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Combining De Bruijn Graphs, Overlap Graphs and Microassembly for *De Novo* Genome Assembly

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In this paper we present a method for *de novo* genome assembly that splits the process into three stages: quasicontig assembly; contig assembly from quasicontigs; contig postprocessing with microassembly. The first stage uses de Bruijn graph, the second one uses overlap graph. We have carried out experiments of assembling the *E. Coli* genome (size ≈ 4.5 Mbp) and *Maylandia zebra* genome (size ≈ 1 Gbp). Advantage of proposed method is a low memory consumption.

Key words: genome assembly, contigs, de Bruijn graph, overlap graph, microassembly.

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