



caLIMS2: a caBIG® Compliant Laboratory Information Management System

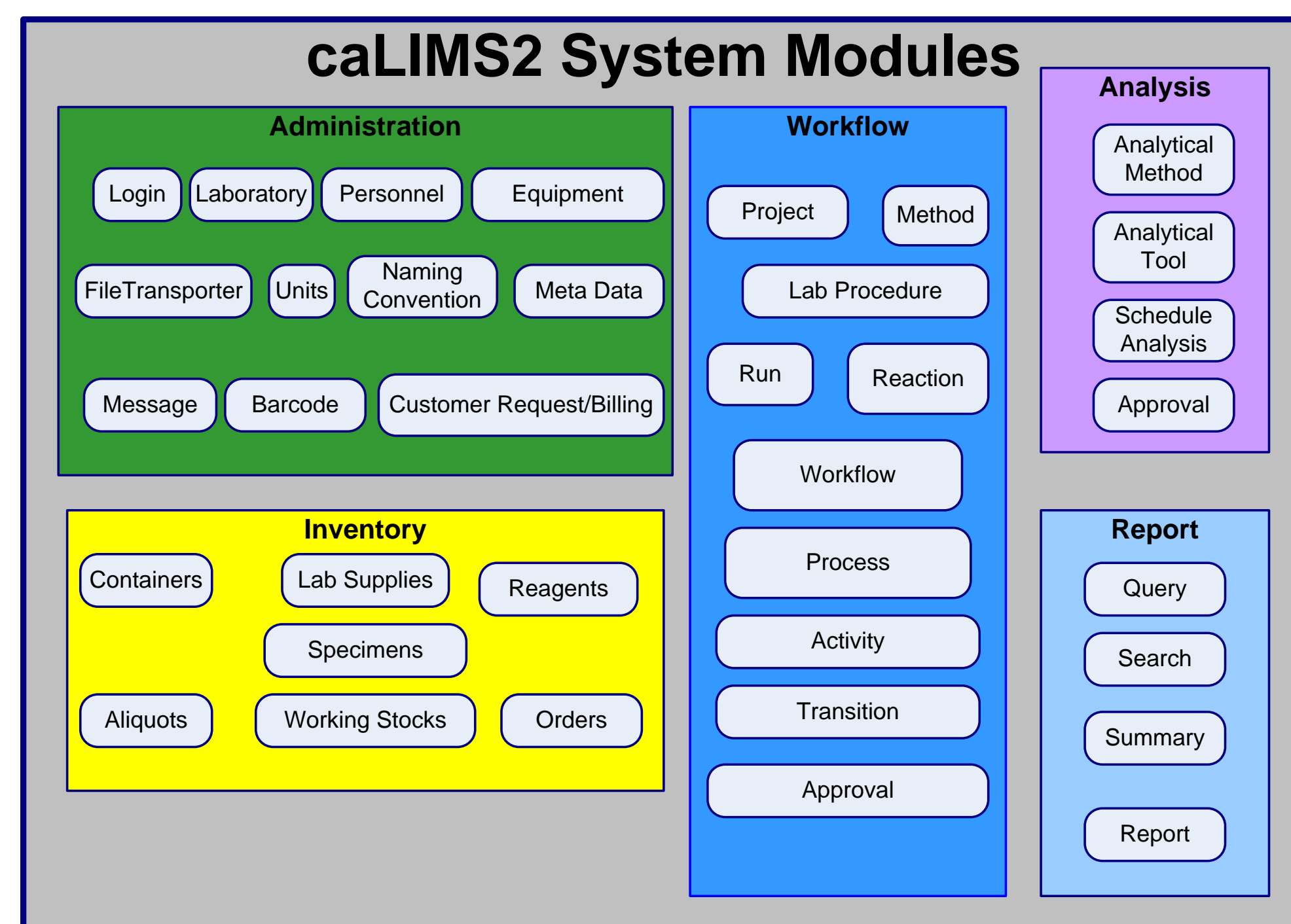
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Background

The purpose of the caLIMS2 initiative is to create a next generation open source Laboratory Information Management System that is caBIG® silver compliant. caLIMS2 will complete the caBIG® bench to bed model by bridging the gap between biospecimen repositories, data repositories and analysis tools. The application is designed to allow easy customization by users and to facilitate integration with laboratory equipment, analytical tools and data sources. caLIMS2 is highly flexible, making it suitable for use by research labs, high throughput core facilities and public health labs. caLIMS2 will help further translational cancer research through the organization of laboratory workflow, tracking of specimens, acquisition of laboratory data and metadata, and the appropriate sharing and dissemination of the data to support subsequent analyses.



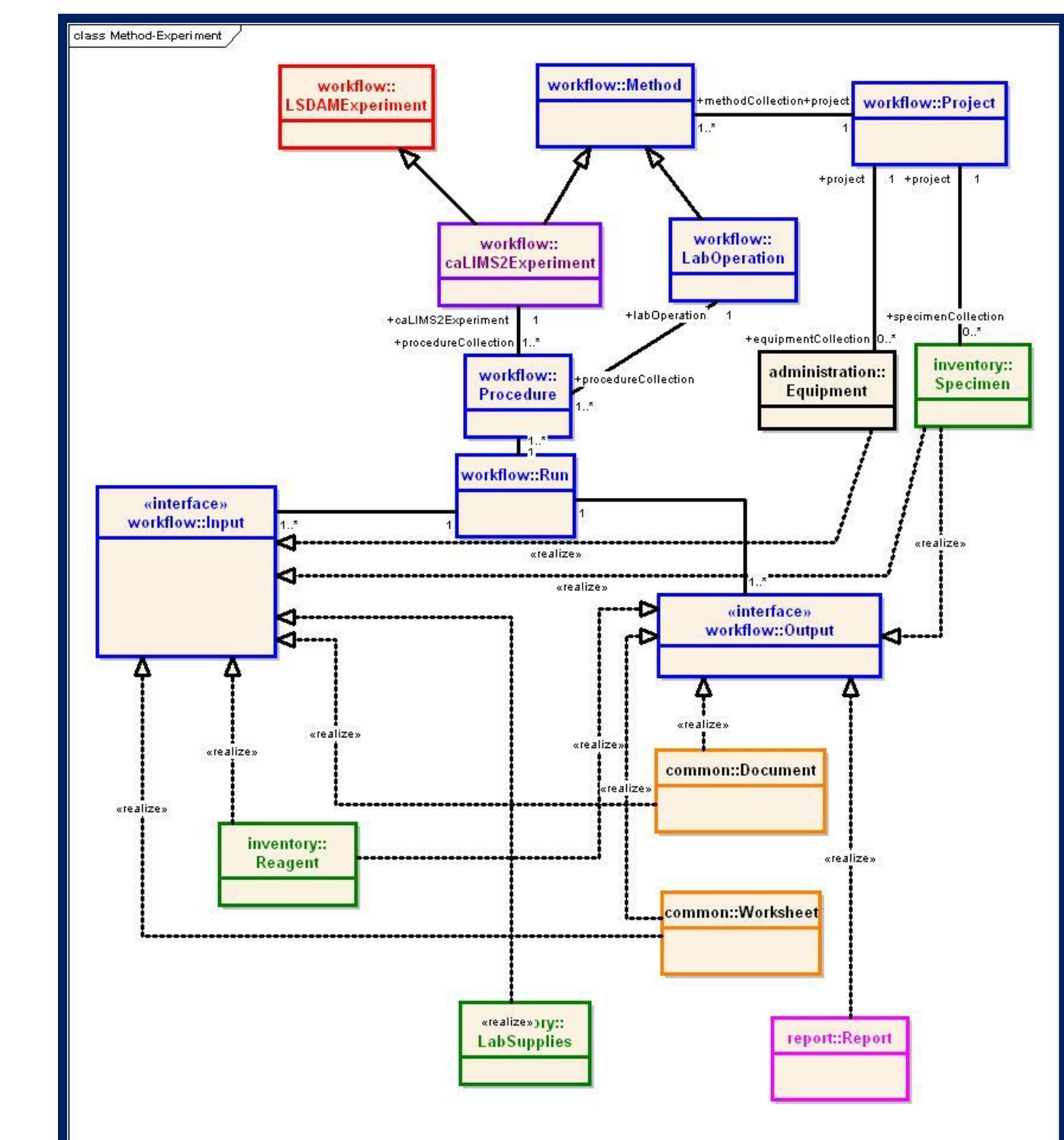
Targeted users of caLIMS2

Laboratories seeking a reliable, cost effective caBIG® compliant LIMS solution and/or one that does not require a large IT resource to implement and maintain.

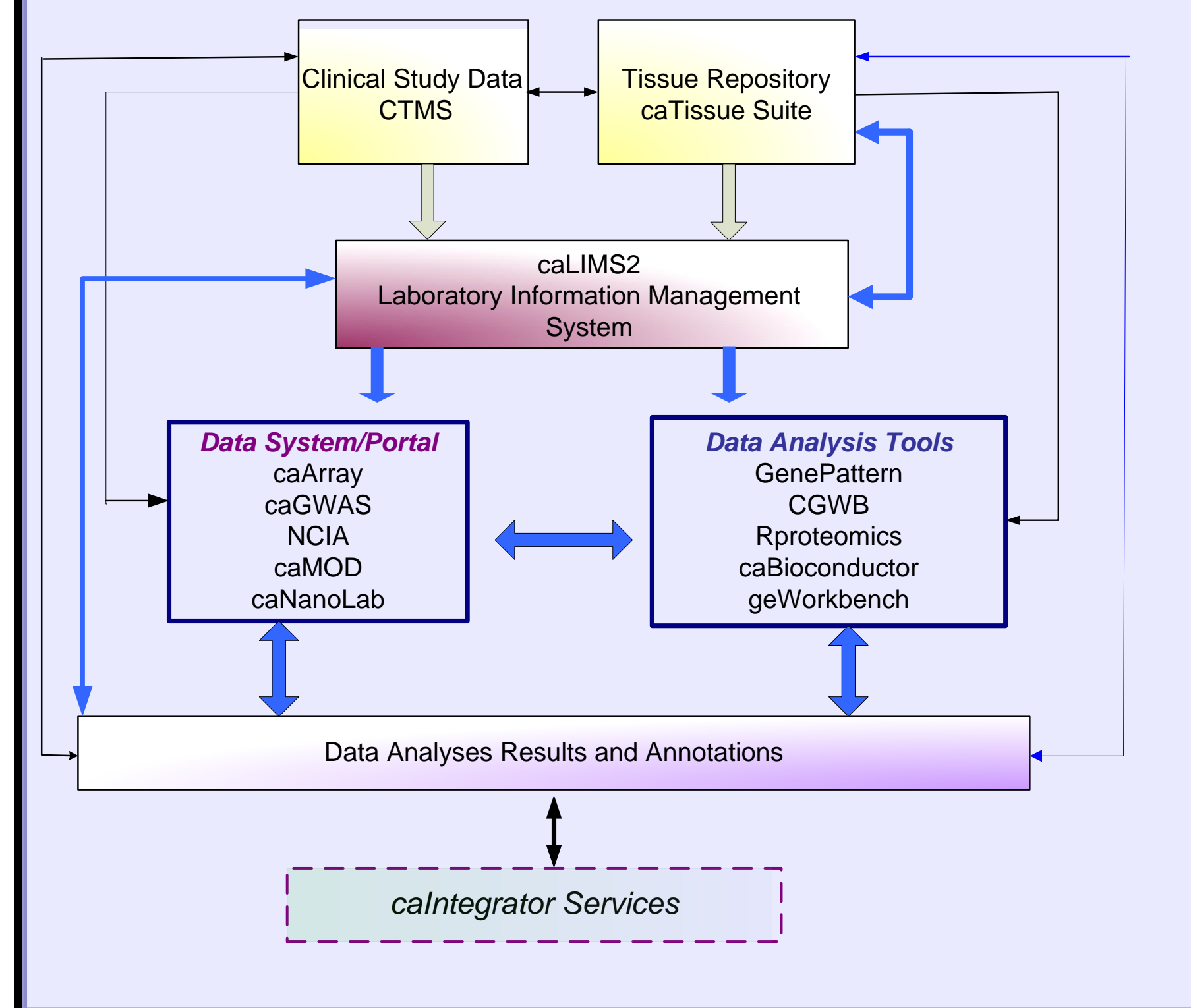
- Basic research laboratory
- Core laboratory facility
- Clinical research laboratory
- Public health laboratory
- BIG-Health disease research laboratory

Features of caLIMS2

- Open source, consortium-based development
- caBIG® integration
- Security management via CSM/UPT
- Generic Experiment model - supports multiple lab domains (genomics, proteomics, nanomaterial, etc.)
- Platform independence
- Customizable UI - lab specific objects
- Laboratory Workflow management – import/export standard workflows
- FileTransporter tool (caAdapter)

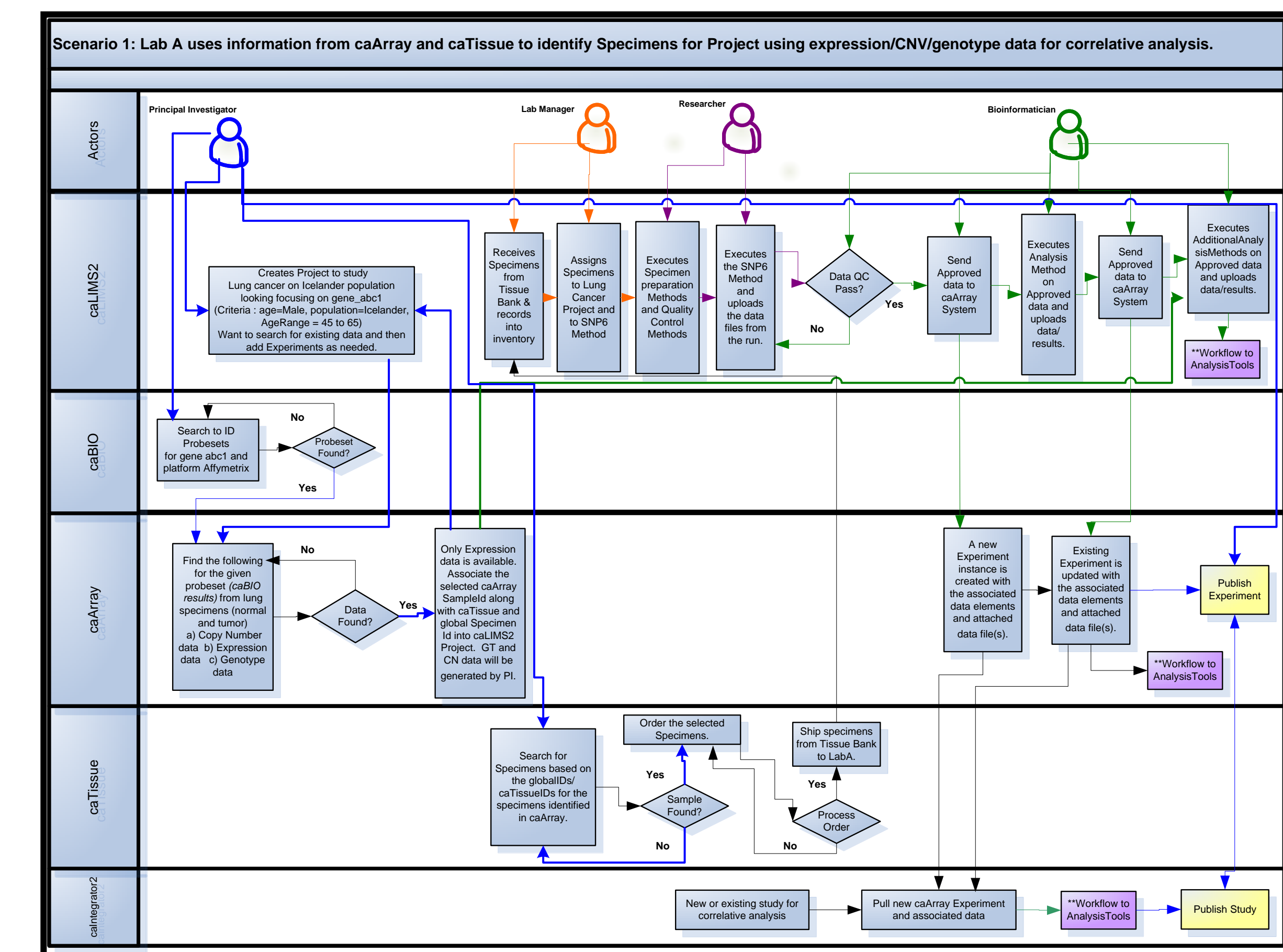


Integration of caLIMS2 in ICR



Use Case for Integrating caLIMS2 with caBIG® applications

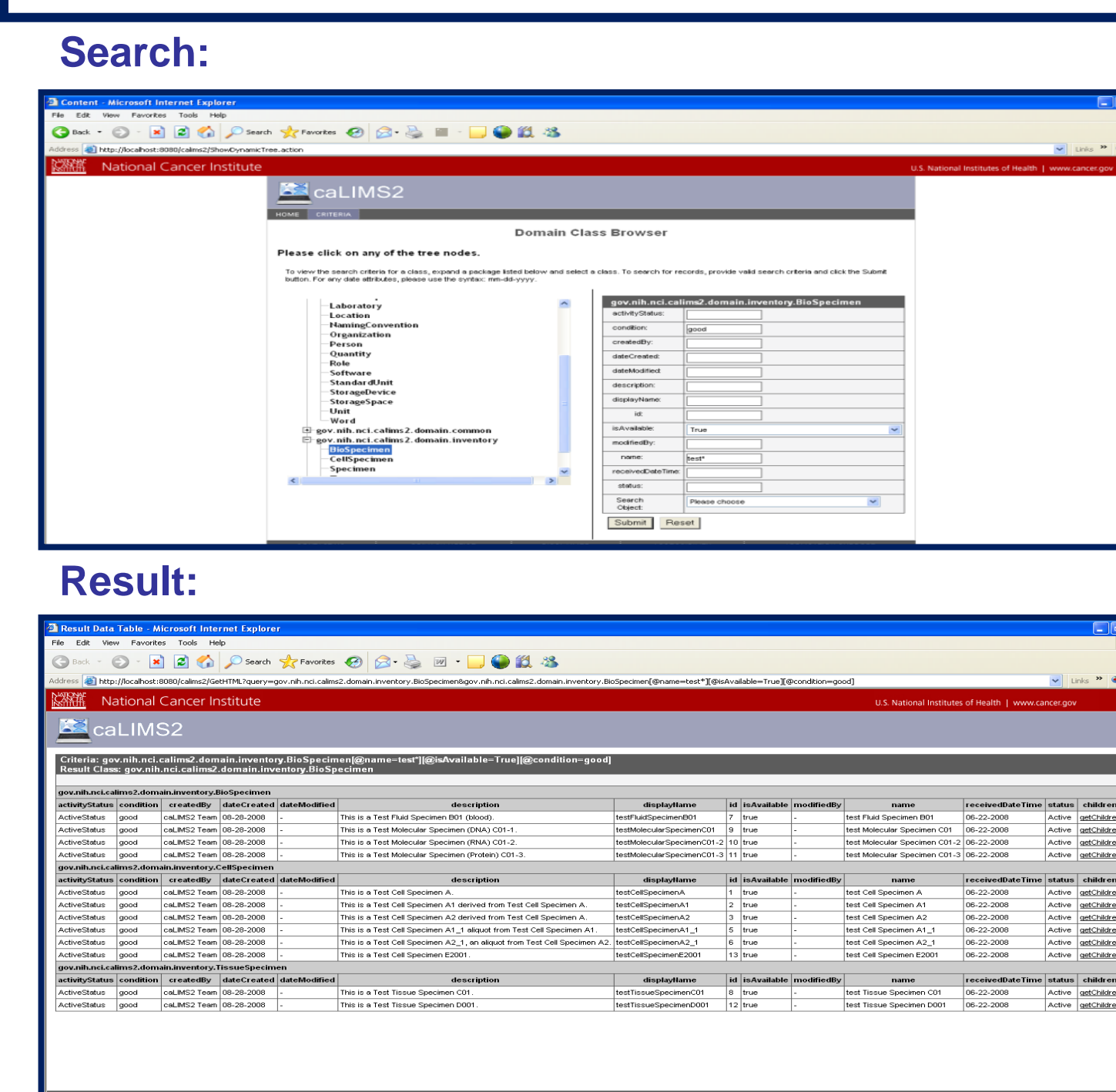
- A Principal Investigator wants to participate in a collaborative study involving the relationship of gene *ABC1* and lung cancer susceptibility in men age 45 – 65. The PI is particularly interested in a population from Iceland.
- PI plans to use multiple data types (copy number, genotype, gene expression) in a new form of correlative analysis and wants to take advantage of existing data and specimen resources.
- PI obtains appropriate tissue specimens from caTissue.
- PI obtains pre-existing gene expression data from caArray and generates new genotype and copy number data in her laboratory.
- PI programmatically submits final data to the caArray repository.



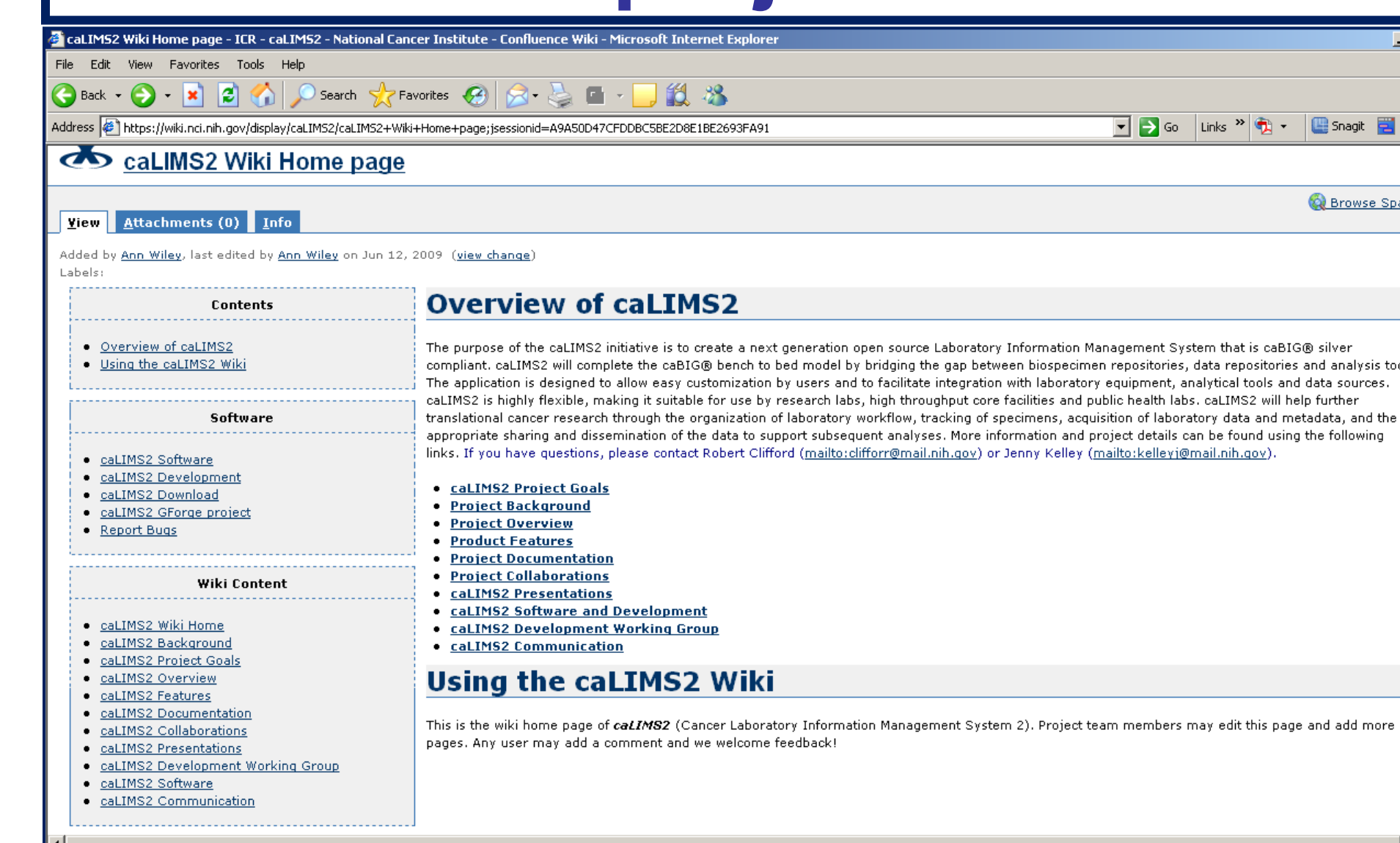
Current Status

- Use Case design phase completed
- Object Model design for beta 0.5 release completed, approved, and registered in caDSR
- Beta 0.5M1.1 release: Java APIs/web services – available
- Basic web UI is under development
- Object Model design for the 1.0 release is near completion and will be submitted Aug. 2009
- Data Model design for 1.0 release is in progress
- Business Model design for 1.0 release is in progress
- Beta 1.0 release: Q3/Q4 2010

Generated Application and Service – caLIMS2 M1.1



caLIMS2 project wiki site



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<https://wiki.nci.nih.gov/display/caLIMS2>