PHASE-CORRELATED DYNAMIC CT

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ABSTRACT

Phase-correlated CT is the measurement of an organ that exhibits quasi-periodic motion. Dedicated image reconstruction algorithms utilize only those data ranges that have been acquired within the desired motion phase and achieve to produce motion free image data. Dynamic CT means covering an organ of interest multiple times to monitor the concentration of contrast agents over the time. Thus information about blood flow or perfusion is obtained. Phase-correlated dynamic CT is the combination of both methods. However it requires to simultaneously measure complete organs during a duration that covers several motion cycles. Although this is far from optimal with today's CT technology we have performed dynamic CT scans of the heart with a 4-slice scanner [1]. In this paper we discuss the application and reconstruction algorithms under the assumption that true cone-beam medical CT scanners with 64 slices or more (as they have been announced for 2004) are available.

1. INTRODUCTION

Scanning objects in motion has been of high interest for a long time. Especially the human heart exhibits difficult motion patterns and high motion frequencies. Early efforts at prospective ECG–gated data aquisition showed limited success and were not continued [2, 3]. Electron–beam tomography with scan times down to 50 ms appeared to be the only approach to be reliable [4]. Due to the high costs and low image quality it never became a wide spread modality. Another attempt to freeze motion and to improve dynamic CT scanning was the introduction of the so–called dynamic spatial reconstructor which comprised 14 X–ray tubes with intensifier screens opposite to them rotating around the patient simultaneously [5]. Its bulky, expensive and error–prone design led to the nick name "Mayo monster" and it remained the only prototype built.

With the introduction of spiral CT a promising new technology became available [6] (see figure 1). Soon first trials of quantification of calcium with 1 s rotation time spiral CT were reported, however without modifying the reconstruction algorithm [7]. Others attempted the retrospective selection of images of a suitable heart phase [8].

Whereas these approaches still were limited in image quality the introduction of phase–correlated spiral CT — it consists of synchronization and phase selection as illustrated in figures 2 and 3 — with dedicated image reconstruction algorithms immediately showed highly promising results [9]. Soon the approaches were

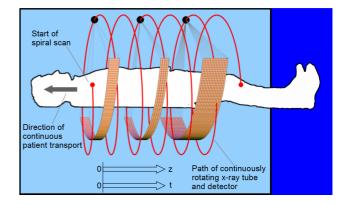


Fig. 1. Spiral CT scanning principle illustrated for single-, fourand 16-slice CT scanners.

generalized to 4–slice spiral CT, to 16 slices and even up to 256 slices [10, 11, 12, 13]. The major CT manufacturers started to implement their own variants of the original algorithms [14, 15, 16, 17, 18] and soon every standard CT scanner became available with a cardiac option [19].

The assessment of cardiac perfusion can be achieved by combining phase–correlated with dynamic CT. A circular trajectory is used to continuously cover a region of the heart. The scan duration and thereby the number of rotations necessary are determined by the speed of the contrast bolus and by the amount of information required to derive functional parameters such as the maximal enhancement, the time to peak enhancement or cardiac perfusion.

2. PHASE-SELECTIVE RECONSTRUCTION

Phase–correlated CT imaging assumes quasi–periodic motion. This means that object motion can be divided into motion cycles and repeats after a cycle is finished. The length of one motion cycle, i.e. the rate of motion (such as the heart rate, for example) can vary from cycle to cycle. The assumption of periodicity is necessary as long as it is necessary to combine data from several cycles to image the complete object. A consistent combination of these data is possible under the assumption of quasi–periodicity. Today, the synchronization information used in clinical CT is either ECG–based [9] or kymogram–based [20, 21].

Let t_n denote the instance at which the *n*-th motion cycle starts and let ϑ_n be the view angle corresponding to t_n . We will refer to the t_n and ϑ_n as the primary synchronization peaks of the object motion. Typically, the instance desired for reconstruction

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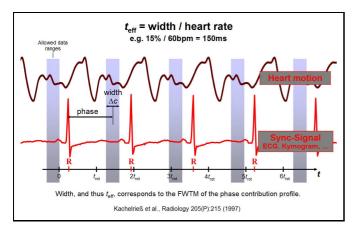


Fig. 2. Synchronization with the motion phase. Only allowed data ranges are to be used for reconstruction. Time *t* is linearly related to the *z*-position and to the view angle ϑ .

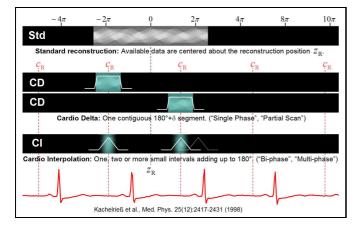


Fig. 3. Phase selection mechanism. The weight functions shown are examples of a wide variety of cardiac weights in use today.

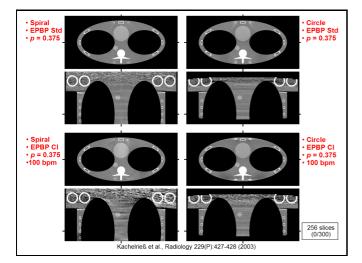


Fig. 4. EPBP reconstruction of spiral and circular 256–slice scans of a simulated thorax phantom with standard and phase–correlated reconstruction.

is specified relative to the sync points. We therefore use the relative reconstruction phase $c_{\rm R}$. It gives the location relative to two adjacent primary sync peaks as follows

$$\hat{\vartheta}_n = \vartheta_n + c_{\mathbf{R}}(\vartheta_{n+1} - \vartheta_n).$$

Although $0 \leq c_{\mathbb{R}} < 1$ seems natural one may use any $c_{\mathbb{R}} \in \mathbb{R}$. Alternatively, absolute triggering is in use. It requires to specify a temporal offset Δt or $\Delta \vartheta$ to define $\hat{\vartheta}_n = \vartheta_n + \Delta \vartheta$.

The so-obtained instances $\hat{\vartheta}_n$ are called the secondary sync peaks. Ideally, reconstruction would only use those data acquired at the projections $\hat{\vartheta}_n$. However, CT image reconstruction requires data intervals that make up a 180° range. Therefore, data ranges have to be attached to the secondary sync peaks in an adequate manner. These so-called allowed data ranges must be sufficiently large to allow to achieve 180° completeness by combining one or more such intervals.

The contribution of the acquired data to the reconstructed image discussed so far can be best modelled using a cardiac weight function $w_{\rm C}(\vartheta)$ which is responsible for phase selection. The weight function is zero everywhere in the forbidden data ranges. One further defines the view range weight function $w_{\rm V}(\vartheta)$ that is positive for those views that measure a given voxel or a desired slice and is zero elsewhere. We will use the view weight below as the temporal window used for dynamic imaging. Usually, the support of the viewing window covers the support of the phase weight function. The compound weight $w(\vartheta) = w_{\rm C}(\vartheta)w_{\rm V}(\vartheta)$ is then used for projection weighting. One defines the 180°–normalized weight

$$\hat{w}(\vartheta) = \frac{w(\vartheta)}{\sum_k w(\vartheta + k\pi)}$$

Proper normalization of \hat{w} can be seen from the following identities:

$$\sum_{k} \hat{w}(\vartheta + k\pi) = 1 \quad \text{and} \quad \int d\vartheta \, \hat{w}(\vartheta) = \pi.$$

Standard image reconstruction, which is not phase–correlated, results when $w_{\rm C}(\vartheta)$ is set to 1 for all ϑ .

A popular phase–weighting technique that avoids transition problems inherent to single–phase or partial scan methods and that promises a high temporal resolution is the cardio interpolation (CI) which is also known as *N*–segment reconstruction. The idea is to use all data within $w_V(\vartheta)$ and to simultaneously adjust the size of all allowed data intervals such that the 180° condition is just met. In general, each interval will be significantly smaller than 180° and only the combination of the intervals fulfills the completeness condition.

3. DYNAMIC CT

Assume information about the object f to be available over several instances in time. Then f = f(x, y, z, t), that can be thought of being a series of images or volumes, can be used for functional assessment. In dynamic CT one aims at detecting an identifier's time-density curve. This information is obtained by repeated scanning of an organ of interest to observe constrast medium kinetics.

Let $\mu_0(t)$ be the reference attenuation measured anywhere in the central blood pool, e.g. in the ventricle, and let $\mu_1(x, y, z, t)$ be the tissue attenuation curve as a function of time which is also known as the tissue time-density curve. The reference curve can

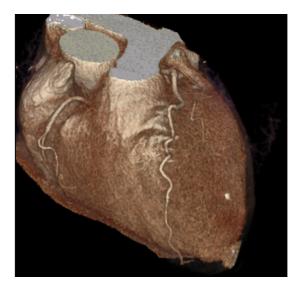


Fig. 5. State–of–the–(he)art image reconstruction. Spiral 16–slice data acquired with 0.375 s rotation time. Data courtesy by Dieter Ropers, Erlangen, Germany.

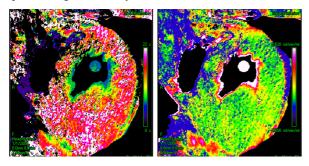


Fig. 6. 4D functional data of the heart [1]. Time to peak enhancement image (left) and perfusion image (right). Color scale in s, and mL/min/mL, respectively.

be obtained by placing an ROI over a vessel carrying contrast media, e.g. at an arteria. μ_0 then describes the flow of contrast media into an organ of interest.

For the measurement of myocardial perfustion, which is one example of what we are interested in phase–correlated dynamic CT, the basic relation states that the flow per volume is proportional to the height of the tissue time–density curve over the area of the reference time–density curve, i.e. proportional to

$$\max_{t} \left| \mu_1(x, y, z, t) - \mu_1(x, y, z, -\infty) \right| \Big/ \int dt \, \mu_0(t)$$

Other parameters, such as the cardiac perfusion, the maximum enhancement (which actually is the numerator of the equation above), time to maximum enhancement and many more can be extracted from the information available. For a thorough review on dynamic CT the reader is referred to reference [22].

4. COMBINING PHASE–SELECTIVITY WITH DYNAMIC CT

To perform dynamic CT studies of an object in motion one can combine the techniques of phase–correlation and dynamic scanning. Basically, this can be achieved by performing circle rather than spiral scans of the heart. Similar to the spiral scan the circle scan must deliver highly redundant data that allows to freely select the motion phase of interest. Consequently, the phase–correlated circle scan must consist of more than one 360° rotation. Quantitatively, at least one heart cycle must be covered during the scan. If $f_{\rm H}$ denotes the heart rate and $t_{\rm rot}$ the rotation time of the scanner, then at least $1/f_{\rm H}t_{\rm rot}$ rotations must be performed for the circle to get phase–correlated information. In general, however, the number of rotations will rather be dominated by the speed of the contrast bolus and by the cardiac perfusion itself (e.g. by the time to the maximum enhancement) than being dominated by the heart rate: it will require several heart cycles until the desired parameters can be measured.

For such a measurement one obtains dynamic information by restricting the view range weight function $w_V(\vartheta)$ to a length of about one to three heart cycles — just enough to perform phase–correlation — and performs several reconstructions with that window sliding over the complete scan time. Under the assumption that the contrast dynamics are much slower than the cardiac motion one thus obtains a five dimensional data set: three spatial dimensions, one dimension for the heart's motion phase c and the temporal dimension showing changes due to the dynamics of the contrast agent. The resulting data are f(x, y, z, c, t).

A modified version of our multi–slice cardio interpolation algorithm 180°MCI and our new cone-beam reconstruction algorithm EPBP are capable of performing such dynamic phase–correlated reconstructions [1, 13].

5. RESULTS

Phase–correlated wide cone angle cone–beam image reconstruction is demonstrated in figure 4. Here, a 256–slice scanner with 0.75 mm slice thickness was simulated. This collimation covers more than 15 cm of the *z*–axis and is therefore sufficient to perform a dynamic study of the heart. For comparison purposes figure 4 also shows the images obtained from a spiral trajectory of the same pitch. Obviously, high image quality can be achieved in all cases, for the spiral and for the circular trajectory as well as for the standard and as for the phase–correlated reconstruction (a synchronization signal corresponding to a heart rate of 100 min⁻¹ was simulated).

The high image quality that is routinely achievable with today's 16–slice scanners (figure 5) is promising with respect to future dynamic CT applications of the heart. Scanners of the next generations will produce similar images in the circular scan mode and allow for precise dynamic studies.

Figure 6 shows an early example of phase–correlated dynamic cardiac CT of a radiotherapy patient. A modified patient table that allows to rotate the patient about the vertical axis by about 20° was used to align the direct imaging planes to anatomical relevant axes. 80 mL of Ultravist 370 contrast agent were injected with a flow rate of 8 mL/s. The data were acquired with a Siemens Sensation 4 scanner collimated to 4×5 mm. Tube settings were 120 kV and 300 mA. A rotation time of 0.5 s was used while the total scan time was 30 s. Image reconstruction was performed with the modified 180°MCI algorithm at the four distinct *z*–positions -7.5, -2.5, 2.5 and 7.5 mm. The color coded images show the time to peak enhancement and the cardiac perfusion of the z = 5 mm slice at 70% of R–R.

6. DISCUSSION

Dynamic studies of periodically moving objects such as the assessment of regional myocardial perfusion with MSCT scanners, for example, are possible with high spatial in–plane resolution. However, to cover complete anatomical regions with high *z*–resolution scanners with far more slices than available today are required. Image reconstruction algorithms capable of handling phase–correlated dynamic tasks with next generation scanners are readily available and promise high image quality (c.f. figure 4).

Future investigations may include the assessment of exact accuracy and reproducibility values in larger patient groups and the comparison to other techniques. Beam hardening artifacts must be reduced to further increase accuracy. Professional amendments (patient table, data acquisition) to the CT-scanners by the manufacturers are necessary to allow more accurate and convenient cardiac perfusion studies in clinical settings.

Phase–correlated dynamic CT of the heart is likely to become particularly attractive with future CT scanner generations that allow to cover complete anatomical regions with one circular scan.

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