**Comparative Genome Assembly**

**Abstract**

Until now, the most complex and computationally intensive tasks of genome sequence analysis is genome assembly we have the resources in both software and hardware that can help us. as we have a great number of sequencing genomes that increase organisms for two or more closely related spices that have been sequenced, that lead to comparative genome assembly

**Introduction**

The most used sequenced genomes as a reference are whole genome shotgun (WGS), which breaks the genome into small fragments and sequence them from both ends to reconstruct the chromosomes of the target organism using latest sequencing technologies. assemblers depended on not only to reconstruct the genome but also to answer basic question. Scientific community has recognized the value of sequencing for example sequencing the genome of (mouse , rat, chimpanzee)and mapping to human to better understand . The algorithm used is overlap layout consensus. Most assemblers use hashing strategies in order to identify those reads that are likely to overlap, another assemblers use (AMOS-Cmp) in this case we skip the overlap step , reads are aligned to the reference genome using modified version called (MUMmer algorithm) ( alignment layout consensus) .

**The goal to be obtained an assembly of this genome using a reference genome as a template**