Mathematical Biology

Preface

Mark Chaplain

It has been a great personal pleasure and honour to be the guest editor for this special issue of the *Journal of Mathematical Biology* devoted to Computational Oncology. "Historically" perhaps one can trace the origins of modelling solid tumours, back to the seminal work of Greenspan [1]. It goes without saying that since the publication of that paper in 1976, many things have changed. Much more is now known biologically about cancer and there have also been many new developments in applied mathematics. Perhaps looking back from a distance of over 30 years and with the benefit of advances in biological understanding, one may find faults in some of the modelling assumptions in Greenspan [1], but not with the spirit of the paper, which still stands out as a beautiful example of the benefit of applying mathematics to a biological problem to gain a deeper understanding of the system. Nonetheless, "nothing is given forever", and as noted by J.H. Newman:

> To live is to change, and to be perfect is to have changed often.

In order to make scientific progress, we must be open to change and willing to change (old mathematical models) when new results, facts and discoveries come to light. The mathematical models of the articles in this special issue are concerned with "cancer", more precisely, solid tumours—their growth, development and treatment. Medically, a (solid) tumour may be defined as follows [2]:

During the course of this special issue being produced, sadly Dr. Judah Folkman, the pioneer and father of modern angiogenesis research and its connections with cancer growth, died (February 24, 1933–January 14, 2008). As a Ph.D. student, I was inspired, upon reading his original papers on tumour-induced angiogenesis from the early 1970s, to focus some of my modelling efforts in this direction. This special edition is dedicated to his memory.

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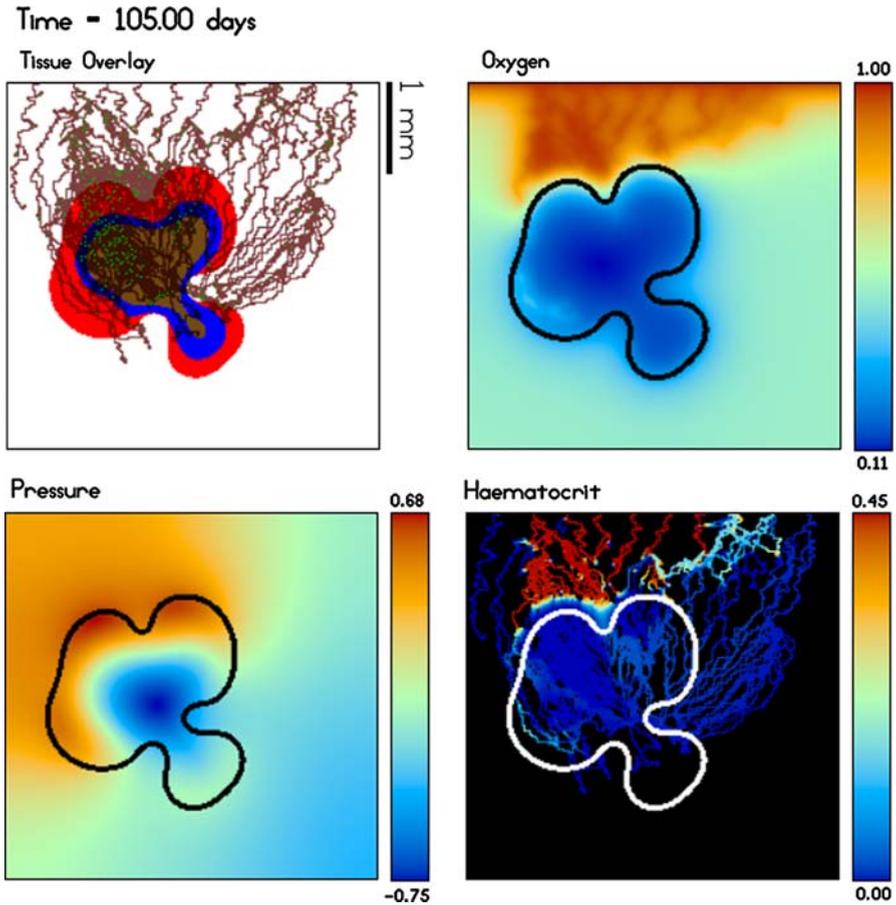
A mass of tissue formed as the result of abnormal, excessive and inappropriate (i.e. purposeless) proliferation of cells, the growth of which continues indefinitely and regardless of the mechanisms which control normal cellular proliferation

In a very real sense then, a tumour lives to change and changes often in order to be perfect, from the point of view of the tumour itself (cf. J. H. Newman). A tumour's successful growth and development depends crucially on its ability to proliferate excessively, to undergo mutations, to adapt to its local environment and to spread from its initial location in the host tissue to distant colonies elsewhere in the body. In this respect, a malignant tumour (i.e. a cancer) "... *may be regarded as a paradigmatic microcosm for all of biology - i.e. as an observable system where mutation and evolution take place.*" [3], and as such offers applied mathematicians possessing different "phenotypic traits" (cf. modellers, applied analysts, numerical analysts, computational scientists, statisticians) many exciting and challenging problems.

The past decade has witnessed enormous advances in our understanding of the molecular basis of cell structure and function. Scientists recognize the spectacular success of the human genome project and the consequent burgeoning interest in the related field of proteomics. Biochemists and cell biologists have made similarly impressive strides in elucidating the mechanisms mediating cell signalling and its consequences for the control of cell proliferation, motility and gene expression. It is, however, abundantly clear that reductionist logic using this impressive "sub-cell-level" information base is not sufficient to deduce an understanding of phenomena operative at the next higher level of biological organisation: the tissue. Employing a literary analogy, the vast "-omic" databases of catalogued genes and proteins, taken together with our growing understanding of the inner workings of individual cells, provide a "dictionary" and a "grammatical syntax" required for the next great challenge, i.e. understanding the "sentences" and "paragraphs" characteristic of emergent tissue-level phenomena. This special issue therefore has an overall aim of quantitative, predictive mathematical modelling of solid tumour growth at all scales, from genetics through to treatment therapy of patients. At the present point in time, the task of accurately modelling solid tumour growth in a comprehensive, multiscale way may seem daunting to say the least. However, perhaps inspired by the words of J. H. Newman:

> Nothing would be done at all if one waited until one could do it so well that no one could find fault with it.

> Let us take things as we find them: let us not attempt to distort them into what they are not... We cannot make facts. All our wishing cannot change them. We must use them.

the articles in this special issue demonstrate just how much has changed (for the better) in the mathematical modelling of solid tumour growth since the paper of Greenspan [1]. Cancer is a global problem, transcending race, gender and creed. It is particularly heartening therefore to see such a diverse spectrum of authorship in the articles, showing that through such international and inter-disciplinary collaboration, we are well on the way to developing genuinely predictive, quantitative mathematical models of solid tumours—*virtual cancers in silico*.

Finally, I would like to personally thank all the authors who have contributed their time and effort to producing the superb state-of-the-art articles in this issue and to the referees who gave up their time to review them.

References

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