CLAIMS

What is claimed is:

1. A gene sequencing analysis method, comprising:

acquiring slice data transmitted from a sequencing platform in real time, the slice data being a set of short sequences read after performing at least one cycle of sequencing on a sequencing library;

inputting the slice data into a memory; and

performing, by calling an encapsulation program pre-set in the memory, data processing and detection analysis on the slice data, to obtain a corresponding analysis result, wherein the encapsulation program is a custom program,

wherein said acquiring the slice data comprises:

acquiring a current central processing unit (CPU) idleness state;

adjusting the slice size based on the current CPU idleness state; and

slicing, based on the slice size, all unsliced short sequences currently transmitted from the sequencing platform and read after a single cycle of sequencing, a set of the sliced short sequences being used as the slice data,

wherein the encapsulation program comprises a data quality control program, a data processing program, and a detection analysis program, and

wherein said performing, by calling the encapsulation program pre-set in the memory, the data processing and detection analysis on the slice data, to obtain the corresponding analysis result comprises:

performing, by calling the data quality control program pre-set in the memory, quality control processing on the slice data, to obtain a quality control result;

performing, by calling the data processing program pre-set in the memory, an alignment between the short sequence in the quality control result and a reference gene, to determine a position of the short sequence on the reference gene;

determining a position tag of the short sequence based on the position of the short sequence on the reference gene;

determining, among pre-set threads in the memory, a target thread that is currently in an idle state;

performing, by calling the target thread and with reference to the position tag of the short sequence, at least one of ordering, deduplication, and re-alignment of the short sequence; and

performing, by calling the detection analysis program pre-set in the memory, detection analysis on the processing result, to obtain a final analysis result.

2. The gene sequencing analysis method according to claim 1, wherein said performing, by calling the data quality control program pre-set in the memory, the quality control processing on the slice data comprises:

by calling the data quality control program pre-set in the memory, calculating a position error rate of short sequences in the slice data, statistically analyzing a base distribution in the slice data, and/or removing low-quality bases from the slice data, wherein the low-quality bases are bases with a base quality below a quality threshold.

3. The gene sequencing analysis method according to claim 1, wherein said performing, by calling the detection analysis program pre-set in the memory, the detection analysis on the processing result comprises:

performing, by calling the detection analysis program pre-set in the memory, mutation detection and interpretation on the processing result.

4. A gene sequencing analysis apparatus, comprising:

a data acquisition module configured to acquire slice data transmitted from a sequencing platform in real time, the slice data being a set of short sequences read after performing at least one cycle of sequencing on a sequencing library;

a slice transmission module configured to input the slice data into a memory; and

a processing analysis module configured to perform, by calling an encapsulation program pre-set in the memory, data processing and detection analysis on the slice data, to obtain a corresponding analysis result, wherein the encapsulation program is a custom program,

wherein the data acquisition module is further configured to:

acquire a current central processing unit (CPU) idleness state;

adjust the slice size based on the current CPU idleness state; and

slice, based on the slice size, all unsliced short sequences currently transmitted from the sequencing platform and read after a single cycle of sequencing, a set of the sliced short sequences being used as the slice data,

wherein the encapsulation program comprises a data quality control program, a data processing program, and a detection analysis program, and

wherein the processing analysis module is further configured to:

perform, by calling the data quality control program pre-set in the memory, quality control processing on the slice data, to obtain a quality control result;

perform, by calling the data processing program pre-set in the memory, an alignment between the short sequence in the quality control result and a reference gene, to determine a position of the short sequence on the reference gene;

determine, a position tag of the short sequence based on the position of the short sequence on the reference gene;

determine, among pre-set threads in the memory, a target thread that is currently in an idle state;

perform, by calling the target thread and with reference to the position tag of the short sequence, at least one of ordering, deduplication, and re-alignment of the short sequence; and

perform, by calling the detection analysis program pre-set in the memory, detection analysis on the processing result, to obtain a final analysis result.

5. A storage medium, having computer readable instructions stored thereon, wherein the computer readable instructions, when being executed by one or more processors, cause the one or more processors to perform steps of the gene sequencing analysis method according to any one of claims 1 to 3.

6. A computer device, having computer readable instructions stored thereon, wherein the computer readable instructions, when being executed by one or more processors, cause the one or more processors to perform steps of the gene sequencing

analysis method according to any one of claims 1 to 3.

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