

Keynote Speaker
Dr Lewis Frey
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caBIG

Abstract: The cancer Biomedical Informatics Grid (caBIG) is a National Cancer Institute (NCI) initiative to promote data sharing in the cancer community. It brings together researchers with diverse expertise in clinical trial management systems, in vivo imaging, integrative cancer research, tissue banks, pathology tools, architecture, population sciences, vocabularies and common data elements. The goal is to develop systems that interoperate and exchange useful information across the grid. The caBIG community has developed a consensus based approach founded on the principles of open source, open access, open development and federation. The community has agreed that semantic integration is an essential component in this development of interoperable systems, because it enables researchers to unambiguously describe the data they are exchanging. Semantic integration uses controlled vocabularies and structured, standards-based metadata as part of its tool set to unambiguously describe diverse data sets. The metadata descriptions of these data sets are then used to coordinate the development of systems that provide analytical services on that data across the cancer community.

Lewis Frey, PhD is an assistant professor in the Department of Biomedical Informatics at the University of Utah. During his two year NLM-funded postdoctoral fellowship at Vanderbilt University in the Biomedical Informatics Department, he specialized in cancer biomedical informatics. Dr. Frey holds a doctorate and masters in computer science with a focus on machine learning from Vanderbilt University and a bachelor of science in mathematics from the University of Pittsburgh. Dr. Frey has worked extensively on the cancer Biomedical Informatics Grid (caBIG) for the National Cancer Institute, helping the Vocabulary and Common Data Elements workspace draft the compatibility checklist for reviews of silver level compliance. He is involved in drafting UML Best Practices for caBIGs model driven architecture. Dr. Frey conducts research in computational biomedical informatics, particularly in methods of combining multiple data sets of different types (e.g., microarray, proteomic) for the purpose of knowledge discovery. He has developed methods for combining prior knowledge of biological pathways with expression data for biomarker discovery. He is currently working on methods for identifying robust biomarker signatures in expression data for diagnosis and prognosis of lung, breast and colon cancers.