



Galaxy as an Integration and Workflow Platform

for Bio-medical Image Analysis and Image Processing Toolkit

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COMPUTATIONAL SIMULATION SCIENCES TCP

www.csiro.au

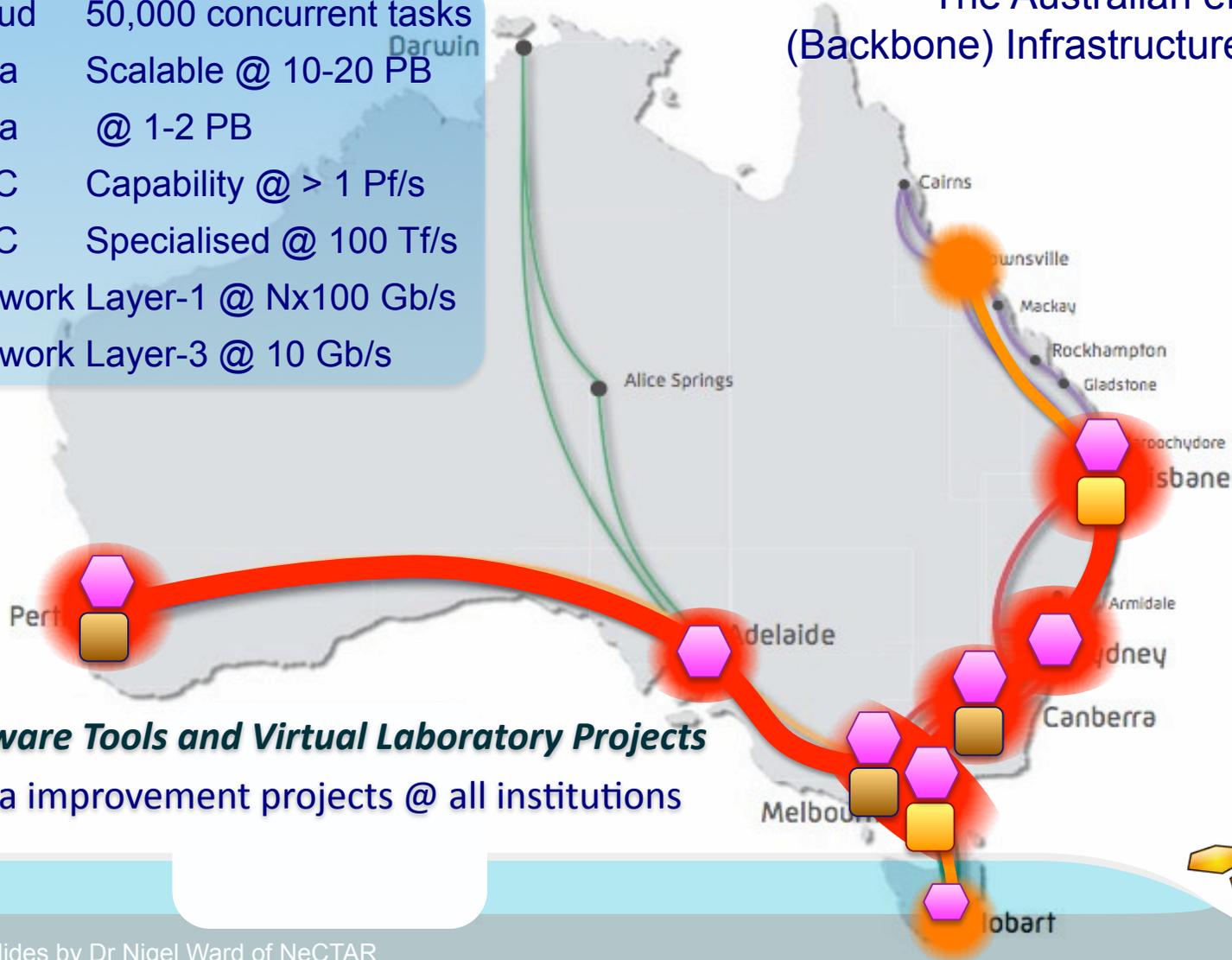
<https://www.nectar.org.au/cloud-based-image-analysis-and-processing-toolbox>
<http://cloudimaging.blogspot.com.au/p/about-project.html>



NeCTAR Research Cloud...

- Cloud 50,000 concurrent tasks
- Data Scalable @ 10-20 PB
- Data @ 1-2 PB
- HPC Capability @ > 1 Pf/s
- HPC Specialised @ 100 Tf/s
- Network Layer-1 @ Nx100 Gb/s
- Network Layer-3 @ 10 Gb/s

The Australian eResearch
(Backbone) Infrastructure @ 2013



40 Software Tools and Virtual Laboratory Projects
250 Data improvement projects @ all institutions



NeCTAR is funding four programs

Research software



Virtual laboratories



eResearch Tools

Computational platforms



Research Cloud



National Server Program

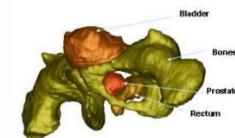
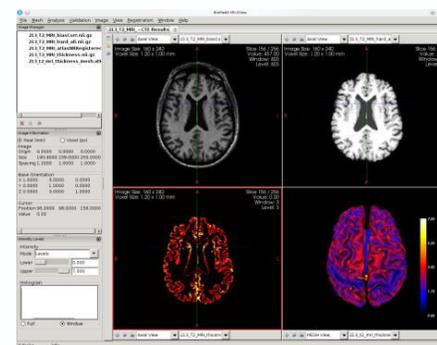
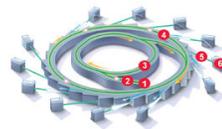
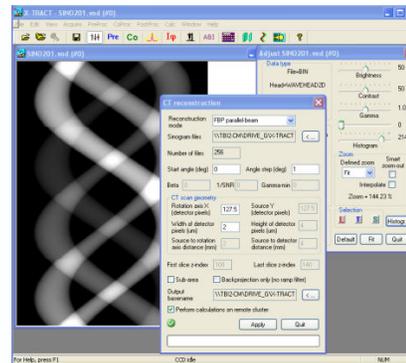
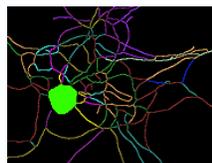
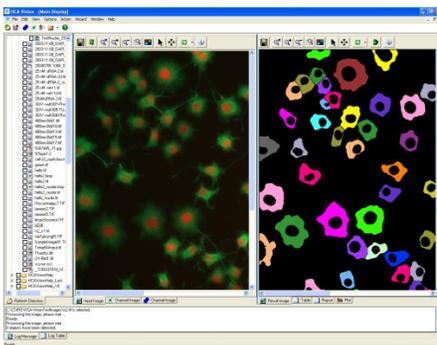
Project Vision

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.

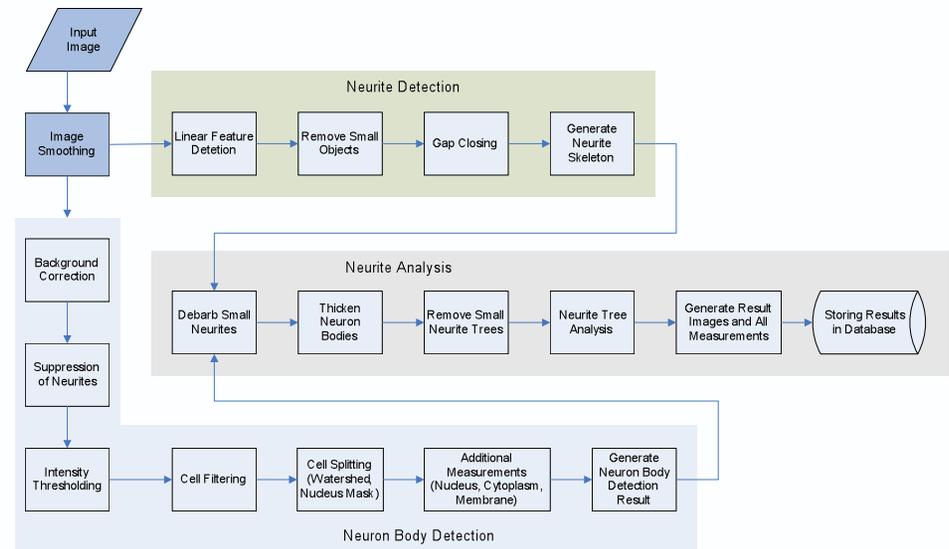
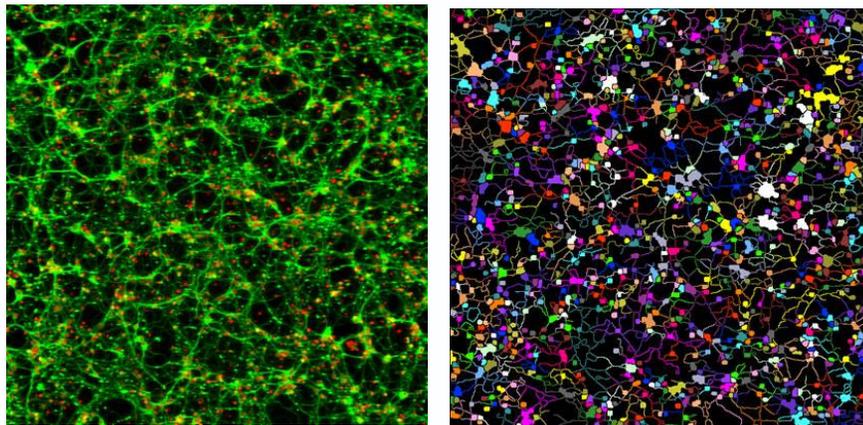


Figure: Neurite Analysis (a) input image; (b) resulted image; (c) diagram of the algorithm.

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.

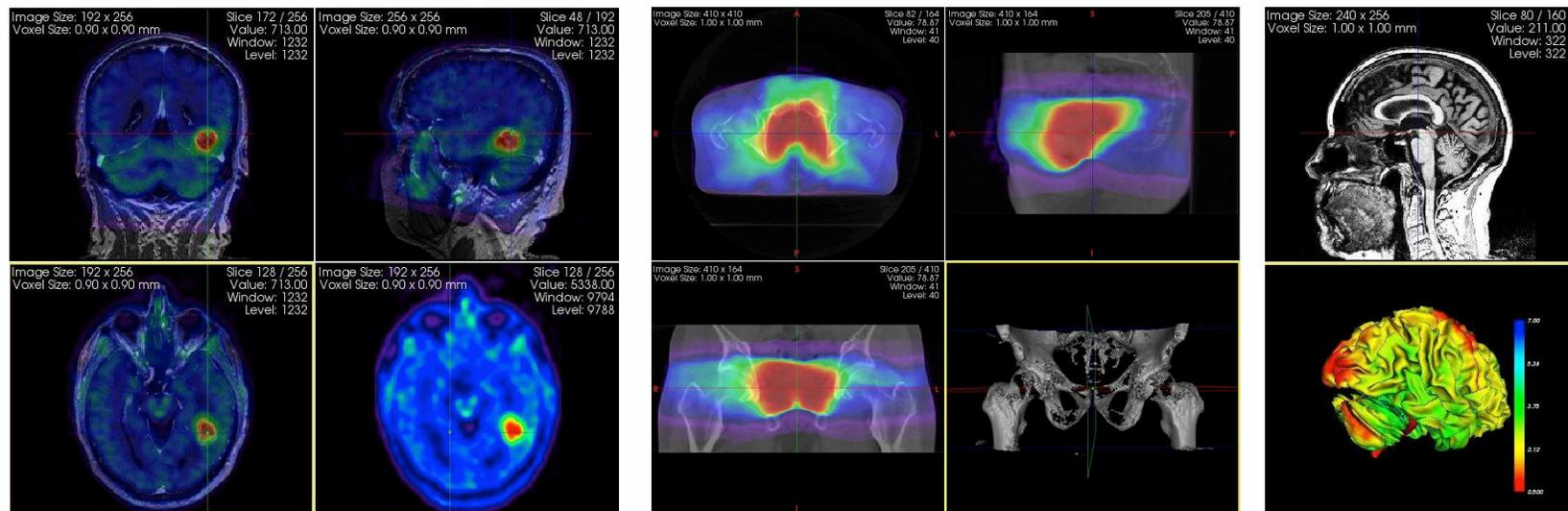
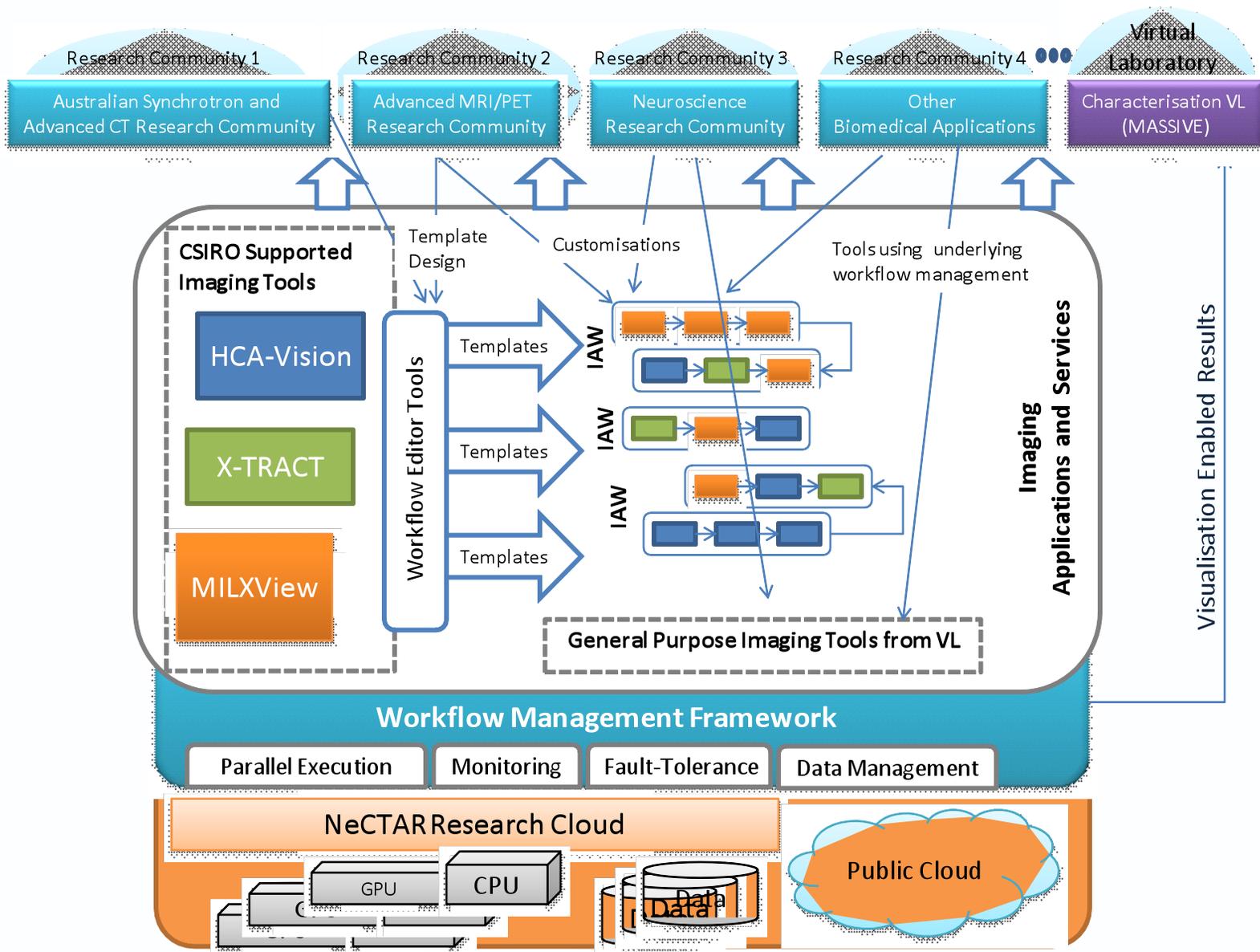
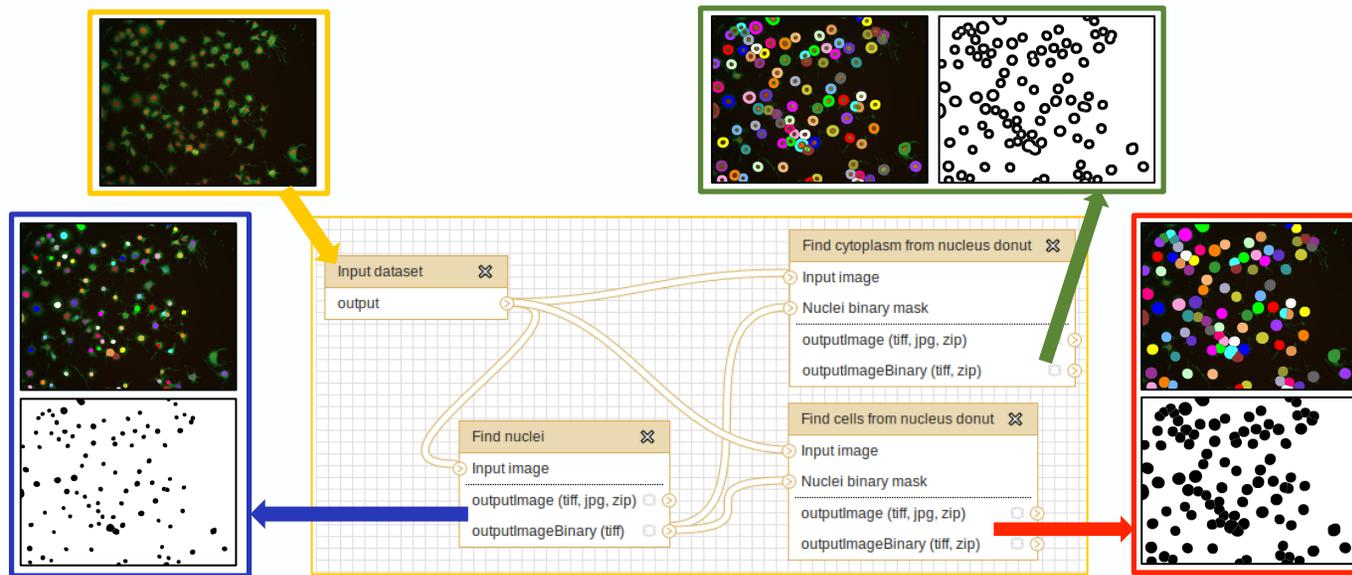


Figure: (a) Brain tumor - PET scan and MRI overlaid; (b) CT scan of a prostate of a patient overlaid with radiation dose; (c) Generated 3D view of a brain allowing study of atrophy pattern characteristics of diseases such as Alzheimer's disease.



Glue = Galaxy



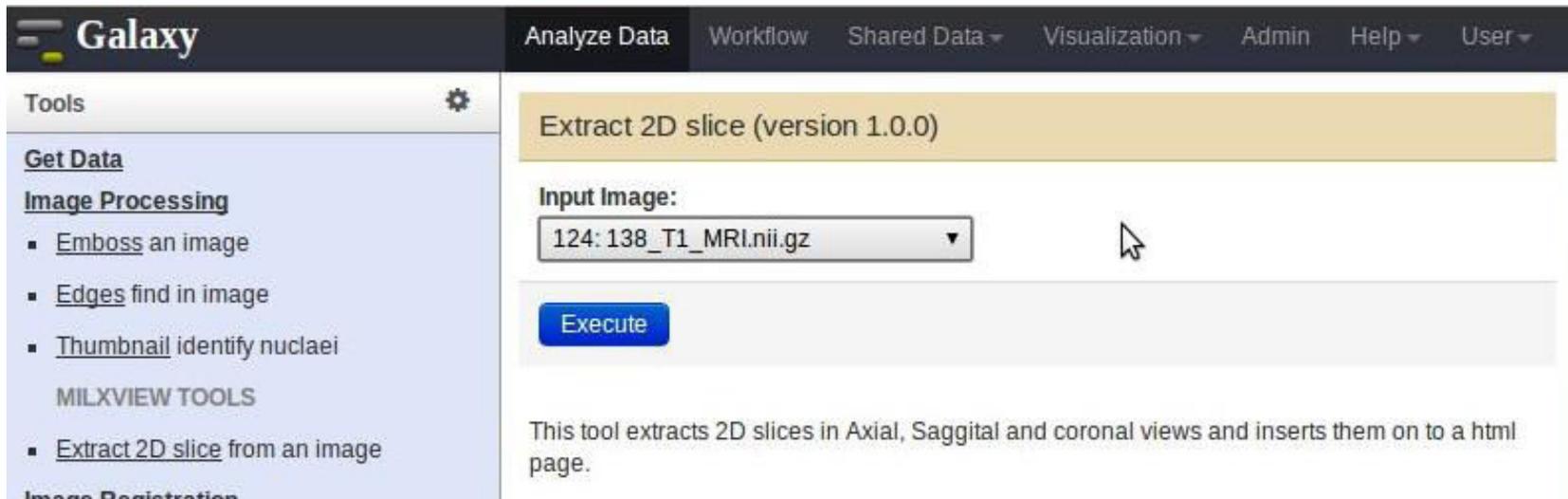
- Tools**
- Thumbnail identify nuclei
 - MILXVIEW TOOLS**
 - Extract 2D slice from an image
 - Image Registration**
 - Register using affine transforms on two images
 - Register using rigid transforms on two images
 - Image Segmentation**
 - Segmentation using wm gm and csf
 - CTE Surface**
 - Reorient 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



The screenshot shows the Galaxy web interface. The top navigation bar includes 'Galaxy', 'Analyze Data', 'Workflow', 'Shared Data', 'Visualization', 'Admin', 'Help', and 'User'. The left sidebar lists tools under 'Tools', 'Get Data', 'Image Processing', and 'Image Registration'. The 'Image Processing' section is expanded, showing 'Emboss an image', 'Edges find in image', 'Thumbnail identify nuclei', and 'Extract 2D slice from an image'. The 'Extract 2D slice from an image' tool is selected, and its configuration panel is shown. The tool title is 'Extract 2D slice (version 1.0.0)'. The 'Input Image' field is a dropdown menu with the value '124: 138_T1_MRI.nii.gz'. Below the input field is a blue 'Execute' button. A description below the button reads: 'This tool extracts 2D slices in Axial, Saggital and coronal views and inserts them on to a html page.'

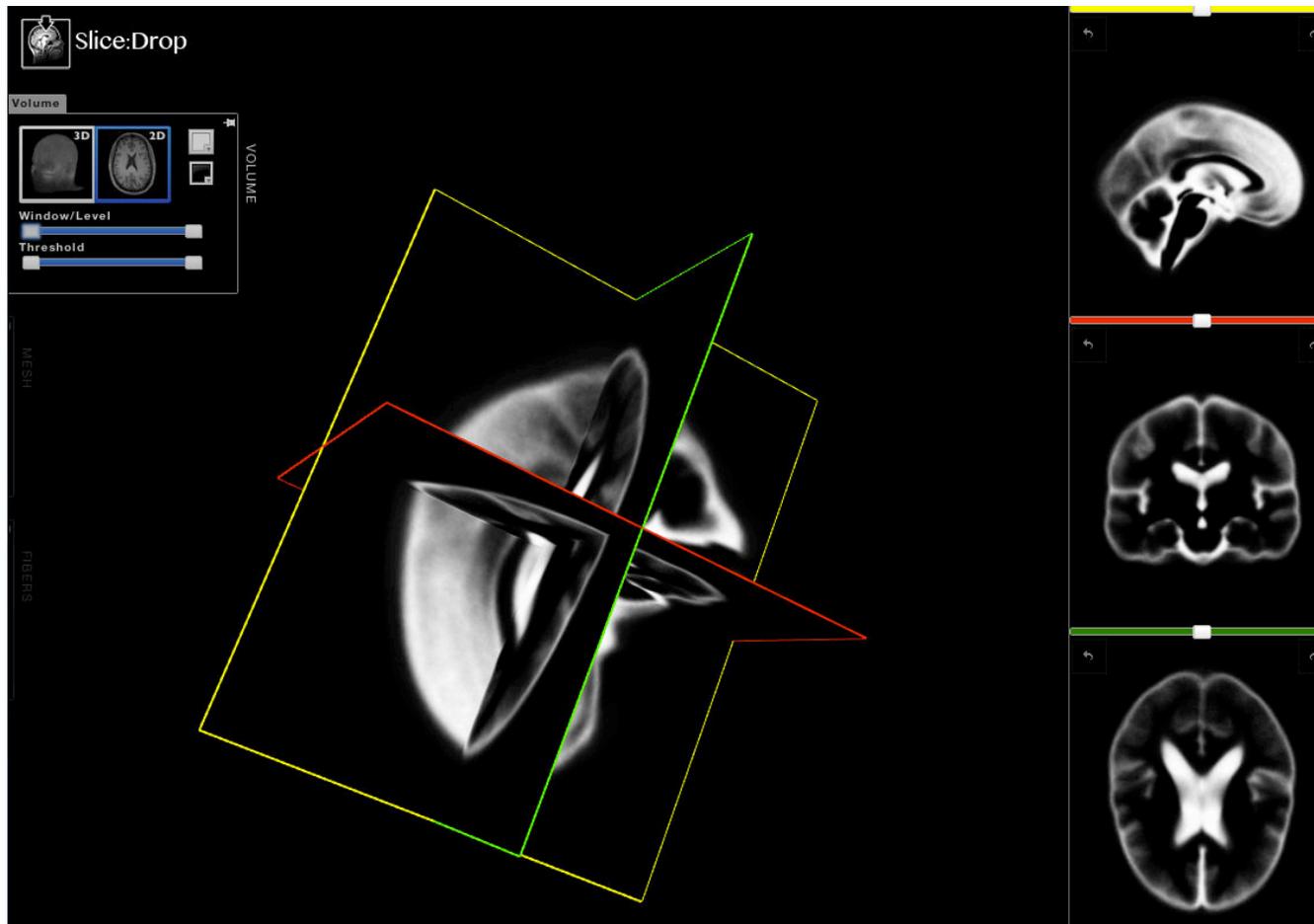
It takes few seconds and a HTML is created to show the user the 2D slices and also lets the user download the images

The screenshot displays the Galaxy web interface. The main content area is titled "Extracted 2D Slices" and shows "Generated 3 PNG output files". Below this, there are three direct links to output files: "Axial_1_output.png", "Coronal_1_output.png", and "Sagittal_1_output.png". The interface also displays two sets of MRI slices: "Axial View" and "Coronal View". The "Axial View" shows three axial slices of a brain, and the "Coronal View" shows three coronal slices. On the right side, there is a "History" panel showing a list of jobs. The top job is "133: Extract 2D slice on 138 T1 MRI.nii.gz at Tue 13:23:48 2012", which is highlighted with a tooltip that says "Display data". Other jobs in the history include "132: Register using affine transforms on 166 T1 MRI 25p.nii.gz and 138 T1 MRI 25p.nii.gz at Tue Nov 6 10:57:44 2012", "131: Create TRSF file on 166 T1 MRI 25p.nii.gz and 138 T1 MRI 25p.nii.gz at Tue Nov 6 10:57:43 2012", "128: Extract 2D slice on aal.nii.gz at Tue Nov 6 10:53:24 2012", "127: Full example pipeline on data 126 at Tue Nov 6 10:48:43 2012", "126: aal.nii.gz", "125: Extract 2D slice on 138 T1 MRI.nii.gz at Tue Nov 6 10:37:55 2012", "124: 138 T1 MRI.nii.gz", "123: 138 T1 MRI 25p.nii.gz", "122: 166 T1 MRI 25p.nii.gz", and "121: CTE create raw data on data 113, data 109, and data 56 at Tue Nov 6 06:40:28 2012". The bottom status bar shows the URL: "140.253.78.44/galaxy/datasets/b90bd8c6882c06dc/display/?preview=True".



Visualisation

WebGL based, Slice:Drop



Cellular imaging in Galaxy

The screenshot shows the Galaxy web interface. The top navigation bar includes 'Analyze Data', 'Workflow', 'Shared Data', 'Help', and 'User', with a 'Using 8.9 Mb' indicator. The left sidebar, titled 'Tools', lists various categories: 'Get Data', 'Image Processing', 'Image Registration', 'Image Segmentation', 'CTE Surface', 'CTE', 'CT Reconstruction', 'Cellular Imaging', 'Text Manipulation', 'Filter and Sort', 'Join, Subtract and Group', 'Graph/Display Data', and 'Workflows'. Under 'Cellular Imaging', several tools are listed with brief descriptions: '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), 'Compute statistics for lines in the image' (identify nuclei), and 'Overlay image with labelled mask' (Find lines). The main panel displays a fluorescence microscopy image of cells with blue nuclei and green cytoplasm. The right sidebar, titled 'History', shows a single entry: '1: Control EAAT1 n1 8a_rgb.tif'.



Building Astrocytes analysis workflow

Step 1. Find nuclei

The screenshot displays the Galaxy web interface with the 'Find nuclei (version 1.1.0)' tool selected. The interface is divided into several sections:

- Tools Panel (Left):** Lists various tool categories such as 'Get Data', 'Image Processing', 'Image Registration', 'Image Segmentation', 'CTE Surface', 'CTE', 'CT Reconstruction', 'Cellular Imaging', 'OBJECTS STATISTICS', 'EXTRAS', 'Text Manipulation', 'Filter and Sort', 'Join, Subtract and Group', 'Graph/Display Data', and 'Workflows'. The 'Find nuclei' tool is highlighted under 'Cellular Imaging'.
- Tool Configuration Panel (Center):** Contains the following settings:
 - Input image:** 2: Nuclei binary mas..18a_rgb.tif
 - Nucleoli radius:** 15
 - Largest nuclei radius:** 121
 - Smoothing size:** 1
 - Threshold sensitivity:** 0,5
 - Radius of holes:** 15
 - Split objects:** (checked)
 - Select image channel:** Red channel
- History Panel (Right):** Shows a list of previous jobs. The current job is '2: Nuclei binary mask for Control EAAT1 n1 8a_rgb.tif' and the previous job is '1: Control EAAT1 n1 8a_rgb.tif'.

An 'Execute' button is visible at the bottom of the tool configuration panel. Below the button, a note states: 'This component finds nuclei in an image of cells'.



Building Actrocytes analysis workflow

Output: nuclei binary mask

The screenshot displays the Galaxy web interface. The central panel shows a binary mask of nuclei, represented as black shapes on a white background. The left sidebar contains a 'Tools' panel with various categories: 'Get Data', 'Image Processing', 'Image Registration', 'Image Segmentation', 'CTE Surface', 'CTE', 'CT Reconstruction', 'Cellular Imaging', 'OBJECTS STATISTICS', 'EXTRAS', 'Text Manipulation', and 'Workflows'. The right sidebar shows the 'History' panel, which lists the workflow steps: '1: Control EAAT1 n1 8a_rgb.tif' and '2: Nuclei binary mask for Control EAAT1 n1 8a_rgb.tif'. The '2: Nuclei binary mask for Control EAAT1 n1 8a_rgb.tif' step is highlighted in green, indicating it is the current step. The 'Info' section for this step shows: '2.3 Kb', 'format: tiff', 'database: 2', and 'Starting workspace-batch on Wed Nov 14 03:51:42 2012'. The 'Image in tiff format' button is visible below the history panel.



Building Astrocytes analysis workflow

Step 2. Find lines

The screenshot displays the Galaxy web interface with the 'Find lines (version 1.1.0)' tool selected. The interface includes a top navigation bar with 'Galaxy', 'Analyze Data', 'Workflow', 'Shared Data', 'Help', and 'User'. A 'Using 8.9 Mb' indicator is visible in the top right. On the left, a 'Tools' sidebar lists various categories like 'Get Data', 'Image Processing', and 'Cellular Imaging'. The main panel shows the tool's configuration options: 'Input image' (Control_EAAT1_n18a_rgb.tif), 'Line length' (9), 'Ignore objects smaller than' (5), 'Line sensitivity' (2.06), 'Smoothing size' (5), 'Link Distance' (7), 'Link quality' (50), and 'Ignore lines with intensity lower than' (10.0). The 'Select image channel' is set to 'Green channel'. An 'Execute' button is at the bottom of the configuration area. On the right, a 'History' panel shows a list of jobs, including '2: Nuclei binary mask for Control EAAT1 n1 8a_rgb.tif' and '1: Control EAAT1 n1 8a_rgb.tif'. A status bar at the bottom of the tool panel reads 'This component finds lines in an image'.



Building Astrocytes analysis workflow

Output: lines binary mask

The screenshot shows the Galaxy web interface. The main panel displays a binary mask of astrocyte lines. The left sidebar lists tools under categories like 'Get Data', 'Image Processing', 'Image Registration', 'Image Segmentation', 'CTE Surface', 'CTE', 'CT Reconstruction', 'Cellular Imaging', 'OBJECTS STATISTICS', 'Text Manipulation', and 'Workflows'. The right sidebar shows the history of the workflow, including steps like 'Adding plugin Data analysis version 2.26.1' and 'Adding plugin Mesh version 2.26.1'.



Building Astrocytes analysis workflow

Last step. Compute statistics on lines per each cell

The screenshot displays the Galaxy web interface. The main panel shows the configuration for the tool 'Compute statistics for lines in the image (version 1.1.0)'. The configuration includes:

- Input image:** 1: Control_EAAT1_n18a_rgb.tif
- Lines binary mask:** 5: Lines binary mask..18a_rgb.tif
- Cells binary mask:** 4: Cells binary mask..18a_rgb.tif
- Select image channel:** Green channel (Suitable image channel)

An 'Execute' button is visible below the configuration. Below the button, a text box contains the instruction: 'This compute statistics, such as line length, angle, density etc, for lines found in the image.'

The right-hand side of the interface shows the 'History' panel, which lists the workflow steps:

- 1: Control_EAAT1_n18a_rgb.tif
- 2: Nuclei binary mask for Control EAAT1 n1 8a_rgb.tif
- 3: Filtered objects from Nuclei binary mask for Control EAAT1 n1 8a_rgb.tif
- 4: Cells binary mask from Filtered objects from Nuclei binary mask for Control EAAT1 n1 8a_rgb.tif
- 5: Lines binary mask for Control EAAT1 n1 8a_rgb.tif
- 6: Lines statistics for Control EAAT1 n1 8a_rgb.tif

The top of the interface shows the 'Galaxy' logo, navigation tabs for 'Analyze Data', 'Workflow', 'Shared Data', 'Help', and 'User', and a memory usage indicator 'Using 8.9 Mb'.



Building Actrocytes analysis workflow

Output: lines statistics

number	LineNo	LineMean	LineLength	LineDensity	LineAngle	LineAngleVar
1	7	35.4068	7.57143	0.0155106	77.2432	0.48947
2	32	43.2456	12.4062	0.0448564	-49.0559	0.72009
3	63	44.2267	11.1905	0.0873191	-50.9927	0.866407
4	40	36.3367	14.3	0.083513	-4.05148	0.722066
5	22	32.76	9.86364	0.046273	-41.919	0.477815
6	57	45.3847	13.5088	0.0297461	-9.71154	0.384416
7	81	34.5088	13.4074	0.0372739	7.39296	0.816632
8	7	46.692	8.57143	0.00372208	-33.3049	0.60562
9	39	31.2907	11.6154	0.0386059	75.6941	0.838289
10	35	44.8682	12.6571	0.0705621	-80.1867	0.714489
11	21	33.4321	19.1429	0.016149	17.3238	0.753558
12	24	49.0239	12.7083	0.0896018	-15.2713	0.503202
13	10	31.0749	18.6	0.0458446	56.0637	0.655443
14	70	49.5411	14.8429	0.0730073	-21.0695	0.841014
15	26	43.2417	17.0769	0.0975919	-25.5584	0.427264
16	55	48.3645	11.7091	0.0875772	-11.9956	0.672437
17	8	40.5262	18.625	0.0952381	-20.7891	0.425022
18	53	40.6744	12.6226	0.0594804	-59.2297	0.756359
19	72	47.3853	14.2361	0.0913362	2.8787	0.450188
20	40	48.2595	14.775	0.108431	3.29259	0.524956
21	56	35.3831	14.875	0.0531583	-10.4459	0.885072
22	96	33.1553	13.2917	0.0839103	-6.81754	0.492923
23	220	36.53	13.0455	0.0867957	-7.19961	0.818244
24	23	45.4204	15.1739	0.106338	-8.94512	0.548168
25	32	38.7071	14.75	0.0684685	-16.5571	0.804267
26	57	39.5403	13.7018	0.0914344	-1.13796	0.436127
27	103	43.5583	11.7087	0.0791557	32.5731	0.759171
28	26	41.9683	20.3077	0.109802	27.7305	0.845859
29	79	53.5965	15.0633	0.0738868	-88.1837	0.596194
30	106	40.5542	12.1321	0.0742693	-11.0509	0.693254
31	30	42.3675	12.8333	0.052477	1.93498	0.792295
32	20	42.1232	13.05	0.0819763	81.0819	0.516809
33	137	37.4242	12.0949	0.0682518	-21.1971	0.729491
34	100	40.5995	11.72	0.0946852	1.73017	0.608366
35	34	29.1543	14.0882	0.0623438	65.9247	0.769496
36	78	40.8803	11.4744	0.0726261	-1.64653	0.844919
37	57	41.1741	13.1228	0.0956694	85.0294	0.683739



Complete Astrocytes analysis workflow

Astrocytes analysis workflow can be reused with other image data

The screenshot displays the Galaxy workflow interface. The main window is titled "Workflow Canvas | Astrocytes analysis". The workflow consists of the following steps:

- Input dataset** (output) feeds into **Find nuclei** and **Find lines**.
- Find nuclei** (Input image) outputs **outputImageBinary (tiff)** to **Filter objects by morphology**.
- Filter objects by morphology** (Objects binary mask) outputs **outputImageBinary (tiff, zip)** to **Find cells from nucleus donut**.
- Find cells from nucleus donut** (Nuclei binary mask) outputs **outputImageBinary (tiff, zip)** to **Compute statistics for lines in the image**.
- Find lines** (Input image) outputs **outputImage (tiff)** to **Compute statistics for lines in the image**.
- Compute statistics for lines in the image** (Lines binary mask, Cells binary mask) outputs **outputStats (tabular)**.

The right-hand panel shows the details for the "Compute statistics for lines in the image" tool:

- Tool:** Compute statistics for lines in the image
- Input image:** Data input 'inputImage' (tiff or jpeg or zip)
- Lines binary mask:** Data input 'inputImageLines' (tiff or zip)
- Cells binary mask:** Data input 'inputImageCells' (tiff or zip)
- Select image channel:** Green channel
- Edit Step Actions:** Rename Dataset, outputStats, Create
- Edit Step Attributes:** Annotation / Notes: This compute statistics, such as line length, angle, density etc, for lines found in the image.



NeCTAR Imaging Toolkit Production Deploy

The screenshot shows the Galaxy web interface. A green notification box states: "The following job has been successfully added to the queue: 9: CT Reconstruction on sino_000.grd at Fri May 10 05:03:54 2013". Below this, a history table shows the job details:

Job ID	Name	User	State	Submit/Start At	Queue
9	CT Reconstruction on sino_000.grd	galaxy	r	05/10/2013 05:04:08	all.q@server-71d48e7b-bc94
4	sino_000.grd				

Below the history table, a terminal window shows the output of the `qstat` command:

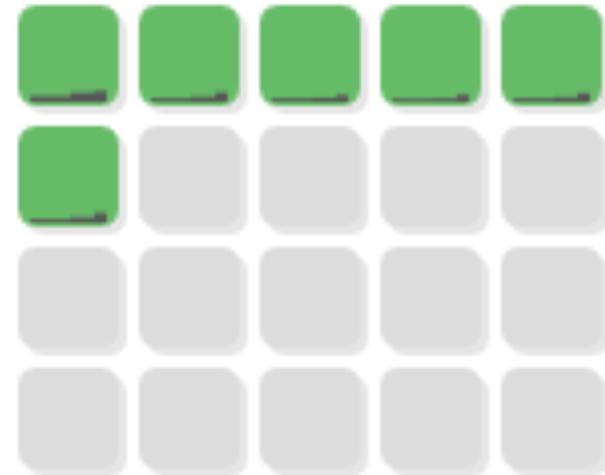
```
Every 1.0s: qstat          Fri May 10 05:04:48 2013
job-ID prior name      user      state submit/start at   queue
-----
      8 0.55500 g12_xtract galaxy    r    05/10/2013 05:04:08 all.q@server-71d48e7b-bc94
-426   5
```

The screenshot shows the CloudMan Console interface. It displays the following information:

- Cluster name:** default
- Disk status:** 1.3G / 40G (4%)
- Worker status:** Idle: 5 Available: 5 Requested: 5
- Service status:** Applications Data

The console also shows a cluster status log:

```
05:14:30 - Master starting
05:14:33 - Attempt to convert unknown role name from string: galaxyShared
05:14:53 - Completed the initial cluster startup process. Configuring a previously existing cluster of type Galaxy
05:15:02 - PostgreSQL data directory '/mnt/galaxyData/db' does not exist (yet?)
05:15:02 - SGE service prerequisites OK; starting the service
```



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



Thank you

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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**