

1. Record Nr.	UNINA9910523003403321
Autore	Wijtvliet Mark
Titolo	Blocks, towards energy-efficient, coarse-grained reconfigurable architectures // Mark Wijtvliet, Henk Corporaal, Akash Kumar
Pubbl/distr/stampa	Cham, Switzerland : , : Springer, , [2022] ©2022
ISBN	3-030-79774-0
Edizione	[1st ed. 2022.]
Descrizione fisica	1 online resource (X, 220 p. 158 illus., 117 illus. in color.)
Disciplina	004
Soggetti	Adaptive computing systems
Lingua di pubblicazione	Inglese
Formato	Materiale a stampa
Livello bibliografico	Monografia
Nota di bibliografia	Includes bibliographical references and index.
Nota di contenuto	Introduction -- CGRA background -- Concept of the Blocks architecture -- The Blocks framework -- Energy, area, and performance evaluation -- Architectural model -- Case study: the BrainSense platform -- Conclusion.
Sommario/riassunto	This book describes a new, coarse-grained reconfigurable architecture (CGRA), called Blocks, and puts it in the context of computer architectures, and in particular of other CGRAs. The book starts with an extensive evaluation of historic and existing CGRAs and their strengths and weaknesses. This also leads to a better understanding and new definition of what distinguishes CGRAs from other architectural approaches. The authors introduce Blocks as unique due to its separate programmable control and data paths, allowing light-weight instruction decode units to be arbitrarily connected to one or more functional units (FUs) over a statically configured interconnect. The discussion includes an explanation of how to model architectures, resulting in an area and energy model for Blocks. The accuracy of this model is evaluated against fully implemented architectures, showing that although it is three orders of magnitude faster than synthesis the error margin is very acceptable. The book concludes with a case study on a real System-on-Chip, including a RISC architecture, the Blocks CGRA and peripherals. Provides a comprehensive overview of many coarse-grained reconfigurable architectures (CGRAs) proposed in the last 25 years, as well as a classification of those CGRAs; Offers a new view on the

positioning of CGRAs; Provides an in-depth description of structure of the Blocks CGRA and its unique aspects; Includes an extensive evaluation of various performance aspects of Blocks, such as performance, energy and area, as well as a comparison with various traditional approaches; Uses a case study showing how Blocks can be used in a real system on-chip, and how performance of this system-on-chip can be estimated using the proposed model.

2. Record Nr.	UNINA9910346752703321
Autore	Sandra Torriani
Titolo	Game Changer - Next Generation Sequencing and its Impact on Food Microbiology
Pubbl/distr/stampa	Frontiers Media SA, 2018
Descrizione fisica	1 online resource (302 p.)
Collana	Frontiers Research Topics
Soggetti	Microbiology (non-medical)
Lingua di pubblicazione	Inglese
Formato	Materiale a stampa
Livello bibliografico	Monografia
Sommario/riassunto	Advances in next-generation sequencing technologies (NGS) are revolutionizing the field of food microbiology. Microbial whole genome sequencing (WGS) can provide identification, characterization, and subtyping of pathogens for epidemiological investigations at a level of precision previously not possible. This allows for connections and source attribution to be inferred between related isolates that may be overlooked by traditional techniques. The archiving and global sharing of genome sequences allow for retrospective analysis of virulence genes, antimicrobial resistance markers, mobile genetic elements and other novel genes. The advent of high-throughput 16S rRNA amplicon sequencing, in combination with the advantages offered by massively parallel second-generation sequencing for metagenomics, enable intensive studies on the microbiomes of food products and the impact of foods on the human microbiome. These studies may one day lead to

the development of reliable culture-independent methods for food monitoring and surveillance. Similarly, RNA-seq has provided insights into the transcriptomes and hence the behaviour of bacterial pathogens in food, food processing environments, and in interaction with the host at a resolution previously not achieved through the use of microarrays and/or RT-PCR. The vast un-tapped potential applications of NGS along with its rapidly declining costs, give this technology the ability to contribute significantly to consumer protection, global trade facilitation, and increased food safety and security. Despite the rapid advances, challenges remain. How will NGS data be incorporated into our existing global food safety infrastructure? How will massive NGS data be stored and shared globally? What bioinformatics solutions will be used to analyse and optimise these large data sets? This Research Topic discusses recent advances in the field of food microbiology made possible through the use of NGS.
