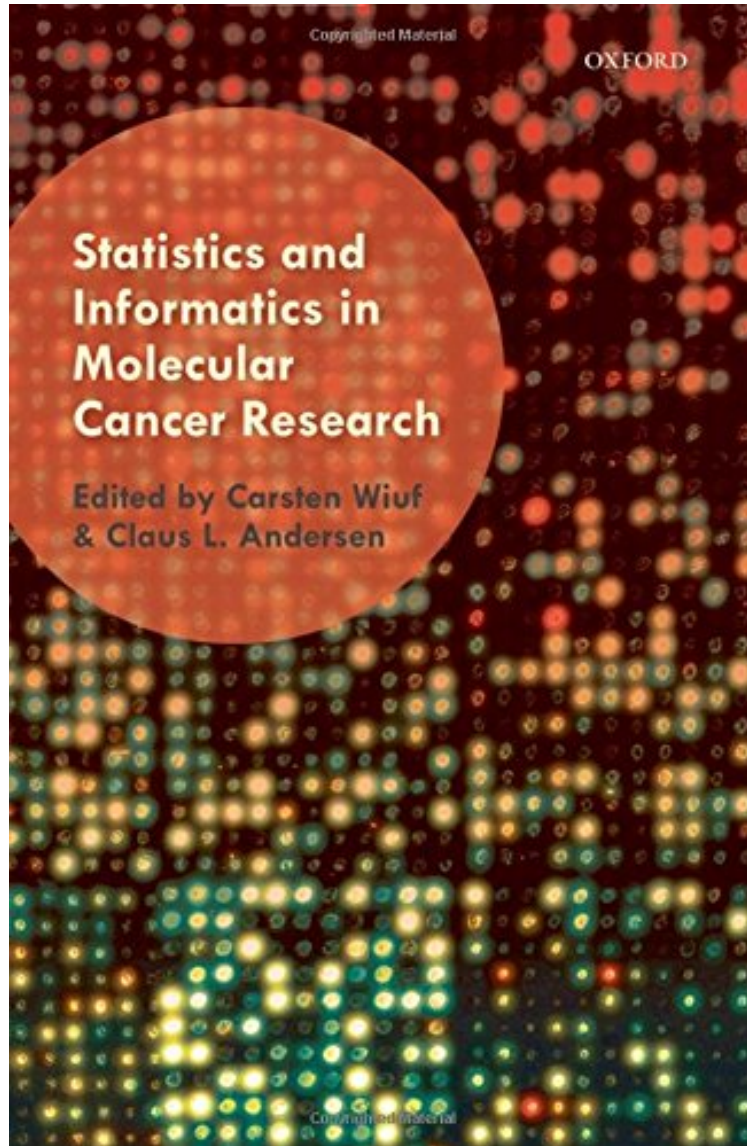


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1 of 1 people found the following review helpful. This book is already out of date. By W. YIP The biomedical technology has been moving in lightning speed for the last few years, and that makes some of the information in the book out of date. The book is useful overall. For example, the example in the DNA methylation chapter uses 8

methylation sites. Nowadays, the Illumina 450 human beadchip can sample 485,000 sites at once. The overall theory is still correct but the techniques to handle the information may not be applicable anymore.

Molecular understanding of cancer and cancer progression is at the forefront of many research programs today, and high-throughput array technologies and other modern molecular techniques produce a wealth of molecular data about the structure, organization, and function of cells, tissues and organisms. Complex mathematical, statistical and bioinformatics tools are required to extract, handle and process data and this book, edited by two leading researchers with contributions from carefully chosen experts, makes these tools available to a wide range of researchers, in a single coherent book volume.

About the Author Carsten Wiuf obtained his PhD in mathematical biology from the University of Aarhus in 1998. Afterwards he spent 4 years in Oxford at the Department of Statistics before joining a biotech company in Boston. In 2003 he became Professor of Bioinformatics at the University of Aarhus. He has co-authored the book *Gene Genealogies, Variation and Evolution* (OUP). Claus L. Andersen earned his PhD in cancer biology from the University of Aarhus in 2002. In 2002, he became an assistant professor at the University of Aarhus and later in 2005 an associate professor. Today he is heading the colorectal cancer research group at the Molecular Diagnostic Laboratory, Aarhus University Hospital. Both have worked on informatics approaches to the analysis of molecular cancer data and have practical as well as theoretical experience with development of bioinformatics and statistical methods for analysis of molecular data.