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A novel signal sparse decomposition based on modulation correlation partition

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ABSTRACT

The prohibitive computational complexity caused by redundant dictionary which is used in signal sparse decomposition has always been perplexing researchers of signal processing all the time. However, large over-complete dictionaries are essential to approximate the signal. In this paper, a decomposition algorithm based on modulation correlation partition (PBMC) is introduced, which improves the process of searching matched atoms in the redundant dictionary of functions. Through analyzing the structure of signals, we unite the frequency factor and phase factor to obtain the 2D modulation factor. The over-complete dictionary is partitioned into several sub-dictionaries according to the modulation correlation of atoms. Each sub-dictionary is represented by a single selected atom which is used in the greedy algorithm. At the end of this paper, experimental results show that the computational complexity of signal sparse decomposition can be adequately reduced by partitioning over-complete dictionary without impacting the decomposition result.

1. Introduction

Sparse representation acts as an important role in signal processing and analyzing. It has been used to solve the problems brought by traditional decomposition [1] of expressing signal in a single way. However, the computational complexity is the bottleneck problem of improving the efficiency of decomposition.

In the traditional methods, signals are projected onto completely orthogonal bases such as Fourier or wavelet transform [2,3]. However, the linear expression of signals with only one basis is not flexible enough. Fourier transformation, for instance, provides a poor representation of functions which is only located in time domain. Similarly, wavelet bases have the limitations of representing signals with narrow bands in high frequency. Therefore, it would be difficult to detect and identify the signal patterns by utilizing the traditional representing coefficients because the information of signal is dispersed throughout the whole basis.

Furthermore, if the structure of signal is complex in time domain and frequency domain, a more efficient algorithm is needed to decompose the signal. Therefore, small signals called time–frequency atoms are generated and the time–frequency characters of atoms are matched to signal structures. For example, pulse signals are decomposed onto bases which have concentrated structures in time domain, while spectral lines are represented by atoms which have a narrow frequency band. Large numbers of atoms constitute a redundant system called over-complete dictionary. Over-complete dictionary has been proposed and used for representing sparse signals. There are two necessary premises for building an efficient over-complete dictionary. Firstly, the diversity of atoms in dictionary should be guaranteed as well as time–frequency information. Secondly, the distinction between different atoms should be kept as clear as possible and the similar atoms should be removed. If the structure of signal is complicated, the size of the over-complete dictionary could be very large. Therefore, it is necessary to find an algorithm to select the best-matched time–frequency atoms to decompose signals.

One important branch of these decomposition algorithms is greedy algorithms. Matching Pursuit (MP) is a classical greedy algorithm proposed by Stephane G. Mallat [4]. In each iteration, MP algorithm selects the best-matched atom to minimize the signal residual. However, MP algorithm has a high computation complexity which reduces the efficiency. The reason is that the dictionary is too large to compute all the inner product and find the maximum. The method of matching pursuit and related contents are elaborated in references [5,6]. Orthogonal complementary matching pursuit (OCMP) proposed by Gagan Rath increases the convergence speed of pursuit algorithm by using a

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dynamic modified dictionary [7]. Similar methods can be found in [8–10]. However, the speed of pursuit algorithms is still not very fast.

In order to reduce the computation complexity, Laurent Daudet composes similar atoms as one molecular to represent these atoms. The Molecular Matching Pursuit (MMP) algorithm has good experimental results on audio signals [11]. MMP algorithm brings about the inspiration of structuring the over-complete dictionary. Philippe Jost proposes a tree-based pursuit algorithm which is also based on structuring strategy [12]. The Iteration-Tuned and Aligned Dictionary (ITAD) presented by Joaquin Zepeda is used in image processing as a learned and structured dictionary [13]. The excellent performance of structured dictionary proves it an efficient method to reduce the high complexity of greedy algorithm. In this paper, we introduce a novel sparse decomposition algorithm, which partitions over-complete dictionary according to the correlations of atoms. This algorithm decomposes signals onto a linear expansion of atoms of a redundant dictionary. By partitioning the over-complete dictionary, the enormous redundant dictionary is cut apart into some sub-dictionaries. After a two-step searching procedure for choosing the best-matched atoms, the decomposition can be improved obviously.

The remainder of this paper is organized as follows. Section 2 reviews the definition of time–frequency decomposition and the Gabor dictionary, while the MP algorithm is introduced too. We then propose a novel method based on partition strategy to reduce computational complexity in Section 3. The experimental results and numerical analysis are given in Section 4. Finally, this paper is concluded in Section 5.

2. Time–frequency atomic decompositions and matching pursuit

Decomposing signals onto bases well localized both in time domain and frequency domain is an important stage of signal processing or harmonic analysis. These bases consist of time–frequency atoms. To extract information from complex signals, we should choose the matched atoms from these bases according to the structural characteristics of signals.

A general family of Gabor time–frequency atoms can be generated by changing the scale, location and modulation of a single window function $g(t)\in L^2(R)$, where the space $L^2(R)$ is the Hilbert space of complex valued functions such that

$$\|f\| = \int_{-\infty}^{+\infty} |f(t)|^2\, dt < +\infty \tag{1}$$

$g(t)$ is a real function, it is continuously differentiable and $O(1/(t^2+1))$. It also should be guaranteed that $\|g\|=1$, where the integral of $g(t)$ is nonzero and $g(0)\neq 0$. For any scale of $s>0$, the Gabor atom can be represented by a parameter group $\gamma=(s,u,v,w)$. Namely define

$$g_\gamma(t) = \frac{1}{\sqrt{s}} g\left(\frac{t-u}{s}\right)\cos(vt+w) \tag{2}$$

$\gamma$is an element of the set $\Gamma = R^+ \times R^2$. The factor $1/\sqrt{s}$ normalizes the norm of $g_\gamma(t)$ to 1. If $g(t)$ is even symmetrical, as a common case, $g_\gamma(t)$ is centered at the coordinate u. Its energy is mostly concentrated nearby u, of which size is proportional to s. $g(t)=e^{-\pi t^2}$ is a window Gauss function and $\gamma=(s,u,v,w)$ is a time–frequency parameter, where s, u, v and w denote the scale factor, translation factor, frequency factor and phase factor respectively. Certainly, γ should be discretized to help executing algorithm simulation on computer.

After that we have $\gamma=\left(a^j, pa^j\Delta u, ka^{-j}\Delta v, i\Delta w\right)$ and $a=2$, $\Delta u=1/2$, $\Delta v=\pi$, $\Delta w=\pi/6$, $0<j<\log_2 N$, $0\le p\le N2^{-j+1}$, $0\le k\le 2^{j+1}$, $0\le i\le 12$. It has previously been researched in reference [14].

Due to the extremely redundancy of $\mathcal{D}=(g_\gamma(t))_{\gamma\in\Gamma}$, an appropriate countable subset of atoms $(g_{\gamma n}(t))_{n\in N}$ must be selected to represent any functions $f(t)$ with $\gamma_n=(s_n,u_n,v_n,w_n)$, then $f(t)$ can be written as

$$f(t) = \sum_{n=-\infty}^{+\infty} a_n g_{\gamma n}(t) \tag{3}$$

Depending on the choice of the atoms $g_{\gamma n}(t)$, the representation coefficients a_n give explicit information about certain $f(t)$.

The general problem of adaptive time–frequency decomposition is how to expand functions onto a set of atoms appropriately selected from a huge redundant dictionary. Matching pursuit performs well as an adaptive decomposition. Let $\boldsymbol{H}$ be a Hilbert space. A dictionary is defined as a family $\mathcal{D}=\left(g_\gamma\right)_{\gamma\in\Gamma}$ of vectors in $\boldsymbol{H}$, such that $\|g_\gamma\|=1$. For the dictionary of time–frequency atoms described in Section 2, $\boldsymbol{H}=L^2(R)$ and each vector g_γ is an atom defined by (2). This dictionary is complete because finite linear decomposition of time–frequency atoms is dense in $L^2(R)$.

Let $g_{\gamma 0}\in\mathcal{D}$. The vector $\boldsymbol{f}$ can be decomposed like

$$\boldsymbol{f} = \left\langle \boldsymbol{f}, g_{\gamma 0}\right\rangle g_{\gamma 0} + Rf \tag{4}$$

where Rf is the residual vector after approximating $\boldsymbol{f}$ in the direction of $g_{\gamma 0}$. Clearly $g_{\gamma 0}$ is orthogonal to Rf, hence

$$\|\boldsymbol{f}\|^2 = \left|\left\langle \boldsymbol{f}, g_{\gamma 0}\right\rangle\right|^2 + \|Rf\|^2 \tag{5}$$

To minimize $\|Rf\|$, $g_{\gamma 0}\in\mathcal{D}$ must be determined such that $\left|\left\langle \boldsymbol{f}, g_{\gamma 0}\right\rangle\right|$ is maximum. In some cases, it is only possible to find a vector $g_{\gamma 0}$ that is almost the best in the sense that

$$\left|\left\langle \boldsymbol{f}, g_{\gamma 0}\right\rangle\right| \ge \alpha \sup_{\gamma\in\Gamma}\left|\left\langle \boldsymbol{f}, g_{\gamma}\right\rangle\right| \tag{6}$$

where α denotes a fixed weakness parameter that satisfies $0<\alpha\le 1$.

Let $R^0 f=\boldsymbol{f}$. It is supposed that we have computed the nth order residue $R^n f$, for $n\ge 0$. An element $g_{\gamma n}\in\mathcal{D}$ is chosen, with the choice function $\mathbf{C}$, which closely matches the residue $R^n f$

$$\left|\left\langle R^n f, g_{\gamma n}\right\rangle\right| \ge \alpha \sup_{\gamma\in\Gamma}\left|\left\langle R^n f, g_{\gamma}\right\rangle\right| \tag{7}$$

the residue $R^n f$ is sub-decomposed into

$$R^n f = \left\langle R^n f, g_{\gamma n}\right\rangle g_{\gamma n} + R^{n+1} f \tag{8}$$

which defines the residue at the order $n+1$. Then this decomposition is carried up to the order m. $\boldsymbol{f}$ is decomposed into the concatenated sum

$$\boldsymbol{f} = \sum_{n=0}^{m-1}\left\langle R^n f, g_{\gamma n}\right\rangle g_{\gamma n} + R^m f \tag{9}$$

The original vector $\boldsymbol{f}$ is decomposed onto a group of atoms which are selected to best match signal residues. The procedure of finding the best-matched atoms costs quite a long time by computer calculating. In the next section, a method which reduces the computational complexity and shortens the runtime of iteration algorithm is discussed.

3. Partition of the over-complete dictionary based on modulation correlation

In this section we introduce a method to partition the over-complete dictionary based on modulation correlation (PBMC) to simplify the sparse decomposition of signals. The PBMC approach is described as follows.