

Chapter 1 System Description 1

Context	1	
Flowcharts	5	
Features	7	
Data tracking for the Sequencing Application		7
Plate Tracking	8	
Location Tracking	9	
Receiving and Purchasing		10
Protocol Tracking	11	
11		
Plugins	13	
Issue Tracking	13	
DNA Sequencing	13	
SAGE Library Construction		14
DNA Fingerprinting and Sizing		14
Architecture and Technologies		15
Architecture view of the alDente LIMS system		16
Users	17	
Lab users	17	
Lab administrators		17
Administrators	17	
Programmers	18	

Appendix A Release 2.7 i

List of Primary Changes i
Minor Changes iii

Group Specific Improvements	vii
LIMS Background Improvements	ix
Deferred Requests	ix
Future Development	ix
Hotfix Patches since previous release	ix
Hotfixed:	ix
Not Hotfixed:	x

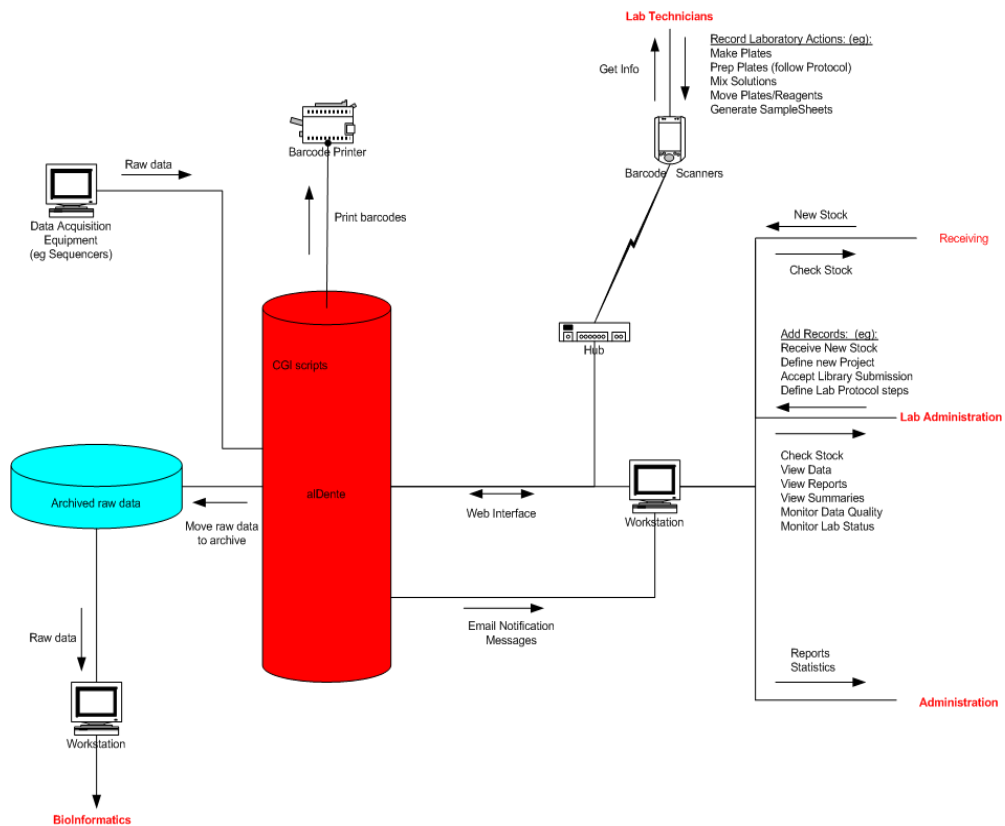
Chapter 1

System Description

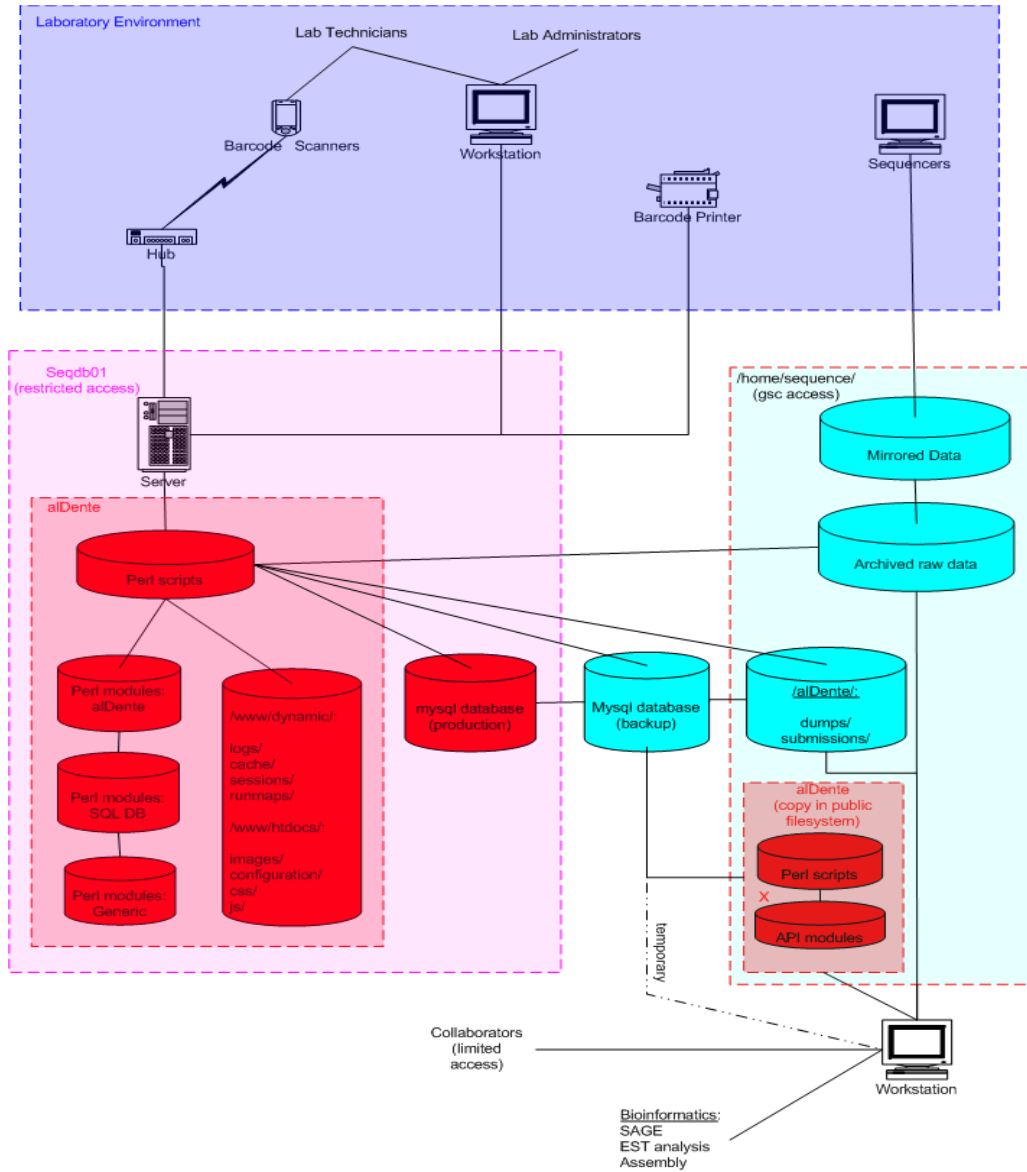
.....

Context

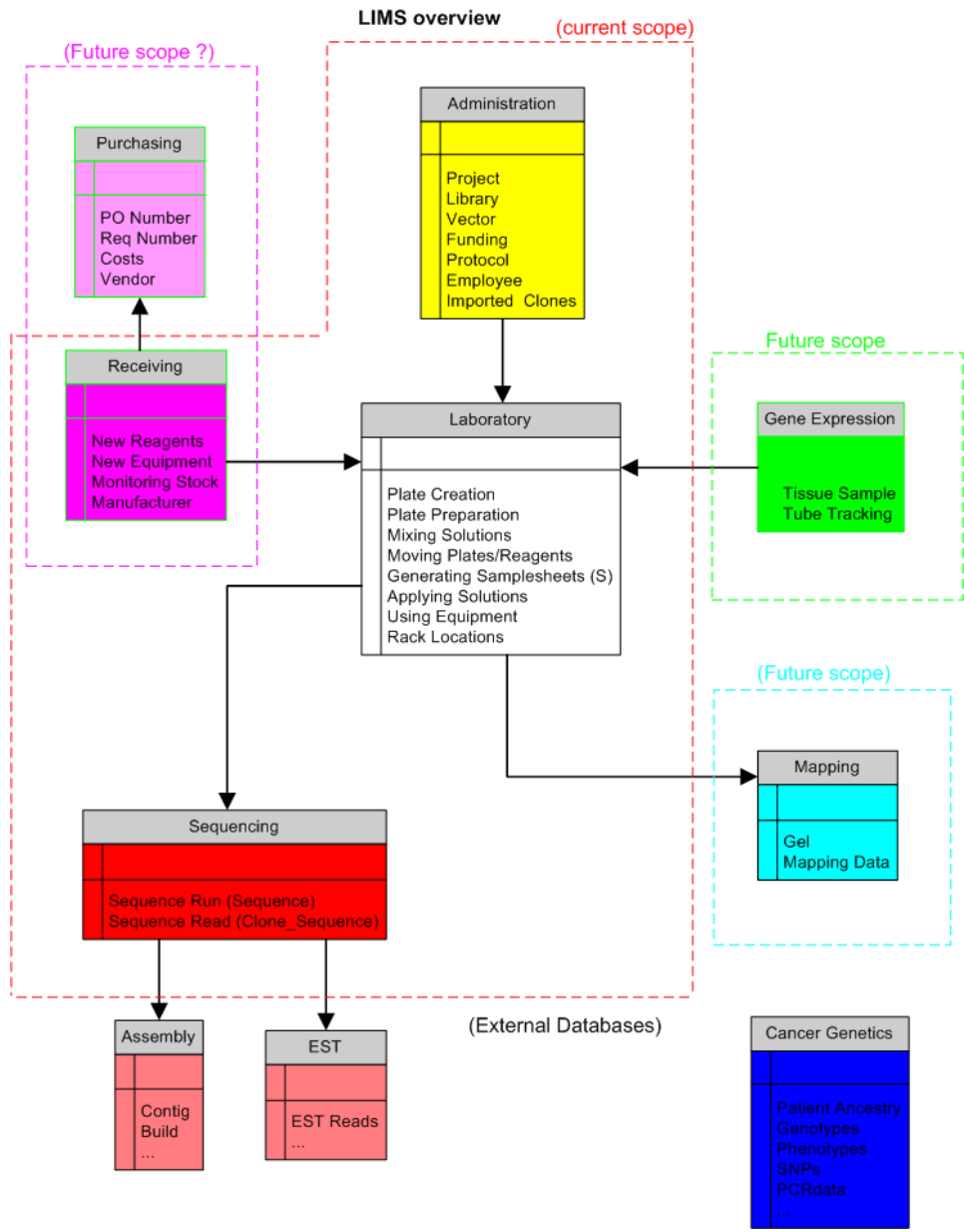
The context of LIMS system within a laboratory



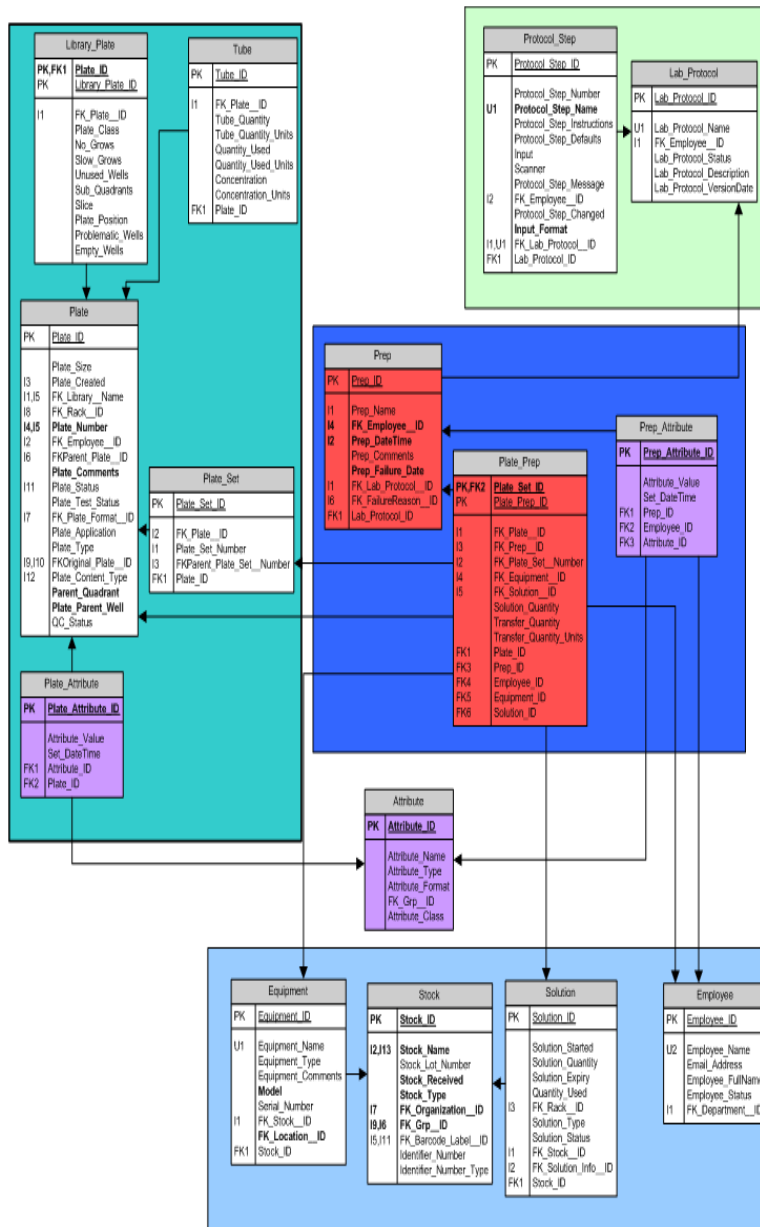
More detailed view of alDente within the LIMS context



Context diagram of alDente LIMS

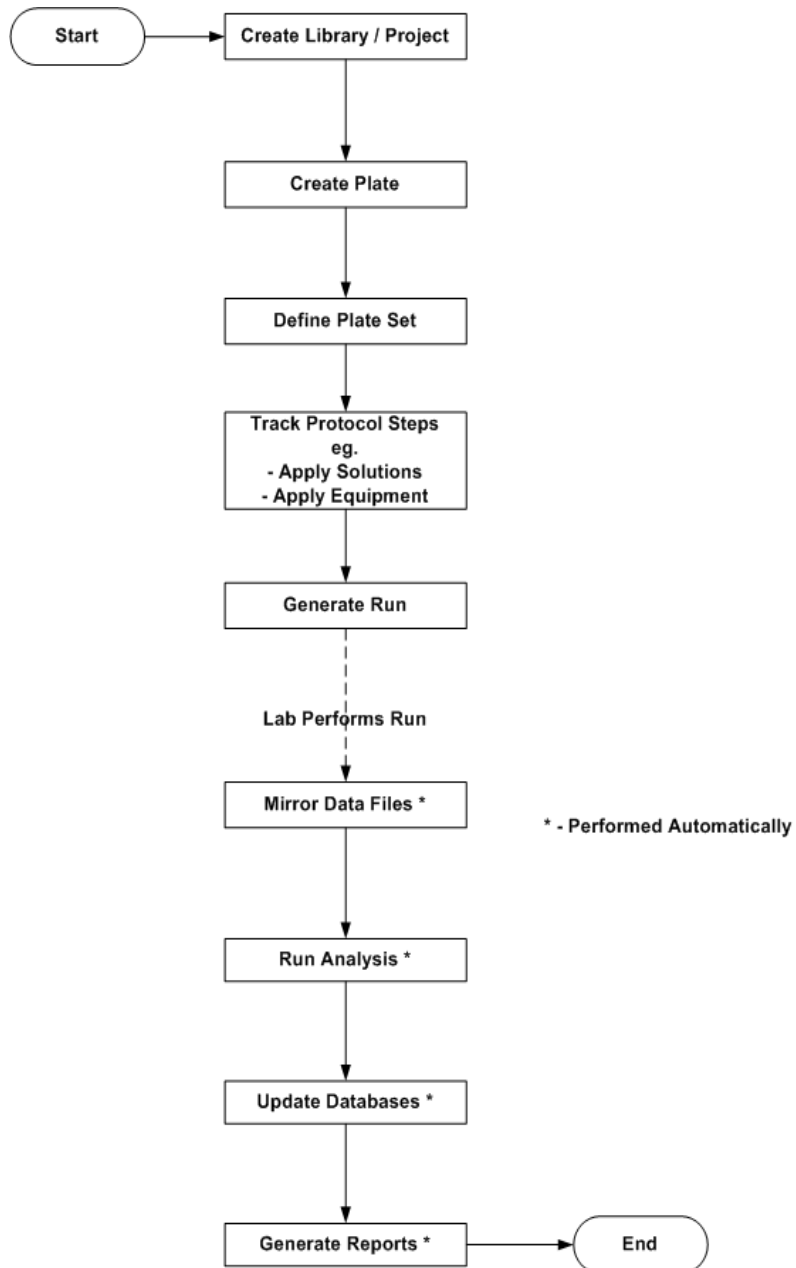


Context of laboratory function within alDente LIMS

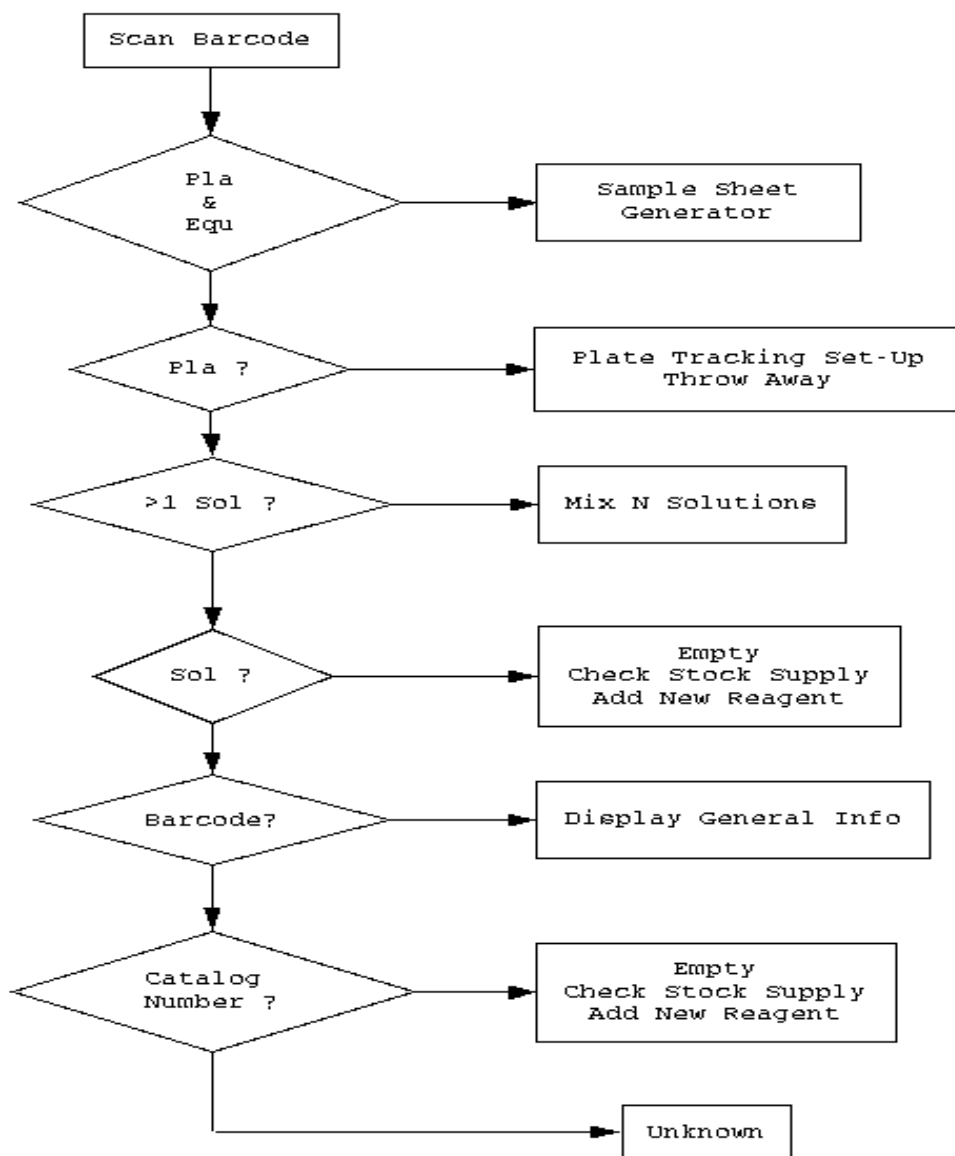


Flowcharts

Run flowchart

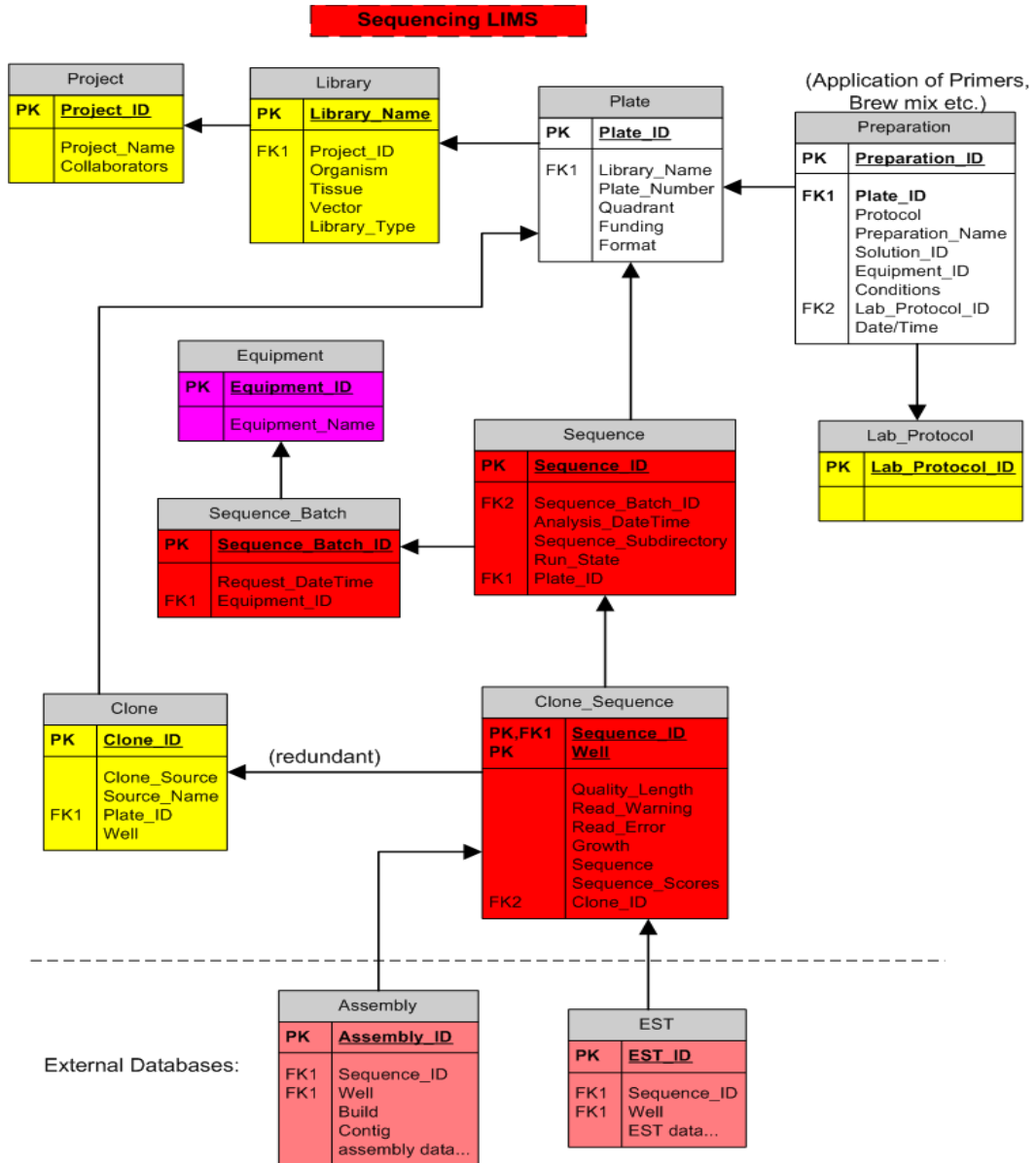


Scan flowchart



Features

Data tracking for the Sequencing Application



alDente LIMS has a number of data tracking processes such as plate tracking, location tracking, protocol tracking, receiving and purchasing.

The following sections explain some of them in more detail.

Plate Tracking

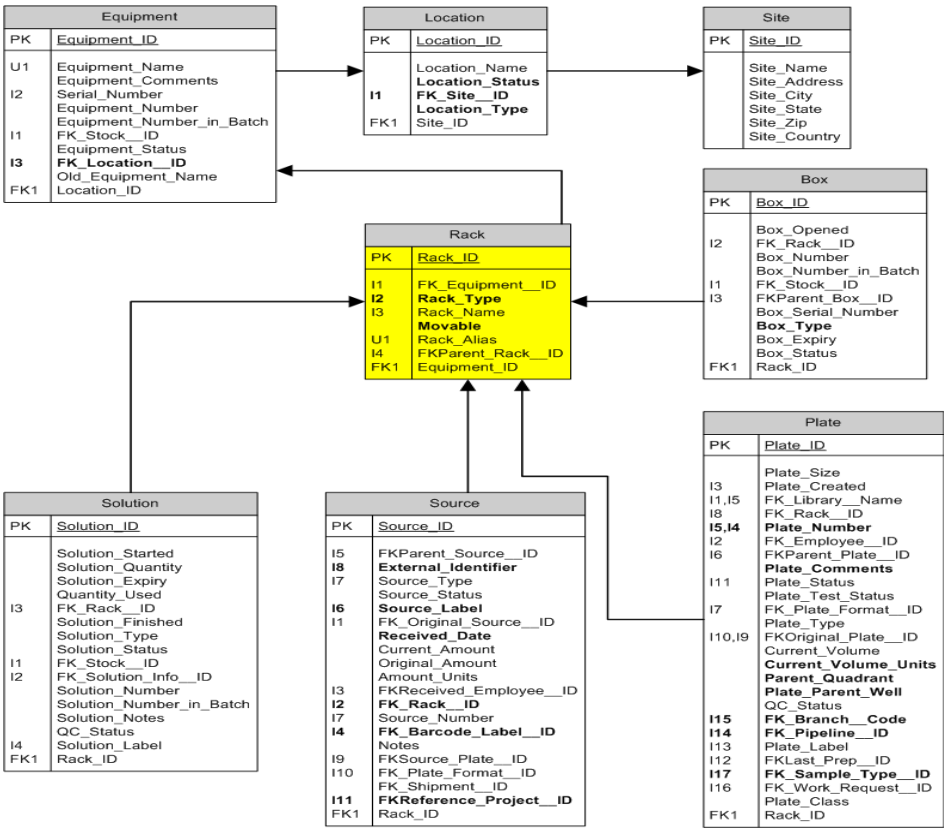
Plate tracking (including the tracking of all laboratory processes applied to samples within plates) allows records to be maintained which represent essentially a lab history of everything that has happened to a sample. This is particularly valuable to monitor the distribution of large numbers of tasks. It also proves very useful in optimizing laboratory procedure by allowing specific processes, reagents, or equipment to be correlated with data quality - something that can quickly identify troublesome aspects such as contaminated reagents, malfunctioning equipment, or ineffective processes. See the schema diagram below.

Refer to the diagram of context of laboratory function within alDente LIMS.

Location Tracking

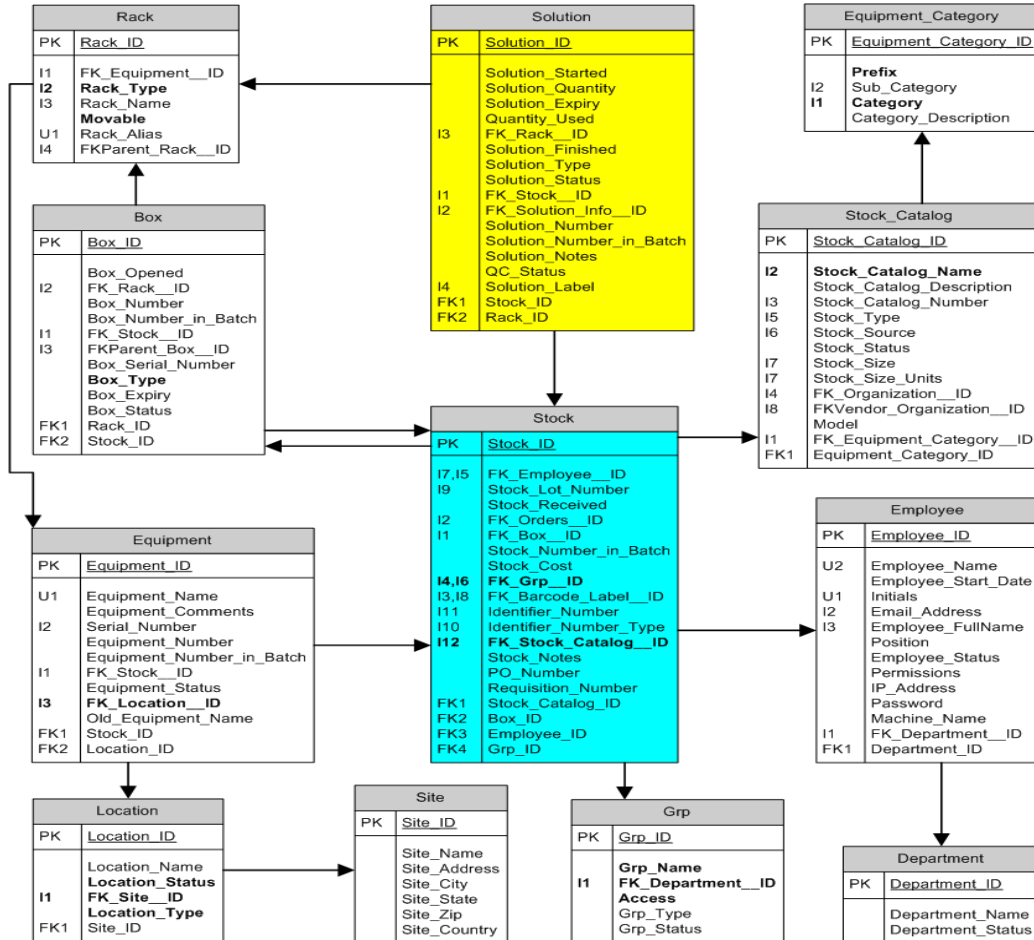
A location is referred to in the database as a 'Rack', and is bar-coded with the prefix 'Rac'. A rack has to be assigned to a single piece of equipment (usually a freezer), and can contain plates, sources, or stock objects (solutions, kits, or boxes). Racks themselves may also contain other racks that are of a type lower on the hierarchical chain.

The following schema diagram illustrates the object relationship in the context of location tracking.



Receiving and Purchasing

Schema diagram for receiving and purchasing.



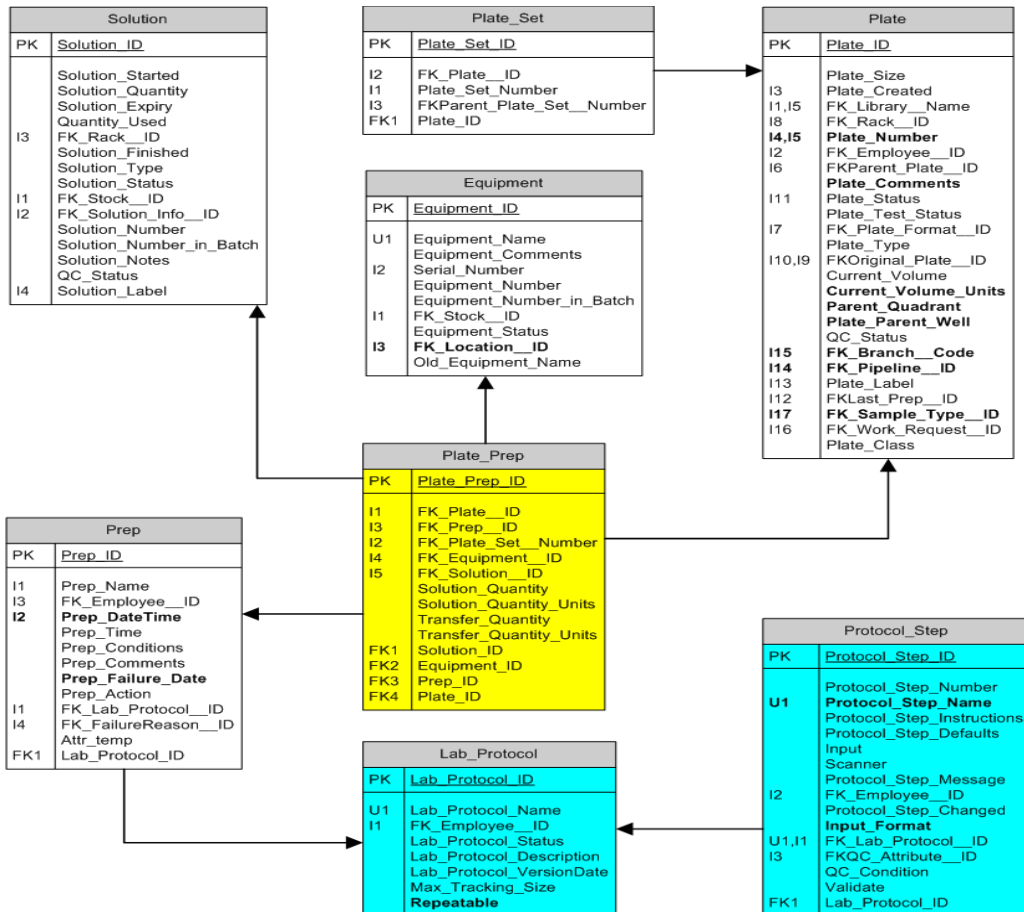
Protocol Tracking

A protocol is a series of pre-defined series of steps that the user follows during sample handling within the lab.

Before tracking can take place, a detailed protocol is written up and stored in the database which includes details for each step such as:

- The name of the step
- The Step number within the protocol
- Whether or not users should be prompted for the step.
- A brief message (to be displayed for each step)
- Detailed instructions that may be made available for each step.
- Input required (eg. Equipment, Solution, Comments etc)
- Default values (if applicable)
- Formatting restrictions (if applicable)

The input of this information is handled through the Protocol Administrator page. Steps of the protocol may be monitored and edited regularly to ensure that it is always up to date.



Plugins

alDente LIMS also offers a number of optional plug-ins in addition to the core features. They include:

Issue Tracking

Tracking issues is crucial for the maintenance of the LIMS in general, both to monitor possible bugs in the system (whether due to inherent code bugs, or due to data entry bugs). It also allows users an easy method of communication problems or suggestions to the on-site LIMS administrators or to request help.

alDente allows issue tracking either by interfacing with a JIRA issue tracking which may exist on-site, or by using its built in issue-tracker. The JIRA system is a highly configurable and powerful issue tracker that can be used company wide.

DNA Sequencing

alDente was originally designed for a DNA Sequencing lab and has a number of tools that are suited particularly well not only for lab tracking but for DNA Sequencing analysis and data monitoring including:

- Colour coded run maps which enable users to quickly and easily identify the general quality of a given run across the entire plate.
- Colour coded run maps which enable users to quickly and easily identify the general quality of a given run across the entire plate.
- Tools to quickly and easily generate fasta files for single runs or batches of runs.
- Tools to view alternative representations of run results including views that clearly identifies sections of each read that are identified as vector.
- Automated run analysis using phred, and storage of sequence scores associated with each called base pair.

- Built in checks for inserts containing: repeating sequence only, yeast or e-coli contamination, poor quality reads.

SAGE Library Construction

For labs in which SAGE libraries are constructed on-site, alDente allows extensive tracking of samples during the construction of the 'SAGE Library'. Downstream sample data may later be tracked all the way back to the original starting material.

DNA Fingerprinting and Sizing

Functionality specific to DNA fingerprinting is also supported within the alDente system, including automatic generation of thumbnails of TIFF images of gel runs. Advanced functionality is also available to perform special tasks such as picking out individual bands from gels and defining them as new samples.

Architecture and Technologies

The alDente LIMS has a client-server architecture that requires essentially three elements: web browser, Perl code, and MySQL database.

A more detailed list of technologies that the system uses is as follows:

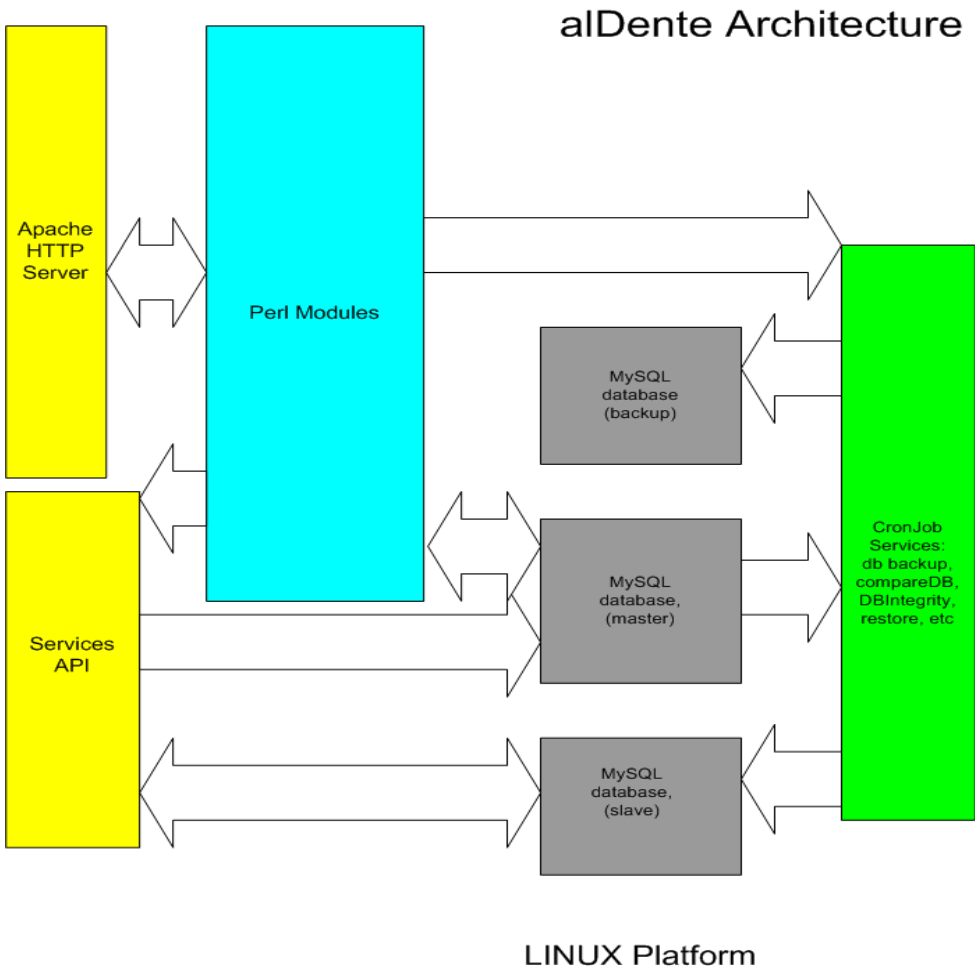
- HTML
- Javascript
- Linux
- Apache
- MySQL
- Perl code with CGI libraries

The system can be accessed through either a web browser or a services API. The web API supports both standard HTTP and secured HTTPS protocols.

Data is stored in a few different places including both the MySQL database, and in various locations on the local file system.

An architecture view of the alDente LIMS system is illustrated in the following diagram.

Architecture view of the alDente LIMS system



Users

A number of people stand to benefit including:

Lab users

This system can make their lives hell ...or a lot easier.

(though usually a subtle combination of both).

To ensure that the edge is given to the 'make their lives easier' camp, it is crucial that constant feedback is supplied to database administrator's, who in turn must appreciate the effect of the system's smooth functionality upon those constantly using the system. With a continuous cycle of feedback and a concerted effort on the developers part to address concerns, lab users stand to gain much more than the cost of having to use barcode scanners or to enter data onto the computer.

Lab administrators

Lab administrators, generally stand to gain much more, since they stand to benefit much more from the potential tools at their disposal such as data viewing pages, report pages, and validation settings which can prevent mistakes before they occur. Similarly, however, to maximize their ability to make use of the system, they should be in close communication with the database administrator to ensure that they both understand how to make best use of it, and to enable them to provide valuable feedback to make the system more effective.

Administrators

Administrators can benefit from the potential of the system to generate detailed cost reports or data summaries that may be used in broader reports. It may allow them to more clearly understand and monitor how projects are proceeding and pass on results directly to collaborators.

Once again, this may be made most effective by communicating with database administrators to ensure needs are met, and to learn how best to retrieve information desired.

Programmers

There are various aspects of the system which can also be utilized by programmers for use with other parallel database systems. The 'SDB' module is designed to be used generically with any 'SQL' database. While its use outside of alDente has currently been limited, there are valuable tools that may simplify the design of interfaces to other databases. Included are modules which simplify the generating of HTML tables, the generation of forms for adding records, and the navigation between related records via hyperlinks on foreign keys. Also included are the filters used to maintain data integrity during the updating, appending, or deleting of records in the database.



Appendix A Release 2.7

.....

Note: This Document may change slightly, and will be accompanied by snapshots providing an indication to real changes to the look of the system where applicable.

List of Primary Changes

(new functionality or large scale changes visible to the end user)

- Added shipping manifold for exporting plates or generating freezer content reports (with options to dump to an excel spreadsheet and/or include a full sample list)

Printable Page *(extracts only this table)*

Shipping Manifest

Date: 2009-07-06 11:03:20

Shipper: LabAdmin

To:
BC Generations Project
2775 Laurel St.,
Vancouver, BC
V5Z 1M9

From:
BC Generations Project
7.208 - 675 West 10th Ave,
Vancouver, BC
V5Z 1L3

Content Summary

Type: Human Blood Specimens

Subject Records: 22

First Subject: BC000110

Last Subject: BC000348

<u>Sample Type</u>	<u>Samples per Subject</u>	<u>Samples</u>	<u>Total Volume in mL</u>
Blood Plasma	8.18	180	720
Blood Serum	5.45	120	0.36
Red Blood Cells	2.73	60	240
Urine	3.00	66	264
White Blood Cells	2.73	60	240
Whole Blood	2.73	60	0.18
Totals (6 Records)	24.82	546.00	1464.54

- Added Queueing system for managing Illumina scheduling priorities [hotfixed]
- Automated validation of Primers based upon Vector Sequences (removing need for admins to do this, and enabling instant access to all 'valid' primers)
- Added distinct Department Tab for QC group [hotfixed]
- Added QC_Batch functionality to track batches of items for QC'ing (including report pages and history views) [hotfixed]
- Added detailed tracking of Shipments received from collaborators
- Added tracking of Internal Shipments including logging of manifests for both SRC and PLA records and separate shipping records for each object shipped
- Refactored Tissue, Histology information for Original Sources to enforce structured vocabulary and help ensure key information is tracked for all incoming samples.
- Set up BioSpecimen Core Department with responsibility to receive & enter imported sample information.
- Set up TCGA Department to enable easy access to project specific views for administrators
- Set up Prostate_Lab department and additional tracking for CLIPR data (as a new Run Type).
- Added minimum standards for user passwords
- Enhanced view module to enable more powerful generation of customized reports
- Added basic graphing functionality to query and views
- Added Patient tracking
- Added capability of tracking information specific to xenograft samples

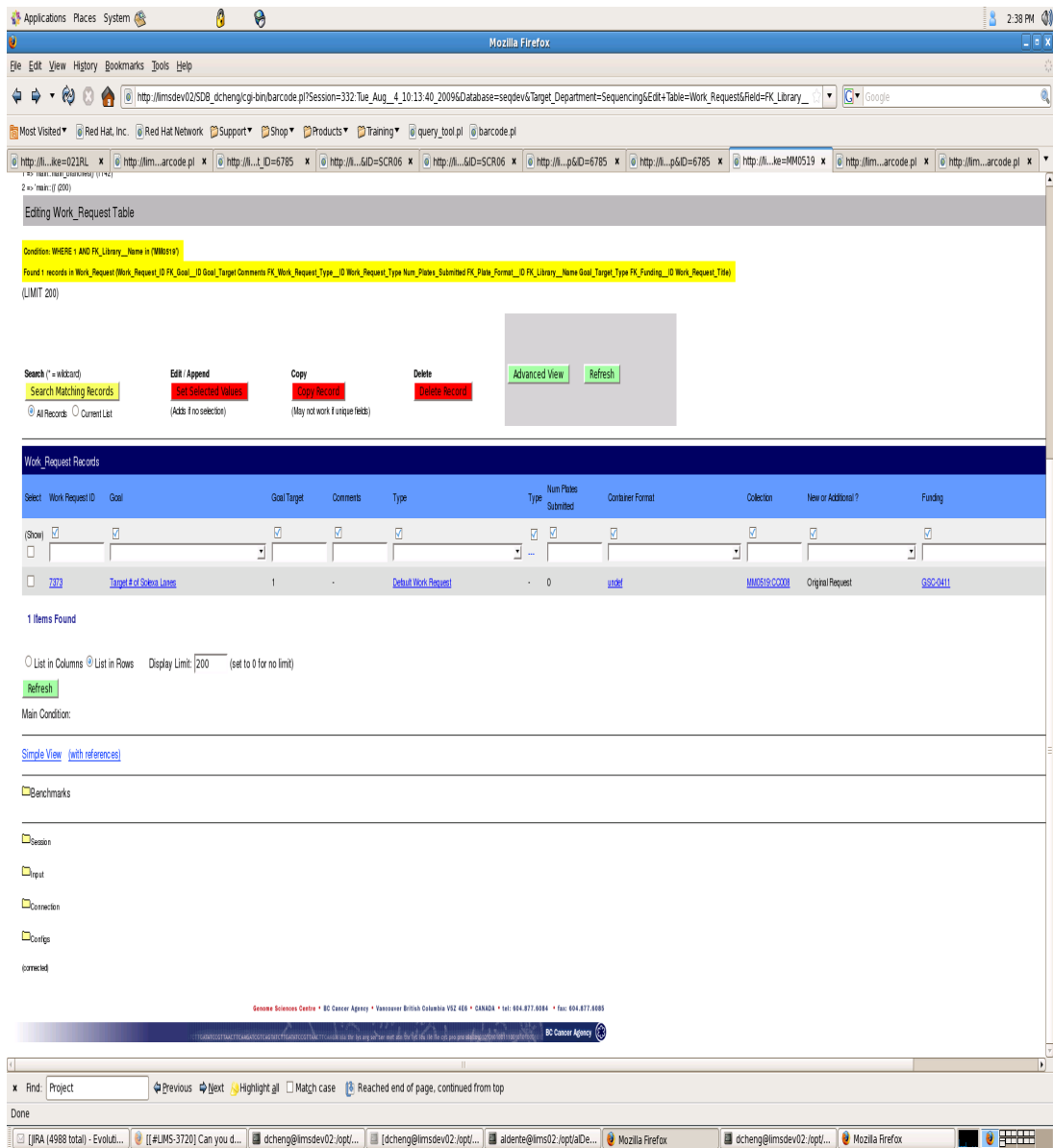
Minor Changes

(improvements to existing core functionality visible to the end user)

- Add ability to Transfer/Aliquot samples 'out' to a new container without shifting focus from current containers.

- Adjust Split function to prompt for split number for **each** container. (ie if splitting 8 tubes into 16, users specify **Split each container into: 2** rather than (previously) 'Split into: 16'). This is more intuitive and removes the chance of 'invalid' numbers being chosen. (hotfixed)
- Prompt enabling users to change the Pipeline during a transfer step within a protocol will only appear if multiple applicable Pipelines include the current Lab Protocol
- Enable movement of items into multiple boxes at one time
(<items_for_box_1><box_1><items_for_box_2><box_2> ... etc)
- Enable loading of slots in boxes in ascending or descending order for columns and/or rows.
- Enabled user to pick the type of label to print when re-printing source barcodes.
- Enable bulk sample redistribution across boxes (enabling users to scan N boxes and extract all samples of a particular type into one or more target boxes)
- Smarter sample relocation into slotted boxes. Confirmation step auto-fills target slots (by row or column; asc or desc order) , and providing feedback wrt first slot used, last slot used & occupied slots that were skipped.

- When only editing a single record that went through the multi-page edit form, it will now go to the single page edit form by default.
Before:



After:

The screenshot shows a Mozilla Firefox browser window with the address bar displaying a URL: http://lmsdev02SD8_dchenglcp-binbarcode.pl?Session=332_Tue_Aug_4_10_13_40_2009&Database=seqdev&Target_Department=Sequencing&Edit+Table=Work_Request&Field=FK_Library_.... The browser's address bar also shows a search bar with the text "Google".

The main content area displays a form titled "Edit Work Request Form". The form includes the following fields and controls:

- Goal**: A dropdown menu with "Target # of So" selected.
- Goal Target**: A text input field with the value "1".
- Comments**: A large text area for comments.
- Type**: A dropdown menu with "Default Work S" selected. There are radio buttons for "Search" and "Filter".
- Num Plates Submitted**: A text input field with the value "0".
- Container Format**: A dropdown menu.
- Collection**: A dropdown menu with "MM0519 CC008" selected, with "(Auto Completed)" in parentheses.
- New or Additional?**: A dropdown menu with "Original Request" selected.
- Finding**: A dropdown menu with "GSC-0411" selected. There are radio buttons for "Search" and "Filter".
- Work Request Title**: A text input field.

Below the form, there is a link "Referenced By: Material Transfer Plate".

At the bottom of the form, there are three buttons: "New Search" (green), "Update Work Request" (red), and "Save as New Work Request Record" (red).

Below the buttons, there are several sections with checkboxes and labels:

- ☐ Benchmarks
- ☐ Deviation
- ☐ Input
- ☐ Connection
- ☐ Configs

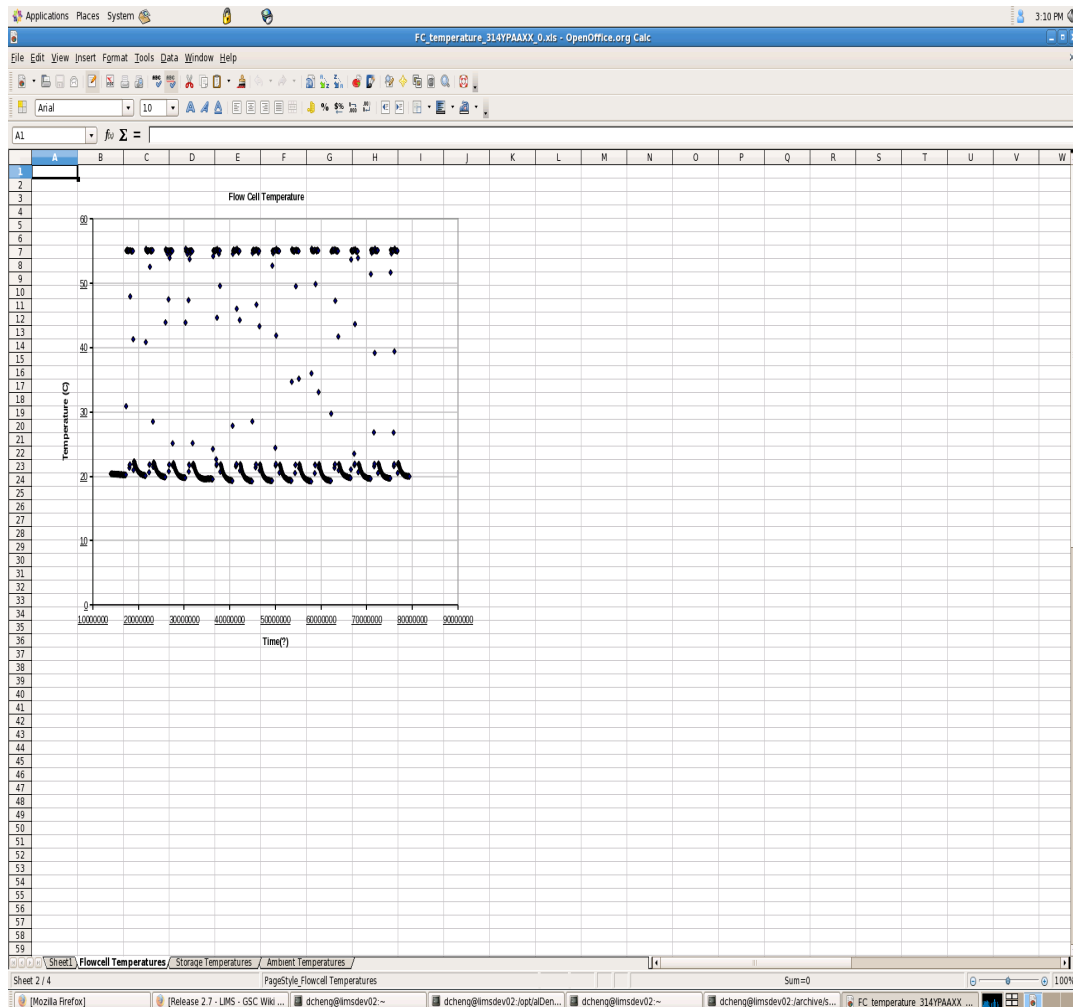
The bottom of the browser window shows a search bar with the text "Find: Project" and a "Done" button. There are also links for "Previous", "Next", "Highlight all", "Match case", and "Reached end of page, continued from top".

- More transparent ancestry information supplied on main pages for Library, Original_Source, Source records

Group Specific Improvements

(Changes applicable only to specific groups)

- Added plugin for SOLID run analysis along with views to monitor SOLID data
- Added plugin for LS_454 data (to enable tracking of externally generated data of this format)
- Automated the process to generate flowcell temperature plot and quality graph.





LIMS Background Improvements

(Changes that may be invisible to users such as database schema changes, performance upgrades, refactoring etc)

- Refactored Prep module to utilize CGI_Application model (added Prep_App, Prep_Views modules)
- Added ability to submit Illumina/SOLID/454 data to Short Read Archive (SRA) and Epigenomics Data Analysis and Coordination Center (EDACC)
- Added ability to submit Whole Genome Assembly (WGA) sequencing data to Trace Archive

Deferred Requests

(Improvement requests that we are aware of, but which are being deferred due to relatively lower priority)

Future Development

(larger scale improvements which would require implementation only at release time, but which may not be available in the near future)

Hotfix Patches since previous release

(list of patches that have been implemented as upgrades from the prior release. These may or may not have been applied prior to the new release)

Hotfixed:

- Installation.pat
Upgrades to the installation process.
- Queue_Core.pat
Set up a queueing system for prioritizing runs

