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| Soggetti | Electronic circuits Bioinformatics Electronics Microelectronics Circuits and Systems Computational Biology/Bioinformatics Electronics and Microelectronics, Instrumentation |
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| Note generali | Description based upon print version of record. |
| Nota di bibliografia | Includes bibliographical references at the end of each chapters and index. |
| Nota di contenuto | Introduction -- Related Work -- Methodology for Implementing Accelerators -- FPGA based Acceleration of Protein Docking -- FPGA based Acceleration of De Novo Genome Assembly -- Design of Accelerators with HEBs -- System Level Design Space Exploration -- Future Directions. |
| Sommario/riassunto | This book presents an evaluation methodology to design future FPGA fabrics incorporating hard embedded blocks (HEBs) to accelerate applications. This methodology will be useful for selection of blocks to be embedded into the fabric and for evaluating the performance gain that can be achieved by such an embedding. The authors illustrate the use of their methodology by studying the impact of HEBs on two important bioinformatics applications: protein docking and genome assembly. The book also explains how the respective HEBs are designed and how hardware implementation of the application is done using these HEBs. It shows that significant speedups can be achieved |

over pure software implementations by using such FPGA-based accelerators. The methodology presented in this book may also be used for designing HEBs for accelerating software implementations in other domains besides bioinformatics. This book will prove useful to students, researchers, and practicing engineers alike.
