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(54) Title: SYSTEM, METHOD, AND APPARATUS FOR COPY-NUMBER ESTIMATION OF GENETIC SEQUENCES FOR GENERATION OF RECOMBINANT PROTEINS FOR USE IN THERAPEUTIC APPLICATIONS

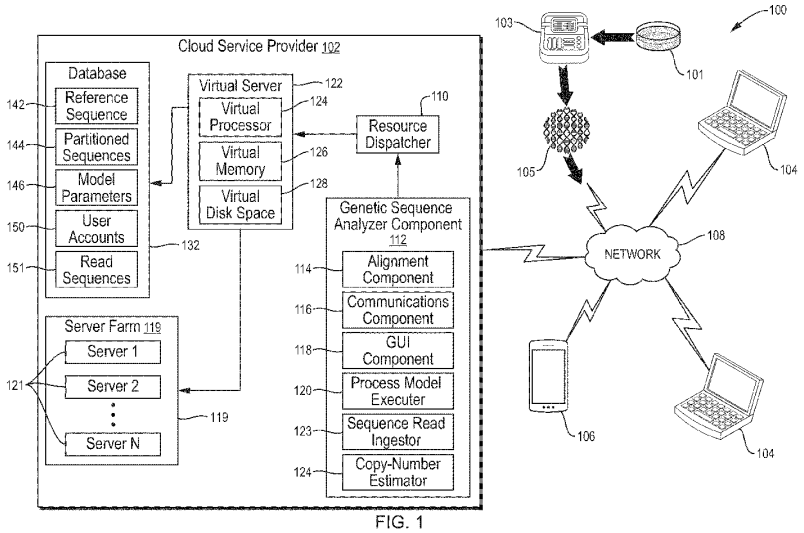


FIG. 1

(57) Abstract: A method is disclosed for determining genomic-region copy number. The method may involve isolating and purifying a sample of genomic nucleic acids, followed by creating a shotgun library from the sample. The shotgun library is then sequenced, and the generated reads are aligned to a reference sequence consisting of a reference genome and a vector sequence. The reference genome is partitioned into multiple sizes, and a mean read coverage is determined for each size until a predetermined number of consecutive mean-read coverage peaks form, with an equal coverage distance between them. A respective copy number is determined for each of these consecutive peaks. Additionally, a model is developed to estimate the copy number of a target sequence. The method utilizes a processor for performing the alignment, partitioning, determination of mean read coverage, copy number determination, and model configuration.

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