NCI Center for Bioinformatics

Informatics Seminar Series

The Role of the Foundational Model of Anatomy for the Cross-Correlation of Neoplasia and Anatomical Entities

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9:00 AM until Noon
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6130 Executive Blvd. (EPN)
Conf. Room H

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The classification of neoplasm is largely based on the anatomical structures affected by the neoplastic process. Therefore, a logical and computable representation of anatomical entities is prerequisite for the symbolic modeling of neoplasms and the effects they exert on parts of the body. In the traditional, hard copy literature anatomy has been represented from a variety of viewpoints to meet the specific needs of clinical and other application domains. Emerging medical terminologies have continued this trend, evidenced by the divergent representation of anatomy in UMLS and other vocabularies, none of which seems to comprehensively meet the needs of knowledge modelers at NCI.

The Foundational Model of Anatomy (FMA) is being developed as a reference ontology that can accommodate all views of anatomy and provide the anatomical information called for by any domain or application. To meet this goal, the FMA will accommodate all anatomical entities ranging from biological macromolecules to cells, organs, organ systems and parts to the entire body. This scope of the FMA is assured by a novel and unifying theory of anatomy, which embraces not only human anatomy but also the anatomy of other species. Such a comprehensive and broad representation, however, requires that this reference ontology be filtered and partitioned to meet the specific

viewpoints and practical needs of application domains such as the correlation of neoplasia and anatomy.

The intent of the presentation and interaction will be to illustrate how the FMA can be partitioned and filtered to provide the view and granularity that meets the needs of NCI knowledge modelers. Particular examples will be used as mockups to show the kinds of neoplasias that can affect certain kinds of anatomical entities and how the FMA can provide the framework for associating gene expression data and other etiological information with particular anatomical entities.

Following the presentation there will be an open discussion.