Institute of Molecular Biology

IMB TechTalk

Prof. Dr. Bertil Schmidt

Head of Parallel and Distributed Architectures,
Institute of Informatics,

Johannes Gutenberg-University Mainz

"Parallel Algorithms and Tools for NGS and Sequence Analysis"

19 June 2012, 14:00 h (*s.t.*)

Please note: different time than usually

Venue: 2nd Floor Seminar Room
Institute of Molecular Biology (IMB)
Johannes Gutenberg University Campus Mainz

All are welcome to attend

Host: Dr. Bernhard Korn, IMB
For further information, please contact: Bianca Steinbach, E-mail: b.steinbach@imb-mainz.de, tel.: +49-(6131)-39-21510

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Parallel Algorithms and Tools for NGS and Sequence Analysis

High-throughput techniques for DNA sequencing have led to a rapid growth in the amount of digital biological data. The current state-of-the-art technology produces 600 billion nucleotides per machine run. Furthermore, the speed and yield of NGS (Next-generation sequencing) instruments continue to increase at a rate beyond Moore's Law, with updates in 2012 enabling 1 trillion nucleotides per run. Correspondingly, sequencing costs (per sequenced nucleotide) continue to fall rapidly, from several billion dollars for the first human genome in 2000 to a forecast US$1000 per genome by the end of 2012. However, to be effective, the usage of NGS for medical treatment will require algorithms and tools for sequence analysis that can scale to billions of short reads. In this talk I will demonstrate how parallel computing platforms based on CUDA-enabled GPUs, multi-core CPUs, and heterogeneous CPU/GPU clusters can be used as efficient computational platforms to design and implement scalable tools for sequence analysis. I will present solutions for classical sequence alignment problems (such as pairwise sequence alignment, BLAST, multiple sequence analysis, motif finding) as well as for NGS algorithms (such as short-read error correction, short-read mapping, short read assembly, short-read clustering).