

Institutskolloquium

Thema: Development of Prognostic Model Based on Estimation of Degree of Tumor Regression

**Referent: Dr. Aliaksandr Nedzvedz, project manager
Deputy Head of Image Processing and Recognition Lab.,
United Institute of Informatics problems,
National Academy of Sciences of Belarus**

**Ort: Hörsaal 6
Erdgeschoss des Universitätsklinikums Aachen,
Pauwelsstr. 30, 52074 Aachen**

Zeit: Dienstag, den 16. November 2010, 14.15 bis 15.45 Uhr

Abstract:

Medical imaging is increasingly electronic in terms of image acquisition and display. Image detectors have become so sensitive that the amount of information acquired is greater than can be displayed at any one time without using special purpose hardware. Research in image processing methods is essential to fully exploit the information that has been acquired. Furthermore, the ability to extract quantitative information from images is becoming increasingly important, requiring algorithmic processing. In CT image processing, texture is especially important, because it is difficult to classify human organ tissues using shape or gray level information.

Some of the challenges are:

- 1) the shape of each organ is not consistent through out all slices of a 3D medical image and may change quickly where the inter-slice distance is large,
- 2) the gray level intensities overlap considerably for soft tissues.

On the other hand, organs are expected to have consistent and homogeneous textures within tissues.

The significance of the research presented here lies in its contribution to the image feature quantification and classification of normal tissue in Computed Tomography (CT) scans. The quantification will apply various features analysis methods to the collection of data about the tissues. The classification step will involve the application of statistical categorization to learn numerical descriptions of human tissue characteristics. In result a software system can classify semiautomatic and automatically normal tissues in CT scans using image information from organs regions.

The 3D image data consisted of 2D DICOM consecutive slices, each slice being of size 512 by 512 and having 12-bit gray level resolution. Using the Contour Models algorithm, we segmented five organs from coronial slices: lungs, great vessels, liver, renal and splenic parenchyma, and backbone. Separate segmentation allows to extract tumor regions. At this stage, in order to generate more organ data, each organ was then subdivided into 4 equal sized regions within the square convex hull of the organ; therefore, segmented regions were generated to be used for analysis and classification. We divided this dataset into a training set and a testing set.



The Institute of Electrical
and Electronics Engineers
Deutsche Sektion
Joint Chapter EMB

<http://ewh.ieee.org/r8/germany/emb/>

