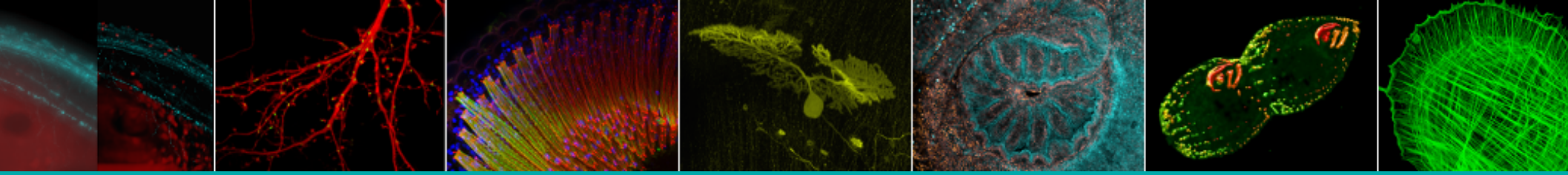


Huygens and OMERO

Multi-user batch deconvolution with web-based HRM via OMERO connection

Remko Dijkstra, Msc.
Imaging Specialist
remko@svi.nl

Scientific Volume Imaging

Deconvolution – Visualization - Analysis

Huygens Software

Huygens Remote Manager

Open-Source www.huygens-rm.org

Collaborators:

EPF Lausanne BioImaging and Optics platform

Friedrich Miescher Institute Facility For Advanced Imaging and Microscopy

Montpellier RIO Imaging

ETH Zurich Single Cell Unit

Scientific Volume Imaging

Leibniz Institute for Neurobiology Magdeburg

Biozentrum Basel University of Basel The Center for Molecular Life Sciences

Combinatorial Neuroimaging Magdeburg

Multi-user access
Provide easy multi-user access to Huygens deconvolution

Web-based solution
Huygens Remote Manager allows easy access to Huygens deconvolution via the web-browser

Easy user management
Easily add new users, and keep track of the usage

Link to OMERO
Exchange data between HRM and OMERO

High-throughput
Ideally suited for high-throughput deconvolution batch jobs

Visualization & Coloc
Peform Colocalization Analysis in batch mode, and visualize deconvolution results

HRM queue manager & GPU acceleration

Image Processing & Deconvolution

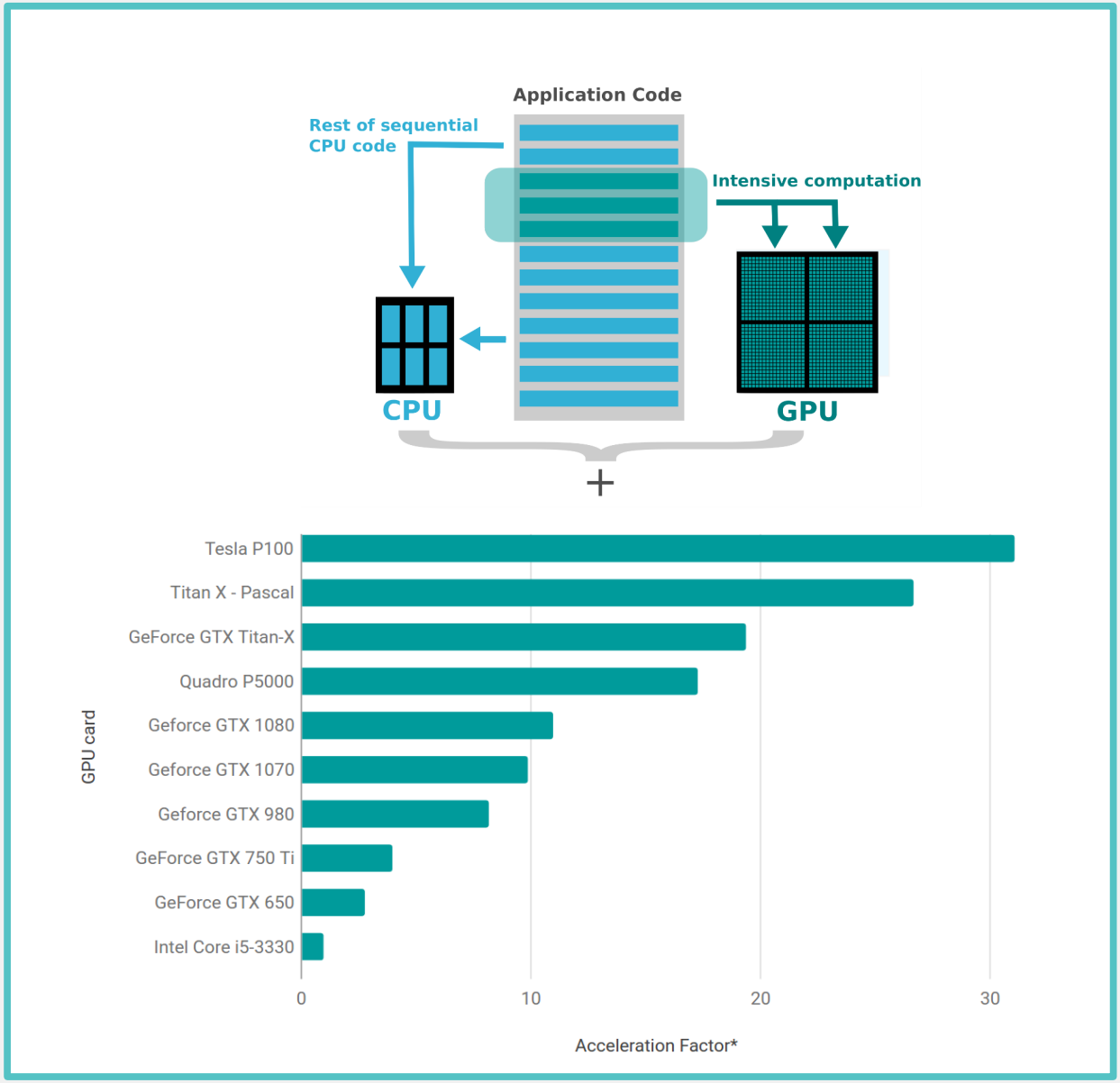
- Powered by Huygens Core
- Theoretical PSF
- Measured PSF

Batch jobs

- Managed by queue manager
- Each user can submit many jobs

Multi-GPU support

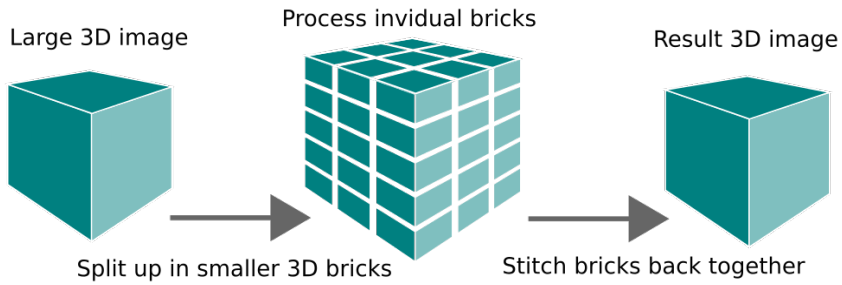
- CUDA GPU acceleration
- Deconvolve jobs on multiple GPU cards in parallel
- https://svi.nl/HuygensGPU



Supports many microscope types

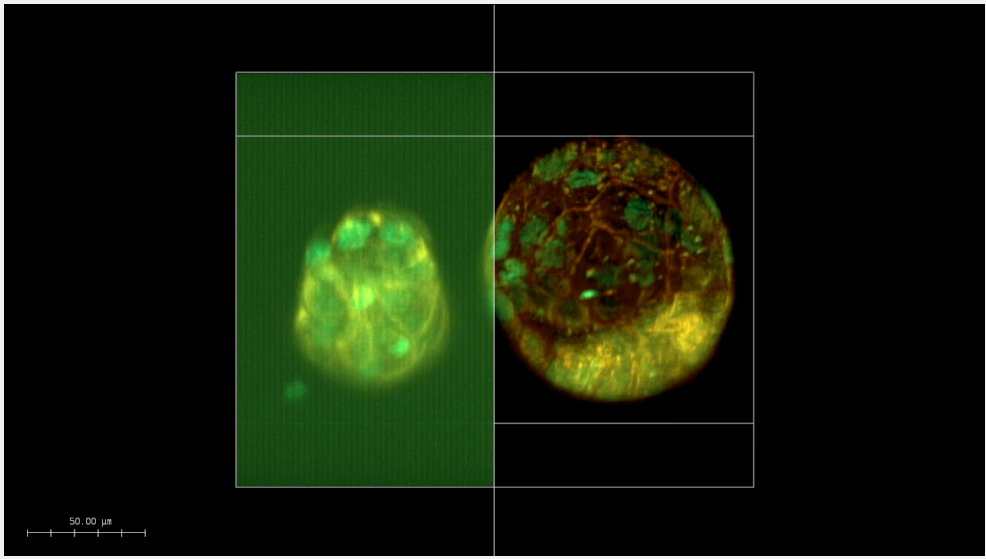
- Widefield
- Confocal
- STED (3D)
- Multi-photon
- Spinning-disk
- SPIM/light-sheet

Unique Huygens bricking:



- Image size is not a problem in Huygens
- multi-PSF handling
- GPU deconvolution

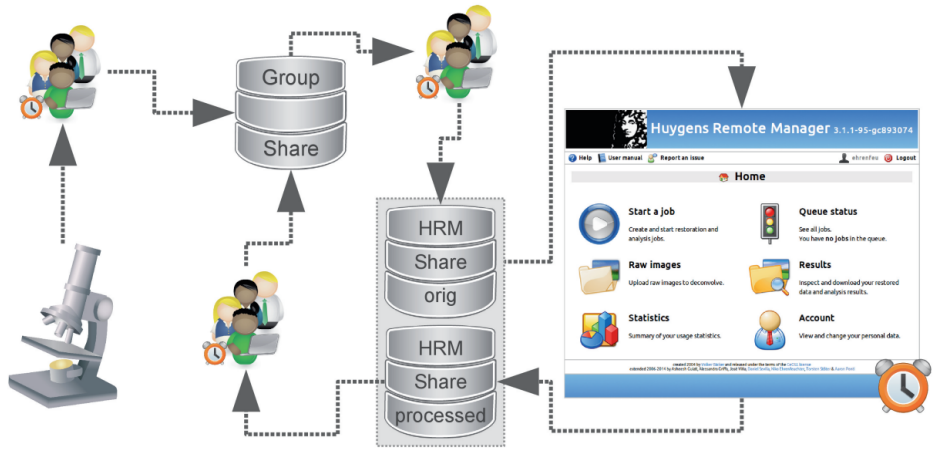
Light-sheet Raw Deconvolved



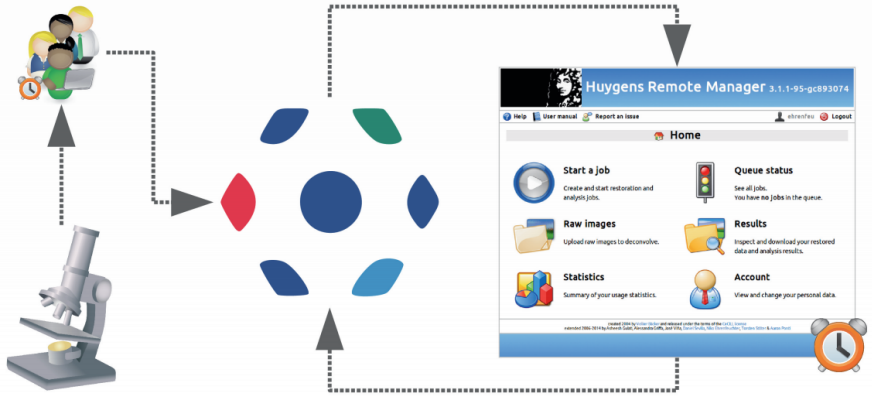
Leica Digital Light Sheet microscope.
Maximum Intensity Projection of a 3D image from mouse blastocyst.
Courtesy of Dr. Marc Duque Ramirez and Dr. Ritsuya Niwayama (Hiiragi group) and Dr. Stefan Terjung (ALMF) from the EMBL Heidelberg, Germany.

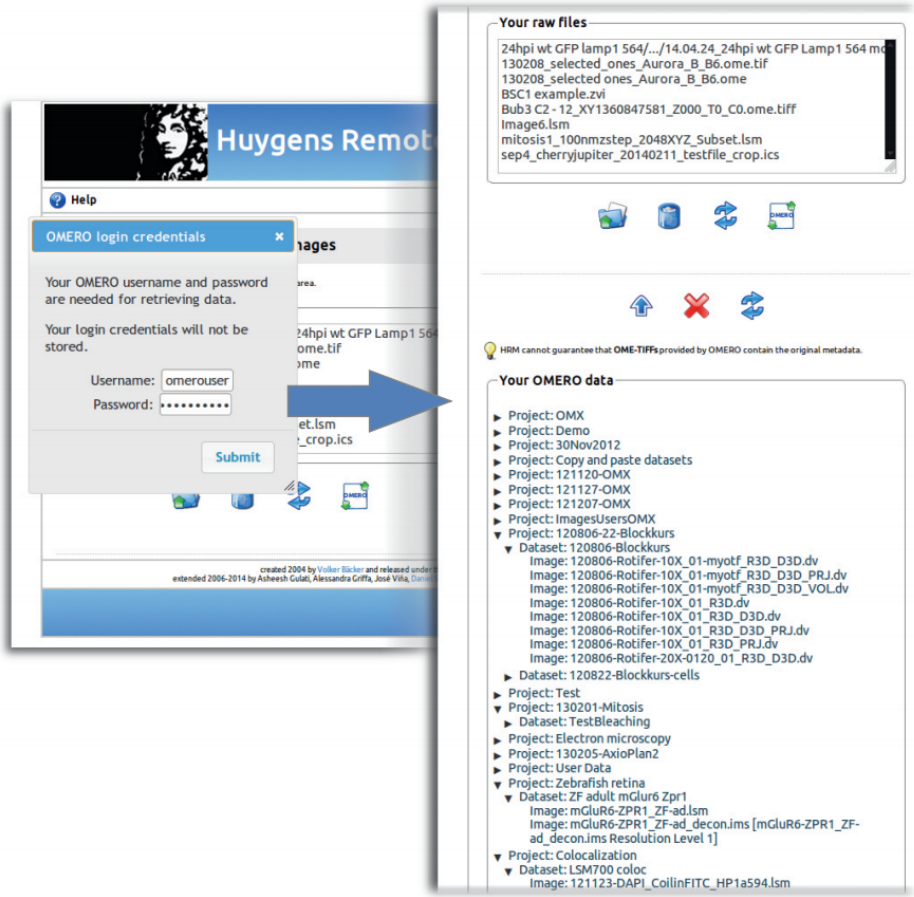
OMERO connection

Conventional workflow



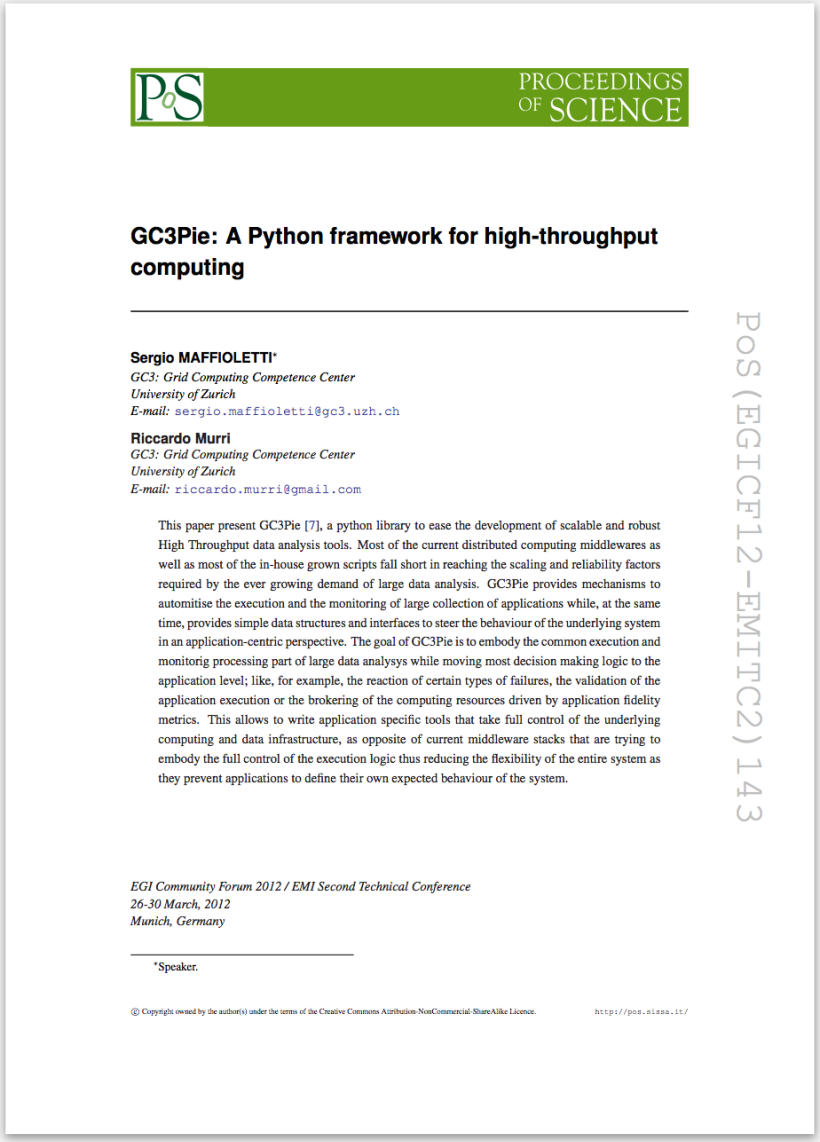
Integrated workflow





HRM future outlook

- New interface – responsive
- Queue manager for clusters (gc3pie)
- Improved OMERO import/export
- PSF distiller
- Image stabilization (z and/or time)
- Tile stitching
- Fusion (light-sheet)



PROCEEDINGS OF SCIENCE

GC3Pie: A Python framework for high-throughput computing

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This paper present GC3Pie [7], a python library to ease the development of scalable and robust High Throughput data analysis tools. Most of the current distributed computing middlewares as well as most of the in-house grown scripts fall short in reaching the scaling and reliability factors required by the ever growing demand of large data analysis. GC3Pie provides mechanisms to automitise the execution and the monitoring of large collection of applications while, at the same time, provides simple data structures and interfaces to steer the behaviour of the underlying system in an application-centric perspective. The goal of GC3Pie is to embody the common execution and monitorig processing part of large data analysys while moving most decision making logic to the application level; like, for example, the reaction of certain types of failures, the validation of the application execution or the brokering of the computing resources driven by application fidelity metrics. This allows to write application specific tools that take full control of the underlying computing and data infrastructure, as opposite of current middleware stacks that are trying to embody the full control of the execution logic thus reducing the flexibility of the entire system as they prevent applications to define their own expected behaviour of the system.

EGI Community Forum 2012 / EMI Second Technical Conference
26-30 March, 2012
Munich, Germany

*Speaker.

 http://pos.sissa.it/

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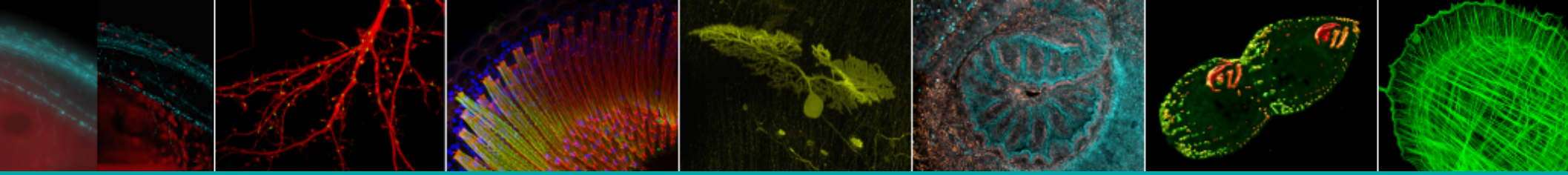

Any Questions?

Authors and contributors

Original concept and implementation

Pierre Travo and Volker Bäcker, Montpellier RIO Imaging (CNRS).
Patrick Schwarb, now at Imagic AG, brought the original version of HRM to the Friedrich Miescher Institute (Basel).

Current developers

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Olivier Burri, BioImaging and Optics Platform, EPFL (Lausanne);
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Former developers

Asheesh Gulati, BioImaging and Optics Platform, EPFL (Lausanne);
Alessandra Griffa, BioImaging and Optics Platform, EPFL (Lausanne);
José Viña, Scientific Volume Imaging (Hilversum).

Free HRM demo:
hrm.svi.nl

More info:
www.huygens-rm.org
https://svi.nl/HuygensCore

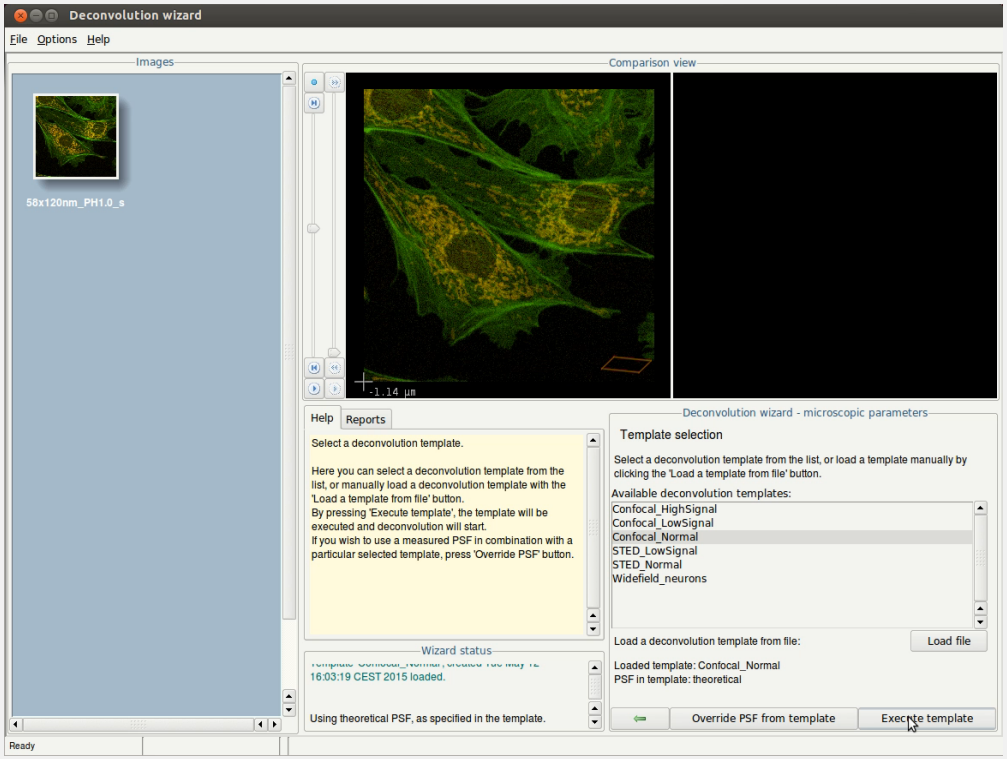
Scientific Volume Imaging

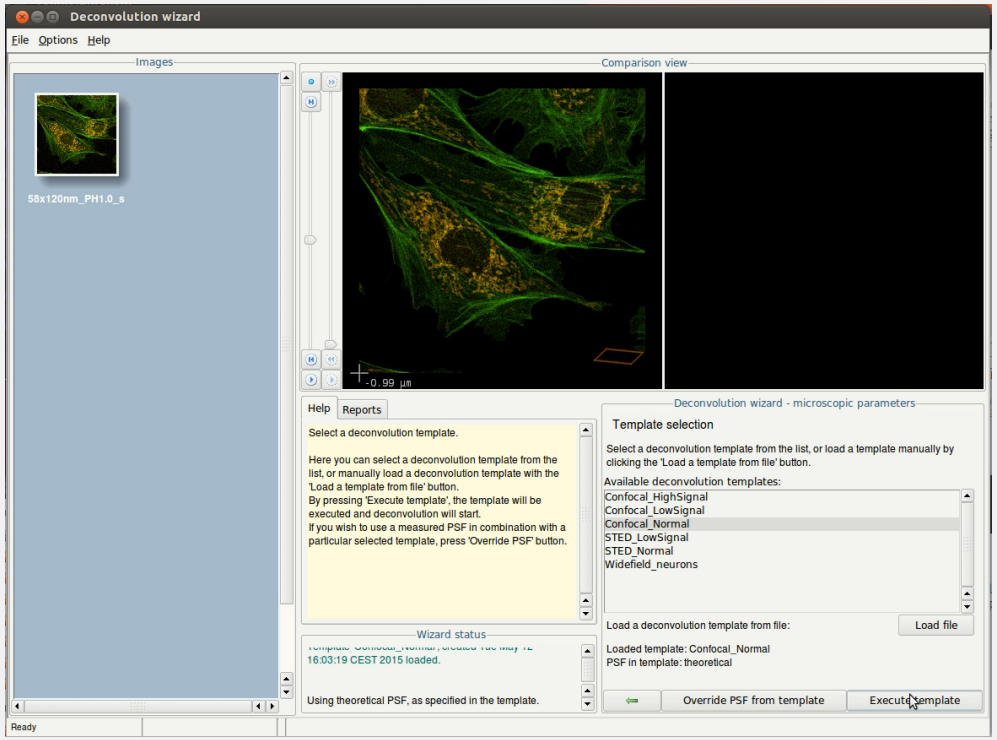
Deconvolution – Visualization - Analysis

Huygens Software

Huygens GPU acceleration

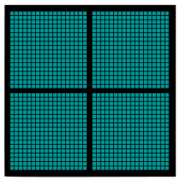
Confocal dataset: 2 channels, 1445 * 1439 * 18 (X*Y*Z) pixels





Using CPU:
Intel Xeon E5-2667 v3
(4 cores @ 3.2 GHz)

+



Geforce GTX Titan-X
3072 CUDA cores
12 GB video-RAM