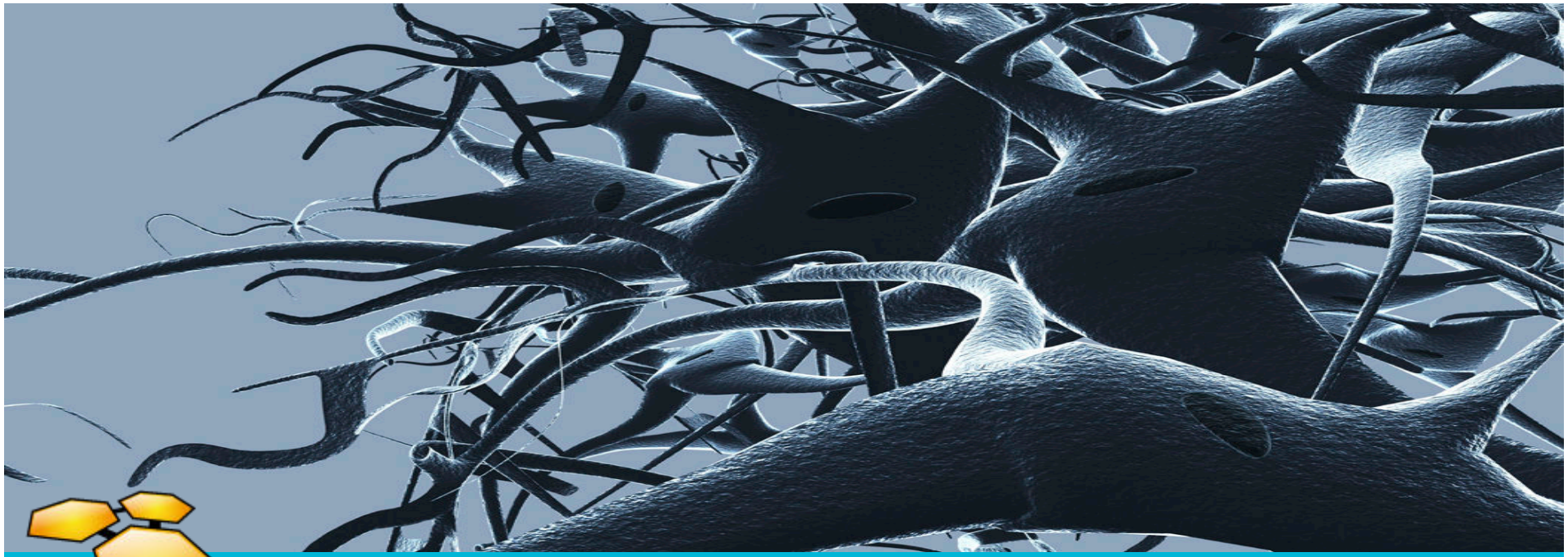


Galaxy as an Integration and Workflow Platform

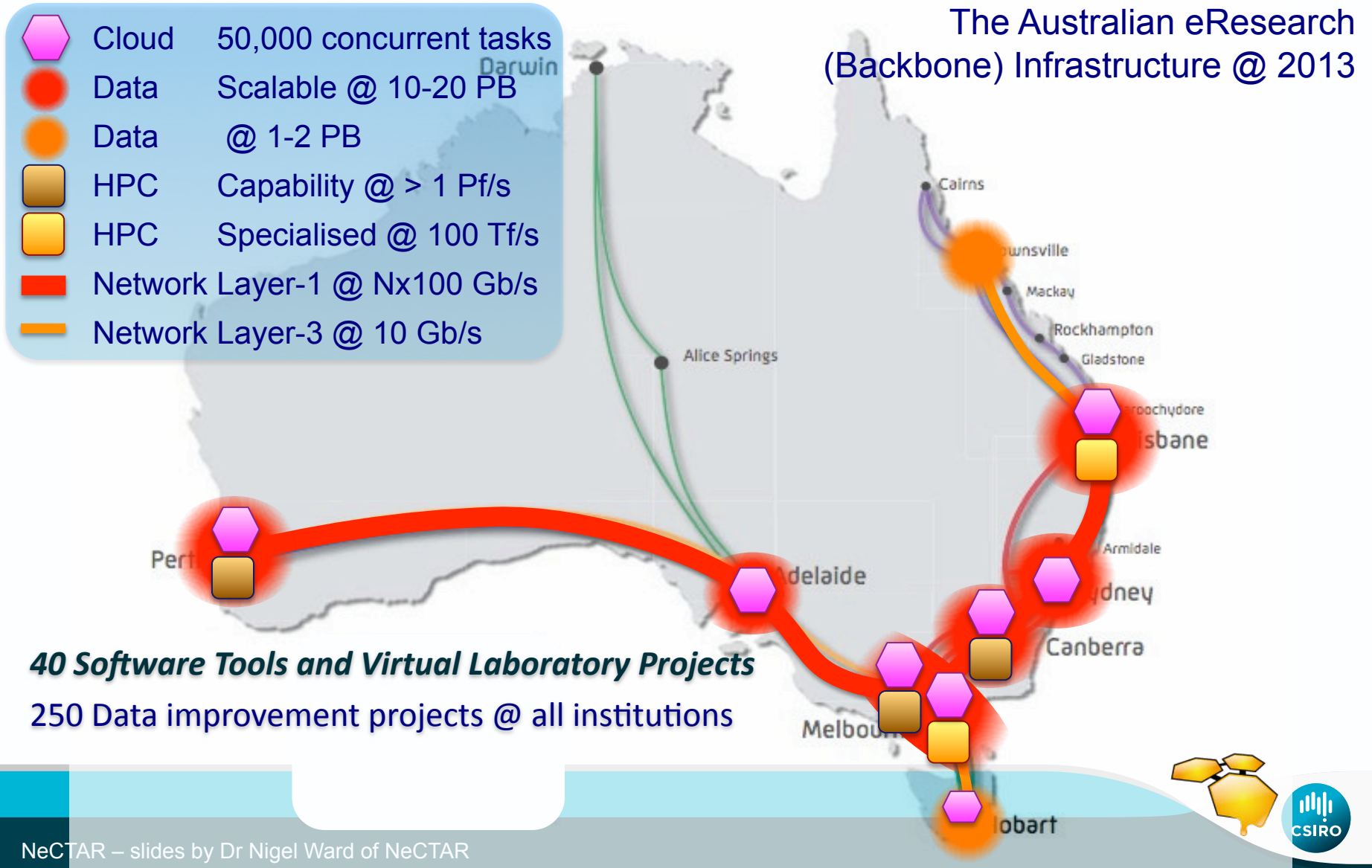
for Bio-medical Image Analysis and Image Processing Toolkit

Piotr Szul, Dadong Wang, Yulia Arzhaeva, Shiping Chen, Alex Khassapov, Neil Burdett, Timur Gureyev, John Taylor, Tomasz Bednarz

COMPUTATIONAL SIMULATION SCIENCES TCP
www.csiro.au

https://www.nectar.org.au/cloud-based-image-analysis-and-processing-toolbox
http://cloudimaging.blogspot.com.au/p/about-project.html

NeCTAR Research Cloud…



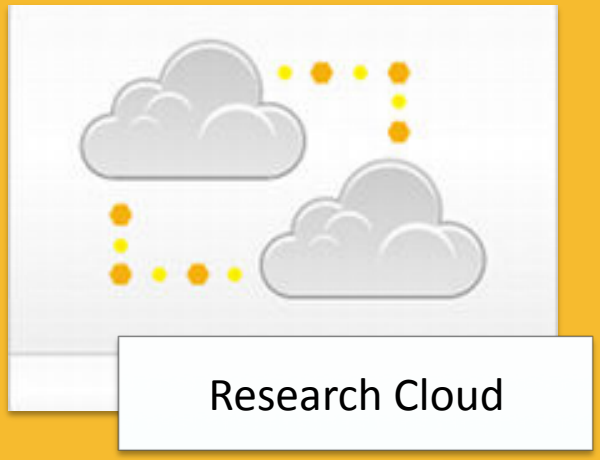
NeCTAR is funding four programs

Research software

Virtual laboratories

eResearch Tools

Computational platforms



Research Cloud

National Server Program

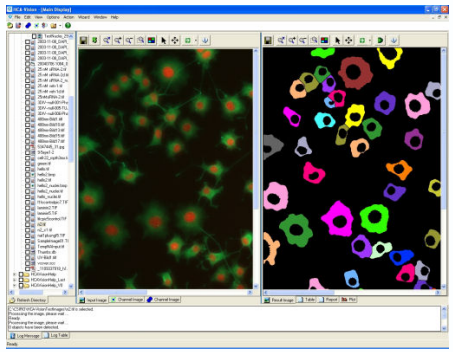
Project Vision

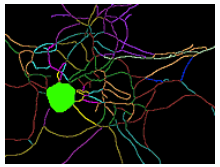
We have 2-3 / 3D data coming from different image modalities

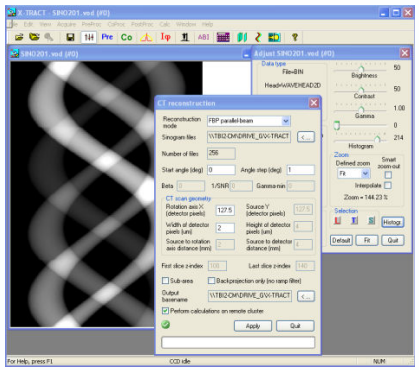
Need: image analysis, image processing, image reconstruction tools

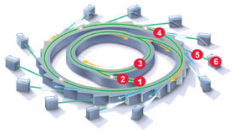
Need: fast, coherent cloud-based image analysis & processing tools integrating existing CSIRO software packages:

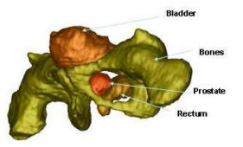
- HCA-Vision, X-TRACT, MILXView,
- Workspace.











HCA-Vision

Developed by CSIRO Quantitative Imaging group for automating process of quantifying cells features in microscopy images. It can reproducibly analyse complex cell morphologies. Recently, extended to 3D enables the analysis of neuron structures in vitro (in cells cultured in a 3D gel matrix) and in vivo (e.g. in exposed rat brains or viable rat brain tissue sections).

It has great value in particular for the pharmaceutical and neuroscience research community.

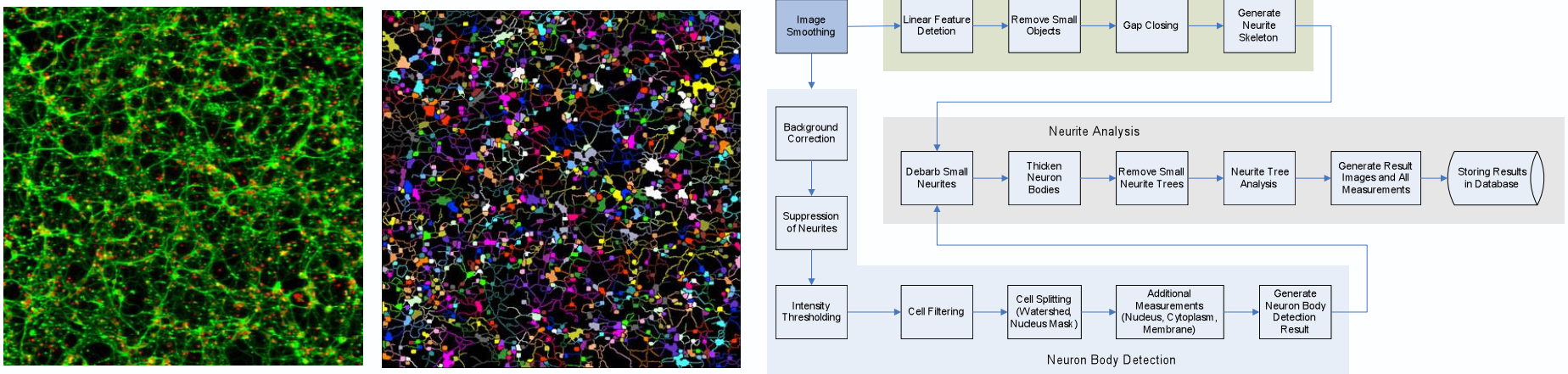


Figure: Neurite Analysis (a) input image; (b) resulted image; (c) diagram of the algorithm.

X-TRACT

A software for advanced X-ray image analysis and Computed Tomography currently in use on the MASSIVE cluster at the Australian Synchrotron, ANU and at the Shanghai Synchrotron in China.

X-TRACT implements a large number of conventional and advanced algorithms for 2D and 3D X-ray image reconstruction and simulation.

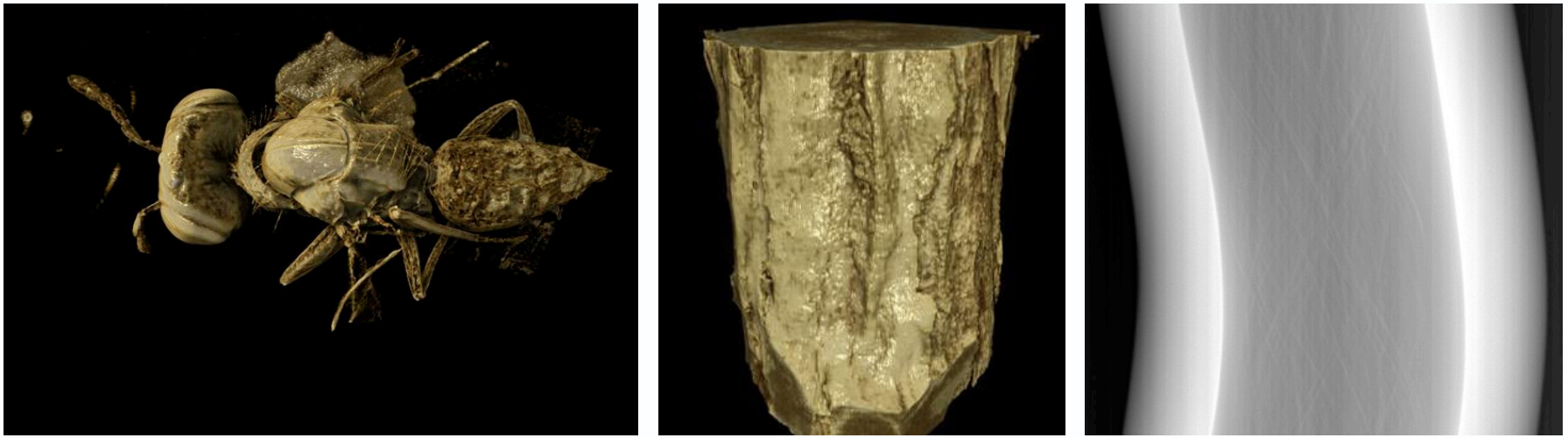


Figure: (a) Insect, reconstruction and rendering by Sherry Mayo (CSIRO); (b) Acacia plant, sample (~1 mm across) provided by Mel Linton (CSIRO), collected, reconstructed and rendered by Sherry Mayo; (c) Sample input Sinogram.

MILXView

A 3D medical imaging analysis and visualisation platform increasingly popular with researchers and medical specialists working with MRI, PET and other types of medical images.

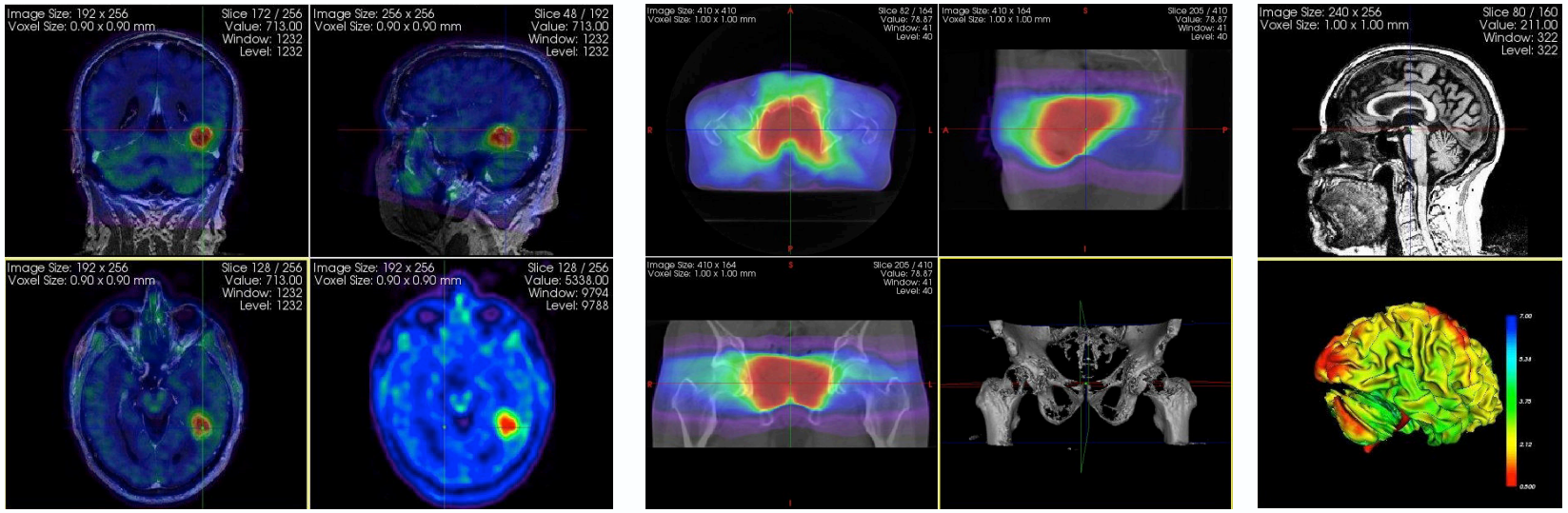
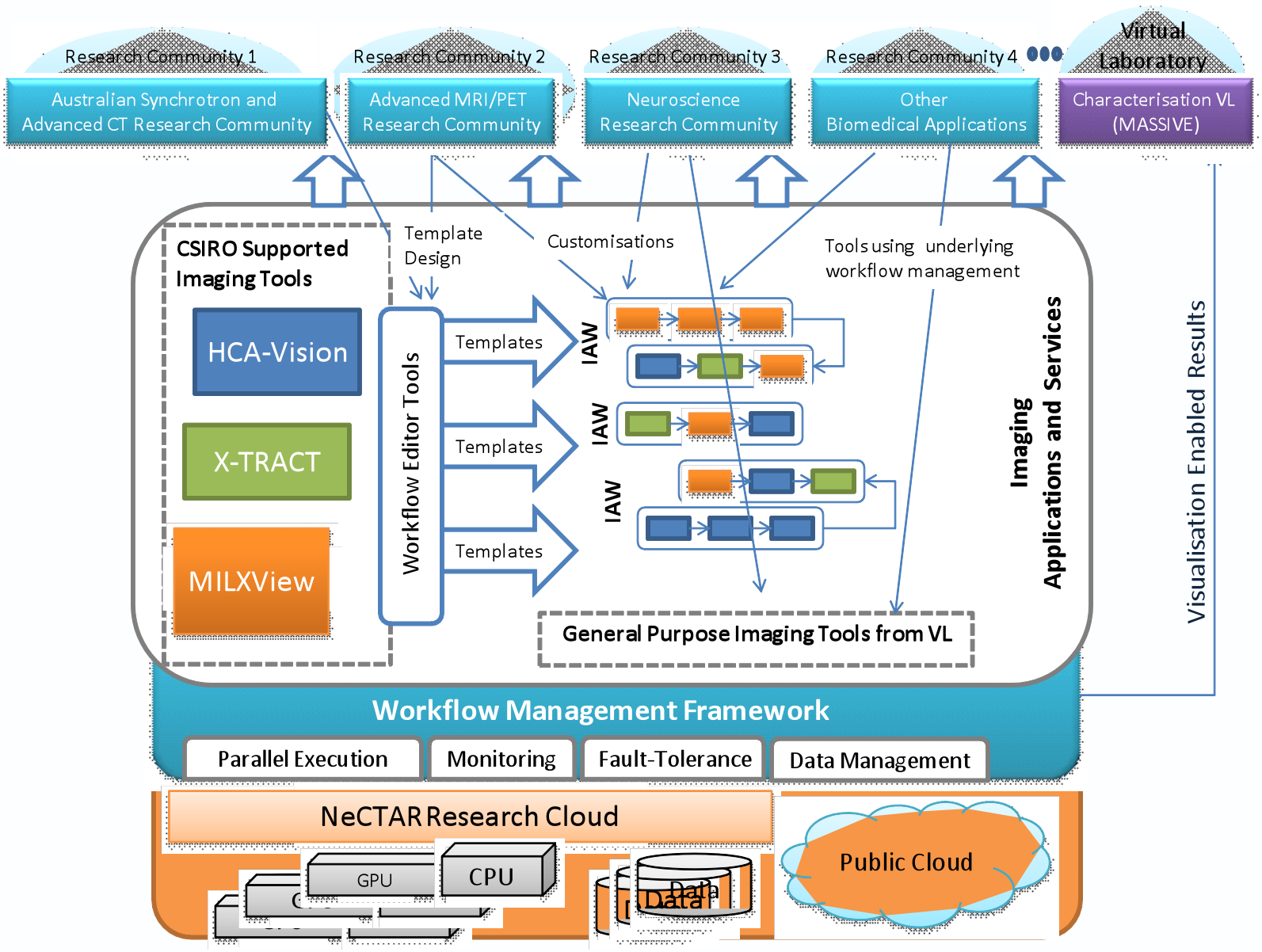
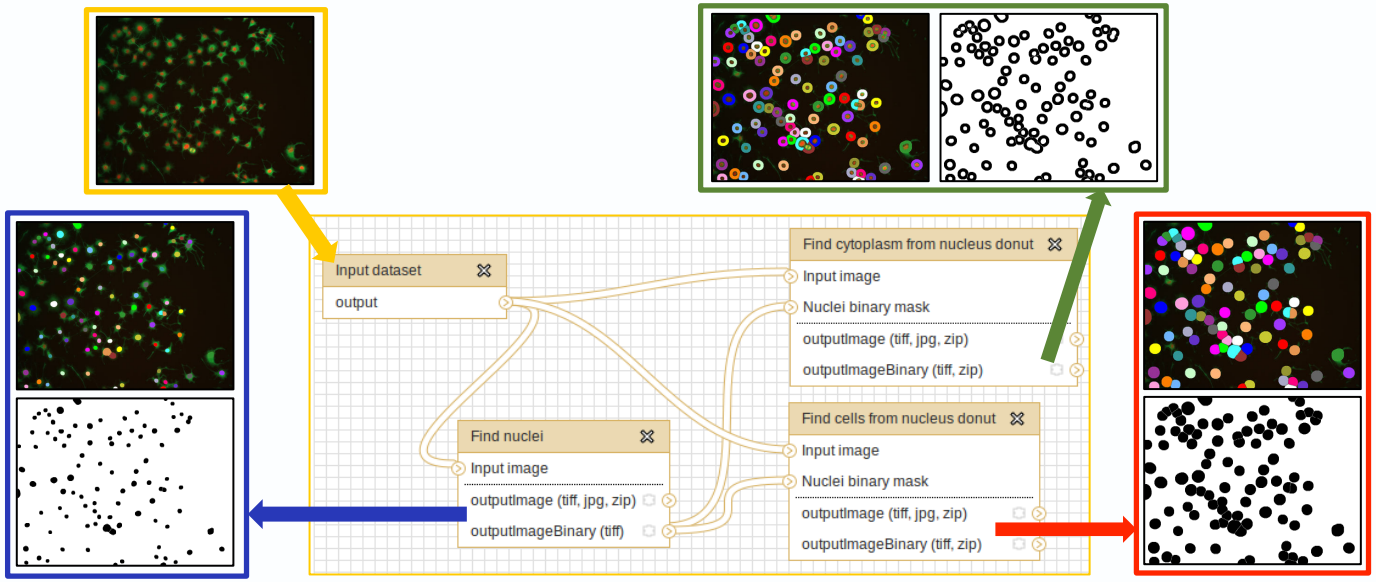


Figure: (a) Brain tumor - PET scan and MRI overlaid; (b) CT scan of a prostate of a patient overlaid with radiation dose; (c) Generated 3D view of a brain allowing study of atrophy pattern characteristics of diseases such as Alzheimer's disease.


Research Community 1
Australian Synchrotron and Advanced CT Research Community
Research Community 2
Advanced MRI/PET Research Community
Research Community 3
Neuroscience Research Community
Research Community 4
Other Biomedical Applications
Virtual Laboratory
Characterisation VL (MASSIVE)
CSIRO Supported Imaging Tools
HCA-Vision
X-TRACT
MILXView
Workflow Editor Tools
Template Design
Customisations
Tools using underlying workflow management
Templates
Templates
Templates
IAW
IAW
IAW
Imaging Applications and Services
General Purpose Imaging Tools from VL
Visualisation Enabled Results
Workflow Management Framework
Parallel Execution
Monitoring
Fault-Tolerance
Data Management
NeCTAR Research Cloud
GPU
CPU
Data
Public Cloud

Glue = Galaxy



Tools

- Thumbnail identify nuclaei

MILXVIEW TOOLS

- Extract 2D slice from an image

Image Registration

- Register using affine transforms on two images
- Register using rigid transforms on two images

Image Segmentation

- Segmentation using wm gm and csf

CTE Surface

- Reorient images for CTE surface
- Full CTE Surface pipeline on list of images

CTE

- CTE create raw data on list of images

CT Reconstruction

X-TRACT TOOLS

- CT Reconstruction Create a slice from a sinogram

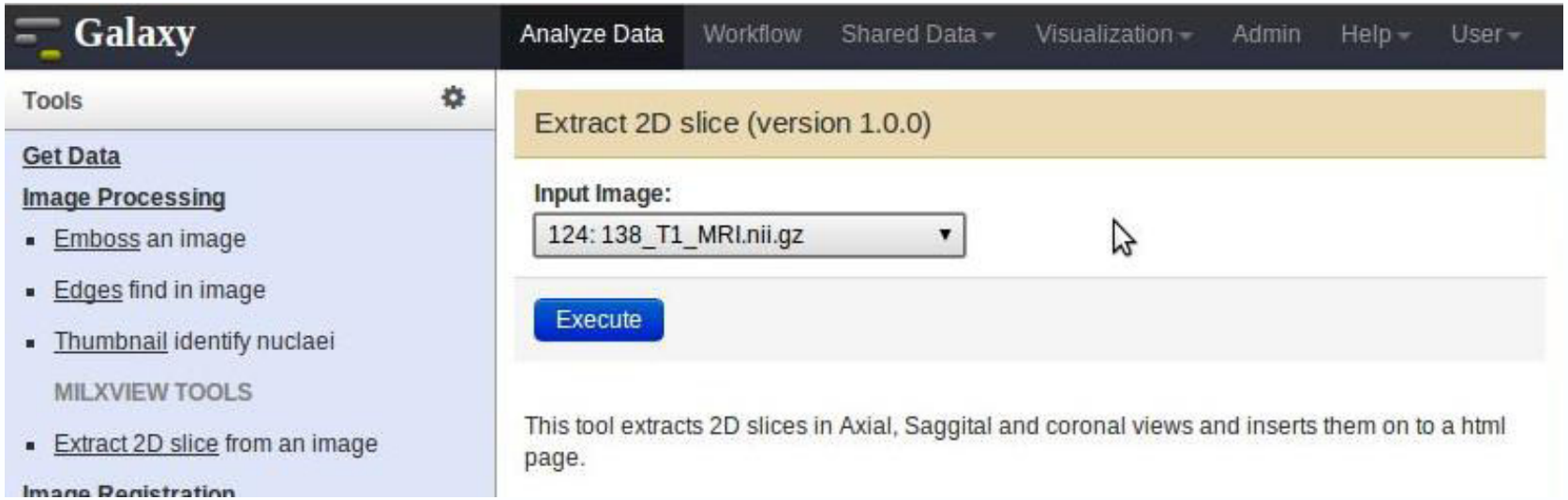
Cellular Imaging

- Find nuclei identify nuclei
- Find cells from nucleus donut Identify cells given a mask of nuclei
- Find cytoplasm from nucleus donut Identify cytoplasm given a mask of nuclei
- Filter objects by morphology filter objects in an image by their morphological properties
- Find lines Find lines
- Find dots Find dots

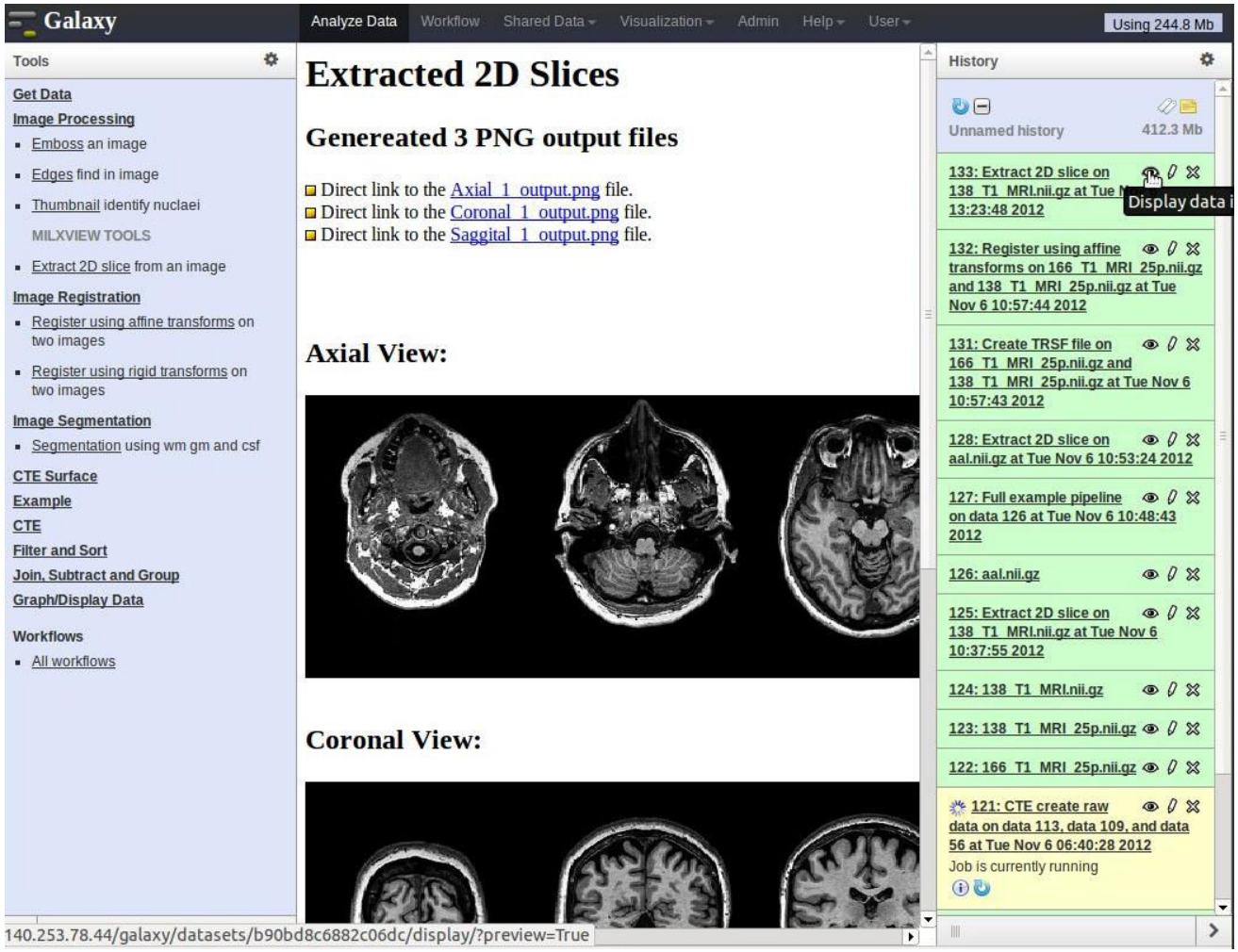
Extract 2D Slices

Extracts 2D slices in three directions from a 3D image

Input image ← 138_T1_MRI.nii.gz

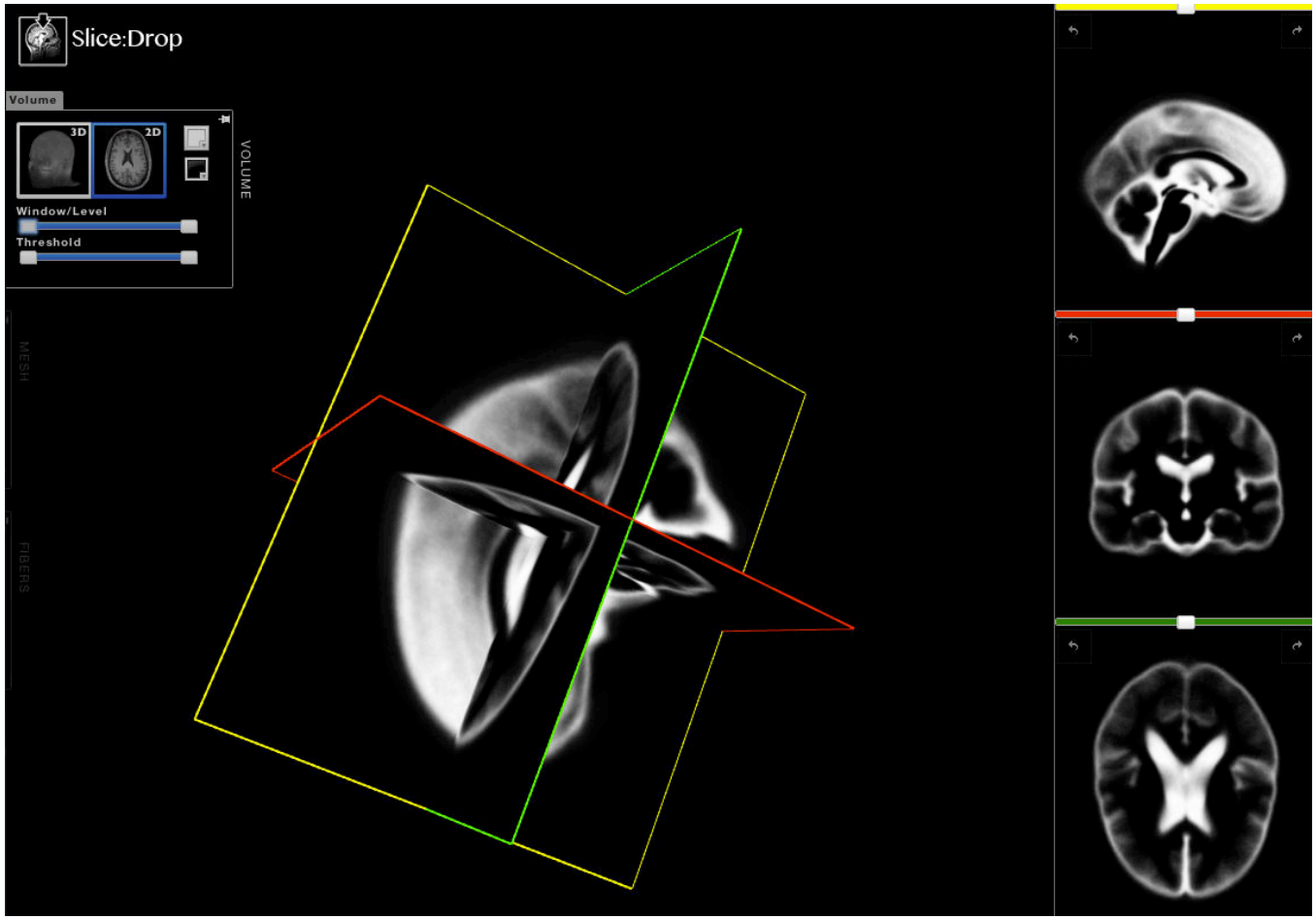


It takes few seconds and a HTML is created to show the user the 2D slices and also lets the user download the images

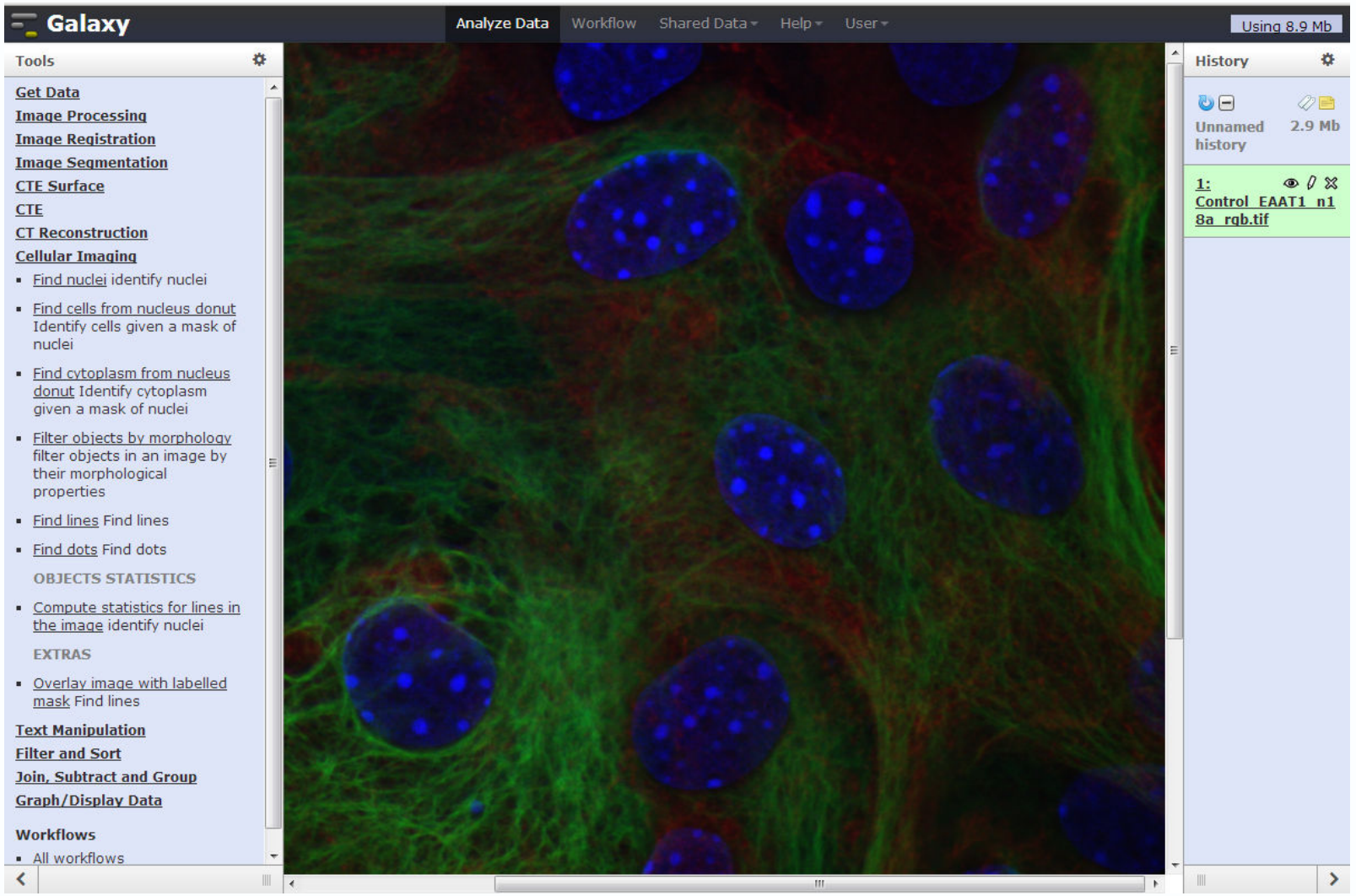


Visualisation

WebGL based, Slice:Drop

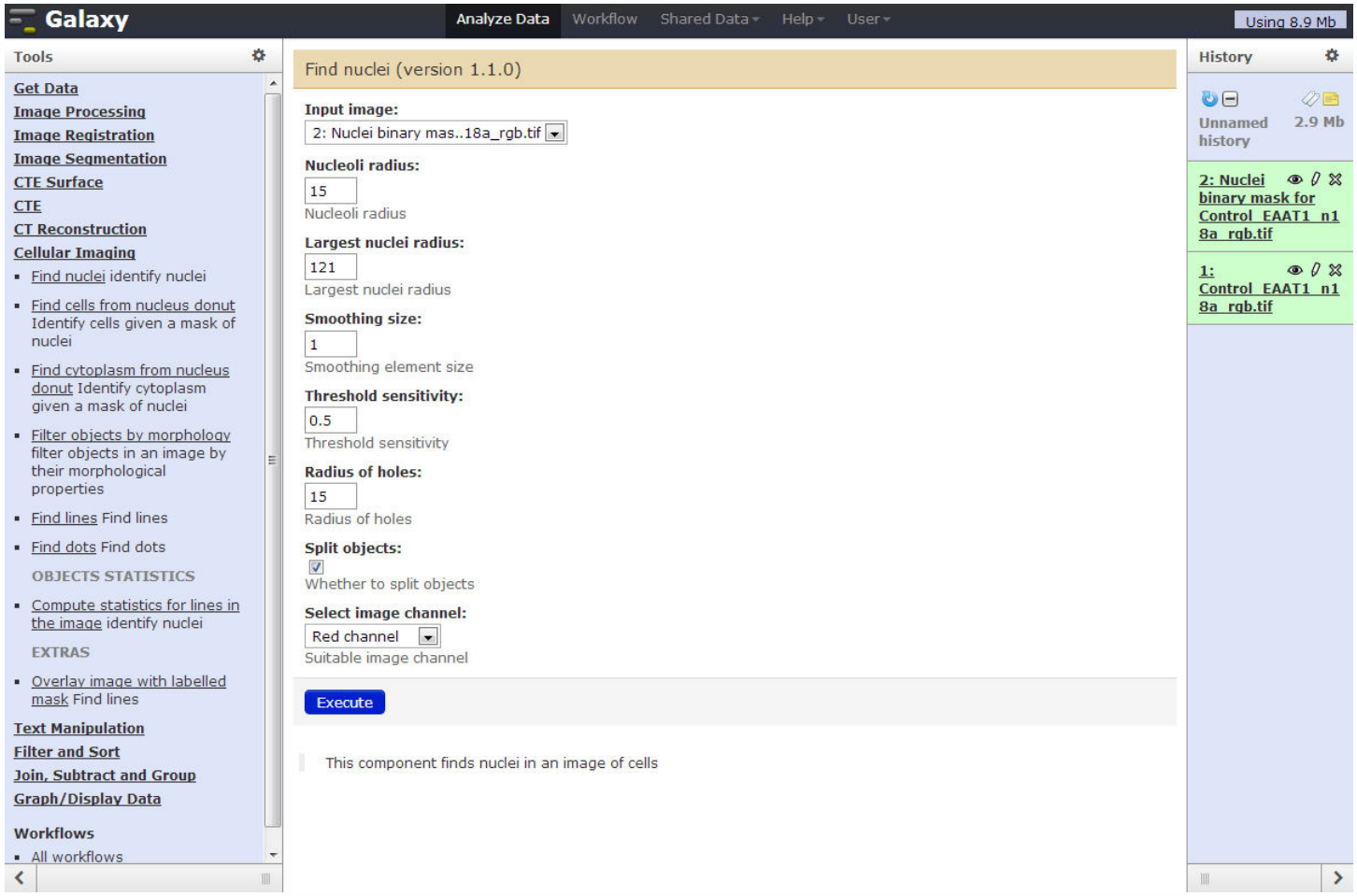


Cellular imaging in Galaxy



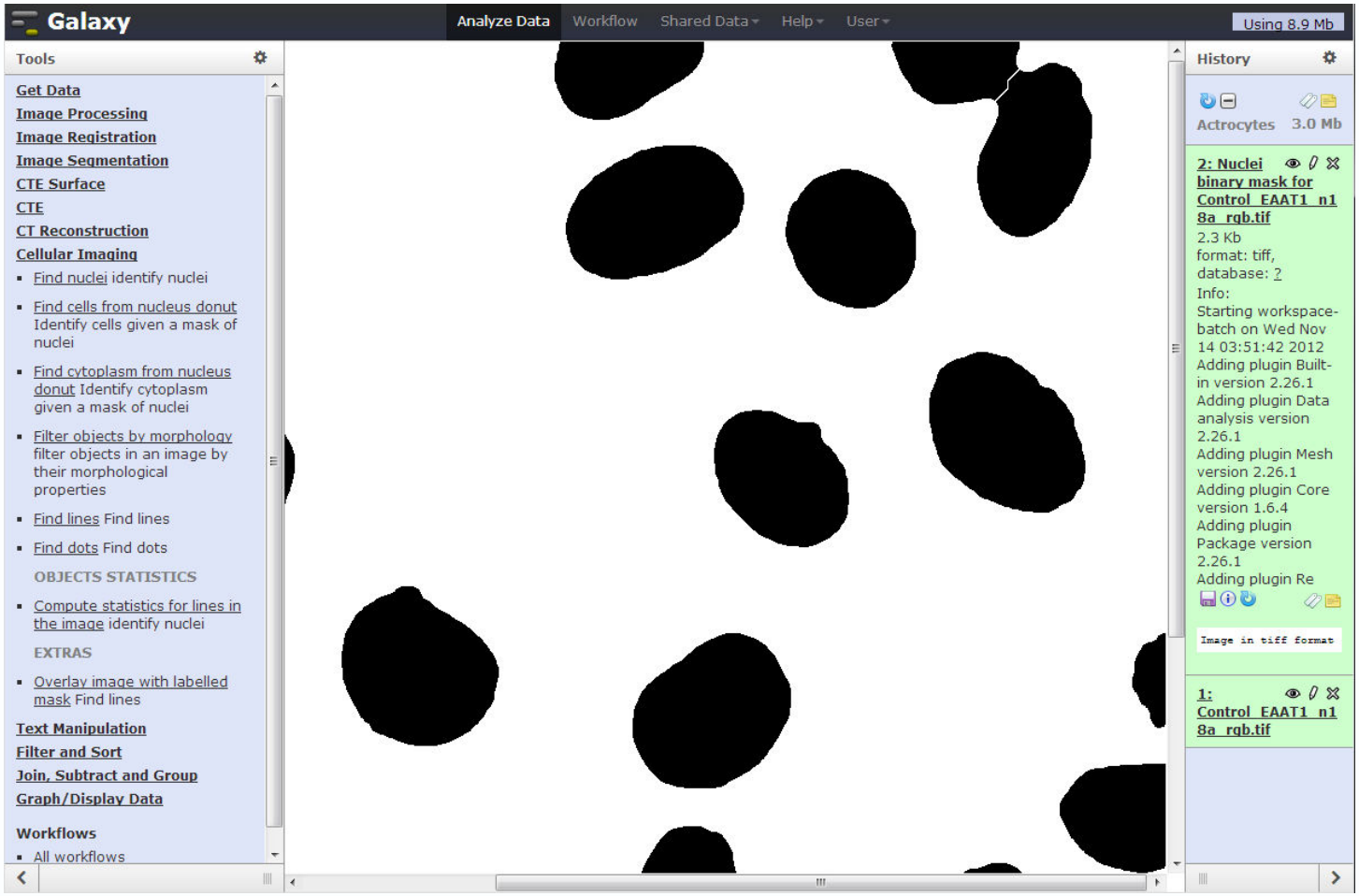
Building Astrocytes analysis workflow

Step 1. Find nuclei



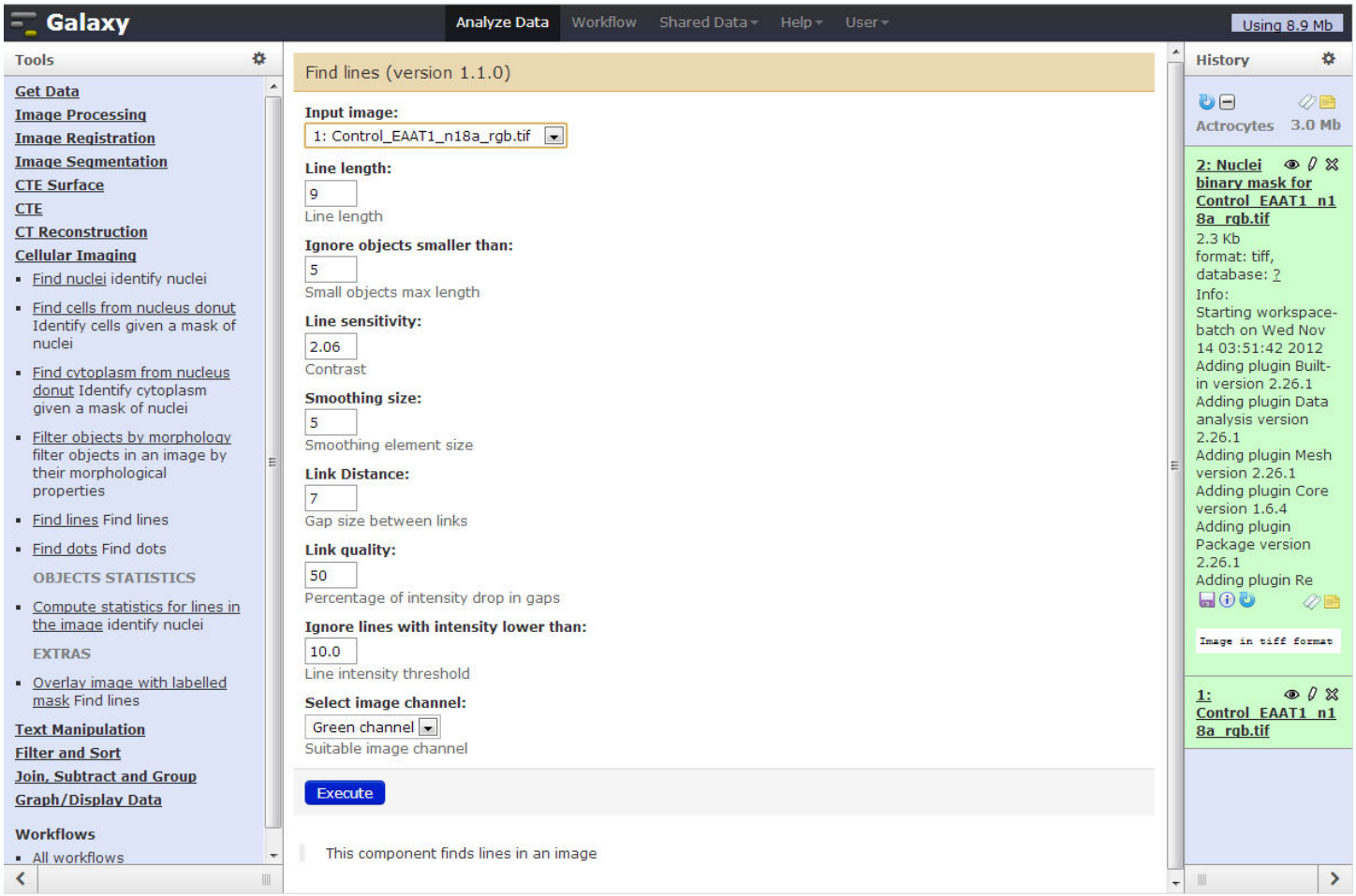
Building Actrocytes analysis workflow

Output: nuclei binary mask



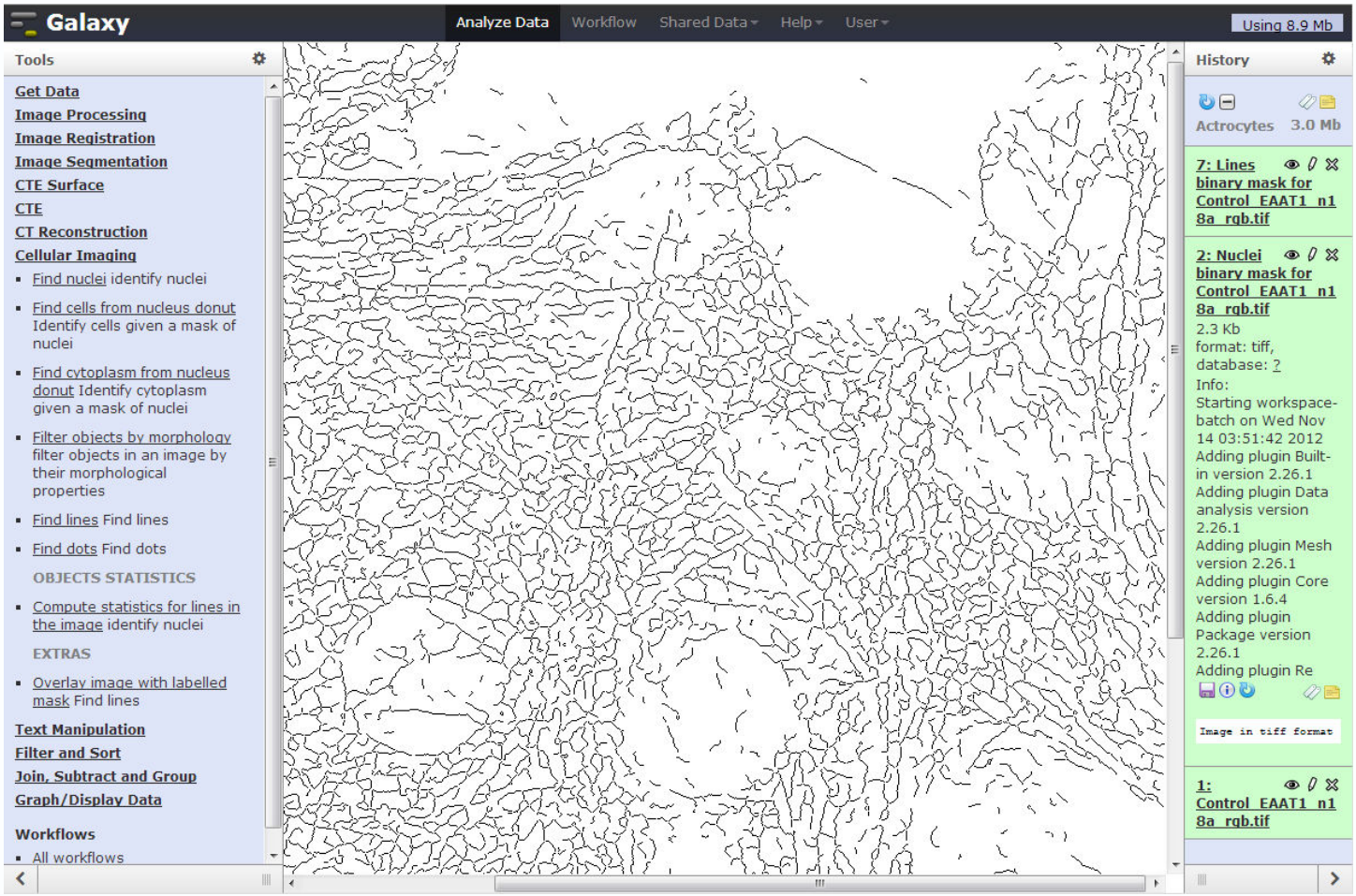
Building Astrocytes analysis workflow

Step 2. Find lines



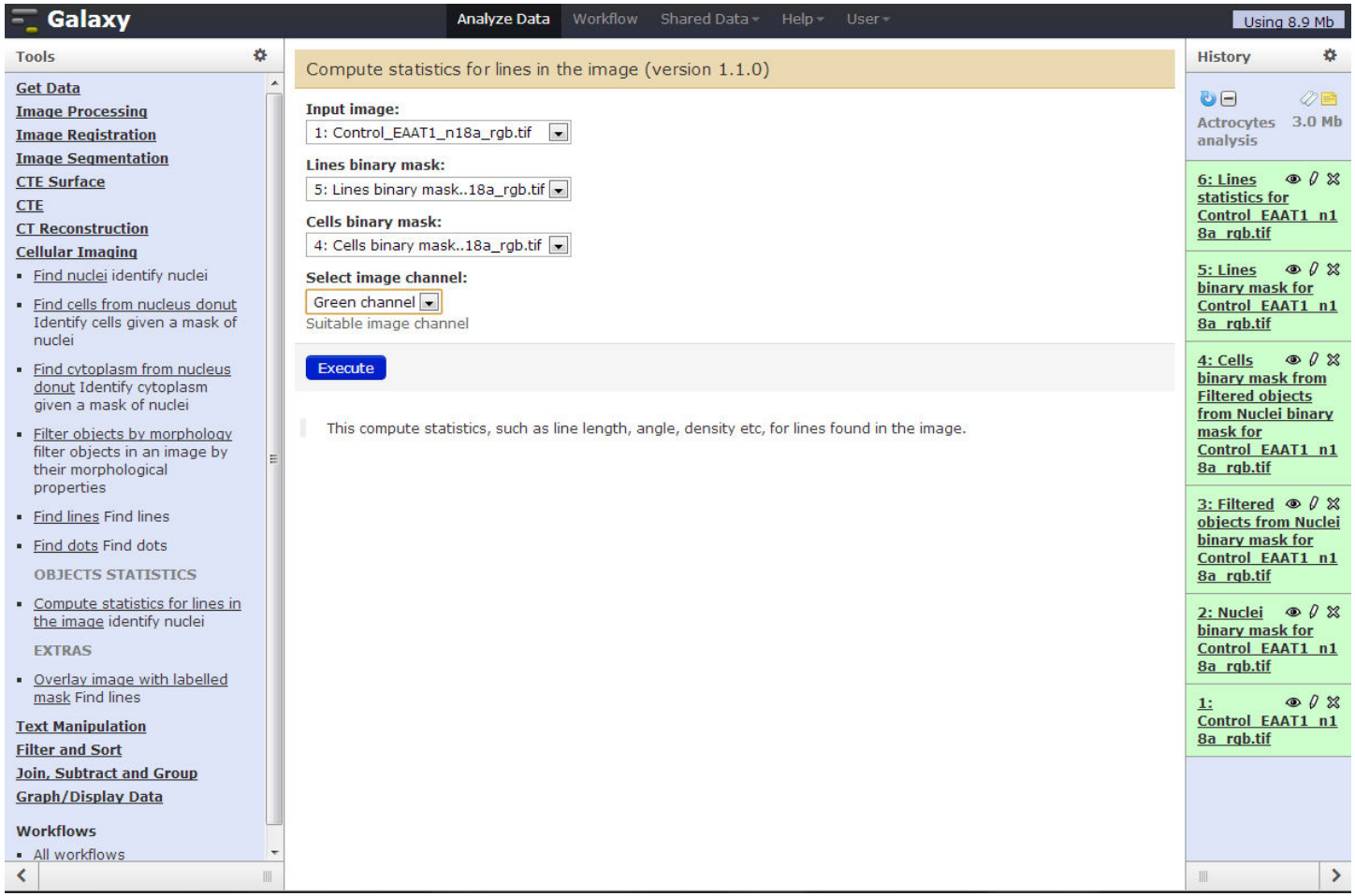
Building Astrocytes analysis workflow

Output: lines binary mask



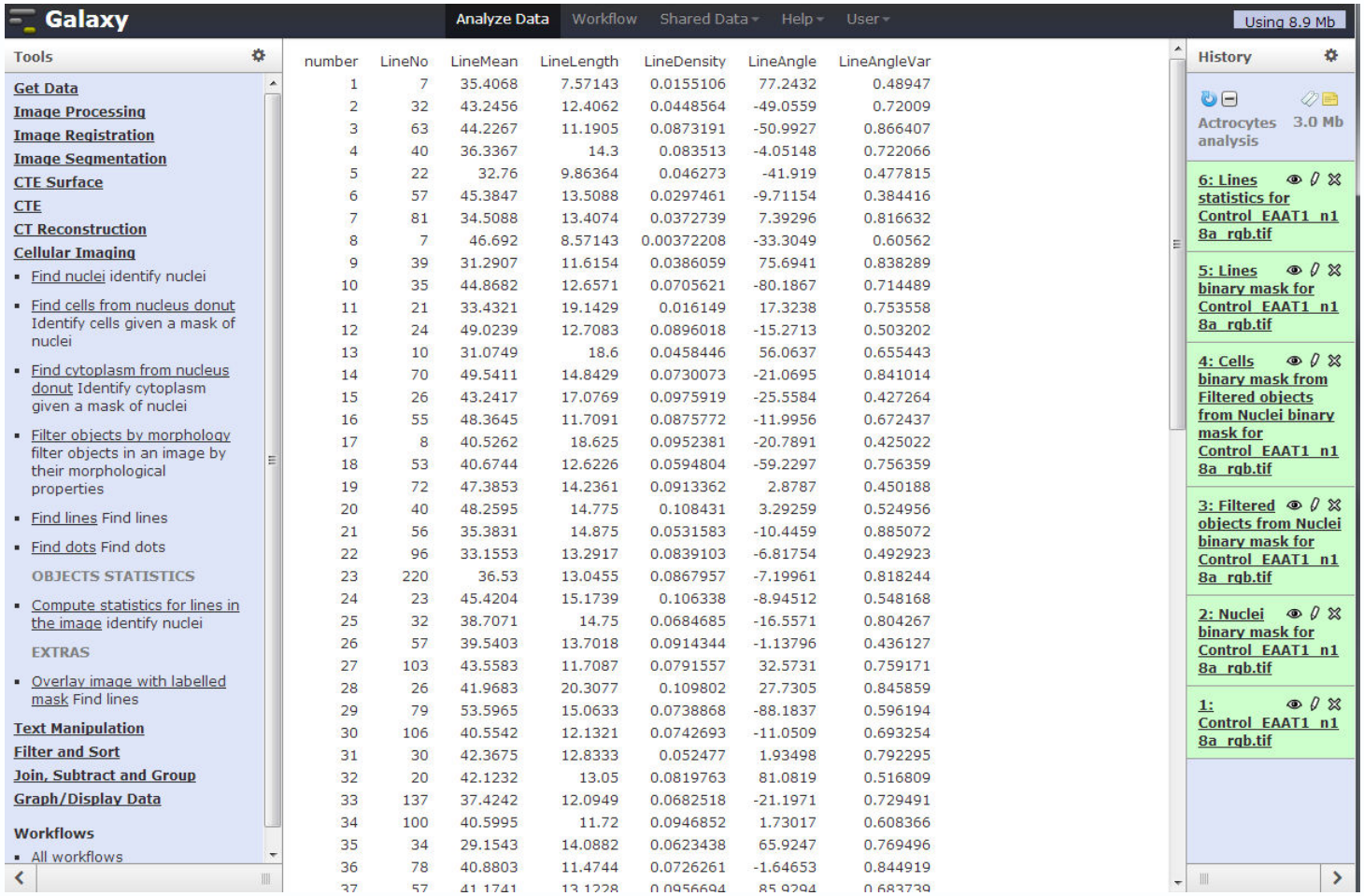
Building Astrocytes analysis workflow

Last step. Compute statistics on lines per each cell



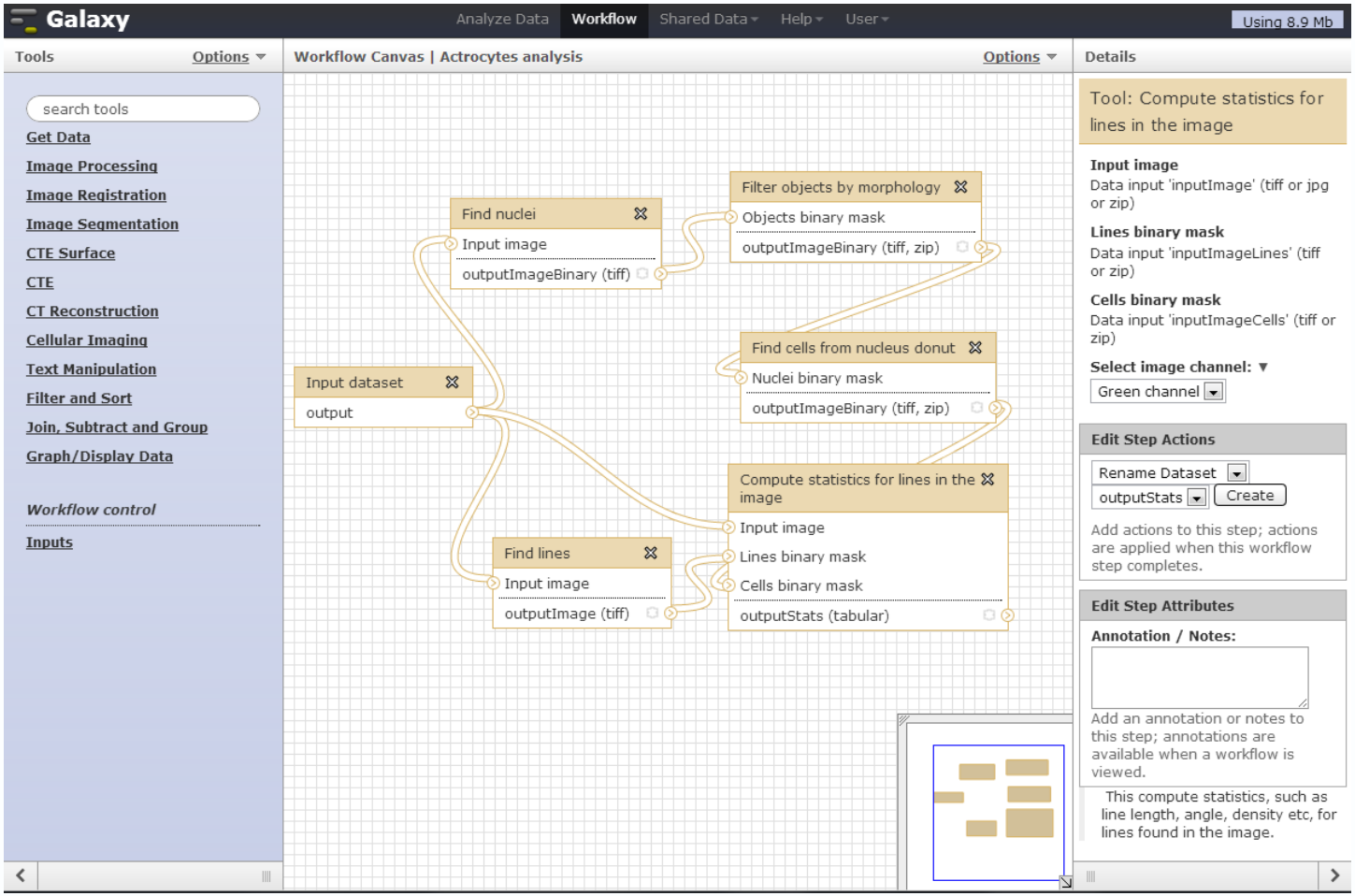
Building Actrocytes analysis workflow

Output: lines statistics

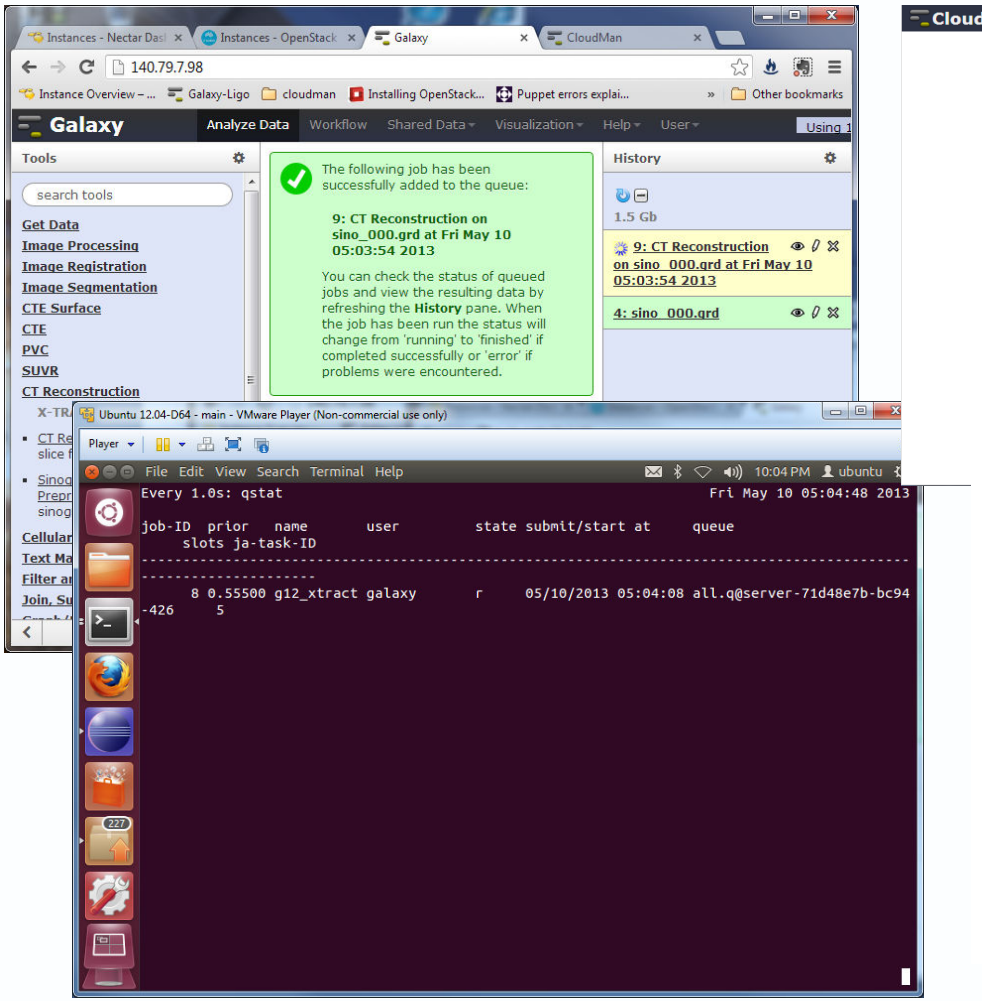


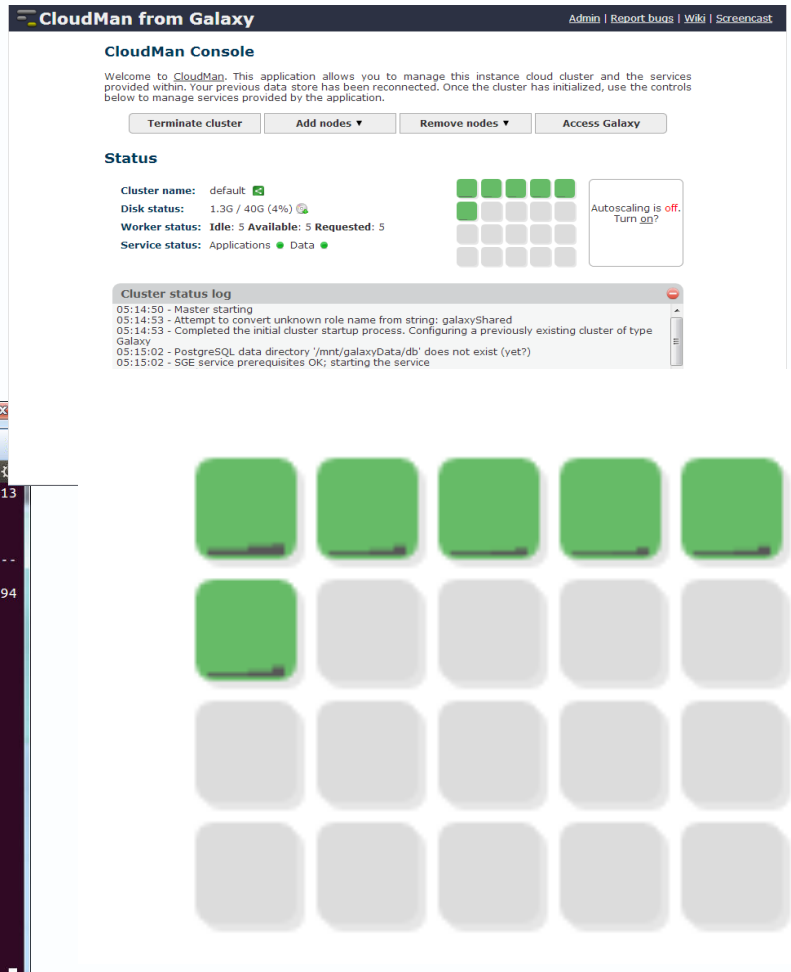
Complete Astrocytes analysis workflow

Astrocytes analysis workflow can be reused with other image data



NeCTAR Imaging Toolkit Production Deploy





Where are we …

So far:

- Migrated all the packages to Linux platform
- Defined domain specific data types and developed most of the tools
- Small scale cloud deployments for pilot users
- Prepared training materials for the users
- Gathered initial feedback from the user communities

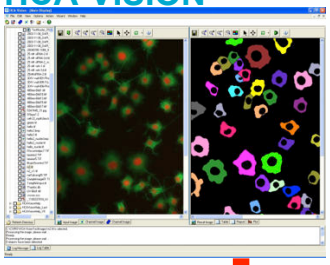
Next steps:

- Full scale deployment on the Research Cloud
- Bringing more users on and ongoing improvement of the platform
- Create a ToolShed and refactor the toolkit
- Develop and share workflows

Cloud-Based Image Analysis and Processing Toolbox

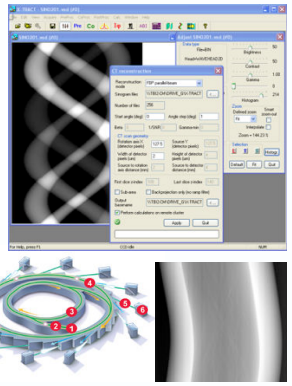
http://cloudimaging.blogspot.com.au

HCA-VISION

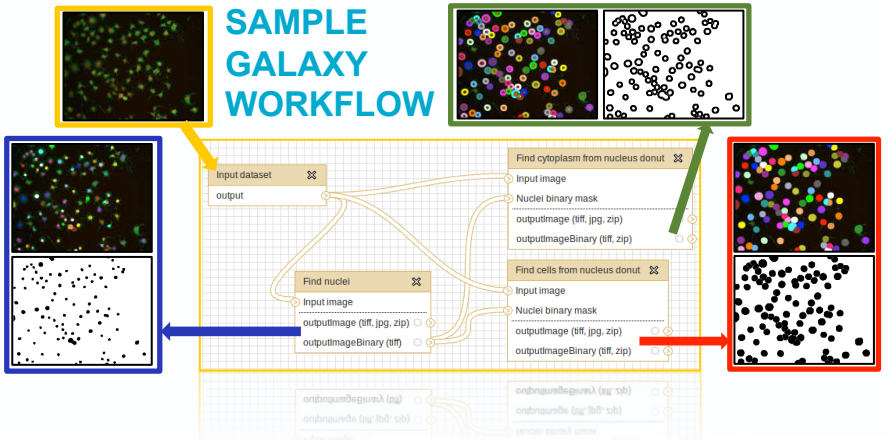


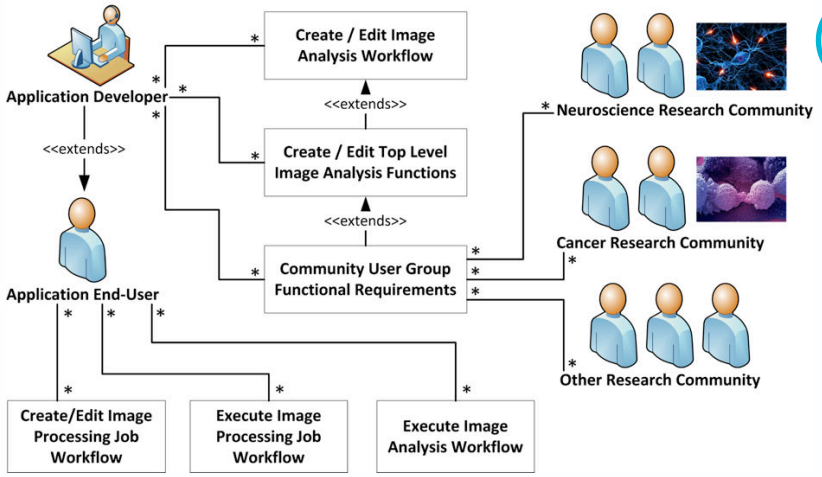
MILXVIEW

X-TRACT



SAMPLE GALAXY WORKFLOW





PROJECT TEAM

Thank you

CMIS / CSS TCP
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w www.csiro.au/cmis

HCA-Vision High Level Functionality

ID	FUNCTION	SHORT DESCRIPTION
H.01	Detect nuclei	Detect nuclei in a 2D microscope image
H.02	Detect nuclei from cytoplasm holes	Detect nuclei from absence of stain of cytoplasm
H.03	Detect cells with nuclei	Detect cells using nucleus image as a mask
H.04	Detect cells without nuclei	Detect cells without using nucleus image as a mask
H.05	Detect neurons with nuclei	Detect neurons from a neurite outgrowth image using nucleus image as a mask
H.06	Detect neurons without nuclei	Detect neurons from a neurite outgrowth image without using nucleus image as a mask
H.07	De-clump touching objects	Separate any touching objects in an image, such as touching nuclei or cells
H.08	Label objects	Label objects such nuclei or cells in a binary image
H.09	Get object stats	Retrieve statistical features of individual objects in a segmented image, including area, perimeter, origin, width and height of the bounding box, coordinate of the centroid, major and minor axis of best fit ellipse, approximate of area of convex hull etc.
H.10	Detect cell from nucleus donuts	Get an anisotropic doughnut which is a region around a cell nucleus that is not uniformly thick. The extension of the doughnut is larger along the major axis of the nucleus than perpendicular to it.
H.11	Detect dots	Detect dots in a 2D image or a cell
H.12	Detect lines	Detect line structures in a 2D image or a cell
H.13	Get dot stats	Retrieve statistical features of the detected dots, including area, perimeter etc.
H.14	Get line stats	Retrieve the statistical features of detected line structures
H.15	Cell Scoring	Count negative and positive cells, measure integrated and average intensity of negative and positive cells.

IDs H.xx – Application area: cell features of microscopy images

X-TRACT High Level Functionality

ID	FUNCTION	SHORT DESCRIPTION
XP.01	Sinogram creation	X-ray projection data must first be converted into sinograms before CT reconstruction can be carried out. Each sinogram contains data from a single row of detector pixels for each illuminating angles. This data is sufficient for the reconstruction of a single axial slice (at least, in parallel-beam geometry).
XP.02	Ring artefact removal	Ring artefacts are caused by imperfect detector pixel elements as well as by defects or impurities in the scintillator crystals. Ring artefacts can be reduced by applying various image processing techniques on sinograms or reconstructed images.
XP.03	Dark current subtraction	Dark current subtraction compensates for the readout noise, ADC offset, and dark current in the detector. The dark current images are collected before and/or after CT measurements with no radiation applied and with the same integration time as the one used during the measurements. The dark current image is subtracted from each CT projection.
XP.04	Flat field correction	Flat-field images are obtained under the same conditions as the actual CT projections, but without the sample in the beam. They allow one to correct the CT projections for the unevenness of the X-ray illumination.
XP.05	Positional drift correction	The function is used for correction of transverse drift between related experimental images. Image drift is assessed by cross-correlating pairs of images.
XP.06	Data normalisation	Data normalisation Including normalisation to a user-defined region
XP.07	TIE-based phase extraction	The TIE algorithm allows the recovery of the optical phase of an electromagnetic wave (e.g. an X-ray beam) from a single near-field in-line image by solving the Transport of Intensity equation under the assumption that the phase shift and absorption distributions are proportional to each other. This method is usually applied in propagation-based in-line CT imaging (PCI-CT).
XCT.01	FBP CT reconstruction	Filtered back-projection (FBP) parallel-beam CT reconstruction
XCT.02	FDK CT reconstruction	Feldkamp-Davis-Kress (FDK) cone-beam CT reconstruction
XCT.03	Centre of rotation	Automated calculation of the centre of sample rotation in a CT scan from experimental X-ray projections, sinograms or reconstructed axial slices.
XCT.04	CT Reconstruction Filters	The choice of available CT reconstruction filters will include at least the Liner-Ramp, Shepp-Logan, Cosine, Hamming and Hann filters.
XCT.05	ROI reconstruction	This option enables the user to select a subset of axial slices to be reconstructed and/or limit the reconstruction area to a user-defined rectangular subarea of the axial slice. The option reduces the reconstruction time and the size of the output data.

IDs XP.xx – Application area: data processing functions
IDs XCP.xx – Application area: CT reconstruction functions

MILXView High Level Functionality

ID	FUNCTION	SHORT DESCRIPTION
MC.01	Atlas registration	Align an atlas image to a target image
MC.02	Segmentation	Segment the MRI into grey matter (GM), white matter (WM) and cerebrospinal fluid (CSF)
MC.03	Bias Field Correction	Estimate and remove the noise on the image
MC.04	Partial Volume estimation	Quantify the amount of partial voluming inside each voxel
MC.05	Topology Correction	Create the topology of the brain to ensure that it is genus zero
MC.06	Thickness Estimation	Compute the thickness of the cortex for each Grey matter voxel
MS.01	Cortical surface extraction	Extract a 3D mesh from the brain segmentation
MS.02	Topological correction	Remove holes and handles from the mesh
MS.03	Biomarker mapping on cortical surface	Mapping of various values on the mesh i.e. thickness, PET values, MR intensity etc ...
MS.04	Surface registration	Align the meshes of any given subject to a template to obtain a correspondence across subjects
MS.05	Transfer of biomarkers on template surface	Map all the values from all subjects to a common space where they can be compared
MP.01	PVC Registration	Registration of the PET image to its corresponding MRI
MP.02	Segmentation	Segmentation of the MRI into GM, WM, and CSF
MP.03	Partial Volume correction (PVC)	Correction for spill in and spill over of the PET image using the MRI segmentation
MR.01	SUVR Registration	Registration of the PET image to its corresponding MRI
MR.02	Segmentation	Segmentation of the MRI into GM, WM and CSF
MR.03	Atlas Registration	Registration of an atlas to the MRI to define a reference region on the MRI
MR.04	Image Normalisation	Normalising the PET intensity with the intensity of the reference region

IDs MC.xx – Application area: neuro-imaging analysis, cortical thickness estimation (CTE)
IDs MS.xx – Application area: neuro-imaging analysis, CTE surface
IDs MP.xx – Application area: neuro PET analysis, PET PVC
IDs MR.xx – Application area: neuro PET analysis, PET SUVR