

Assembly of Small Microbial Genome

Instructor

Abdullah Al Nahid

facebook.com/abdnahid

Brought to you by

**Community of
Biotechnology**

Part of

**COB Genomics Learning
Program 2022**

De novo assembly

1. Ideal approach
2. Recreate original genome sequence through overlapping sequenced reads
3. More accurate
4. Not biased towards reference genome unlike mapping-based approach
5. Expensive, need a lot of reads
6. Time and memory consuming

Paired-end sequencing

1. Sequencer starts reading from one end till specified read length
2. Reads from the opposite direction again
3. improves ability to identify relative read position in genome
4. much more effective than single-end seq. in resolving gene insertions, deletions etc.
5. improves assembly of repetitive regions

Tools

1. sra-tools (fastq-dump)
2. fastqc
3. trimmomatic
4. megahit or other assemblers
5. quast

Practical

Let's assemble sequenced SARS-CoV-2 genome

Thank You