LETTER

Fast Algorithm for Computing Analysis Windows in Real-Valued Discrete Gabor Transform

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SUMMARY Based on the completeness of the real-valued discrete Gabor transform, a new biorthogonal relationship between analysis window and synthesis window is derived and a fast algorithm for computing the analysis window is presented for any given synthesis window. The new biorthogonal relationship can be expressed as a linear equation set, which can be separated into a certain number of independent sub-equation sets, where each of them can be fast and independently solved by using convolution operations and FFT to obtain the analysis window for any given synthesis window. Computational complexity analysis and comparison indicate that the proposed algorithm can save a considerable amount of computation and is more efficient than the existing algorithms.

key words: *convolution, analysis window and synthesis window, real-valued discrete Gabor transform, sub-equation set*

1. Introduction

The Gabor transform is an important and commonly utilized time-frequency analysis tool [1] which plays a crucial role in nonstationary signal processing. Although Gabor transform has been proven useful in diverse areas such as speech and image processing and interpretation, real-time applications are challenging due to the high computational complexity of the discrete Gabor transform coefficients and reconstruction of the original signal from the transform coefficients. A number of approaches have been proposed to solve the problem, such as complex-valued discrete Gabor transform (CDGT) [2]–[7]. Generally these methods for computing the Gabor transforms all involve complex operations and are complicated to implement in software or hardware. For real-valued signals, such as sampled speech and images, real-valued discrete Gabor transform (RDGT) permits a computationally faster implementation [8]–[11].

Because the basis functions of the discrete Gabor tranform are not orthogonal, for the completeness of the transform, a dual window, called the analysis window corresponding to the synthesis window in the basis functions of the transform, must be introduced. The analysis window for any given synthesis window can be computed by solving a linear equation set related to the biorthogonal relationship between analysis window and synthesis window. A wealth of research investigating the subject of the dual windows can be found [12]–[19]. Currently, there are several main methods for computing the canonical dual windows. One such method, proposed by Strohmer [15] and Søendergard [16], is based on the Moore-Penrose pseudoinverse of duality and support conditions as well as fundamental factorization. Qian and Chen [17], [18] presented another method for finding analysis windows based on minimum of ℓ_2 norms, but involving the inverse matrix calculation with high computation complexity if the matrix dimension is too large. Werther, Subbanna and Eldar [19] also proposed an efficient algorithm to compute the analysis window based on discrete Fourier transforms and a non-minimum norm of dual windows for integer oversampling.

In this paper, a fast algorithm for computing the analysis window in the RDGT is presented for any given synthesis window based on the new biorthogonal relationship between analysis window and synthesis window, which can be derived in terms of the completeness of the RDGT. We shall simplify a linear equation set related to the new biorthogonal relationship and separate it into a certain number of independent linear sub-equation sets, so that each of them can be fast and independently solved by using convolution operations [20] and FFT in order to obtain the analysis window for any given synthesis window. In this way, the proposed algorithm can save a large amount of computation and is more efficient than the existing algorithms. The proposed algorithm can be easily generalized and applied to the traditional CDGT and the multiwindow discrete Gabor transform.

2. Review of Real-Valued Discrete Gabor Transform

Let $x(k)$ denote a real finite periodic sequence with period L. The real-valued discrete Gabor expansion is defined by [10], [11]:

$$x(k) = \sum_{m=0}^{M-1} \sum_{n=0}^{N-1} a(m,n) g(k - m\bar{N}) \cdot \mathrm{cas}\left(\frac{2\pi kn}{N}\right) \tag{1}$$

an the coefficients $a(m,n)$ can be obtained by

$$a(m,n) = \sum_{k=0}^{L-1} x(k) \gamma(k - m\bar{N}) \cdot \mathrm{cas}\left(\frac{2\pi kn}{N}\right) \tag{2}$$

where $\mathrm{cas}(\cdot) = \sin(\cdot) + \cos(\cdot)$, $M\bar{N} = N\bar{M} = L$. Equation (2) defines the RDGT for periodic sequences and (1) also defines its inverse RDGT. Note that the synthesis window $g(k)$ and the analysis window $\gamma(k)$ are all periodic with L. In (1) and (2), M and N are the numbers of Gabor sampling points in time and frequency domains, respectively.

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$\bar{M}$ and $\bar{N}$ are the Gabor frequency and time sampling intervals, respectively. The condition $MN > L$ must be satisfied to ensure stable reconstruction and the oversampling occurs when $MN > L$. The critical sampling occurs when $L = MN = \bar{M}\bar{N}$. There may be a loss of information in the undersampling condition ($MN < L$). The oversampling rate $\beta = MN/L = M/\bar{M} = N/\bar{N} > 1$. Properly choose the sampling parameters M and $\bar{M}$, or N and $\bar{N}$ to make the oversampling rate β a positive integer. Comparing with the traditional CDGT [3], one can easily prove the relationship between RDGT coefficients $a(m,n)$ and CDGT coefficients $c(m,n)$ as follows:

$$\begin{aligned} c(m,n) = [&a(m,n) + a(m,N-n)]/2 \\ &+ j[a(m,N-n) - a(m,n)]/2 \end{aligned} \tag{3}$$

where $j = \sqrt{-1}$. Therefore, the RDGT also offer an efficient method to compute the CDGT coefficients.

3. Fast Algorithm for Computing Analysis Windows

3.1 New Biorthogonal Relationship between Analysis Window and Synthesis Window

To derive a new biorthogonal relationship different from that in [10], [11], substituting (2) into (1) yields the following relation

$$\begin{aligned} x(k) &= \sum_{k'=0}^{L-1} x(k') \sum_{m=0}^{M-1} \sum_{n=0}^{N-1} g(k - m\bar{N})\gamma(k' - m\bar{N}) \\ &\quad \cdot \operatorname{cas}\left(\frac{2\pi kn}{N}\right) \operatorname{cas}\left(\frac{2\pi k'n}{N}\right) \\ &= \sum_{k'=0}^{L-1} x(k') \sum_{m=0}^{M-1} g(k - m\bar{N})\gamma(k' - m\bar{N}) \\ &\quad \cdot \sum_{n=0}^{N-1} \operatorname{cas}\left(\frac{2\pi kn}{N}\right) \operatorname{cas}\left(\frac{2\pi k'n}{N}\right) \end{aligned} \tag{4}$$

recalling

$$\sum_{n=0}^{N-1} \operatorname{cas}\left(\frac{2\pi kn}{N}\right) \cdot \operatorname{cas}\left(\frac{2\pi k'n}{N}\right) = N \cdot \sum_{p=0}^{\bar{M}-1} \delta[k - k' - pN] \tag{5}$$

and substituting (5) into (4) leads to

$$\begin{aligned} x(k) =& N \sum_{k'=0}^{L-1} x(k') \sum_{m=0}^{M-1} g(k - m\bar{N})\gamma(k' - m\bar{N}) \\ &\cdot \sum_{p=0}^{\bar{M}-1} \delta[k - k' - pN] \\ =& N \sum_{k'=0}^{L-1} x(k') \sum_{u=0}^{M-1} g(k + u\bar{N})\gamma(k' + u\bar{N}) \\ &\cdot \sum_{p=0}^{\bar{M}-1} \delta[k - k' - pN] \end{aligned} \tag{6}$$

For the completeness of the transform, the following biorthogonal relationship should be satisfied:

$$\begin{aligned} N \sum_{u=0}^{M-1} g(k + u\bar{N})\gamma(k' + u\bar{N}) &\sum_{p=0}^{\bar{M}-1} \delta[k - k' - pN] \\ &= \delta(k - k') \end{aligned} \tag{7}$$

Due to the periodicity of $g(k)$ and $\gamma(k)$, (7) can be rewritten as:

$$\begin{aligned} \delta(p) &= N \sum_{u=0}^{M-1} g(k' + pN + u\bar{N})\gamma(k' + u\bar{N}) \\ &= N \sum_{u=0}^{M-1} g(i + l\bar{N} + pN + u\bar{N})\gamma(i + l\bar{N} + u\bar{N}) \\ &= N \sum_{u=0}^{M-1} g(i + pN + (l+u)\bar{N})\gamma(i + (l+u)\bar{N}) \\ &= N \sum_{q=l}^{M+l-1} g(i + pN + q\bar{N})\gamma(i + q\bar{N}) \\ &= N \sum_{q=0}^{M-1} g(i + pN + q\bar{N})\gamma(i + q\bar{N}) \end{aligned} \tag{8}$$

where $0 \le p \le \bar{M}-1$, $k' = i + l\bar{N}$, $0 \le i \le \bar{N}-1$, $0 \le l \le M-1$, and $L = M\bar{N}$. Equation (8) is obviously a linear equation set that is used to solve the analysis window $\gamma(k)$. The matrix form of (8) can be expressed as:

$$\begin{pmatrix} \boldsymbol{G}^{(0)} & 0 & \cdots & 0 \\ 0 & \boldsymbol{G}^{(1)} & \cdots & 0 \\ \vdots & \vdots & \ddots & \vdots \\ 0 & 0 & \cdots & \boldsymbol{G}^{(\bar{N}-1)} \end{pmatrix} \begin{pmatrix} \boldsymbol{\gamma}^{(0)} \\ \boldsymbol{\gamma}^{(1)} \\ \vdots \\ \boldsymbol{\gamma}^{(\bar{N}-1)} \end{pmatrix} = \frac{1}{N} \begin{pmatrix} \boldsymbol{e} \\ \boldsymbol{e} \\ \vdots \\ \boldsymbol{e} \end{pmatrix} \tag{9}$$

where $\boldsymbol{\gamma}^{(i)}$ is a vector with length M, $i = 0, 1, \cdots, \bar{N}-1$ and $\boldsymbol{G}^{(i)}$ is a real value matrix by $\bar{M} \times M$. $\boldsymbol{e}$ is a unit vector with length $\bar{M}$, i.e., $\boldsymbol{e} = [1, 0, \cdots, 0]^{\mathrm{T}}$.

$$\boldsymbol{\gamma}^{(i)} = \begin{pmatrix} \gamma(i) \\ \gamma(i + \bar{N}) \\ \vdots \\ \gamma\big(i + (M-1)\bar{N}\big) \end{pmatrix} \tag{10}$$

$$\boldsymbol{G}^{(i)} = \begin{pmatrix} g^i_{0,0} & g^i_{0,1} & \cdots & g^i_{0,M-1} \\ g^i_{1,0} & g^i_{1,1} & \cdots & g^i_{1,M-1} \\ \vdots & \vdots & \ddots & \vdots \\ g^i_{\bar{M}-1,0} & g^i_{\bar{M}-1,1} & \cdots & g^i_{\bar{M}-1,M-1} \end{pmatrix} \tag{11}$$

where $g^i_{p,q} = g(i + pN + q\bar{N})$, $0 \le p \le \bar{M}-1$, and $0 \le q \le M-1$. Equation (9) can be separated into $\bar{N}$ independent sub-equation sets:

$$\boldsymbol{G}^{(i)}\boldsymbol{\gamma}^{(i)} = \frac{1}{N}\boldsymbol{e} \tag{12}$$

3.2 Fast Algorithm for Computing Analysis Window in Integer Oversampling Case

By choosing the sampling parameters M and $\bar{M}$ properly, the oversampling rate $\beta = MN/L = N/\bar{N} = M/\bar{M} > 1$ could be a positive integer. However, the rank of $\boldsymbol{G}^{(i)}$ is less than the number of columns in the oversampling case, so (12) could have an infinite number of solutions. Equation (12) can be rewritten in the following form:

$$\left(\boldsymbol{G}_0^i, \boldsymbol{G}_1^i, \cdots, \boldsymbol{G}_{\beta-1}^i\right)\begin{pmatrix}\boldsymbol{\gamma}_0^i\\ \boldsymbol{\gamma}_1^i\\ \vdots\\ \boldsymbol{\gamma}_{\beta-1}^i\end{pmatrix} = \frac{1}{N}\boldsymbol{e} \tag{13}$$

where $\boldsymbol{G}_\alpha^i$ is a $\bar{M} \times \bar{M}$ real left circulant matrix and $\boldsymbol{\gamma}_\alpha^i$ is a vector with length $\bar{M}$, $0 \le \alpha < \beta$, and

$$\boldsymbol{\gamma}_\alpha^i = \begin{pmatrix}\gamma(i + \alpha\bar{N})\\ \gamma(i + N + \alpha\bar{N})\\ \vdots\\ \gamma\left(i + (\bar{M}-1)N + \alpha\bar{N}\right)\end{pmatrix} \tag{14}$$

$$\boldsymbol{G}_\alpha^i = \begin{pmatrix} g_{0,0}^{i,\alpha} & g_{0,1}^{i,\alpha} & \cdots & g_{0,\bar{M}-1}^{i,\alpha}\\ g_{1,0}^{i,\alpha} & g_{1,1}^{i,\alpha} & \cdots & g_{1,\bar{M}-1}^{i,\alpha}\\ \vdots & \vdots & \ddots & \vdots\\ g_{\bar{M}-1,0}^{i,\alpha} & g_{\bar{M}-1,1}^{i,\alpha} & \cdots & g_{\bar{M}-1,\bar{M}-1}^{i,\alpha}\end{pmatrix} \tag{15}$$

where $g_{p,g}^{i,\alpha} = g(i + pN + qN + \alpha\bar{N})$, $0 \le p \le \bar{M} - 1$, and $0 \le q \le \bar{M} - 1$. Then rewrite (13) as:

$$\hat{\boldsymbol{G}}_\alpha^i \hat{\gamma}_\alpha^i = \frac{1}{N}\boldsymbol{g}_\alpha^i \tag{16}$$

$$\hat{\boldsymbol{G}}_\alpha^i = (\boldsymbol{G}_\alpha^i)^{\mathrm{T}}\boldsymbol{G}_\alpha^i \tag{17}$$

$$\boldsymbol{\gamma}_\alpha^i = \lambda_\alpha \hat{\boldsymbol{\gamma}}_\alpha^i \tag{18}$$

$$\boldsymbol{g}_\alpha^i = \begin{pmatrix} g(i + \alpha\bar{N})\\ g(i + N + \alpha\bar{N})\\ \vdots\\ g\left(i + (\bar{M}-1)N + \alpha\bar{N}\right)\end{pmatrix} \tag{19}$$

where $\sum_{\alpha=0}^{\beta-1} \lambda_\alpha = 1$. Thus, (16) also can be written as a circular convolution ($\hat{\boldsymbol{g}}_\alpha^i$ is the first column of $\hat{\boldsymbol{G}}_\alpha^i$).

$$\hat{\boldsymbol{g}}_\alpha^i * \hat{\boldsymbol{\gamma}}_\alpha^i = \frac{1}{N}\boldsymbol{g}_\alpha^i \tag{20}$$

By utilizing the results of the circular convolution theorem [20], the discrete fast Fourier transform (FFT) can then be used to compute $\hat{\boldsymbol{\gamma}}_\alpha^i$.

$$\hat{\boldsymbol{\gamma}}_\alpha^i = \frac{1}{N}F_{\bar{M}}^{-1}\left(\frac{F_{\bar{M}}(\boldsymbol{g}_\alpha^i)}{F_{\bar{M}}(\hat{\boldsymbol{g}}_\alpha^i)}\right) \tag{21}$$

where $F_{\bar{M}}$ is the $\bar{M}$-point FFT and $F_{\bar{M}}^{-1}$ is the $\bar{M}$-point inverse FFT. Because the Gabor analysis window must satisfy the localization property [21], $\boldsymbol{\gamma}^{(i)}$ should satisfy the minimum of ℓ_2 norms:

$$\begin{aligned}\arg\min\left\{\|\boldsymbol{\gamma}^{(i)}\|_2^2\right\} &= \arg\min\left\{\sum_{\alpha=0}^{\beta-1}\|\boldsymbol{\gamma}_\alpha^i\|_2^2\right\}\\ &= \arg\min\left\{\sum_{\alpha=0}^{\beta-1}\lambda_\alpha^2\|\hat{\boldsymbol{\gamma}}_\alpha^i\|_2^2\right\}\end{aligned} \tag{22}$$

Equation (22) can be solved with the Lagrangian method by transforming it to the following optimum problem:

$$J(\lambda_\alpha) = \frac{1}{2}\sum_{\alpha=0}^{\beta-1}\lambda_\alpha^2\|\hat{\boldsymbol{\gamma}}_\alpha^i\|_2^2 + \mu\left(1 - \sum_{\alpha=0}^{\beta-1}\lambda_\alpha\right) \tag{23}$$

where $\mu \in \mathbb{R}^1$. Taking a derivative of $J(\lambda_\alpha)$ with respect to λ_α leads to.

$$\frac{\partial J(\lambda_\alpha)}{\partial \lambda_\alpha} = \lambda_\alpha\|\hat{\boldsymbol{\gamma}}_\alpha^i\|_2^2 - \mu = 0 \tag{24}$$

Equation (24) can be rewritten as matrix form as follows:

$$\begin{pmatrix}\|\hat{\boldsymbol{\gamma}}_0^i\|_2^2 & 0 & \cdots & 0\\ 0 & \|\hat{\boldsymbol{\gamma}}_1^i\|_2^2 & \cdots & 0\\ \vdots & \vdots & \ddots & \vdots\\ 0 & 0 & \cdots & \|\hat{\boldsymbol{\gamma}}_{\beta-1}^i\|_2^2\end{pmatrix}\lambda = \mu\begin{pmatrix}1\\1\\ \vdots\\1\end{pmatrix} \tag{25}$$

where $\boldsymbol{\lambda} = \left[\lambda_0, \lambda_1, \cdots, \lambda_{\beta-1}\right]^{\mathrm{T}} \in \mathbb{R}^\beta$. Then we can obtain the solution of λ from (25) and substituting this solution into the constraint $\sum_{\alpha'=0}^{\beta-1}\lambda_{\alpha'} = 1$ to solve μ leads to.

$$\lambda = \frac{1}{W}\left[1/\|\hat{\gamma}_0^i\|_2^2, 1/\|\hat{\gamma}_1^i\|_2^2, \cdots, 1/\|\hat{\boldsymbol{\gamma}}_{\beta-1}^i\|_2^2\right]^{\mathrm{T}} \tag{26}$$

where $W = \sum_{\alpha'=0}^{\beta-1} 1/\|\hat{\boldsymbol{\gamma}}_{\alpha'}^i\|_2^2 = 1/\mu$. Note that the proposed algorithm also can be easily applied to the critical sampling case ($\beta = \lambda = 1$).

4. Computational Complexity Analysis and Comparison

Because the total computational complexity of the proposed set of algorithms is equal to that of the total independent sub-equation sets, the computation time of the proposed algorithm is dependent on the computational complexity of each sub-equation set. The single sub-equation set carries $\bar{M}^2$ multiplications, two $\bar{M}$-point fast DFT (with computational complexity $\bar{M}\log_2\bar{M}$), one $\bar{M}$-point fast IDFT (with computational complexity $\bar{M}\log_2\bar{M}$), and the computational complexity of λ (can be ignored under critical sampling case) is the order of $\beta\bar{M}$. Table 1 gives a comparison between the proposed algorithms and the main existing algorithms, which clearly demonstrates that the computational complexity of the proposed algorithm is lower than that of

Table 1 Comparison of computational complexity related to total computation time

References	Computational complexity	Applicability
[16]	$C\bar{M}(\bar{M}^2/D^2 + \bar{M}\log_2 D) + L^2$	CS,OS
[17]	$(\bar{M}\bar{N})^3 + 2(\bar{M}\bar{N})^2 L + (\bar{M}\bar{N})L$	CS,OS
[18]	$\bar{M}^3\bar{N} + 2\bar{M}^2 L + L\bar{M}$	CS,OS
[19]	$2L\log_2\bar{M} + 2\bar{M}\bar{N} + L^2$	CS,OS
Proposed algorithms	$3L\log_2\bar{M} + \bar{M}L$	CS
	$3L\log_2\bar{M} + \bar{M}L + L$	OS

Table 2 Numeric comparison of total number of multiplications related to total computational time

L	M	N	β	Total number of multiplications				
				[16]	[17]	[18]	[19]	Proposed algorithms
	16	16	1	82176	50397184	200704	68096	7168
256	32	16	2	73856	110518528	167936	67840	7424
	32	32	4	67136	2375680	38912	67200	4608
	16	32	1	295424	402915328	401408	267264	14336
512	32	32	2	278784	84017152	335872	266752	14848
	32	64	4	265344	18939904	77824	265472	9216
	32	32	1	1213440	3.2223×10^9	3178496	1060864	48128
1024	64	32	2	1131008	671612928	2654208	1059840	49152
	64	64	4	1065216	151257088	606208	1057280	29696

the others. In Table 1, the symbols CS and OS denote the critical sampling case and the oversampling case respectively. $C = \gcd(N, \bar{N})$, $D = \gcd(M, \bar{M})$, where gcd denotes greatest common divisor. A numeric comparison on the total number of multiplications related to the total computational time between the proposed algorithms and the main existing algorithms is given in Table 2, which is calculated by using the formulas in Table 1.

5. Conclusions

Solving the analysis window for any given synthesis window is a crucial step in Gabor time-frequency analysis. This paper proposed a fast algorithm for solving analysis window for any given synthesis window in the RDGT based on the new biorthogonal relationship between analysis window and synthesis window, which can be derived in terms of the completeness of the RDGT. We decomposed the linear equation set, related to the new biorthogonal relationship, into a certain number of independent sub-equation sets so that each of them could be fast and independently solved by using convolution operations and FFT to obtain the analysis window for any given synthesis window. Computational complexity analysis and comparison showed that the proposed algorithm can compute the analysis window efficiently with much less computational complexity as compared to other existing algorithms.

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