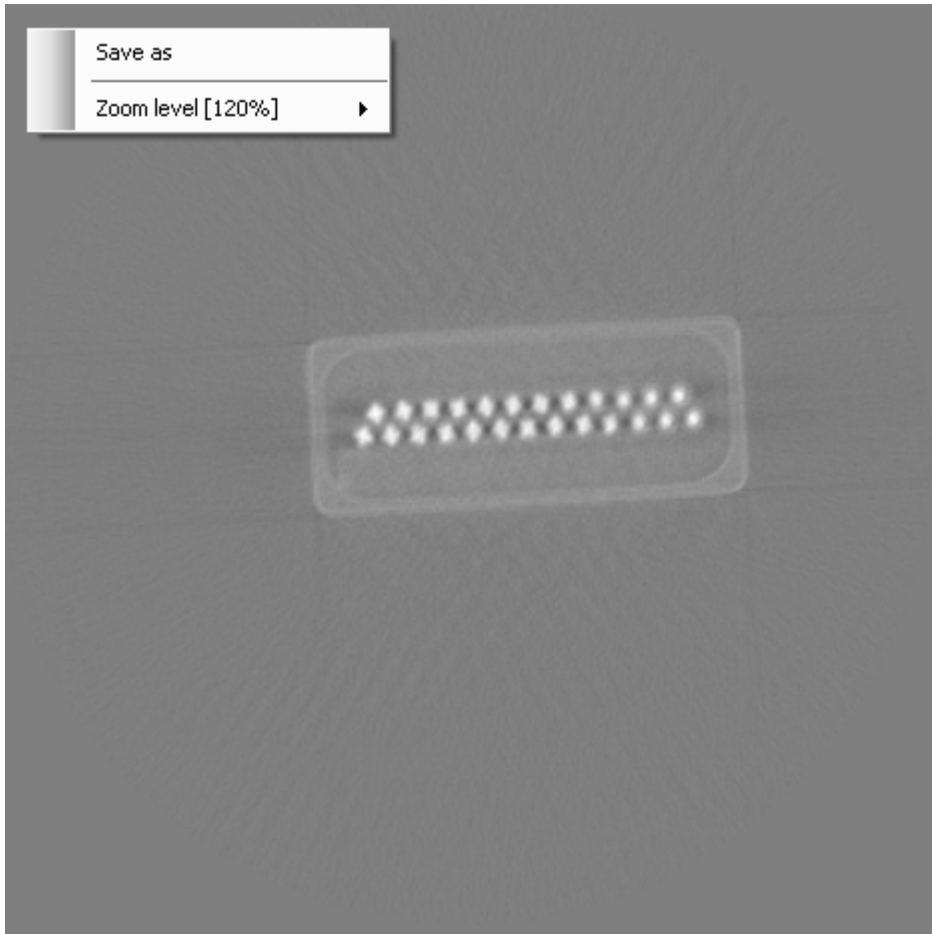
Right clicking on the image gives access to a number of facilities detailed in the Context Menu topic

3.7.1 Right Click Context Menu

Right clicking on the menu, depending on the image control in question brings up a menu of various options to give extra facilities.

Other special facilities are detailed in sub-topics:

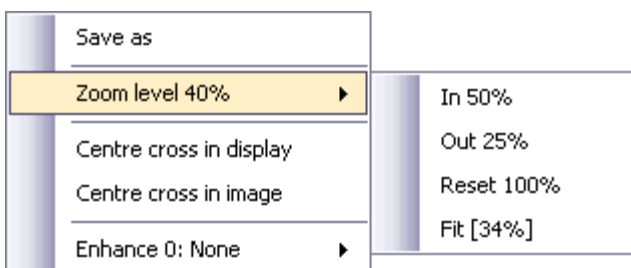
Common Context Menu Items



All Image dialogs have the following facilities:

Save As: Save the current image as shown to a file

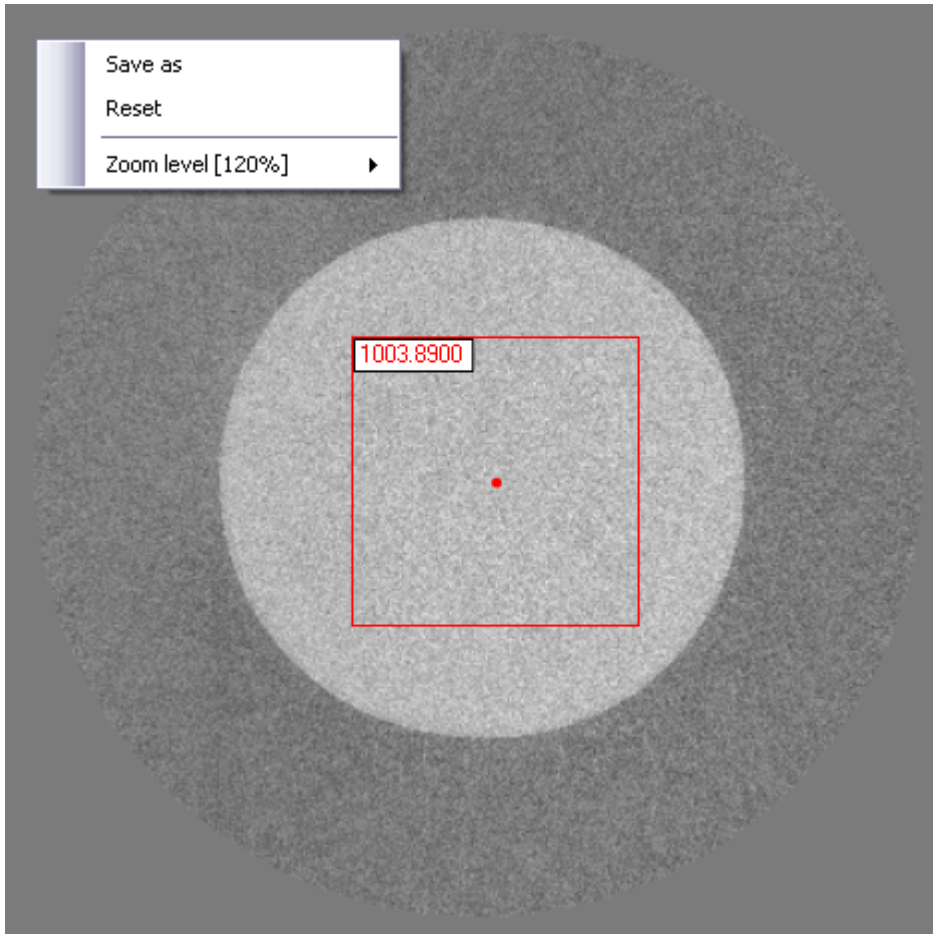
Zoom Level: This acts in the same way as the normal zoom level controls, ie



3.7.1.1 Reconstruction: Reset

Right clicking on the menu, depending on the image control in question brings up a menu of various options to give extra facilities.

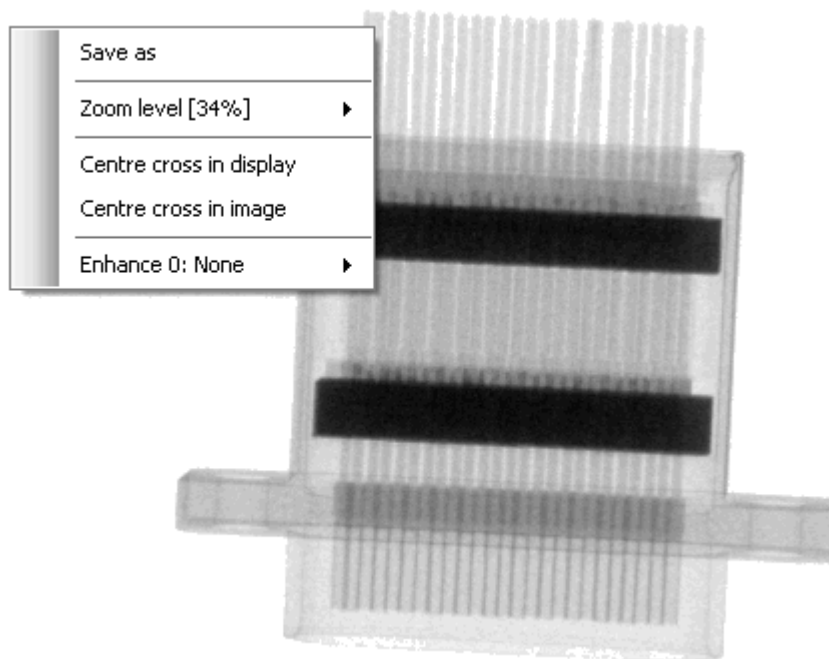
For most Reconstruction image display controls where an area measurement can be made, this may be dismissed by selecting Reset:



3.7.1.2 Image Tab: Extra Context Menu Items

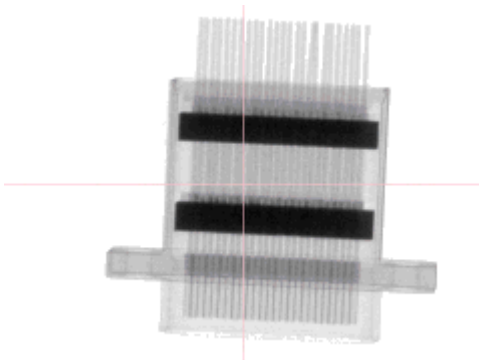
Right clicking on the menu, depending on the image control in question brings up a menu of various options to give extra facilities.

For the Image tab, the extra facilities are:

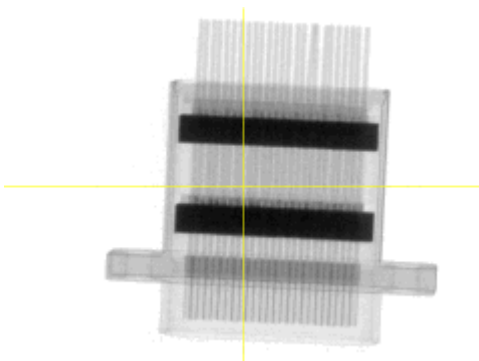


Centre Cross

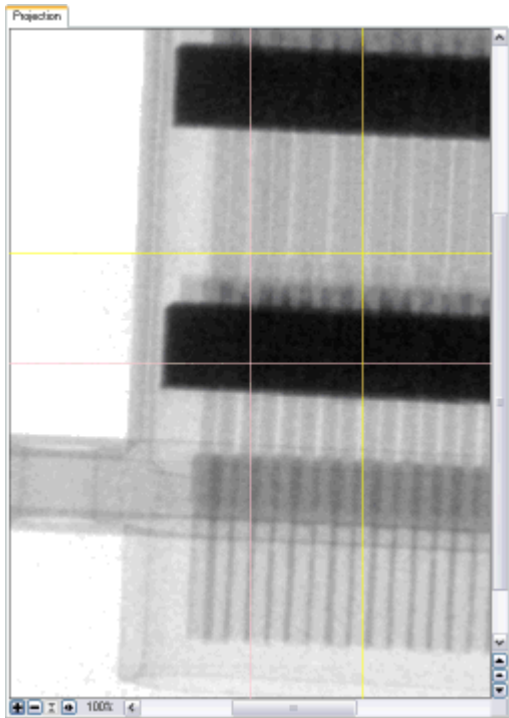
Centre Cross in Display: Paints a cross in the display to enable you to determine where the centre of the control is.



Centre cross in image: Paints a cross in the image to enable you to determine where the centre of the image is.

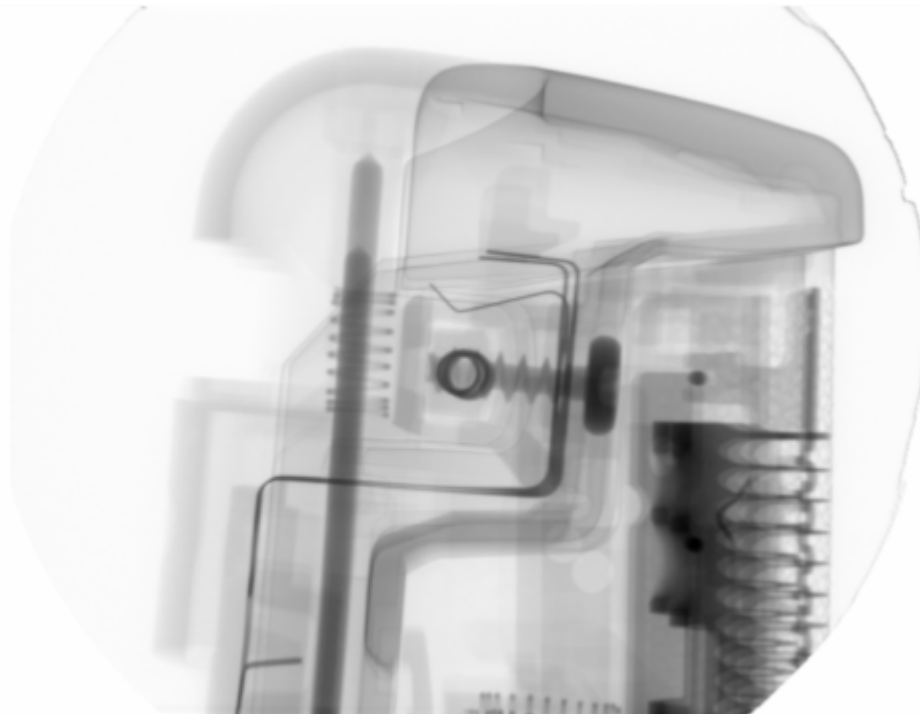


Combined: This can be useful when combined with the centre cross in display for examining alignments

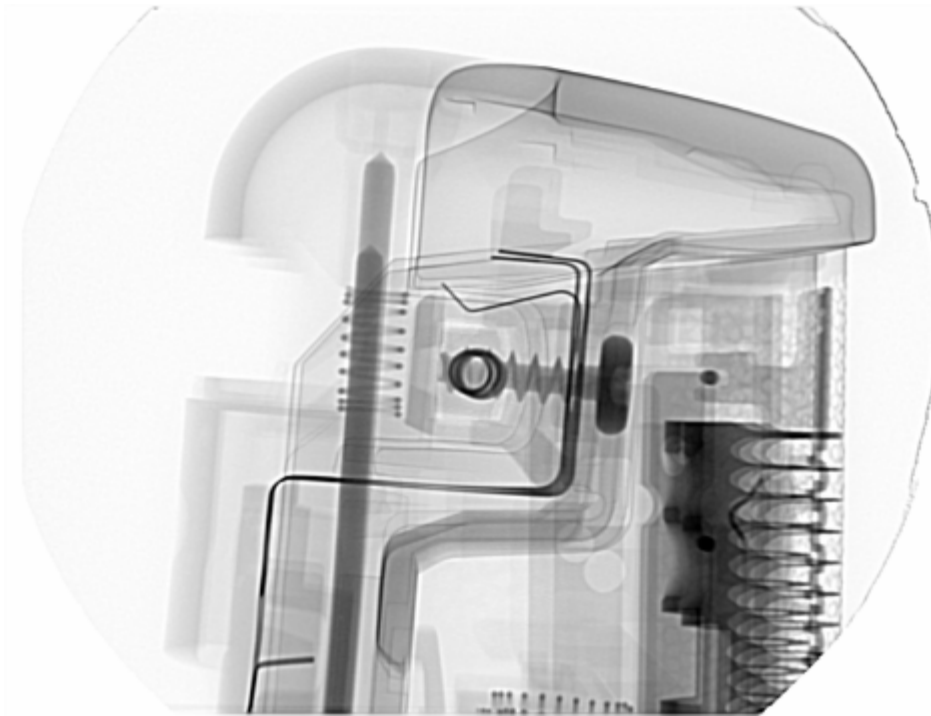


Enhancement

This sharpens the image if you wish to examine detail, however this significantly slows down the rate of display of images.



Enhancement of 0



Enhancement of 3

3.8 Menu

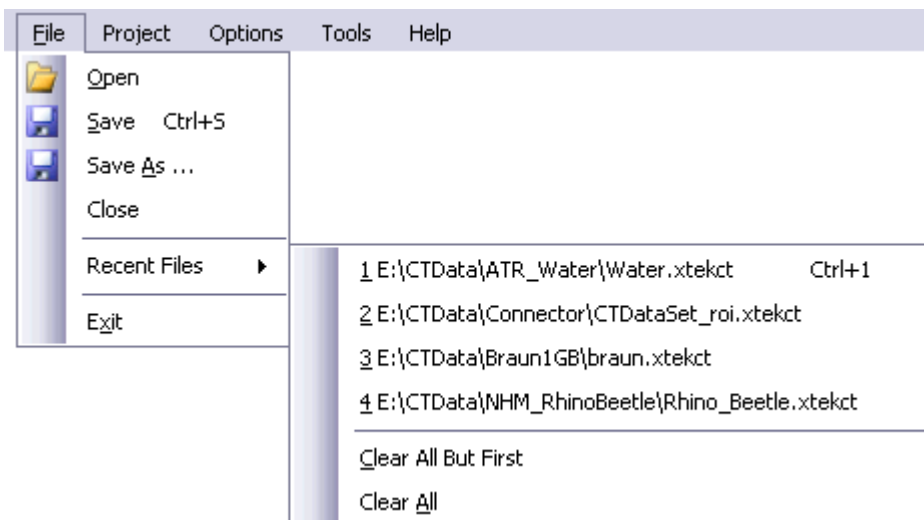
The following menu items are available

File Project Options Tools Help

File

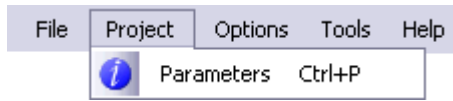
The usual project open, save, close items are available.

Additionally the list of recent files may be accessed.



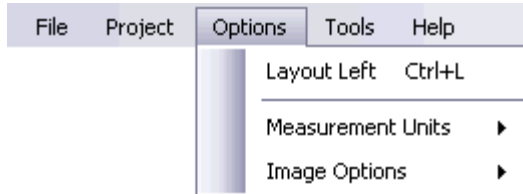
Project

Here the project itself may be examined



Options

These manipulate application properties or are tools to use in an opened project



Measurement Units: As shown below, the measurement units for the indicated items may be chosen to suit individual requirements. The normal units are selected by default.

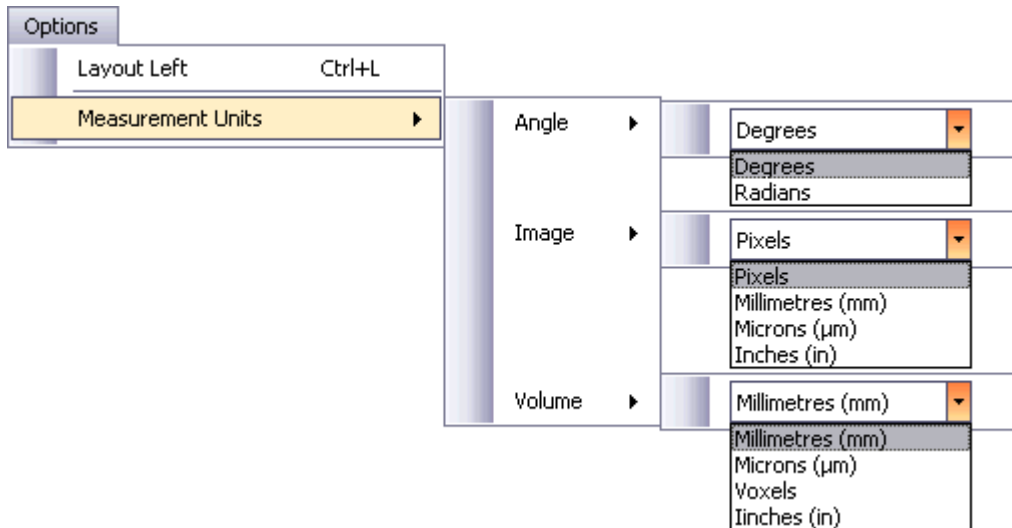
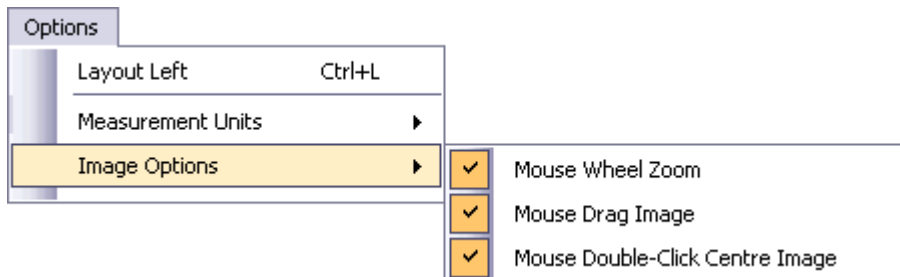


Image Options: For the Image Tab, projection of radiographs image control, these affect manipulation of the image within the control.



Tools

Tone Curve: This allows the tonal rendition of the displayed image to be altered if certain grey level information is not clear see the Tone Curve topic.

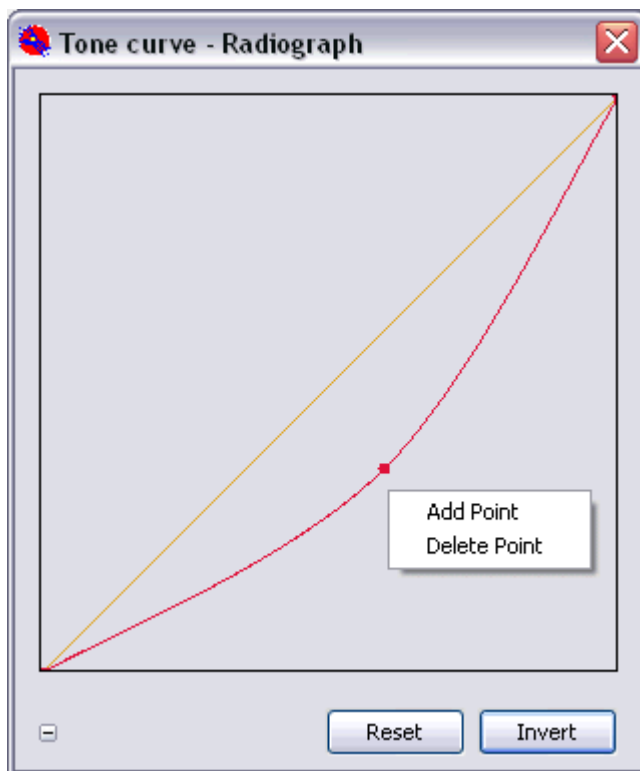
Advance Options

Advanced Options: these are password protected options not available to normal customers.

3.8.1 Tone Curves

Tone curves for Radiograph images and reconstructions can be defined independently, but work in identical manner.

From the Menu, Tools & Options, select either of the Tone Curve items. This displays the following graph. You may right click the line to insert or delete points which allow you to modify the shape of the curve. The ends of the curve may also be moved.



The Orange line shows the shape of the curve before you modified it. The Rest button resets the curve to be a linear line. The Invert button inverts the shape of the line vertically.

Clicking the navigation control opens additional controls showing the value of a point on the line, and the facility to save and load tone curves if necessary.



SECTION 4

Help

4 Help

This has two topics.

Troubleshooter: Diagnoses common problems.

Glossary: Explains terminology and in depth exploration of topics mentioned elsewhere.

Further information can be found by asking for documents

144TN178 Format of Data in CT Volumes.doc

4.1 Glossary

A glossary of explanations and terms for topics which do not require a sperate topic page

Voxels

A voxel is a 3D pixel, and in our case refers to the voxels contained in the reconstruction volume.

Reconstruction Resolution

Q What is the best resolution to reconstruct at?: The expected answer is a 1:1 selection where the size of a voxel in the reconstruction volume matches the size of a collected radiograph pixel when projected from source, through the volume to the detector (i.e. the demagnified pixel size). However this is not quite true, because each voxel in the reconstruction volume is derived from the cumulative addition back projection of density lines through its volume from radiographs at small rotational angles about it. Therefore each volume element has been sub-sampled by several pixels and so using smaller voxels could result in higher resolution than simply the demagnified pixel size. A gain of about 40% on resolution can be obtained this way, providing enough projection angles are collected.

Q So how do we improve resolution?: Take more projection angles or use a higher resolution detector.

X-ray capitalisation

Q Should X-ray always be capitalised?: Yes, X is a symbol not a letter of the alphabet, so we always write X-ray with a big X.

4.2 Reconstruction

How a volume is built up

CT reconstruction works by capturing an X-ray image of the object through a series of angles, and then back projecting lines of density through a 3D reconstruction volume. When line intersect they reinforce each other gradually producing an image. Where they don't intersect, the value generated is low and appears in the image as general background noise. The more projections you take originally, the better quality image you get as a result as the signal to noise ratio improves (up to a certain limit). If only a few projections are used, the edges are blurred as the contribution of projection lines at various angles causes a high degree of noise very close to the intersection point. More projections reduce this effect.

Fast Order display of a slice

As each projection is processed, the display is updated. If the processing is very fast, then the number of projections in each update will be greater than one. You will observe how each new projection improves the definition of the output. To render a viewable output faster, the order of projections processed is in *fast order*. What this means is that instead of going round from the projection at angle 0 to the next in turn, a pyramid order of processing is performed, ie {0,90} degrees, then {45, 135, 225, 315} then the next bisecting angles etc. In this way a rough but identifiable image appears quickly. You will observe that after about half of the projections have been processed that the image quality will not appear to change visually. However - the quality of the rendered 3D volume will continue to improve.

4.3 File types

This version of software stores parameter data in .xtekct files .The xtekct file contains all the information, such as acquisition geometry, volume of interest selection, beam hardening and any other parameters used to reconstruct the volume. This file should NOT be deleted.

Previous parameters were stored in a .PAR or .PAR.XML file. When selected it is immediately converted to a .xtekct file of the same name and that file is subsequently used. If an xtekct file of the same name exists it is overwritten.

List of Input files:

*.par	Old NGI CT file.
*.par.xml	Old V1 CT Pro CT file
*.xml	Old V1 CT Pro file (renamed to .par.xml to avoid confusion with other xml files)
*.xtekct	Fast CT files (a version without this setup user interface for batch processing)
*.ang	Lists the angles that each projection image was acquired at. This is really only necessary if continuous CT capture is used, when it is not possible to guarantee the linear angular increment of each projection.
*.lsf	Lateral shift file (stores the lateral shifts used during ring artefact suppression - is needed to recorrect raw data files)
*.log	Details the CT reconstruction activity. Generated only when concurrent reconstruction with data acquisition is performed (this file may be deleted if no longer required)
*.cpt	Inspection Machine setup, i.e. X-ray conditions, manipulator positions and other
*.xct	qualifying parameters.
file0001. atn	Output radiograph: Attenuation image - from iXS or IMPS
file0001. tif	Output radiograph: Image - from Inspect-X
_geompl ate.tif	Setup: Geometric plate correction image
_black. tif	Setup: Black and white reference images
_white.tif	
_rod0. atn	Setup: Rod images used to calculate the exact projection position of the axis of
_rod90. atn	rotation in the images
_water. tif	Setup: An image of a water bottle collected with the same X-ray conditions as the projection images - used to calibrate the Hounsfield units calculation

Parameter file: These files describe the physical geometry of the collection system. The conditions of collection are described in a .CPT file if this exists. The geometry for the angle of collection may be further detailed in a .ANG file if the dataset was collected by continuous rotation where the angle of successive radiographs may not be uniform as in a step and collect collection mode.

Output files

Before a reconstruction commences, an output name for this is chosen, usually based upon the input name and extended with a number to distinguish it from any other set with the same name. You may choose a different output name if you require. Thus an input dataset called NAME may become NAME_00001, and we will use this below.

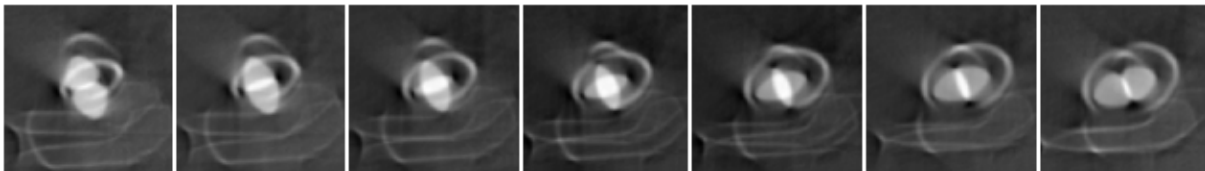
After a reconstruction has completed, an output .XML file, NAME_000001.xml will contain the parameters used for that reconstruction. This can be used later as an input file if you wish. The other files produced will be:

NAME_000001.vgi	Volume graphics description file - used to import the CT volume file into the volume viewing software, VGStudioMAX
NAME_000001.vol	Volume graphics data file (usually a large file)
NAME_000001.log	Log of activity for this reconstruction (may be discarded later)
NAME_000001.xtekct	Saved parameter file with the settings used to generate this volume (may be discarded but is a useful reference)

4.4 Incorrect Geometry

Source to Object or Detector Incorrect

These kinds of error do not normally cause much of a problem, and while they should be correct, as small error of up to 10mm is not normally very noticeable. However if the error is very extreme, the following kind of error is observed as shown in this strip. Here we have reconstructed a small rod with a centre of rotation varying from -6 to +6 pixels. The centre picture is the correct image normally, but when the Source to Detector distance is deliberately set incorrectly to almost 3 times the correct value, giving ellipses rather than a perfect circle.



In this example the Source to Detector distance has been changed to show the effect.

	Original	Incorrect
Source to Object distance	167.3 mm	167.3 mm
Source to Detector distance	618.0 mm	1718.0 mm

4.5 Continuous Image Collection

Start and End Image Determination

Normal image collection acquires images through a 360 degree rotation of the object table using a repeated sequence of: turn, stop, image capture. While this produces high quality radiographs, the downside is that acquisition is slow, especially if a large number of radiographs are being captured (ie 1500 radiographs at 1 second per capture is 25 minutes).

Continuous rotation keeps the turntable stage rotating while image capture takes place, and can be up to 3 times faster. This increases throughput on a machine, however the downside is that a) each

image capture must be made before the stage has turned any one pixel in the object by more than its own size and b) that the image correction and reconstruction must still be carried out offline, thus increasing the overall time to generate a volume.

There are a number of factors which govern which technique to use. The main ones are image exposure time, image correction and reconstruction time. The details of this choice will not be further discussed here.

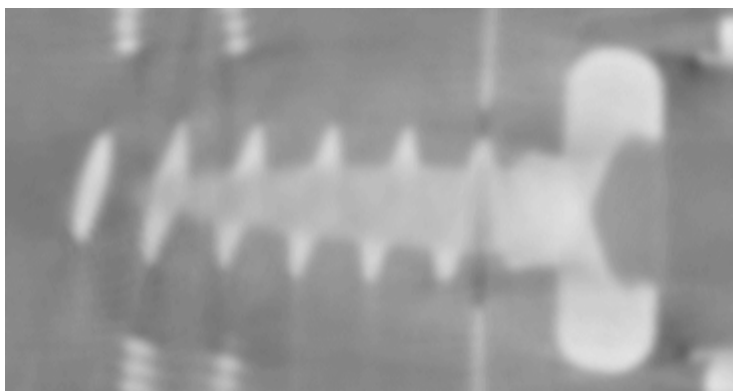
When continuously capturing images, you normally capture through 370 degrees. This is because the first 5 degrees of images may not have a uniform angular increment as the turntable is speeding up and settling down to a uniform rotation speed. You thus choose to discard the first 10 images and reset the 11th image as the first or 0 degree image. You now have the problem of determining which image forms the last image in the 360 degree rotation. You need to find the image which most closely matches the start image, and then use the previous image as the end of the set. Dividing 360 by the number of selected images in the set give you the angular increment per image.

4.6 Effect of Projections on Quality Reduction

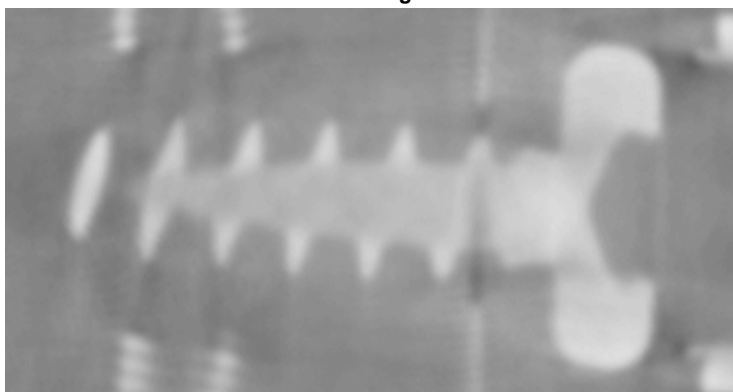
To speed up reconstruction there are two techniques that may be used. Firstly to reconstruct the first 180 degrees only, and secondly to reconstruct with a subset of the projections, ie every 1:2 or 1:4 of the projection set. In either case quality is diminished, however this may be desirable if a lesser quality will satisfy a particular application along with the time saved.

1) 180 degree reconstruction

The comparison of the first two images show only a slight deterioration in quality when reconstructing 360 degrees and 180 degrees. However, to show the effect of only reconstructing 90 degrees, this is clearly unusable.



Full 360 degrees



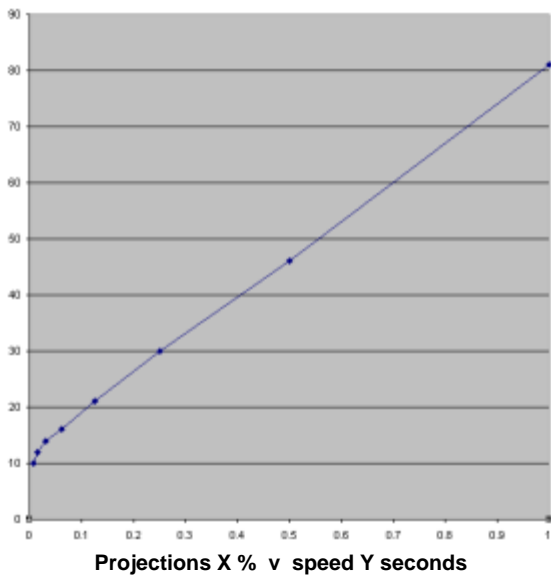
Half 180 degrees



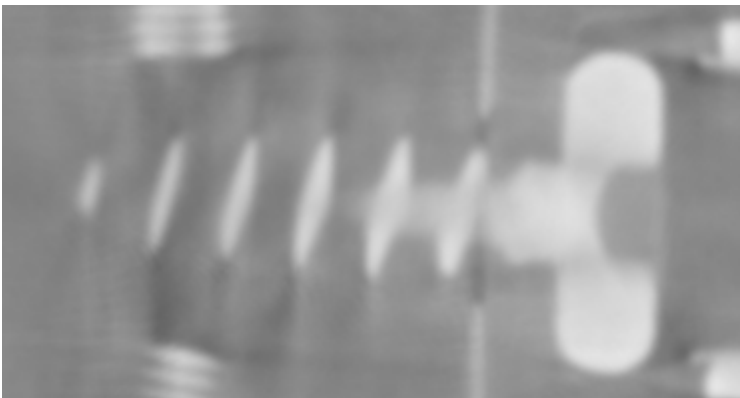
Quarter 90 degrees (for comparison)

1) Subset reconstruction.

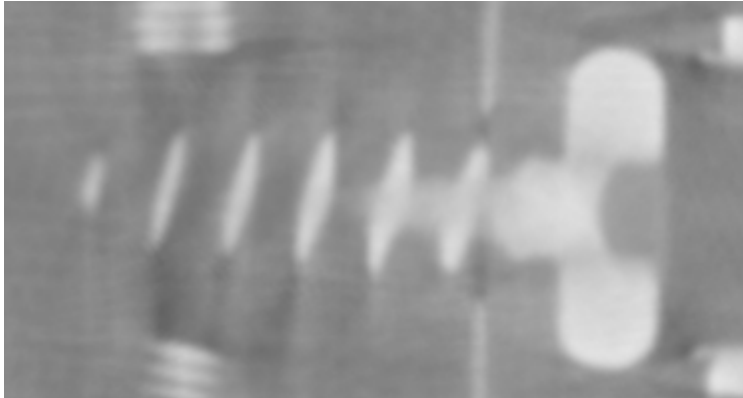
Normally we choose to reconstruct every projection giving 1:1 quality. However a speedup can be obtained by doing 1:2 (or every other projection). Further reductions of 1:4 and 1:8 can save considerable time, but quality starts to degrade quickly. Also edge pixels at the circumference will be more poorly reconstructed and may be less than the minimum number of projections to satisfactorily reconstruct these. However the technique is useful in order to obtain a quick overview of the data taken.



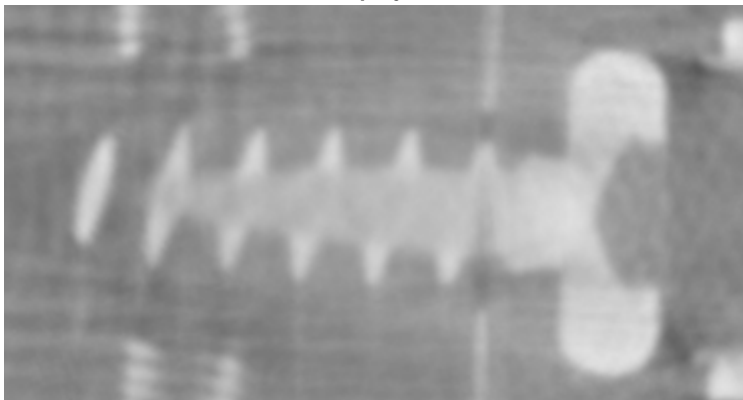
An example reconstruction quality when comparing quality range 1:1 (good) to 1:16 (poor & quick) below:



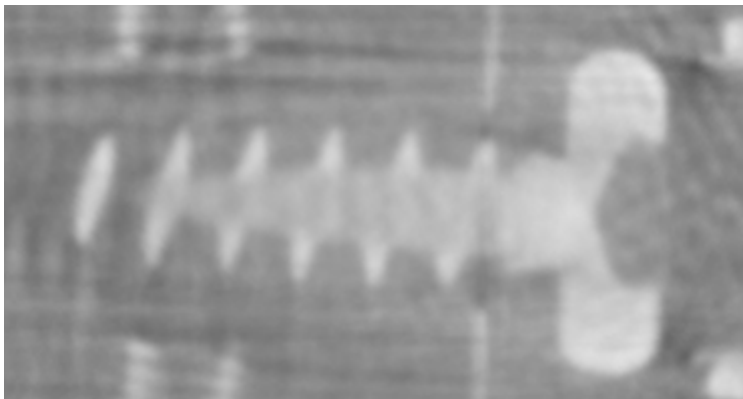
1:1 full # projections



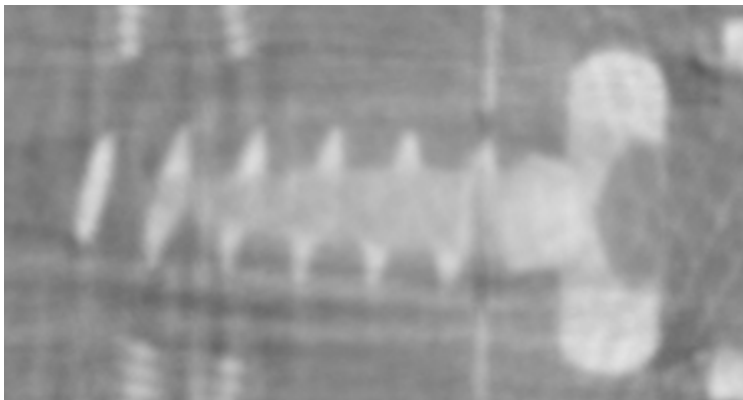
1:2 Half projections



1:4



1:8



1:16

4.7 Minimum Number of Projections Required

1) There is a minimum number of projections required to reconstruct a volume. At a minimum, you require one projection ray to pass through a voxel. At the centre of rotation this is not a problem, however as the distance from the centre increases, then less projections will potentially pass through a voxel. So taking the furthest point from the centre of rotation to be reconstructed, If we assume the angles are small, the approximate calculation is:

$$\text{Num Projections} = \text{Circumference} / \text{Voxel resolution}$$

Thus a sample of 10mm radius reconstructed at 0.1mm Voxel resolution requires 628 projections minimum, ie

$$628 = (3.14 * 2 * 10) / 0.1$$

2) The number of projections should be **odd**.

The reason for this is that for the 0 degree and 180 degree positions, near the centre, if you have an even number of projections, then for the 180 degree beam, the centre rays projects along the same line in the opposite direction; thus not gaining any new useful information. By using an odd number you avoid this situation. The effect is however usually very small.