

ON THE CROSS-BIORTHOGONAL REPRESENTATION

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ABSTRACT

A novel cross term deleted Wigner representation can be obtained by expanding the Wigner Distribution (WD) in terms of two complementary Gabor coefficients of the signal and a translated set of Wigner basis functions. Two such complementary Gabor coefficients of a signal can be obtained by reversing the role of Gabor synthesis window $h(t)$ and its biorthogonal function $b(t)$. Such a representation is defined here, as Cross-Biorthogonal representation (XBIO). Details of derivation of this new representation is provided in this paper. The choice of the synthesis functions and their corresponding biorthogonal functions with respect to (i) concentration/resolution capabilities, (ii) redundancy vs. minimum-dimension tradeoffs, (iii) noise reduction and (iv) basis set properties of the XBIO representation are also discussed. Simulation results are provided to substantiate the theoretical findings.

1. INTRODUCTION

It is very well known in the signal processing community that the inherent bi-linear characteristics of the Wigner Distribution (WD) introduces artifacts (cross terms) which complicates the extraction of the required information from the WD of a multi-component signal. Therefore, several methods were developed to suppress or filter the cross terms. Each technique has its own advantages and disadvantages. Recently, in [1, 2], the authors have shown that the WD can be decomposed into terms that contribute only to auto and cross WD via Gabor expansions. If the terms that affect the cross-WD are deleted, we get a time-frequency representation without the cross-WD term. Such a representation which is devoid of cross-terms is defined as the Cross-term Deleted Wigner Representation (CDWR) [1]. The XBIO, a new time-frequency representation that is introduced in this paper, can be free of cross-terms and is an alternative method to decompose the WD using two complementary Gabor coefficients of a signal and a translated set of Wigner basis functions.

Initially, the concept of cross-biorthogonal was used for the synthesis problem in [3] based on the observation that the cross-WD of a window and its biorthogonal function generate an orthogonal set in time-frequency plane under the appropriate translations. Further, the basic idea of XBIO representation originates with the recognition that a Gabor synthesis window $h(t)$ and its biorthogonal function $b(t)$

generate two complementary Gabor expansions one using $h(t)$ as the synthesis window and $b(t)$ as the analysis window, and the other using $b(t)$ as the synthesis window and $h(t)$ as the analysis window.

It is known that a signal $s(t)$ can be expanded using the Gabor coefficients $G_{m,n}$ as:

$$s(t) = \sum_m \sum_n G_{m,n} h_{m,n}(t) \quad (1)$$

where $G_{m,n} = \int_{-\infty}^{\infty} s(t) b_{m,n}^*(t) dt$ and $h_{m,n}(t) = h(t - \alpha m) e^{j2\pi n \beta t}$. Here α and β are constant time and frequency sample intervals, respectively, $\star$ is the complex conjugation operator and $b_{m,n}(t)$ is defined similar to $h_{m,n}(t)$. It can be shown that if $G_{m,n}$ s are complete $b_{m,n}$ s are also complete which implies that $s(t)$ can also be expressed as a weighted sum of translates of $b(t)$. That is,

$$s(t) = \sum_p \sum_q \hat{G}_{p,q} b_{p,q}(t) \quad (2)$$

where $\hat{G}_{p,q} = \int_{-\infty}^{\infty} s(t) h_{p,q}^*(t) dt$ is the set of biorthogonal basis expansion coefficients. From the above two equations, it can be seen that $G_{m,n}$ s and $\hat{G}_{m,n}$ s, the complementary Gabor coefficients of $s(t)$ are generated by reversing the role of $h(t)$ and $b(t)$. It has been shown that these complementary Gabor coefficients are related through a linear transformation whose kernel is the ambiguity function of the window or biorthogonal function. By decomposing the WD using these complementary Gabor coefficients, the XBIO representation (continuous and discrete) can be derived; details of which are given in the next section.

2. DERIVATION OF THE XBIO REPRESENTATION

2.1. Continuous case:

The continuous WD of a signal $s(t)$ is defined as:

$$WD_s(t, \omega) = \int_{-\infty}^{\infty} s(t + \frac{\tau}{2}) s^*(t - \frac{\tau}{2}) e^{-j\omega\tau} d\tau \quad (3)$$

By substituting $s(t)$ with its complementary Gabor expansions (Eqs. (1) & (2)) in the above equation, the WD can be decomposed into:

$$WD_s(t, \omega) = \sum_{m,n} \sum_{p,q} G_{m,n} \hat{G}_{p,q} WD_{h_{m,n}, b_{p,q}}(t, \omega) \quad (4)$$

where $WD_{h_{m,n},b_{p,q}}(t, \omega)$ is the cross-WD of windows $h(t)$ and $b(t)$, and is a set of basis functions for the expansion of $WD_s(t, \omega)$. By algebraic manipulations, the above equation can be reduced to:

$$WD_s(t, \omega) = \sum_{m,n} \sum_{p,q} G_{m,n} \hat{G}_{p,q}^* WD_{h,b}(t - \frac{n+q}{2}T, \omega - \frac{m+p}{2T}) \times e^{j\pi \left\{ \frac{(m+p)(n-q)}{2} + \frac{(m-p)t}{T} - (n-q)T \right\}} \quad (5)$$

Note that no special relationship between h and b is required for the above equation to hold. However, we are particularly interested in the above equation when h and b are a biorthogonal pair.

From the above equation, it can be seen that it exhibits both auto and cross-WD terms. The auto-WD terms correspond to the case when $m = p$ and $n = q$. Therefore, by retaining only the terms that affect auto-WD terms, we get the cross-term deleted X BIO time-frequency representation $XB_s(t, \omega)$ of a signal $s(t)$. That is,

$$XB_s(t, \omega) = \sum_{m,n} G_{m,n} \hat{G}_{m,n}^* WD_{h,b}(t - nT, \omega - \frac{m}{T}) \quad (6)$$

where T is the sampling rate. Note that if h replaces b above, then $\hat{G}_{m,n} = G_{m,n}$ and the X BIO representation (the above equation) is equivalent to the CDWR. Therefore, the CDWR is a special case of the X BIO representation.

2.2. Discrete case:

Similarly, the discrete version of the X BIO (DXBIO) representation can be obtained by considering the discrete-time, discrete-frequency definition of the WD which for a signal $s(k)$ is defined as [4]:

$$DWD_s(\eta, \mu) = \frac{1}{2p_1} \sum_{k=0}^{p_1-1} s(k) s^*(\eta - k) e^{-j\frac{\pi}{p_1} \mu (2k - \eta)} \quad (7)$$

where p_1 is the period of $s(k)$. Using the complementary Gabor expansions $x_{m,n}$ and $\hat{x}_{p,q}$ of a discrete signal $s(k)$, the above equation can be written as:

$$DWD_s(\eta, \mu) = \frac{1}{2p_1} \sum_{k=0}^{p_1-1} \left(\sum_m \sum_n x_{m,n} h_{m,n}(k) \right) \times \left(\sum_p \sum_q \hat{x}_{p,q}^* b_{p,q}^*(\eta - k) \right) \times e^{-j\frac{\pi}{p_1} \mu (2k - \eta)} \quad (8)$$

where $h_{m,n}(k)$ and $b_{p,q}(k)$ are:

$$\begin{aligned} h_{m,n}(k) &= h(k - m\bar{Q}) e^{j\frac{2\pi}{\bar{Q}} nk} \\ b_{p,q}(k) &= b(k - p\bar{Q}) e^{j\frac{2\pi}{\bar{Q}} qk}, \end{aligned} \quad (9)$$

respectively. Substituting for $h_{m,n}(k)$ and $b_{p,q}(k)$ in Eq. (8) and after some algebraic simplifications, it can be shown that:

$$\begin{aligned} DWD_s(\eta, \mu) &= \sum_{m,n} \sum_{p,q} x_{m,n} \hat{x}_{p,q}^* \\ &\times DWD_{h,b} \left(\eta - (m+p)\bar{Q}, \mu - \frac{p_1}{\bar{Q}}(n+q) \right) \\ &\times e^{-\left[2\pi m\bar{Q} \left(\frac{\mu}{p_1} - \frac{(n+q)}{\bar{Q}} \right) - \frac{\pi\eta(n-q)}{\bar{Q}} \right]} \\ &- (m+p)\bar{Q}\pi \left(\frac{\mu}{p_1} - \frac{(n+q)}{\bar{Q}} \right) \end{aligned} \quad (11)$$

Here, $DWD_{h,b}$ is the cross-DWD of $h(k)$ and $b(k)$. Similar to the continuous case, the above equation exhibits a mix of auto and cross-terms. The auto-DWD terms are those that correspond to $m = p$ and $n = q$. Hence, by retaining only the autoterms in the above equation, we get a cross term deleted DXBIO representation $DXB_s(\eta, \mu)$ which is given by:

$$DXB_s(\eta, \mu) = \sum_{m,n} x_{m,n} \hat{x}_{m,n}^* DWD_{h,b}(\eta - 2m\bar{Q}, \mu - 2\bar{P}n) \quad (12)$$

In the above set of equations, $\bar{Q}$ and $\bar{P}$ define the time and frequency sampling intervals, and $m\bar{Q}$ and $n\bar{P}$ define the sampling points of the Gabor expansion in the time-frequency plane. In addition, $P, Q, \bar{Q}$ and $\bar{P}$ are positive integers constrained by: $p_1 = P\bar{Q} = \bar{P}Q$. The selection of these integers determine the sampling rate of DXBIO representation. For example, when $P = \bar{P}$, $Q = \bar{Q}$ and $p_1 = PQ$, the DXBIO representation is said to be critically sampled. In the following sections, some properties of the X BIO representations, and selection of synthesis window and its biorthogonal function are discussed.

3. PROPERTIES

Both continuous and discrete X BIO representations have some interesting characteristics. These are discussed in the following sections.

3.1. Property # 1 Completeness:

The WD basis functions ($WD_{h,b}(t - nT, \omega - \frac{m}{T})$ and $DWD_{h,b}(\eta - 2m\bar{Q}, \mu - 2\bar{P}n)$) should satisfy completeness for synthesizing the signal from its X BIO representation. The WD basis functions form a complete orthogonal set in $L^2(R^2)$ if h and b are complete in $L^2(R^2)$. This permits a development of a large number of orthogonal bases for the time-frequency plane and implies that near-orthogonal sets can be obtained when b is sufficiently close to h in the least square sense. In [5], an algorithm is described to design b which is close to h in least square sense. This procedure is equivalent to designing b with minimum energy constraint [6]. When b is designed at the maximum oversampling rate with minimum energy constraint, it can be shown that it is a scaled version of h . For the proof refer to [7, 8]. Therefore, we use this methodology to design b which is close to h . In Figure 1, we plot h (a Gaussian window) and b which is designed as described above. From this figure, it

can be seen that b is indeed a scaled version of h . In addition, since h and b are biorthogonal to each other they are complete in $L^2(R^2)$ [8]. Therefore, using the described method we can generate the WD basis functions which are complete in $L^2(R^2)$. This implies that the signal $s(t)$ can be resynthesized from its XBIO/DXBIO representation.

3.2. Property # 2 Destructive interference:

From Eqs. (6) and (12), it can be seen that in the computation of the XBIO representation, the cross-WD of the windows and the complementary Gabor coefficients are involved. Both cross-WD ($WD_{h,b}$ and $DWD_{h,b}$), and weights ($\{G_{m,n}, \hat{G}_{m,n}^*\}$ and $\{x_{m,n}, \hat{x}_{m,n}^*\}$) are complex valued unlike in the case of the CDWR. Therefore, it is conceivable that destructive interference between adjacent expansion terms is possible. This implies that, this property could be exploited in detection or noise reduction problems. In Figure 2, (i) the synthetic signal that consists of three modulated Gaussian signal components with additive white Gaussian noise of SNR = -6dB and (ii) its CDWR and XBIO representations at four different sampling rates are plotted, respectively. From this figure, it is clear that the three signal components are better detectable in the XBIO representation (in particular, at maximum oversampling rate) of the noisy signal as compared to the CDWR. This indicates that the destructive interference of the adjacent terms of the XBIO representation is helping in noise reduction. Therefore, it should be advantageous to use XBIO TFR for signal detection when it is embedded in noise as compared to the CDWR.

3.3. Property # 3 Dimension of the XBIO:

The dimension in other words the number of auto-terms of the XBIO/DXBIO representation can be controlled by the choice of h and b pair because:

- a signal will have a certain dimension which is approximately equal to the number of significantly large expansion coefficients $\{G_{m,n}\}$ or $\{x_{m,n}\}$ when the signal is expanded using a given window function,
- the same signal will have a different dimension when the biorthogonal window is used as the basis function in the expansion of a signal and
- the dimension or the number of auto-terms of the XBIO/DXBIO is then less than or equal to the minimum dimension of the weights $\{G_{m,n}\}$ and $\{\hat{G}_{m,n}\}$ or $\{x_{m,n}\}$ and $\{\hat{x}_{m,n}\}$ since any zero term of the weights cause the XBIO/DXBIO weight at (m,n) , i.e. the product $G_{m,n}\hat{G}_{m,n}$ or $x_{m,n}\hat{x}_{m,n}$ to be zero.

Therefore, by designing b appropriately, we can either get maximum or minimum dimension XBIO/DXBIO representation. In the following sections, design details of maximum and minimum dimension b are provided.

3.3.1. Maximum dimension

We can get highly redundant or maximum dimension XBIO/DXBIO representation if the maximum dimensions of b and h are the same. It can be shown that their dimensions are the same when b is designed such that it is a scaled version of h . In section 3.1. it was mentioned that

b is a scaled version of h only when b is designed at maximum oversampling rate with minimum norm constraint. Therefore, maximum dimension XBIO representation can be obtained by designing b of a given h at maximum oversampling rate.

The main advantage of maximum dimension XBIO/DXBIO representation is that it has the best time-frequency resolution since it can be shown that the cross-WD of h and b has the best concentration in the time-frequency domain when the maximum oversampled b is used [7]. In addition, as observed from Figure 2, the noise effect is reduced and thus signal can be enhanced.

3.3.2. Minimum dimension

Similarly, minimum dimension XBIO/DXBIO representation can be obtained if the dimension of b is minimized for a given h or vice versa. The minimum dimension b can be designed by minimizing the mutual information between h and b in information theoretic sense. The mutual information between h and b , $I(b, h)$ is defined as [9]:

$$I(b, h) = H(b) - H(b|h) \quad (13)$$

where H is the entropy. Therefore, for a given h , the mutual information can be minimized by minimizing the information or entropy of b . In oversampled case, this can be achieved by forcing certain components of b to zero. These components can be chosen by minimizing the variance J_e :

$$J_e = \sum_i (b_i - \xi)^2 \quad (14)$$

where ξ is the mean of b . This approach was used to design a minimum dimension b for a given Gaussian window h . In Figure 1(a) and 1(c), h and b are plotted, respectively. From these two figures, it can be seen that b has only three non-zero components and hence has a dimension of three.

4. SIMULATION

From the discussion in the above section, it is clear that an expansion based on cross-biorthogonal function may lead to crossterm deleted representation in which the number of autoterms maybe smaller than the CDWR. Therefore, an experiment was conducted to compare the concentration/resolution capabilities of the minimum, maximum dimension XBIO and the CDWR representations by considering a non-linear chirp signal, $s(t) = (1 - e^{-at})\sin 2\pi(f_c + f(t))t$ where $f(t) = -f_0 e^{-ct}$. The parameters a , carrier frequency f_c , f_0 and c are set to 2.3×10^7 , 10^7 , 1.5×10^6 and 3.0×10^4 , respectively. The contour plots of the CDWR, maximum and minimum dimension XBIO representations of this non-linear chirp signal are as shown in Figure 3. From this figure, it can be seen that the highly redundant XBIO representation has the best concentration/resolution since its energy is concentrated along the time-varying instantaneous frequency of the signal whereas the CDWR has the least resolution/concentration.

5. CONCLUSIONS

We have derived a novel XBIO time-frequency representation. We have shown that the CDWR is a special case

of the XBIO TFR. Some of the properties of this representation are discussed. These properties have lead to two new design techniques for the biorthogonal analysis window which are described in this paper. The signal enhancement and resolution/concentration capabilities of the XBIO and the CDWR TFRs are compared with simulation examples. From the experimental results, it can be seen that the highly redundant XBIO representation has better noise reduction and resolution/concentration capabilities. This implies that the XBIO TFR is a potential tool for signal detection and classification problems.

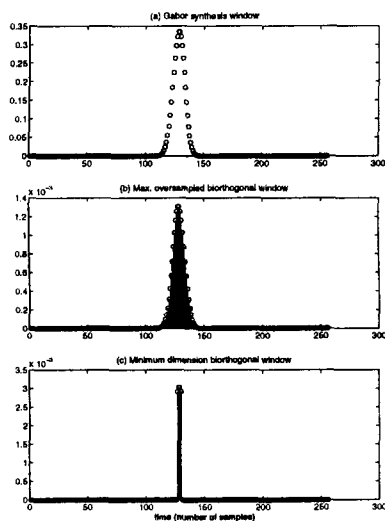


Figure 1. Gaussian synthesis window and its maximum and minimum dimension biorthogonal functions

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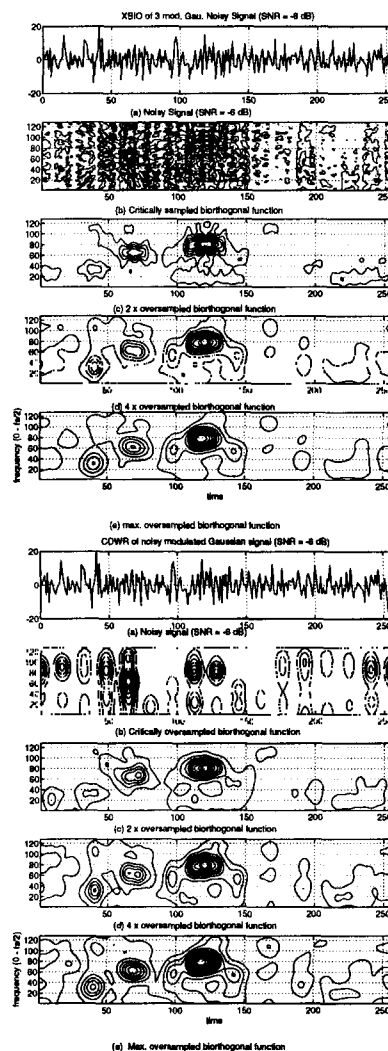


Figure 2. The noisy synthetic signal with additive white Gaussian noise (SNR = -6 dB), and contour plots of its XBIO and CDWR representations.

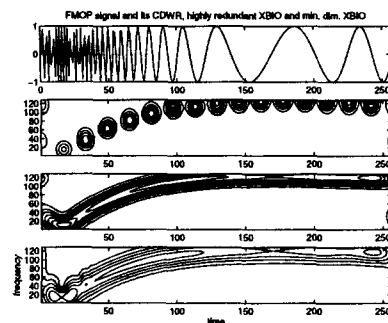


Figure 3. Non-linear chirp signal and contour plots of its CDWR, highly redundant and minimum dimension XBIO representations