



Univerzitet u Sarajevu
Prirodno-matematički fakultet
ODSJEK ZA MATEMATIKU

NAUČNI KOLOKVIJ

Abstract

Sequencing projects involving thousands of individual genomes are underway and the need for algorithmic speedup is bigger than ever. We will go through some of the algorithmic developments introduced by my lab to address challenges in big data genomics, especially for cancer research. These algorithms involve one or more techniques in data compression, streaming, memory hierarchy awareness and parallelization. Application areas range from read mapping to variant calling, novel isoform and fusion gene identification to clonality inference.

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**Data driven research in
(cancer) genomics**

Petak, 11. decembar 2015. godine, 11:00 sati
Prirodno-matematički fakultet
Odsjek za matematiku, sala RC