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A core data model to effectively support major use cases in precision oncology

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Terminologies and ontologies are broadly used in biomedicine, such as the International Classification of Diseases and the Systematized Nomenclature of Medicine, and more specifically in oncology, such as the National Cancer Institute's Thesaurus. Significant efforts are also invested in developing and maintaining concrete data standards like the Observational Medical Outcomes Partnership by the Observational Health Data Sciences and Informatics program and the Fast Healthcare Interoperability Resources by the Health Level 7 organization. Overall, data standardization is paramount in biomedicine but vital in precision oncology, where large volumes of clinical-genomic data are collected and combined with external knowledge to allow for a thorough evaluation of patient cases and the delivery of personalized care. Standardization can further support other tasks, such as information reuse, secondary analysis, and interoperability across different systems. Several efforts have attempted to build data models for successfully standardizing data in precision oncology. For example, the American Society of Clinical Oncology's Minimal Common Oncology Data Elements model (mCODE) assembles several data elements to consistently capture clinical and genomic information from oncology electronic health records (EHRs). In this talk, we will discuss the importance of data standardization in precision oncology by presenting existing common data models and referring to their application to the real clinical setting. To this end, we will use the example of Molecular Tumor Boards (MTBs) that analyze clinicalgenomic data from EHRs and combine them with external knowledge to recommend molecularly-guided therapies for patient cases. We also review the JHU Precision Oncology Core Data Model (Precision-DM), initially developed to fill existing gaps and fully support the MTB and other use cases in precision oncology.

Biography

Taxiarchis Botsis is an Assistant Professor of Oncology and Medicine at the Division of Quantitative Sciences at The Sidney Kimmel Comprehensive Cancer Center at Johns Hopkins University. His background lies in Medical Informatics with a focus on precision oncology, natural language processing of clinical texts, normalization and standardization of clinical information, construction of decision support systems, integration of data from multiple sources, generation of efficient and compelling information visualizations, and development of advanced methods and approaches in pharmacovigilance. Among his other funding in these areas, Dr. Botsis has received awards to improve the efficiency and rigor of pharmacovigilance at the U.S. Food and Drug Administration and develop decision-support solutions to enhance clinical trial recruitment, and personalized medicine approaches in precision oncology.