

Related work:

In the past, genome assembly methods were designed for brief reads (i.e. de Bruijn graph approach) but it not suitable for nanopore reads due to the high error rates for the previous nanopore sequencing devices, in order that they used OLC algorithms start with finding the reads -to read overlap, which is that the second step of the pipeline. read-to read overlap is defined to be a typical sequence between two reads. GraphMap and MiniMap are the commonly used state-of -the art tools for this step.