A Statistical Technique to Assess Overall Cardiac Ventricle Contraction Dyssynchrony[1]

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Dyssynchrony between patterns of strain developed by different cardiac ventricular regions can indicate an activation abnormality or the failure of activated tissue to contract. To quantify overall chamber dyssynchrony with one number, we implemented a cross-correlation technique first developed with Doppler velocity images [1-2], and applied the method to calculate time delays between strain (σ) waveforms of paired tissue regions [3]. We then derived one average time delay (TD avg) from all region strain pairs distributed through an image.

The method acquired a long axis two-dimensional echocardiographic view from a Philips ultrasound scanner. Image acquisition was followed by strain calculation at seven adjacent regions of the myocardium by Philip's QLAB software. From each region x and y pairing, a cross-correlation function $Rxy(j) = \sum_{i=0}^{M-1} \sigma x(i) * \sigma y(i+j)$ between σ waveforms was assessed over M samples spanning the RR interval, and normalized time delay (TD xy) was computed based on the correlation's index of maximum (jmax). With strain measured from all seven regions of the myocardial wall, the TD xy results collected from 42 possible region pair combinations were combined to form the TD avg.

$$TD\ xy = \frac{index\ jmax\ \ of\ the\ Rxy(j)\ maximum}{M-1}\ ,\quad \text{TD avg} = \sum_{x=1}^{7}\sum_{y=1, y\neq x}^{7} |\text{TD xy}|\ /42 \qquad (1)$$

The TD avg output of calculation was applied to numerically gauge timing of subjects having no apparent functional abnormality (Normal group: 291 data sets from 291 patients with one time point measure each), and subjects undergoing cardiac resynchronization therapy (CRT group: 149 data sets from 22 patients with multiple time point measures during pacing adjustment). Comparing means of the TD avg results between groups, Normal strain development was synchronous (Normal TD avg = .014 ± .007), whereas CRT group strain was comparatively dispersed between different regions of the myocardium (CRT TD avg = .036 ± .031, $p < 10^{-6}$ unpaired). The Normal group's 95% confidence interval of the TD avg measure (0< =TD avg <=.028) was also exceeded by at least one time point in 18 CRT patients.

The developed software presents a simple user interface for the selection of strain waveform pairs and the associated display of correlations within a matrix of TD xy results. The software also generates a structured report of different calculation endpoints including TD avg and the maximum of all TD xy measures. Applying the TD avg endpoint, our results now suggest a further investigation to examine whether the general differences we observed between Normal and CRT groups can be refined into an index with useful diagnostic sensitivity. The development of a sensitive measure based on strain, might also benefit from a well-defined model of the normal strain waveform, and the application of such a model to interpret data collected from one or more image views. As strain data is conveniently captured from the echo image, the ability for rapid post-processing based on strain may then facilitate an easily applied basis to assess dyssynchrony, diagnose the need for CRT, or measure the effectiveness of adjustments to different modes of CRT pacing.

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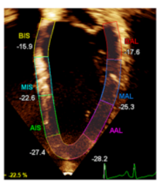
Introduction

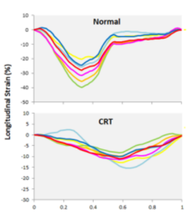
Different regions of the cardiac chamber are normally activated to contract simultaneously, but interregional activations can become dyssynchronous and lead to the need for pacing interventions by Cardiac Resynchronization Therapy (CRT). To assess timing properties indicating CRT patient timing differences from normal functioning patients, we applied a method to calculate cross correlation time delays (TD xy) between different tissue region strain (σ) waveforms, and computed one average time delay (TD avg) from all measurable region pairs distributed through an echocardiogram image.

Methods



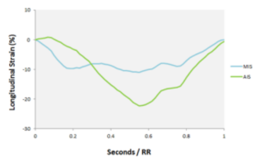
- Each data set was formed by a left ventricle echo image acquired from a Philip's scanner, and seven adjacent image regions defined the myocardium locations of strain waveform measurement by Philips QLAB software.

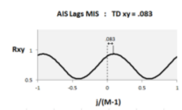
- The waveforms were processed to gauge timing from a Normal group of 291 data sets collected from 291 different patients, and a CRT group of 149 data sets from 22 patients with multiple measures performed during the CRT pacing adjustment. One representative data set from each patient group is shown.



Processing

- Measures of strain from each image region pair (x and y) were then provided as the waveform inputs to calculate correlation $Rxy(j) = \sum_{i=0}^{M-1} \sigma x(i) * \sigma y(i+j)$ over M samples spanning the RR interval. Normalized time delay $TD\ xy = \frac{jmax}{M-1}$ is computed based on the correlation function's index of maximum (jmax).



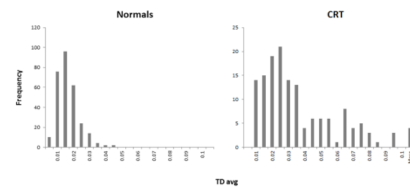


- 42 TD xy calculations from all pairings between different image regions will form entries to a synchronization result matrix, and from all entries the average interregional time delay factor is calculated.

$$TD\ avg = \sum_{x=1}^{7} \sum_{y=1, y\neq x}^{7} |TD\ xy| / 42$$

Rxy Wrapped	BIS	MIS	AIS	Apex	ApL	MAL	BAL
BIS		-0.03	0.03	0.02	0.00	0.02	0.00
MIS	0.03		0.08	0.07	0.03	0.05	0.05
AIS	-0.03	-0.08		-0.02	-0.03	0.00	-0.02
Apex	-0.02	-0.07	0.02		-0.02	0.02	0.00
ApL	0.00	-0.03	0.03	0.02		0.03	0.02
MAL	-0.02	-0.05	0.00	-0.02	-0.03		-0.02
BAL	0.00	-0.05	0.02	0.00	-0.02	0.02	

Results



Applying the technique, the Normal results : TD avg = .014 ± .007 and the CRT results : TD avg = .036 ± .031 demonstrated a statistical difference between mean values ($p < 10^{-6}$) . With 18 of the 22 CRT patients, the 95% confidence interval (0 < = TD avg <=.028) of the Normal group was also exceeded by at least one CRT procedure time point.

Conclusions

Our results indicate measurable trends of TD avg differences between the normal and CRT patient groups and suggest future work to now refine a reliable index with diagnostic sensitivity useful for diagnosis and effectiveness monitoring of the CRT pacing adjustment. The strain analysis might also benefit from a well-defined model of a normal σ waveform, with the model's application as a template for correlation.

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