Adapting caArray to a Cancer Center's Workflow

Fangxia (Scott) Li, M.S., Karl J. Smalley, B.B.A, Jack W. London, Ph.D.
Kimmel Cancer Center, Thomas Jefferson University, Philadelphia, PA

The Kimmel Cancer Center (KCC) microarray facility and its research community will be adopting NCI's recently released version 1.0 of caArray for annotation and management of microarray experimental results. It is our desire to publish microarray data generated for our zebra fish facility to the grid. However, first development efforts will be directed towards utilizing a local instance of caArray's APIs to better incorporate caArray in the microarray workflow of our cancer center. Specifically, EJBs and MAGE-OM APIs will be carefully tested in order to generate center-based requirement and system specification documents for extensions to caArray. These documents describing caBIG-compliant tools to be built on top of the caArray 1.0 platform, will include a service-oriented system called caArray-MIAME Service Toolkit (caArray-MST). In this way the caArray platform can be extended to address the following workflow use case scenarios:

- How different "actors" (e.g., researchers, microarray staff) can locally enter different portions of the MIAME annotation, at different times.

- How research labs and the microarray facility can dynamically update any previous locally entered annotation based on tailored project views.

This poster and demonstration will provide details on the planned work, and present any progress in caArray API integration realized to date. We will also discuss the KCC's caBIG-compliant tool system for potential integration of our legacy microarray results virtual file directory system, MAGGIE, with caArray in the grid computing environment. It is felt that the requirements and specifications collected in KCC's initial efforts in this process will be valuable at other cancer centers.