SLIMS—a user-friendly sample operations and inventory management system for genotyping labs

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ABSTRACT

Summary: We present the Sample-based Laboratory Information Management System (SLIMS), a powerful and user-friendly open source web application that provides all members of a laboratory with an interface to view, edit and create sample information. SLIMS aims to simplify common laboratory tasks with tools such as a user-friendly shopping cart for subjects, samples and containers that easily generates reports, shareable lists and plate designs for genotyping. Further key features include customizable data views, database change-logging and dynamically filled pre-formatted reports. Along with being feature-rich, SLIMS' power comes from being able to handle longitudinal data from multiple time-points and biological sources. This type of data is increasingly common from studies searching for susceptibility genes for common complex diseases that collect thousands of samples generating millions of genotypes and overwhelming amounts of data. LIMSs provide an efficient way to deal with this data while increasing accessibility and reducing laboratory errors; however, professional LIMS are often too costly to be practical. SLIMS gives labs a feasible alternative that is easily accessible, user-centrically designed and feature-rich. To facilitate system customization, and utilization for other groups, manuals have been written for users and developers.

Availability: Documentation, source code and manuals are available at http://genapha.icapture.ubc.ca/SLIMS/index.jsp. SLIMS was developed using Java 1.6.0, JSPs, Hibernate 3.3.1.GA, DB2 and mySQL, Apache Tomcat 6.0.18, NetBeans IDE 6.5, Jasper Reports 3.5.1 and JasperSoft's iReport 3.5.1.

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1 INTRODUCTION

Genetic studies of complex diseases that interrogate the human genome are known as genome-wide association (GWA) studies. They require both high-throughput genotyping platforms and large samples sizes—with thousands of subjects from multiple sources and time points—to clearly define the contributions of common alleles associated with common complex diseases. To obtain the large sample sizes needed, GWA studies have led to international consortia formed from smaller studies, with differences in study designs and quality control procedures. If not dealt with appropriately, these situations can lead to decreased data accessibility, increased laboratory errors and an overall reduction in operational efficiency. Laboratory information management systems (LIMSs) provide solutions for these situations; however, the perception that learning to use new software will be time-consuming and difficult can be a significant barrier to the adoption of a LIMS (Anderson *et al.*, 2007). This situation is worsened by the high turnover rate of research staff—resulting in recurrent training costs—and the lack of user-centric designs in open source LIMS—resulting in steep learning curves. In searching for a solution to the challenges we faced managing our biological samples, we failed to find any open-source systems that would provide adequate functionality for our needs. We developed Sample-based LIMS (SLIMS) to make available a feature-rich system capable of handling longitudinal data and to increase the presence of user-centric design in LIMSs. SLIMS is based on a previously published LIMS: PASSIM (Viksna *et al.*, 2007).

2 FUNCTIONALITY

SLIMS manages information for subjects, the biological samples they have provided and the containers (plates or boxes of tubes) used to store and ship them. Each level of abstraction provides the user with more power; they can choose to deal with wells individually, all the wells of a plate, all the samples from one subject, all the plates containing a sample from one subject, etc. At each level, users can view, edit and create new entries. Data integrity is protected by validating input and controlling which users' accounts have privileges to edit and create different fields. Accounts also specify their users' roles in the lab. Because statisticians and database administrators (so-called 'dry lab' staff) may be interested in very different information than laboratory (or 'wet lab') staff, SLIMS has tailored default view schemes that are fully customizable. This cuts down on the confusion caused by information overload. A user's preferred view scheme is remembered every time they log in, so that a user can make the system their own and maximize its efficiency.

SLIMS features several new tools that expedite experiment operations while ensuring complete record keeping and facilitating intra-lab communications. The most broadly successful of these is a 'shopping cart' that allows users to create, store and share lists of subjects, samples and containers. Lists can be created by anyone in the lab and populated by selecting elements singly, adding the results of a search or uploading a file. Being able to share these lists directly through SLIMS can be useful in labs spread over

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several rooms, buildings or disciplines because it imposes structured veins of communication with set vocabularies. It also reduces the use of personal spreadsheets, which can become out of sync or indecipherable if the creator leaves.

Lists allow wet lab staff to perform batch operations such as volume updates or plate creations. When a new plate is designed in SLIMS, record keeping is automatically linked with the production of documents that aid in plate creation (a map of a plate's samples and a 'recipe' of sources detailing how much of which samples from where are to be used). Lists of plates can be used to design plates, serving cases such as the mechanical combination of four 96-well plates into one 384-well plate for TaqMan genotyping (Heid *et al.*, 1996). SLIMS integrates record-keeping and lab operations for this process by giving the user a tool to design their new 384-well plate, which in one stroke makes a record in the database and creates an import file necessary for machine operation. New plates can also be created without the use of lists, simply from pre-existing plates. A plate cloning tool allows the user to make a new plate and sample records, adjust the volumes of the source well records and print off documents for plate creation, all in one step.

To facilitate preparation for genotyping, SLIMS features a customizable, criteria-based sample selector and plate layout design tool. Given a list of subjects in a study, the sample selector allows a user to define a hierarchical tree of criteria that SLIMS uses to retrieve the most appropriate sample for each subject. Once the initial selection process has been performed, the user can then manually curate the results: if they reject a particular sample, the 'next-best' will be presented and so on. When the final set of samples is ready, it is stored in a 'shopping cart' list. This list can then be used with the plating tool, which designs plate layouts, makes plating documents for the wet lab and updates records of the new plate and the source samples.

All of the data updates that occur while using these tools—or any other SLIMS function—are logged in the supporting database. This automatic, detailed and reversible record keeping encourages lab members to use the system even if they are as yet unfamiliar with it by providing them with a safety net. Higher level data tracking is made possible by the availability of dynamically filled, preformatted reports created using Jasper Reports technology (JasperSoft, 2009). Further, any search result or 'shopping cart' list can be exported to a delimited text file.

Providing users with a powerful, feature-rich system—such as SLIMS—empowers them to increase their efficiency and productivity. However, if a system appears complex and feels overwhelming it can have the exact opposite effect. To ensure a high level of user-acceptance, all interfaces were designed with formal user testing and a detailed user manual describing all views, tools and features was produced.

3 DISCUSSION

The consequences of incomplete user acceptance of a LIMS are very serious. Even the best professional systems lose value—and can even become detrimental—if they fall out of date because of inconsistent use. In a busy laboratory, instructing staff to use a new system can only have so much effect; successfully achieving consistent usage requires incentives in addition to instruction. To this end, SLIMS aims to combine record-keeping with features that save time and simplify daily

Table 1. Summary of SLIMS's features, this table summarizes the general features adapted from PASSIM as well as those newly developed now being presented

General features
Manages subjects, samples and containers
Data browsing and simple or complex searching
Manual creation and editing of entries
Input validation and user-based editing privileges
New features
Widely applicable for sample-based laboratories
Shopping cart for subjects, samples and plates
Database change-logging
Dynamic, pre-formatted reports
Tailored and fully customizable views
Plate cloning tool
Dynamic 'to do' lists for lab procedures
Sample upload tool for wet lab
Manuals for users and developers
Targeted for genotyping laboratories
Criteria-based sample selector and plate creation tool
Plate combiner for 384-well plate TaqMan genotyping

laboratory tasks. We have taken a three-pronged approach to achieve this goal. First, facilitation of bench-top procedures is integrated with record keeping in SLIMS by the automatic production of documents required for procedure completion. Second, we have ensured that the user's experience is as easy and efficient as possible by formally involving a broad spectrum of users in the development process from requirements analysis to interface design and testing. This approach allowed us to map different user-groups' mental models of a LIMS system and incorporate them in our design, making the system more intuitive for users. Though focusing development on users instead of programmers reduces a system's learning curve, it cannot be erased. Our third prong focused on easing and accelerating the learning process with user manuals and instructional text throughout the system. Though SLIMS' applicable scope may be limited by a setup targeting sample-based laboratories and tools targeting genotyping workflows, the approaches to LIMS development described above incorporate widely applicable, well-established techniques (Debbie Stone *et al.*, 2005) that are lacking in existing open-source LIMS. Documentation, source code, and manuals are available at http://genapha.icapture.ubc.ca/SLIMS/index.jsp.

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