

## Time-Frequency Domain Signal Processing for 3D Acoustic Impedance Microscopy and Its Application to Human Skin Observation

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### 1. Introduction

The acoustic impedance microscope technology has enlarged the capability to observe the biological matters in a very small scale, such as the cultured cell and human cheek skin. In the recent years, the scale of observation has reached the depth direction and the cross-sectional acoustic impedance section of the subject had successfully been obtained [1-2]. In the human cheek skin assessment by means of its acoustic impedance value, deconvolution process had become the most important step in order to reconstruct the reflection intensity that comes only from the interface between the skin and the substrate dish. The previous research also showed that the combination of the deconvolution performed in both time and frequency domain could retain most of the essential frequency components that existed inside the signal [1]. During the process of dual domain deconvolution, the low-frequency part calculated from the time domain deconvolution is combined with high-frequency part calculated from the frequency domain deconvolution by specifying a threshold level in order to reconstruct a full-resolution signal. In addition to that, a down-sampling operation is applied to the target and the reference signal to save the computation time. In this study, the amount of subjected low-frequency components by means of the threshold level and also the effect of performing a down-sampling operation will be discussed. As a result, a 3D reconstruction of human cheek skin that consists of 50 stacks of cross-sectional acoustic impedance image and also the estimation of the shape of horny and papillary layer was successfully calculated.

### 2. System Setup

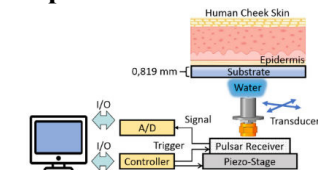


Fig. 1. The setup of the system

**Fig. 1** illustrates the setup of measurement system. A focused ultrasound wave with the center

frequency of 80 MHz is transmitted by a transducer to the object through a plastic substrate (polystyrene dish). A human cheek skin is attached to the other side of the substrate. A distilled water is used as the coupling medium. The transducer is controlled by a piezoelectric stage to scan the area along the x and y axis with the size of 2 x 0.5 mm, with the area resolution of 300 x 50 x 400 points for x, y and z direction (1 ns sampling interval), respectively.

### 3. Signal Processing

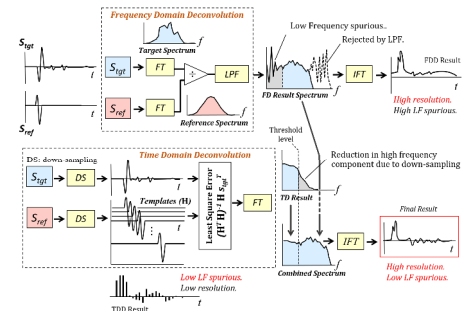


Fig. 2. The stream of signal processing

**Fig. 2** illustrates the stream of signal processing. The process begins by deconvolving the target signal (signal acquired from the interface between the substrate and the skin) with the reference signal (signal acquired from the interface between the substrate and water) in both time and frequency domain, separately. The down-sampling operation is applied to both signals before the time domain deconvolution. A threshold level is then specified in order to combine the high-frequency parts from the frequency domain deconvolution with the low-frequency parts from time domain deconvolution. The detail of dual domain deconvolution is precisely discussed in the previous research [1]. Since a template matrix is created by shifting the reference signal in time domain before the time domain deconvolution process, this will create a huge matrix if the sample size of the signal is large, which will slow down the computation time. **Fig. 3.a** shows the effect of performing down-sampling with the factor of  $2^n$  to the execution time. As the number of samples is decreased, the required time for calculation becomes shorter (the calculation time without

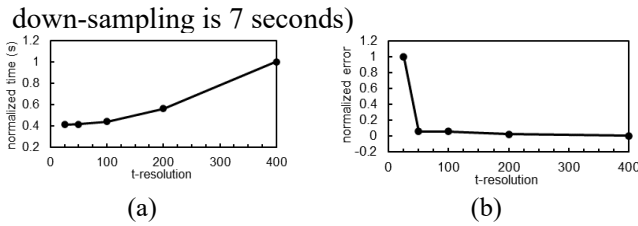


Fig. 3.a. (Normalized) The impact of down-sampling to the computation time. 3b. The impact of down-sampling and its corresponding error.

However, if the level of down-sampling factor is too high, as shown by **Fig.3.b**, it will alter the profile of the resulting signal because the number of samples required for the least square operation is too small. The terms of error in the graph is the absolute error or the difference of RMS between the down-sampled signal with the full-sized signal (without being down-sampled) which is used as a reference.

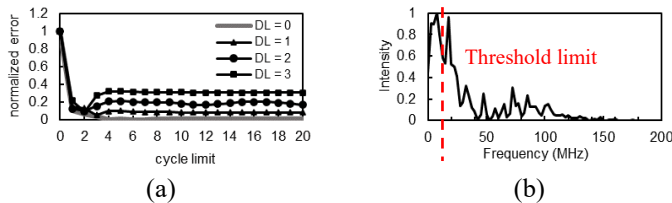


Fig. 4.a. The effect of the selected threshold value and its corresponding error. 4b. The spectrum as the output of dual domain deconvolution (ideal condition)

On the other hand, the amount of subjected low-frequency components into the signal by means of threshold level is shown by **Fig. 4.a** (DL: Down-sampling Level). Each limit value corresponds to one cycle of the window length (400 ns in time domain), which is equal to 2.5 MHz in the frequency domain. In this study, a full resolution signal (without down-sampling) with the cycle limit of 6 are set as the ideal condition for the number of low-frequency components, this corresponds to 15 MHz in the frequency domain, as the spectrum is shown by **Fig. 4.b**. In practice, before the down-sampling operation, a moving average is applied in order to retain the detail of the signal. However, as the number of samples are reduced by down-sampling, the spectrum resolution of the signal especially on the high frequency components will be reduced. This will create a large error when the number of cycles is increased, especially if the selected down-sampling factor is high. As shown by **Fig. 4.a**, the number of errors will increase along with the higher number of cycle limit and the level of down-sampling. This is because as the frequency resolution becomes smaller while the number of cycles is increase, there will be a zero gap between the low and high-frequency components which also becomes larger in the combined spectrum, resulting a distorted waveform. In the ideal condition, when the selected limit is too low (below 6), the number of low-frequency components subjected into the

signal is small, this means that the deconvolution is almost performed fully in the frequency domain. This will create an artifact in the acoustic impedance image because the low-frequency components are unstable.

#### 4. Result and Discussion

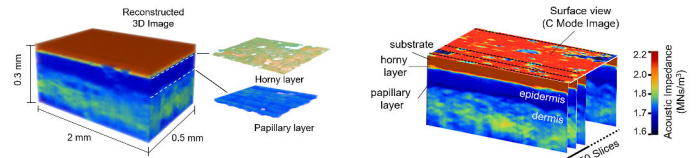


Fig. 5. The 3D reconstruction of the skin and the estimation of the shape of horny and papillary layer.

The deconvoluted signal is then transformed into the acoustic impedance distribution by utilizing an algorithm similar to the Time Domain Reflectometry (TDR) [1-2]. **Fig. 5**. Shows the result of the 3D reconstruction of human cheek skin calculated from the stacks of the cross-sectional acoustic impedance image. By observing the 3D result, the shape estimation of the horny and papillary layer could be generated. The average thickness of the horny layer is estimated to be as thin as 4.8  $\mu\text{m}$ .

#### 5. Conclusion

There are two important parameters that need to be specified carefully during the dual domain deconvolution, that is the level of down-sampling and the amount of the low-frequency components that are subjected into the signal. This study showed that performing down-sampling to the signal can reduce the computation time to be 50% faster. However, if the level of the down-sampling is extremely small, it will alter the profile of the signal. In this study, the best down-sampling level is 1 (200 samples), which is half of the original samples. The ideal condition to subject the low-frequency into the signal is as much as 6 cycles, which corresponds to 15 MHz in frequency domain. Since there is not a significant error even when increasing the number of cycles (on ideal condition), this means that the deconvolution in the frequency domain is actually not necessary, however, if the number of samples in the signal is large, the generated template matrix will also be large and it will make the computation time longer. By observing the generated 3D reconstruction image, the shape of the horny and papillary layer can be estimated. A further analysis based on the generated 3D acoustic impedance value can also be performed, which will be the continuation of the research in the future.

#### References

1. E. B. Prastika: J. Appl. Phys. 59 (2020) SKKB06-1.
2. T. W. Chean: J. Appl. Phys. 56 (2017) 07JF18.