

## **iLAP: a novel work flow oriented approach for microscopy data management and protocol development**

**G. Stocker<sup>1</sup>, M. Fischer<sup>1</sup>, D. Rieder<sup>1</sup>, G. Bindea<sup>1</sup>, J.G. McNally<sup>2</sup>, Z. Trajanoski<sup>1</sup>**

<sup>1</sup> **Institute for Genomics and Bioinformatics, Graz University of Technology,  
Petersgasse 45/V, 8010 Graz, Austria**

<sup>2</sup> **NCI (LRBGE), National Institute of Health, Bethesda, USA**

**E-mail: gernot.stocker@tugraz.at, zlatko.trajanoski@tugraz.at**

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Both quantitative and high-throughput microscopy confront scientists with the daunting challenge of storing heterogeneous data in a structured and organized way. Among the available data management solutions there is no intuitively usable system which covers the complete work flow of microscopy experiments. Therefore we have developed the web application iLAP (Laboratory data management, Analysis and Protocol development) which combines experimental protocol development, wizard-based data acquisition and high-throughput data analysis into one single, integrated system.

A unique feature of iLAP is that it supports the experimental design phase. The working protocols that scientists develop for wet lab experiments can be stored and modified within iLAP. Eventually, these protocols lead to the acquisition of image data. iLAP then provides a data acquisition wizard to assist the scientist in associating the acquired image data with steps in the protocol. Standardization initiatives, such as MISFISHIE[1] for DNA fluorescence in situ hybridization, can be supported by enforcing the input of required parameters during this data acquisition. Further processing and analysis of the raw image data can be performed either with analysis modules developed specifically within iLAP or with external third party programs. Interesting visual observations can be documented as notes at any place.

We have realized iLAP as a standard three tier business application using state-of-the-art JEE (Java Platform, Enterprise Edition 5) software technologies. Due to this flexible software architecture we were able to develop an intuitive web interface as well as a generic SOAP (Simple Object Access Protocol)- based programming interface. This platform independent programming interface allows external image processing applications like ImageJ[2] to access the files stored in iLAP. Computationally intensive tasks like three-dimensional deconvolution of image stacks[3] are transparently distributed on high-performance computing infrastructure, and results are stored within the underlying relational database management system. These results are associated automatically with the original experiment data. To facilitate ease of use, this complexity of data management and IT infrastructure is completely hidden from the user.

iLAP is an open source project which is freely available for the microscopy community. It has been tested extensively in our in-house microscopy facility and continuous user feedback has led to improvements in functionality, usability and responsiveness. A distinctive virtue of iLAP is that it inherently leads to structured recording of experiments, conserving the complete experimental context of data records throughout the history of the research project.

[1] E.W. Deutsch et al., "Development of the Minimum Information Specification for In Situ Hybridization and Immunohistochemistry Experiments (MISFISHIE)", *OMICS*, Vol. 10, 205-208 (2006)

[2] M.D. Abramoff et al., "Image Processing with ImageJ", *Biophotonics International*, Vol 11 Issue 7, 36-42 (2004)

[3] J.G. McNally et al., "Three-dimensional imaging by deconvolution microscopy", *Methods*, Vol 19, 373-385 (1999)