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(71) Applicant: **GENOMICS PLC** [GB/GB]; King Charles House, Park End Street, Oxford OX1 1JD (GB).

(72) Inventors: **MOORE, Rachel**; C/o Genomics PLC, King Charles House, Park End Street, Oxford OX1 1JD (GB).

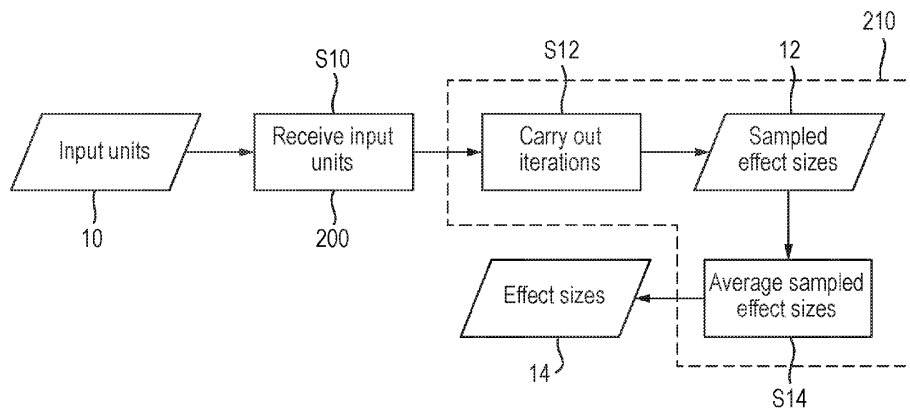
PLAGNOL, Vincent Yann Marie; C/o Genomics PLC, King Charles House, Park End Street, Oxford OX1 1JD (GB). **RIVEROS-MCKAY, Fernando**; C/o Genomics PLC, King Charles House, Park End Street, Oxford OX1 1JD (GB). **WEALE, Michael**; C/o Genomics PLC, King Charles House, Park End Street, Oxford OX1 1JD (GB). **WELLS, Daniel**; C/o Genomics PLC, King Charles House, Park End Street, Oxford OX1 1JD (GB).

(74) Agent: **J A KEMP LLP**; 80 Turnmill Street, London Greater London EC1M 5QU (GB).

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(54) Title: COMPUTER-IMPLEMENTED METHOD AND APPARATUS FOR ANALYSING GENETIC DATA

Fig. 1



(57) Abstract: Disclosed is a method of analysing genetic data about an organism comprising receiving a plurality of input units. Each input unit comprises information about the association between genetic variants in a region of the genome and a target phenotype. One or more iterations are carried out comprising, for each variant, determining whether the variant is causal for the target phenotype. If the variant is causal, a sampled effect size is determined for each input unit based on the input units and correlations between the plurality of genetic variants in the region. The sampled effect size is non-zero for all of the input units. For each variant, a prediction effect size is determined for each input unit based on an average across the iterations of the sampled effect sizes for the input unit or of posterior effect sizes for the input unit calculated using the sampled effect sizes.

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