

CAVEman: Standardized anatomical context for biomedical data

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A software system called the CAVEman has been created for the visual integration and exploration of heterogeneous anatomical and biomedical data. The CAVEman can be applied for both education and research tasks. The main component of the system is a three-dimensional digital atlas of the adult male human anatomy, structured according to the nomenclature of Terminologia Anatomica. The underlying data-indexing mechanism uses standard ontologies to map a range of biomedical data types onto the atlas.

The CAVEman system is now used to visualize genetic processes in the context of the human anatomy and to facilitate visual exploration of the data. Through the use of Javatrade mark software, the atlas-based system is portable to virtually any computer environment, including personal computers and workstations. Existing Java tools for biomedical data analysis have been incorporated into the system. The affordability of virtual-reality installations has increased dramatically over the last several years. This creates new opportunities for educational scenarios that model important processes in a patient's body, including gene expression patterns, metabolic activity, the effects of interventions such as drug treatments, and eventually surgical simulations.

The CAVEman Project aims to create visual maps of information about diseases that have a genetic component, such as cancer, diabetes, and Alzheimer's. Using an immersive virtual reality environment called the CAVE, the research team will integrate a high-

resolution digital atlas of a human body with medical data related to specific diseases. The final result will be a next-generation 4D (space and time) visual system to "see" disease processes and the effects of interventions, such as drugs, on these processes.



The mapping results are visualized within the virtual reality environment offered by the CAVEman system. After the desired anatomical systems are loaded into the visualization scene, the user loads the text file that contains the ADME data of a particular drug, which triggers the series of mapping processes required for visual integration of the data. Semantic mapping is accomplished by either using a simple term mapper or an ontology reasoning engine to process semantic relationships contained in the ontologies.

Sources:

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