

**Automation of Microscopy Image Analysis  
via Kepler Scientific Workflows and ImageJ**

Harriet Hu

Pacific Rim Undergraduate Experiences Program, 2012

University of California, San Diego || Host Institution: Monash University

Mentors: Dr. David Abramson (Monash) and Dr. Ilkay Altintas (UCSD)

**Abstract**

The advent of modern biological microscopy has led to the integration of visualization software with computational tools in order to analyze microscopy images. Through the use of Kepler Scientific Workflow System, a combined workflow graphical user interface and a background execution engine that allows non-computer scientists more ease in analyzing scientific data, image processing can be streamlined for more routine analysis through the construction of microscopy workflows. The primary goal in this project is to incorporate ImageJ scripts into Kepler Scientific Workflows v2.3 in order to automate the image analysis of microscopy images using workflows that can be variably changed per experiment.

**Background**

Image analysis of microscopy images often involves routine tasks per experiment that can be automated using workflows for increased efficiency. This project is conducted in collaboration with Dr. Mary Vail of the Department of Biochemistry and Molecular Biology at Monash

University, who provided sets of microscopy images that can be used for analysis experimentation and testing.

Kepler workflows can be designed to acquire and process microscopy images routinely, beginning by scanning a given microscope image up until the final analysis of composite images. At Monash University, members of the Monash eScience and Grid Engineering Laboratory (MeSsAGE lab) are using Nimrod/K, a workflow system built upon Kepler for the purpose of automating scientific tasks. Throughout the project, I used the Nimrod/K project that contains sets of directors and actors and ImageJ to create workflows that can be utilized specifically for microscopy image analysis.

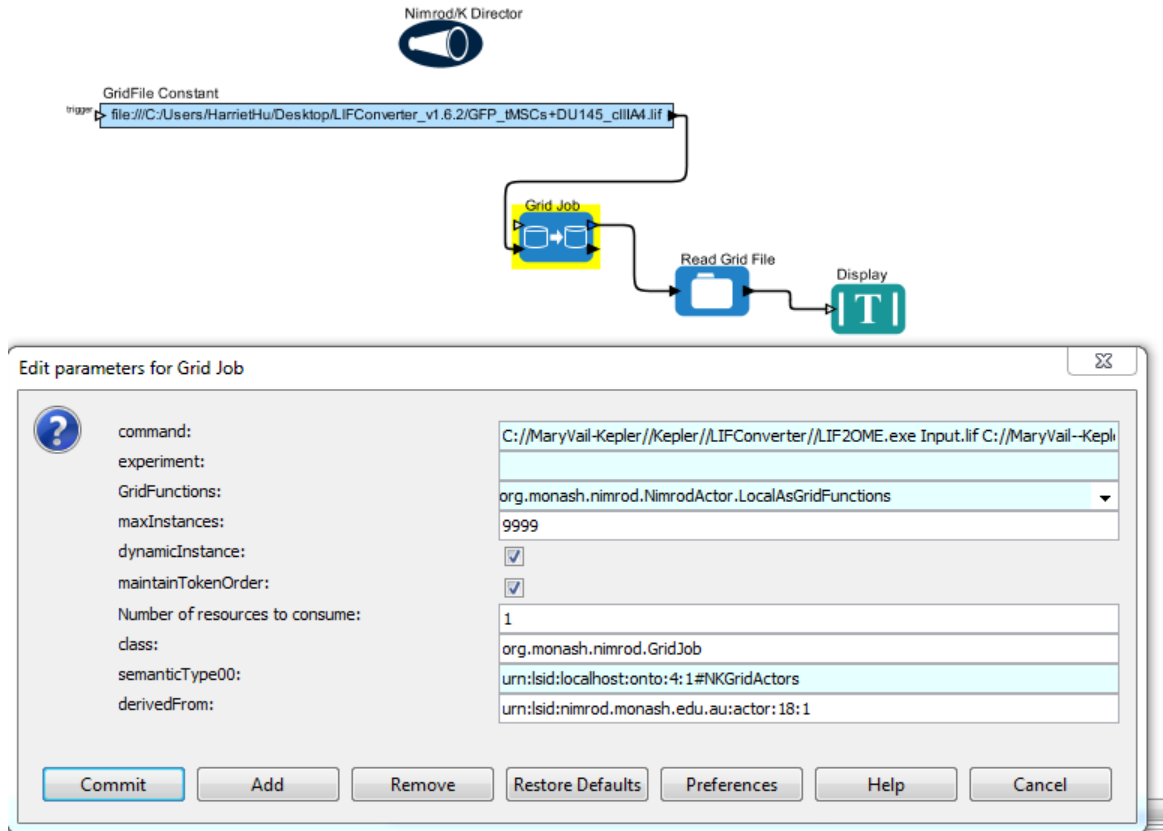
## **Methods and Contributions**

There are currently three workflows on the department computer: 1. LIF converter, 2. individual channel analysis with imageJ scripts, and 3. composite merging with imageJ scripts. The original goal was to have one single workflow in which all three steps could be completed, but due to issues with Kepler and parallel processing, multiple gridjobs cannot currently be executed on a single workflow.

### **1. LIF Converter Workflow**

This workflow allows for external execution of a .lif converter designed by Minh Dinh of the MeSsAGE lab. This workflow converts .lif type images into editable .tif images that can be exported onto ImageJ. It requires a file location, input name, and an output

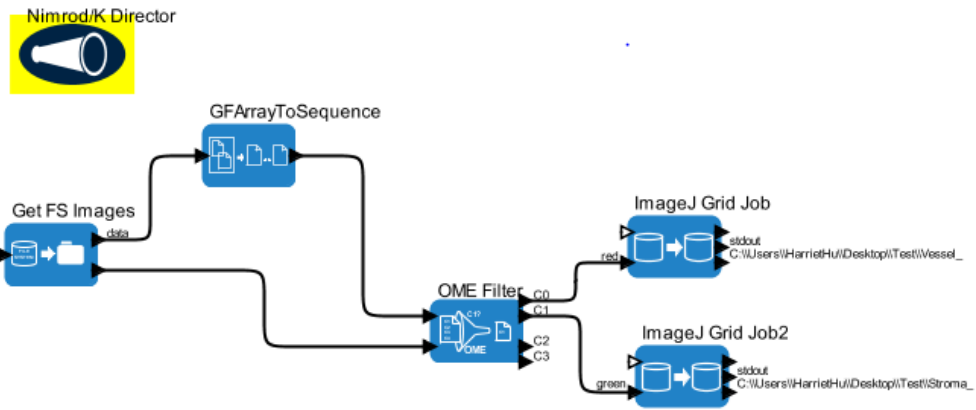
location.



**Figure 1: Workflow one allowing for external execution of LIF exporter**

## 2. IndivAnalysis.kar Workflow

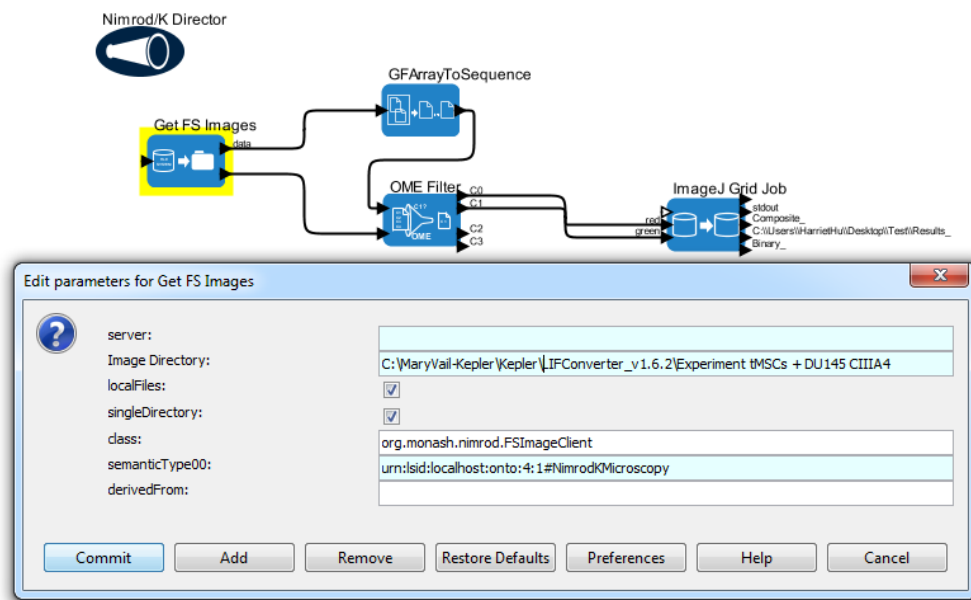
This workflow uses inputted images as designated by “get FS images”, sorts it as a sequence and filters it by channels determined by the C0-C4 outputs from OMEFilter. These respective channels can then be analyzed/modified via the ImageJ Gridjob, and outputted.



**Figure 2: Workflow that allows for individual analysis of various channels**

### 3. Composites.kar Workflow

This workflow takes a directory that contains subdirectories of the converted .tif images, sorts it into a sequence and filters it into ImageJ Gridjob. This final ImageJ gridjob will create the composite images with RGB after analyzing the total particles.



**Figure 3: Workflow that creates composite images and analysis**

## **Conclusions**

The workflows developed in this project have been properly documented and installed onto a department computer at the Department of Biochemistry and Molecular Biology lab. Due to issues with GridJob functions in Kepler Workflows, I had to modify the workflows from my desired approach, and have instead separated the workflows per function. These workflows can be further developed based on the analysis that needs to be conducted per experiment, and provide the beginning foundations to more workflows that can be used for image analysis.

Further questions can be directed to Harriet Hu at [h9hu@ucsd.edu](mailto:h9hu@ucsd.edu).

## **Acknowledgements**

This summer research experience was made possible through the tremendous support and vision of Dr. Gabriele Wienhausen, Dr. Peter Arzberger, Teri Simas, Jim Galvin, and Tricia Taylor of the Pacific Rim Undergraduate Experiences Program. I would also like to thank Dr. David Abramson of Clayton School of IT at Monash University and Dr. Ilkay Altintas of the San Diego Supercomputer Center for their mentorship and technical advice throughout the internship. I would also like to thank Slavisa Garic, Dr. Mary Vail of Monash University, and the Monash eScience and Grid Engineering Laboratory team for their patience and assistance in technical aspects of the project. This summer research experience was supported through the generous donation from the Eurkea! Summer Undergraduate Scholarship Foundation and the National Science Foundation (IOSE-0710726).

## References

1. Abramson, D., Bethwaite, B., Dinh, M., Enticott, C., Firth, S., Garic, S., Harper, I., Lackmann, M., Nguyen, H., Ramdas, T., Russel, A.B.M., Schek, S. and Vail, M.: Virtual Microscopy and Analysis using Scientific Workflows, IEEE e-Science 2009, Oxford, UK (December 2009)
2. Abramson, D., Enticott, C and Altinas, I. “Nimrod/K: Towards Massively Parallel Dynamic Grid Workflows”, IEEE Supercomputing 2008, Austin, Texas, November 2008.
3. ImageJ Project, <http://rsbweb.nih.gov/ij/>
4. “Getting Started with Kepler”. Kepler Project, <https://kepler-project.org/>
5. Taylor, I.J.; Deelman, E.; Gannon, D.B.; Shields, M. (Eds.), “Workflows for e-Science: Scientific Workflows for Grids”, 530 p., Springer.
6. Vail, M. “An anti-EphA3 antibody, chIIIA4, targeting bone marrow-derived mesenchymal stroma attenuates tumour growth by disrupting the stromal and vascular architecture.” 2011, October, Melbourne, AU