

IT предизвикателства при анализ на данни от паралелно секвениране

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Абстракт. The development of algorithmic ideas for next-generation sequencing data analysis is a major challenge and new breadth in bioinformatics development and applications. The strongly IT dependent high-throughput sequencing technologies require both new and review of old solutions. A crucial set of problem in N&S is the assembly algorithms and the software tools used for these purposes. They are heavy in development and handling and open a significant space for implementation of new information technologies, algorithms and software development. The purpose of the seminar will be a discussion about the opportunity to merge the goals and to make some suggestions how to meet the requirements of NGS data analysis in the IT context.