The second wave of quantitative pathology

The first decade of the new millennium has passed, and we have witnessed exciting progress in medical science. The first two human genomes were sequenced, and many more followed [4,9]. Genome technology has developed at an astonishing speed and before the end of the second decade current high end sequencing capacity will probably be available as turn key desktop solutions. All of this has caused an enormous boost in the speed with which we now are able to unravel biological processes as mechanisms of disease and translate this new knowledge into powerful diagnostic assays, both laboratory tests and molecular imaging applications, as well as new therapeutic agents like the targeted therapies that now are entering clinical practice in medical oncology.

Exactly these developments in 2004 have lead the International Society for Cellular Oncology to change the scope of the journal affiliated with the society, Analytical Cellular Pathology, to this new and exciting area of biomedical science and hence Analytical Cellular Pathology underwent a metamorphosis to become Cellular Oncology [5]. This turned out to be a successful expedition, Cellular Oncology has been among the top pathology journals in the ISI Thompson ranking over the last couple of years with an impact factor that has increased from around 1.5 to an average of around 3.5. The high rejection rate of around 65% indicates that authors consider Cellular Oncology as a journal that they are keen to publish their work in, and feedback from the readership reflects that the Cellular Oncology content is highly appreciated.

At the same time, exciting developments have also been ongoing in other areas. A true technological revolution has affected everyday life. Computers have become omnipresent, and even more important, neither in a professional environment nor at home, hardly any computer can be found nowadays that is not connected to a network, which mostly also includes the world wide web. Immense amounts of data travel over this network, and the speed and extent at which this now is possible have been facilitated by an enormous progress made in the areas of signal processing, image and data analysis, data compression, digital imaging, broad band computing, standardization of interfaces and data formats, etc. As a result we now have minute devices called MP3 players loaded with digital music and images, complex mobile phones with speech recognition, huge LCD TV screens, cheap digital cameras with enormous image resolutions and smart software full of image analysis algorithms that, for instance, provide face recognition.

Especially the developments in the field of capturing, storing, processing, viewing, analyzing and interpreting images now turns out to have an enormous impact on pathology. Pathology is the medical discipline that aims to generate as much relevant information as possible from cell and tissue specimens taken from patients in order to come to the best diagnosis and subsequent therapy for individual patients. Throughout the 20th century, interpreting images of these cells and tissues through the microscope has been the main approach to do this. As mentioned, over the last decade molecular pathology, the subject of Cellular Oncology, has become an important new adjunct to our arsenal, but interpreting images has been and will be for long the backbone of diagnostic pathology. The growing awareness that issues in diagnostic pathology related to standardization, reproducibility and interpretation of microscopic images could be improved upon by computerized image analysis and quantification have lead in the last decades of the 20th century to a very productive area of research devoted to image analysis and quantitative pathology. The two predecessors of the International Society for Cellular Oncology, i.e. the European Society for Analytical Cellular Pathology and the International Society for Diagnostic Quantitative Pathology were important platforms, bringing together researchers on this subject from all over the world. This work built upon concepts, many of which already predated the area of image analysis [2].

Principles related to quantitative analysis of cell and tissue specimens addressing issues related to, e.g., sampling schemes and segmentation problems in fields as stereology, morphometry and digital image processing were turned into practice. That is to say, into solutions that would work in research practice, but large scale deployment of these methods in routine diagnostic pathology was hampered by complex technology that required dedicated operators and ran at considerable costs.

Now we see that many of the issues that have restricted the development of quantitative pathology have been overcome in other areas, mainly concerning products for large consumer markets like digital photo cameras, software for processing digital images like Photoshop and alike, and, for instance, scanning technology that rapidly has moved from simple flat bed document scanning to high resolution 35 mm slide scanners. It is not hard to imagine that from there, the step to microscope slide scanning has been a minor one.

So, development of consumer products has revitalized the field of digital microscopy, and that shows. Or to put it differently, it has taken the pressure of the market to get technology at a stage that it finally is able to catch up with ideas and demands that bright scientists in the field of quantitative microscopy already had decades ago [3,7].

At the moment, on a wide scale a renewed interest exists in digital microscopy. Old issues are addressed with all the new tools available today, and these indeed do provide exciting new opportunities. For instance, one of the major challenges for doing measurements on tissue slides concerned sampling of microscopic fields of vision within a slide, and this required dedicated hardware like an automated scanning stage. Nowadays, this issue can be overcome by simply scanning a whole microscope slide and then performing the sampling in silico. This second wave of quantitative pathology also results in a new wave of research being done, some of which recently has been published in *Cellular Oncology* [1,7,8].

Against this background, IOS press and the International Society for Cellular Oncology have taken on to relaunch Analytical Cellular Pathology as the platform for publishing high quality papers produced in this second wave of quantitative pathology. In 2010, Analytical Cellular Pathology will appear as a section in Cellular Oncology, and from 2011 onward Cellular Oncology and Analytical Pathology will continue as two independent journals. It is my strong belief that these two journals will be able to fulfill an important role in communicating the advancements of science in the two respective areas they are devoted to, and I am confident that authors and readers will appreciate these two journals for the quality of their content.

> Gerrit Meijer Editor in Chief

References

- F. Albregtsen, How to calculate the goodness-of-fit of a fractal dimension, *Cell. Oncol.* 31 (2009), 501.
- [2] J.P.A. Baak (ed.), Manual of Quantitative Pathology in Cancer Diagnosis and Prognosis, Springer-Verlag, Heidelberg, 1991.
- [3] P. Hamilton and D. Allen (eds), *Quantitative Clinical Pathology*, Blackwell Science, Oxford, 1995.
- [4] E.S. Lander, L.M. Linton, B. Birren, C. Nusbaum, M.C. Zody, J. Baldwin et al., Initial sequencing and analysis of the human genome. International human genome sequencing consortium, *Nature* 409 (2001), 860–921.
- [5] G.A. Meijer, The future of *Cellular Oncology, Cell. Oncol.* 26 (2004), 271–273.
- [6] G.A. Meijer, J.A. Belien, P.J. van Diest and J.P. Baak, Origins of . . . image analysis in clinical pathology, *J. Clin. Pathol.* 50 (1997), 365–370.
- [7] K. Metze, I. Lorand-Metze, N.J. Leite and R.L. Adam, Goodness-of-fit of the fractal dimension as a prognostic factor, *Cell. Oncol.* **31** (2009), 503–504.
- [8] M.C. Osterheld, R.N. Laurini, E.P. Saraga and F.T. Bosman, Evaluation of DNA-ploidy heterogeneity in gastric cancers, *Cell. Oncol.* **30** (2008), 511.
- [9] J.C. Venter, M.D. Adams, E.W. Myers, P.W. Li, R.J. Mural, G.G. Sutton et al., The sequence of the human genome, *Science* 291 (2001), 1304–1351.