Assessing Normality of Heart Sound by Matching Pursuit Residue with Frequency-domain-based Templates

Hong-Hui Chen, Tung-Chien Chen and Liang-Gee Chen

Abstract— The healthiness of the heart is import to human for leading a healthy life. Some of the abnormal conditions of heart could be detected by the heart sound. For example, heart murmur is one of the conditions possibly resulting from the illness of heart valves. In this work, we propose a new template family used in the matching pursuit (MP) algorithm to assess the degree of normality of the heart sound. Not only the rating of normality is generated but also an intuitive visual feedback with abnormal interval highlighted is outputted. In this way, the condition like heart murmur is well-identified by inspecting the matching residue. Comparison with previous work which adopts different template family is also given. Experiment results indicate that the proposed family is more effective to matching the normal heart sound to achieve better assessing result.

I. INTRODUCTION

Human heart sound [1], also called phonocardiography (PCG) [2], is composed of several components. These components are S1, S2, S3 and S4 as shown in Fig. 1. S1 and S2 are more prominent than the rest of 2 components. S3 and S4 may be lack in PCG for most of the people. The closings of the heart valves result in the S1 and S2 sounds. If there is any anomaly happening to the heart valves, extra noise, called heart murmur, is often generated within the quiet period of the heart sound. The anomaly of the valves might lead to undesired conditions of humans including the difficulty of breath, faint after exercise, and lacking of blood in partial human body. For patients with serious conditions, the valve is required to be replaced with an artificial one.

To find out if there is any condition of the valves, traditionally we resort to doctors to conduct the inspection. The doctors use stethoscope to receive the heart sound from human body surface, including chest and back. Well-trained and experienced doctors can detect if there is any anomaly within the whole sound period and even more they could tell which part, systole or diastole, the abnormal conditions happen. One with detected abnormal condition can then be arranged to do further diagnosis like echocardiography to confirm the harmfulness of the condition.

In this work, we propose a new frequency-domain-based template family used with the matching pursuit (MP) algorithm [3]. The main idea is to assess the normality of

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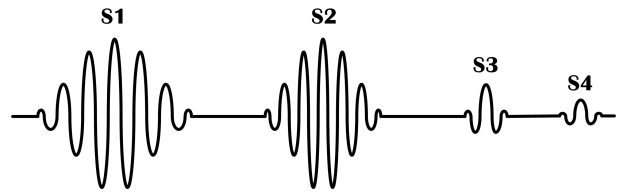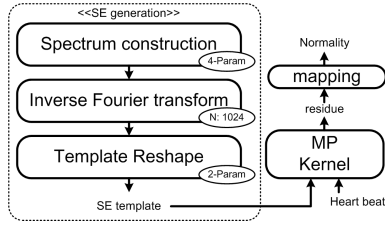
Fig. 1. Heart sound of human

the heart sound by applying suitable algorithm. If the result indicates that there is a high possibility of the abnormal conditions, one could then seek to inspect the exact condition by the doctors in the hospitals. Our algorithm does not try to classify which abnormal condition it is because it is risky to do an automatic diagnosis of human whose individual differences is quite high. Our goal is to provide a pre-screening tool like [4]. If the tool is affordable and easily accessible, everyone could pay more attention to the health of the heart in a more regular basis and benefit from it.

There are several advantages of selecting matching pursuit as the primary resort to assess normality of heart sound. First, it is friendly to parallel computation, which fits adequately in current prevailing computation architecture, for example, generic homogeneous processors and cloud computing with balanced peer computing capability. Compared to other common computing schemes [5][6] adopted in medical applications which are mainly composed of feature extraction and classification processes, the computational load and bottleneck of MP are more predictable. The computation time of feature extraction processes vary from feature to feature. Besides, the computational order of growth of the classification process if realized by advanced classifier, like SVM [7] is normally more than linear. This is generally not desired for large-scale data set. Secondly, if the matching templates are well partitioned to different computation nodes, matching pursuit algorithm is more robust to node malfunction. That is if the neighborhood matching templates, which have similar MP searching parameters, are invoked in different nodes, the assessing result is not seriously affected if some of the node is out of service. On the contrary, classification results from the schemes with classifiers might be altered significantly when certain important feature is wrong. Thirdly, in our desired application, matching pursuit algorithm results in a more intuitive assessing result presentation. In addition to a rating of degree of normality of the heart sound, the suspicious portion of abnormal heart sound interval is identified within the out-of-matching windows of

Fig. 2.   Generation procedure of proposed SE template family

Fig. 3.   Example of one SE template

TABLE I
PSEUDO CODE OF SE TEMPLATE GENERATION

Auxiliary functions
LineSpace(A,B,K): linearly sample K points from A to B
NormalDist(X,A,B): normal distribution with mean A, and standard deviation B, X: input vector
IFFT(A,B): inverse Fourier transform with amplitude part A, phase part B
BarrelShift(A,B): rotate B times by shifting a sample from A's tail to its head
Amplitude outline
(K_Fs = 1024 for N == 1024)
X = LineSpace(0, $\frac{K\_Fs}{2}$, $\frac{N}{2}$+1);
AmpOutline[1:1:$\frac{N}{2}$+1] = NormalDist(X, μ, σ)
AmpOutline[$\frac{N}{2}$+2:1:N] = AmpOutline[$\frac{N}{2}$:-1:2]
Phase outline
PhaseOutline[1:1:$\frac{N}{2}$] = LineSpace($s\theta$, , $e\theta$, $\frac{N}{2}$)
PhaseOutline[$\frac{N}{2}$+1:1:N] = -PhaseOutline[$\frac{N}{2}$:-1:1]
SE template
T = IFFT(AmplitudeOutline, PhaseOutline);
SE = α * BarrelShift(T, β);
≪ **Matching window of SE: active region of SE [see Fig. 3]** ≫

the original heart sound. A graphical representation with suspicious portion could be highlighted as a feedback for the user. The schemes with feature extraction and classification presenting an integrated classifying result and lose track of the relationship between the time span and the classifying result. Therefore, it is more difficult for these kind of schemes to give an intuitive feedback to the users.

In a more broad point of view, MP could be regarded as only a single feature to the mentioned schemes in [5][6]. Though owing to the computational complexity, MP is not generally used as feature extraction means. From our point of view, this single MP feature is just enough to assess the normality of heart sound. It is overkill to use too many features to achieve our assessing goal. However, it is necessary for classifying purpose to use as many features as possible. The classifier works great if some of the input features are decisive to the classifying procedure. In our application, knowing degree of normality is first priority, therefore MP is a quite suitable algorithm for our purpose.

The previous work [8] of MP uses Gabor dictionary as matching templates to decompose the heart sound. It is a time-domain-based template family. In this work, we propose a new template family which is a frequency-domain-based one. The proposed template family matches the normal heart sound better and is well qualified for the assessing purpose of our application. The reminder of this paper is organized as follows. First the proposed templates and matching pursuit algorithm are introduced. Then the experimental results and comparison are presented. Finally the conclusions and future works are given.

II. PROPOSED SE TEMPLATES FOR MP AND HEART SOUND NORMALITY ASSESSMENT

The generation procedure of proposed template family is depicted in Fig. 2. We denote the proposed family as SE (S elimination where S is acronym from heart sound) family and the family from [8] as GB (GB is acronym from Gabor) family in the following context. To generate a SE template, the first step is to compose a spectrum with its amplitude outline as normal distribution and its phase outline as straight line with predefined slope. Figure 3(a)(b) illustrate these two outlines. The second step applies the inverse Fourier transform (IFFT) to produce time domain representation from the two input outlines. The sampling points of the two outline is the same as the point count N used in IFFT. Point count N is selected to be 1024 after a
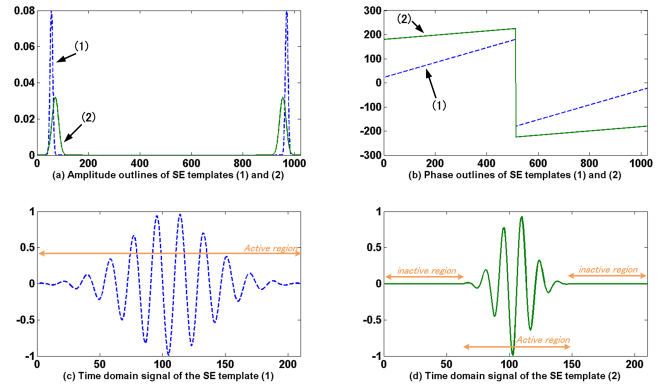
heuristic search of possible N number. 1024 is a trade-off between IFFT computational complex and the smoothness of the SE template in time domain representation after IFFT. Larger N gives better smoothness of the time domain signal while the computation time increases drastically. The third step applies gain and offset parameters to reshape the time domain signal and the generation of one single SE template now completes. Examples of SE templates are given in Fig. 3(c)(d).

Table I gives the pseudo code of the generation procedure. There are totally six parameters for generating a SE template. We define a possible range of parameters for normal heart sound, as listed in Table II, while searching the best matching patterns in the input heart sound with the MP procedure. Pseudo code of a complete search run with MP for heart sound components S1 and S2 is given in Table III.

In the thorough MP procedure, the algorithm tries to eliminate the 2 prominent heart sound component, S1 and S2.

TABLE II
SEARCH RANGE OF NORMAL HUMAN HEART SOUND

μ (search range of frequency mean) :	55 - 85
σ (search range of frequency standard deviation) :	5 - 20
$s\theta$ (search range of phase start) :	0 - 359
$e\theta$ (search range of phase end) :	0 - 359
α (search range of time-domain gain) :	0.1 - 1
β (search range of time-domain displacement) :	0 - N

TABLE III
MATCHING PURSUIT WITH SE TEMPLATES

B: resampled input heart sound

T = B **// for S1**
For S1, S2
 • In range(μ)
  In range(σ)
  In range($s\theta$)
   In range($e\theta$)
    In range(α)
     In range(β)
       S = SE(μ, σ, $s\theta$, $e\theta$, α, β)
       BDiff = B - S
       Residue = Sum(Abs(BDiff))
       if(Residue < MinResidue)
        MinResidue = Residue
        MinBDiff = BDiff
 • end of all loops
 T = MinBDiff **//update T for S2**
(**MinResidue**: for normality mapping)

The absolute values of the remaining samples are summed to form the MP residue which is used to assessing the normality of the heart sound. The normality is rated via a mapping curve with the residue input as the seed.

There are multiple choices of normality mapping curves. Some examples are depicted in Fig. 4. Curve (I) is more pessimistic than others and is more sensitive to the remaining residue. The curve should be selected based on the recording capability of applied devices (ex: signal-to-noise ratio) and operating condition (ex: quietness of the environment, measuring spot of the PCG, stillness of the measured target). Curve (II) is selected for the assessing experiments in the following section for illustrative purpose.

III. EXPERIMENTAL RESULT AND COMPARISON

In previous work [8], the GB template family is generated using the following formula:
$$h_i(t) = \beta_i \cdot (2^{\frac{1}{4}} \cdot e^{-\pi \cdot (t - p_i/s_i)^2}) \cdot cos(2\pi f_i + \phi_i)$$
There are 5 parameters involved in the above formula. Their meanings are: β_i: gain, p_i: displacement, s_i: scale, f_i: frequency, ϕ_i: phase. Both the GB and SE families are used in the following experiments. The resolution (step of increment) of the looping parameters are selected on a best
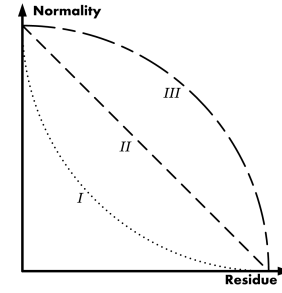

Fig. 4.   Mapping curves of matching pursuit residue for assessment
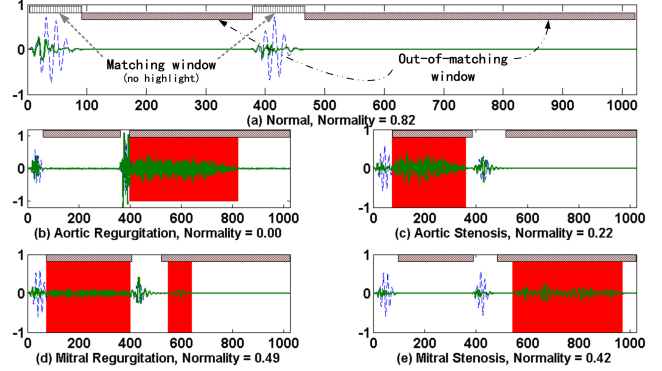

Fig. 5.   MP results of different input heart sounds [solid line: residues; dash line: original beats (visible if not overlaid by residue)]

effort basis, the MP algorithm stops further dividing of the looping increments if no significant residue reduction could be achieved. The run time of the GB differ SE families is different. Run time of SE is always longer for getting a minimal residue because it has more parameters to be searched than GB. Here we are trying to prove that SE is also a good approximation of heart sound originally derived from the frequency-domain spectrum. As for dealing the run time overhead, an accelerated version of the MP with SE family is under development and seems promising without signification performance degradation. We do not discuss how to accelerate the algorithm here and leave it for future work.

The heart sound database from [9] is used to conduct the experiments. Heart sound is manually segmented to only a single beat before input to the MP procedure. Though automatic segmentation like [10] could also be used, we choose not to let the MP result be affected by the segmentation algorithm. The input heart beat is first resampled to the same length as IFFT point count N. Then the MP process starts with the parameters search range listed in II. Results of the MP procedure with different input heart sounds are shown in Fig. 5.

In Fig. 5, the suspicious interval resulting in the decreasing of normality rating is highlighted automatically as an intuitive feedback. The applied procedure not only effectively assesses the normality of heart sound but also gives back understandable hints of why the normality rating it is. It is

Residue remaining ratio (RRR)

Family	SE	GB
Normal	25.13%	26.18%
Aortic Regurgitation	95.73%	88.63%
Aortic Stenosis	72.50%	71.59%
Mitral Regurgitation	66.59%	63.84%
Mitral Stenosis	56.06%	56.93%

The residue remaining ratio (RRR) is defined as follows:

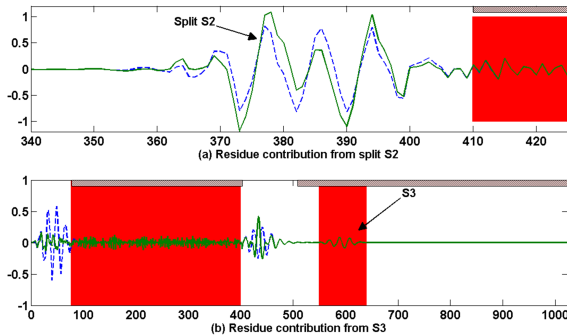**RRR** $= \sum_i |\text{residue(i)}| / \sum_i |\text{input beat(i)}| * 100\%$

Fig. 6. MP residues contribution from the split S2 and the existing S3 [solid line: residues; dash line: original beats (visible if not overlaid by residue)]

worth mentioning that some of the spectrum of the murmur segments is very similar to the S1 and S2 parts. Therefore it is not easy to separate this kind of spectrum by using simpler scheme like filtering.

The comparison of the MP residue of SE and GB are listed in Table IV. The residues of the MP result from SE and GB are very similar judged based on the residue remaining ratio (RRR) values. While the GB family is slightly better when pursuing the cases with heart murmur, SE family is 4% $((26.18 - 25.13)/26.18 * 100)$ better in RRR with a lower matching residue when pursuing the normal heart sound. Most of the residues from SE related to the cases with heart murmur are higher than that from GB. This means that SE do a better job when distinguish normal cases from abnormal cases than GB. There are several kinds of sources, in addition to the heart murmur, which contribute to the residue. In Fig. 6(a), which is the "Aortic Regurgitation" case listed in Table IV, there is a heart sound split in S2, therefore, the RRR is much higher than other cases. In the mean time, the existence of S3 on some cases resulting in higher RRR. As the denoted part in Fig. 6(b), the residue comes from this interval is quite a few. Previous research [11] points out that S3 might be harmful for certain situations but is not always true. The intuitive graphic feedback from the MP provides a handy means to inspect S3. One may further consult medical professionals, like doctors, to decide whether the highlighted part of the residue is harmful or not.

In our work, we put a higher priority on assessing the normal heart sound. Therefore SE family is more appealing to our targeted application because it fits normal heart sound well and makes normal cases distinguishable from the abnormal ones. However both the computation loads of the MP with GB and SE family are high. The MP algorithm with GB conducts 5-parameter search loops, while the one with SE has 6 parameters to search in the looping. The IFFT of SE templates introduce another computational burden. Therefore, total computational load of SE is surely higher than GB. However, the SE family can be deemed as a heart modeling means derived from frequency domain. It is a good complement to the existing time domain counterparts.

IV. CONCLUSIONS AND FUTURE WORKS

In this work, we propose a new template family, SE family, suitable for using in the MP algorithm to assess the normality of human heart sound. According to our experiments, MP algorithm with SE family is effective for judging the normality of heart sound. Compared to the previous work, SE family is better for representing the normal heart sound. However, its run time might be too long for practical use. Future works are to develop fast pursuing algorithm without significant performance degradation and deploy the accelerated MP algorithm to the targeted cloud-based platform for further experiments involving computational load balancing, feedback latency observation and error robustness of the whole system.

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