



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 (Figs 1-3).

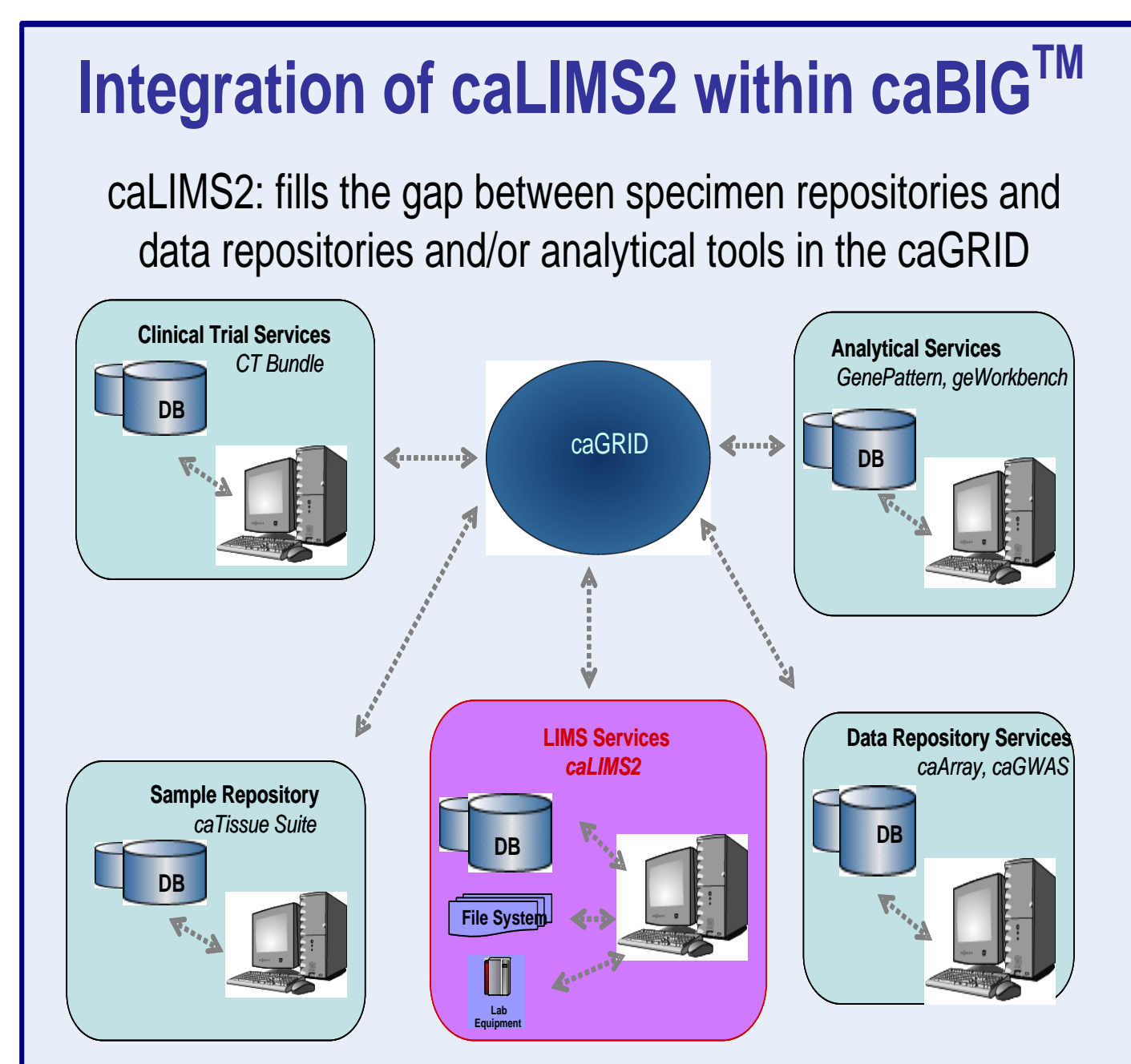


Fig. 1

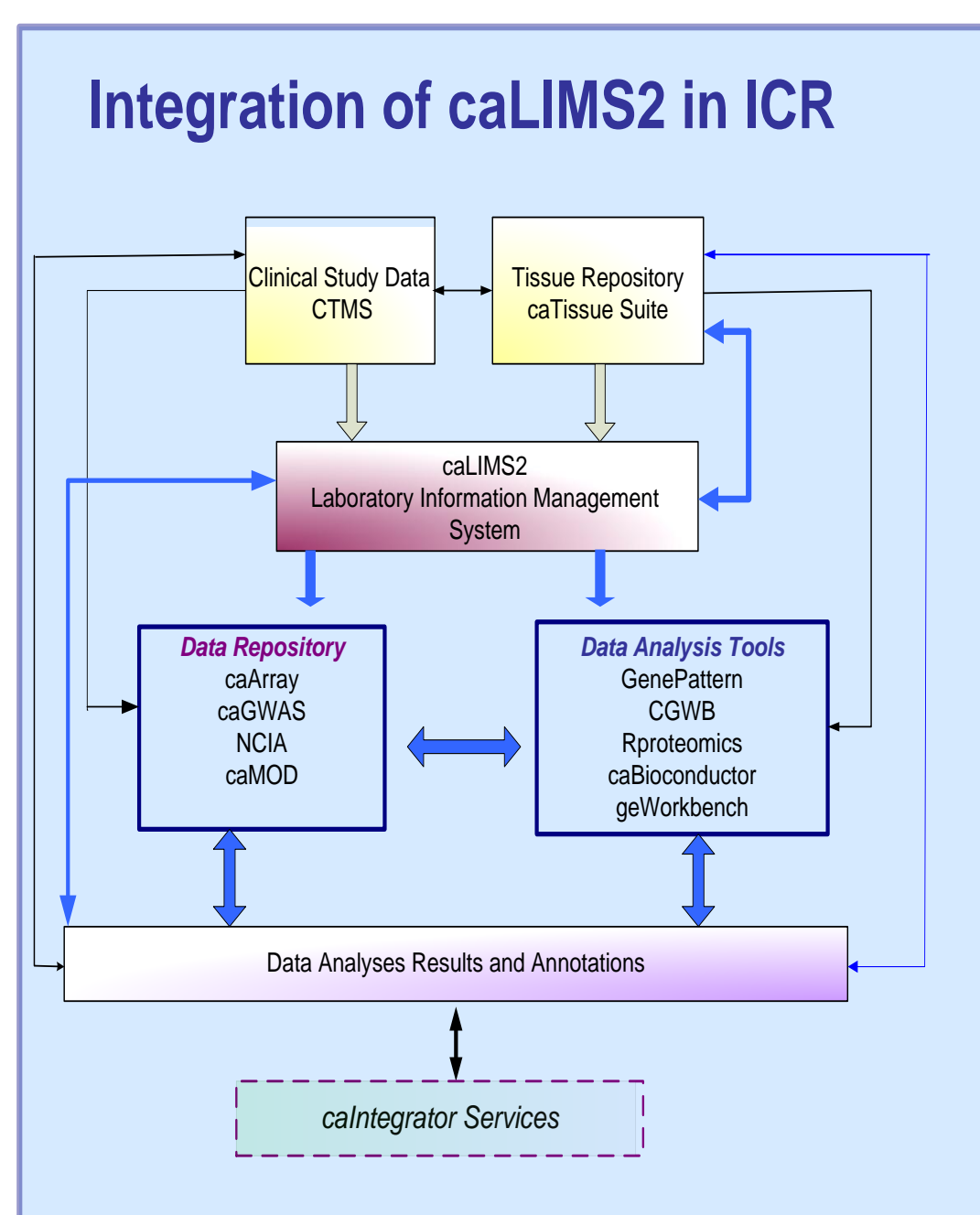


Fig. 2

Targeted Users

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

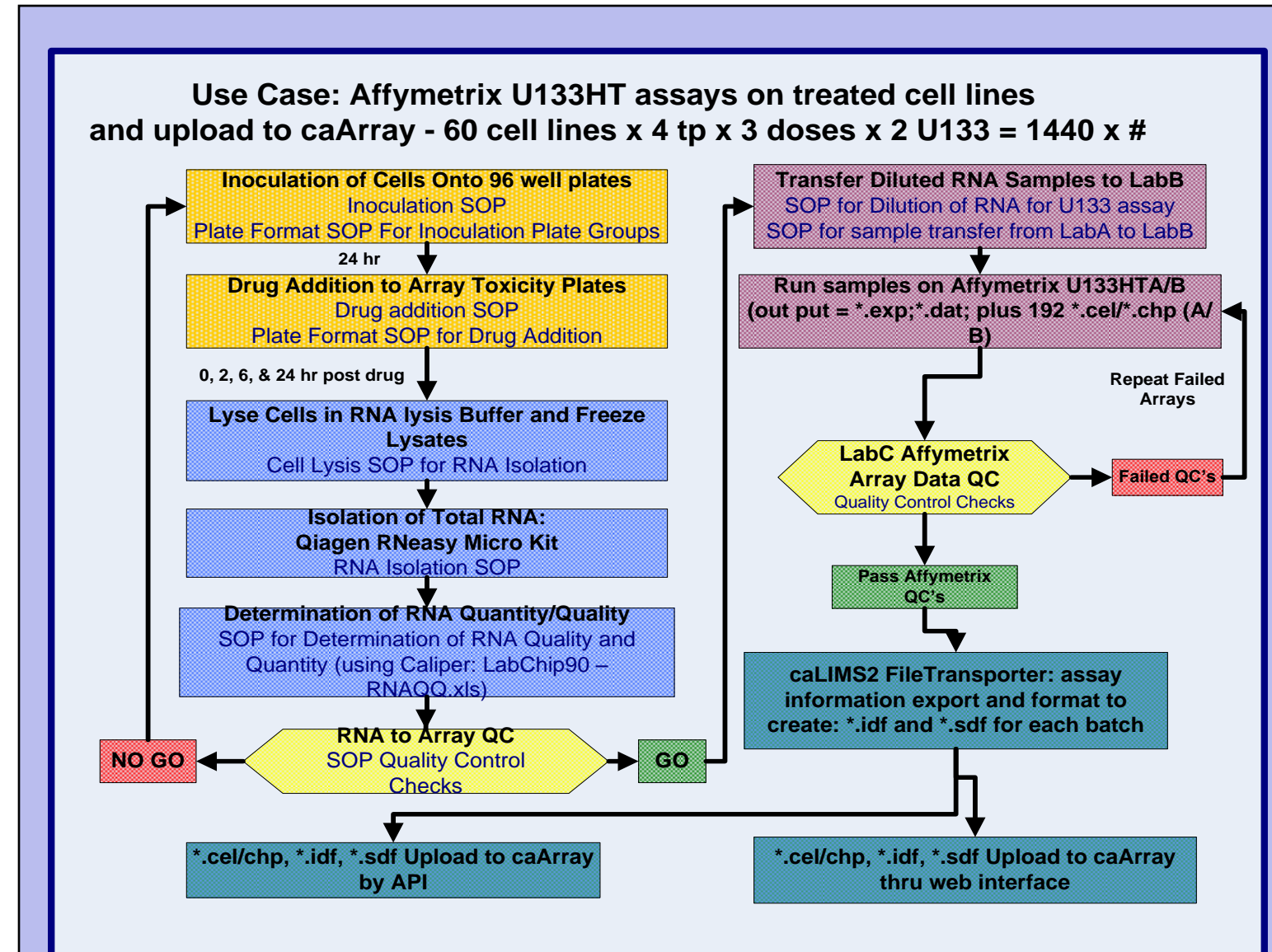
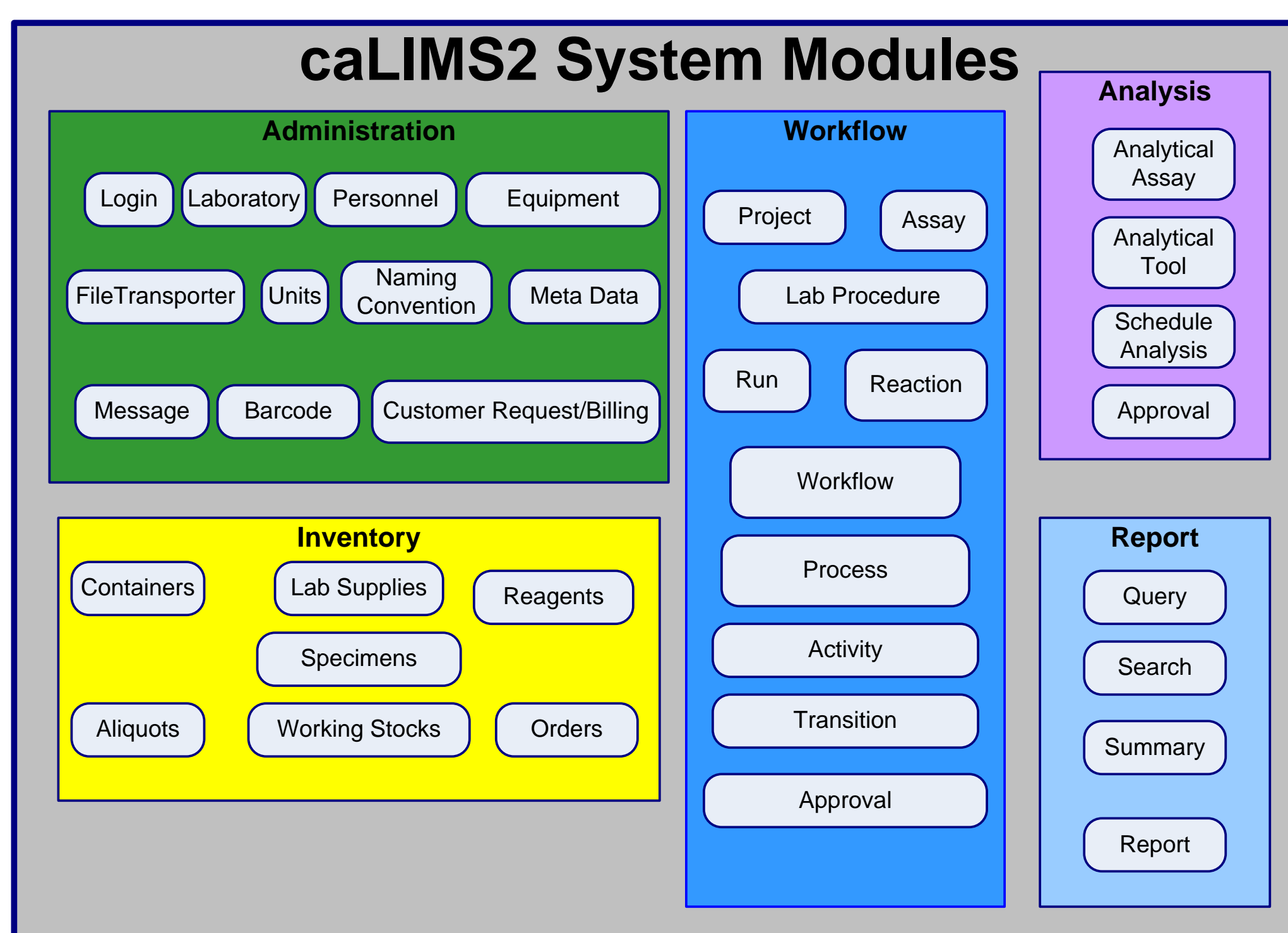


Fig. 3

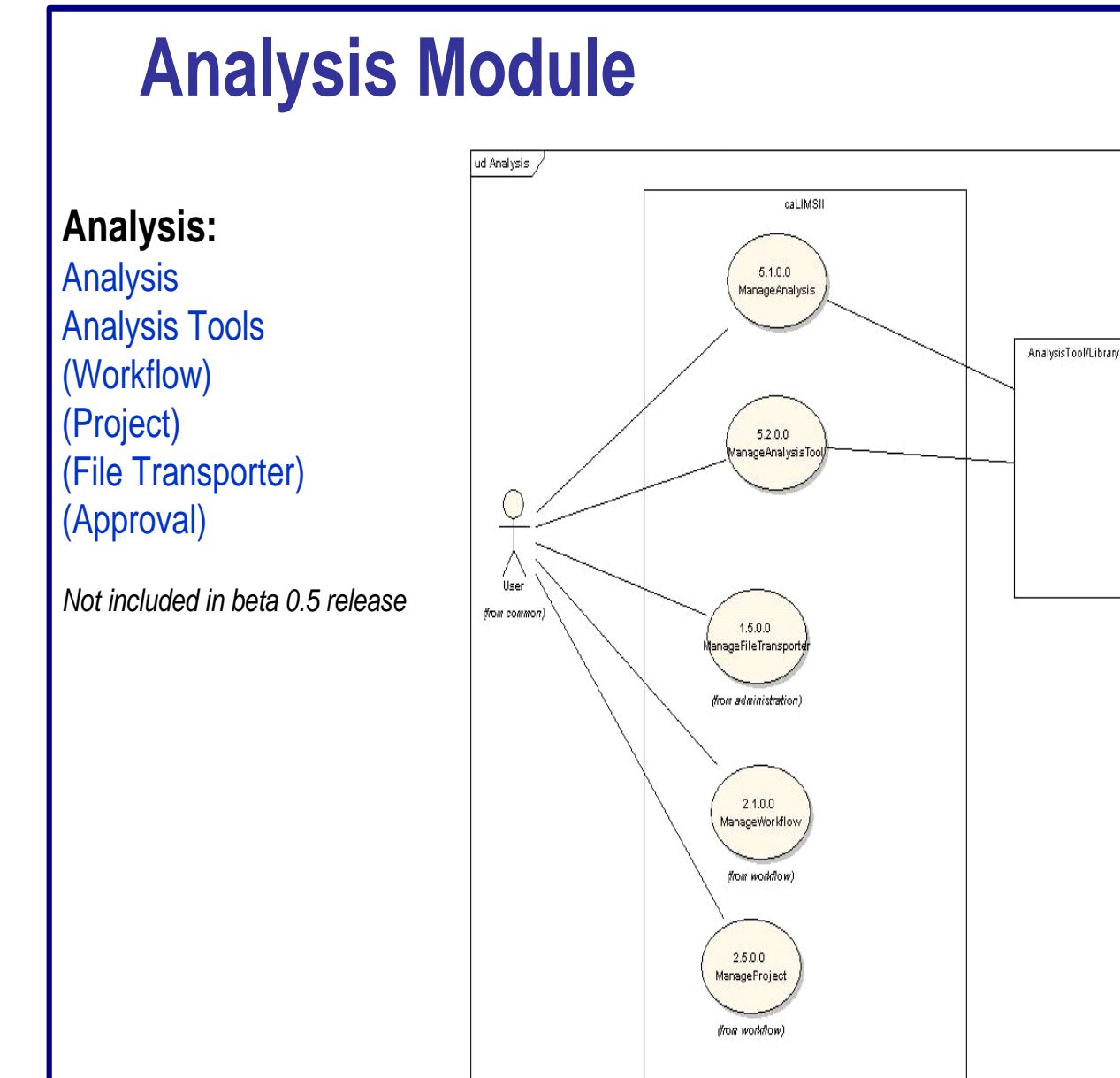
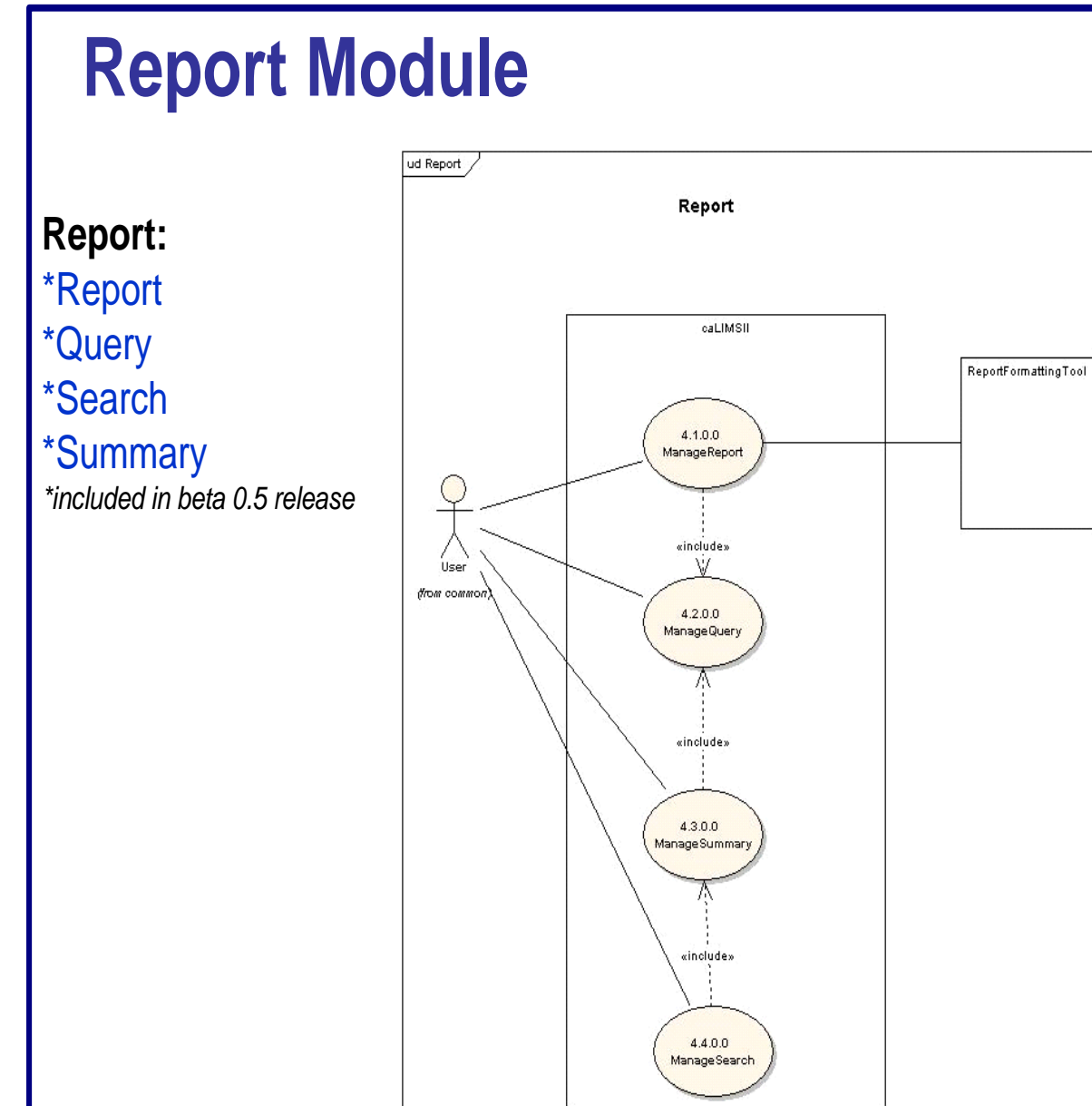
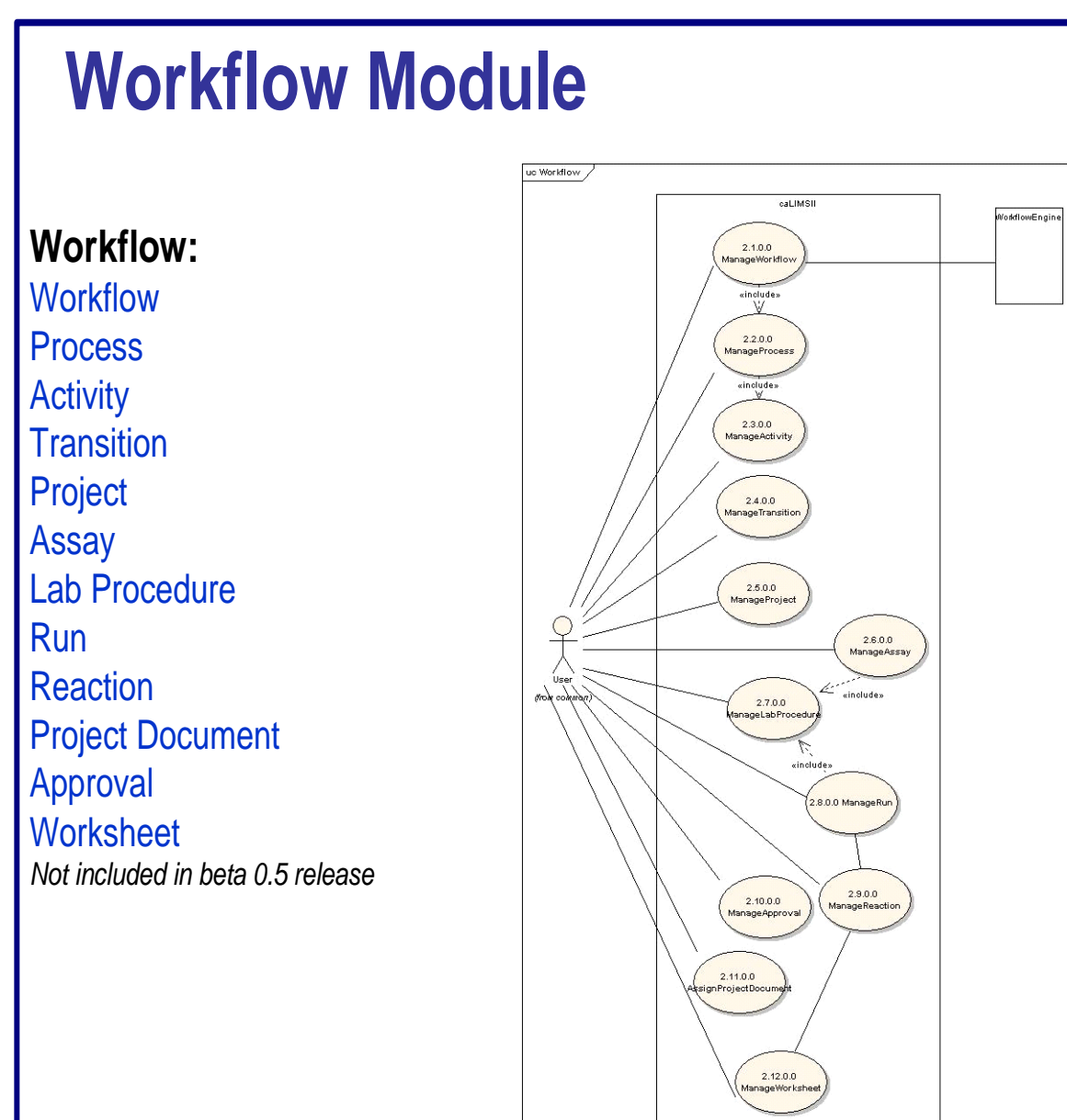
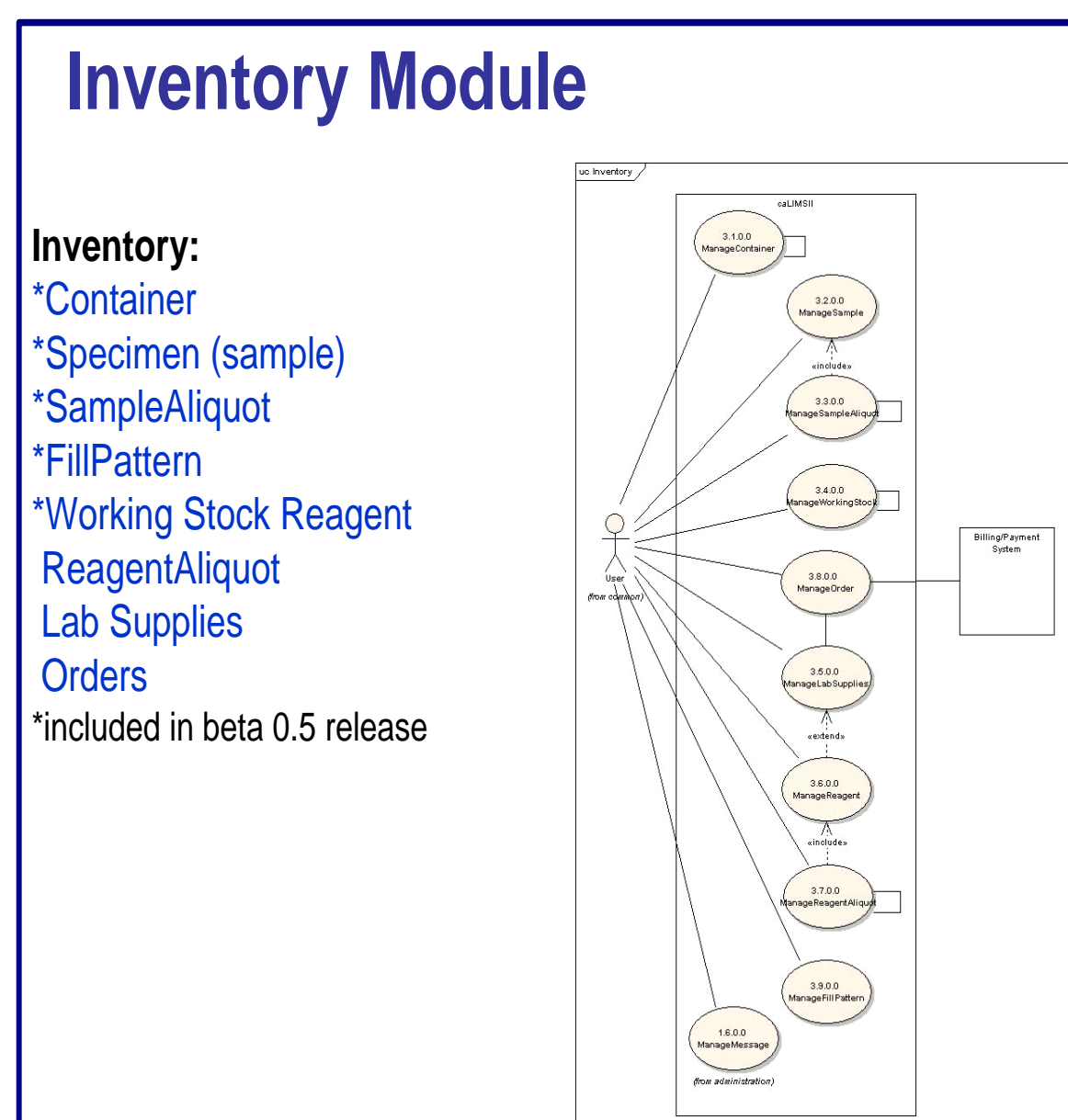
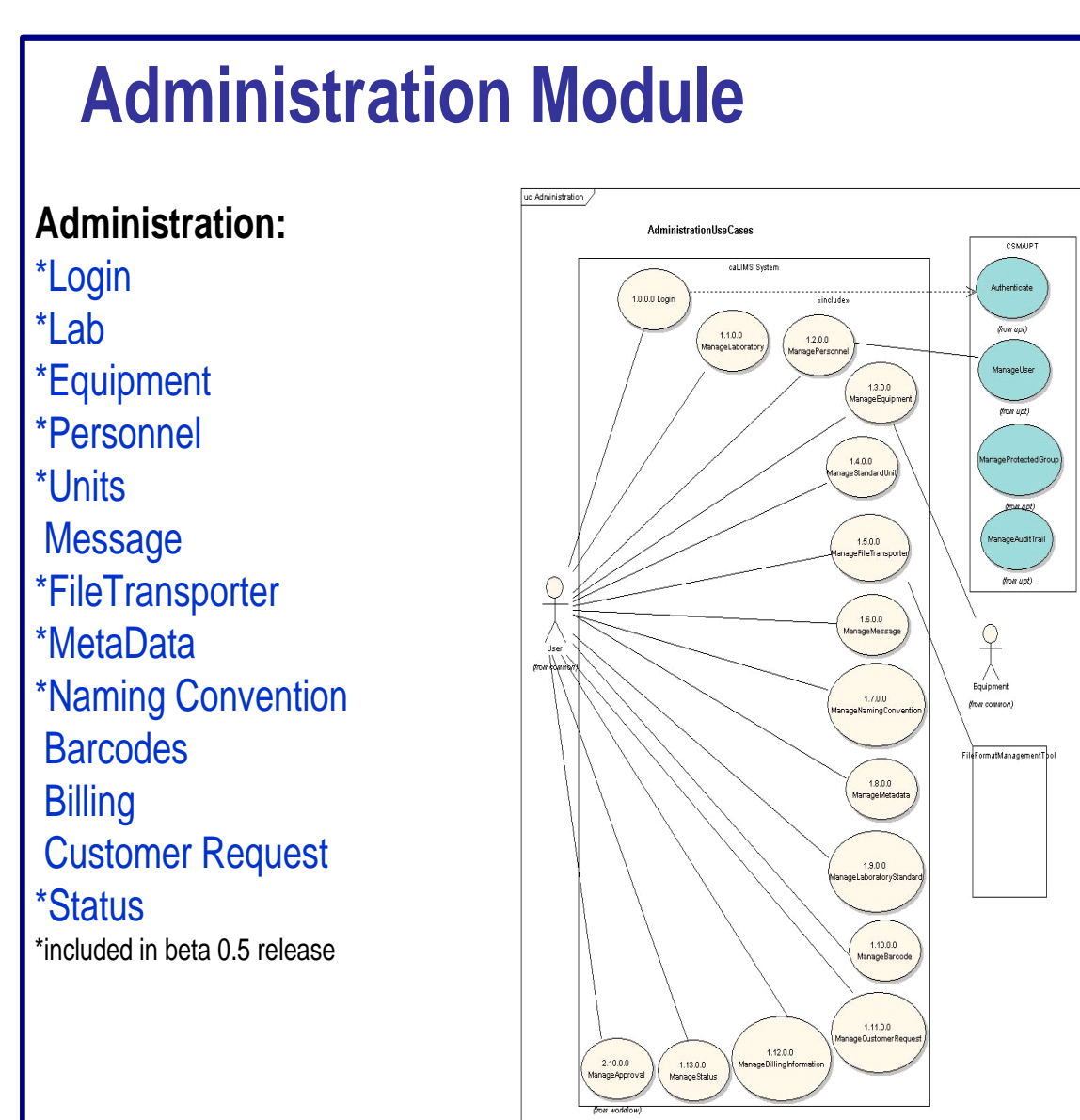
Features

- Open source with caBIG™ integration
- Customization – custom lab specific objects and UI
- Consortium-based development* - supports multiple lab domains (genomic, proteomic, nanoparticle, etc.)
- Security management: CSM/UPT
- Workflow management – import standard workflows (Taverna)
- FileTransporter tool (caAdapter)
- Platform and database independent



Example Use Case for caLIMS2 (Fig. 3): Cells - U133HT - caArray

- Sample plates and assays tracked through Project/Assays/LabProcedures/Runs and SOPs,
- QC tracked for each sample and approvals required to proceed or samples tracked to repeat,
- Transfer events track LabA - LabB -LabC to caArray,
- FileTransfer: upload output files, parse data, reformat and create files; archive raw data files, create the specific *.idf and *.sdrf files from information stored in caLIMS2 and then create the appropriate set of upload zip files that include the data cel/chp files with the experiment idf/sdrf files.
- Execute the upload of the exported files to caArray by using either the caArray web interface (currently available)
- Or ultimately – by using a caLIMS2 API to export directly to caArray



NCI CBIIT LIMS Consortium

Contributing members:

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SAIC: Sashi Thangaraj, Brian Levine
CBIIT: Anand Basu, Clint Malone
LMT: Bob Stephens, Jin Chen
ARL: Nirav Merchant, Dave Thompson
DFCI: Jomol Mathew, Deven Atnoor, Andrey Belozarov, Erica Jones
APHL/MN PHL: Gary Jones, Christina Tamondong
UMN MSI: Ben Lynch

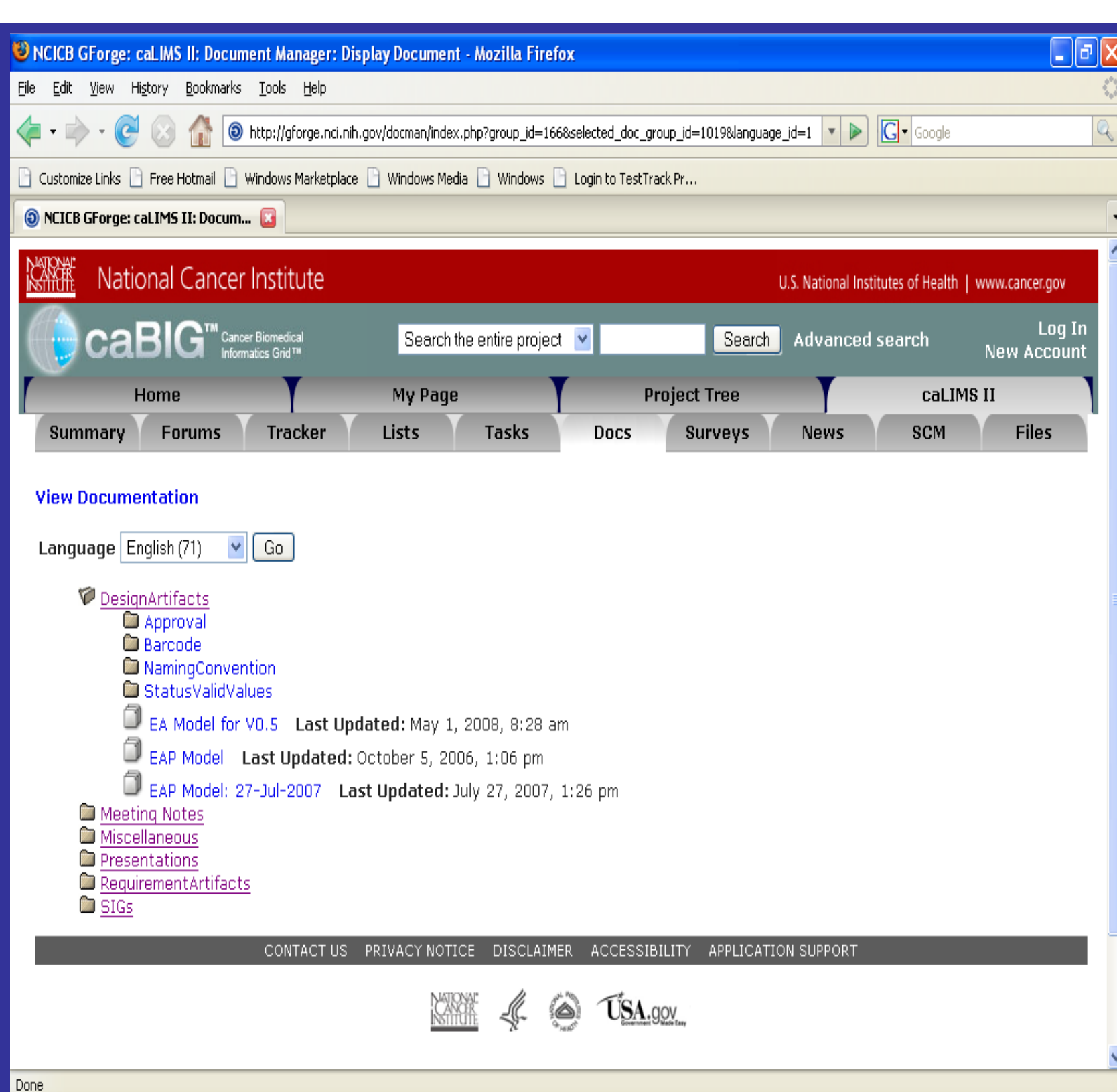
caLIMS2 project site:

<http://gforge.nci.nih.gov/projects/calims2>

caLIMS2 LISTSERV:

<https://list.nih.gov/archives/nci-lims-consortium.html>

caLIMS2 gForge site: Documentation



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Current Status

- Use Case design phase completed
- Object Model design for beta 0.5 release completed, approved by EVS team, and registered in caDSR (more classes will be registered for the full 1.0 release)
- Data Model for beta 0.5 release completed; will need to complete additional data tables for 1.0; will need to optimize and normalize as the application is tested
- Coding for beta 0.5 release (core system and specimen management) is in process
- Beta 0.5 release: Java APIs/web services - July 2008
- Basic web UI is under development
- Beta 1.0 release: December 2008