Proposed Classification of Cells in the Foundational Model of Anatomy

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A logical and principled representation of cell types and their component parts could serve as a framework for correlating the various ontologies that are emerging in bioinformatics with a focus on cells and subcellular biological entities. In order to address this need we have extended the Foundational Model of Anatomy (FMA)^{1,2} from macroscopic to cellular and subcellular anatomical entities. The poster will provide a live demonstration of this implementation.

Although Schleidig and Schwan proposed the cell theory over 150 years ago, a satisfactory and comprehensive classification of cells remains to be established. The varied and inconsistent classification schemes implied by traditional and contemporary hard-copy sources in biology and medicine are adequate for human usage, but fall short of the requirements for supporting machinebased inference.

Although much information remains to be instantiated, the extension of the Anatomy taxonomy (At) component of the Foundational Model of Anatomy (FMA) to microscopic and macromolecular levels establishes the information space for accommodating the diverse attributes of the large variety of cell types that constitute the human body. The frame-based Protégé-2000 knowledge acquisition system, in which the FMA is implemented, supports seamless navigation from organs and organ systems to tissues, cells and their microscopic and macromolecular components. Consistent with the structural context of the FMA. we relied on inheritable structural attributes for classifying cells and their parts.

The class *Cell* inherits the defining attributes of its superclass *Anatomical structure* (Material physical anatomical entity which has inherent 3D shape; is generated by coordinated expression of the organism's own structural genes) and is distinguished from its sibling classes by its own set of defining attributes (Anatomical structure that consists of cytoplasm surrounded by a plasma membrane, with or without the cell nucleus). These defining attributes are represented as slots in a concept frame. In addition to structural attributes shown in Figure 1, the frame of a cell can

also accommodate cell specific attributes, such as proliferative vs. nonproliferative state, somatic vs. germ cell lineage, and tissue type. Many cell parts and biological macromolecular structures have been instantiated and their inherited attributes and values have been included.



Figure 1. A section of *Anatomical Taxonomy* with the attributes of the class Cell, displayed through the Foundational Model Explorer (FME),³ a web-browser providing a simplified view of Protégé frames.

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References

- 1. C Rosse et al "Motivation and organizational principles for the Digital Anatomist Symbolic Knowledge Base: an approach toward standards in anatomical knowledge representation" JAMIA 1998, 5:17-40.
- C Rosse, L Shapiro, J Brinkley, "The Digital Anatomist Foundational Model: principles for defining and structuring its concept domain" Proc AMIA Symp 1998:820-824.
- L Detwiler, J Mejino, C Rosse, "Web-Based Browsing of the Foundational Model of Anatomy" Proc AMIA Symp 2003. Submitted.