WHAT IS CLAIMED IS:

1. A method for processing gene sequencing data, wherein the method is applied to an apparatus for processing gene sequencing data, the apparatus is a heterogeneous multi-core architecture, comprising an advanced Reduced Instruction Set Computer machine (ARM) architecture, a graphics processing unit (GPU) architecture, and a peripheral component interconnect (PCI) bus; the ARM architecture is connected to the GPU architecture through the PCI bus; the ARM architecture comprises at least one central processing unit (CPU) module; the GPU architecture comprises at least one GPU module; and the method comprises:

S1, obtaining, by a CPU module in an idle state, batches of gene sequencing data by reading gene sequencing data in batches;

S2, obtaining, by the CPU module in the idle state, a first algorithm and a second algorithm by dividing a gene analyzing method;

S3, obtaining, by the CPU module in the idle state, a plurality of reads by dividing each batch of gene sequencing data based on the first algorithm, and sending the plurality of reads and the second algorithm to a GPU module in an idle state;

S4, performing, by the GPU module in the idle state, a calculation on each read based on the second algorithm, and sending respective calculation results to the CPU module in the idle state;

S5, obtaining, by the CPU module in the idle state, a batch processing result based on the calculation results and the first algorithm; and

repeating S1 to S5 until processing the gene sequencing data is completed, and obtaining, by the CPU module in the idle state, a final processing result by integrating the batch processing results.

2. The method according to claim 1, wherein the CPU module in the idle state determines the number of the GPU modules in the idle state and a data processing amount corresponding to each GPU module in the idle state by scanning the at least one GPU module, and reads the gene sequencing data in batches based on the number of the GPU modules in the idle state and the respective data processing amount.

3. The method according to claim 1, wherein a gene analyzing algorithm comprises a gene alignment algorithm, a Dotplot algorithm, a blast algorithm, a partition around medoids, PAM, algorithm, a hidden Markov model, HMM, algorithm, and an artificial intelligence, AI, inference algorithm.

4. The method according to claim 3, wherein the gene alignment algorithm comprises a Burrows-Wheeler transform (BWT) algorithm, and the first algorithm comprises an anchor point cutting algorithm; and the method further comprises:

performing, by the CPU module in the idle state, an anchor point positioning operation on each batch of gene sequencing data through the anchor point cutting algorithm, and obtaining the plurality of reads by extending for a length of N × bp forward and backward respectively with the anchor point as a center and dividing each batch of gene sequencing data by a length of (2N+1) × bp based on a NEON instruction, where N is a positive integer.

5. The method according to claim 4, wherein obtaining the plurality of reads comprises:

obtaining the plurality of reads using a following a formula:

$$（2 * N + 1） * x < L$$

where x represents the number of anchor points, N represents the number of extended bps, and L represents a length of each batch of gene sequencing data.

6. The method according to claim 3 or 4, wherein the second algorithm is a Hash algorithm; and the method comprises:

preforming, by the GPU module in the idle state, a Hash operation on each of the plurality of reads based on the Hash algorithm to obtain a Hash calculation result, and sending the Hash calculation result to the CPU module in the idle state, wherein the Hash calculation result is a value of a BWT algorithm matrix, used for calculation of the BWT algorithm matrix.

7. The method according to claim 6, wherein the first algorithm further comprises a BWT matrix transformation algorithm; and the method further comprises:

performing, by the CPU module in the idle state, a transformation operation on the BWT algorithm matrix based on the BWT matrix transformation algorithm, to obtain a BWT transformation result of the plurality of reads.

8. The method according to claim 3, wherein the gene alignment algorithm comprises a Smith-Waterman algorithm, and the second algorithm comprises a scoring matrix algorithm; and the method further comprises:

obtaining, by the GPU module in the idle state, a Smith-Waterman scoring matrix based on the scoring matrix algorithm, the plurality of reads, and a reference species sequence, and sending the Smith-Waterman scoring matrix to the CPU module in the idle state.

9. The method according to claim 8, wherein obtaining the Smith-Waterman scoring matrix

comprises:

obtaining the Smith-Waterman scoring matrix using following formulas:

$$M=R*C$$

$$R=a*L^2+b$$

where, M represents the Smith-Waterman scoring matrix, R is a length of a candidate section of reference species sequence, C represents a length of a read generated by screening and splicing reads received from the CPU module in the idle state, L represents a length of each batch of gene sequencing data, and a and b are constants.

10. An apparatus for processing gene sequencing data, configured to execute a method for processing gene sequencing data according to any one of claims 1-9.