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This book is written by the collaborators of the center of excellence BIOPATTERN and reports on research which attempts to bring the clinical management of cancer together with machine learning and statistical modeling. More specifically this book focusses on the prediction of survival using Artificial Neural Networks (ANNs). Currently, the clinical management of cancer is based on empirical data from the literature (clinical studies) or based on the expertise of the clinician. Approximately one decade ago microarray technology emerged and has the potential to revolutionize the clinical management of cancer. Since then other technologies have emerged (i.e. proteomics, metabolomics, methylation) which promise an even greater flood of data. This book describes the use of advanced statistical and machine learning techniques to predict the outcome in cancer and potentially provides solutions to the data deluge that will submerge clinicians in the future.

The first section of the book describes the clinical problem of outcome prediction in cancer. First, traditional methods for providing prognosis such as TNM staging are described. Subsequently the problem of competing risks is discussed. The second section discusses biological and genetic factors associated to cancer. The first chapter in this section discussese environmental and genetic risk factors of lung cancer while the second chapter discusses the use of an ANN based on host, tumour and treatment parameters in laryngeal cancer to predict survival. Section three describes the mathematical background for prognosis models, specifically focusing on ANNs. A comparison is made between traditional models and ANN models. The following section describes applications of ANNS and other machine learning methods. The final section discusses the issue of dissemination of information which is often overlooked.

We regret that this book focusses on the use of ANNs to predict outcomes in cancer. Recent research has shown that these models are somewhat outdated and currently are overshadowed by the rise of kernel methods (e.g. Support Vector Machines (SVMs)). This class of models is very flexible; due to the choice of kernel any type of data can be modeled. Moreover, SVMs have few parameters that have to be specified and trained, certainly compared to ANNs where the architecture of the ANN (i.e. the number of hidden layers and hidden nodes) has to be specified beforehand, and many weight parameters have to be trained. Therefore, SVMs are less endangered by overfitting. Finally, and most importantly, SVMs do not suffer from the many local optima that exist when learning ANNs. This complicates training of ANNs whereas training an SVM results in only one solution which is optimal given the data.