

Communications

Efficient Computation of Amplitude and Phase Maps in Nuclear Medicine Equilibrium-Gated Cardiac Studies

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Abstract—The Goertzel algorithm is proposed as a method to obtain the first harmonic coefficient of time activity curves from equilibrium gated cardiac studies. The coefficients are used to produce functional images. The algorithm achieves an important reduction in the number of operations and memory accesses needed to compute the coefficients.

Index Terms— Cardiovascular system, discrete Fourier transforms, discrete time filters, functional analysis, nuclear cardiography, nuclear imaging.

I. INTRODUCTION

Equilibrium-gated blood pool imaging of the heart is used to visualize and quantify cardiac function [1]. Quantification of global ventricular function is usually based on the determination of a time-activity curve (TAC) over the left ventricle, from which parameters such as ejection fraction, stroke volume, and filling rate can be obtained [2]. The complexity of the cardiac cycle can be presented in a more comprehensive way with functional images: images where each pixel represents the parameter of interest obtained after Fourier analysis of every individual TAC [3]. The main parameters are the amplitude and phase of the first harmonic, from which three functional images are generated: the amplitude and phase maps, and the phase histogram.

- 1) The amplitude image shows the change of activity in each pixel, without regard to the timing of these variations within the cardiac cycle. It is useful to show abnormalities of the wall movement [4].
- 2) The phase image represents approximately the relative variations in the timing of the movement of the heart regions. Delays of the blood circulation in different parts of the heart can be easily seen. This image may be used to detect delays in contraction and shows areas working asynchronously [5].
- 3) The phase histogram has two peaks in a healthy heart: the higher one arises from the activity of the ventricles; the smaller one from the atria. Between the two peaks exists a difference of approximately 180°. The width of each peak shows the synchronization of the contractions.

The computation of the first harmonic coefficient of every pixel's TAC requires a number of operations, proportional to the number of time samples. The number of images per cardiac cycle is a compromise between temporal resolution and acquisition time: as the signal-to-noise ratio (SNR) depends on the Poisson statistics of

Manuscript received December 19, 1995; revised September 5, 1996.
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Publisher Item Identifier S 0018-9294(97)01474-2.

the nuclear data acquisition for a given time, increasing the number of images per cardiac cycle means reducing the number of counts per image and the SNR accordingly. A typical study has between 16 and 32 (64×64 pixels) images per cycle; this represents a good compromise between spatial resolution and acquisition time. Then, 4096 TAC's have to be analyzed.

In this Communication we present an efficient method to estimate the first TAC Fourier coefficient. Several methods are available to compute the fast Fourier transform (FFT) when a limited number of coefficients are needed [6], but they are efficient only for a large number of time points. Here, however, we need to compute many FFT's with a few time points at the input; then, the reduction in the number of operations provided by fast algorithms is not significant, and simpler algorithms can be more efficient, as will be shown.

II. METHOD

Using a commercial gamma camera, images are acquired synchronously with the R wave and stored in the LIST mode (in this mode, acquisition coordinate pairs x and y for each scintillation are stored together with a time reference in a list format [7], [8]). After cine-sequence reconstruction, a TAC is obtained for every pixel. To minimize the quantization noise, and due to the finite number of points obtained (one from each image) in typical studies, temporal interpolation or smoothing is needed for good representation of the TAC's. From the different interpolation methods available, cubic spline interpolation is chosen due to its global smoothness, that produces a function continuous up to its second derivative. The smoothing step is needed only to display the TAC's prior to computation of the functional images, since the coefficients themselves generate the smoothest version of the TAC's.

The amplitude and phase of the first harmonic is the first Fourier coefficient of each raw TAC, and can be obtained by different methods: directly from the discrete Fourier transform (DFT) formula

$$X(k) = \sum_{n=0}^{N-1} x(n)W_N^{kn} \quad (1)$$

where $W_N = e^{-j2\pi/N}$, or with any algorithm that computes the FFT. We propose to use the Goertzel algorithm because it has several advantages, as will be shown.

Once the coefficients have been calculated, the amplitude and phase maps can be produced. The generation of the amplitude map is straightforward, but for the phase maps two observations can be made.

- 1) Points with negligible amplitude should not be represented in the phase map as these points are usually static (extracardiac) structures. A mask that includes the points with amplitude less than 10% of the maximum value in the image can be used to skip such points.
- 2) The phase image should preserve the periodic nature of the phase values, thus, a cyclic color scale has to be used. There should be also the possibility to shift this scale when the boundary between two colors is near a peak in the phase histogram: a more meaningful representation can be obtained if similar values are represented in the same color.

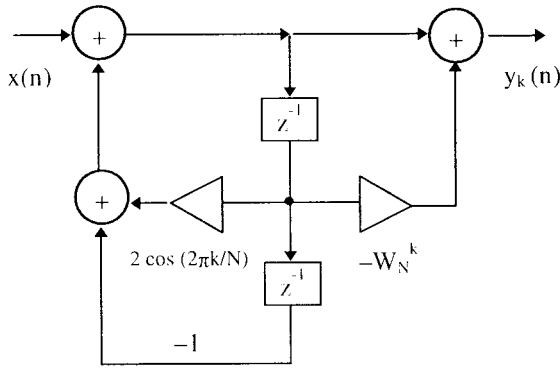


Fig. 1. Implementation of the Goertzel algorithm as a linear filter.

A. The Goertzel Algorithm

The Goertzel algorithm is an efficient way to compute a reduced number of DFT values [9]. It can be implemented as a linear filtering operation with only two complex coefficients. To derive it, (1) can be expressed as

$$X(k) = \sum_{n=0}^{N-1} x(n) W_N^{-k(N-n)} \quad (2)$$

where the second term has been multiplied by W_N^{-kN} (which is always equal to one). Equation (2) can also be seen as the N th value of convolution of the N samples of $x(n)$ with a filter that has the impulse response

$$h_k(n) = W_N^{-kn} u(n). \quad (3)$$

Then $X(k)$ is simply the output of this filter at time N , when its input is $x(n)$

$$X(k) = x(n) \otimes h_k(n)|_{n=N}. \quad (4)$$

Thus, to compute the DFT parameters, a filter could be implemented with the system function expressed as

$$H_k(z) = \frac{1}{1 - W_N^{-k} z^{-1}} = \frac{1 - W_N^k z^{-1}}{1 - 2 \cos(2\pi k/N) z^{-1} + z^{-2}}. \quad (5)$$

The direct form implementation of the filter is shown in Fig. 1. As can be seen, only one real coefficient and one complex coefficient are needed. As just the N th value of the output is needed, the forward branch of the filter has to be computed only at time N .

III. RESULTS

Tables I–III show the number of real operations (noncomplex multiplications or additions) needed to compute the DFT coefficients from a noncomplex input signal. The split-radix algorithm [10] is the best among nine different ways to compute the DFT [11]. Except for the FFT algorithm, the tables reflect the number of operations performed on the computation of a single (complex) coefficient (as needed in this application to produce the amplitude and phase maps). The split-radix algorithm produces the N FFT coefficients, and thus in this case the figures given are the number of operations needed to compute the N coefficients. Table I shows the number of nontrivial real multiplications (multiplications by 1, -1 , j , and $-j$ are excluded). Table II shows the number of real additions.

Table III shows one of the main advantages of the Goertzel algorithm: it needs just one real and one complex coefficient while the computation of the DFT needs N complex coefficients (this table excludes again the *trivial* coefficients).

TABLE I
NUMBER OF NONTRIVIAL REAL MULTIPLICATIONS FOR
DIFFERENT ALGORITHMS (N/A : NOT APPLICABLE)

N	Split-radix FFT	DFT (per coef.)	Goertzel (per coef.)
16	10	24	14
24	N/A	40	22
32	34	56	30

TABLE II
NUMBER OF REAL ADDITIONS FOR DIFFERENT ALGORITHMS

N	Split-radix FFT	DFT (per coef.)	Goertzel (per coef.)
16	60	30	32
24	N/A	46	48
32	164	62	64

TABLE III
NUMBER OF REAL COEFFICIENTS NEEDED FOR EACH ALGORITHM

N	DFT	Goertzel (per coef.)
16	24	3
24	40	3
32	56	3

IV. DISCUSSION AND CONCLUSIONS

From the previous tables, it can be seen that the Goertzel algorithm is an efficient way to compute the amplitude and phase maps. Time savings are 34% with a 486 central processing unit (CPU), and go up to 40% with a Pentium. When these savings are applied to the computation of the individual time-activity curves (4096 for 64×64 pixels images; 16384 for 128×128 images), the reduction in the number of operations becomes significant. For example, for a sequence with 24 images (64×64 pixels), the direct DFT method needs 163840 real-number multiplications while with the Goertzel algorithm this figure is reduced to 90112. This reduction of CPU cycles together with the reduction of memory access allows implementation of functional image analysis on smaller computers with reasonable execution times. The Goertzel algorithm has the additional advantage of being efficient for any N (time points), while FFT-based methods lose efficiency when N is not an integral power of two.

In a practical clinical case, we have measured that our algorithm takes 3 s for a 32-image sequence, 128×128 pixels per image, on a Sun 4/370 system, while the same process in our standard equipment used in clinical routine needs between 15 and 30 s, depending on the CPU used. In both cases, the coefficients obtained are exactly the same.

The proposed method will be more useful with functional maps obtained from magnetic resonance images. In that case, the number of individual TAC's will be in the order of 256×256 , and hence the reduction in the number of operations will be very significant.

REFERENCES

- [1] C. Schiepers and J. J. Almasi, "Equilibrium gated blood pool imaging at rest and during exercise," in *Effective Use of Computers in Nuclear Medicine*, M. J. Gelfand, S. R. Thomas, Eds. New York: McGraw-Hill, 1988.
- [2] S. Bacharach and M. Green, "Data processing in nuclear cardiology: measurement of ventricular function," *IEEE Trans. Nucl. Sci.*, vol. 29, no. 4, pp. 1343–1354, Aug. 1982.

- [3] S. Bacharach, M. Green, D. Vitale, G. White, M. Douglas, R. Bonow, and S. Larson, "Optimum Fourier filtering of cardiac data: A minimum-error method," *J. Nucl. Med.*, vol. 24, pp. 1176–1184, 1983.
- [4] J. Candell and D. Ortega, *Cardiologia Nuclear*. Barcelona, Spain: Ediciones Doyma, 1992.
- [5] M. Green and S. Bacharach, "Functional imaging of the heart: Methods, limitations and examples from gated blood pool scintigraph," *Progress Cardiovasc. Diseases*, vol. 28, no. 5, pp. 319–348, Mar/Apr. 1986.
- [6] H. Sorensen and S. Burrus, "Efficient computation of the DFT with only a subset of input or output points," *IEEE Trans. Signal Processing*, vol. 41, no. 3, pp. 1184–1200, Mar. 1993.
- [7] S. Bacharach, M. Green, and J. Borer, "Instrumentation and data processing in cardiovascular nuclear medicine: Evaluation of ventricular function," *Seminars in Nucl. Med.*, vol. 9, no. 4, pp. 257–274, Oct. 1979.
- [8] J. Lear and J. Pratt, "Real-time list-mode processing of gated cardiac blood pool examinations with forward-backward framing," *Eur. J. Nucl. Med.*, vol. 19, pp. 177–180, 1992.
- [9] J. Proakis and D. Manolakis, *Digital Signal Processing: Principles, Algorithms and Applications*. New York: Macmillan, 1992.
- [10] P. Duhamel, "Implementation of 'Split-Radix' FFT algorithms for complex, real, and real-symmetric data," *IEEE Trans. Acoust., Speech, Signal Processing*, vol. ASSP-34, no. 2, pp. 285–295, Apr. 1986.
- [11] H. Sorensen, D. Jones, M. Heideman, and S. Burrus, "Real-valued fast Fourier transform algorithms," *IEEE Trans. Acoust., Speech, Signal Processing*, vol. ASSP-35, no. 6, pp. 849–863, June 1987.

Estimation of Slowly Changing Components of Physiological Signals

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Abstract—A method for the estimation of slowly changing components of physiological signals is presented in this communication. The method is based on a sequential approximation of slowly changing components by a low-order polynomial function. The polynomial coefficients are obtained by minimizing the distance between the expected zero crossing density (ZCD) value of the fast components of the physiological signal and the estimated ZCD value of these components. The method has been tested and preliminary results were satisfactory.

Index Terms—Baseline, drift, ECG.

I. INTRODUCTION

The estimation of the slowly changing components of physiological signals is of both theoretical and practical importance. In biomedical signal processing, these components can be associated with trend signals in monitoring systems [1], baseline wander in electrocardiogram (ECG) signals [2]–[5], [12], [13], electrode drift [8], [11], [13], and other signals [6], herein referred to as underlying signals. These signals can generally be described as any component that can be represented as a slow and consistent monotonic change; however, the change does not necessarily have to be slow [1], [13]. A physiological signal can be defined as the combination of the underlying signal, the fast components of a physiological signal,

Manuscript received February 2, 1995; revised September 30, 1996. Asterisk indicates corresponding author.

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Publisher Item Identifier S 0018-9294(97)01475-4.

and additive noise that can include artifacts, transients, and other anomalies. Relative to the underlying signal, the fast components and the noise can be distributed asymmetrically (asymmetric density function); for example, relative to baseline, the ECG signal and the noise are generally distributed asymmetrically. Standard methods of underlying signal estimation usually concentrate on linear filtering methods [1], [3], however these distort the low-frequency components of a physiological signal [2], [3], [12]. One reason for using nonlinear methods is that these methods have been shown to be effective and robust [2], [4], [5], [12]. Sequential modeling by polynomial functions [2], [12] are preferred for estimating the underlying signals, but, for asymmetrically distributed fast components and noise, an estimation based on well-known criteria such as least square error (LSE) or least absolute deviation (LAD) can bias the estimation of polynomial coefficients. The bias is derived from incompatibility between criteria (estimation based on LSE or LAD is optimal for signals with symmetric density function) and the fast components and noise conditions (asymmetric density function) [7], [9]. Biased estimation can be effectively solved by using only selective data points with methods such as those described by Meyer and Kaiser [2], which were developed to remove baseline wander in ECG signals using only the points (knots) on P–R segments (isoelectrical levels) and baseline approximation by cubic spline interpolation between the knots. The block scheme, shown in Fig. 1, describes this method. One drawback of this method is that it assumes the P–R segments are well defined, recognizable, and with known positions; otherwise, this method fails [3], [12]. On the other hand, visual evaluation (often known as the draftsman method) is easily performed by drawing an underlying signal curve through the data points [9], [12]. This could be seen as a trivial operation, but its transformation to an algorithm can be complex. The proposed method is similar, in some respects, to the draftsman method and the underlying signal is estimated according to human intuition and perception. An intuitive interpretation of the main idea behind this method is to find the smooth curve that is crossed the maximum number of times by the original signal. The proposed method is described and a brief summary of the algorithm is presented in Section II, and its performance is tested in Section III. The advantages, disadvantages, and computational complexity of the method is discussed in Section IV.

II. THE METHOD

The proposed method for estimating the underlying signal is based on the central assumption that the underlying signal, in general, changes slowly relative to the other components of the physiological signal. Let us define the physiological signal $s(n)$ as the sum of the underlying signal $u(n)$, the fast components of physiological signal $x(n)$, and the additive noise $w(n)$, expressed as

$$s(n) = u(n) + x(n) + w(n) \quad n = 0, \dots, M \quad (1)$$

where M is segment length.

The approximation function $f(a, i)$ is defined as follows: $f(a, i) = a_0 + a_1 i + \dots + a_j i^j$ where a_j are polynomial coefficients, j indicates the power of the polynomial, and $i = -M/2, -M/2 + 1, \dots, M/2$.

The error, $e(i)$, between $s(i)$ and $f(a, i)$ is expressed as

$$e(i) = s\left(\frac{M}{2} + i\right) - f(a, i) \quad i = -\frac{M}{2}, \dots, \frac{M}{2} \quad (2)$$

where $e(i)$ is an approximation of $x(i) + w(i)$; $f(a, i)$, of $u(n)$.