



Medical image analysis – the key to personalized medicine? IEEE Fellow Professor Ewert Bengtsson

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Images have a central role in medicine both for clinical diagnoses and for research. There are rapid developments of new imaging methods with many different technologies. In radiology digital imaging and image handling has since a couple of de-cades completely replaced the older film based imaging. In pathology we are beginning to see that shift today, whole slide scanning techniques are making the information earlier available only directly at the microscope now available to store and display in computer systems. This is creating challenges for efficient data handling a typical microscope slide leads to a couple of gigabytes of digital data. Radiology is also facing similar problems even though a single 2D image there only are a few megabytes the tomographic scanners typically delivers several hundred or thousands of 2D slices to capture the 3D information of the body. Here research on effective visualisation methods plays an important role

Traditionally most medical imaging has been showing anatomy, e.g. a broken bone or clogged vessel in radiology or a tissue that has turned cancerous in pathology. To an increasing extent the imaging is now becoming functional. Showing how the brain reacts to different stimuli or where a medicine is being taken up in the body. Through fluorescent microscopy it is possible to mark individual genes and proteins with stains that make it possible to see where in the tissue they are expressed, down to the subcellular or even molecular level.

There has also for several decades been research on how to analyse images with computers. The purpose may be to obtain more quantitative information, to extract features for more objective and reproducible diagnoses or to automate tedious tasks. The impact on biomedical research and medicine has not yet been as great from this image analysis research as from the imaging research. But we are currently seeing rapid progress also in this field. The recent developments in machine learning of methods based on deep convolutional neural networks are also greatly influencing medical image analysis.

The hope is that detailed imaging is going to make personalized medicine reality. The individual patient should then be characterized through various kinds of imaging and image analysis techniques (as well as genomic techniques) to the level

where it becomes possible to see exactly what is wrong in the fundamental cellular processes and what molecules should be given as drugs that can interfere with the disease processes and cure that particular patient not just based on what usually works for the average patient with that disease but specifically for that individual. Genomics is revolutionising biomedical understanding and will have a great impact on future medicine. But conventional genomic techniques only give information of what genes are present and active not where in the body they are expressed. There is currently a lot of research going on where the goal is to find out where in the body the genes are expressed, down to the cellular or subcellular level. Here computerized image analysis is an indispensable tool. There will be a review article on this topic in our flagship publication, IEEE Proceedings coming out about the same time as this newsletter written by a team at Uppsala University headed by my colleague Carolina Wählby (Title: Bridging Histology and Bioinformatics –Computational Analysis of Spatially Resolved Transcriptomics.)

Medical image analysis research is strong in Sweden. At our Centre for Image Analysis in Uppsala we are around 25 persons working in that field. There are strong groups also at KI, KTH, LiU, LU, Chalmers and GU. Some of the groups have been active almost as long as there has been possible to create digital images. Personally I started in 1973 and was last year honoured by becoming IEEE Fellow “for contributions to quantitative microscopy and biomedical image analysis”.