# Abstract

In the postgenomic era, high-throughput screening methods have identified a large number of genes which still lack functional characterization. Fluorescence microscopy can be used to localize labeled proteins from those genes in determining their functional role in cellular processes. In order to perform a systematic analysis of the generated microscopy images, structured storage of the data and organized documentation of its experiments are inevitable.

To address this problem a platform independent computational environment for handling microscopy data, named Scientific MIcroscopy Laboratory Environment (SMILE), was developed. The project oriented workflow of a typical experiment guides the design of the software for data storage, data retrieval and consistent chronological documentation. This approach inherently leads to structured recording of the experiment, conserving the complete experimental context of data records at any time. State-of-the-art software technology was used to implement a multi-tiered J2EE application offering an intuitive Web-based user interface. The SMILE application back-end can be accessed through a generic programming interface and is open for integration of external imaging tools, such as ImageJ. Computationally intensive tasks for server-side image processing and analysis are transparently delegated to an adequate high performance computing infrastructure, and results are stored within the underlying relational database management system.

The SMILE computational environment offers researchers an integrative software platform for scientific collaboration, while hiding the necessary complexity of data management and IT infrastructure. Because of its modular and flexible architecture, SMILE is ready to face the future challenges of microscopy data management.

**Keywords:** microscopy, experiment workflow, SMILE database, J2EE, high performance computing