# Assignment 1: Abstract and Introduction summary

- Research in bioinformatics has changed rapidly since the advent of next-generation sequencing that want to sequecing data in small time and less memory and it is the challenge for every generation.
- There are many 2 types for sequencing biological data first is alignment and second is assembly first must be refrence genome and second no refrence genome we will talk about assembly  called De Novo Fragment Assembly
- the problem is,  De Novo Fragment Assembly doesn't have any information about genome ,transcriptome , proteins
- The genome assembly problem arises because it is impossible to sequence a whole genome directly in one read using current sequencing technologies.
- so we will study the Classification of de Bruijn Graph Approaches.
- we will talk about the solution to reduce the execution time and memory in de Bruijn graph using k-mers method.
- we find the k-mers of every read without repetion of every reads
- so de Bruijn graph layout is to find the eulerian path in the graph
- in this paper, we apply those concepts in Protein, DNA and RNA, using for that effect,
- examples : velvet , ABySS , ALLPATH-LG , SOAPdenovo