APPLICATION OF DIAMETRICAL CLUSTERING TO TREE-BASED MATCHING PURSUIT FOR SINUSOIDAL MODELING

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ABSTRACT

This paper deals with the application of Diametrical Clustering to the design of structured dictionaries in order to reduce the computational complexity of the Matching Pursuit algorithm for sinusoidal modeling. Diametrical Clustering organizes the dictionary in clusters, so that the similarity measure (average squared correlation coefficient between two atoms) is maximized. The optimal centroids are the dominant right singular vectors of the average correlation matrix of the atoms in the cluster. Some experiments are presented which show the suitability of this clustering algorithm, because the correlations of the atoms in a cluster with its centroid are much higher than the correlations with the centroids of other cluster. A dictionary of sinusoids has been divided in four clusters, and the centroids have been obtained and represented.

1. INTRODUCTION

The classical sinusoidal or harmonic model [1] comprises an analysis-synthesis framework that represents a signal, $x[n]$, as the sum of a set of K sinusoids with time-varying frequencies, phases, and amplitudes:

$$x[n] \approx \hat{x}[n] = \sum_{k=1}^{K} A_k[n] \cdot cos\left(\omega_k[n] \cdot n + \phi_k[n]\right) \quad (1)$$

where $A_k[n]$, $\omega_k[n]$ and $\phi_k[n]$ represent the amplitude, the instantaneous frequency and the instantaneous phase of the k-th sinusoid, respectively. This is a linear model, whose parameters must be estimated using the available data.

Assuming that the parameters of expression (1) do not change considerably along the analysis frame, the signal can be reconstructed from the harmonic parameters with expression (2):

$$x[n] \approx \hat{x}[n] = \sum_{k=1}^{K} A_k \cdot cos\left(\omega_k \cdot n + \phi_k\right) \quad (2)$$

The length of the analysis frame should be signal dependent so as to achieve an adapted multi-resolution analysis [2].

A large number of methods have been proposed for estimating the parameters of the sinusoidal model. Estimation of parameters is typically accomplished by peak picking the Short-Time Fourier Transform (STFT). Usually, analysis by synthesis is used in order to verify the detection of every spectral peak.

When the parameters of the sinusoidal model vary with time, the harmonic synthesis model involves a peak-tracking process, which is usually carried out by means of linear interpolation of the amplitudes, while cubic interpolation is used for the phases [1, 3]. This type of interpolation supposes an important limitation due to the need to overlap adjacent frames so as to track changes in the input signal.

Assigning tones to spectral peaks is a direct and simple method to obtain the parameters of the sinusoidal model. Nevertheless, the accuracy of the model, specially in frequency, is limited by frequency sampling, inherent to the discrete Fourier transform.

Another possibility is the definition of over-complete dictionaries which contain enough elements to obtain a precise model. Finding the best linear expansion using a redundant dictionary is a hard problem, that can be NP-hard in the general case. Suboptimal solutions can be sufficiently good. Among them, the Matching Pursuit (MP) algorithm proposed by Mallat and Zhang [4] which has been applied with success for sinusoidal modeling. Unfortunately, the computational complexity of this algorithm is so high, that real time implementations are difficult. Several proposals have appeared in the literature in order to save operations to implement the MP algorithm with particular over-complete dictionaries, like sinusoidal or wavelet functions [5] [6].

Another interesting approach, that can be applied to any kind of dictionary, is the organization of the elements in clusters, in order to implement a *Tree-Based Pursuit* (TBP) [7]. Highly redundant sub-dictionary of atoms are represented by a unique element, called *molecule*. In the original proposal of TBP, the authors studied how to structure redundant dictionaries in clusters, and the computational complexity of tree-based search, compared with MP. In this paper, the use of *Diametrical Clustering* [8] to organize the over-complete dictionary of sinusoidal functions is proposed. The obtained clusters have molecules whose correlation has been minimized, but the correlation with the atoms of the cluster is maximized.

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2. MATCHING PURSUIT

The Matching Pursuit algorithm was introduced by Mallat and Zhang. So as to explain the basic ideas concerning this algorithm, let's suppose a linear expansion approximating the analyzed finite length signal, represented by vector $\mathbf{x}$ in terms of vectors $\mathbf{g}_i$ chosen from a over-complete dictionary $D = \{\mathbf{g}_i;\ i = 0, 1, \ldots, L-1\}$. The L elements of the dictionary span $\mathbf{C}^L$ and are restricted to have unit norm. It is possible to build the approximation one term at a time by selecting at each step the atom which best correlates with the residual vector. Greedy algorithms, like MP, extend this idea to general dictionaries. It offers a suboptimal solution for decomposing a vector $\mathbf{x}$ in terms of unit norm expansion vectors $\mathbf{g}_i$ chosen from an overcomplete dictionary D. At the first iteration, the atom $\mathbf{g}_i$ with the largest inner product with the analyzed signal is chosen. The contribution of this vector is then subtracted from the signal, and the process is repeated on the residual.

The problem of choosing the vector $\mathbf{g}_i$ which represent the largest part of energy of the analyzed signal or vector is computationally very complex. MP is an algorithm that offers a sub-optimal solution by means of an iterative algorithm. Every step of the iterative procedure the vector in the set D which gives the largest inner product with the signal ($< \mathbf{x}, \mathbf{g}_i >= \mathbf{x}^T\mathbf{g}_i$) is chosen. The iterative procedure is repeated on the subsequent residue $\mathbf{r}^m$:

$$\begin{aligned} \mathbf{r}^0 &= \mathbf{x} \\ \mathbf{r}^m &= \alpha_{i(m)} \cdot \mathbf{g}_{i(m)} + \mathbf{r}^{m+1} \end{aligned} \tag{3}$$

$$\mathbf{g}_{i(m)} = \arg\min_{\mathbf{g}_i \in D} \|\mathbf{r}^{m+1}\|^2 \tag{4}$$

The orthogonality principle ($< \mathbf{r}^{m+1}, \mathbf{g}_{i(m)} > = 0$) allows us to compute the value of $\alpha_{i(m)}$:

$$\alpha_{i(m)} = \frac{< \mathbf{g}_{i(m)}, \mathbf{r}^m >}{< \mathbf{g}_{i(m)}, \mathbf{g}_{i(m)} >} = \frac{< \mathbf{g}_{i(m)}, \mathbf{r}^m >}{\|\mathbf{g}_{i(m)}\|^2} \tag{5}$$

where $\alpha_{i(m)}$ is the weight associated to the the optimum function (or atom) $\mathbf{g}_{i(m)}$ at the m-th iteration.

This algorithm is quite suitable for signal representation because the procedure converges to the vector $\mathbf{x}$ [4], and the signal energy is conserved:

$$\|\mathbf{x}\|^2 = \sum_{m=0}^{M-1} | < \mathbf{r}^m, \mathbf{g}_{i(m)} > |^2 + \|\mathbf{r}^M\|^2 \tag{6}$$

3. COMPUTATIONAL COMPLEXITY OF THE MATCHING PURSUIT ALGORITHM

The computational complexity of the MP algorithm is very high, and is caused by the following factors:

- For initializing the algorithm, correlations of signal to be decomposed with the dictionary atoms must be calculated, which results in a computational complexity of $O(Mlog(M))$ [9]. If the dictionary is composed of complex exponentials or wavelets, an efficient algorithm can be found in order to calculate correlations [5] [6].
- Correlations must be updated every iteration of the algorithm, which results in a computational complexity of $O(M)$.
- At each iteration, the possible coefficients of the linear expansion must be calculated and the optimum one, must be selected.
- The computational complexity grows up with the number of extracted atoms. On the other way, the quality of the signal model can be related to this number of atoms. Therefore, a trade-off relation between complexity and accuracy must be taken into consideration.

In order to reduce the complexity, several approaches have appeared in the literature, that use orthogonal transforms, like DFT or wavelet transform, to calculate the coefficients at each iteration. Another interesting approach to reduce the computational complexity is to organize the dictionary. Similar atoms are grouped together, and represented by a unique atom, which is called *molecule*. The reduced complexity does not have a penalty on the approximation accuracy [7]. The advantages of using this idea become more evident if two dimensional signals are considered, such as Synthetic Aperture Radar images [10].

4. DIAMETRIC CLUSTERING

Jost et al. [7] studied the properties of subdictionaries in order to be used to obtain sparse approximations of signals using greedy algorithms. They established that if the atoms in the dictionary D are sufficiently uncorrelated, a simple greedy algorithm is able to recover a sparse approximation of the signal. Unfortunately, overcomplete dictionaries are highly correlated redundant dictionaries. The idea behind Tree-Based Pursuit is the representation of correlated dictionaries by molecules, minimizing the correlation among molecules at the same time.

First of all, let set the nomenclature in the same way used in [7]. Let the elements of the dictionary $D = \{\mathbf{g}_i\}_{i \in \Gamma}$ be labeled by the index set Γ. A subdictionary is defined as the set of elements such as $i \in \Lambda$, where $\Lambda \subset \Gamma$. The subdictionaries have the following properties: $\cup_i \Lambda_i = \Gamma$ and $\Lambda_i \cap \Lambda_j = \emptyset, \forall i \neq j$. The subdictionary or cluster is represented by a molecule or centroid ($\mathbf{m}$), which minimizes the mean distance to all the elements of the cluster:

$$\mathbf{m}_\Lambda = \arg\min_m \sum_{i \in \Lambda} d(\mathbf{m}, \mathbf{g}_i) \tag{7}$$

In order to minimize coherence of a subdictionary, defined by:

$$\lambda_\Lambda = \min_{i,j \in \Lambda} | < \mathbf{g}_i, \mathbf{g}_j > | \tag{8}$$

the distance between two unit energy atoms is defined by [7]:

$$d(\mathbf{g}_i, \mathbf{g}_j) = 1 - | < \mathbf{g}_i, \mathbf{g}_j > |^2 \tag{9}$$

Therefore, for the defined distance to be minimum, the magnitude of the correlation between atoms must be maximum.

The Diametrical Clustering algorithm proposed by I.S. Dhillon [8], is used to find clusters containing vectors that are highly positively correlated or highly negatively correlated. The square of the correlation coefficient $S(\mathbf{g},\mathbf{h}) = (\mathbf{g}^T\mathbf{h})^2$, where $\mathbf{g}$ and $\mathbf{h}$ are vectors with mean zero and norm one, is known as *similarity measure*. This measure is high if the vectors have high positive or negative correlation. Our objective is to find the representative vector $\mathbf{x}_j$ that maximizes the similarity measure:

$$\max_{\mathbf{x}_j} \sum_{\mathbf{g}\in\mathbf{C}_j} (\mathbf{g}^T\mathbf{x}_j)^2 = \max_{\mathbf{x}_j} \sum_{\mathbf{g}\in\mathbf{C}_j} \mathbf{x}_j^T(\mathbf{g}\mathbf{g}^T)\mathbf{x}_j \qquad (10)$$

The optimal solution to this problem was provided by Golub and Loan [11]. It is achieved when $\mathbf{x}_j$ is the dominant right singular vector of the matrix $\sum_{\mathbf{g}\in\mathbf{C}_j} \mathbf{g}\mathbf{g}^T$. A measure of quality is given by the total squared correlation coefficient, being $\mathbf{v}_j$ the dominant vectors mentioned above:

$$Q(\mathbf{C}_1,\mathbf{C}_2,...,\mathbf{C}_k) = \sum_{j=1}^{k} \sum_{\mathbf{g}\in\mathbf{C}_j} (\mathbf{g}^T\mathbf{v}_j) \qquad (11)$$

Diametrical clustering is implemented as an iterative process, with two main tasks: singular vector analysis, and reorganization of clusters, according to the similarity measure.

5. EXPERIMENTS

In order to illustrate the performance of diametrical clustering and its potential utility to implement TBP, we have carried the following experiment. A dictionary of sinusoids has been built, with 512 atoms of 128 samples each. The set of functions can be modeled as follows:

$$g_m[n] = cos\left(\frac{m\pi n}{512}\right) \qquad (12)$$

being $m \in \{1,...,512\}$ and $n \in \{1,...128\}$.

We have implemented the necessary code to divide the dictionary in four clusters. The clusters and centroids have the following properties:

- Correlation between the centroid and each atom in its cluster must be higher than the correlation with the atoms of other clusters.
- If the correlation is maximum, the distance defined in expression (9) is minimum. It means that clustering is useful for MP implementation, because we can focus the search to the atoms of the selected cluster, reducing the computational complexity. This idea can be iterated.
- The centroid of each cluster is the dominant right singular vector of the matrix $\sum_{\mathbf{g}\in\mathbf{C}_j} \mathbf{g}\mathbf{g}^T$.

The computational complexity is reduced compared to the direct implementation of Matching Pursuits, once the structure of clusters and centroids is obtained. This reduction is due to the following reasons:

- The first step in the implementation of MP is the calculation of the correlations between the original signal and the atoms. If 2^N atoms are defined in the dictionary, 2^N correlations should be obtained with the direct implementation. If we use TBP, only two correlations are calculated in each layer of the tree, giving rise to $2N$ correlations in total.
- The second step is the calculation of the residue. This residue is obtained by subtracting the projection of the signal in the selected atom (exp. (3)).
- The direct implementation of MP requires to calculate $< r^m[n], g_i[n] >, \forall i$, at each step of the algorithm. This calculation can be substituted by an updating procedure, where the correlations at each step are obtained by updating the correlations used in the previous step. The knowledge of the correlations among atoms is necessary, which demands huge amounts of memory. If TBP is used, we can calculate the $2N$ correlations that are necessary in each step, without the used of any updating procedure.

Figures 1 to 4 represent the centroids of the four clusters. On the other hand, Figure 5 represents the magnitude spectra of the centroids, demonstrating that they concentrate the energy in different frequency bands.

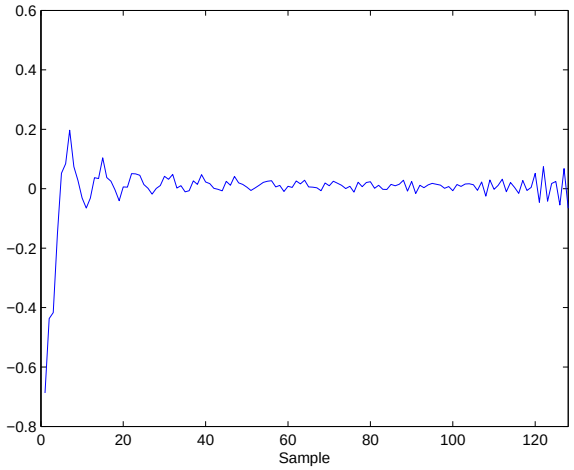

Figure 1: Centroid of the first cluster.

The absolute value of the correlations of the elements of each cluster with the first, second, third and fourth centroids are represented in Figures 6 to 9. It must be highlighted that the correlation between the atom and the centroid of the cluster it belongs to is almost always higher.

6. CONCLUSIONS

In this paper, we have discussed about the applicability of Diametrical Clustering to reduce the computational complexity of Matching Pursuit. The Tree-Based Pursuit algorithm is considered to implement Matching Pursuit.

Diametrical Clustering is proposed for organizing the atoms in clusters and also for calculating the centroids of each cluster. It has been implemented as an iterative process, with two main tasks: singular vector analysis, and reorganization of clusters, according to the similar-

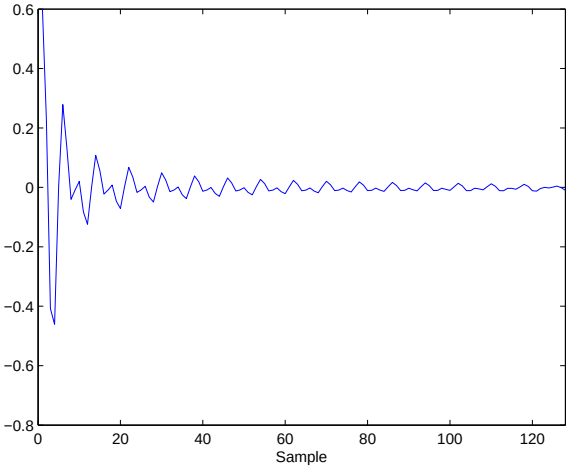

Figure 2: Centroid of the second cluster.

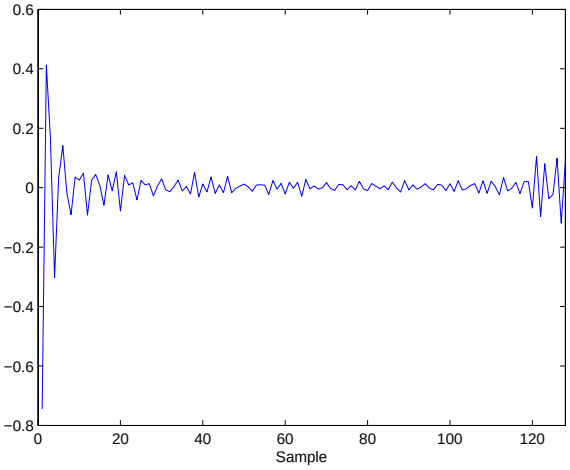

Figure 3: Centroid of the third cluster.

ity measure. This measure is defined as the squared correlation coefficient between two atoms. The result is an organization of the dictionary, where the correlation of the atoms in a cluster with its centroid is higher than their correlation with the other centroids.

To illustrate performance, a simple experiment has been presented, where a dictionary composed of 512 sinusoids is organized in four clusters. Some figures are included in the paper to show the performance of the algorithm, demonstrating its utility in this task.

The centroids of each cluster have been represented in the time domain and the frequency domain, demonstrating that they concentrate energy in non-overlapping bands. We have also obtained the correlations of the elements of each subdictionary with the molecules or centroids, demonstrating that the correlation are higher with the centroid of the corresponding cluster.

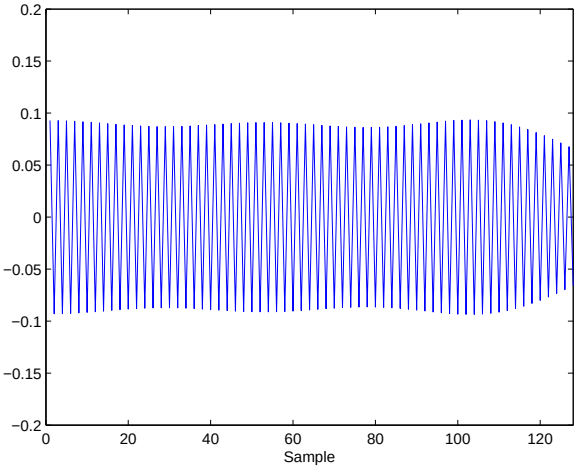

Figure 4: Centroid of the fourth cluster.

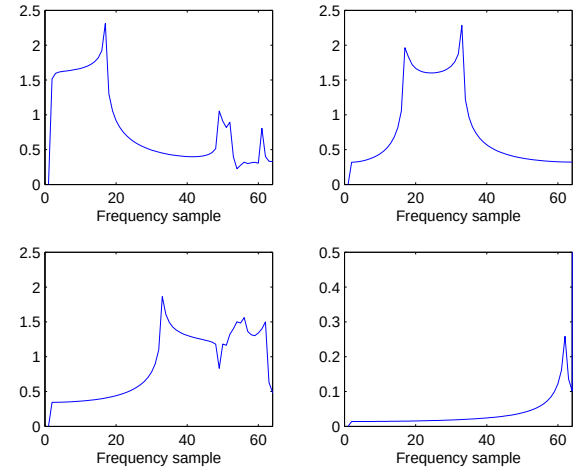

Figure 5: Magnitude spectra of the four centroids.

7. ACKNOWLEDGEMENT

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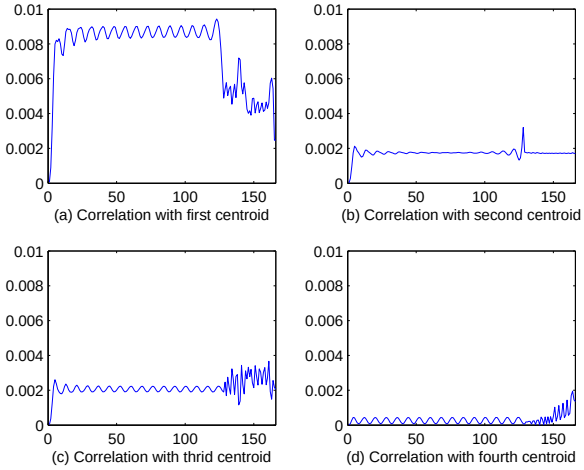

Figure 6: Correlations of the atoms in the first cluster with the four centroids.

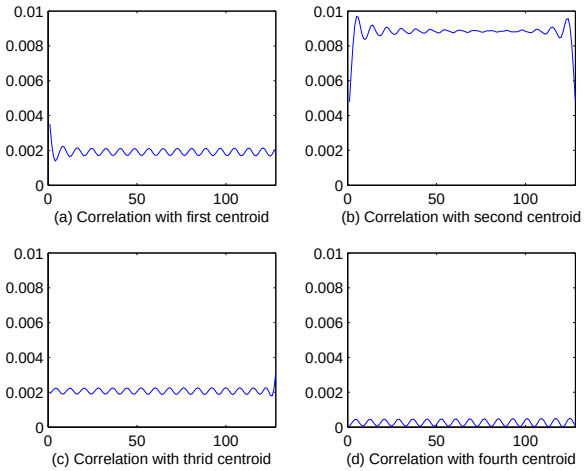

Figure 7: Correlations of the atoms in the second cluster with the four centroids.

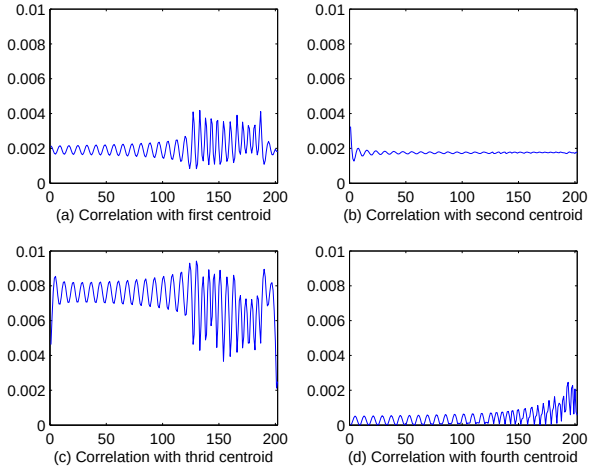

Figure 8: Correlations of the atoms in the third cluster with the four centroids

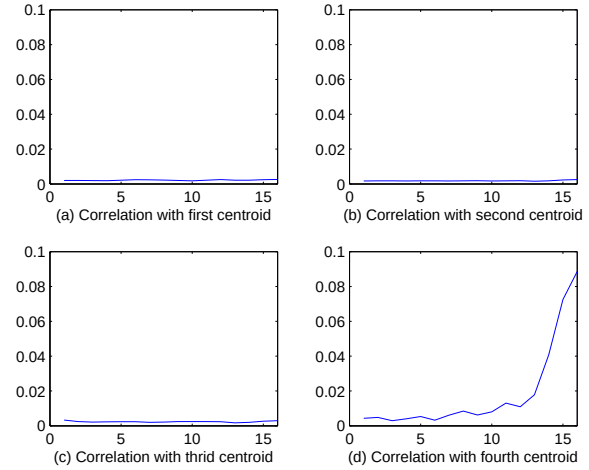

Figure 9: Correlations of the atoms in the fourth cluster with the four centroids.

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