

**CLAIMS**

1. A method, comprising:  
inputting data, wherein the data corresponds to source data for gene sequencing on a sample;  
5 receiving a selected data processing technique;  
performing, using the selected data processing technique, gene sequencing processing on the inputted data based on a pathogen genome of a predetermined pathogen to obtain a data processing result, wherein the data processing result indicates whether the sample includes the predetermined pathogen; and  
10 presenting the data processing result.
2. The method as described in claim 1, wherein prior to the inputting of the data, the method further comprises:  
presenting descriptions of the selected data processing technique, wherein the descriptions include one or more of the following: data formatting requirements, data  
15 processing price, and/or data processing priority level.
3. The method as described in claim 1, wherein prior to the receiving of the selected data processing technique, the method further comprises:  
presenting a plurality of data processing techniques and the corresponding principles, advantages, and disadvantages of the plurality of data processing techniques.
- 20 4. The method as described in claim 1, wherein the performing of the gene sequencing processing on the inputted data comprises:  
converting the data to a gene sequence format to obtain reads;  
comparing the reads to the pathogen genome of the predetermined pathogen;  
determining whether the reads are included in the pathogen genome;  
25 assembling the reads into a sample genome; and  
by aligning the sample genome with the pathogen genome, obtaining the data processing result, wherein the data processing result indicates whether the sample includes the predetermined pathogen.
5. The method as described in claim 1, wherein the presenting of the data processing  
30 result comprises:  
presenting a probability that the sample includes the predetermined pathogen.

6. The method as described in claim 5, wherein the presenting of the data processing result comprises:  
presenting variant sites of the predetermined pathogen.
7. The method as described in claim 1, further comprising:  
5 generating and printing a report including the data processing result.
8. A method, comprising:  
acquiring sequencer output data of a sample, wherein the sequencer output data corresponds to data resulting from sequencing performed on the sample by a sequencer;  
converting the sequencer output data to a gene sequence format to obtain reads;  
10 comparing the reads to the pathogen genome of the predetermined pathogen;  
determining whether the reads are included in the pathogen genome based on the comparison;  
assembling the reads into a sample genome; and  
by aligning the sample genome with the pathogen genome, obtaining a data  
15 processing result indicating whether the sample includes the predetermined pathogen.
9. The method as described in claim 8, wherein:  
the method employs a distributed processing technique and/or a parallel processing technique to compare the reads to the pathogen genome of the predetermined pathogen and determine whether the reads are included in the pathogen genome;  
20 the distributed processing technique comprises distributing a plurality of reads of the sample across a plurality of pieces of server hardware for processing; and  
the parallel processing technique comprises: putting a plurality of reads of the sample in a plurality of tasks of a single piece of server hardware for parallel processing.
10. The method as described in claim 9, wherein the method employs the distributed  
25 processing technique and/or the parallel processing technique to assemble the reads into the sample genome.
11. The method as described in claim 8, further comprising:  
upon determining that the reads are included in the pathogen genome, determining positions of the reads in the pathogen genome.
- 30 12. The method as described in claim 8, further comprising:  
performing at least one of the following:  
determining a degree of similarity between the sample genome and the

pathogen genome and obtaining a probability that the sample includes the predetermined pathogen; and/or

determining variant sites of the predetermined pathogen based on a comparison of the sample genome to the pathogen genome.

- 5 13. The method as described in claim 8, wherein the acquiring of the sequencer output data of the sample comprises:
- performing one or more of the following:
- acquiring the sequencer output data of the sample through single-end sequencing;
- 10 acquiring the sequencer output data of the sample through paired-end sequencing; and/or
- acquiring the sequencer output data of the sample through sequencing that uses different sequence lengths.
14. The method as described in claim 8, wherein the predetermined pathogen comprises a novel coronavirus or a severe acute respiratory syndrome (SARS) associated coronavirus.
- 15 15. A system, comprising:
- a processor; and
- a memory coupled with the processor, wherein the memory is configured to provide the processor with instructions which when executed cause the processor to:
- 20 input data, wherein the data corresponds to source data for gene sequencing on a sample;
- receive a selected data processing technique;
- perform, using the selected data processing technique, gene sequencing processing on the inputted data based on the pathogen genome of a predetermined pathogen to obtain a data processing result, wherein the data processing result
- 25 indicates whether the sample includes the predetermined pathogen; and
- present the data processing result.
16. A computer program product being embodied in a tangible non-transitory computer readable storage medium and comprising computer instructions for:
- 30 input data, wherein the data corresponds to source data for gene sequencing on a sample;
- receiving a selected data processing technique;

performing, using the selected data processing technique, gene sequencing processing  
on the inputted data based on the pathogen genome of a predetermined pathogen to obtain a  
data processing result, wherein the data processing result indicates whether the sample  
includes the predetermined pathogen; and  
5 presenting the data processing result.