Abstract

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Breast Cancer has been a threatening disease for decades and numerous research have been done to emprove its diagnosis and treatment, but all the current method are based on a qualitative analysis of the tumor and the pathology results may take days or weeks. Unfortunately, if the results from surgery comes out positive, the patient is much likely to undergo a second surgery.

This research focuses on a quantitative analysis of a terahertz image of a freshly excised breast tumor in order to produce results in almost real time. The san data consists of the signal at each pixel location in the image. Previous research have shown that these signals will be different based on the type of tissue cells at the pixel location. Therefore, it possible to classify tissue types as cancer, fat or muscles based on the distribution of poxel signals in the image.

Knowing that pixels in the same tissue type have the same signal and assuming that tissues of same type are morelikely to be in the same location, we can conclude that there is an spatial autocorrelation between pixels, wich led us to suggest an patial autoregressive model for our data. Moreover, pixels can have different distribution based on the type of tissues cells in the human breast. Therefore, we have also proposed a Gaussian mixture model (GMM) to analyze terahertz image data of breast cancer tumor.

Our first model, CAR model was used to analyze a terahertz image of pathology block in order to compare the patholo a murine tumor sample and compared