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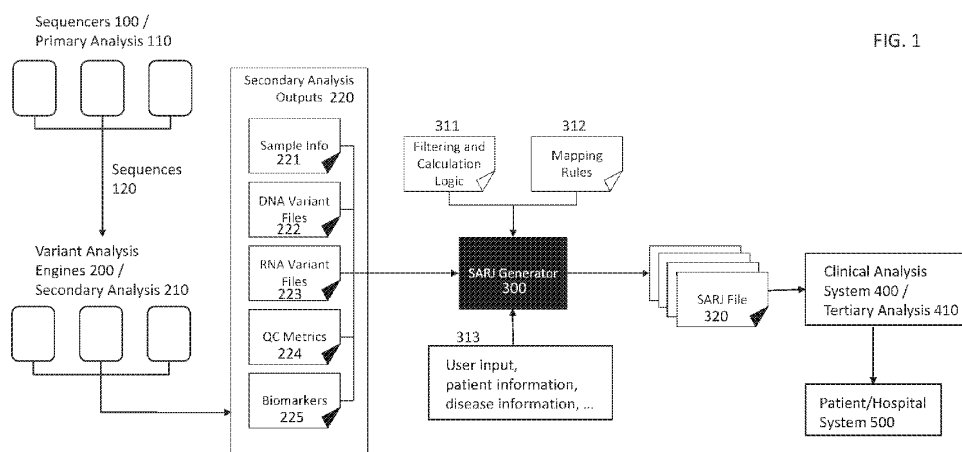


FIG. 1

(57) **Abstract:** Methods and systems are disclosed which can gather large data sets from nucleic acid sequencing technologies and devices, filter relevant genomic information and sequence variant information of biological samples from files of various formats, generate a custom data file having only relevant information in a standardized format, and provide the generated information to downstream analysis for personalized medicine use.