Content-Based Analysis of Medical Image Data for Augmented Reality Based Health Applications

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Novel 3D sensors and augmented reality-based visualisation technology are being integrated for innovative healthcare applications to improve the diagnostic process, strengthen the doctor-patient relationship and open new horizons in medical education. Our aim is to help doctors and patients explain and visualise medical status using computer vision and augmented reality.

Data from medical 3D sensors, such as computer tomography (CT) and magnetic resonance imaging (MRI), give 3D information as output, thereby creating the opportunity to model 3D objects (e.g., organs, tissues, lesions) existing inside the body. These quantitative imaging techniques play a major role in early diagnosis and make it possible to continuously monitor the patient. With the improvement of these sensors, a large amount of 3D data with high spatial resolution is acquired. Developing efficient processing methods for this diverse output is essential.

Our "Content Based Analysis of Medical Image Data" project, conducted with Pázmány Péter Catholic University, Faculty of Information Technology and Bionics (PPKE ITK) [L1], concentrated on the development of image processing algorithms for multimodal medical sensors (CT and MRI), applying content-based information, saliency models and fusing them with learning-based techniques. We developed fusion methods for efficient segmentation of medical data, by integrating the advantages of generative segmentation models, applying traditional, "handcrafted" features; and the currently preferred discriminative models using convolutional features. By fusing the two approaches, the drawbacks of the different models can be reduced, providing a robust performance on heterogeneous data, even with previously unseen data acquired by different scanners.

The fusion model [1] was introduced and evaluated for brain tumour segmentation on MRI volumes, using a novel combination of multiple MRI modalities and previously built healthy templates as a first step to highlight possible lesions. In the generative part of the proposed model, a colour- and spatial-based saliency model was applied, integrating a priori knowledge on tumours and 3D information between neighbouring scan slices. The saliency-based output is then combined with convolutional neural networks to reduce the networks' eventual overfitting which may result in weaker predictions for unseen cases. By introducing a proof-of-concept method for the fusion of deep learning techniques with saliency-based, handcrafted feature models, the fusion approach has good abstraction skills, yet can handle diverse cases for which the net was less trained.

In a similar manner, we also implemented a technique for liver segmentation in CT scans. First, a pre-processing was introduced using a bone mask to filter the abdominal region (this is important in the case of whole-body scans). Then a combination of region growing, and active contour methods was applied for liver region segmentation. This traditional feature-based technique was fused with a convolutional neural network's prediction mask to increase segmentation accuracy (Figure 1).

The proposed techniques [2] have been successfully applied in the "zMed" project [L2], a four-year project run by Zinemath Zrt., the Machine Perception

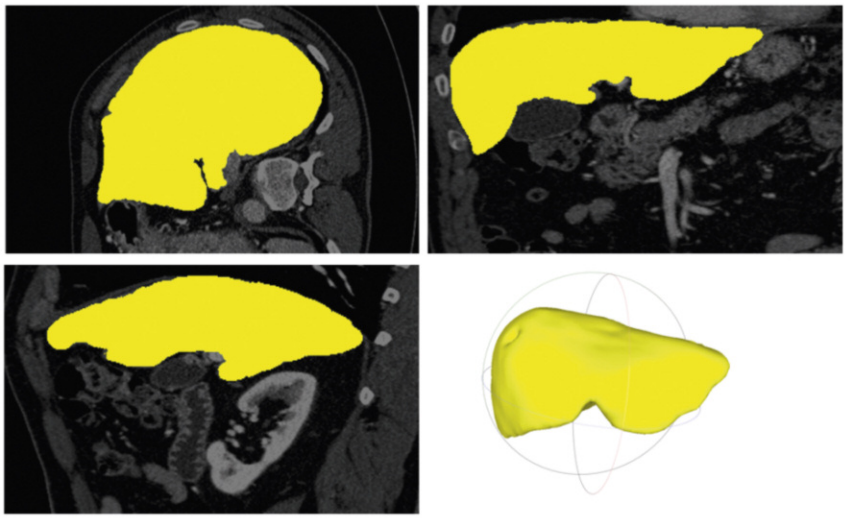

Figure 1: Liver segmentation and 3D modelling on CT data: Segmentation result in axial, coronal, sagittal view and the rendered 3D model of the liver.

Figure 2: The main motivations of the zMed project [L2].

Research Laboratory in the Institute for Computer Science and Control of the Hungarian Academy of Sciences (MTA SZTAKI) [L3] together with the University of Pécs (PTE). The Department of Radiology at PTE provides input data of different modalities (CT and MRI) for the segmentation algorithms, developed by the computer vision researchers of MTA SZTAKI. Based on these tools, Zinemath Zrt is developing a software package, which provides 3D imaging and visualisation technologies for unified visualisation of medical data and various sorts of spatial measurements in an augmented reality system. By creating a completely novel visualisation mode and exceeding the current display limits, the software package applies novel technologies, such as machine learning, augmented reality and 3D image processing approaches.

The developed software package is planned to be adaptable to multiple medical fields: medical education and training for future physicians, introducing the latest methods more actively; improving the doctor-patient relationship by providing explanations and visualisations of the illness; surgical planning and preparation in the pre-operative phase to reduce the planning time and contributing to a more precisely designed procedure (Figure 2).

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Links:

[L1]: https://itk.ppke.hu/en
[L2]: http://zinemath.com/zmed/
[L3]: http://mplab.sztaki.hu

References:

[1] P. Takacs and A. Manno-Kovacs: "MRI Brain Tumor Segmentation Combining Saliency and Convolutional Network Features", Proc. of CBMI, 2018.
[2] A. Kriston, et al.: "Segmentation of multiple organs in Computed Tomography and Magnetic Resonance Imaging measurements", 4th International Interdisciplinary 3D Conference, 2018.

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Artificial Intelligence: Understanding Diseases that People Cannot Understand?

by Marleen Balvert and Alexander Schönhuth (CWI)

Many diseases that we cannot currently cure, such as cancer, Alzheimer's and amyotrophic lateral sclerosis (ALS), are caused by variations in the DNA sequence. It is often unknown which characteristics caused the disease. Knowing these would greatly help our understanding of the underlying disease mechanisms, and would boost drug development. At CWI we develop methods based on artificial intelligence (AI) to help find the genetic causes of disease, with promising first results.

Identifying disease-causing genetic characteristics starts with analysing datasets containing the genetic information of both healthy individuals and patients with a disease of interest. The data analysis provides direction to disease experts and lab researchers, who can experimentally test whether a genetic variant indeed causes disease. Validated disease-causing genetic variants provide insight into the cellular processes involved in disease, which is the starting point for drug development.

Today's predominant technique for analysing genome datasets, called genome-wide association studies (GWAS), ensures that cause (genetic variant) and effect (disease) can be linked in a way the human mind can grasp. GWAS examine each individual genetic variants for correlation with disease, following well-understood statistical principles. GWAS allows the researcher to easily interpret findings and has been very successful: many potentially disease-causing variants have been detected for various diseases.

However, several diseases stubbornly resist such "human intelligence-based approaches", as their genetic architecture is difficult to unravel. One architectural feature that complicates analyses considerably is epistasis[1]: genetic variants do not necessarily just add up their effects to establish effects, but operate in terms of logical combinations. Consider, for example, three variants A, B and C, which establish the disease-causing effects if (and only if) A is not there, or B and C are both there. Such complex logical relationships reflect common biochemical gateways.

Analysing diseases with a more involved genetic architecture, such as cancer, type II diabetes or ALS, in terms of "human mind perceivable" approaches clearly has reached certain limits. So, an immediate question is: if the human mind is struggling, can AI help out?

This motivated CWI researchers Marleen Balvert and Alexander Schönhuth to develop new, AI-based techniques for identifying complex combinations of genetic characteristics that are associated with disease. The challenge is twofold.

First, genome datasets contain millions of genetic variants for thousands or tens of thousands of individuals. Deep neural networks - currently established among the most successful classification techniques [2] - offer enhanced opportunities in processing large datasets. This motivated Balvert and Schönhuth to employ deep neural networks.

Second, deep neural networks have been predominantly developed for