

Lecture: «Next-Generation Sequencing: Big Data meets High Performance Computing»

Data: martes, 18 outubro, 2016 - 12:00 - 14:15

Lugar: CITIUS Assembly Hall

Poñente(s): Bertil Schmidt (Johannes Gutenberg University Mainz)

Idioma: Inglés

Streaming: Non



Abstract

The progress of next-generation sequencing has a major impact on medical and genomic research: this high-throughput technology can now produce billions of short DNA fragments in excess of a few Terabytes of data in a single run. This leads to massive datasets used by a wide range of applications including personalized cancer treatment and precision medicine.

In addition to the hugely increased throughput, the cost of using high-throughput technologies has been dramatically decreasing and low sequencing cost of around US\$1K per genome has now rendered large population-scale projects feasible. However, in order to make effective use of the produced data, the design of big data algorithms and their efficient implementation on modern high performance computing systems is required. In this context, prof. Schmidt will present the design of scalable and parallel algorithms for metagenomic read classification and short read mapping.

About the speaker

Bertil Schmidt is Chair for Parallel and Distributed Architectures at [JGU Mainz](#), Germany. Prior to that he was a faculty member at Nanyang Technological University (Singapore) and at University of New South Wales (UNSW). His research group has designed a variety of CUDA-enabled open-source tools for Bioinformatics mainly focusing on the analysis of large-scale short read datasets. For his research work, he has received a GPU Research Center award, a CUDA Academic Partnership award, a CUDA Professor Partnership award and the Best Paper Award at IEEE ASAP 2009. Furthermore, he serves as the champion for Bioinformatics and Computational Biology on [gpucomputing.net](#).