

# Bio-Formats in C++ applications

Aaron Ponti, Mario Emmenlauer

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# Motivation

## XuvTools



**University of Freiburg – Institute for Computer Science**  
Chair of Pattern Recognition and Image Processing  
<http://lmb.informatik.uni-freiburg.de>

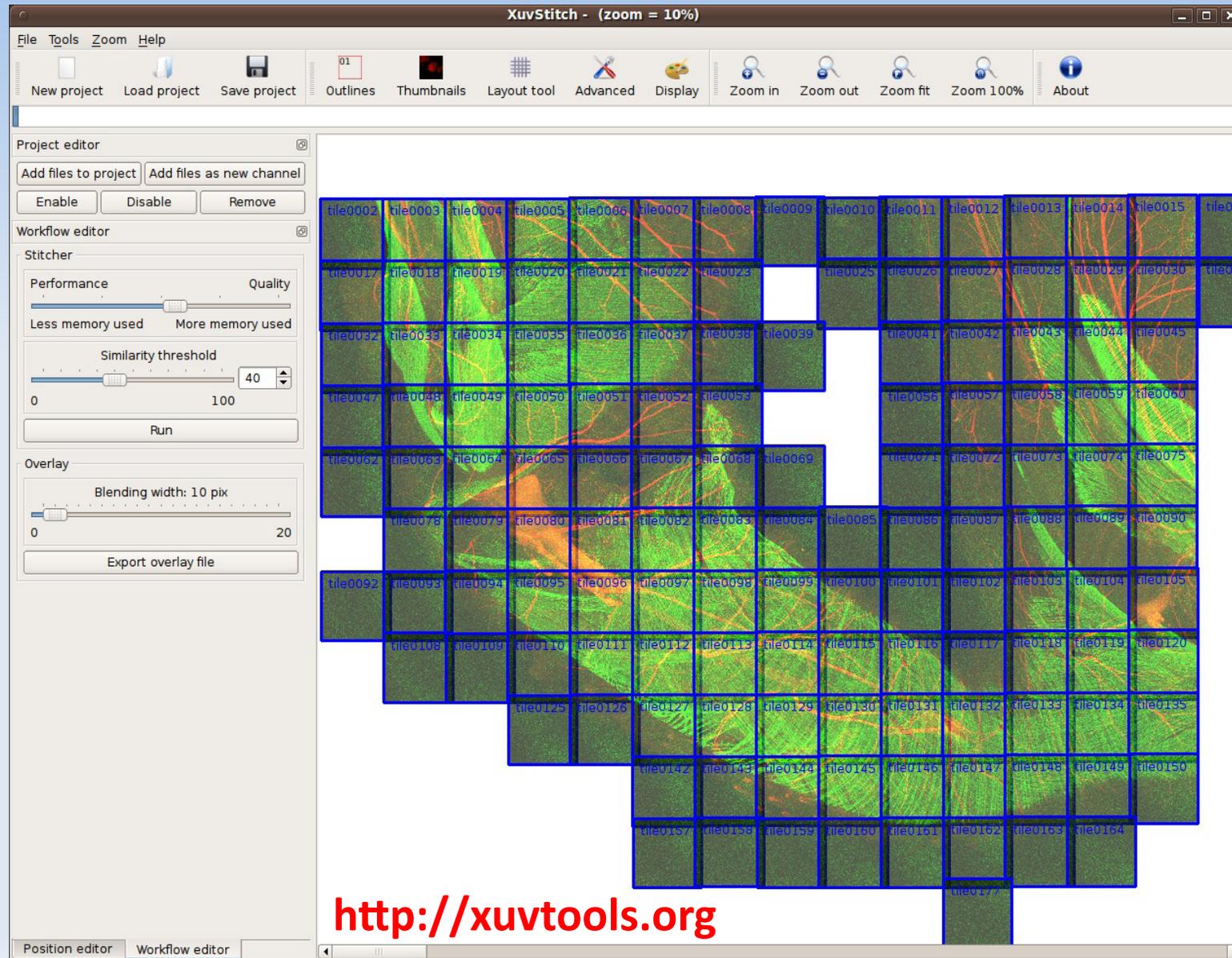


**Friedrich Miescher Institute for Biomedical Research**  
Part of the Novartis Research Foundation  
<http://www.fmi.ch>



**Center for Biological Systems Analysis**  
Developmental Biology  
<http://www.zbsa.uni-freiburg.de>

# Motivation



<http://xuvtools.org>

# Bio-Formats C++ bindings

- ❏ The well-known and long established **LOCI Bio-Formats Java library** supports reading of a long list of file formats. It is unmatched amongst available file reader libraries, and is free and open source software.
- ❏ The goal of this project is to make the LOCI Java library available to C++ software, via a Java-C++-Interface.
- ❏ The resulting C++ library, named “**libBlitzBioFormats**” will integrate in the XuvTools stitching toolkit.
- ❏ The project is founded by the Swiss Initiative in Systems Biology (<http://www.systemsx.ch>), and in particular SyBIT (the Systems Biology IT).
- ❏ Pixel data is read into Blitz++ arrays.

# Bio-Formats C++ bindings

```
#include <BlitzBioFormats.hh>

int main(int argc, char *argv[])
{
    try
    {
        // Create the reader
        BlitzBioFormats* blitzBioReader = new BlitzBioFormats(".", 512);

        // Open the image file
        blitzBioReader->setId("some.image.file");

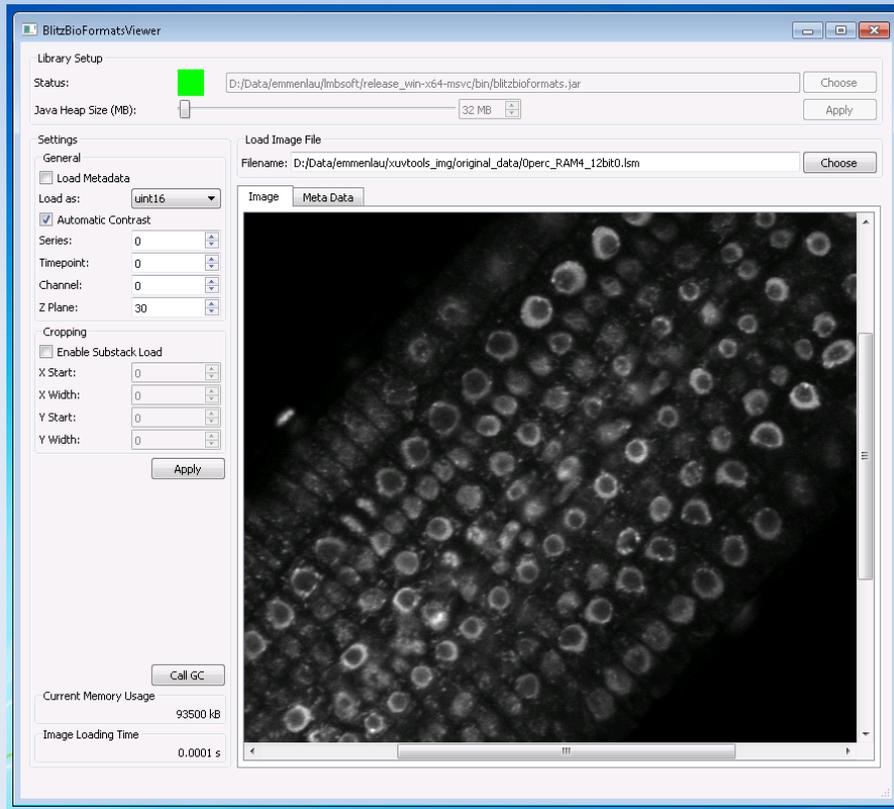
        // Go to the last series
        blitzBioReader->setSeries(blitzBioReader->getSeriesCount()-1);

        // Check pixel type
        if (blitzBioReader->getPixelType() == BlitzBioFormats::PixelType::Int8)
        {
            // Allocate a blitz array
            blitz::Array<char,3> image;

            // Read image data of the top z-level into array
            blitzBioReader->readArray(image, blitzBioReader->getSizeZ()-1);
        }

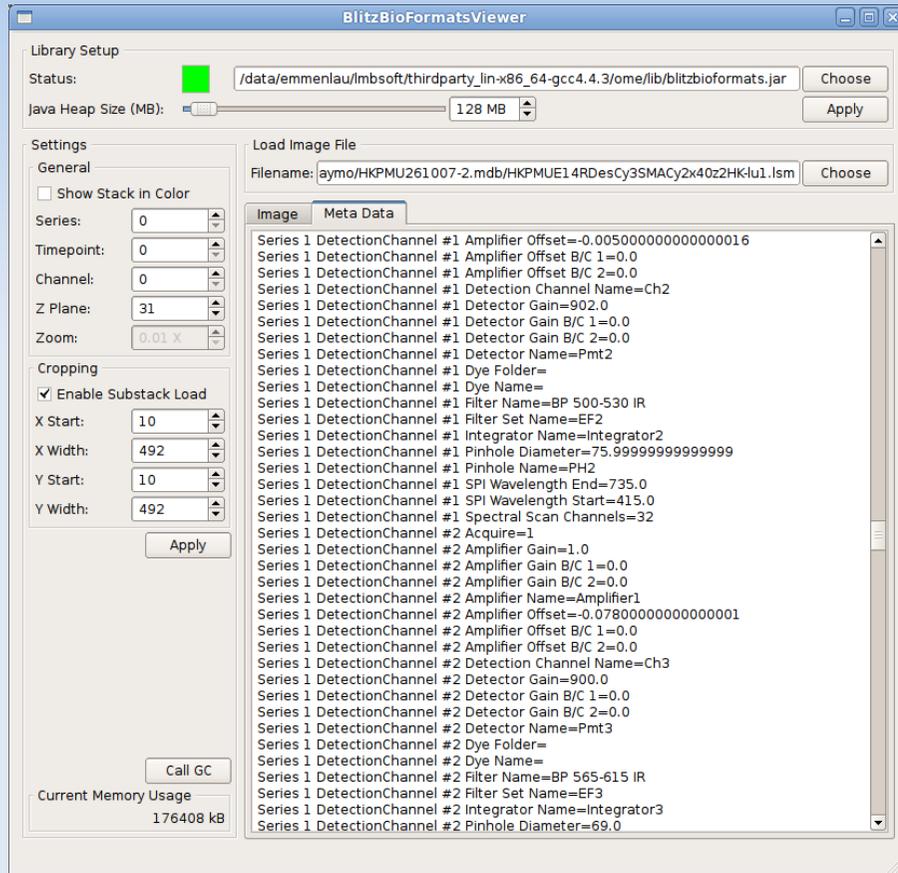
        // close (all) image files and free memory
        bbReader->close();
    }
    catch (BlitzBioFormatsException& bbfe)
    {
        std::cout << bbfe.what() << std::endl;
    }
}
```

# Image Viewer



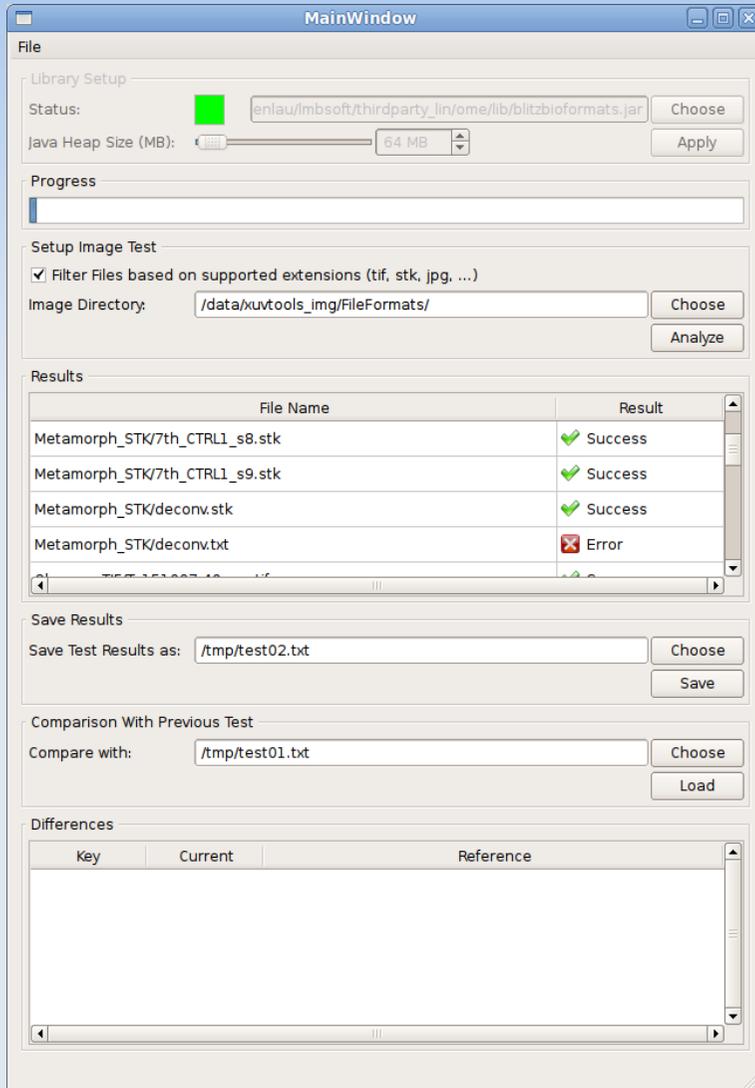
- ❑ Uses libBlitzBioformats
- ❑ GUI uses Nokia Qt
- ❑ Allows for manual setting of many parameters of the ImageReader class
- ❑ Allows for manual setting of classpath and JVM Heap
- ❑ Loads and displays 2D single channel images

# Metadata Viewer



- Part of the Image Viewer
- Displays ungrouped metadata of files
- Useful to inspect availability of metadata, i.e. stage coordinates
- A new "Properties" tab (not shown) groups the most relevant metadata (for visualization and, in particular, stitching)

# Automatic Test Suite



- Following Bio-Formats version updates, we can perform fully automatic testing
- Batch loading and inspection of all image files in a directory tree (recursive)
- Batch comparison against earlier test runs

# Specification

- ❏ The libBlitzBioFormats library provides a plain C/C++ interface, with no Java/Jace/LOCI header inclusion:

```
#include <BlitzBioFormats.hh>
```

- ❏ Compiles on Linux gcc (4.2-4.4), MS Visual Studio, Apple Xcode
- ❏ All data is copied bitwise from/to Java, i.e. no shared data structures
- ❏ Uses Bio-Formats **SVN r5847** (due to compilation problems with current head)
- ❏ An issue in Jace was patched to avoid a severe crash in JVM creation on Windows (missing destructor)
- ❏ Available at:

<http://www.xuvtools.org/doku.php?id=devel:libblitzbioformats>