

Assignment1(Abstract and Introduction)

- ☐ Humans have coexisted with pathogenic microorganisms throughout its history of evolution. We have never halted the exploration of pathogenic microorganisms.
- ☐ With the improvement of genome-sequencing technology and the continuous reduction of sequencing costs, an increasing number of complete genome sequences of pathogenic microorganisms have become available.
- ☐ Our problem that is Genome annotation of this massive sequence information has become a daunting task in biological research.
- ☐ This paper summarizes the approaches to the genome annotation of pathogenic microorganisms and the available popular genome annotation tools for prokaryotes, eukaryotes and viruses.
- ☐ Although we have accumulated much useful understanding of the emergence, evolution, pandemic and pathogenic mechanism of pathogenic microorganisms, there are still some crucial gaps in our knowledge.
- ☐ Since the first complete genome sequence of the microorganism *Haemophilus influenza* was published in 1995 , the whole-genome era's arrival has brought a new dawn for us to fill these gaps.
- ☐ Genome annotation has become a critical element for us to understand genomic biology, especially the genomes of pathogenic microorganisms. Over the years of efforts, genome annotation has flourished. Today, we know not only protein-coding genes but also many other functional elements, such as promoters, enhancers, noncoding RNAs and DNA methylation sites.