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(54) **Title:** METHOD AND APPARATUS FOR ANALYSIS OF CHROMATIN INTERACTION DATA

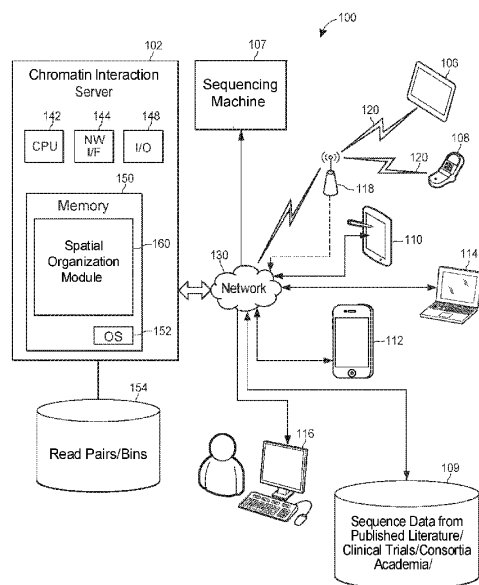


FIG. 1A

(57) **Abstract:** To analyze spatial organization of chromatin a computing device may compile genomic element contacts or reads into variable size bins using a binary search tree. The bins may be selected to each represent a different outside increment or functional element within a genome, such as a gene, TAD, chromatin state segment, loop domain, chromatin domain, etc. Two sets of bins are selected to generate a squared genome matrix of bin pairs, where each set represent an axis of the matrix. Then a normalization method is applied to the interaction frequencies for the bin pairs having variable size and/or shape to generate normalized interaction frequencies for each bin pair. The normalized interaction frequencies may be used to identify bin pairs having enriched and depleted contacts for a variety of analyses, including the detection of target genes of genomic variants, as well as genome wide analysis of contacts.

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