

# Respiratory motion management for CT

## Summary

The topic of using CT for respiratory motion assessment in preparation for radiation therapy treatment has generated hundreds of published manuscripts in the literature and numerous talks at conferences. To cover this subject in a comprehensive manner is well beyond the scope of this white paper. However, this document will provide an overview of the basics of respiratory correlated (or gated) CT (aka 4D-CT). It provides a detailed description of this functionality as implemented on the Philips Brilliance CT Big Bore. Respiratory devices, workflow, geometric and temporal accuracy, theoretical basis for 4D-CT, and image processing tools are all topics covered in this white paper.

Both prospective techniques where the respiratory device triggers a scan and retrospective methods where the respiratory waveform is utilized in binning the acquired CT data will be explained. For retrospective acquisitions, the pros/cons of binning in sinogram vs. image space and using cine axial vs. low pitch helical will be explained. Two binning algorithms will be explored. This includes the common linear phase method which is time based on the percentage of the breathing cycle and an algorithm which uses the waveform amplitude as a basis for binning images. Though this document is quite lengthy, it is divided into sections by subject allowing the reader to focus on his area of interest.

## Background

Over the past decade, many papers<sup>1-3</sup> have been published concerning the challenges of respiratory movement during radiation therapy. It is well known that normal breathing can cause severe motion artifacts during a CT scan. For diagnostic scans, the patient is usually scanned during a deep inspiration breathhold which minimizes internal motion. This option is unsatisfactory for CT Simulation which is being performed in preparation for radiation treatment. Since radiation treatment times are of longer duration, patients cannot maintain a stable breathhold throughout the treatment session. Therefore, it is highly desirable that CT image volumes are generated for the entire respiratory cycle. This enables the clinician to observe the tumor movement relative to other anatomical structures during a normal breathing cycle. The most commonly employed method is to perform a very slow acquisition process that is correlated to the respiratory signal via some external surrogate.<sup>4-5</sup> Retrospectively, the acquired data is binned into data volumes that represent different phases of the respiratory cycle. This procedure is often referred to as 4D-CT.

There are two main acquisition modes in use for 4D-CT. One is called cine axial where the CT scanner scans continuously for the duration of at least one breathing cycle with the CT couch being stationary. The couch then increments one detector collimation width and repeats the process until the desired longitudinal extent is covered.<sup>11</sup> The other method is a helical scan with an ultra low couch speed or very low pitch factor. The pitch is set low enough that each slice of the volume remains illuminated at least for the duration of one respiratory cycle.<sup>5</sup> The Philips Brilliance CT Big Bore utilizes this low pitch helical mode for 4D-CT acquisitions. Some comparisons of these scanning modes have been previously published.<sup>4</sup> This document will discuss both the differences in acquisition modes and its impact on the geometric accuracy of the reconstruction process.

Besides these retrospective scanning modes, another approach is to trigger a CT scan prospectively based on the respiratory signal. This type of acquisition will only generate a single phase or a snapshot of the internal anatomy at some user selected point in the respiratory cycle. This may be sufficient for gated radiation therapy where the linear accelerator beam is only turned on for a short period of time at a particular phase point in the breathing cycle.

However, the physician usually desires to view the entire range of tumor motion throughout the breathing cycle. One approach is to perform two prospective scans, one at full exhale and the other at full inhale. In this way, the extremes of tumor motion can be visualized. The deficiency of this approach is that respiratory motion is not linear and it can have hysteresis. This means that the exhale and inhale trajectories can differ. Therefore, many clinicians prefer the retrospective mode where the full extent of anatomical motion can be observed and accounted for during treatment planning.

On the Brilliance CT Big Bore, the trigger mode of scanning is referred to as Prospective Axial. When the breathing signal reaches a pre-determined threshold, an axial multi-slice scan is performed and the couch will increment by the size of the detector collimation (typically 24mm). This process is repeated for the next breath. Each couch increment requires another breathing cycle.

An alternative approach to the respiratory movement issue is to scan with breathhold and gate the treatment with the patient's breathhold. On the Brilliance CT Big Bore, the Prospective Spiral scan mode is best suited for this type of acquisition. The user can manually start a helical scan when the patient has reached the targeted respiratory level and the patient's breathhold has stabilized. Helical scanning requires the couch to accelerate to the desired speed before scanning initiates. Since this delay (~3 sec.) is present and the breathing must be stable at a specific level, the Brilliance CT Big Bore does not automatically trigger this scan. The Brilliance CT Big Bore does record the breathing trace so that when the clinician reviews the images, it can be retrospectively determined if the patient maintained the desired level of breathhold.

## Respiratory monitoring devices

To perform any type of respiratory gating, it is obvious a device to monitor breathing is required. With the strong interest in this field, a plethora of devices have been utilized for recording the respiratory signal. It is beyond the scope of this paper to provide a comprehensive description of all types of respiratory devices. Instead the most commonly used and readily available apparatuses will be covered.

The basis for most respiratory monitors is to measure the external abdominal movement as a surrogate for the internal respiratory induced motion. One device that is supplied with the Brilliance CT Big Bore is the Philips bellows.

This device consists of a rubber air bellows that is attached to a pressure transducer. As the abdomen stretches and contracts, the transducer senses the air pressure changes within the bellows. This signal is digitized and transmitted to the scanner which records the waveform trace. Another common commercially available device is the Varian RPM.<sup>™</sup> It utilizes a plastic block with infrared reflectors that is placed on the patient's abdomen. (See Figure 1). A digital camera is focused on this block and relays the video output to a digital frame grabber. The digital images are analyzed by PC based software which identifies the reflectors in the image and thus can deduce their movement.<sup>9</sup> This movement corresponds to the abdominal motion of the patient. The RPM is also available for gating treatment on the Linac. Other devices of this genre that measure abdominal motion may use abdominal pressure,<sup>12</sup> optical camera<sup>14</sup> or lasers<sup>13</sup> to monitor movement of the abdominal skin. Another approach to measuring the respiratory wave is to monitor air flow via a spirometer.

Some studies have been performed comparing the accuracy of these various devices.<sup>12</sup> In general, the conclusions are that there are no significant differences in accuracy between these various methods. The Philips bellows has the unique virtue of being integrated with the Brilliance CT Big Bore scanner. This provides a distinct simplicity in workflow since the user does not need to interact with another computer system when performing

respiratory correlated CT. A second monitor with keyboard and different user interface is eliminated and the concomitant problems of transferring data between computer systems are mitigated.

### Workflow for prospective scanning

There are two prospective acquisition modes available on the Brilliance CT Big Bore. Prospective axial is used to acquire a single phase of the breathing cycle. In this mode, the scanning is triggered at the user selected point in respiratory signal and the scanner performs a single multi-slice acquisition. The common protocol is to use a collimation of 8x3.0mm. The couch will increment by the detector collimation (24mm) and when the subsequent trigger point is reached the next set of slices are acquired.

Prospective axial mode is compatible with both the bellows and RPM devices. However, the process for each is different. With the RPM, the trigger signal is sourced from the RPM computer. Therefore, the setup for the generation of this signal is performed on the RPM. The user observes the respiratory signal and designates a threshold or phase point on the RPM system. When the trigger pulse is received by the Brilliance CT Big Bore, it will perform a single multi-slice acquisition. The user can select a full (360°) rotation for the axial scans or for increased temporal resolution a partial angle(240°) axial scan can be performed.

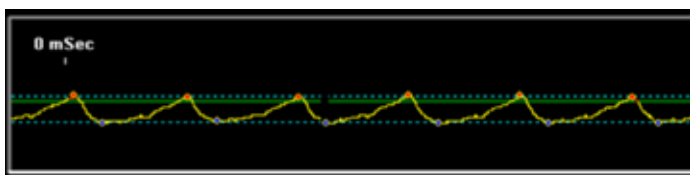


Bellows

RPM

**Figure 1:** Respiratory devices for the Brilliance CT Big Bore.

In contradistinction to the RPM, the bellows device is integrated into the Brilliance CT Big Bore scanner. Therefore, the setup menu is displayed on the CT console and is part of the scan protocol interface. The user has the option of selecting the inhale or exhale phases or a user defined phase which is based on the amplitude of the breathing waveform. The maximum inhale point is the local maximum and the maximum exhale is the local minimum for the respiratory signal. The user menu is shown below.



**Figure 2:** Real time view of respiratory waveform in Prospective Axial mode.

When selecting user defined, the user is required to enter a threshold value that will trigger the scan. The units are based on the patient's average breathing pattern. Therefore, this feature requires a 'learning' phase at which time the system will determine the extent of the patient's respiratory signal. The value of +1 is nominally set to the max. inhale point and -1 to the max. exhale point. The user can enter a range of +2.0 to -2.0. In this way, a threshold can be set beyond the normal breathing range and allow the system to trigger on a large inhale or exhale breathhold. Furthermore, the system can trigger on the amplitude crossing when sloping upward or sloping downward. This is controlled by the radio buttons in the menu above. On the waveform window, a solid horizontal line will be displayed that will correspond to the user defined level. Its position will change whenever a new level is entered. Two dotted horizontal lines are placed at the nominal +1.0 and -1.0 positions. See Figure 2.

The prospective spiral mode is a targeted breathhold scanning protocol. In this procedure, the goal is to perform a rapid scan when the patient has reached a

pre-determined respiratory threshold and maintains that level throughout the scan. Since there is a ~3 sec. delay before a helical scan is initiated, the system does not automatically trigger the acquisition when the threshold is crossed. Furthermore, the scan should only be initiated when the patient's breath has stabilized at this targeted level. Therefore, the user must manually start the scan. For the bellows, the respiratory trace is displayed on the screen. When the RPM is used, the waveform will be transferred after the acquisition is completed. The waveform data is also archived with the images.

### Workflow for retrospective spiral

The Brilliance CT Big Bore supports two modes of operation for 4D-CT. One uses an interface compatible with the Varian RPM and the other designated for the Philips bellows. The user can switch modes at any time between studies by accessing the User Preferences' page and modifying the field for Respiratory Device. There is a different interface cable for each of these two modes. These cables are connected to the same connector on the back of the scanner gantry.

When using the RPM device, the user places the plastic reflector block on the patient's abdomen and positions the infrared camera to be focused on this block. Before the RPM can record the respiratory waveform, it needs to complete the 'tracking' phase. During this step of the procedure, the RPM computer 'learns' the extent and typical pattern of the patient's respiratory cycle. The end of this phase is indicated on the screen and then the RPM proceeds to record the respiratory data. The waveform is only visible on the RPM computer while the scan acquisition is in progress. During the recording stage, the RPM will transmit real time pulses indicating that a maximum inhale position (0%) has been detected. These pulses are displayed on the CT host computer monitor. The pulses serve a dual purpose. They ensure that the RPM is operational prior to scanning and these pulses can also be utilized by the reconstruction system as a backup for the respiratory waveform data should the network transfer of the RPM waveform file fail.

It should be noted, that the tag points identified in the RPM file may not coincide with the real time pulses. The pulses transmitted during the scan are based on the internal predictive algorithm of the RPM and this can cause inhale points to be missed when the patient's breathing deviates from the predicted pattern. However, these inhale points are properly identified in the RPM file. Furthermore, if the Recalculate Phase on Export option is set (recommended), the RPM may re-position the inhale points significantly post acquisition.

At the conclusion of the scan, the RPM now has the benefit of hindsight in analyzing the waveform and need not rely on predictive algorithms that are the requisites of real time analysis and therefore, the inhale points may be shifted to a more accurate position.

At the end of the scan, the recording on the RPM ceases and the user exports the waveform file to a network shared disc location that is accessible to the CT computer. The CT system imports this file and will then display the contents of the file as a waveform. The maximum inhale points are displayed as red dots (aka tags) and the user has the ability to edit these points in case the RPM missed an inhale point or erred in identifying the true inhale point.

The workflow usage of bellows is more streamlined as compared to the RPM. There is no 'tracking' stage per se, though the user should allow for 3-4 breaths to occur so that the internal auto-scaling of the bellows has stabilized. During the scan the user can observe the waveform in real time on the CT host computer while with RPM only pulses will be displayed. After the scan completes, the waveform is immediately available for editing inhale points if necessary. No exporting of the waveform file is required since the bellows is an integrated device. While the respiratory data is being collected, the system will display the red dots at the presumed inhale points. When the scan terminates, a post analysis is performed on the waveform data which results in a more accurate identification of the inhale points. This procedure is automatic and transparent to the user.

Irrespective of the breathing device that is utilized, it is important that each voxel remains illuminated by the CT X-rays for the entire breathing cycle.<sup>5</sup> Otherwise, some breathing phases will be missing data and we will not have a complete 'motion' picture of the total scanned anatomy. For helical scans, the controlling parameter is the pitch factor which implicitly determines the couch velocity of the scan. The couch velocity must be low enough that the duration of every voxel that passes under the detectors is at least one breathing cycle. This establishes an upper limit to the pitch factor which is inversely proportional to the couch speed. However, setting the pitch factor too low will limit the longitudinal extent of the scan due to the 120 sec. maximum X-Ray ON time limit of the Brilliance CT Big Bore. Therefore, it is desirable to keep the pitch factor only as low as necessary. Figures 3 and 4 show the recommended pitch factors for different breathing rates (Brilliance CT Big Bore only).

The minimum pitch available on the Brilliance CT Big Bore is 0.04. This enables the scanner to accommodate the slow breathers (10BPM). Note, even a normal breather (15BPM) should be scanned with pitch factor <0.1. A more in depth derivation of pitch factors will be covered later.

#### 0.5 sec rotation time

Breathing rate (BPM)	Pitch
20	0.1
15	0.08
14	0.075
13	0.06
12	0.055
11	0.05
10	0.04

Figure 3: Maximum pitch factors for different breathing rates.

#### 0.44 sec rotation time

Breathing rate (BPM)	Pitch
20	0.09
15	0.07
14	0.066
13	0.053
12	0.05
11	0.045
10	0.04

Figure 4: Maximum pitch factors for different breathing rates.

Using the 120sec. time limit of the Brilliance CT Big Bore, it is possible to calculate the maximum longitudinal extent of an acquisition based on the pitch factor selected. This data is presented in Figure 5. This plot assumes a rotation time of 0.5 sec.

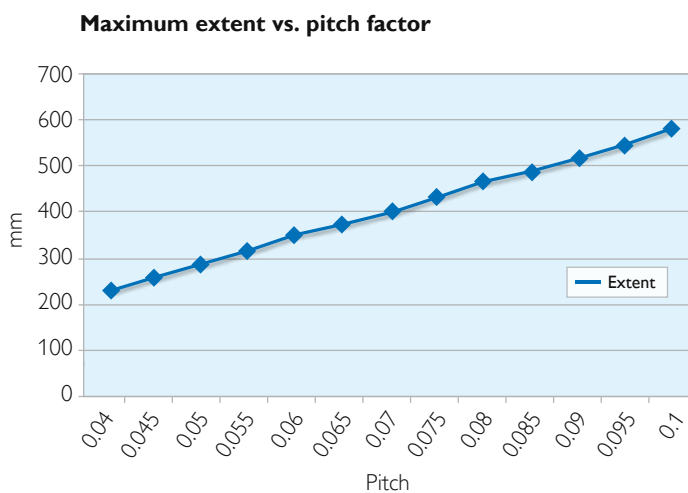


Figure 5

The Brilliance CT Big Bore is capable of reconstructing up to 10 phase bins of data at a time. The user can perform multiple reconstructions with a different set of 10 phases thus any number of phase bins can be generated by the system. It is important to note, the number of phases has no impact on the temporal resolution of the 4D-CT data sets. The reconstruction will always optimize temporal resolution which is nominally equal to half of the rotation time regardless of the particular phase selected or number of phases requested. For example, a reconstruction of 10 equally spaced phases and a single reconstruction of the 10% phase, will result in the two 10% phase volumes being identical.

### Breathing statistics

The breathing waveform viewer on the Brilliance CT Big Bore has a tab called INFO. Selecting this tab will display various statistics of the breathing trace. This information may be useful in identifying and classifying the irregularities in the breathing waveform. Below is a list of data that is displayed and a brief description of its derivation.

**Scan length:** This is the total length of the helical in seconds. The length of the respiratory data usually exceeds this value because the scanner records this signal both prior to and post scan.

**Mean BR:** This is the average breathing rate of the patient in breaths per minute (BPM). Only data samples recorded while scanning are included in the calculation of this average.

**Breath rate range:** This displays the limits of the breathing rate variations for this patient. It shows the lowest breathing rate and fastest breathing rate that occurred during this scan. A very wide range is indicative of a patient whose breathing is very irregular. The low breathing rate can be verified against the pitch factor of the scan. A breathing rate that is too low can potentially cause image artifacts.

**Average full exhalation phase:** The system will identify the local minimum for each breathing cycle. The value displayed here is the average location of all of local minima. This time location is expressed in percentage of breathing cycle. With amplitude binning this value will be very near to 50%. With phase binning this number can vary greatly depending on the patient's breathing pattern.

**Average full inhalation phase:** This is the average location in time for the local maxima. When using the bellows or the RPM with Recompute Phase on Export set, this number shall be close to 100%. If this number is in the range of 3%-97%, it indicates that the user may want to re-examine the waveform and edit the 'tag' points.

**Amplitude range:** Since the respiratory waveform is stored as a unitless vector, the system calculates the average local maximum and assigns it the nominal value of 1.0. The average local minimum is assigned the value of 0.0. A wide range indicates that there was irregular breathing during the acquisition.

**Amplitude standard deviation (SD):** From the values of all of the local maxima, the system calculates the SD from the mean value. A high SD implies that the patient has a very erratic breathing pattern. If the amplitude range is wide and the SD is low, this characterizes the case where only one or two breaths deviated substantially from the norm. The user can locate these points on the waveform and be alerted that the corresponding anatomy may be impacted.

### Scan protocol parameters

**Slice thickness:** The standard protocol for 4D-CT on the Brilliance CT Big Bore uses a 3mm slice thickness. This value is based on the current standard of practice for CT Simulation. Since the acquisition is performed with a collimation of 16x1.5mm, the minimum slice thickness is 2mm. On the Brilliance CT Big Bore, the slice thickness entered is the "effective" slice thickness which includes a broadening factor inherent in the spiral weighting vector. The actual detector size is 1.5mm but due to the nature of helical acquisition there is slice broadening.

**Increment:** With helical scanning, the user can reconstruct slices that are highly overlapped. The default mode is to generate contiguous slices i.e. slice increment equal slice thickness. Using overlapped slices may improve the visualization of very small structures. It is especially beneficial when any form of 3-D rendering will be performed. This includes the generation of Digitally Reconstructed Radiographs (DRR). The Brilliance CT Big Bore allows the user to select increments as low as 0.25mm. The main drawback in using small increments is that it can greatly increase the number of slices.

**Field of view (FOV):** For Oncology protocols, the default FOV is 600mm. This size allows that in most cases the air/skin boundary is visible for all slices. The user can select a smaller FOV which will generate images with an improved lateral resolution. This may be beneficial in visualizing more intricate anatomy.

**Matrix:** The default image matrix size is 512 pixels. By increasing the matrix size, the user can generate images with higher resolution without using a smaller FOV. Some RTP (Radiation Treatment Planning) systems do not support images larger than 512x512 pixels.

### Cine axial vs. Low pitch helical

As was discussed in the introduction to this document, there are basically two acquisition modes for 4D-CT: low pitch helical (used by the Brilliance CT Big Bore) and cine axial. In cine axial mode, the couch is stationary when the scanning is in process. The scan time is set to exceed the period of one breath. At the conclusion of a cine cycle, the couch increments by the detector collimation width and another cine cycle is initiated. At every couch position, axial slices are reconstructed at a fixed time interval. The binning is performed in image space on these reconstructed slices. The phase point locations on the respiratory waveform can be expressed as offsets in time from the start of the acquisition. Since the images are time stamped, the binning process consists of selecting the image closest to each phase point. However, these images are centered at a pre-determined point time which may differ to some extent from the targeted phase point in time. This will result in a phase error. This is illustrated in Figure 6. The orange squares represent the time points of the pre-reconstructed slices. In this case, a 400msec. increment was used. The green triangles are the phase points corresponding to 0%, 25%, 50%, 75%.

As seen from this plot there might be a significant time difference between the desired phase point (▲) and available image (■). This causes a recon phase error. With helical mode scanning, the binning is performed on the sinogram data and therefore the temporal center of any image can be placed at exactly the desired phase point in time. Therefore, there are no phase errors with helical mode.<sup>17</sup>

One advantage of utilizing an axial scan for 4D-CT is that the effective slice thickness is equal to the detector width. When performing helical scanning, there is the effect of slice broadening which does increase the effective slice thickness. However, this advantage for axial scans is only true for pixels near the center of FOV or centered within the detector rings. For pixels near the periphery of the FOV and detector rings, the effective slice thickness will widen significantly.

### SSP

The acquisition and reconstruction sub-systems of the Brilliance CT Big Bore were designed to support the low pitch helical scan mode for 4D-CT. It is imperative that the longitudinal resolution or effective slice thickness is maintained at the ultra low pitch factors used for 4D-CT.<sup>4</sup> The standard method to measure effective slice thickness is to use the slice sensitivity profile (SSP) test (See AAPM RPT-1). The full width at half maximum (FWHM) of the SSP is considered to be the effective slice thickness.

A series of experiments were performed on the Brilliance Big Bore using a 1.5mm detector width (16x1.5mm collimation). The CT-SSP Phantom (Model 76-412 Fluke Biomedical) was used. Helical scans were performed while varying the pitch from 0.04 to 0.2. The results were that the FWHM of the SSP graphs never exceeded 2.0mm for all pitch factors tested. This demonstrates that the Brilliance CT Big Bore will maintain longitudinal resolution even at ultra low pitch factors.

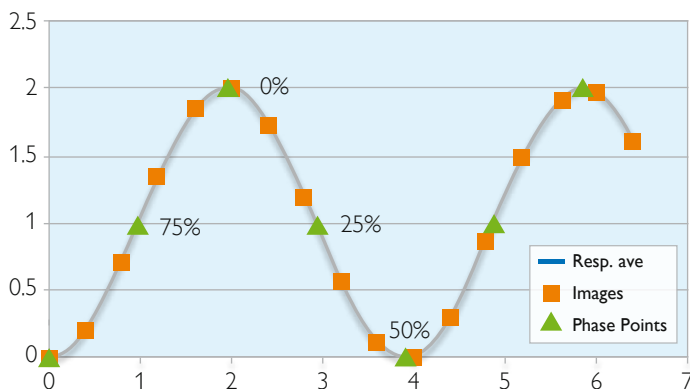


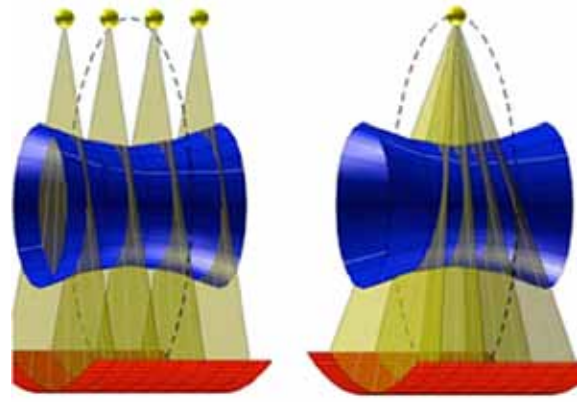
Figure 6: Temporal location of cine axial images and desired phase points.

### Off center SSP

The above SSP experiments were all performed with the phantom well centered within the scan plane.

Another set of tests were executed with the phantom at varying distances from the isocenter of the CT gantry. For helical scans, both pitch factor and offsets were varied. In axial scans, pitch is meaningless. For axial scans, the position of the phantom relative to the center of the detector rings was altered. The detector width on the Brilliance CT Big Bore is 24mm. The ball bearing was positioned between 0-12mm offset from the center detector in 3mm increments. For both axial and helical scans, the phantom was moved vertically in the scan plan from 0-25cm from CT isocenter in 5cm increments. For all these scans, the SSP graphs generated and the FWHM was recorded. The results for both helical and axial scans are shown in Figure 7.

As can be observed from these plots, helical scanning does have a slight broadening of the SSP width and axial mode scanning will have better longitudinal resolution near the center of the scan field of view (FOV). However, the SSP width degrades significantly for pixels offset from the CT isocenter and nearer to the edge of the detector collimation. This can be explained by the fact that axial scans are reconstructed without accounting for beam divergence. With helical scanning, the Brilliance CT Big Bore invokes the cone beam reconstruction algorithm (COBRA) which performs a divergent backprojection. As can be observed from the above results, the deleterious effects of ignoring beam divergence is most pronounced near the edges of the detector collimation and offset from the center of the scan FOV. Figure 8 is a 3D illustration of non-divergent parallel beam geometry while in reality an MDCT has single source divergent x-ray beam.

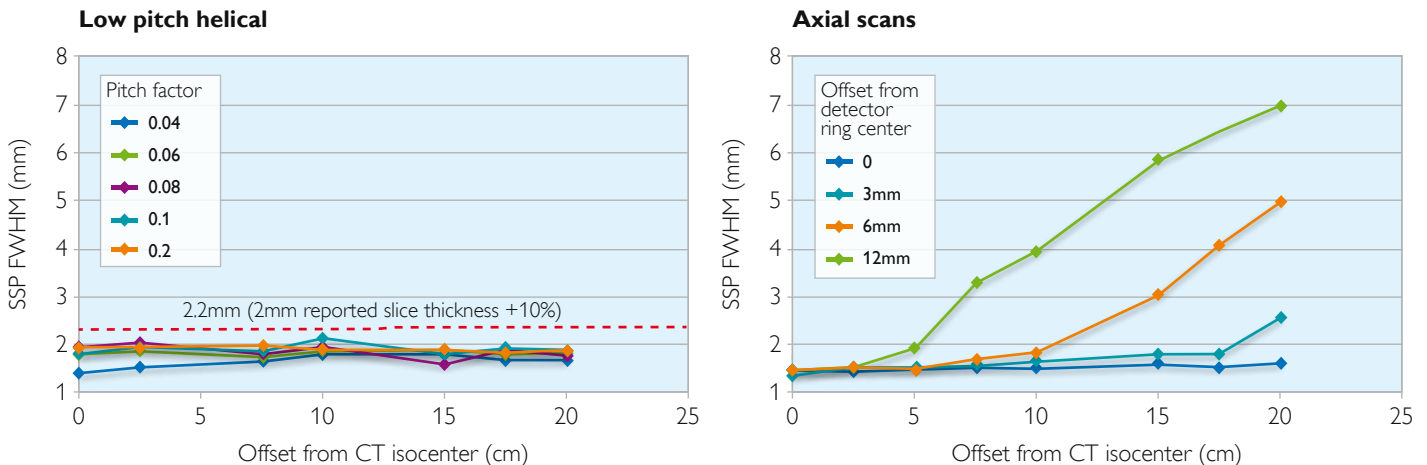


Axial 2D reconstruction. Helical cone beam reconstruction.

**Figure 8:** Non-divergent beam vs. divergent beam.

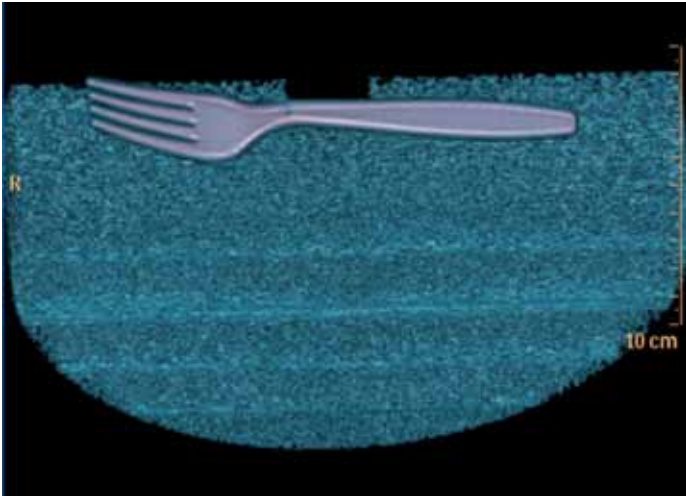
It should be noted that performing a low pitch helical acquisition does not per se ensure that beam divergence is being handled properly. The key point is that the reconstruction system performs the proper calculations to account for the fact that the beam is not parallel. When the binning process is combined with the divergent beam correction, it is very computational intensive for the reconstruction system.<sup>16</sup> This can have an impact on reconstruction time. With the advent of newer high performance ASIC's, there is no longer any need to compromise as evident with the RapidView 4D feature in the Brilliance CT Big Bore. A 10 phase reconstruction of typical 4D-CT (400mm extent) using COBRA can be completed in less than 4 minutes.

An ideal phantom that can illustrate the consequences of assuming that the divergent beam is parallel would be a plain mundane plastic fork. Several scans were performed using this type of fork. In all cases, the fork was stationary as the goal of these experiments was to verify the geometric accuracy of the scan protocol and



**Figure 7**





**Figure 9:** 3-D rendering of plastic fork placed atop of low density foam.

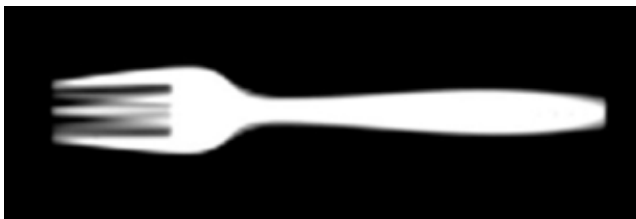
not to test temporal response. The fork was placed on top of low density foam with height of ~5cm. The fork was positioned laterally in the scan field so that the scan direction was perpendicular to the tines. Figure 9 is a 3-D volume render of a fork. This scan was performed with a pitch factor of 0.08 and reconstructed with a 0.25mm slice increment which optimizes 3-D image quality.

For the images below, axial scans were performed with the fork in the center of the FOV and at a 15cm offset from the center. A Coronal MIP of the volume was generated. Since the fork is surrounded by air or low density foam, this process projects the entire fork to a plane. The scan

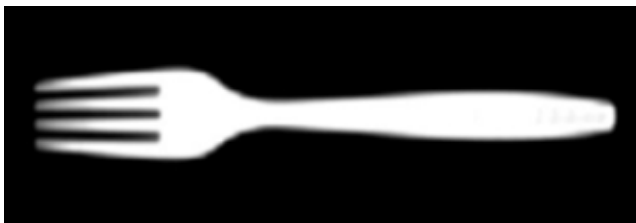
start position was set to be near the edge of the fork for Figure 10A and at the center of the fork tines in Figure 10B. The severe artifacts in the figures are caused by the axial reconstruction which did not correct for beam divergence. The location of the artifacts is near to the edge of the detector ring. Figure 10C is the same fork scanned at a 15cm offset from the center using a helical protocol with a pitch factor of 0.04. Since this is a helical scan, the reconstruction software can invoke COBRA and apply the proper corrections for beam divergence. The outstanding off-axis longitudinal resolution was one of the factors considered in choosing low pitch helical mode for the Brilliance CT Big Bore.



**A.** Axial acquisition.  
Centered within detector rings.



**B.** Axial acquisition.  
Fork center on edge of detector rings.



**C.** Low pitch helical.  
Helical scan, fork in any position.

**Figure 10:** Volume MIPs of plastic fork.

### Pitch factor/BPM dependency

One of the main challenges in 4D-CT is not acquisition speed but rather it's the ability of the scanner to capture sufficient data for the entire respiratory cycle. Respiratory frequency is typically between 10-20BPM. This is much slower than cardiac motion. When using a low pitch helical scan, it is imperative that the pitch factor be set low enough so that the entire scan volume is illuminated throughout the cycle. In the past, the pitch factor relationship was simply derived based on the illustration in Figure 11. The couch speed must be slow enough so that a voxel entering the detector area does not exit until one respiratory cycle or breathing period has been completed. The breathing period (BP) must be less than the transit time (TT).<sup>3</sup>

However, the above formula is not valid for the actual geometry of a MDCT (Multi-Detector CT). A more accurate depiction of the problem is in Figure 12. It should be obvious that the derived formula is only valid for voxels at the center of the FOV (purple circle) but not for voxels near the edge (red circle).

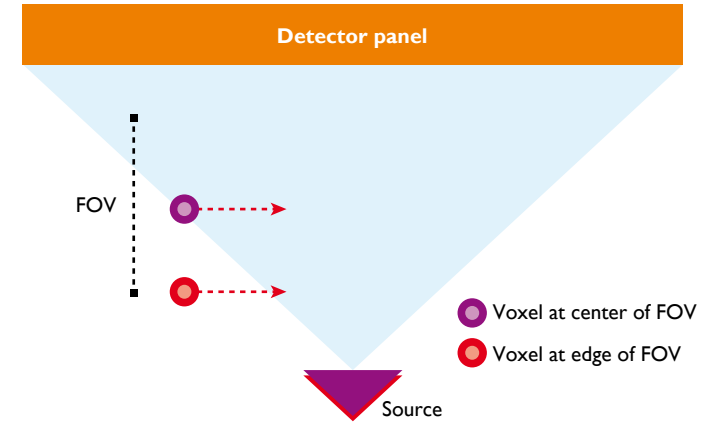


Figure 12: Scanner geometry for divergent beam.

To derive the adjustment factor needed for calculating the maximum PF consider the diagram in Figure 13.

Let,  $R_s$  = distance from x-ray source to CT isocenter.

$Z_{min}$  = longitudinal distance (Z-axis) of beam at edge of FOV.

COLL = detector collimation i.e. beam width at center of FOV.

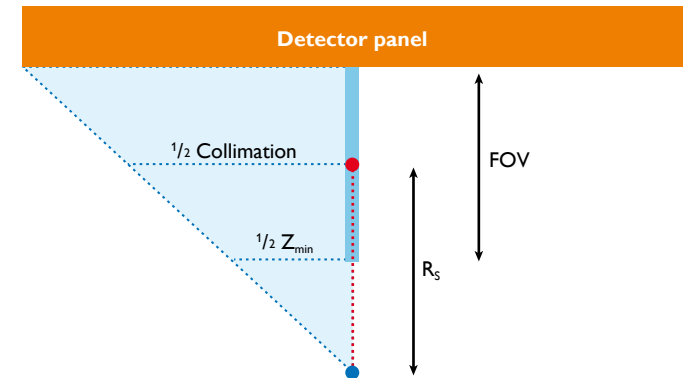


Figure 13: Interaction between FOV and source to isocenter distance.

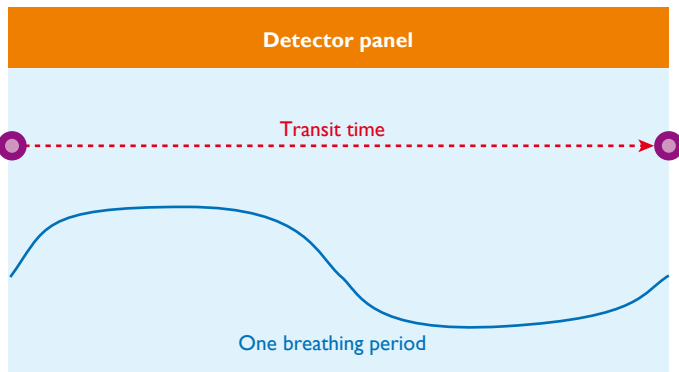


Figure 11: Scanner geometry for non-divergent beam.

The maximum PF (Pitch Factor) can be derived as follows:

NROT = number of rotations, RT = rotation time

$BP < TT$  and  $TT = NROT * RT$

$NROT = 1/PF$  by definition

$BP < RT/PF$  or  $PF < RT/BP$

In order to ensure that a voxel at the edge of FOV remains illuminated for at least one breathing cycle, the speed must be lower by a factor of  $\left(\frac{z_{min}}{COLL}\right)$ . By using similar triangles,

$$\frac{z_{min}}{COLL} = \frac{(R_s - FOV/2)}{R_s} = \left(1 - \frac{FOV}{2R_s}\right)$$

$$PF \leq \left(\frac{RT}{BP}\right) \times \left(1 - \frac{FOV}{2R_s}\right)$$

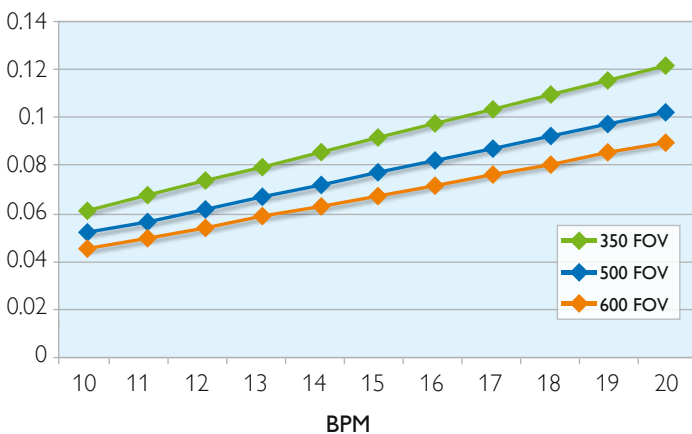
This equation introduces two additional variables that will impact PF, i.e.  $R_s$  and FOV.

The FOV referenced here is the reconstructed FOV not the scanned FOV. Which means if the user reconstructs using a smaller FOV, the PF utilized during the scan can be higher. A larger value for  $R_s$  will also permit a higher PF. Therefore, the larger  $R_s$  (X-ray to CT isocenter distance) on the Brilliance CT Big Bore is actually beneficial for performing 4D-CT. The standard 70cm bore scanner has  $R_s = 570\text{mm}$  vs. the Brilliance CT Big Bore  $R_s = 645\text{mm}$ .

Based on the above equation, we can plot the maximum PF for a given BPM. In Figure 14 below, there are three such plots for different FOV's. This graph assumes  $R_s = 645\text{mm}$  which is correct for the Brilliance CT Big Bore.

In practice, it is usually desirable to slightly exceed the PF limitations based on equation. The reconstruction software will compensate this equation by increasing the temporal window to include sufficient raw data that can produce a geometrically accurate image. This degradation to temporal resolution will be minimal.

**Maximum pitch vs. BPM**

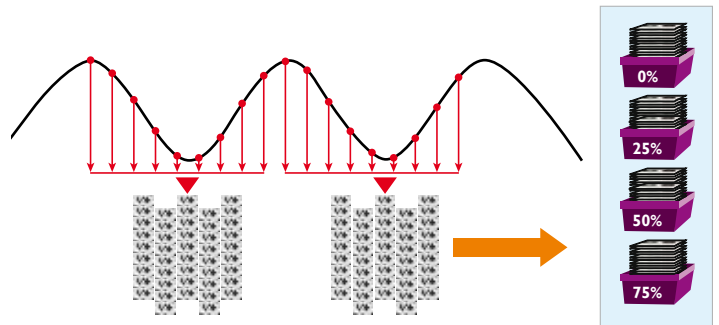


**Figure 14:** Maximum pitch factor based on FOV and breathing rate.

### Amplitude binning

In 4D-CT, binning is the process by which the reconstruction software selects which subset of sinogram data that will be processed to be included in the targeted phase volume. During the low pitch helical scan, spatially redundant data is acquired which is later binned based on the temporal phase of respiratory cycle at the time the data was collected. On an MDCT, multiple slices are being acquired at any point in time. These slices are binned together with other slices that were acquired at the same phase of the respiratory cycle as shown in Figure 15.

The default binning mode on the Brilliance CT Big Bore is referred to as linear phase binning. In this mode, the local maxima (or peak inhale points) of the waveform are identified and designated as the 0% phase. The temporal points of the other phases are determined by calculating the time differences between maxima and selecting the time points that correspond to the phase percentage. For example, 50% is half way between the maxima, 25% would be one quarter distance, etc. This methodology will function properly for a periodic breathing pattern. It is also accurate when breathing frequency varies but the inhale/exhale symmetry (shape) remains constant.

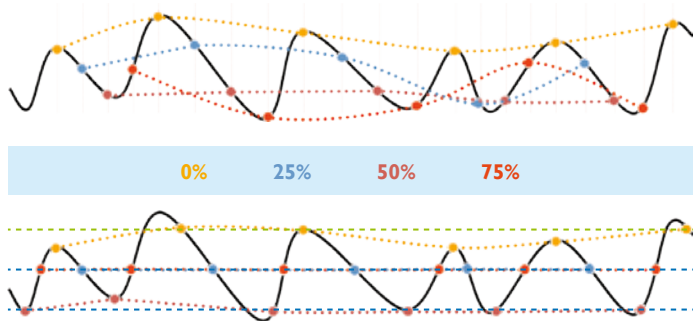


**Figure 15:** Illustration of multi-phase acquisition on multi-slice scanner.

Since the basis of 4D-CT is the assumption that internal movement is correlated with respiratory motion, it is intuitive that a change in the amplitude of the patient's breathing pattern e.g. a deeper inhale will impact the position of the internal anatomy. This has been demonstrated experimentally.<sup>7,8</sup> It is also known that internal motion tends to follow an elliptical path with the inhale and exhale trajectories being different. The phenomenon has been referred to as hysteresis.<sup>10</sup> Therefore, a binning process based purely on amplitude would not suffice. It is important to differentiate data collected during inhale vs. data from exhale.

The Brilliance CT Big Bore does provide another binning algorithm as alternative to phase binning. It is called amplitude binning which utilizes the amplitude of the waveform instead of just its phase during the binning process. This algorithm does account for the hysteresis effect by binning identical amplitudes of inhale (up-slope) and exhale (down-slope) separately. One breathing model that has been proposed<sup>6</sup> is that the position of any voxel of internal anatomy is a function of tidal volume and airflow. The amplitude of the breathing waveform corresponds to the relative tidal volume and airflow is proportional to the slope of the waveform. Amplitude binning on the Brilliance CT Big Bore does not consider the magnitude of the slope only the sign (positive/negative). By far, the major impact on the hysteresis is the direction of breathing. The actual velocity influence is minimal.

Below in Figure 16 is an example of an irregular breathing waveform. The top diagram shows the phase binning processing of this data. In this example, four bins are considered i.e. 0%, 25%, 50% and 75%. The horizontal lines represent equal fraction in time for each breathing cycle. Their spacing is proportional to the length of each breathing cycle. It is obvious that these phase bins will be reconstructed from data taken at widely different amplitude levels. For example, the 25% bin (blue line) is quite close in amplitude to the maximum inhale phase (0%) for the middle breath and is near in amplitude to the maximum exhale phase (50%) in the following breath.

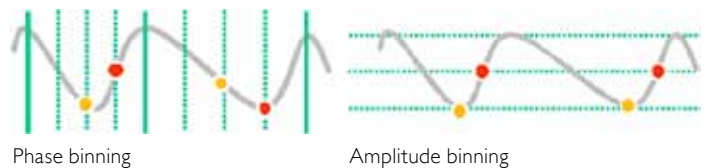


**Figure 16:** Comparison of phase and amplitude binning.

The second waveform in this graph is identical to the one above. The difference is in the placement of the binning points. In this case, amplitude binning is employed. Therefore, all points belonging to the same binning percentage are placed at or near to the same amplitude. For the 25% and 75% bins, the identical amplitude position can be achieved and they only differ in slope. At the extremes i.e. 0% and 50%, the identical amplitude position may not exist since the patient may have a shallow inhale/exhale for some breaths. The initial

step in amplitude binning is to identify the local maxima (peaks) and minima (valleys) points on the waveform. From these points, a 'clean' average peak and valley is determined. In this context 'clean' indicates that outlier points are excluded when calculating the average value. The algorithm will target the 0% and 50% bins to the average peak and valley points respectively. These limits are denoted by the green and blue dotted lines in Figure 16. Any points on the waveform that exceed these boundaries will not be utilized when reconstructing amplitude binned images. When selecting a binning point the algorithm will target the point closest in amplitude that corresponds to the selected percentage.

It is interesting to note, that even when there is no variation in the amplitude of the breathing, phase binning can still cause imaging anomalies. This may occur when the inhale/exhale 'symmetry' is modified. For example, consider the waveform in Figure 17. In this case, the inhale and exhale points do not exhibit any variation in amplitude. However, with phase based binning, it is obvious that the 50% (gold) and 75% (red) points are not aligned at the same amplitude. In Figure 17, the points are placed based on the amplitude binning algorithm and these binning points do correspond to the identical breathing amplitude.



**Figure 17:** Phase binning vs Amplitude binning.

The utilization of amplitude binning in clinical practice can have an impact on reducing artifacts for 4D-CT studies. In this section, several examples will be shown. The artifacts eliminated by the amplitude binning algorithm can be traced to irregularities in the breathing waveform.

Consider the coronal image in Figure 18. This is an image that was reconstructed at the 80% phase. There is an obvious artifact that 'shadows' the diaphragm. With amplitude binning in Figure 18, this artifact is not present. The cause of the artifact can be traced to the 80% points on the breathing waveform. With phase binning they do not correspond to the same amplitude. See Graph in Figure 18. In this example, there is almost no variation in the amplitude of the waveform. The artifact caused by phase binning is due to the change in the patient breathing pattern. The exhale is relatively longer in one of the breathing cycles.

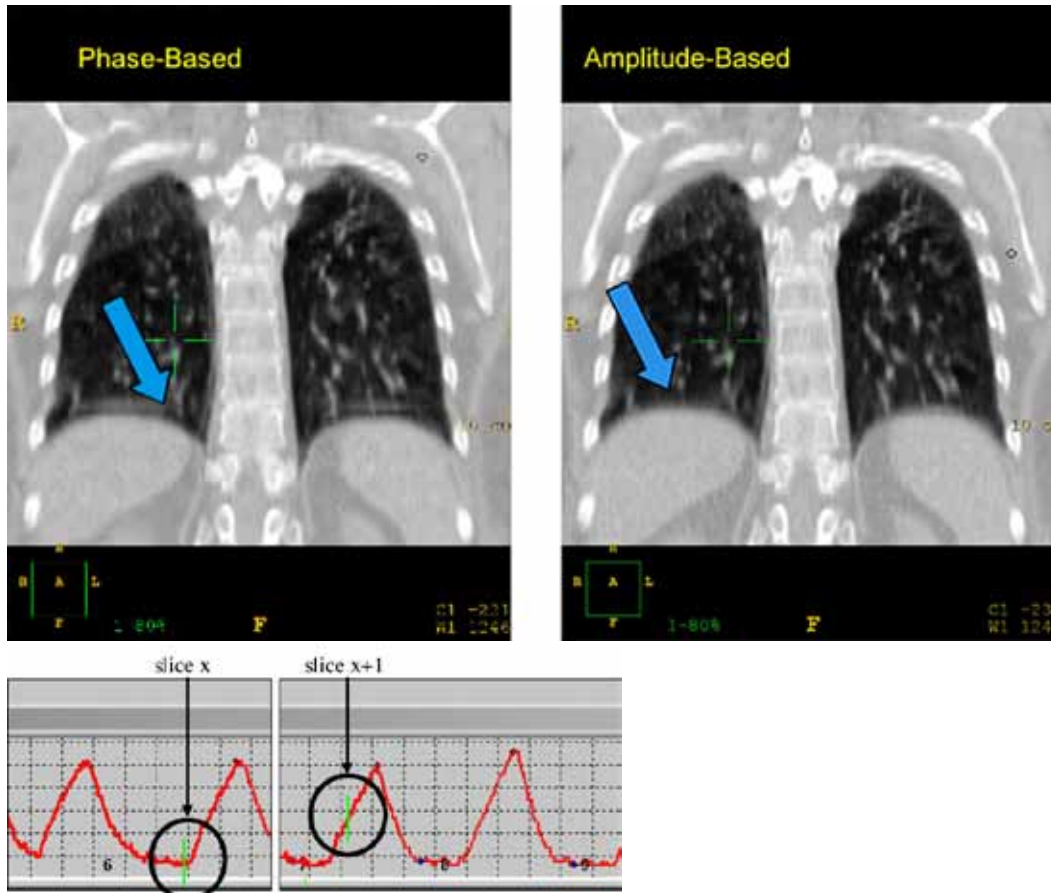


Figure 18: Respiratory wave form.

Amplitude variations most often occur near to the peak inhale points. However, there are instances when a patient may exhale with slightly more force and indeed this can also cause artifacts. Below in Figure 19 is an interesting phenomenon where the part of the rib cage appears to have entered the lung. When the data is reconstructed with amplitude binning, this

anomaly is rectified. (Figure 19). Also, note the slight protrusion of tissue that appears on the left side of the patient for the phase binned image. Upon examining the breathing trace, the obvious forced exhale can be observed and this correlates to the anatomical position of the artifact. With amplitude binning, this deviation in breathing pattern is discarded.

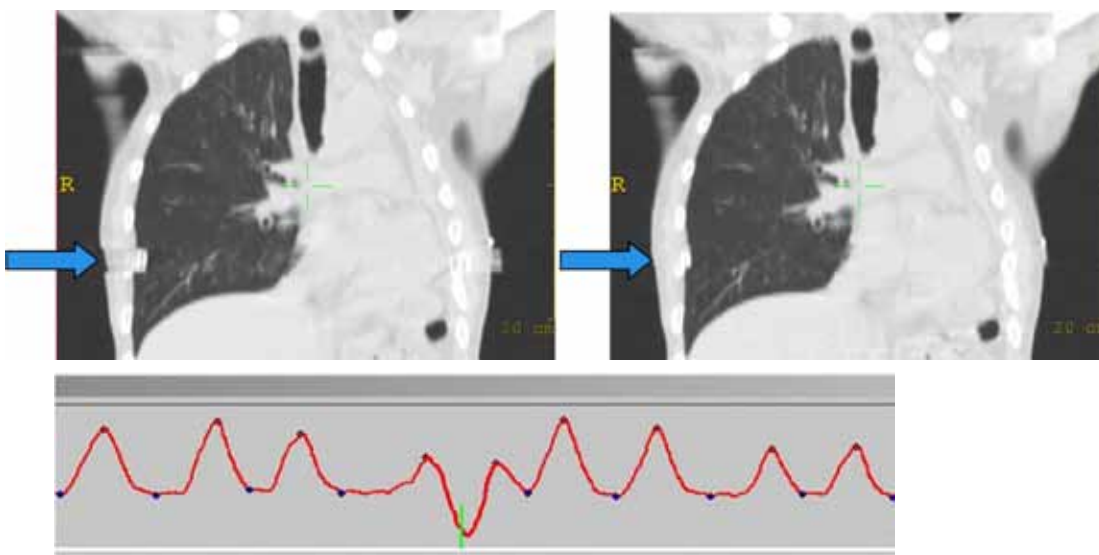
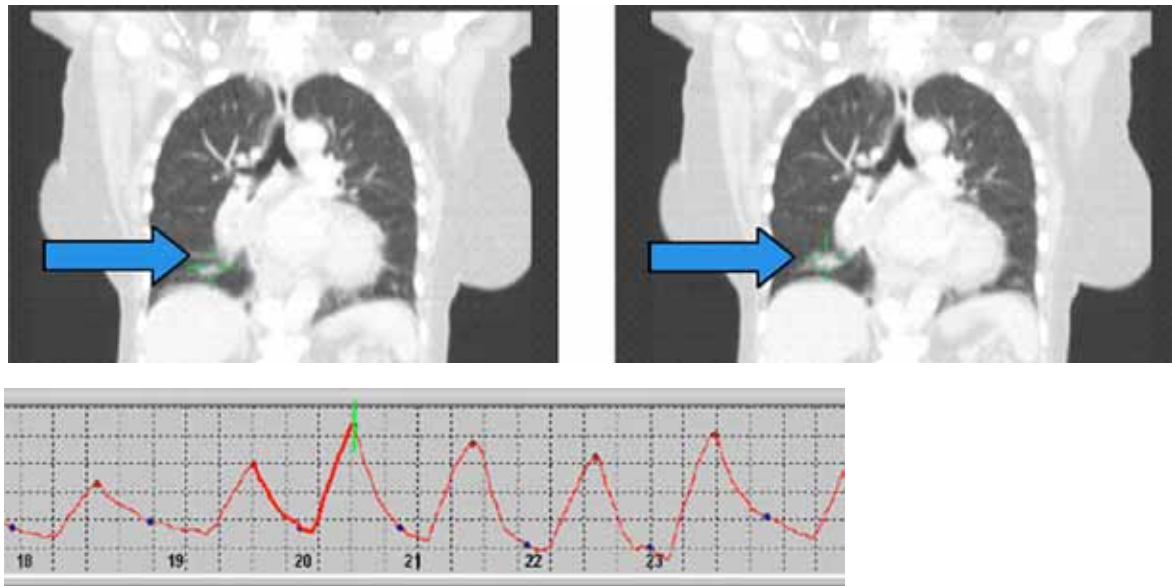


Figure 19: Exhale irregularity in respiratory signal.

A common source of artifacts is fluctuation in the inhale amplitude of the breathing trace. The example in Figure 20 is noteworthy because an amplified inhale caused an artifact in the tumor. The tumor tissue appears bifurcated in the CT image. With amplitude binning this incongruity is avoided. The variation in breathing can be observed in Figure 20 below.



**Figure 20:** Inhale irregularity in respiratory signal.

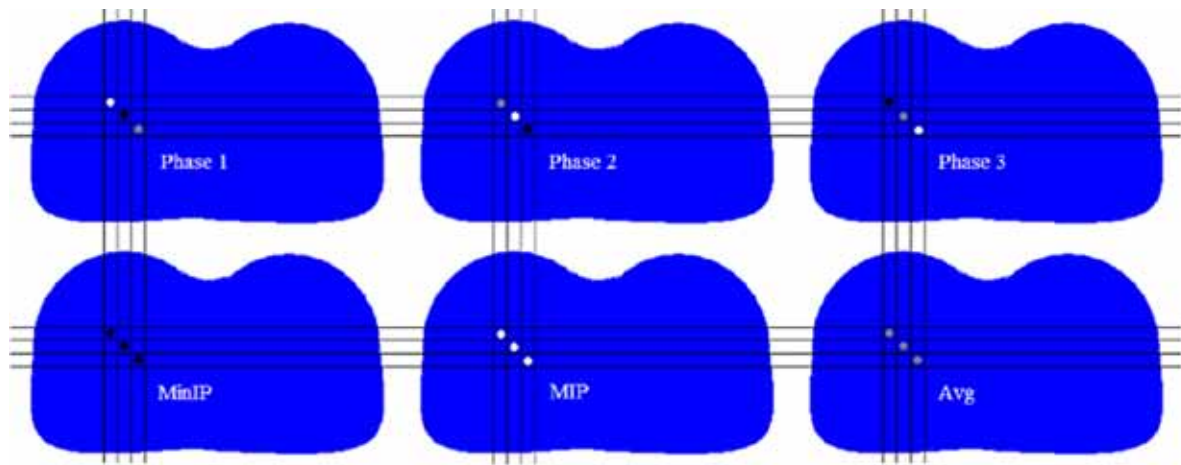
Users may still choose phase binning in some cases. Patients that only have minor irregularities in their breathing pattern may not benefit from amplitude binning. Since phase binning is the most commonly used method, many users may prefer this mode. Since amplitude binning will not reconstruct data outside the normal breathing range of the patient, there may be instances where clinicians may desire to view these anomalous images and therefore reconstruct using phase binning. Another example would be when there is a long pause in the exhale phase of the breathing cycle. This will cause artifacts for both amplitude and phase binned images. However, the phase binned images may have slightly less severe artifacts in these unique cases. On the Brilliance CT Big Bore, phase/amplitude binning is a reconstruction option and the user can select either one whenever the raw data is reconstructed.

#### 4D image processing tools

The Brilliance CT Big Bore is equipped with a plethora of visualization tools geared for 4D studies. There is a Pulmonary Viewer which allows the user to easily scroll through all the 4D phases. It includes a cine mode for any imaging plane e.g. axial, coronal, oblique etc. The user can simultaneously view the respiratory waveform and cross

reference the current cursor position to a time point on the waveform. In this fashion, the user can determine data acquisition point on the waveform for any pixel.

All of the aforementioned functionality also exists in the TumorLOC CT simulation software that is available on the Brilliance CT Big Bore. Additionally, TumorLOC provides the ability to easily view side-by-side images from different phases at any orthogonal plane. The user can easily traverse through the 4D phases using the arrow keys. Cine mode is also available for both DRR's and DCR's (Digitally Composited Radiograph). Contouring of organs or tumor on axial slices can be performed even while these slices are in a cine mode. This allows a user to concurrently edit a contour and observe its projection in the 4D phases in 'real time.' TumorLOC includes a feature that can synthesize a new dataset from the 4D-CT phase data volumes. There are methods offered: MIP (Maximum Intensity Projection), MinIP (Minimum Intensity Projection) and AVG (Average Projection). The MIP evaluates the voxels in the 4D phase and selects the voxels with the maximum CT number (HU) to be included in the new volume. MinIP is similar to MIP except the minimum CT number is used.



**Figure 21:** Image projection types.

The AVG calculates the average HU between each 4D phase volume and uses that value for the voxels in the new dataset. This created dataset can be archived to the disc and transmitted via the DICOM protocol. Figure 21 is an illustration of the MIP, MinIP, AVG processing three sample pixels from three 4D-CT phases. The MIP will select the maximum hence the brightest pixels, the MinIP the darkest pixels and AVG will just average the values.

The MIP volume is typically used for lung tumors which are usually hyperdense as compared to the surrounding lung parenchyma.<sup>18</sup> MinIP can be applied to some liver tumors since they are typically hypodense. The AVG dataset might be used to determine the location where the tumor is most often during the breathing cycle. That area should be brighter.

The MIP can be a very powerful workflow tool by providing a quick and easy estimate of tumor's internal target volume (ITV). Using TumorLOC, the clinician can then cine or scroll through the phases and 'touch-up' the tumor contour as needed. Used in this manner the MIP can significantly facilitate the tumor contouring process.

Another type of 4D-CT dataset available on the Brilliance CT Big Bore is the Untagged volume. This cannot be created in TumorLOC, rather it is a reconstruction feature. The untagged (or untagged) volume will utilize all of the sinogram data to reconstruct the data volume. There is no binning operation. This differs from the AVG dataset in two ways. The 'data averaging' is performed in sinogram space by backprojecting all of the raw data. Furthermore, the AVG volume is an average of the bins that were reconstructed and therefore based on the width and spacing of bins which may not include all of the data collected. Whereas, the untagged volume is always a true representation of the time averaged data that was acquired.

## Conclusions

The 4D-CT capabilities on the Brilliance CT Big bore were designed to provide superb temporal resolution, geometric accuracy, clinical flexibility and an integrated workflow.

Highlights include:

- The use of low pitch helical acquisition of 4D-CT can have benefits in flexibility and accuracy. A prime feature is the ability to perform a geometrically accurate cone beam reconstruction that accommodates beam divergence.
- With the advent of faster hardware, it is not necessary to compromise the accuracy of cone beam reconstruction for the sake of processing speed.
- The availability of pitch factors down to 0.04 is imperative for scanning patients with breathing rates close to 10BPM.
- The Brilliance CT Big Bore includes many features that can facilitate workflow. The tools or features required to generate and analyze 4D-CT studies are resident on the CT console.
- The bellows on the Brilliance CT Big Bore provides an integrated respiratory device which simplifies the 4D-CT scanning procedure. There is no need to setup and interact with another computer system. The tools or features necessary are on the console. The placement of the device itself on the patient is simple and its footprint in the CT room is minimal.
- The Brilliance CT Big Bore offers the option of three different acquisition modes for respiratory CT. There is retrospective helical for a full acquisition of all the breathing phases, prospective axial for acquiring a single phase in a trigger mode and prospective spiral for a breathhold scan that will include monitoring of the patient's breathing.
- The Brilliance CT Big Bore directly supports two respiratory devices i.e. RPM and bellows. The user can easily switch between these devices. With either system, the user can perform phase binning or amplitude binning. Since binning is a reconstruction option, the same scan can be reconstructed using both methods of binning.

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