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Time- and Frequency-Based Approach to Heart Sound Segmentation and Classification

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Introduction

Phonocardiograph (PCG) is a recording of the sounds made by the heart. In this study we describe our approach to analyzing the PCG data set provided by the PhysioNet/Computing in Cardiology Challenge 2016 [1]. Our aim was first to identify the most distinct and repeating fundamental heart sound (FHS) segments [2], and then to analyze the energy content of the signal during FHSs and between them on multiple different frequency bands.

Method

The method we applied was based on our existing ECG event detection algorithms, which we translated to the domain (see figure 1). We created time-frequency surfaces in order to build informational models on the material at hand (see figure 2). The Similarity we created is a combined representative model to denote the interdata concurrent frequency components near FHS segments S1 and S2.

We formed an energy norm based event detector for FHS segment detection and decomposition. We determined the repetitive segments based on adaptive similarity value clusterization by maximizing the similarity value:

$$sim(A,B) = \begin{cases} \frac{cov(A,B)}{cov(A,A)}, cov(A,A) \geq cov(B,B) \\ \frac{cov(A,B)}{cov(B,B)}, cov(A,A) < cov(B,B) \end{cases}$$

Then we named the clusters S1 or S2 based on their relative time distribution. If only one cluster was identified, it was named s. This resulted in three sets of data: a set where both S1 and S2 FHSs were identified (*s1s2*), a set where only s was identified (*ss*), and a set where no repeating sounds were identified reliably enough (*remainder*). Table 1 lists the size of each event set.

Using the set of bandpass filters and inter-segment timings, we created three sets of markers: a total of 3818 markers for the *s1s2* set, 1811 markers for the *ss* set and 429 markers for the *remainder* set. More detailed descriptions on the sets will be published in [3].

Finally, we generated binary tree classifiers where each node used one PCG marker and a limit value. We selected the combinations of markers and limit values by minimizing the split entropy values. The resulting classification trees are detailed in table 2.

Results

As a result, we achieved a score of 0.79 (Se = 0.66 and Sp = 0.92) on a hidden test subset. The precision of event detection for each event type as compared with the reference was 99.8 %, when the ranges defined as noise in the reference were ignored (see table 3. for summary). The inconsistency rate was 2.46 % in the ss set, when we looked for cases where annotation was not consistent on either S1 or S2.

Conclusion and discussion

Our approach was based on methods we had implemented for other signal domains, and we were pleased to confirm that our event detection algorithm was accurate also in PCG context. We were, however, surprised by the considerable differences between the data from different sources (see figure 2.): a single node separated the set *training-f* with 99.2 % accuracy and the set *training-b* with 96.3 % accuracy from the other sets, which was much higher than the accuracy of single nodes in separating normal from abnormal events. We conclude that reliable patient identification with PCG data from multiple sources is likely to require other than only time-frequency based approach, or at least substantial adjustments to balance the measurement position and device-specific differences.

References:
[1] Liu C, Springer D, Li Q, Moody B, Juan RA, Chorro FJ, Castells F, Roig JM, Silva I, Johnson AE, Syed Z, Schmidt SE, Papadaniil CD, Hadjileontiadis L, Naseri H, Moukadem A, Dieterlen A, Brandt C, Tang H, Samieinasab M, Samieinasab MR, Sameni R, Mark RG, Clifford GD. An open access database for the evaluation of heart sound algorithms. Physiological Measurement 2016;37(9).
[2] Leatham A. Auscultation of the Heart and Phonocardiography. Second edition. Churchill Livingstone, 1975.
[3] Mäkelä J, Väänänen H. Time and Frequency -Based Approach to Heart Sound Segmentation and Classification. Computing in Cardiology 2016, submitted.

Summary

The objective was to automatically detect cardiac sound patterns from data and to identify normal and pathological subjects.

Although our software framework was originally developed for electrocardiographic (ECG) data we were pleased to verify that after small tweaks our methods were also applicable to the very different signal domain of heart sounds.

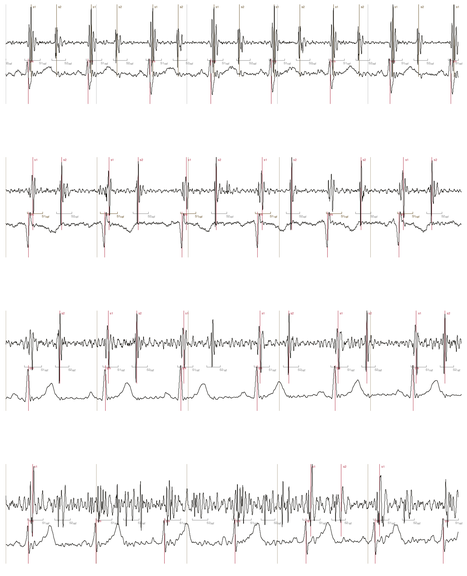


FIGURE 1. Four example cases with QRS detections in ECG, and with repeating FHS detections and reference annotations in PCG

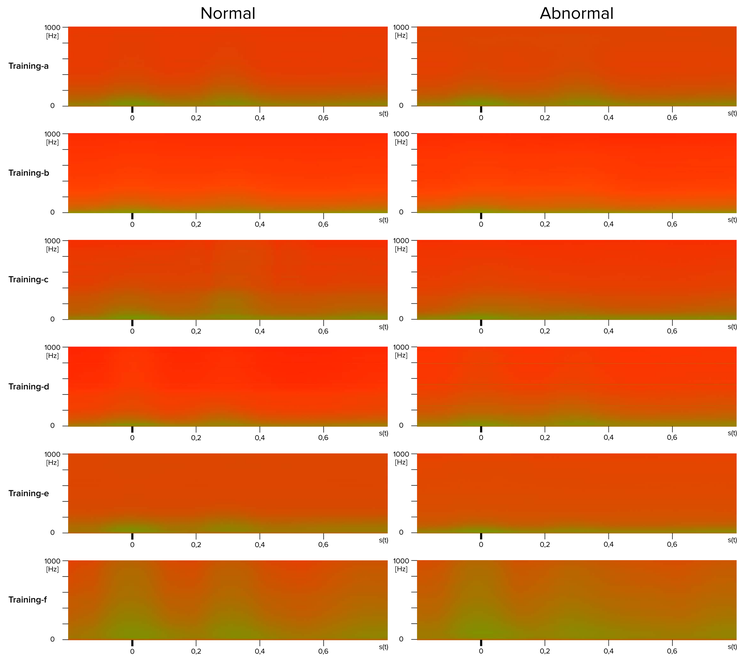


FIGURE 2. Time – frequency distribution of the concurrent energy in normal and abnormal datasets from separate data sources. See [1] for more info about the sources.

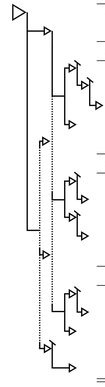
TABLE 1. Distribution of training set data in heart sound decomposition sets by patient groups

Event set	Normals	Abnormals	Total
s1s2	1402	203	1605
ss	761	292	1053
remainder	325	170	495

TABLE 3. Event detection precision (Prec) compared to reference events. Prec is defined as TP / (S1+S2+FP), where TP is S1 for s1, S2 for s2 and S1 or S2 for ss. Noise is the number events detected inside reference noise annotations. False positive (FP) reflects the detected events that don't match any reference event.

Event	S1	S2	Noise	FP	Prec
s1	21793	413	417	14	0.981
s2	611	17369	657	76	0.962
ss	8976	516	517	19	0.998

TABLE 2. The biggest nodes in the three classifier trees. WHAT, WHERE, TO and HOW are type descriptors for node parameters. $Freq_{low}$ and $freq_{high}$ are the filter bandpass frequencies. Limit is the binary limit of the left and right separator. N and Abn are abbreviations for normal and abnormal patient groups. See [3] for more accurate description.



	WHAT	WHERE	TO	HOW	$freq_{low}$	$freq_{high}$	limit	N left	Abn left	N right	Abn right
trunk											
-	NORM	seq	-	max	300	500	0.154				
L	NORM	seq	-	min	0	25	0.596				
s1s2											
LL	NORM	s2s1	-	min	100	200	0.157	141	153	1179	16
LLL	REL	s2s1	s1	minmax	400	600	0.502	62	3	79	150
LLLR	ABS	s1s2	-	min	750	850	0.586	63	53	16	97
LR	NORM	seg	-	min	25	50	0.275	48	0	15	31
R	ABS	s2s1	-	all	-	-	133.5	19	0	0	3
ss											
LL	NORM	ss	-	min	75	100	1.33	69	191	484	15
LLL	REL	ss	s	minmax	500	700	0.486	24	2	45	189
LR	NORM	seg	-	min	25	50	0.256	119	13	50	60
LRR	WIDTH	s	-	50%	125	150	0.052	47	22	3	38
R	ABS	seq	-	min	125	150	0.172	29	1	10	12
remainder											
LL	NORM	seg	-	min	87.5	112.5	0.145	31	68	27	1
LLL	ABS	seg	-	minmax	0	25	442	12	63	19	5
LR	ABS	seg	-	min	350	400	0.601	220	63	0	8
R	NORM	seg	-	min	12.5	37.5	0.218	21	0	26	30
RR	NORM	seg	-	min	225	250	0.020	25	15	1	15