

# CONFERENCIA

## Next-Generation Sequencing: Big Data meets HPC

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**Lugar:** Aula 3.01. Edificio Área Científica (UDC).

**Data:** martes, 4 de abril de 2017

**Hora:** 16:30

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. 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 talk, I will present the design of scalable and parallel algorithms for metagenomic read classification and short read mapping.

Bertil Schmidt is tenured Full Professor and Chair for Parallel and Distributed Architectures at the University of 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 algorithms and tools for Bioinformatics mainly focusing on the analysis of large-scale sequence and read datasets. For his research work, he has received a GPU Research Center award, GPU Education Center Award, CUDA Academic Partnership award, CUDA Professor Partnership award and Best Paper Awards at IEEE ASAP 2015 and IEEE ASAP 2009.