

# LabControl: a LIMS software to manage microbial data

Mariana Teixeira Dornelles Parise<sup>1</sup>, Joarley Ferreira dos Santos<sup>2</sup>, Aristóteles Góes-Neto<sup>1</sup>, Daniela Arruda Costa<sup>1</sup>, Anne Cybele Pinto<sup>1</sup>, Gabriel da Rocha Fernandes<sup>3</sup>,  
Vasco Azevedo<sup>1</sup>

*Federal University of Minas Gerais<sup>1</sup>, Pitágoras College<sup>2</sup>, Research Center Rene Rachou<sup>3</sup>*

Due to NGS sequencing techniques, the amount of genomic data has been increasing exponentially and this rapid growth has created management issues. Thus, Laboratory Information Management Systems (LIMS) have been used to manage this data and other types of laboratory data, such as samples and genomic data. Biological collections are important sources of raw material for genomic studies as well as essential ways to preserve the samples for future studies. In addition to these softwares, data patterns concerning genomic and microbiological fields have been developed and implemented in some LIMS or other kinds of laboratory softwares. Those patterns aim to standardize the information held in the softwares, facilitating information comparison and exchange between different sources or laboratories. However, neither the management utilizing softwares nor the usage of data patterns are common in small academic laboratories, which normally cannot afford for a commercial LIMS or develop their own LIMS. This lack of management support can cause inefficiency in the laboratory environment due to unorganized and unstandardized data in spreadsheets, data loss and difficult knowledge extraction and comparison. Considering this situation, LabControl has been developed as a free LIMS software based on World Federation for Culture Collections and Genomic Standards Consortium recommendations that aims to assist microbial collection management and organization by normalizing and integrating data from different organisms as well as to manage datasets and meta-data generated by *in vitro*, *in vivo* and *in silico* techniques applied to these strains. In addition to these features, the software requirements were based on interviews and investigation of researchers' routine, which generates a more reliable data model providing better assistance from the software to the researchers' real needs. The technologies used in the development are Java programming language in NetBeans IDE integrated with Spring and Hibernate frameworks, using the PostgreSQL database. LabControl software allows users to a faster strain information management through an easy-to-use system, which reduces the impact of the migration from spreadsheets to a web system. This migration process may promote a significant gain in researchers' daily productivity through organized, updated and persistent data of all studied strains and techniques applied to them.