New Frontiers of Genome Assembly with SPAdes 3.1

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Project web site: http://bioinf.spbau.ru/en/spades
Source code available at: http://bioinf.spbau.ru/en/spades
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Despite all the efforts high quality genome assembly is a complex task that so far remains unsolved. It is well known that majority of problems caused by repeats present in all genomes of any nature. The usage of multiple methods of genomic DNA isolation, different sequencing technologies and different types of genomic libraries for research projects introduces additional levels of complication to the genome assembly. The assembler tool SPAdes was originally developed at the St. Petersburg Academic University for the purpose of overcoming the complications associated with single-cell microbial data (uneven coverage and increased level of chimerical reads). The tool was able to successfully resolve these issues for Illumina reads and was recognized by the scientific community as one of the best assemblers working with both isolates and single-cell data. Even though the assembler was specifically designed to work solely with microbial genomes, scientists have tested the tool on a large number of different types of other data.

Their efforts and feedback have inspired us to extend the capabilities of SPAdes to include additional platforms (Ion Torrent, PacBio, Sanger), combinations of platforms, and to work with both paired-end and mate-pair libraries of different insert sizes. In this work we present novel features of SPAdes 3.1: hybrid assemblies including the combination of Illumina/IonTorrent with PacBio (or other long reads technologies), improved algorithms for scaffolding and repeat resolution, and an approach for mate-pair only assembly using new Illumina NexteraMP protocol.