PREFACE

The therapeutic potential of evaluation of molecular parameters will soon start assisting existing clinical factors for the identification of high and low risk groups and in future may even prove to be better markers than classical clinical features. A retrospective look at the basis of human disease pathogenesis almost always reveals an apoptotic component that either contributes to disease progression or accounts for it. What makes this field particularly exciting is the breadth of therapeutic opportunities that are on offer. The pace of apoptosis research has raised expectations that applied therapeutics will follow soon. Practical therapeutics that modulates apoptosis will no doubt appear in the clinic in the next few years.

Oncogenesis of cancer cells depends on a multitude of factors, including proliferation, angiogenesis, metalloproteinases, adhesion molecules, genes controlling metastatic pathways, regulatory factors, DNA repair, regulation of cell movement etc etc. The number of biological players with a role in each of these processes is quite large, and their roles are not completely understood. In addition to the constitutive cross talk among the numerous players of any single process, there is communication between members of the different groups. Thus our efforts to define a potentially dangerous phenotype with a select group of prognostic markers representative of individual members of the various groups is simply working at the tip of the iceberg; it would require ‘neural networking’ to convert the data into any meaningful individual prognostic index.