

**Disbalance of gut microbiota  
during cancer treatment in pediatric patients  
detected using metagenomic sequencing**

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Gut microbiota is essential for human host homeostasis. When the host undergoes chemotherapy, structure of his/her microbiota can change drastically. With short-cycle high-throughput sequencer available, metagenomic sequencing allows monitoring of microbiota composition, particularly, quantitative detection of a wide spectrum of bacterial pathogens. Analysis of temporal variation of community structure during and after the treatment will allow to elucidate microbiota recovery mechanism and means for microbiota modulation in order to increase patient survival rate.

During the pilot project, 16 stool samples were obtained from 4 children undergoing cancer treatment in Federal Scientific Clinical Centre of Pediatric Hematology, Oncology and Immunology named after D. Rogachev at several time points. DNA was extracted and

shotgun metagenomic sequencing was performed on SOLiD 4. Community structure was assessed by alignment of the reads to catalog of reference microbial genomes and subsequent normalization. The analysis detected significant presence of pathogenic bacteria and fungi in most samples, as well as high fraction of human DNA. Analysis of SNP signatures in reference genomes allowed to assess the hypothesis of single source for some of the pathogen strains. Diverse types of data including temporal evolution of patients microbiota and clinical data were visualized as an interactive network graph, providing a potential exploratory tool for both bioinformaticians and clinical experts.

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