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61/361,886 6 July 2010 (06.07.2010) US(71) Applicant (for all designated States except US): **LIFE TECHNOLOGIES CORPORATION** [US/US]; C/O Intellevate, P.O. Box 52050, Minneapolis, MN 55402 (US).

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(54) Title: SYSTEMS AND METHODS TO DETECT COPY NUMBER VARIATION

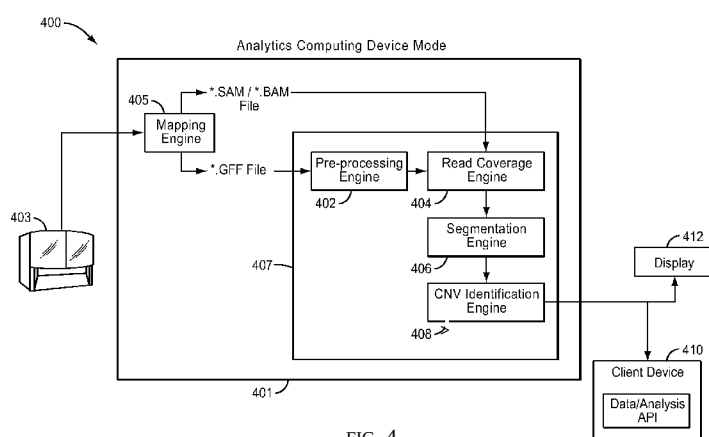


FIG. 4

(57) **Abstract:** In one aspect, a system for implementing a copy number variation analysis method, is disclosed. The system can include a nucleic acid sequencer and a computing device in communications with the nucleic acid sequencer. The nucleic acid sequencer can be configured to interrogate a sample to produce a nucleic acid sequence data file containing a plurality of nucleic acid sequence reads. In various embodiments, the computing device can be a workstation, mainframe computer, personal computer, mobile device, etc. The computing device can comprise a sequencing mapping engine, a coverage normalization engine, a segmentation engine and a copy number variation identification engine. The sequence mapping engine can be configured to align the plurality of nucleic acid sequence reads to a reference sequence, wherein the aligned nucleic acid sequence reads merge to form a plurality of chromosomal regions. The coverage normalization engine can be configured to divide each chromosomal region into one or more non-overlapping window regions, determine nucleic acid sequence read coverage for each window region and normalize the nucleic acid sequence read coverage determined for each window region to correct for bias. The segmentation engine can be configured to convert the normalized nucleic acid sequence read coverage for each window region to discrete copy number states. The copy number variation identification engine can be configured to identify copy number variation in the chromosomal regions by utilizing the copy number states of each window region.

- *before the expiration of the time limit for amending the claims and to be republished in the event of receipt of amendments (Rule 48.2(h))*

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INTERNATIONAL SEARCH REPORT

International application No.
PCT/US2011/042976**A. CLASSIFICATION OF SUBJECT MATTER****G06F 19/10(2011.01)i**

According to International Patent Classification (IPC) or to both national classification and IPC

B. FIELDS SEARCHED

Minimum documentation searched (classification system followed by classification symbols)

G06F 19/10; C07H 21/04; G06F 17/10; G06F 19/00; C07H 21/02; C12P 19/34; C12Q 1/68

Documentation searched other than minimum documentation to the extent that such documents are included in the fields searched

Korean utility models and applications for utility models

Japanese utility models and applications for utility models

Electronic data base consulted during the international search (name of data base and, where practicable, search terms used)

eKOMPASS(KIPO internal) & Keywords: "nucleic acid*", "gene*", "geno*", "copy number*", "CNV*", "sequenc*", "reference"

C. DOCUMENTS CONSIDERED TO BE RELEVANT

Category*	Citation of document, with indication, where appropriate, of the relevant passages	Relevant to claim No.
A	US 2006-0292608 A1 (DANIEL PINKEL et al.) 28 December 2006 See the abstract; and paragraphs [0039]-[0075] .	1-20
A	US 6365353 B1 (THOMAS LORCH et al.) 02 April 2002 See the abstract; column 3, line 40 - column 6, line 33; and figures 2-3.	1-20
A	US 2006-0078917 A1 (BHUBANESWAR MISHRA et al.) 13 April 2006 See the abstract; paragraphs [0005], [0084]-[0087]; and claim 1.	1-20
A	US 2009-0098547 A1 (GHOSH SRINKA) 16 April 2009 See the abstract; paragraphs [0007], [0111]-[0119]; and claim 1.	1-20



Further documents are listed in the continuation of Box C.



See patent family annex.

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"T" later document published after the international filing date or priority date and not in conflict with the application but cited to understand the principle or theory underlying the invention

"X" document of particular relevance; the claimed invention cannot be considered novel or cannot be considered to involve an inventive step when the document is taken alone

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"&" document member of the same patent family

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Information on patent family members

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