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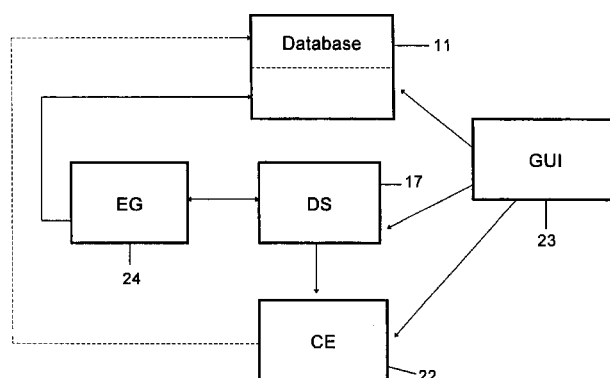
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(54) Title: SYSTEM AND METHOD FOR MODELING GENETIC, BIOCHEMICAL, BIOPHYSICAL AND ANATOMICAL
INFORMATION: IN SILICO CELL



(57) Abstract: Genetic, biochemical, biophysical and anatomical information is integrated at the subcellular, cellular, tissue and organ level. At least one database containing biological information is used to generate at least one data structure having at least one attribute associated therewith. An interface interactively views, edits or links together attributes of the data structures to create at least one hierarchical description of subcellular, cellular, tissue and organ function. The hierarchical description may optionally be an elementary, binary or pathway data structure, or, alternatively, an anatomical data structure capable of being modified to form a structural model. A computational engine mathematically generates at least one data structure from the hierarchical description. Genetic information is accessed, tabulated and combined with functional information on the biochemical and physiological role of gene products. Computational models of genetic, biochemical and biophysical processes within cells and higher order systems are automatically formulated, solved and analyzed based on combination of genetic and functional information adduced. A dynamic tool is thereby provided for achieving discernible objectives, such as increased understanding of biological processes, identification of new drug targets for therapeutic intervention and predictions involving the outcome of drug screening. These objectives are accomplished by the realization of highly complex nonlinear dynamic interactions that occur between each gene or gene product.



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