

Rhadius: a cloud-based framework interfacing with OMERO.server for bioimaging analysis of large scale datasets

Luca Coviello, Marco Mina, Cesare Furlanello

Rhadius is a cloud-based web-service that takes advantage of cloud scalable computational infrastructures to run custom analysis pipelines built with different open source bioimaging software. Rhadius is able to interface to OMERO.server remote imaging repositories.

Cloud architecture



- Fully dockerized
- Installed as a single package on any hardware/software platform
- Require minimal IT knowledge and effort



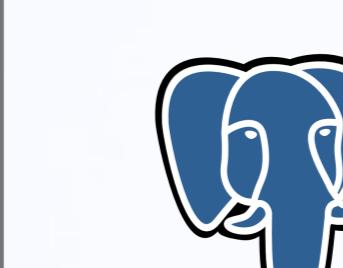
Running on AWS instance

Demo available at rhadius.fbk.eu

Rhadius interface

The Rhadius interface consists of two main parts. The top part shows the "Home" page, which features a large red fluorescence microscopy image of a cell with the text "Rhadius" overlaid. Below this is a sidebar with links: Home, MPBA, Datasets, Script, DeconvolutionLab, and Results. The bottom part shows the "Result" page, which displays a table of analysis tasks. The table includes columns for Submitted date, Task ID, Pipeline Name, Project > Dataset, Status, Result, Download, and Delete. Each row shows a successful task submission, such as "NB > test" or "DeconvolutionLab - Tikhonov-miller".

System solution



PostgreSQL
bootableDB



- Open source web app. framework
- Python-based

- PostgreSQL
- Open source
- Object-relational DBMS

- Asynchronous tasks and jobs queue
- Real-time operations
- Process scheduling
- Open source key-value cache and store
- Message broker

Direct interface to OMERO



- OMERO plugin for exporting images
- Can export images to:
 - Original raw images
 - OME-TIFF files converted by OMERO

The "Upload Images.py" form allows users to upload images to Rhadius. It includes fields for Data Type (Project), IDs, Project Name, Dataset Name, Choose File Type (TIFF), URL (rhadius.fbk.eu), Username, and Password.

The upload images OMERO plugin interface

Custom pipeline support

- Upload and run new custom analysis pipelines
- Support scripts based on open source frameworks (Fiji/ImageJ, Python, R)



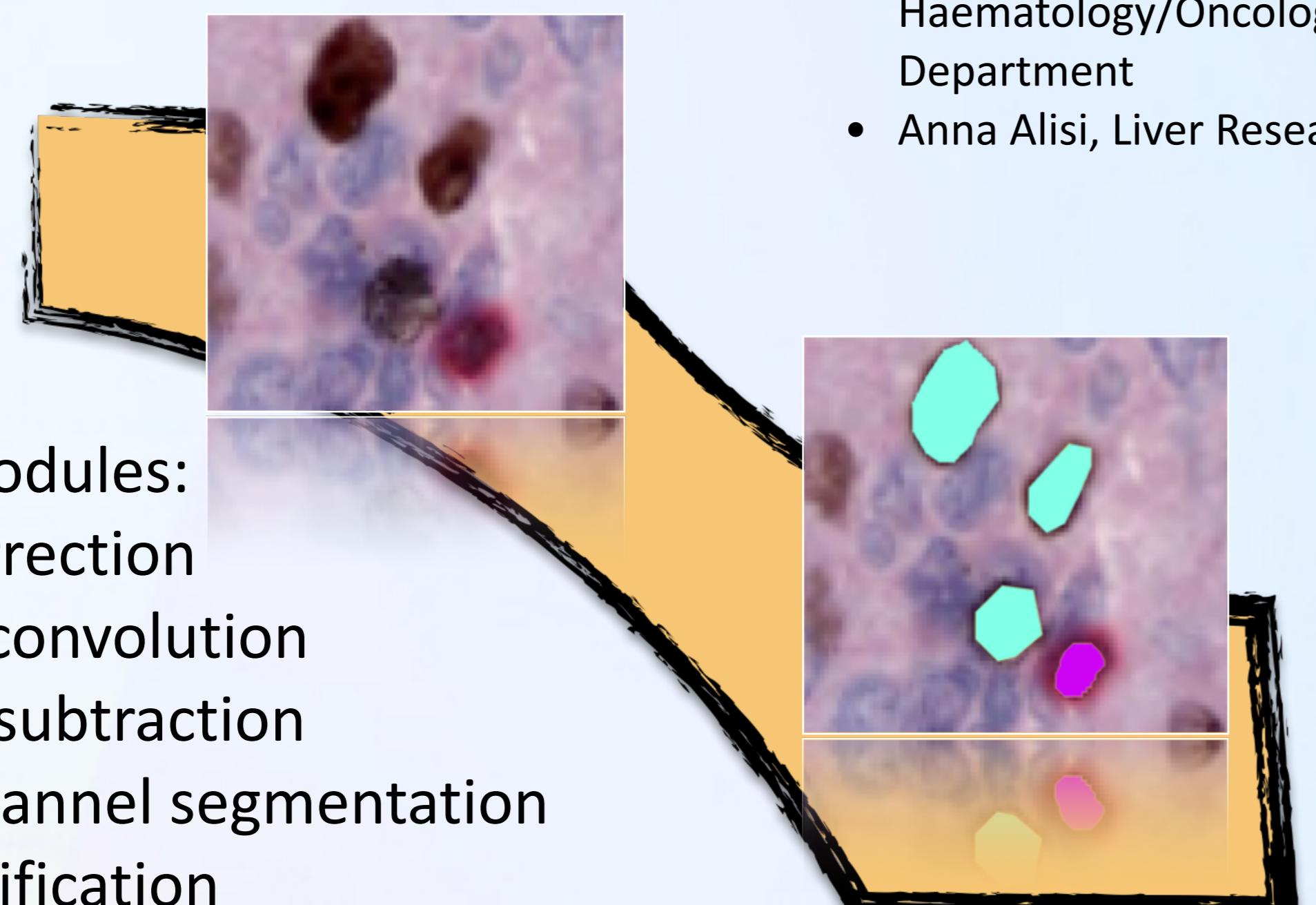
The "Script View" interface of Rhadius shows a script named "Watershed.py". The script imports Fiji and ImageProcessor, opens an image, creates a mask, and saves the result. It also includes comments for the output file and results.

The Script upload interface of Rhadius

A selection of pipelines available in Rhadius

A. Cellular segmentation and classification pipeline

Immunohistochemistry bright field microscopy image acquisition



- Pipeline modules:
- Color correction
 - Color deconvolution
 - Channel subtraction
 - Single-channel segmentation
 - Cell classification

Mina M. et al., Oncoimmunology (2015)

Ceccarelli S. et al., Journal of Hepatology (2014), 60(S1), S159.

- In collaboration with:
- Doriana Fruci, Paediatric Haematology/Oncology Department
 - Anna Alisi, Liver Research Unit

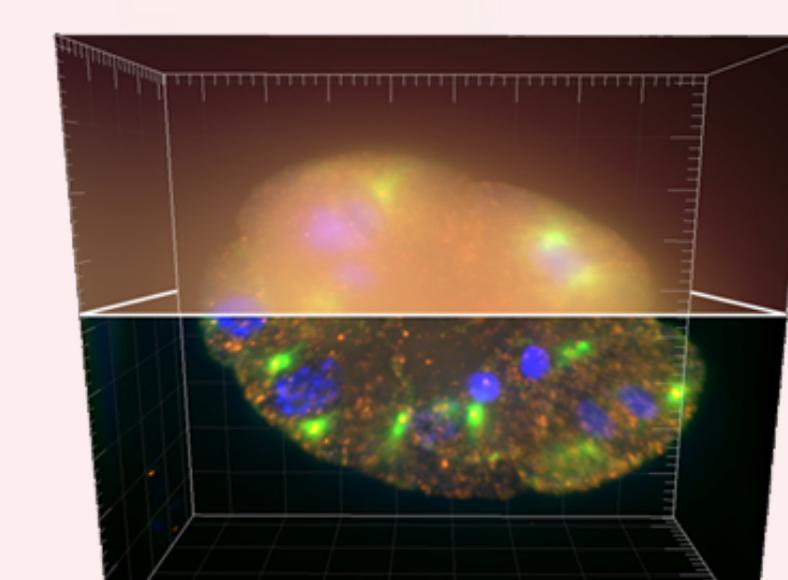


B. 3D image deconvolution package

- Interface to the DeconvolutionLab* ImageJ plugin
- Deconvolve 2D or 3D microscopic images
- Several deconvolution algorithms supported
- We are extending the deconvolution package to support 5D images

The "DeconvolutionLab" interface of Rhadius shows three steps: 1. Select the images to be deconvolved, 2. Select the pdf, and 3. Select the algorithm. The algorithm selected is "Tikhonov-Miller".

The deconvolutionLab interface of Rhadius



*DeconvolutionLab:
bigwww.epfl.ch

In collaboration with:
Daniele Arosio, Molecular Imaging Lab

