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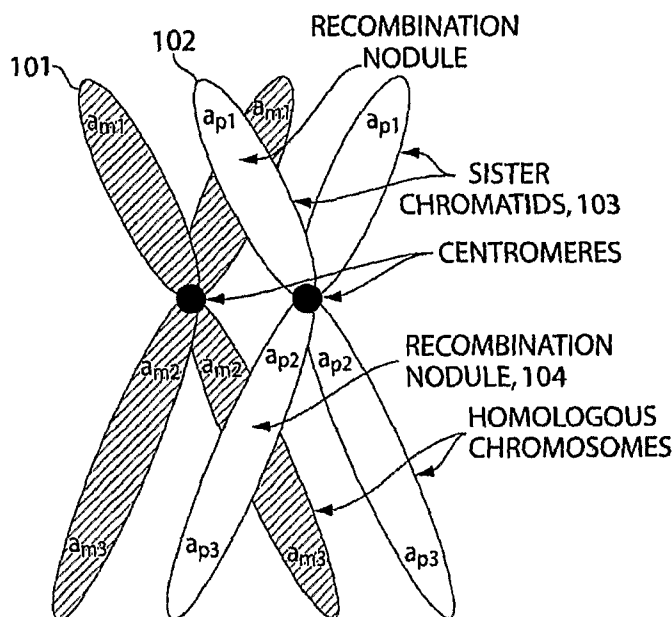
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(54) Title: SYSTEM AND METHOD FOR CLEANING NOISY GENETIC DATA AND USING DATA TO MAKE PREDICTIONS



(57) Abstract: A system and method for determining the genetic data for one or a small set of cells, or from fragmentary DNA, where a limited quantity of genetic data is available, and also for predicting likely phenotypic outcomes using mathematical models and given genetic, phenotypic and/or clinical data of an individual, and also relevant aggregated medical data consisting of genotypic, phenotypic, and/or clinical data from germane patient subpopulations. Genetic data for the target individual is acquired and amplified using known methods, and poorly measured base pairs, missing alleles and missing regions are reconstructed using expected similarities between the target genome and the genome of genetically related subjects.

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C. DOCUMENTS CONSIDERED TO BE RELEVANT		
Category*	Citation of document, with indication, where appropriate, of the relevant passages	Relevant to claim No.
X --- Y	WO 03/031646 A1 (FINDLAY et al) 17 April 2003 (07.04.2003), entire document, especially Fig 4-7, pg 6, ln 8 - pg 36, ln 26, table 6a, 6b	1-4, 6-14, 16-17, 19-25, 28, 30-31, 36-42, 44 ----- 5, 15, 18, 26-27, 29, 32-35, 43
X --- Y	US 2004/0137470 A1 (DHALLAN) 15 July 2004 (15.07.2004), entire document, especially Abstract, Fig 3A-3C, 12, para [0006] - [2693]	45-61 ----- 5, 26-27
Y	US 2004/0236518 A1 (PAVLOVIC et al.) 25 November 2004 (25.11.2004), entire document, especially Fig 4, 5 and Fig 1A-1B, para [0036] - [0060]	15, 18, 29, 32-35, 43
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