INF219 - Interactive visual analysis of renal perfusion data

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ABSTRACT

Four dimensional perfusion data provides medical doctors with a wealth of information and may pose interpretation challenges. For this INF219 project, programs were designed and developed to convert raw 4D perfusion data into a set of shape parameter volumes which simplify the representation of the raw time/intensity curves (TICs), and were used for interactive visual analysis (IVA). IVA using linked views and soft brushing, offers a method of extracting valuable information from large time dependent data sets. One of the programs written for this project allows interactive viewing of a data set, its TICs and shape parameters, and has proved useful in exploring the TICs. This project provided excellent experience with programming C++ with OpenGL and with interactive visualization and analysis.

INTRODUCTION AND RELATED WORK

Perfusion data provides indispensable information for diagnostics. The passage of a contrast agent injected into a patient is registered by scanning the organ of interest over time. Medical doctors then interpret a set of 4D data, for example CT slices taken at (ir)regular time intervals, in order to confirm a diagnosis or to plan surgery. One may look through the data slices for visible changes showing the contrast agent passage, by animating the data back and forth through time, and looking at slices in relation to one another. Interactive visual analysis with linked views and brushing offers a method of extracting valuable information from large multivariate data sets. This project was based on methods from the study *Interactive visual analysis of perfusion data*, Oeltze et al. This project utilizes data from Bergen – a phantom kidney data set provided by the mathematics department of UIB, and a patient kidney data set from Haukeland University Hospital.

PREPARING DATA FOR IVA

DATA CONVERSION

The acquired kidney data can come in many forms, in the case of this project as MATLAB matrix files. These must be converted before they can be used in SimVis, the application chosen for IVA. First the data was converted from original form into a time series of *.vol* files (unsigned short integer 6 byte header: x,y,z dimensions, data array (for z for y for x)) Then converted to *.raw* files (single precision floats 24 byte header: x,y,z dimensions voxelx,voxely,voxelz dimensions, data array (for z for y for x)). Finally the .raw files converted by the program RAWConverter, into .hum format for loading into SimVis. (see INF219_pipeline.doc for more details)

SHAPE PARAMETERS

Shape parameters which simplify the representation of the TICs were generated for each voxel position by the project program ShapeParameters. The program has an interactive display for viewing TICs and shape parameters, as well as slicing through the volumes. The output is a set of shape parameter *.raw* files which serve as input to the program RAWConverter.

- PE (Peak enhancement) – Maximum intensity
- CAA (Contrast agent arrival time) – Scan-time where the intensity >= baseline
- TTP (Time to peak) – Time interval from CAA to PE time
- Slope – Slope from CAA to PE time
- Slope2 – Slope from CAA to time before PE time where intensity <= 90% PE

• Downslope – Slope from PE time to end time
• Downslope2 – Slope from time after PE time where intensity <= 90% PE to end time
• Integral (CAA to End) – Midpoint Riemann-sum from CAA to end time
• Integral(Entire TIC) – Midpoint Riemann-sum from over entire TIC

baseline – Minimum intensity

end time – Time after PE time where intensity <= 50% PE

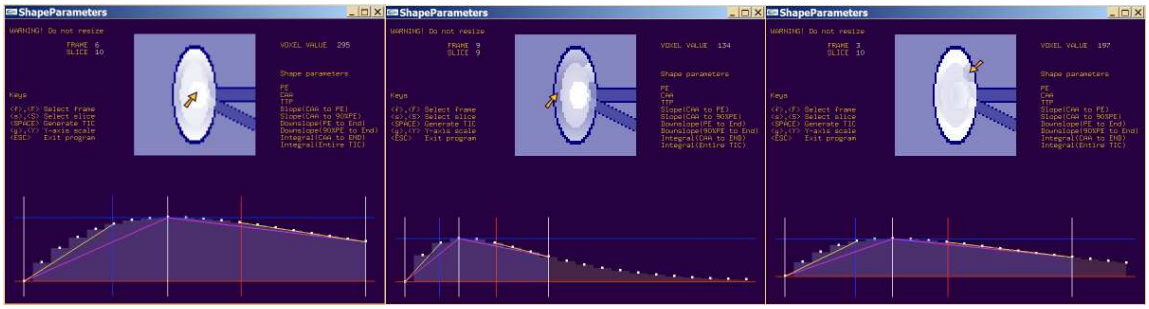

Figure 1 *Three TICs through different voxels. Note the TIC on the right, from an anomalous area of the phantom kidney.*

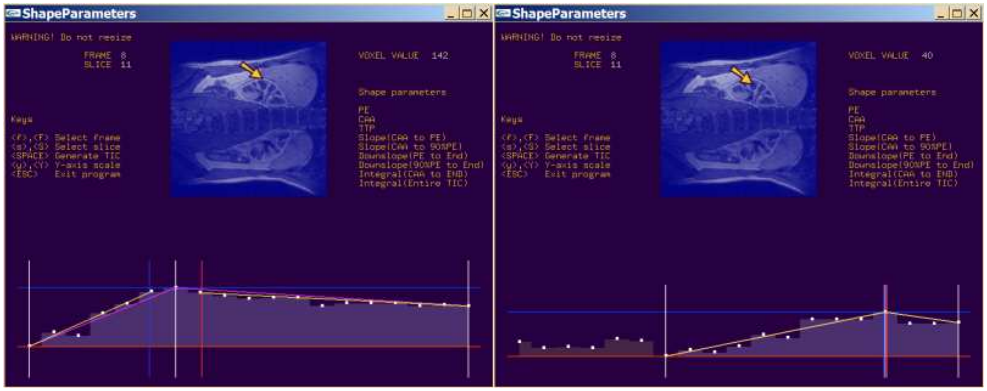

Figure 2 *A cortex TIC and a medulla TIC. These scans were from a healthy volunteer.*

IVA

The IVA in this project was done using SimVis. The converted SimVis .hum files for the entire data set, and for each of the shape parameters were used. Explorative analysis by brushing different variations of linked histograms and scatter plots revealed features in the data, and led to some interesting visualizations.

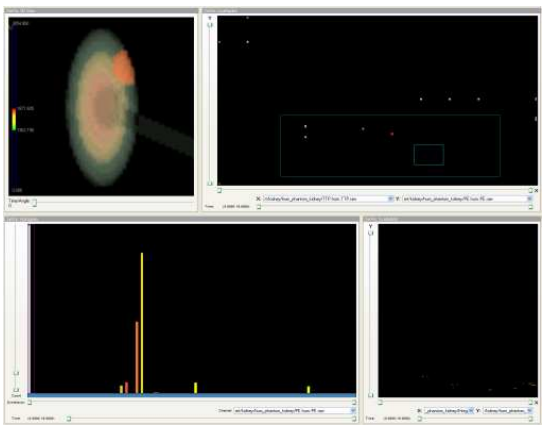

Figure 3 *Phantom kidney visualization, focusing on areas with relatively high TTP and low PE (the anomalous region upper right) The coloration of the volume showed the TIC integral. Soft brushing was used to show the entire kidney for orientation.*

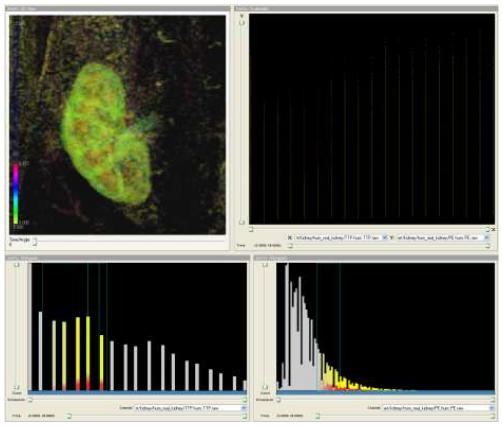

Figure 4 *Kidney visualization focusing on areas of high PE and relatively low TTP. The coloration visualized the CAA time and showed clear differences between the cortex and lower areas of the medulla.*

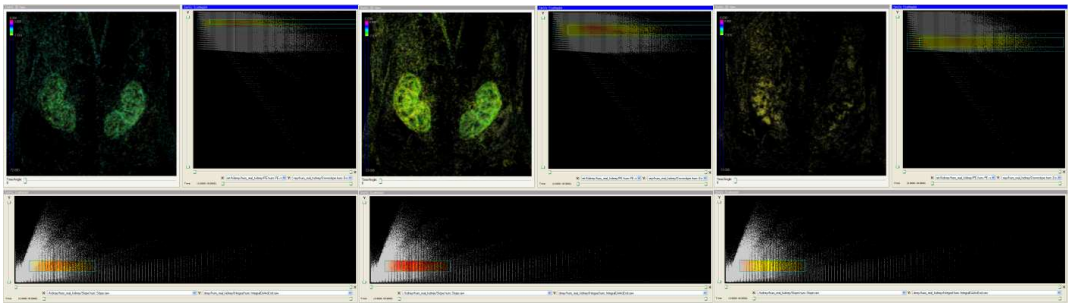

Figure 5 *Areas with a relatively high TIC integral and high PE were selected to focus on the kidneys. IVA with respect to TIC downslope differentiated anatomical structures. Downslope steepness decreased from left to right. Coloration reflected the TIC downslope.*

CONCLUSIONS AND FUTURE WORK

The results from the ShapeParameters program and of the IVA using the SimVis program demonstrated their usefulness in testing hypotheses about the data, as well as revealing expected and sometimes unexpected features in the data. Medical interpretation of the visualization results were not presented. In theory the process described in this project should help further develop the understanding of perfusion in different organ systems. However it remains to be seen if the process can be useful within the relatively short time-span from patient diagnosis to treatment. Data conversion was time consuming and in the future this may be automated. In addition, the shape parameter generating algorithms may be further developed. It would be interesting to try the method on several kidney perfusion data sets, also diseased kidneys and on data such as brain or breast.

REFERENCES

Interactive visual analysis of perfusion data, Oeltze et al., IEEE Transactions on Visualization and Computer Graphics 2007

Model-based measurement of kidney perfusion and glomerular filtration rate (GFR) using dynamic MRI, A Lundervold, BBG seminar 2008

A phantom model for testing registration in kidney perfusion analysis, A Zanna MedViz workshop 2008