MRC Human Genetics Unit

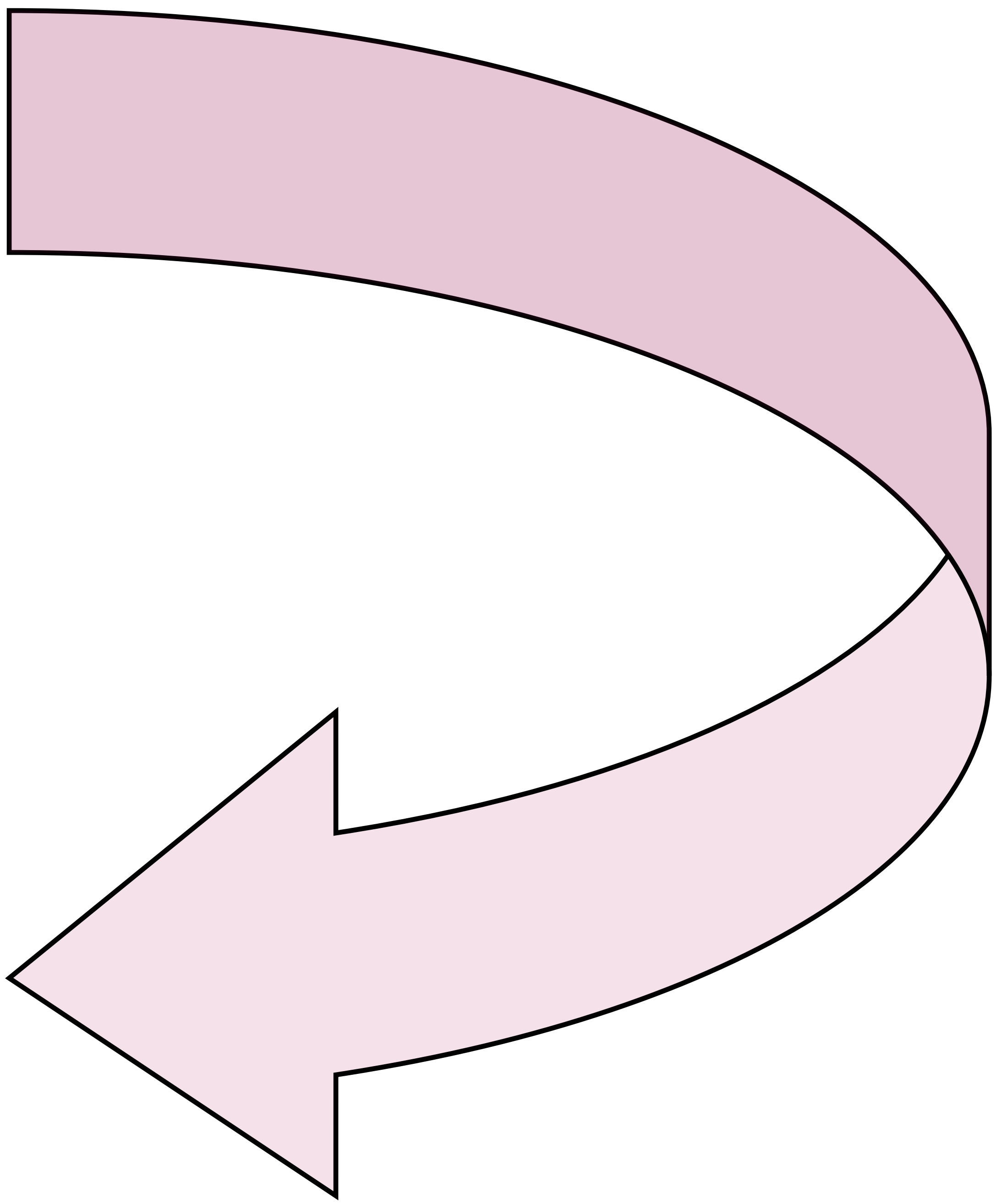
# The Mouse Atlas Database: An Atlas-Based IMage Resource

**Richard Baldock**
*MRC Human Genetics Unit*
*Institute of Genetics and Molecular Medicine*
*Edinburgh, UK*

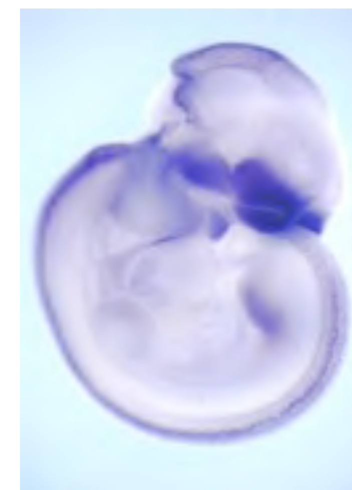
# Credits

- Bill Hill
- Jianguo Rao

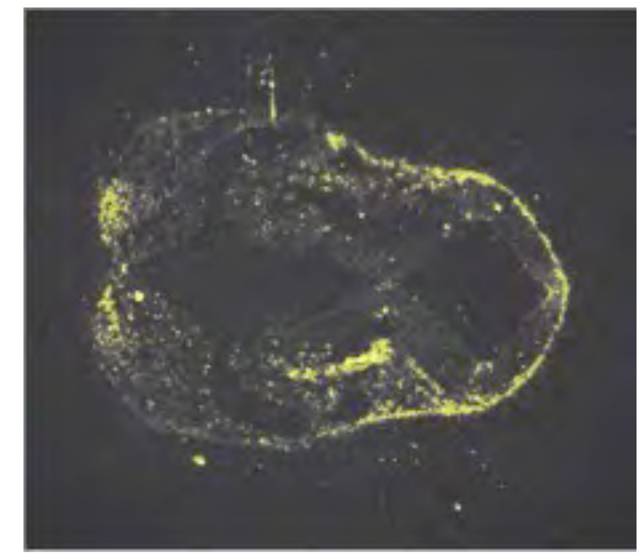
# eMouseAtlas - Development and Gene-Expression

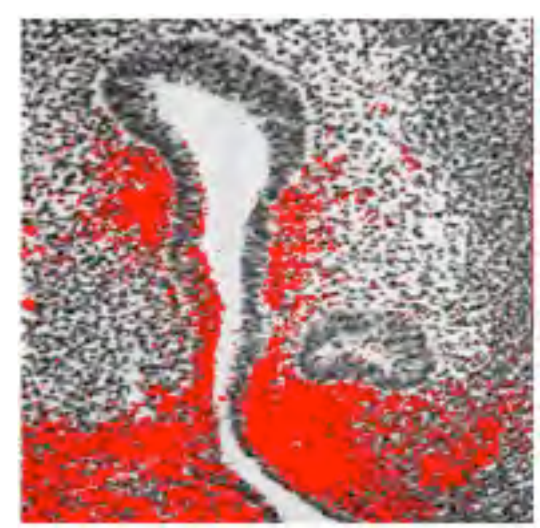


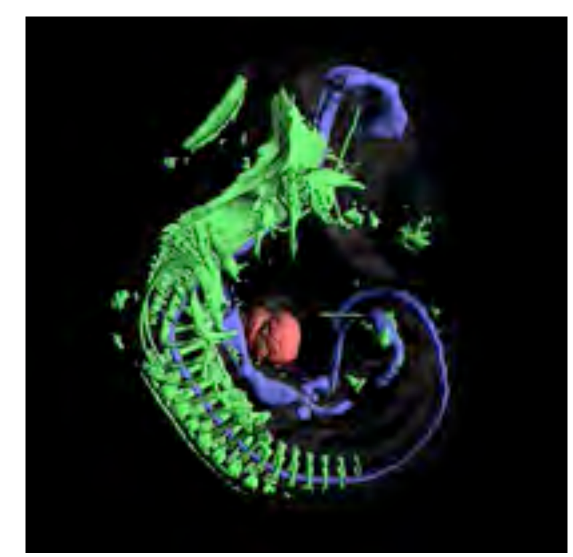
**GENE EXPRESSION**



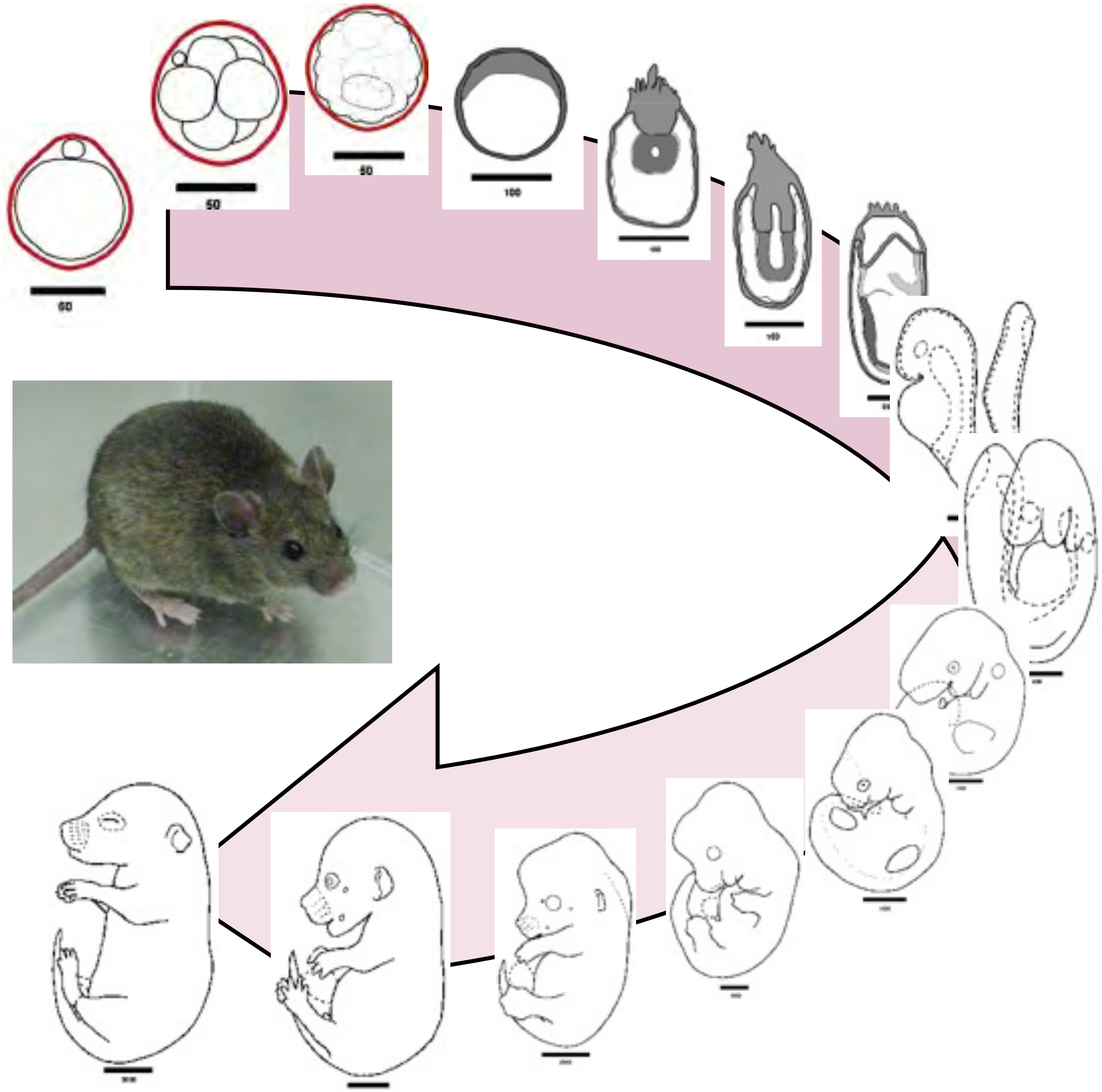
Carol Wicking, University of Queensland



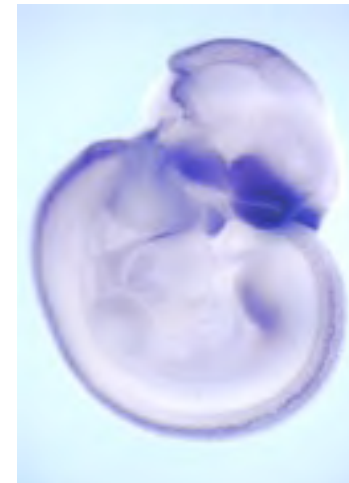




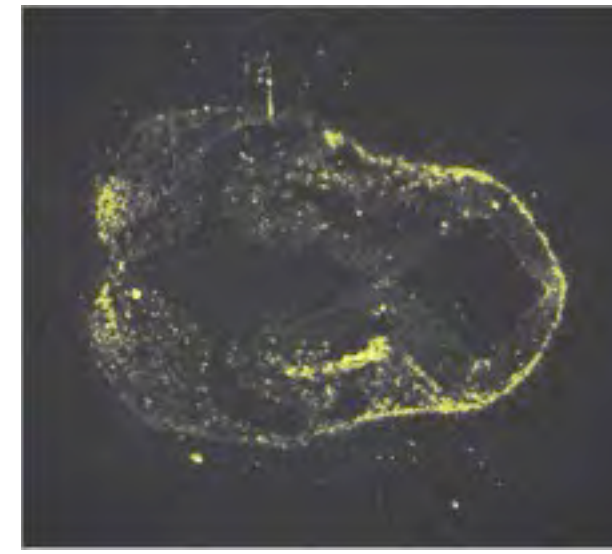
# eMouseAtlas - Development and Gene-Expression

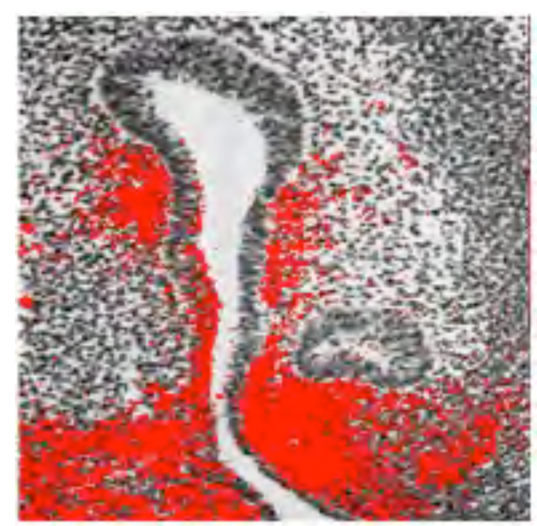


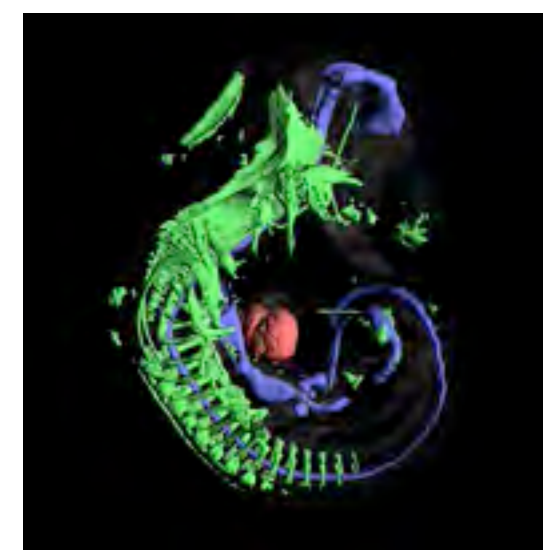
**GENE EXPRESSION**



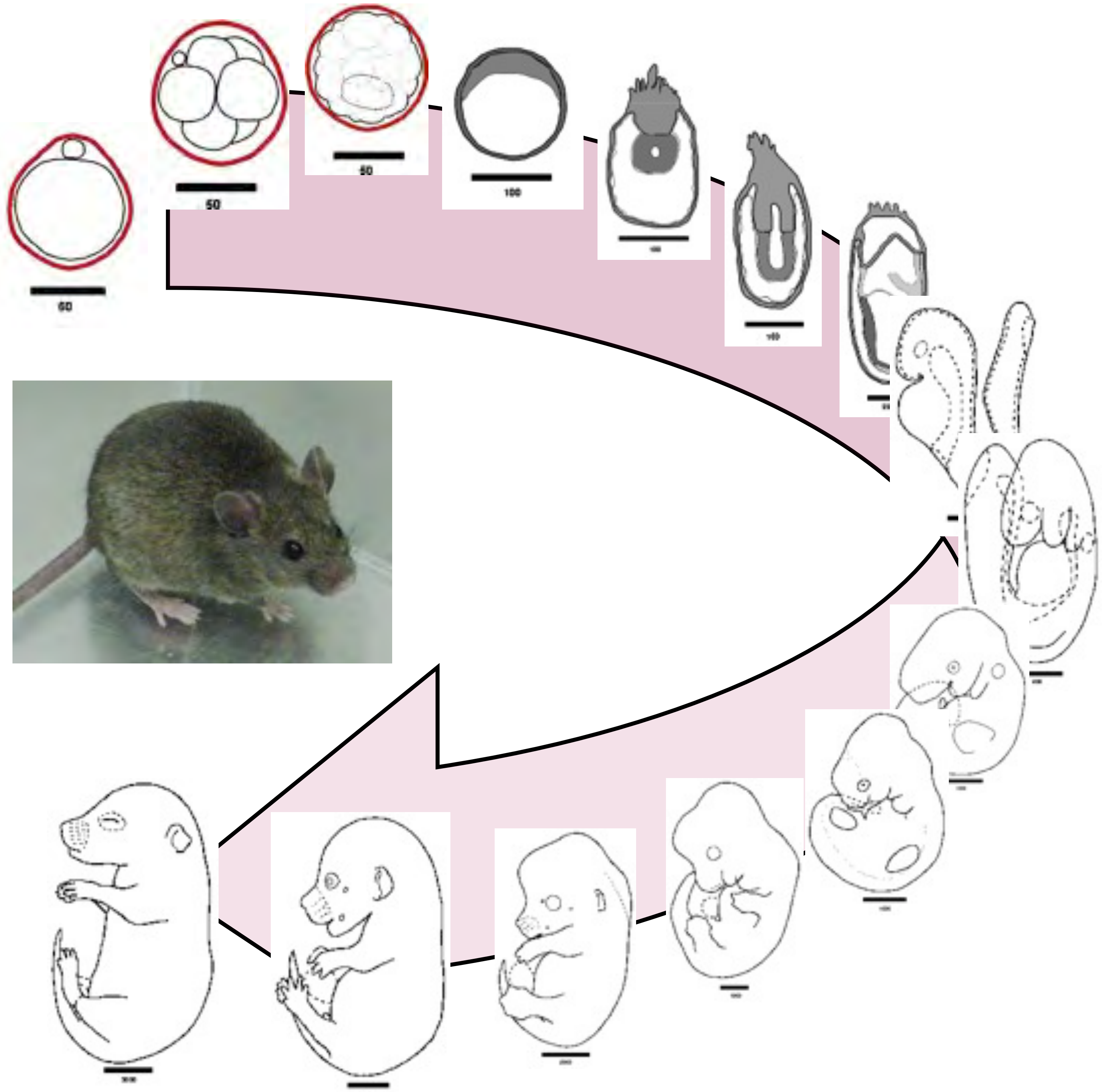
Carol Wicking, University of Queensland



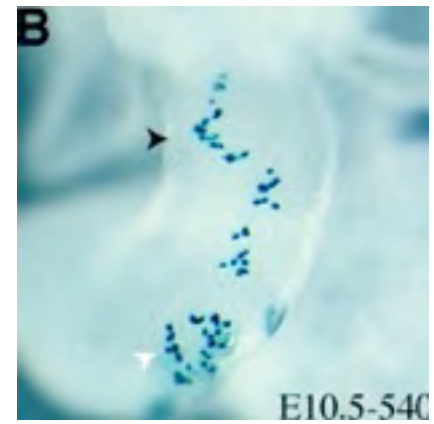




# eMouseAtlas - Development and Gene-Expression

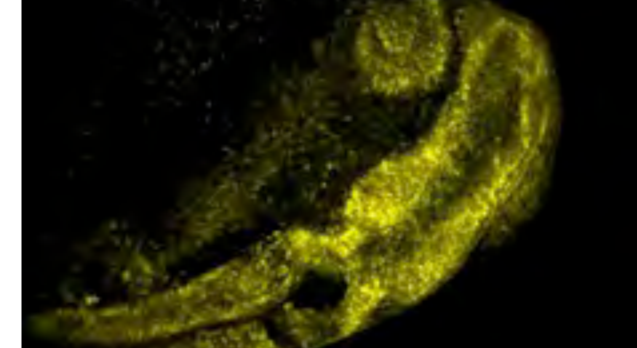


**CELL LINEAGE**




Sigolène Meilhac
Institut Pasteur

**CELL DIVISION**



anti-BrdU staining
J. McDearmid
McGill University

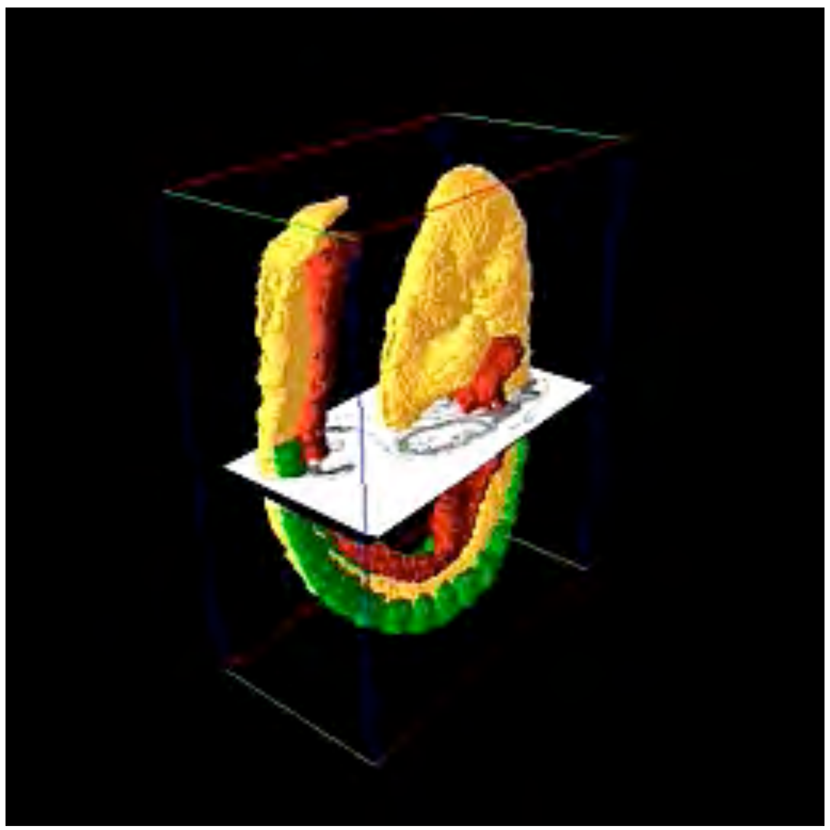
**APOPTOSIS**


Acridine Orange
J. Burns
University of Bristol

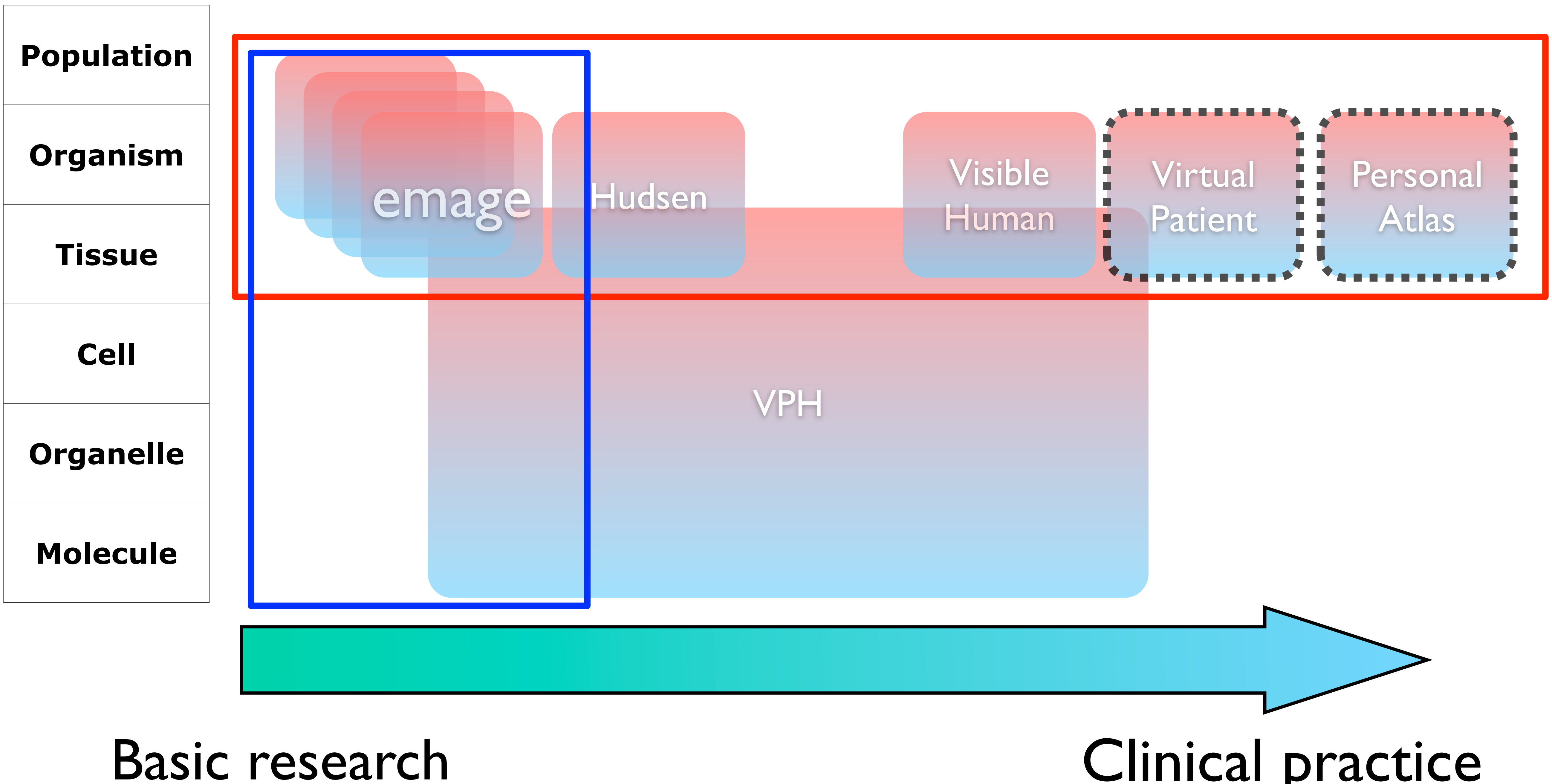
**TRANSGENICS**

cre induced-
LacZ expression
W. Hsu, University of Rochester

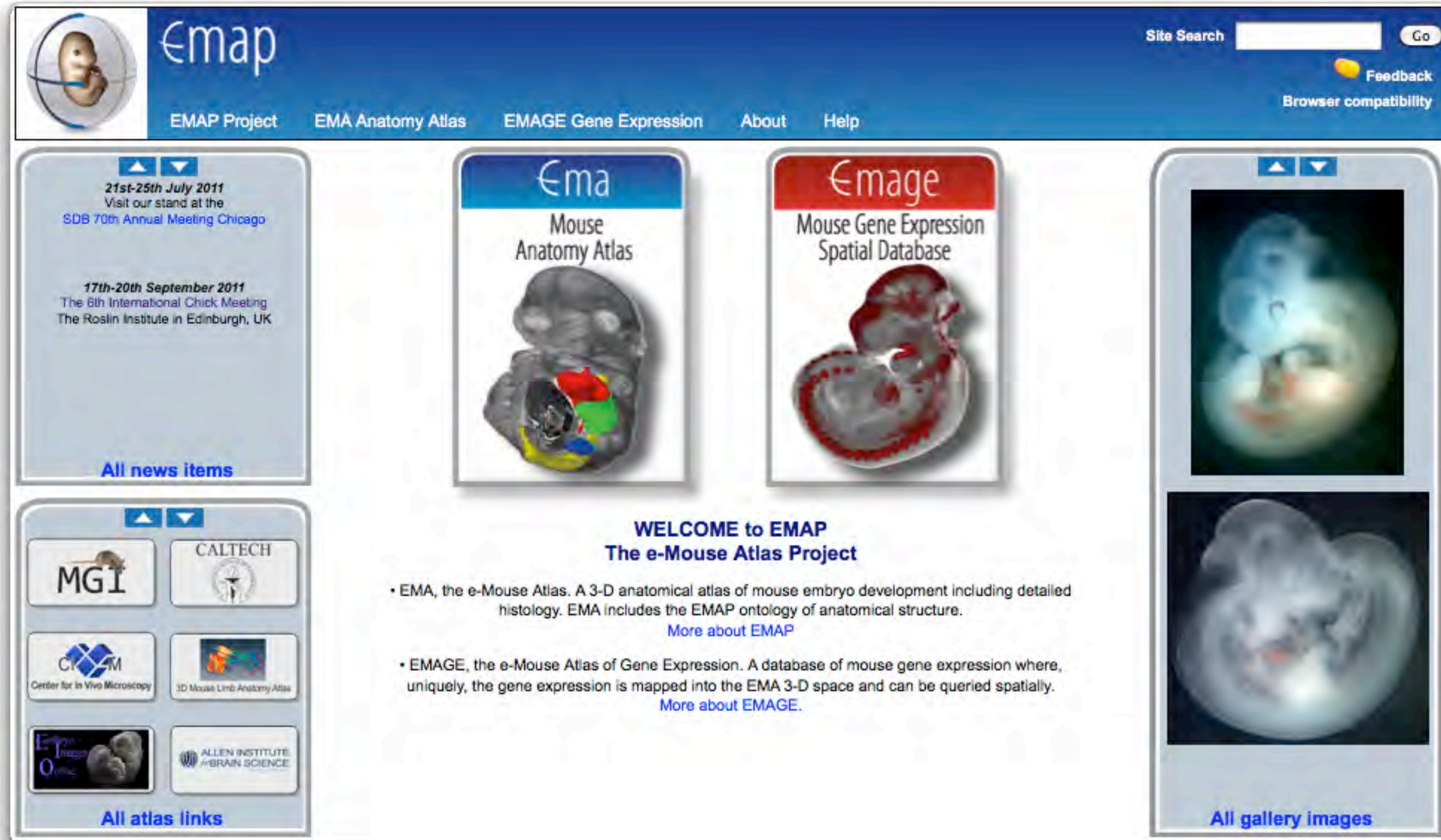
# eMouseAtlas Framework



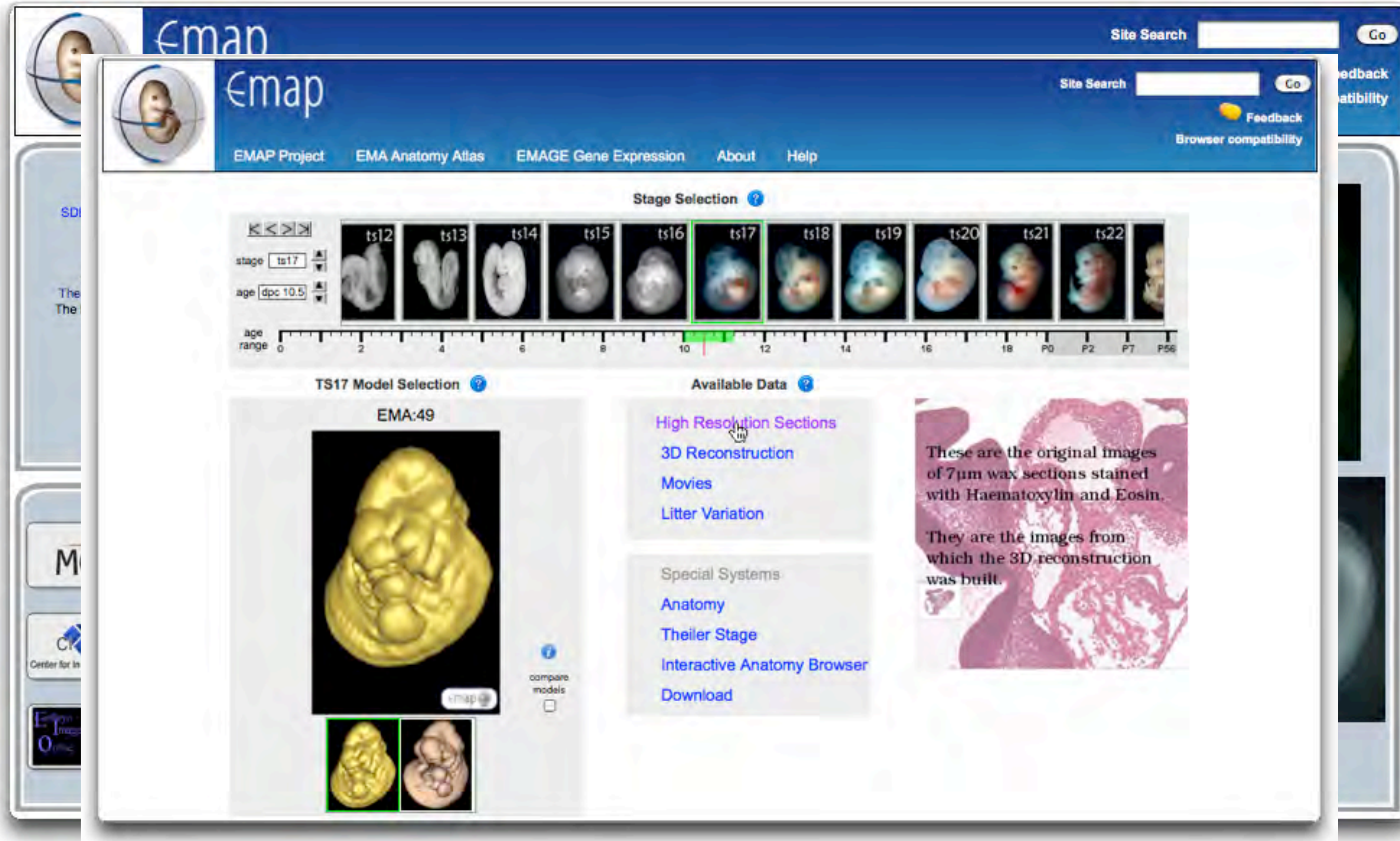
# Atlas-Based Infrastructures



# eMouseAtlas



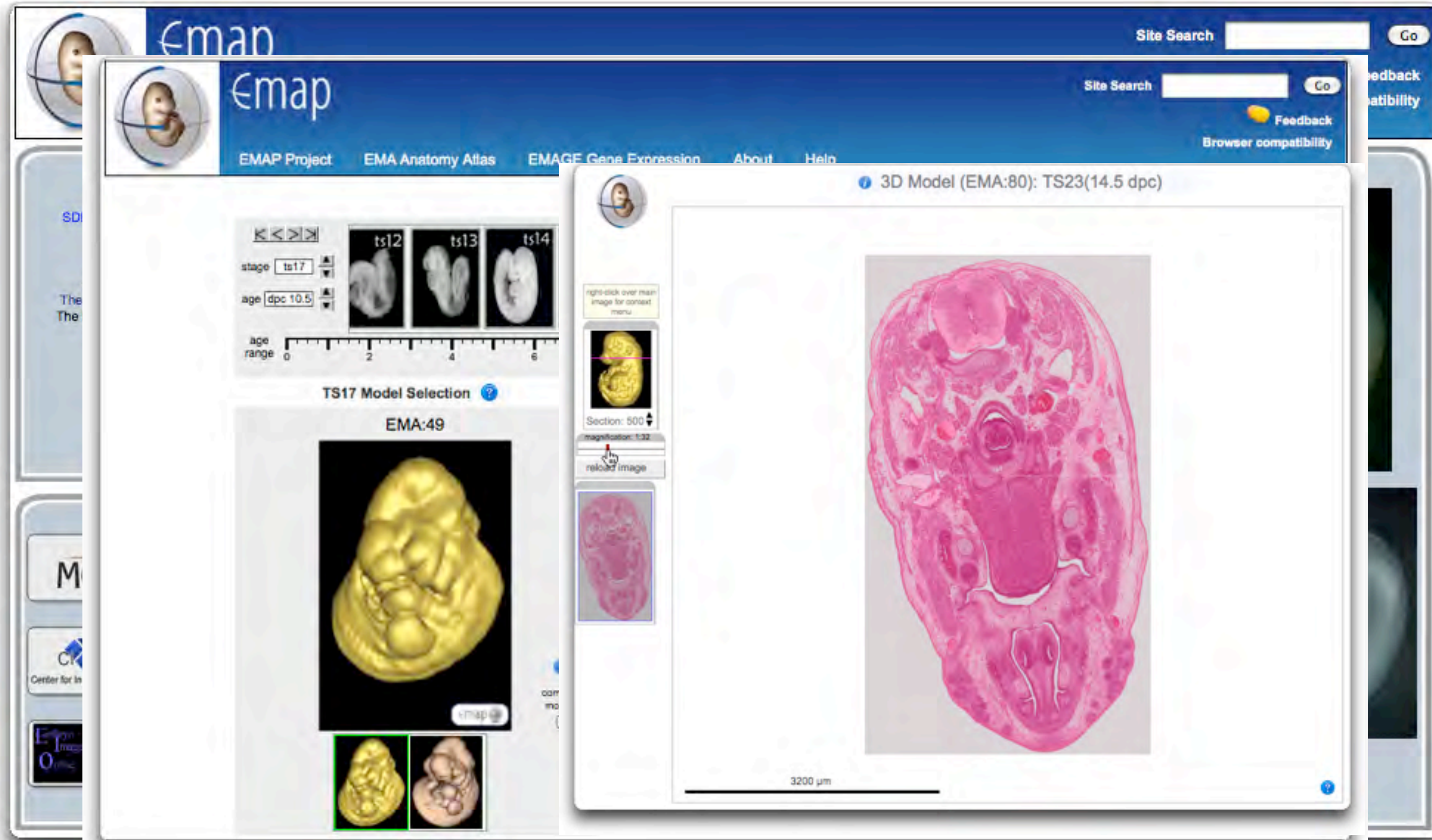
# eMouseAtlas



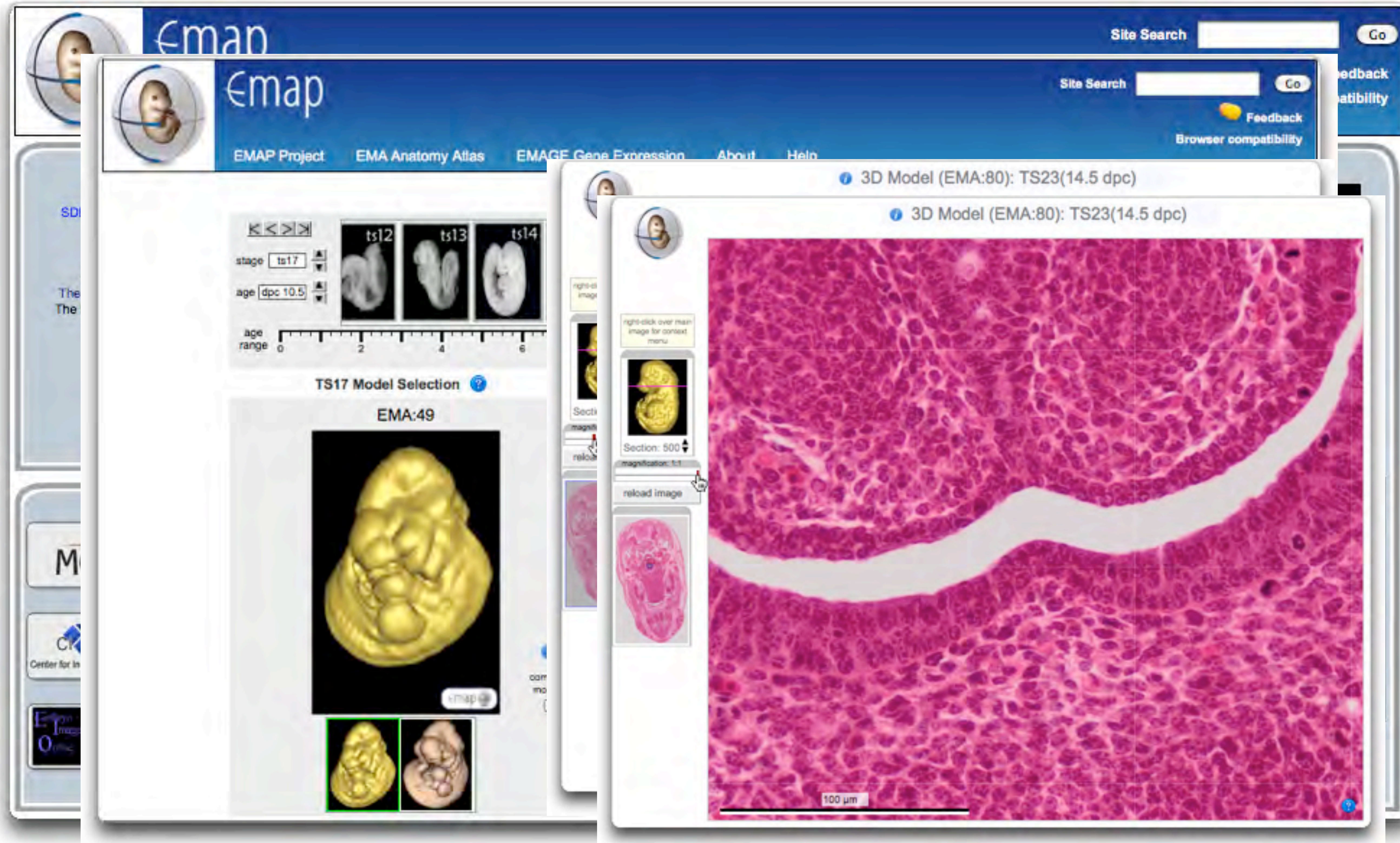



MRC Human Genetics Unit

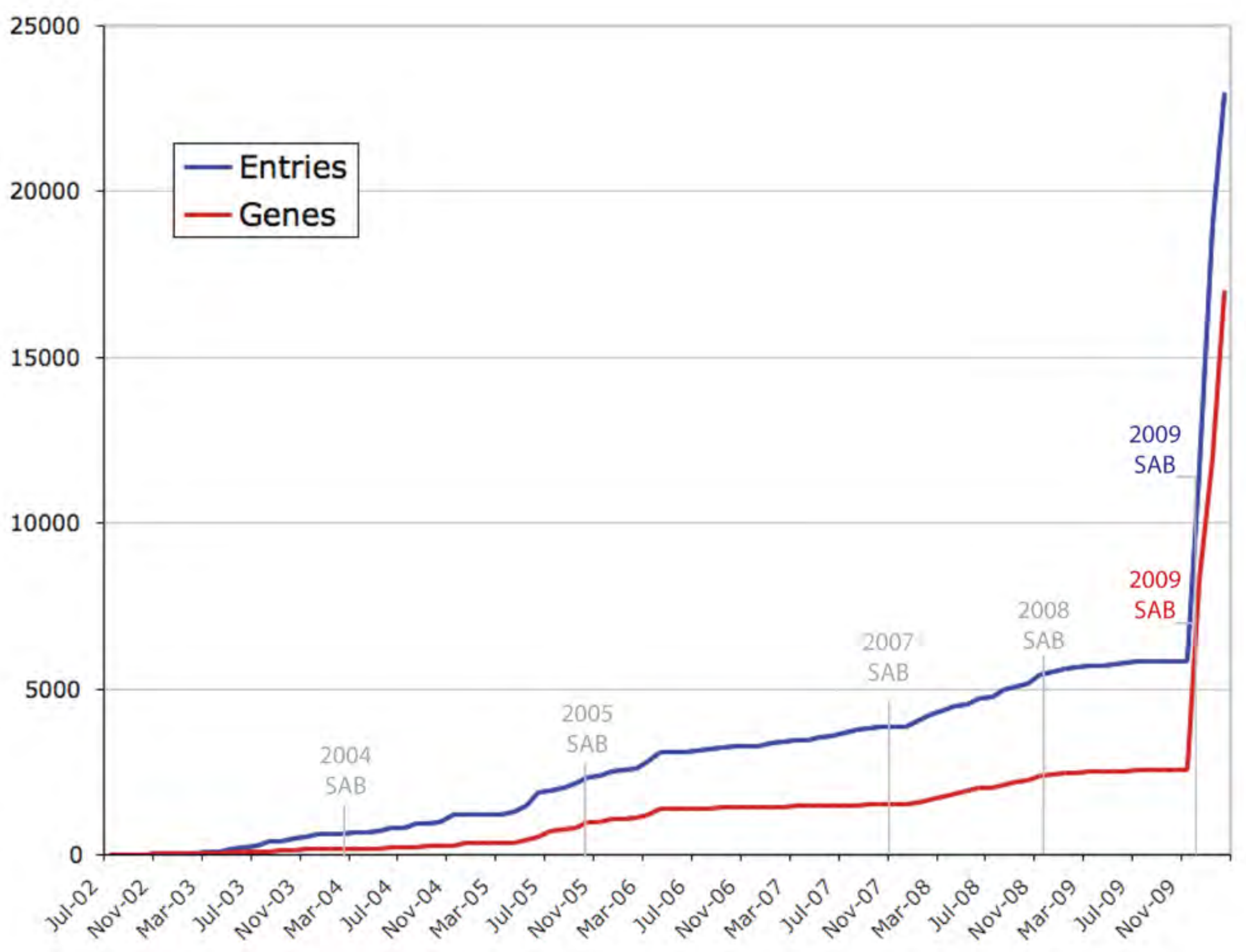
# eMouseAtlas

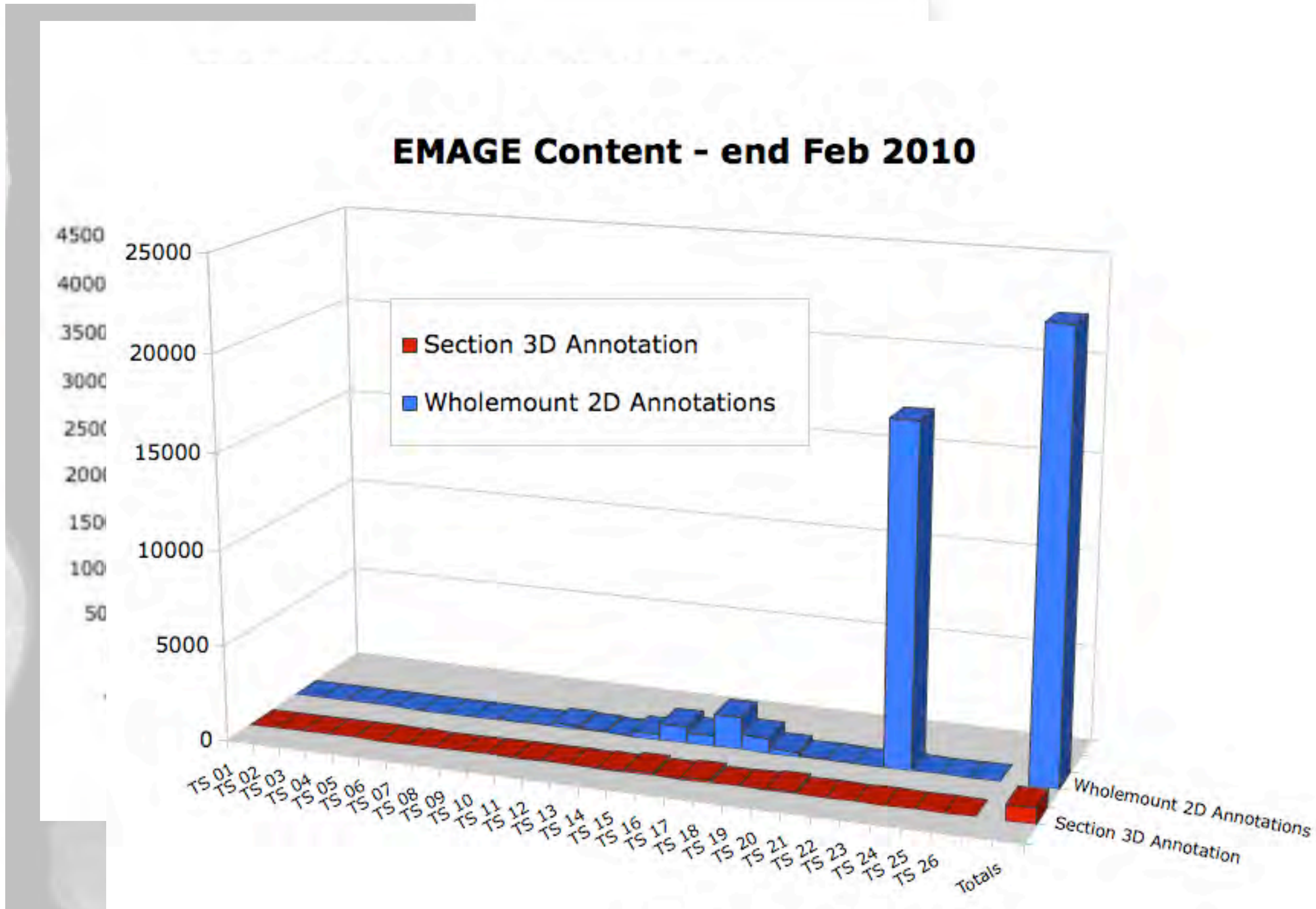


# eMouseAtlas



# EMAGE - current status





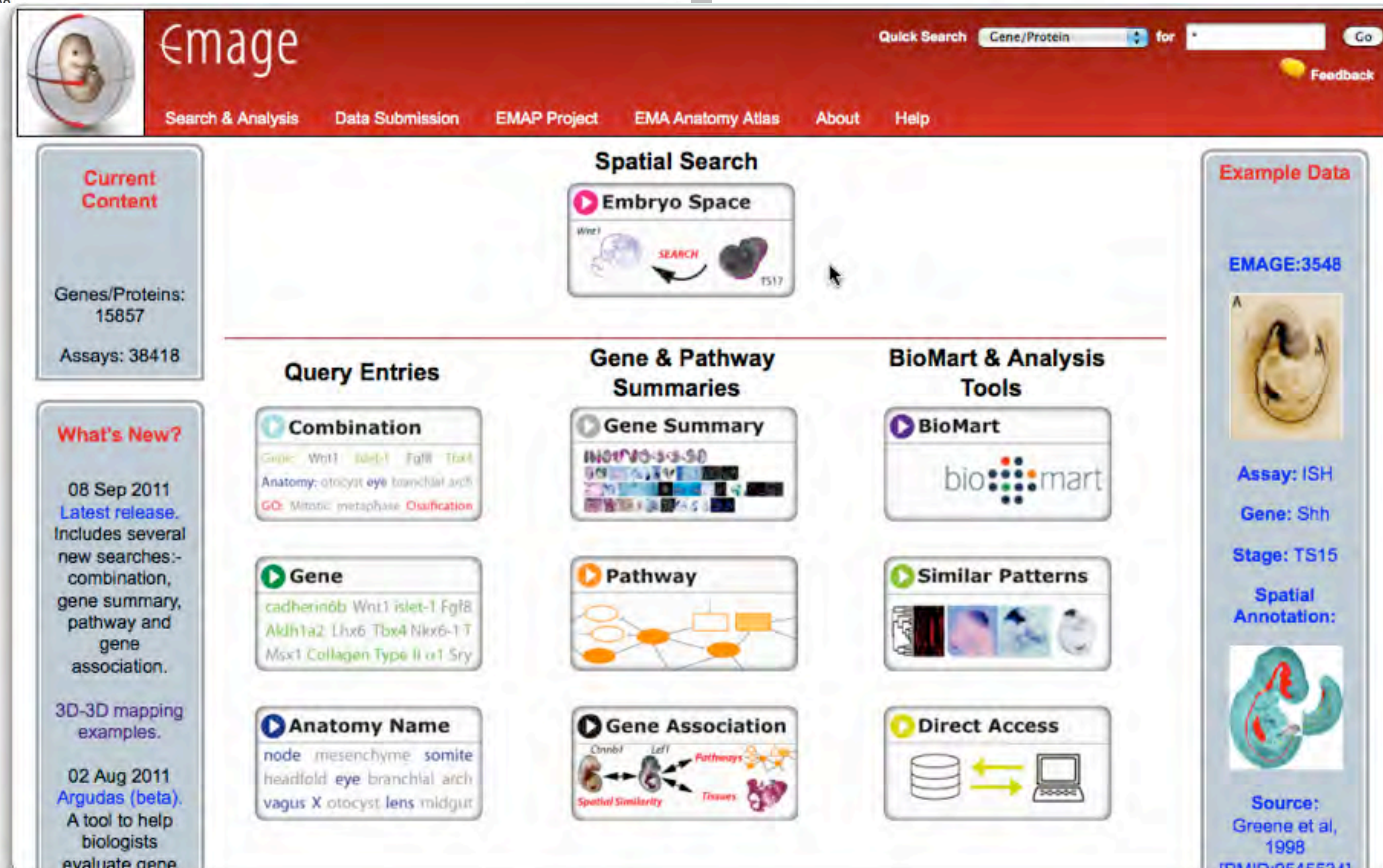
~22K submissions

Range Theiler 7-25

- MGI/GXD (~1,300)
- Direct submission (~300)
- Large scale screens (~16K)

Repository DB: 38.4K entries

# EMAGE - current status

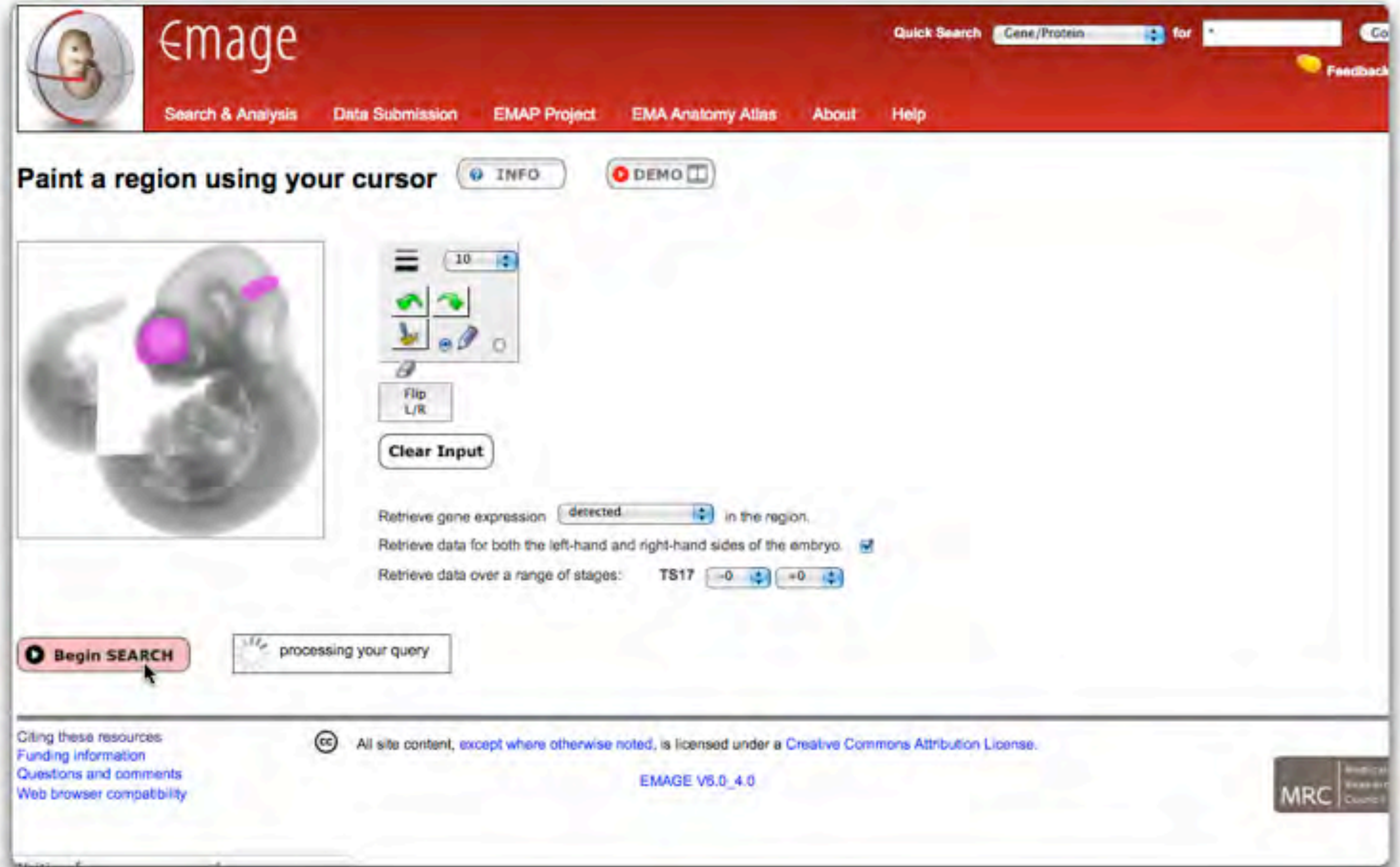




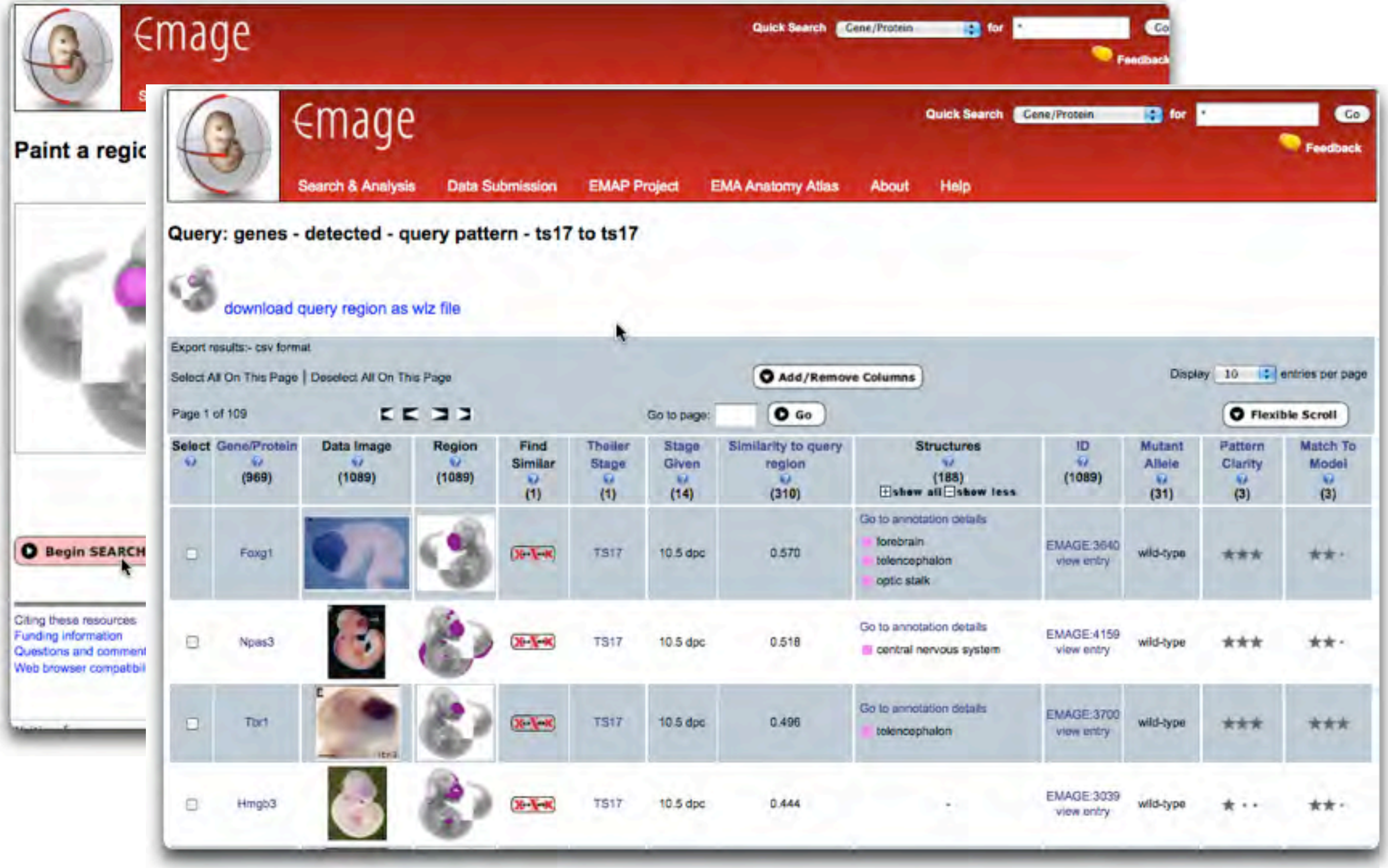

MRC Human Genetics Unit

Thursday, 28 February 2013

# EMAGE Embryo Space



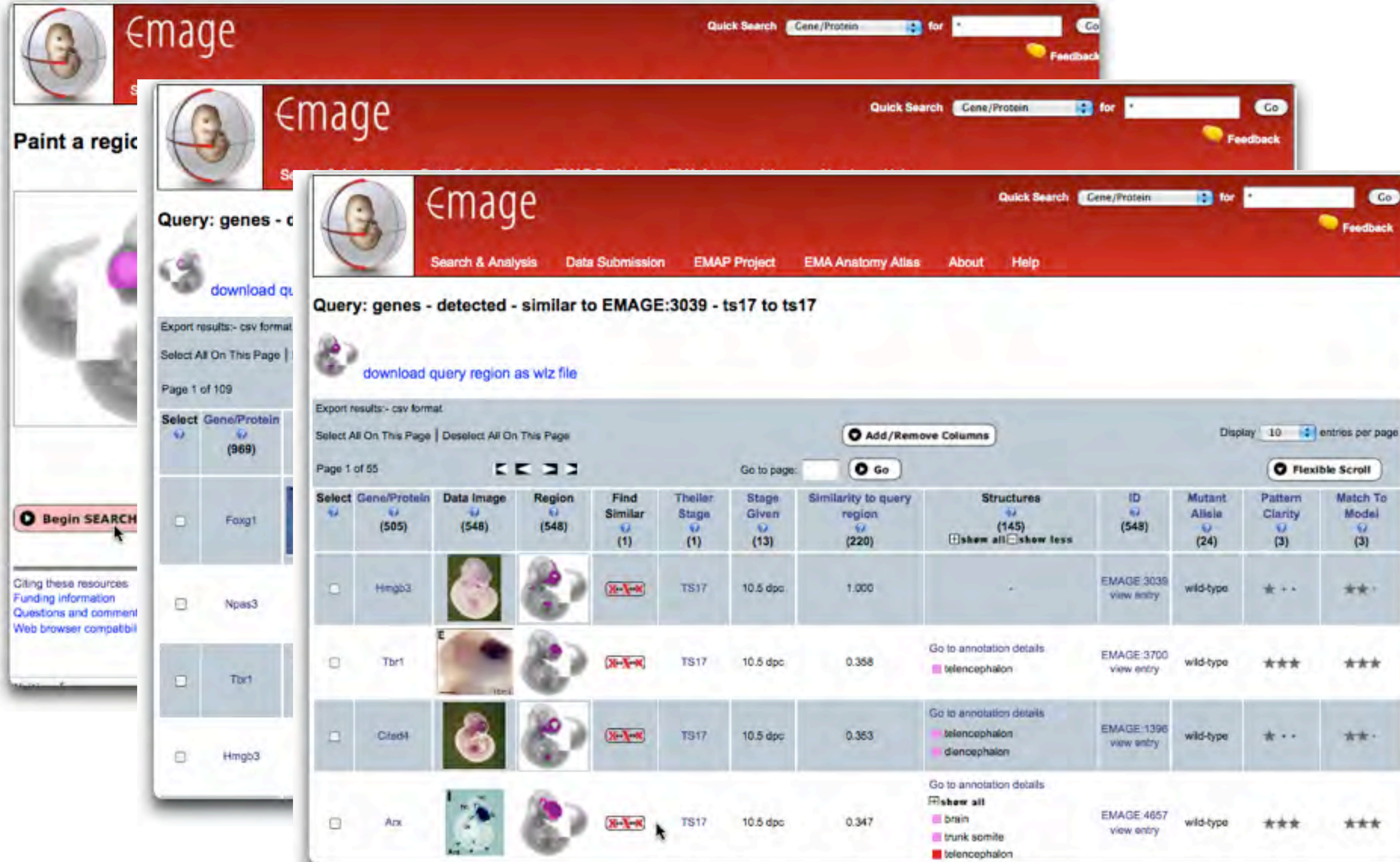
# EMAGE Embryo Space






MRC Human Genetics Unit

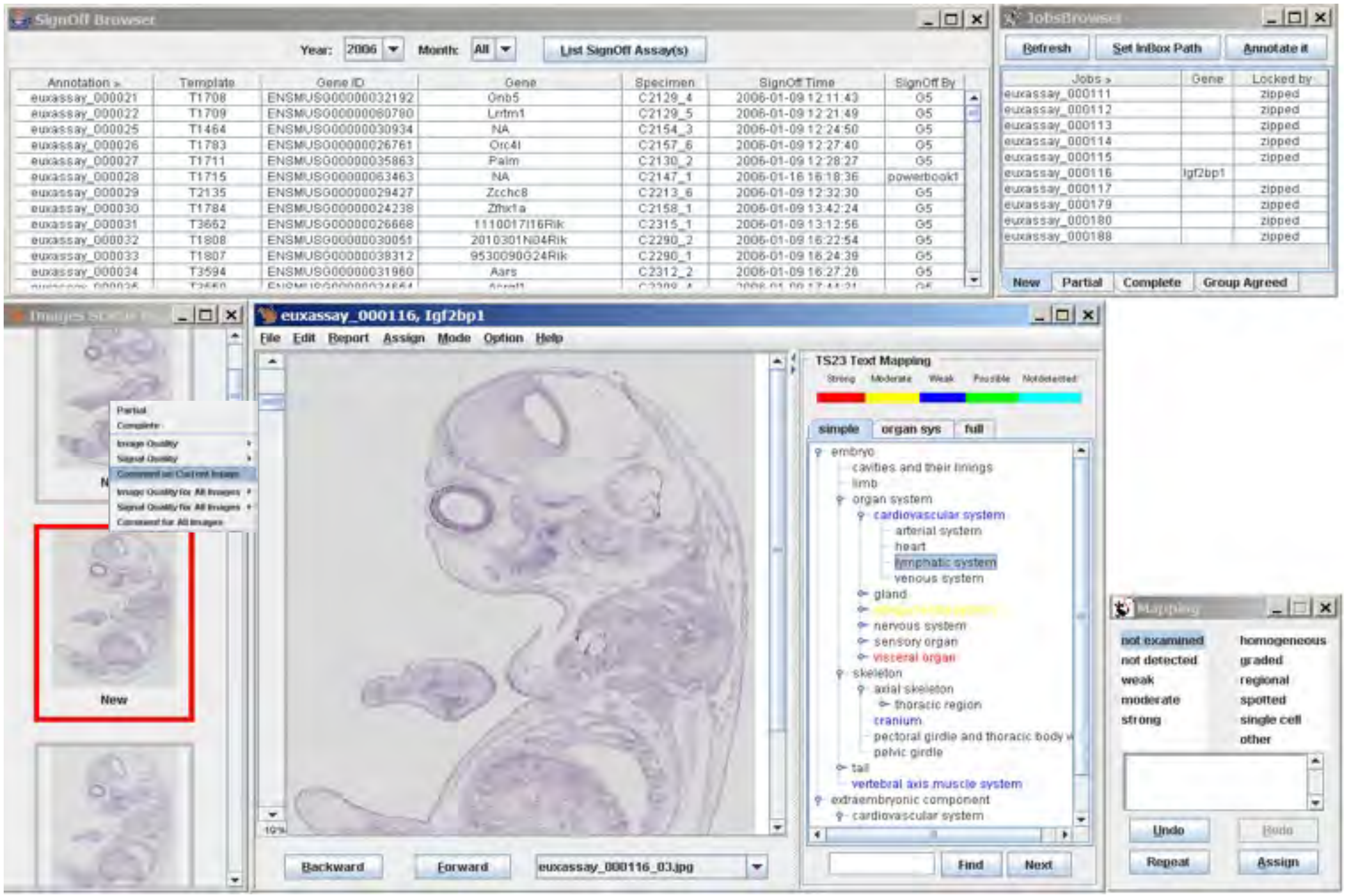
# EMAGE Embryo Space



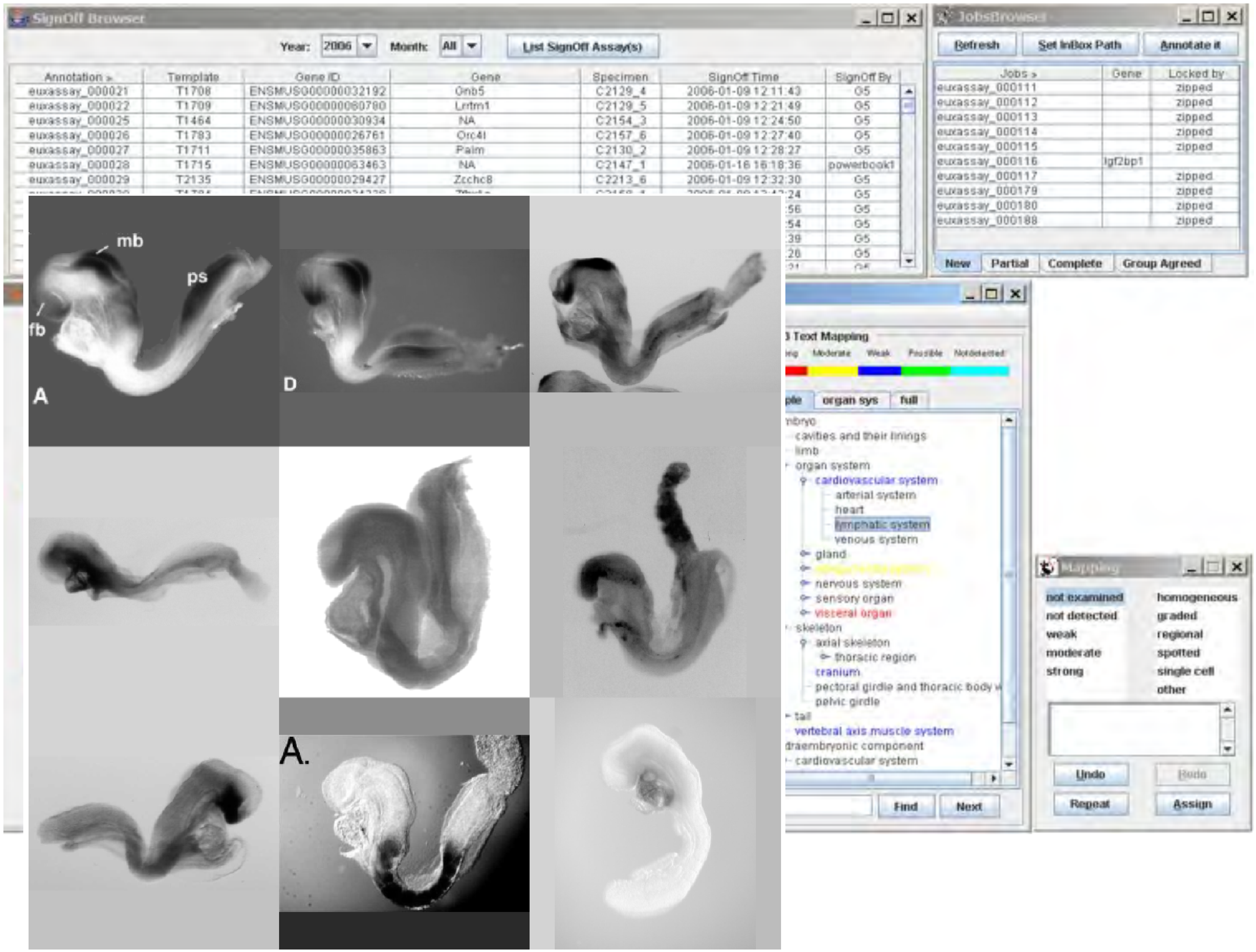
# BioAtlas - data mapping

- image collection - no mapping all spatial interpretation left to user
- implicit mapping - data interpreted and annotated with controlled vocabulary or ontology, image requires interpretation but some query and pattern analysis possible - “simple”
- explicit mapping, full spatial delineation of information e.g. expression pattern.

# BioAtlas - data mapping



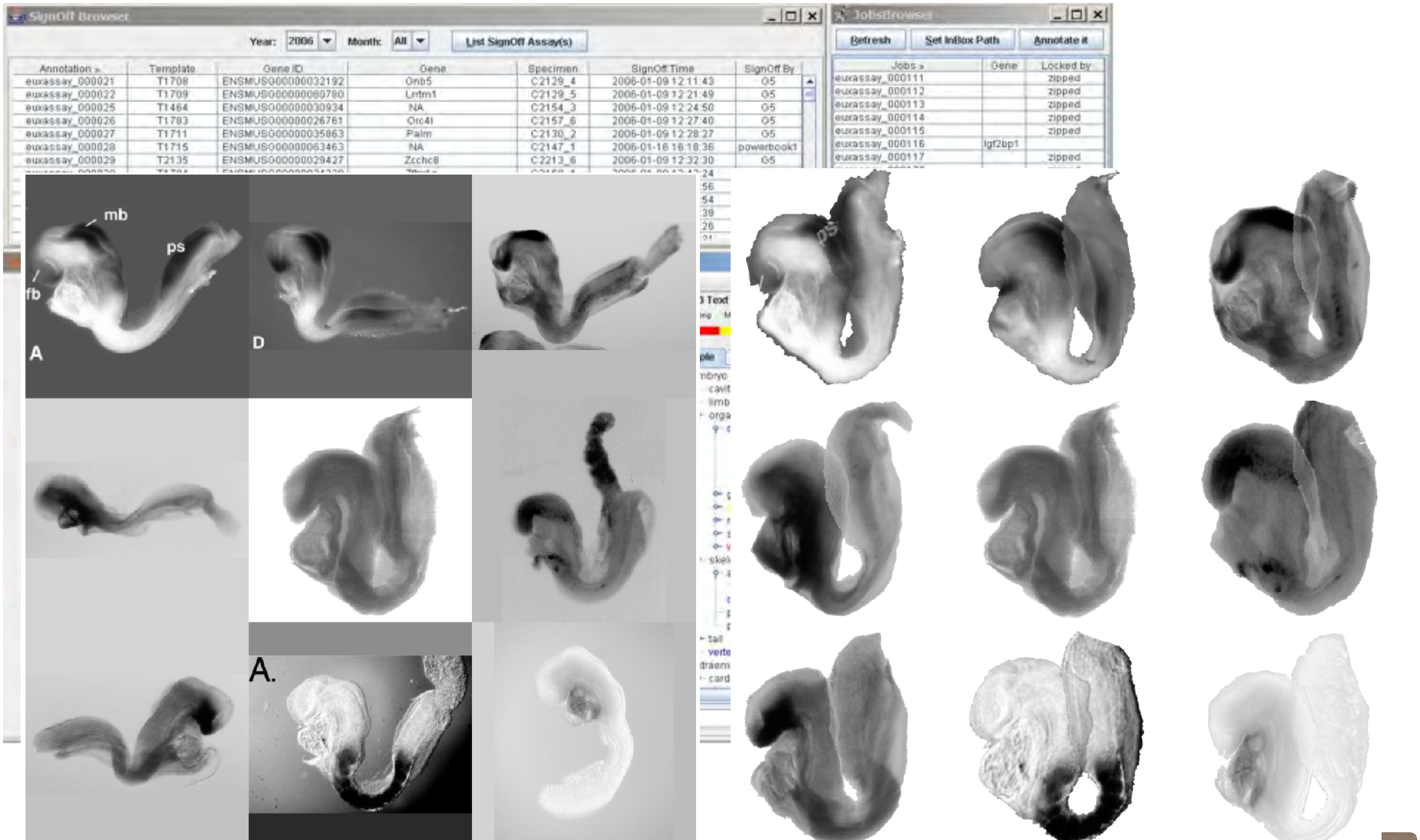
# BioAtlas - data mapping






MRC Human Genetics Unit

# BioAtlas - data mapping



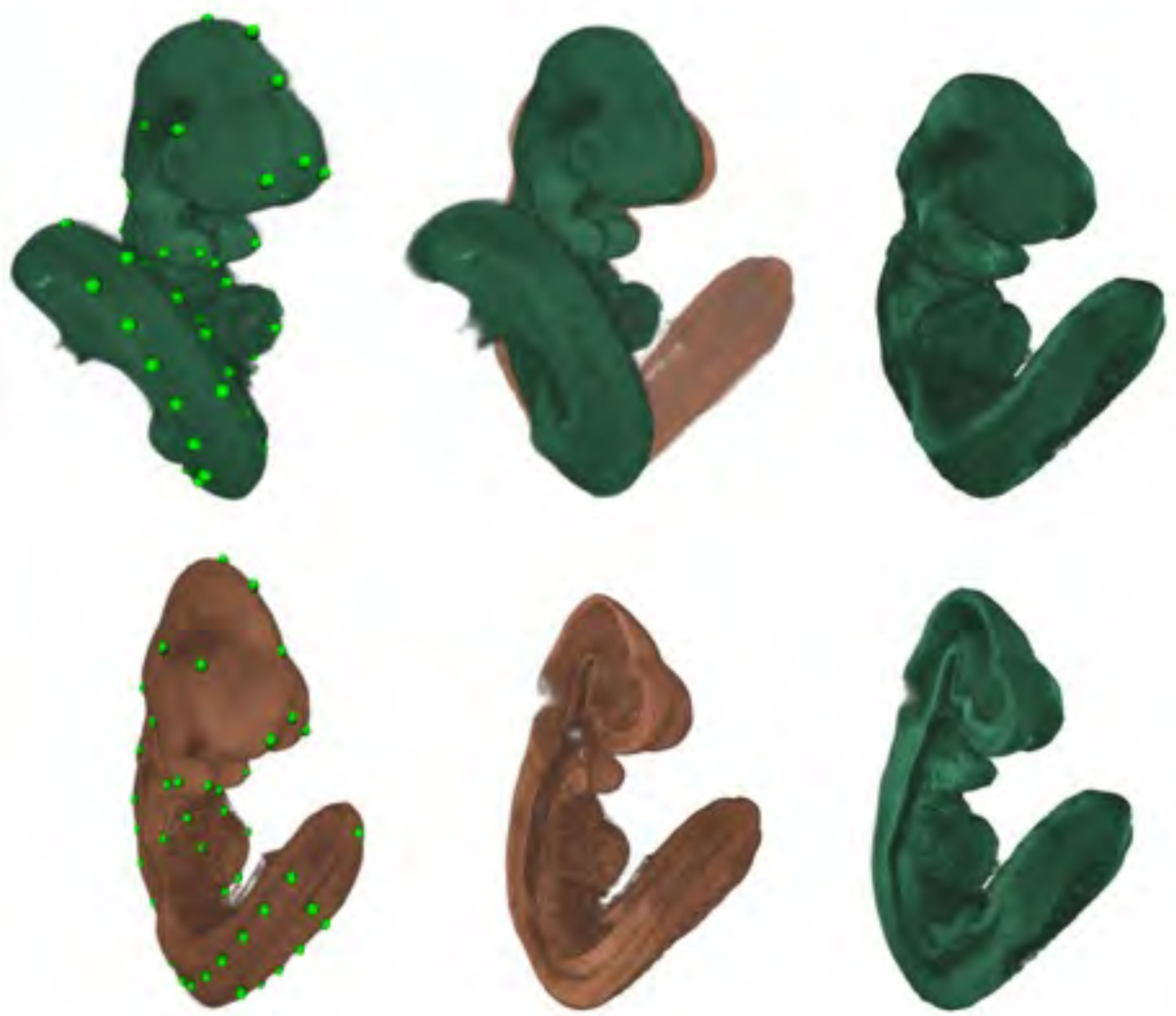



MRC Human Genetics Unit

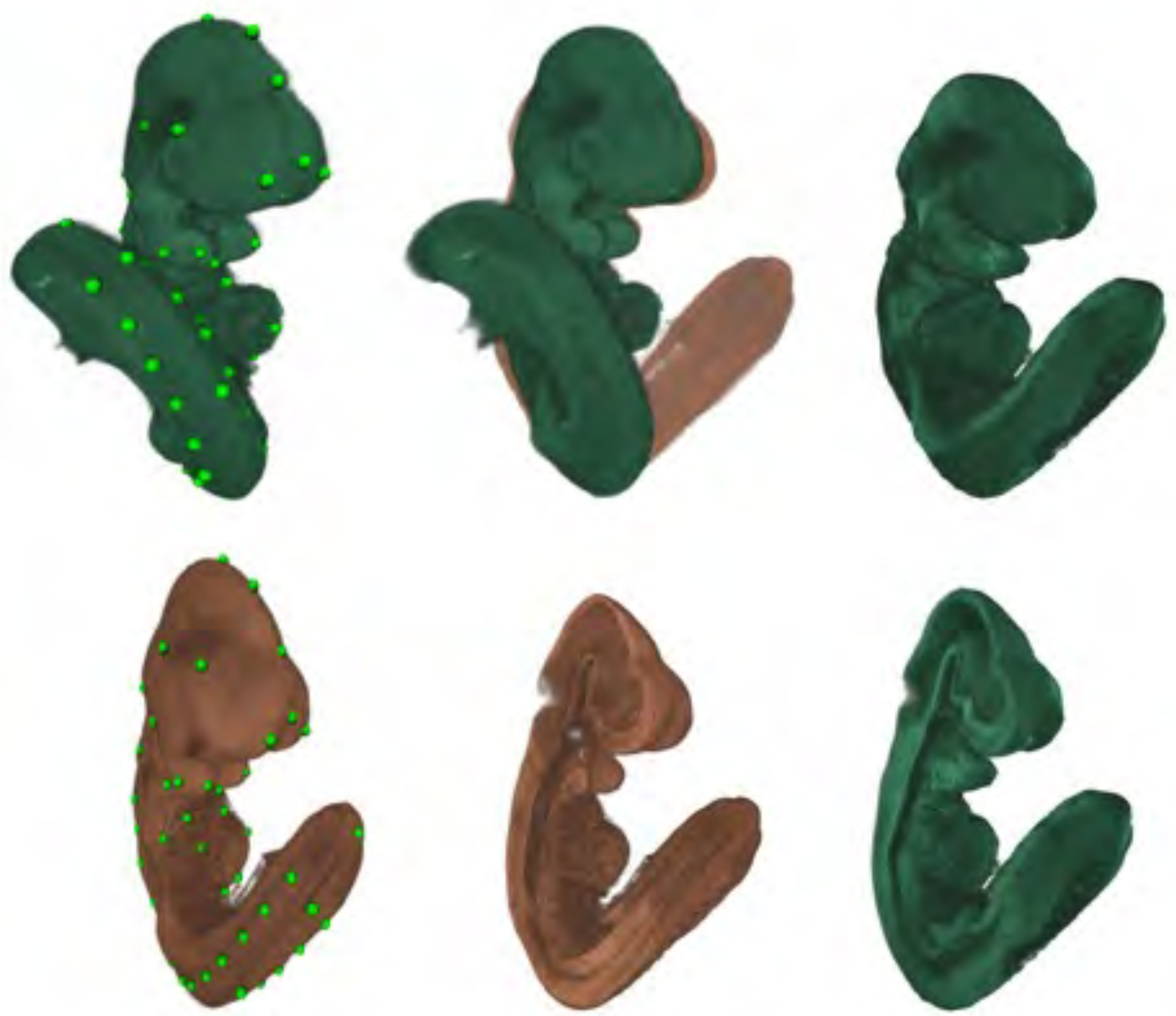
# Spatial Data Mapping

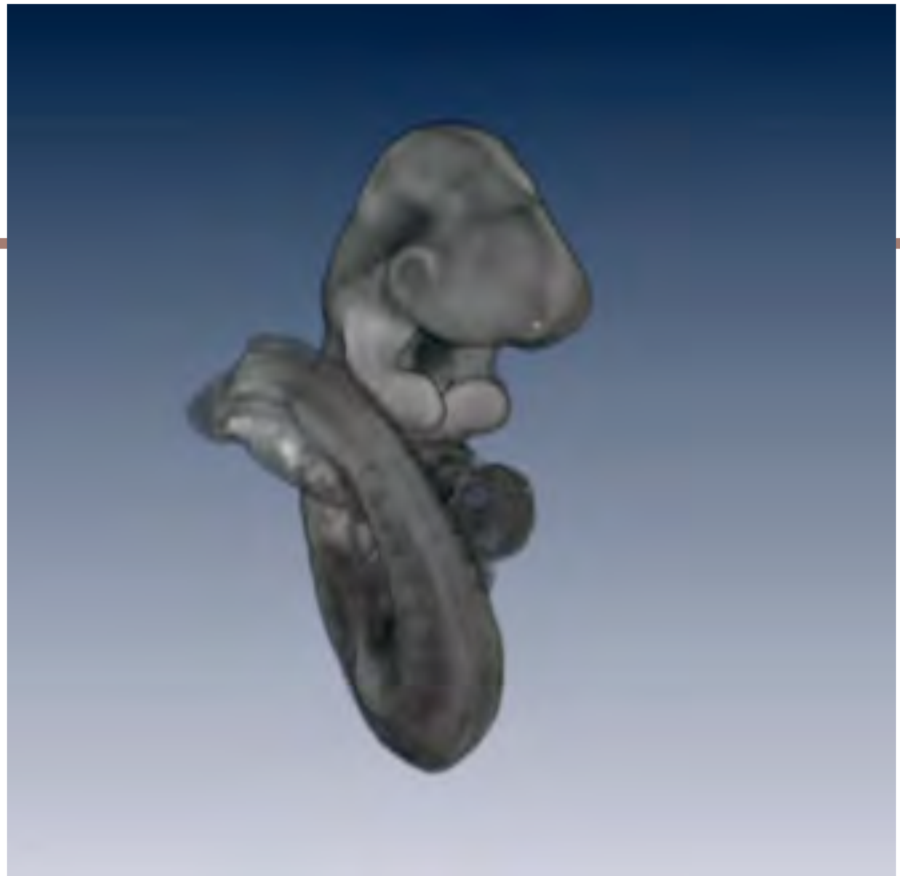
- Manual tie-point alignment (WlzWarp)
  - mesh-based constrained distance transform
  - interactive
  - arbitrary complexity
- Automated fine tuning (ITK/ANTS)
- Editor review

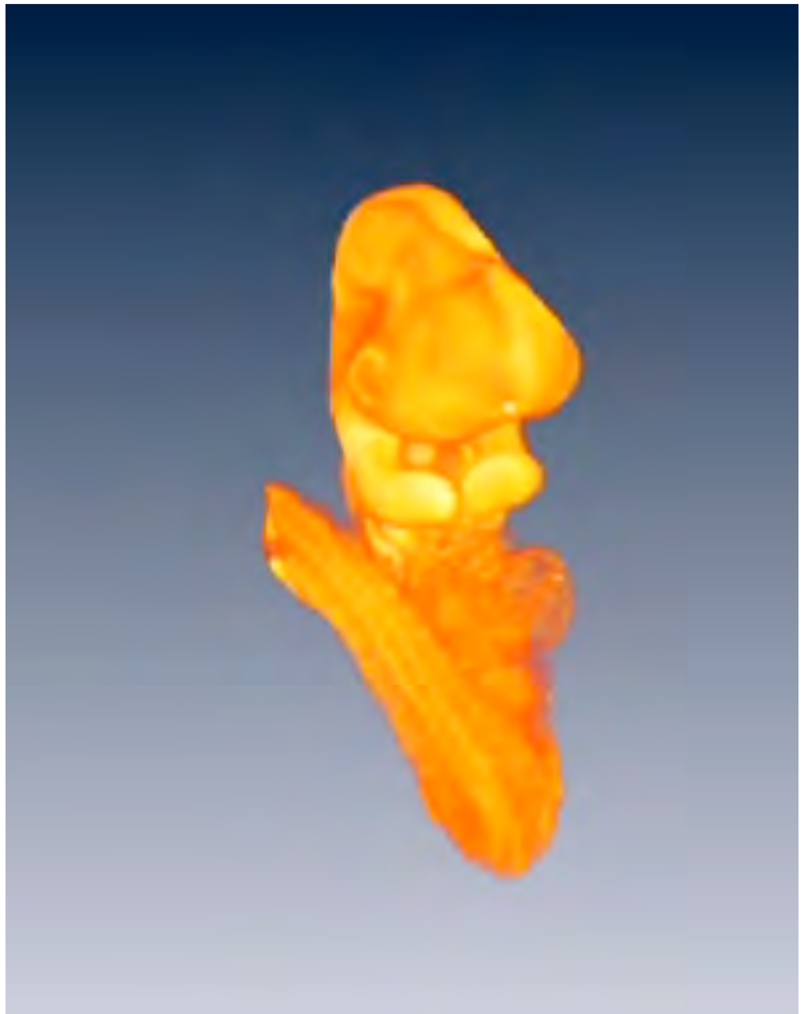
# 3D Data Mapping - WlzWarp



# 3D Data Mapping - WlzWarp



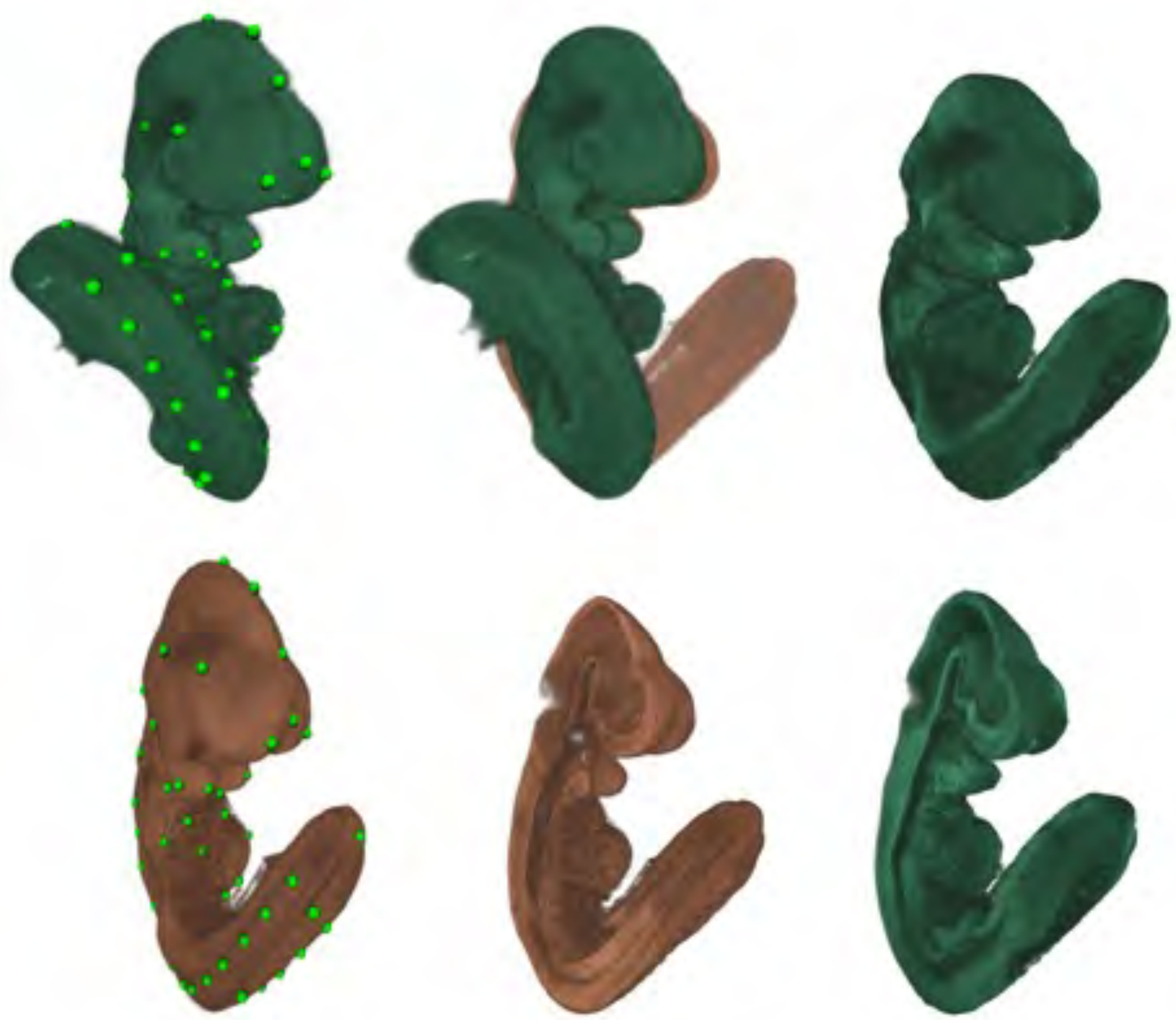


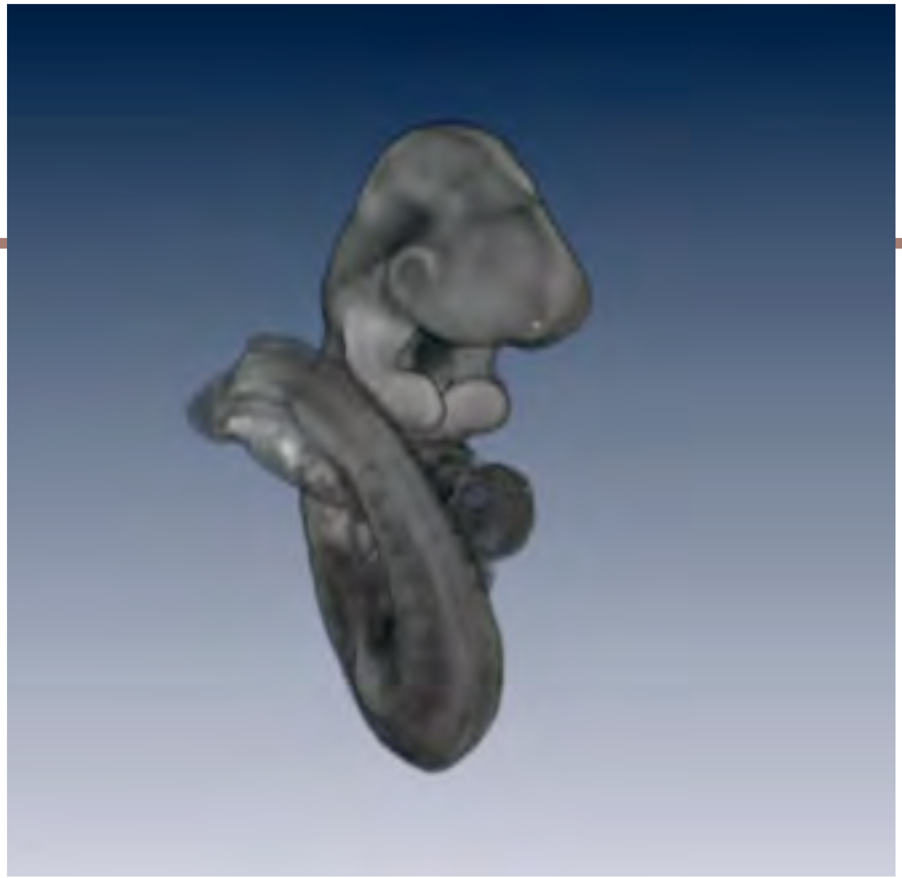


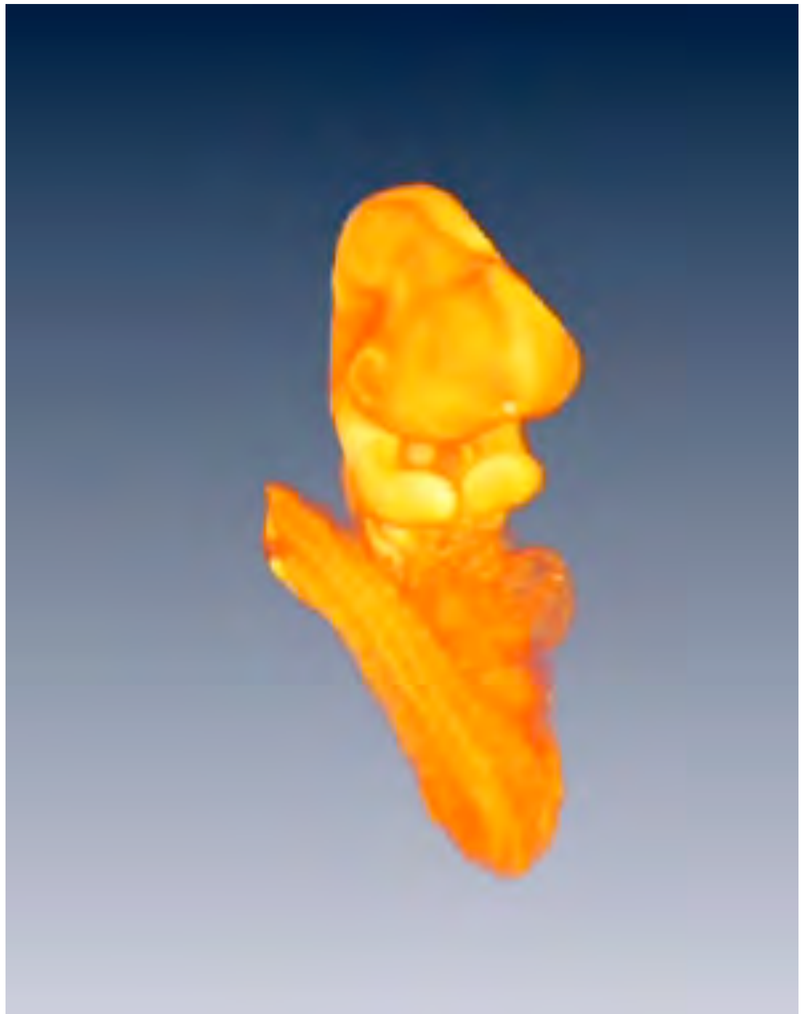


Human Genetics Unit MRC

# 3D Data Mapping - WlzWarp







# 3D Mapping - Wnt signalling pathway

| | | | | | |
|---|---|---|---|---|---|
| Wnt1 |  | TS17 | 10.5dpc | 3D View | EMAGE:6132 |
| Wnt2 |  | TS17 | 10.5dpc | 3D View | EMAGE:6134 |
| Wnt3 |  | TS17 | 10.5dpc | 3D View | EMAGE:6138 |
| Wnt3A |  | TS17 | 10.5dpc | 3D View | EMAGE:6141 |
| Wnt4 |  | TS17 | 10.5dpc | 3D View | EMAGE:6142 |
| Wnt5A |  | TS17 | 10.5dpc | 3D View | EMAGE:6144 |
| Wnt6 |  | TS17 | 10.5dpc | 3D View | EMAGE:6148 |
| Wnt7A |  | TS17 | 10.5dpc | 3D View | EMAGE:6150 |

**Data Images**

3D reconstructed object showing signal. | All sections along the X-axis, as movie. | All sections along the Y-axis, as movie. | All sections along the Z-axis, as movie. | Photograph prior to 3D imaging.

View 3D opt image

Download 3D images in woolz format.

Expression pattern clarity: ★★-

# 3D Mapping - Wnt signalling pathway

| | | | | | |
|---|---|---|---|---|---|
| Wnt1 | | TS17 | 10.5dpc | 3D View | EMAGE:6132 |
| Wnt2 | | TS17 | 10.5dpc | 3D View | EMAGE:6134 |
| Wnt3 | | TS17 | 10.5dpc | 3D View | EMAGE:6138 |
| Wnt3A | | TS17 | 10.5dpc | 3D View | EMAGE:6141 |
| Wnt4 | | TS17 | 10.5dpc | 3D View | EMAGE:6142 |
| Wnt5A | | TS17 | 10.5dpc | 3D View | EMAGE:6144 |
| Wnt6 | | TS17 | 10.5dpc | 3D View | EMAGE:6148 |
| Wnt7A | | TS17 | 10.5dpc | 3D View | EMAGE:6150 |


Wnt1

# 3D Visualisation

- Applications:
  - SectionBrowser, JAtlasViewer
  - Format conversion -> a.n.other
- Browser-Based
  - canned views & movies
  - Tiled zoom-viewer
    - Extended to 3D protocol (IIP3D)
    - Multi-layer
    - Interactive overlays
    - WebGL

# OME Project Objectives

To use and extend OMERO to meet mouse atlas *et al* and IGMM requirements:

- Embed woolz images
- Sparse reconstruction & mapping
- large image data
- Annotation overlay and visualisation
- 3D mapping - e.g. OPT images
- Project image archiving - EMAP, GUDMAP etc.
- IGMM imaging - archiving and analysis

# Woolz images

## A fast interval processor

G.A. Shippey[a], R.J.H. Bayley[a], A.S.J. Farrow[a], D.R. Rutovitz[a] and J.H. Tucker[a]

[a]MRC Clinical and Population Cytogenetics Unit, Edinburgh, U.K.

Received 22 December 1980. Available online 19 May 2003.

**Abstract**

The advent of high resolution Linear Image Sensors, and high p.r.f. steppin…
development at the MRC Edinburgh is intended to scan a conventional micr…
The high pixel data rate (8 MHz peak) easily saturates most computer config…
threshold, pixels (i.e. 'intervals') into a set of interval parameters. These inter…
microprocessors to give object parameters from which the cells can then be …
The paper describes the hardware and software architecture, with comment…
The linkage procedure used to reconstitute contiguous object descriptions i…
the order of 1 ms.

**Keywords:** Interval; Image sensor; Stepping motor; Auto-focus; Metaphase; Ce…

**Pattern Recognition**
Volume 14, Issues 1-6, 1981, Pages 345-356
1980 Conference on Pattern Recognition

# Woolz images

Pattern Recognition Letters
Volume 3, Issue 2, March 1985, Pages 119-129

## Data structures for image processing in a C language and Unix environment ☆

Jim Piper[a] and Denis Rutovitz[a]

[a]MRC Clinical and Population Cytogenetics Unit, Western General Hospital, Crewe Road, Edinburgh EH4 2XU, Scotland

Received 14 December 1983; revised 12 July 1984. Available online 19 May 2003.

**Abstract**

A variety of single-address image, graphic, and image-operator data structures and a library of support subroutines have been implemented in the C programming language. These facilitate efficient and representation-independent procedure implementation, and have been used to construct a set of image processing tools in a Unix environment which make a flexible interactive image processing system.

**Keywords:** Image data; image domain; C language type structure; pointer variable; interactive image processing; shell programming

☆This work was supported entirely by the UK Medical Research Council.

# Woolz images

Cytometry. 1994 May 1;16(1):7-16.

## Automatic fluorescence metaphase finder speeds translocation scoring in FISH painted chromosomes.

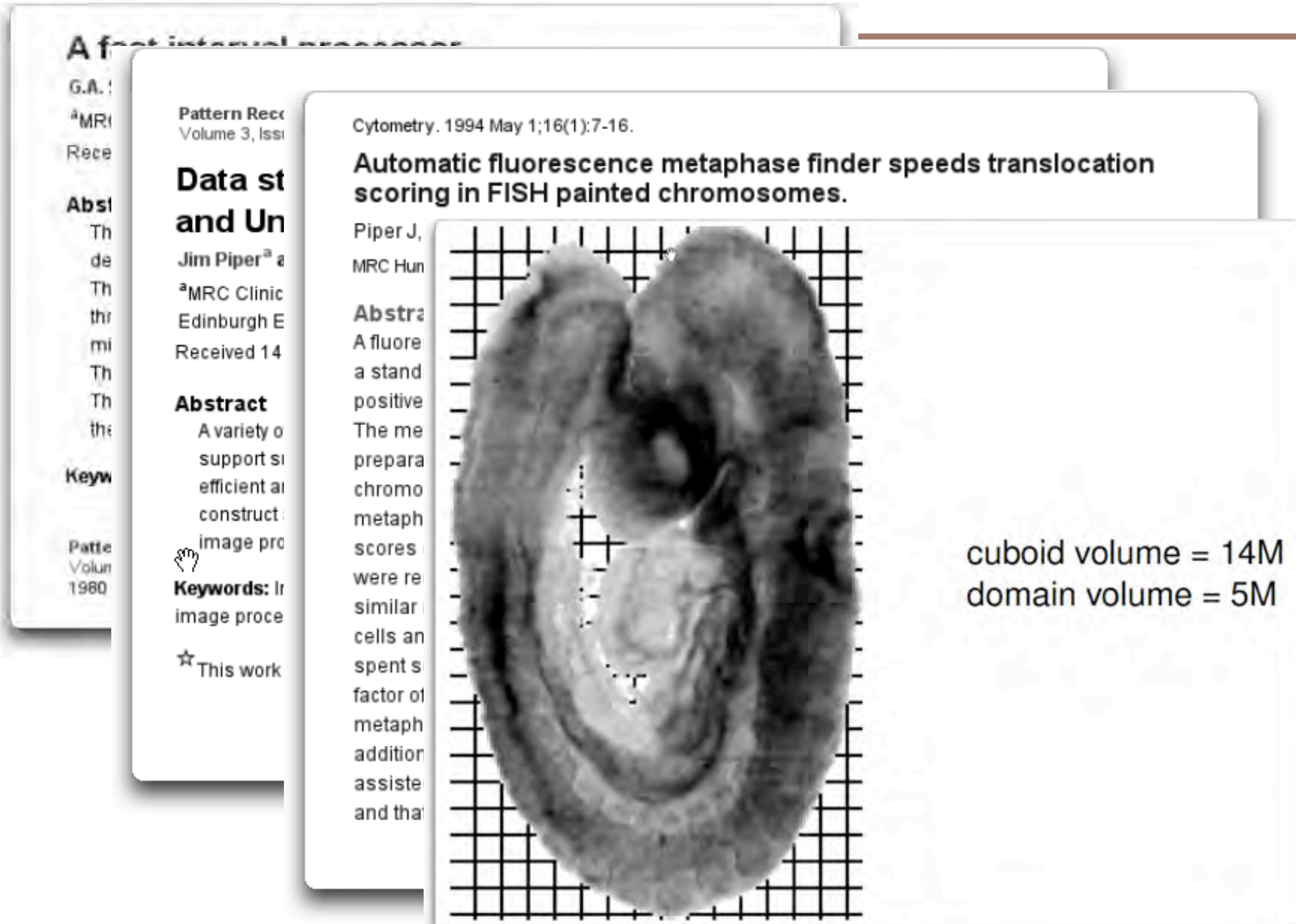
Piper J, Poggensee M, Hill W, Jensen R, Ji L, Poole I, Stark M, Sudar D.

MRC Human Genetics Unit, Edinburgh, Scotland.

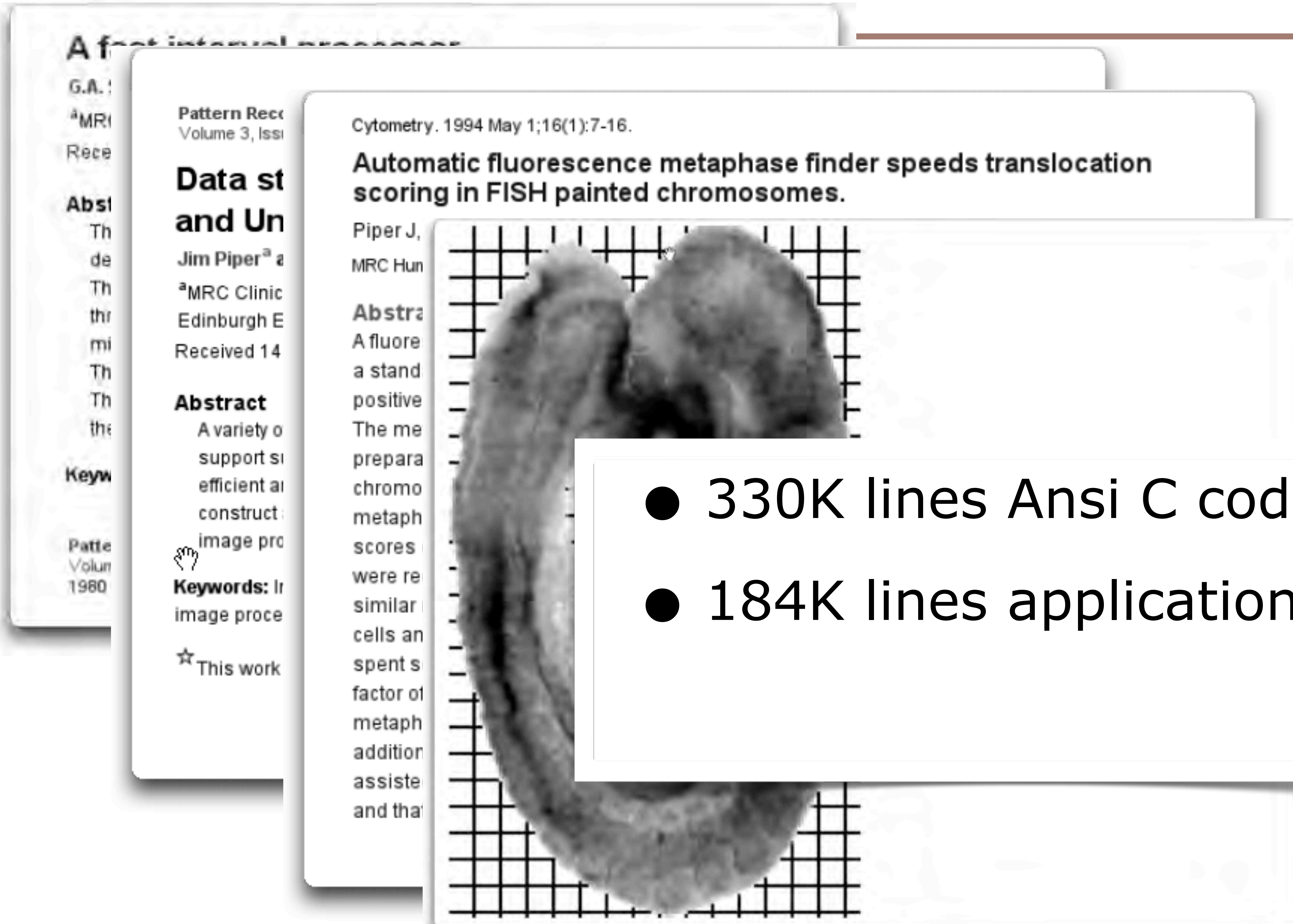
### Abstract

A fluorescence metaphase finder was constructed with commercially available hardware and a standard Unix workstation. Its accuracy was measured in terms of the number of false positive and false negative detected metaphases on a variety of different slide preparations. The metaphase finder was used in a translocation scoring experiment in which metaphase preparations of human peripheral blood lymphocytes were hybridized with whole chromosome probes to chromosomes #1, #2, and #4. The automatic finder presented metaphases to the cytogeneticist, centered in the eyepieces at x63. The cytogeneticist's scores of analyzable metaphases and of painted chromosomes involved in rearrangements were recorded. The time for the analysis was recorded and compared to the time to analyze a similar number of cells in a purely visual experiment in which the cytogeneticist scanned for cells and analyzed them, both at x63. The results showed that, neglecting the machine time spent scanning unattended, the amount of time required for the analysis was reduced by a factor of three. Furthermore, in this experiment the metaphase finder found more scorable metaphases than the cytogeneticist found by visual scanning. Machine-assisted scoring had additional, less quantifiable, benefits; notably that digital images of metaphases sometimes assisted the analysis of chromosome rearrangements, that cells could be revisited easily, and that the analysis was much less fatiguing.

# Woolz images



# Woolz images




- 330K lines Ansi C code
- 184K lines application code

# Woolz Images

- Domain
  - Rectangle based
  - Interval based
  - 3D planewise domains

# Woolz Images

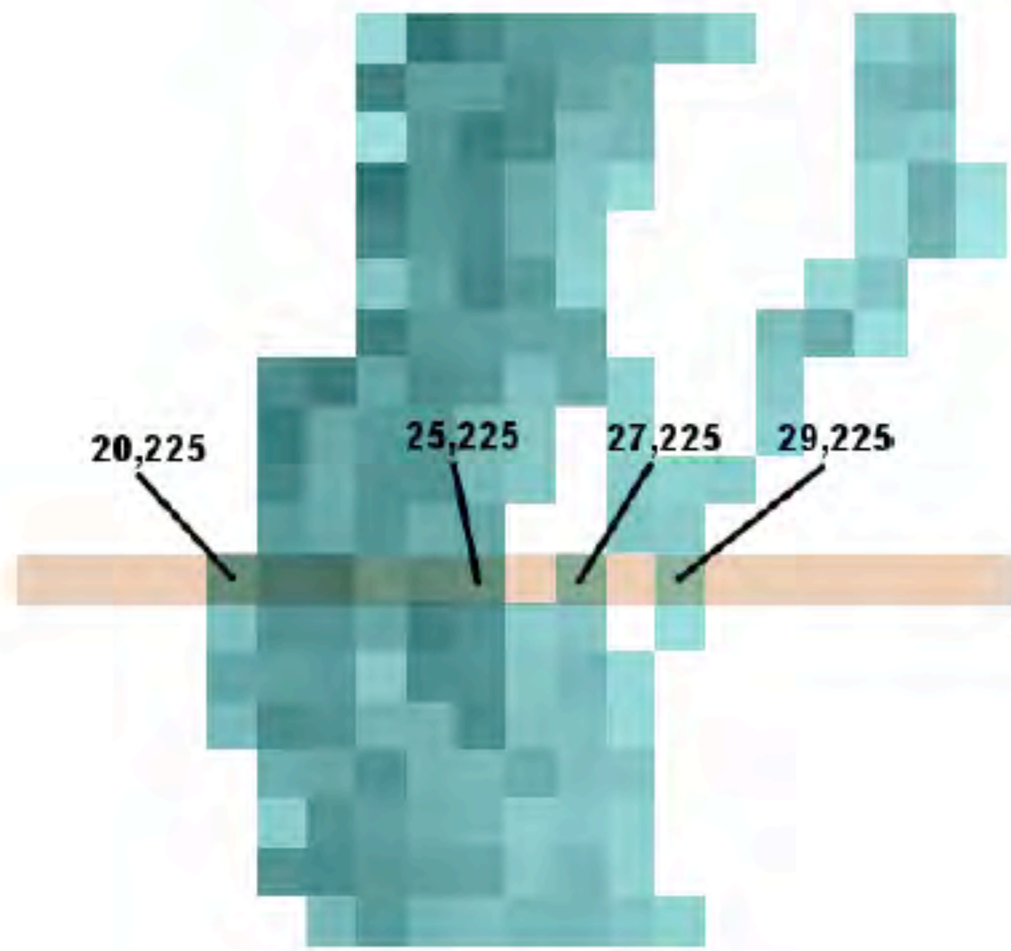
- Domain
  - Rectangle based
  - Interval based
  - 3D planewise domains
- Values
  - Rectangle based
  - Raged and interval based
  - Tiled

# Woolz Images

- Domain
  - Rectangle based
  - Interval based
  - 3D planewise domains

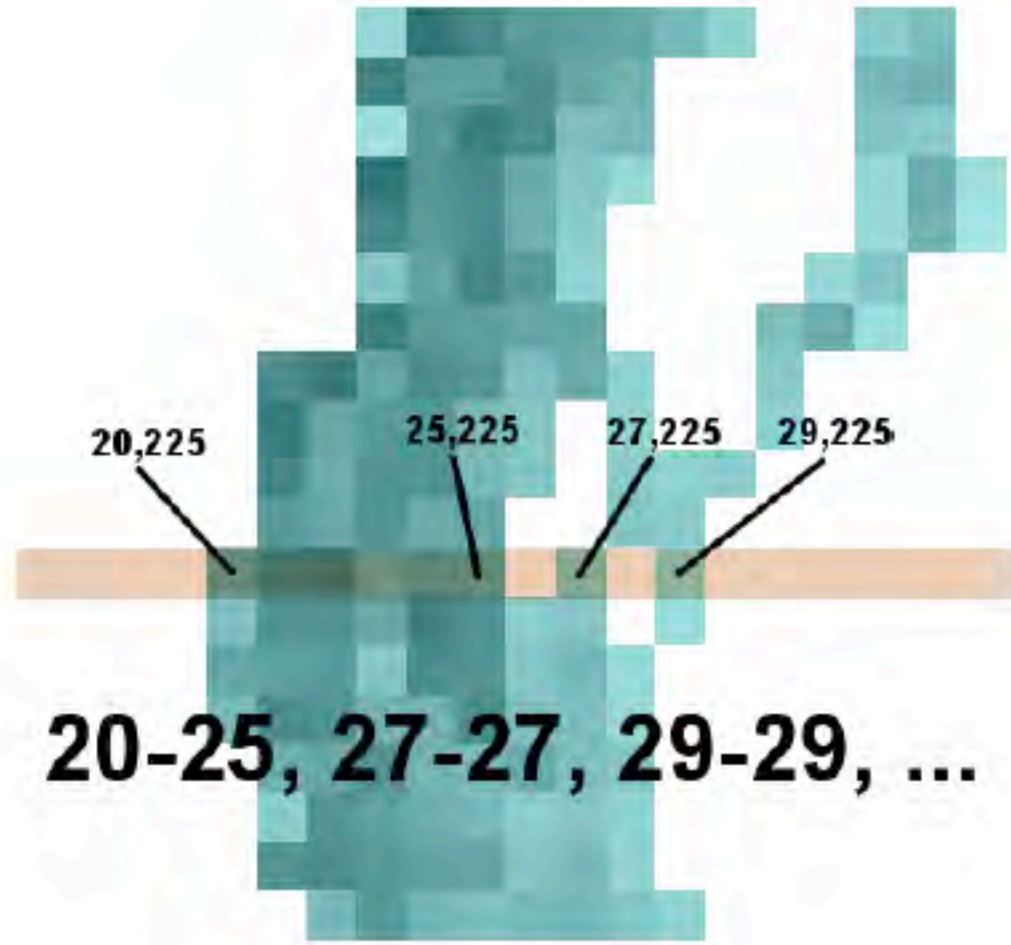
# Woolz Images

- Domain
  - Rectangle based
  - Interval based
  - 3D planewise domains
- Values
  - Rectangle based
  - Raged and interval based
  - Tiled



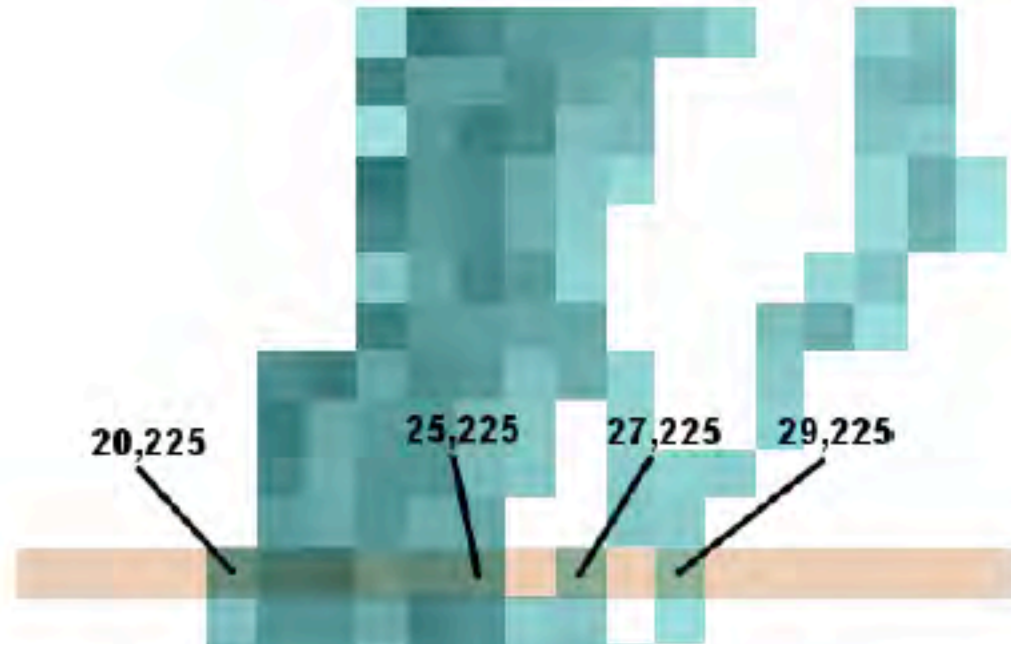
# Woolz Images

- Domain
  - Rectangle based
  - Interval based
  - 3D planewise domains
- Values
  - Rectangle based
  - Raged and interval based
  - Tiled



# Woolz Images

- Domain
  - Rectangle based
  - Interval based
  - 3D planewise domains
- Values
  - Rectangle based
  - Raged based
  - Tiled



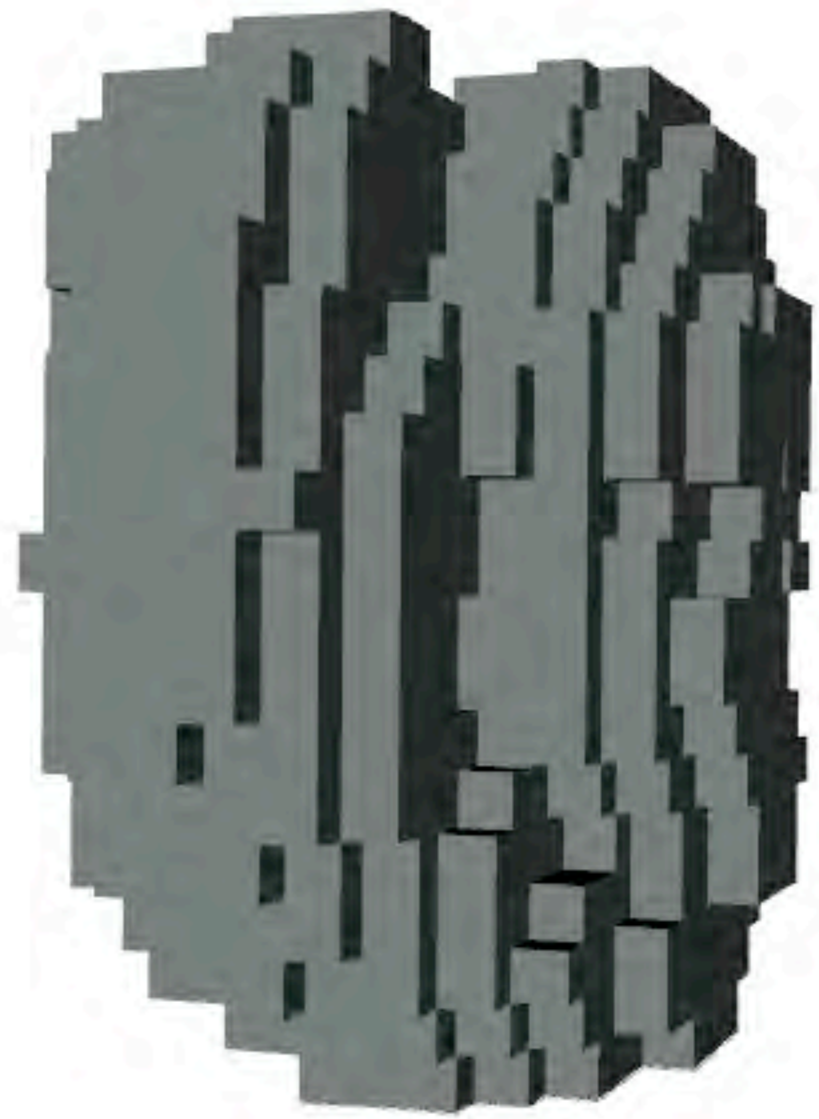

- Arbitrary bounding box
- Interval coding - compact
- Fast binary & morphological operations
- Separation of domain from values enables value data sharing

# Woolz Images

- Domain
  - Rectangle based
  - Interval based
  - 3D planewise domain
- Values
  - Rectangle based
  - Raged and interval based
  - Tiled

# Woolz Images

- Values
  - Rectangle based
  - Raged and interval based
  - Tiled



# Woolz Images

- Values
  - Rect
  - Rage base
  - Tiled

- value types: ubyte, short, int, float, double, rgba, bitmap
- Value table can be shared by many objects
- Compact coding without compression
- Iterators to navigate data
- Tiled data can be memory mapped for very fast access  - minimal coding change

# Woolz image objects

- Polylines, boundary lists
- histograms
- meshes - 2D & 3D
- transforms
  - affine
  - basis function
  - mesh
  - conforming mesh

# Woolz image objects

- Polylines, boundary lists
- histograms
- meshes - 2D & 3D
- transforms
  - affine
  - basis function
  - mesh
  - conforming mesh

$$\begin{pmatrix} t_{00} & t_{01} & t_{02} & t_{03} \\ t_{10} & t_{11} & t_{12} & t_{13} \\ t_{20} & t_{21} & t_{22} & t_{23} \\ 0 & 0 & 0 & t_{33} \end{pmatrix}$$

# Woolz image objects

- Polylines, boundary lists
- histograms
- meshes - 2D & 3D
- transforms
  - affine
  - basis function
  - mesh
  - conforming mesh

$$\Delta u = u - x$$

$$\Delta u = P_u(x, y) + \sum_{i=1}^{i=N} \lambda_i b(r_i)$$

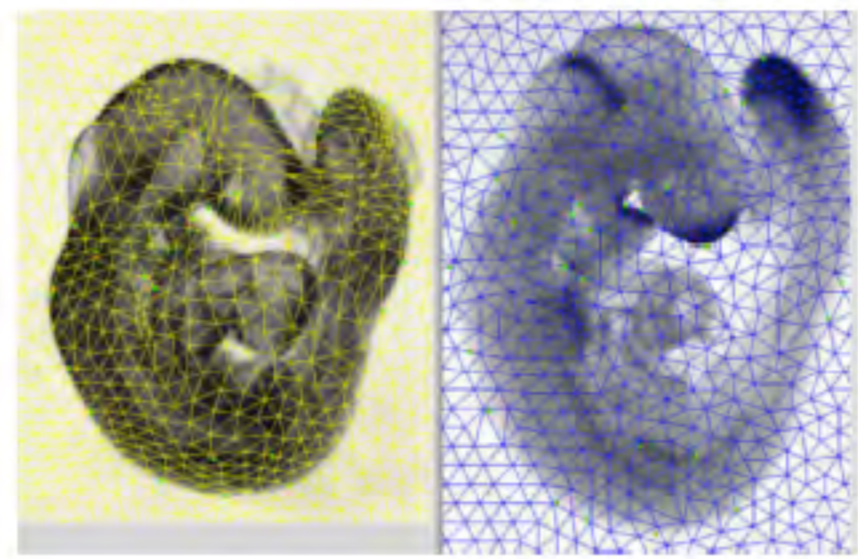
$$b_{TPS}(r) = r^2 ln(r^2)$$

$$b_{MQ}(r) = \sqrt{r^2 + \delta^2}$$

$$b_{IMQ}(r) = \frac{1}{\sqrt{r^2 + \delta^2}}$$

# Woolz image objects

- Polylines, boundary lists
- histograms
- meshes - 2D & 3D
- transforms
  - affine
  - basis function
  - mesh
  - conforming mesh



# Woolz image objects

- Polylines, boundary lists
- histograms
- meshes - 2D & 3D
- transforms
  - affine
  - basis function
  - mesh
  - conforming mesh

## Woolz image objects

- Review of OME image structures
- Woolz to GitHub
- JavaWlz re-instated
- Incorporation into ImageJ (Fiji)
- Issue of expressivity - arbitrary spatial domain location and offsets
- to be continued....

# Sparse Image Reconstruction & Mapping

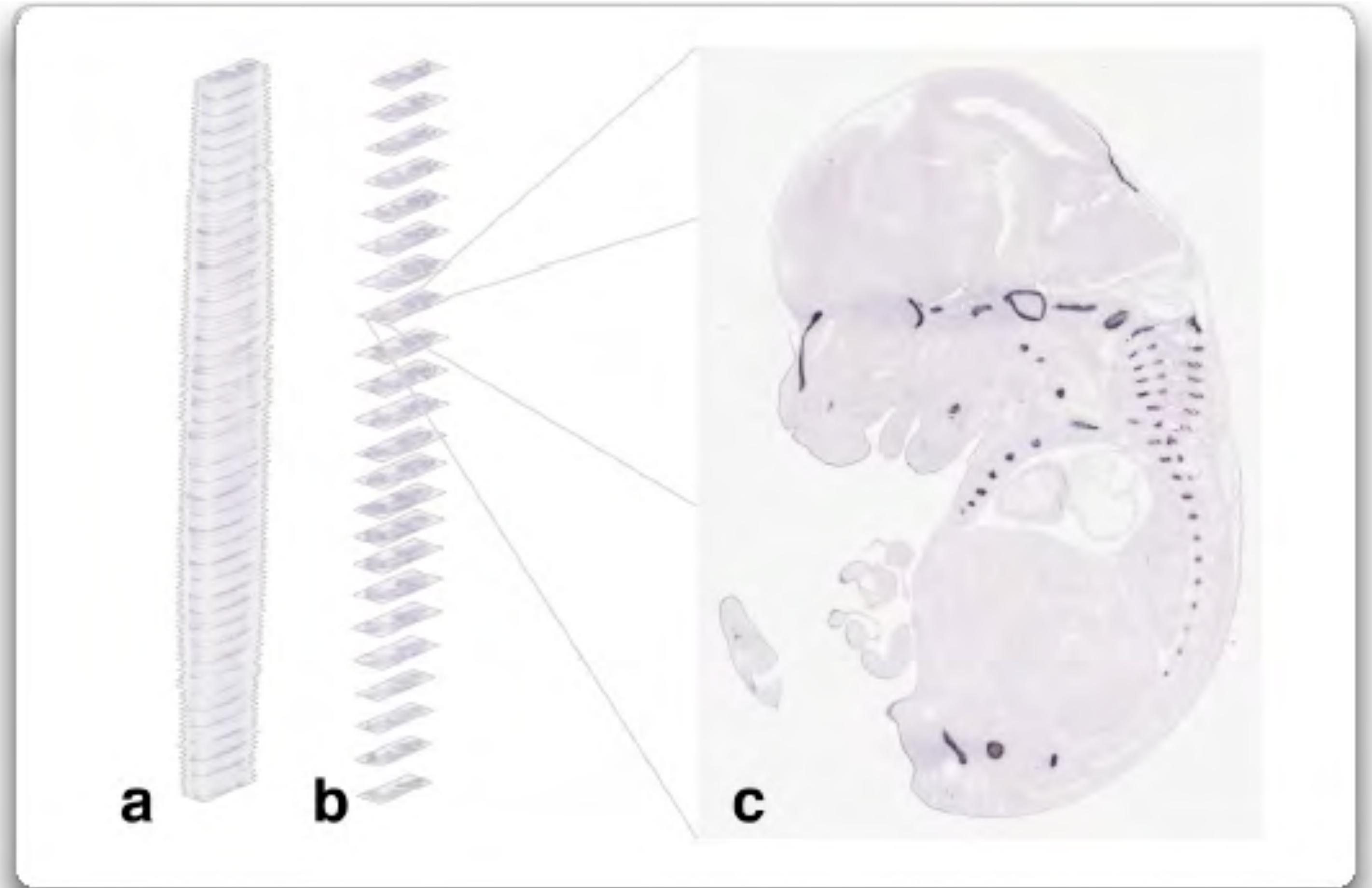
- EurExpress project
  - 19.5K in situ probes, 350K images
  - ~24 images per in situ probe
  - ~0.5 micron resolution in plane
  - 150 micron plane separation
- EmbryoExpress - 20K images
- Allen Brain Atlas - 200K images
- Require automation - Advanced Normalisation Tool (ANTs)
  - sparse image, matching mask
  - Full 3D affine then non-linear warping.

# Pseudo Wholemount Mapping to Emap - done

- Semi-automatic reconstruction
- Automated segmentation
- Manual mapping
- 2D pseudo wholemount
- full 3D in progress

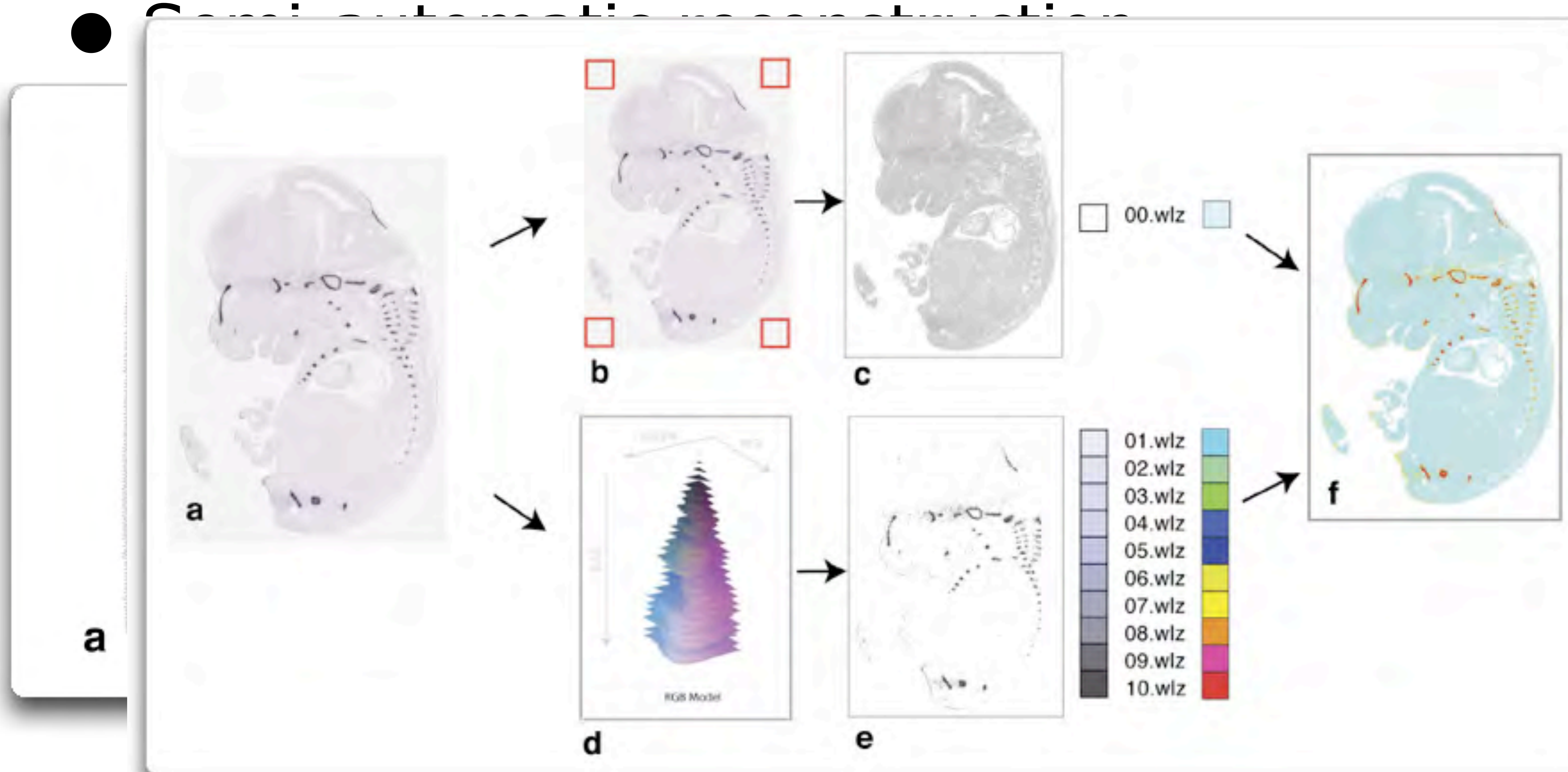
# Pseudo Wholemount Mapping to Emap - done

- Semi-automatic reconstruction



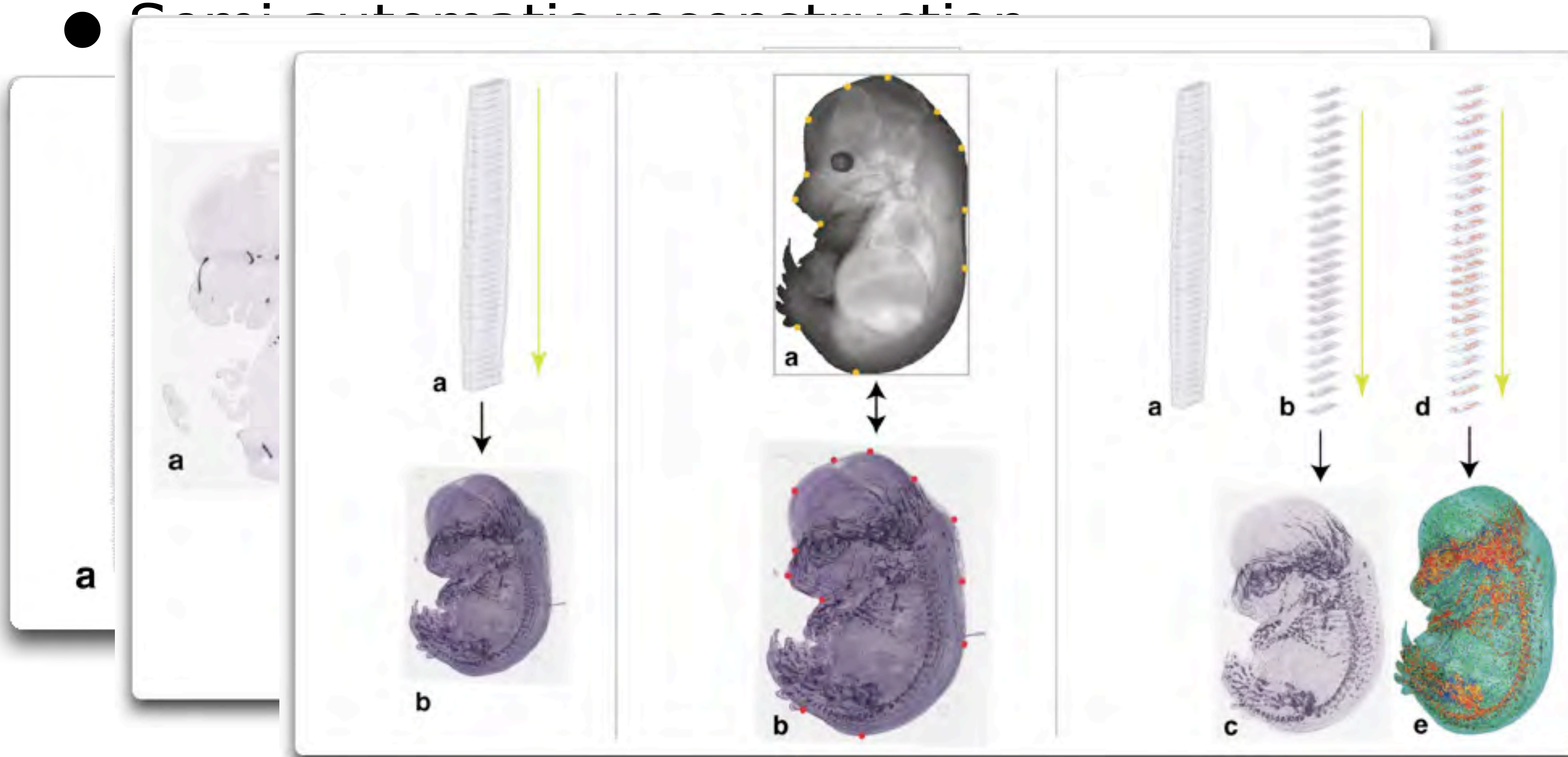
# Pseudo Wholemount Mapping to Emap - done

- Semi-automatic reconstruction

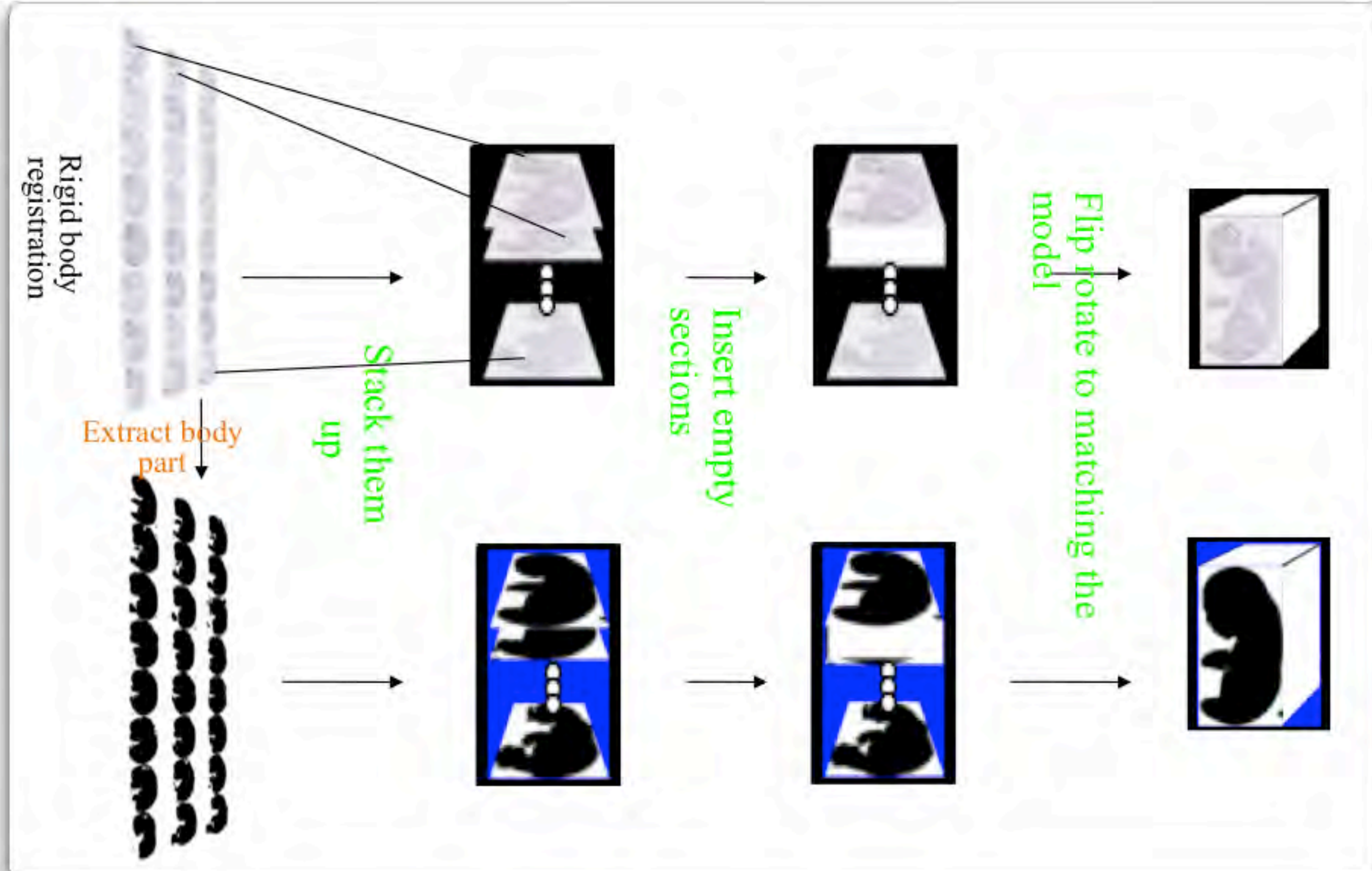


# Pseudo Wholemount Mapping to Emap - done

- Semi-automatic reconstruction



# 3D Mapping to emap

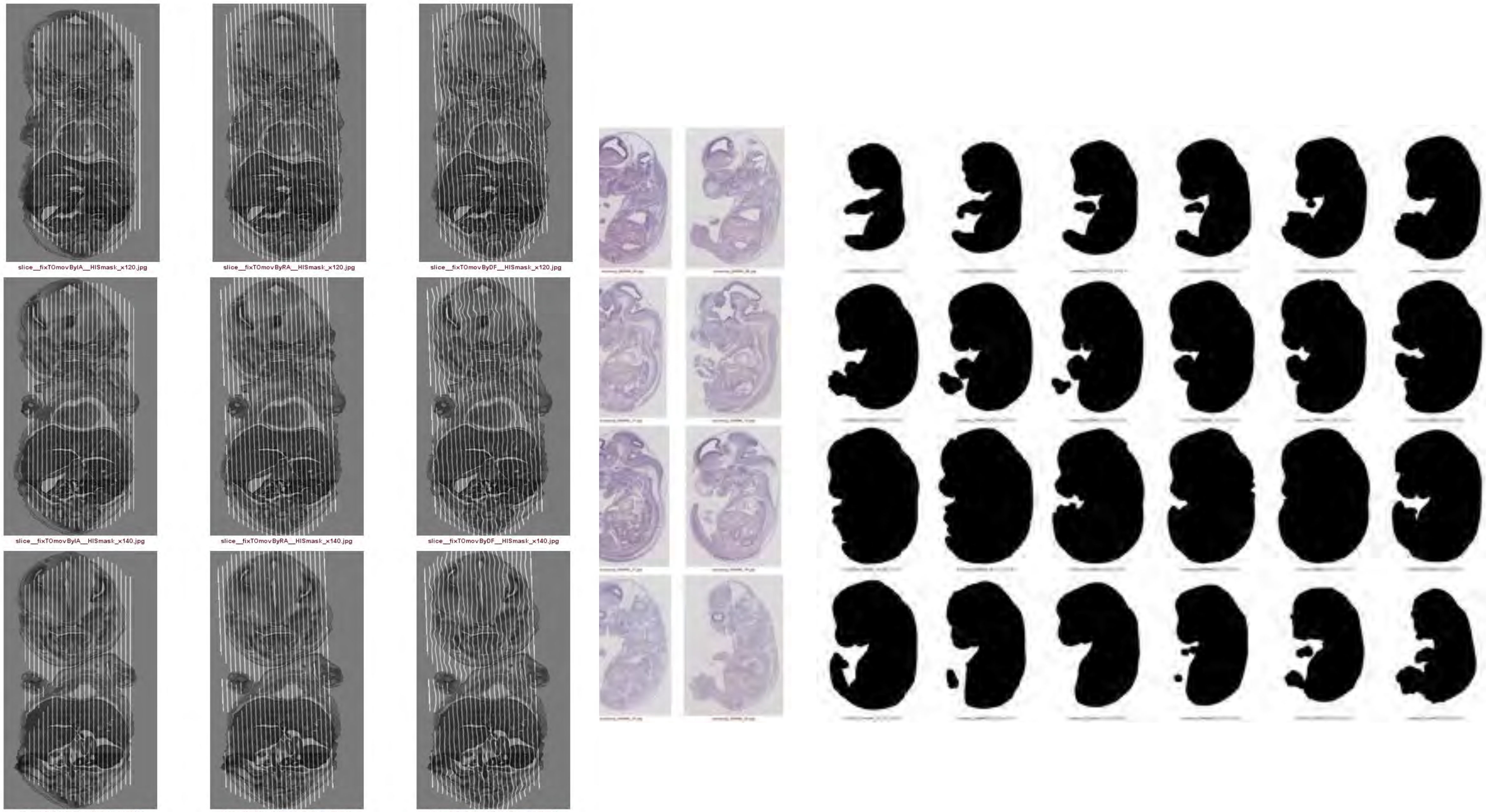


# 3D Mapping to emap

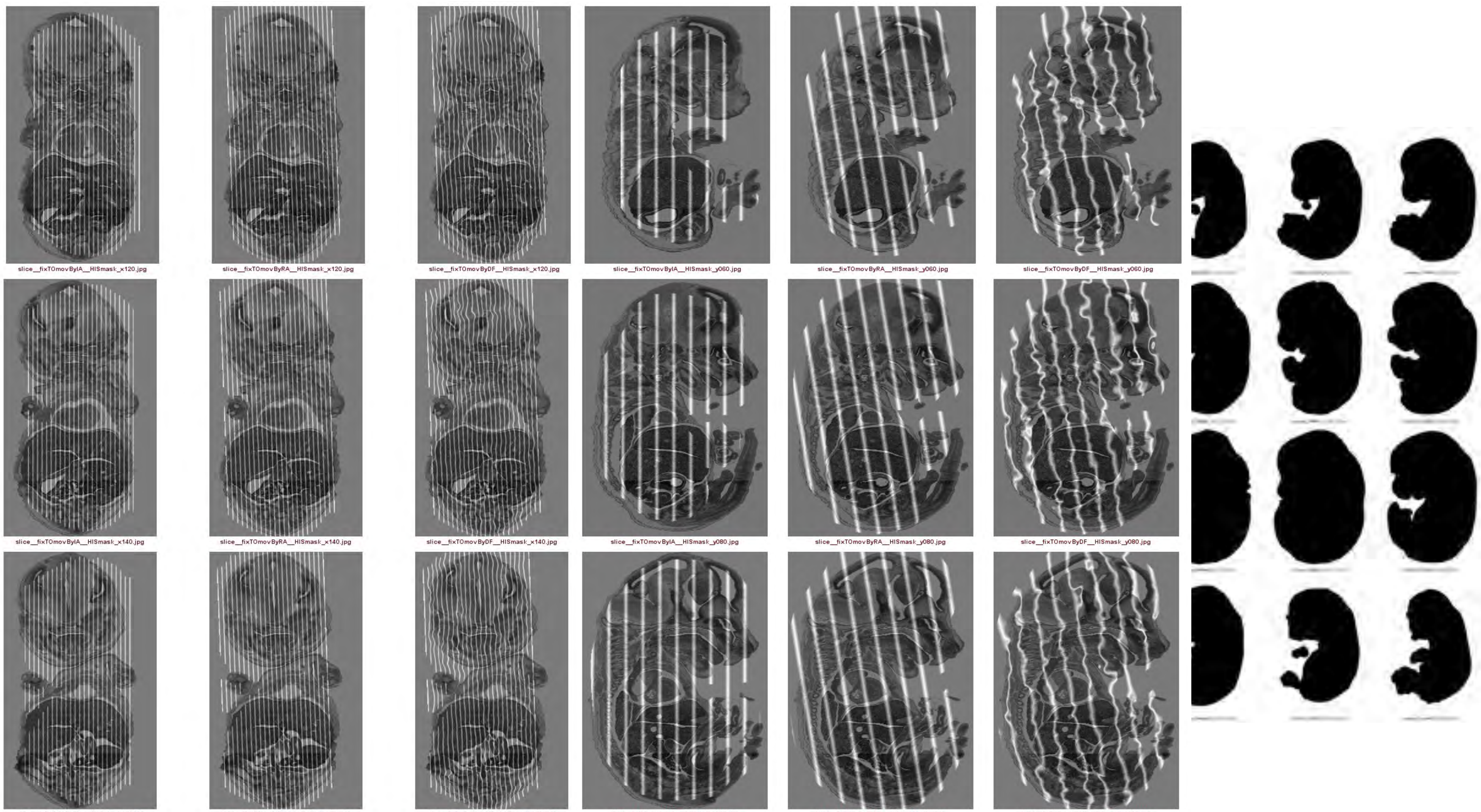


Thursday, 28 February 2013

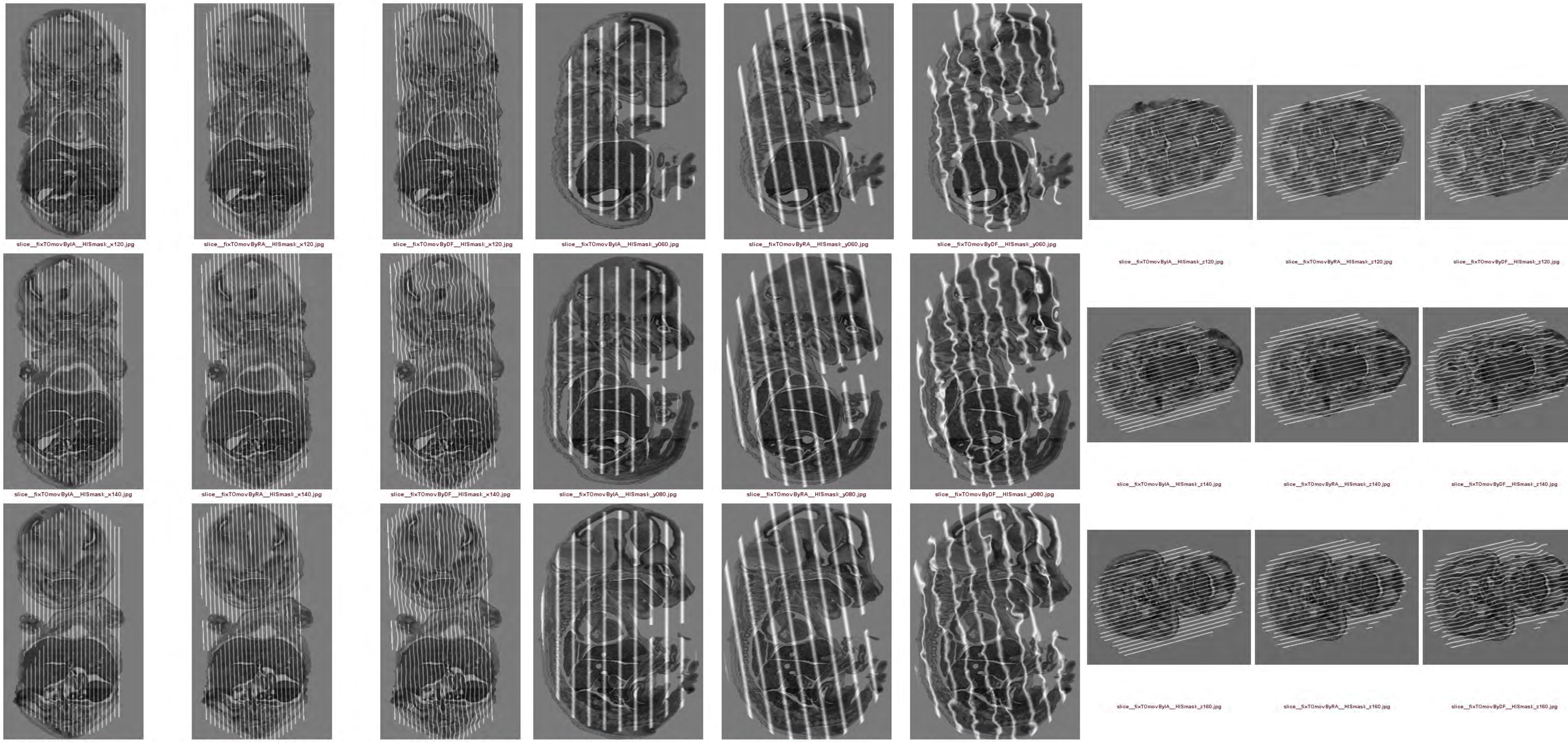
# 3D Mapping to emap



# 3D Mapping to emap



# 3D Mapping to emap

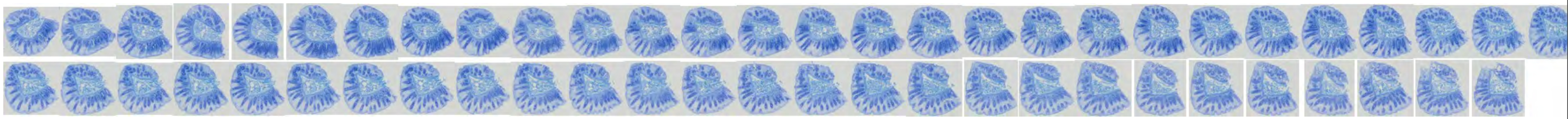


# Serial Section Reconstruction

- Typical task:
  - 2D high-res (.3 micron) histology
  - serial sections (1-2 micron)
  - 3D image for tissue module geometry and stats
  - reconstruction using non-linear registration
  - “user-friendly” i.e. no developer intervention

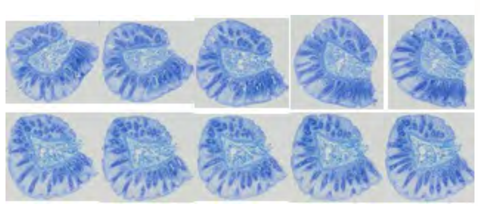
# Serial Section Reconstruction

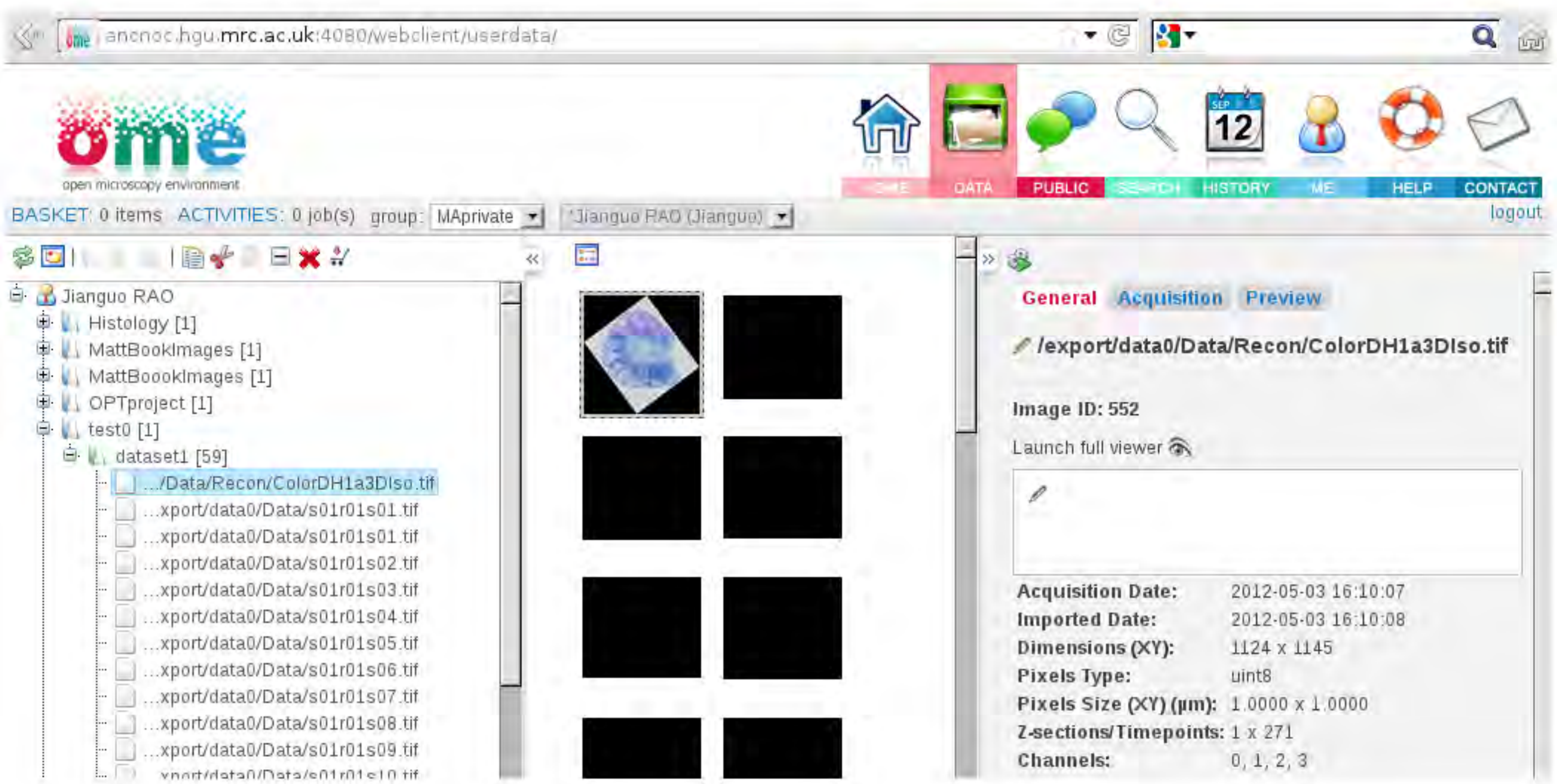
- Typical task:
  - 2D high-res (.3 micron) histology
  - serial sections (1-2 micron)
  - 3D image for tissue module geometry and stats
  - reconstruction using non-linear registration
  - “user-friendly” i.e. no developer intervention

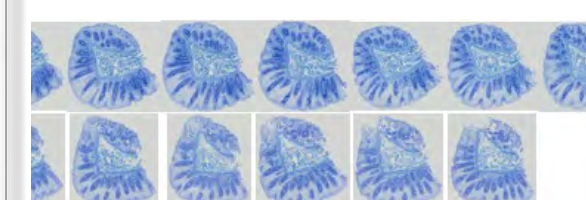


# Serial Section Reconstruction

- Typical task:
  - 2D high-res (.3 micron) histology
  - serial sections (1-2 micron)
  - 3D image for tissue module geometry and stats
  - recon on
  - “user- tion





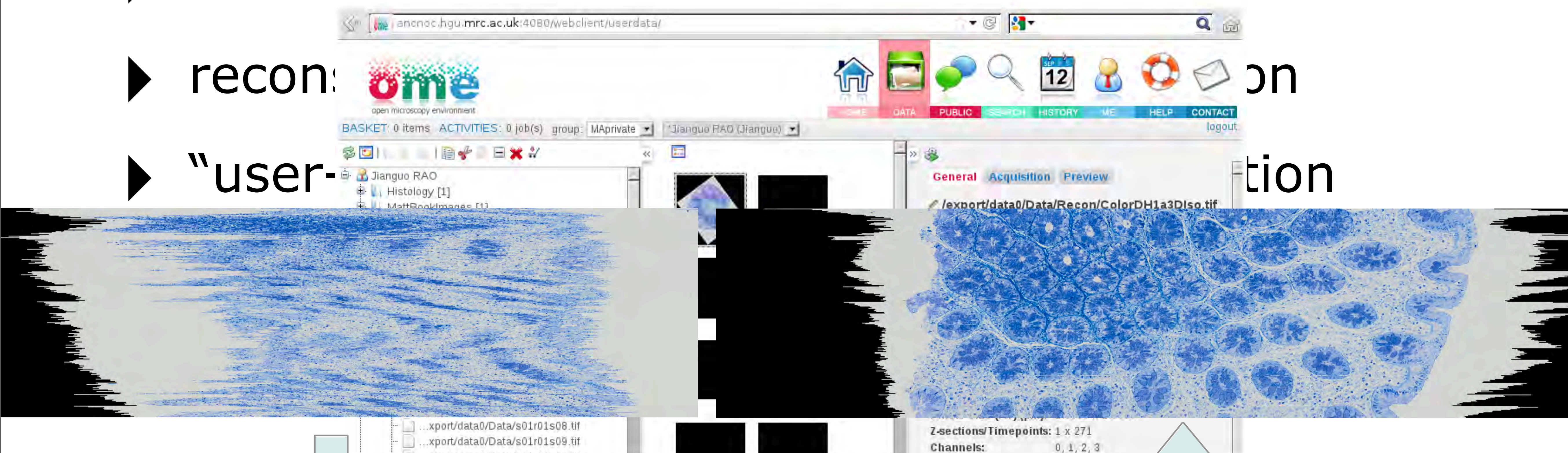





Thursday, 28 February 2013

# Serial Section Reconstruction

- Typical task:
  - 2D high-res (.3 micron) histology
  - serial sections (1-2 micron)
  - 3D image for tissue module geometry and stats
  - recon… on
  - “user-… tion

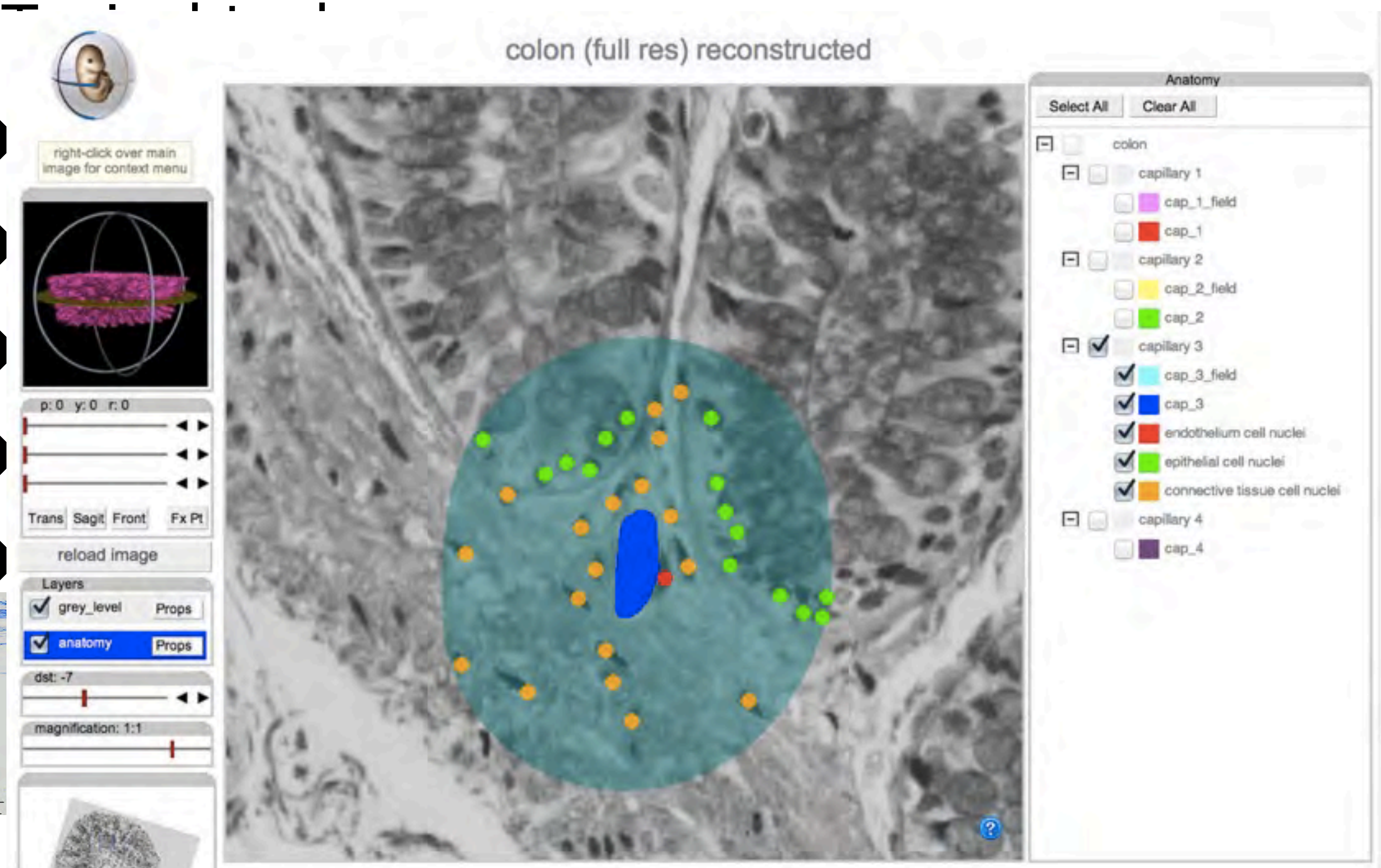



ITK based registration



MRC Human Genetics Unit

# Serial Section Reconstruction



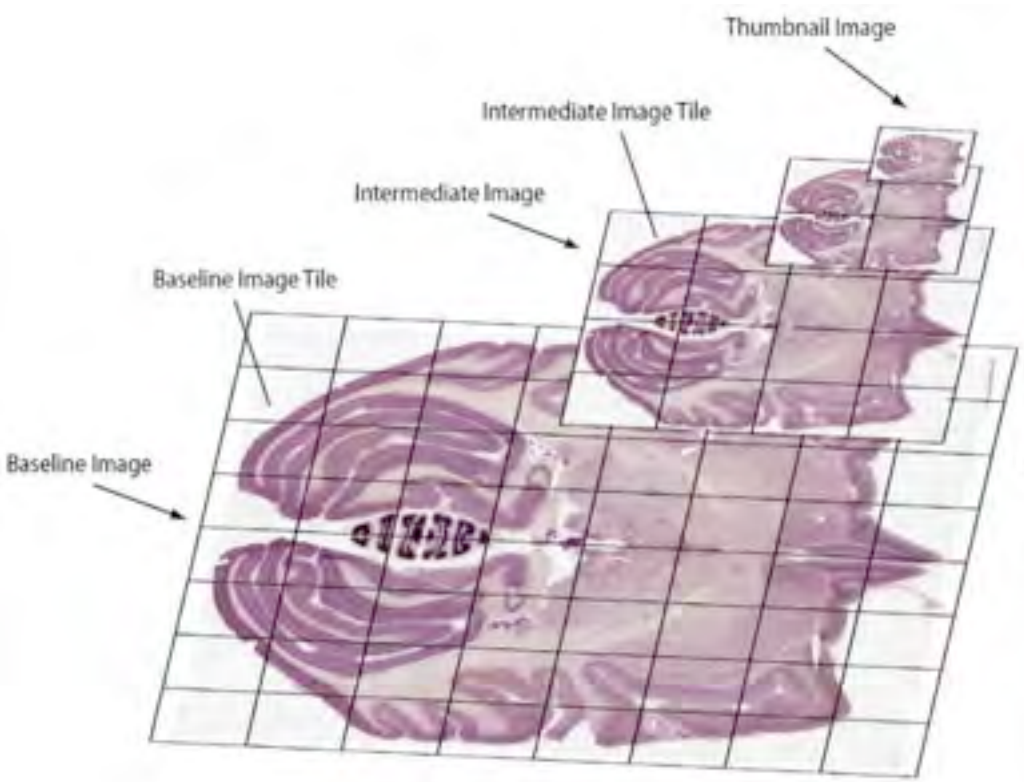

ITK based registration

# Large Image Data

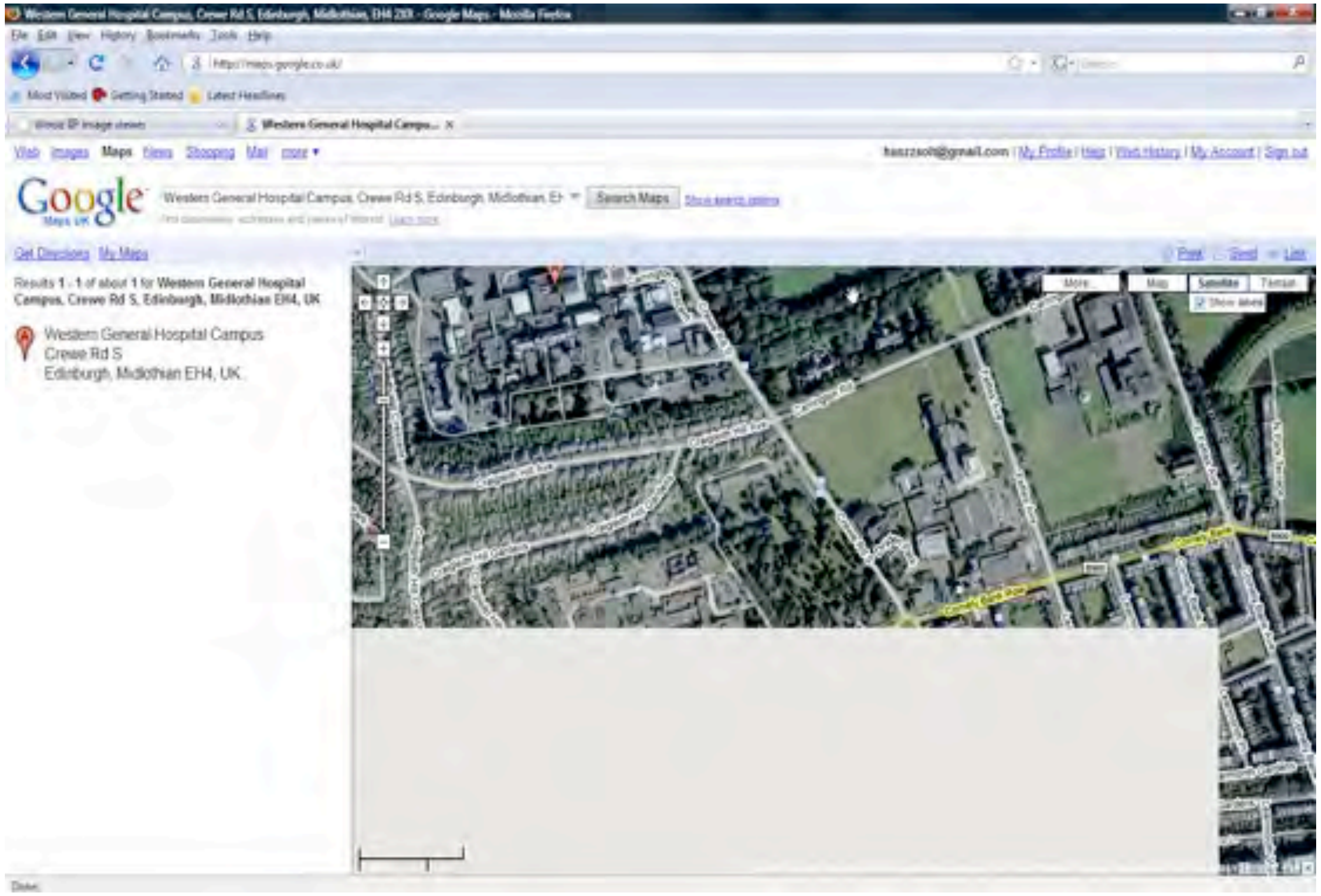
- Single light microscopy reconstructions already 30+GB, microCT sets ~200GB
- New EM embryo data ~0.5TB
- OPT data - small (200MB) but many - 5K
- Typical requirement to browse as sections
- Require arbitrary angle re-sectioning

- BLB - want to browse online using no more that a web-browser

# Tiled Image Servers



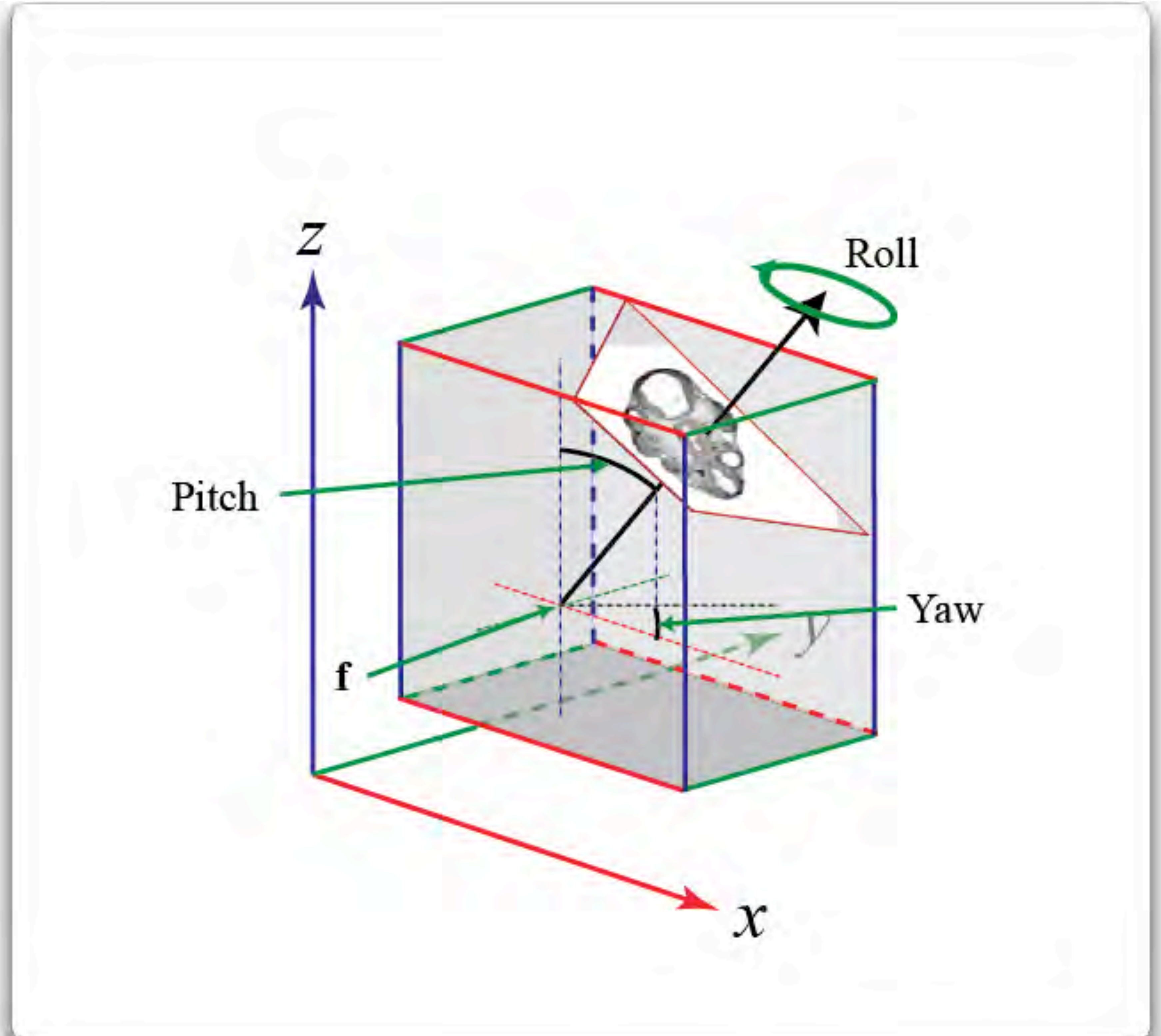

[Shawn Mikula, Issac Trotts, James M. Stone, and Edward G. Jones,Internet-Enabled High-Resolution Brain Mapping and Virtual Microscopy, Neuroimage, vol 35(1), p. 11, 2007]



[maps.google.com]

# Sectioning Parameters

- Angles:
  - Pitch, Yaw, Roll
- Position:
  - Fixed point (f) & distance
- Scale
- Tiling depends on orientation & scale



# IIP3D - Extensions

| Command | Purpose | Syntax |
|---|---|---|
| **WLZ** | Specify the Woolz object | `WLZ=`*path* |
| **DST** | Specify the distance of the sectioning plane | `DST=`*dis* |
| **FXP** | Specify the fixed point of the viewing section rotation | `FXP=`*X,Y,Z* |
| **FXT** | Specify the second fixed point of the viewing section rotation | `FXT=`*X,Y,Z* |
| **MOD** | Specify the projection mode | `MOD=`*mode* |
| **PIT** | Specify the pitch angle of the sectioning rotation | `PIT=`*angle* |
| **PAB** | Specify the 3D query point absolute in the object coordinate | `PAB=`*X,Y,Z* |
| **PRL** | Specify the 2D query point relative in tile or display or tile co-ordinate | `PRL=`*T,X,Y* |
| **ROL** | Specify the roll angle of the sectioning rotation | `ROL=`*angle* |
| **SCL** | Specify the scale used in the sectioning transformation | `SCL=`*scale* |
| **UPV** | Specify the up vector for the **UP_IS_UP** mode | `UPV=`*X,Y,Z* |
| **YAW** | Specify the yaw angle of the sectioning rotation | `YAW=`*angle* |

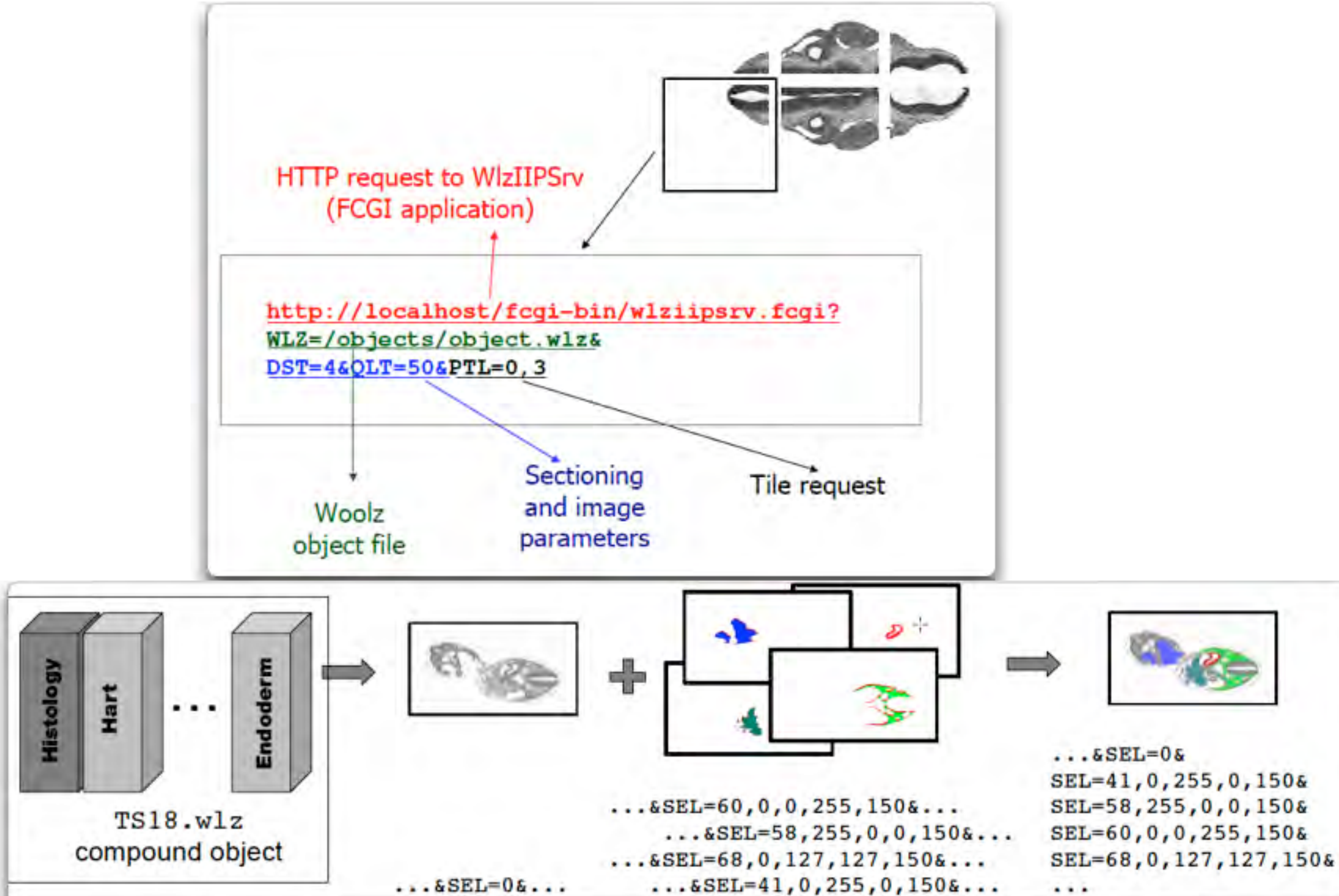
Table 1: Extended command overview

| Object | Purpose |
|---|---|
| **IIP-server** | Identify if WLZ-IIP is running |
| **Max-size** | The size of the section |
| **Tile-size** | The size of a tile |
| **Wlz-true-voxel-size** | The voxel size of the object |
| **Wlz-volume** | The volume of the object |
| **Wlz-distance-range** | The range of the sectioning plane distance |
| **Wlz-sectioning-angles** | The pitch, yaw and roll angles of of the sectioning plane |
| **Wlz-3d-bounding-box** | The first and last plane, line and column number of the object |
| **Wlz-coordinate-3D** | The 3D coordinates defined in 2D by the **PRL** command |
| **Wlz-grey-value** | The grey or RGB value of a point specified either the **PRL** or the **PAB** commands |

Table 2: Extended object overview

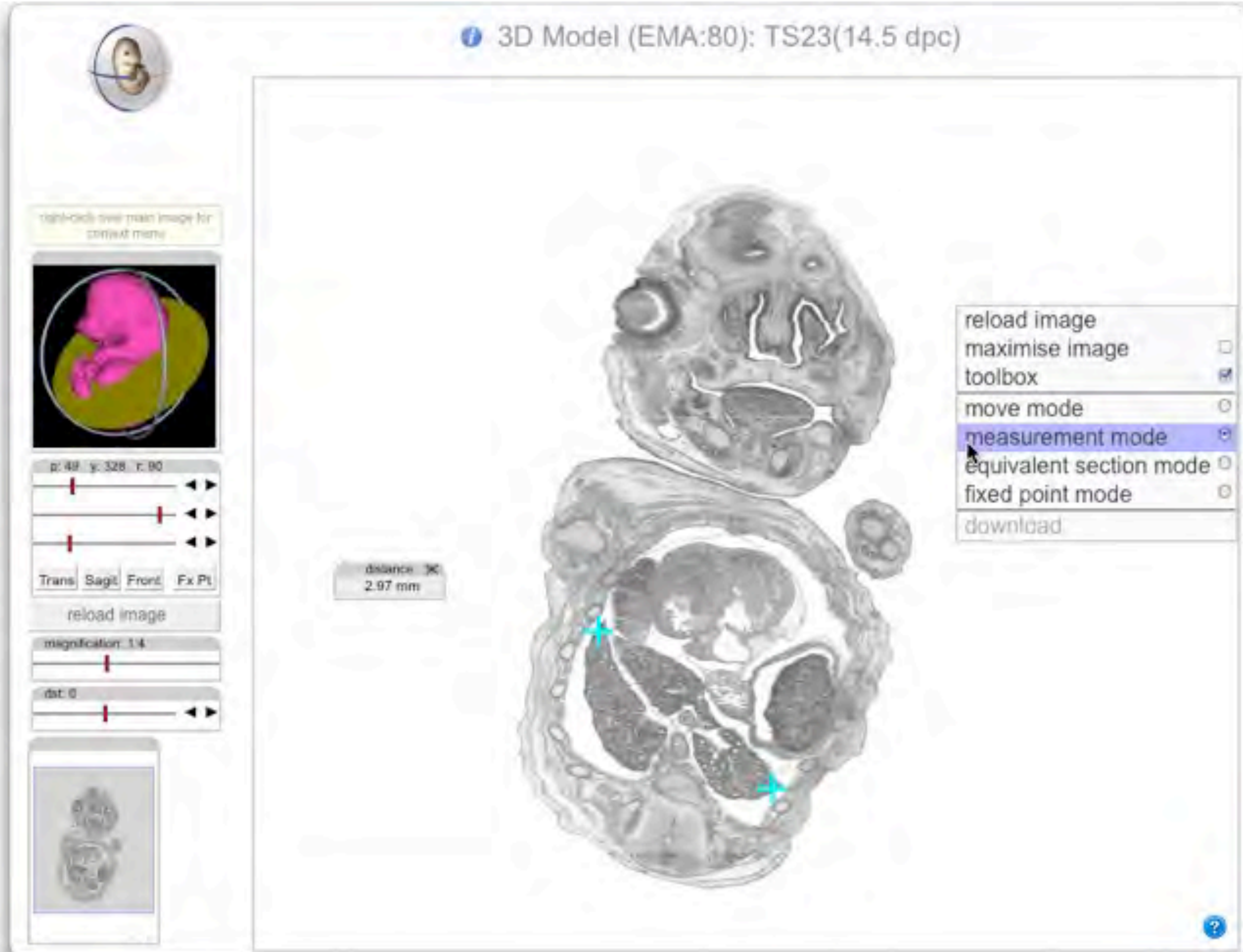
R A Baldock

# IIP3D

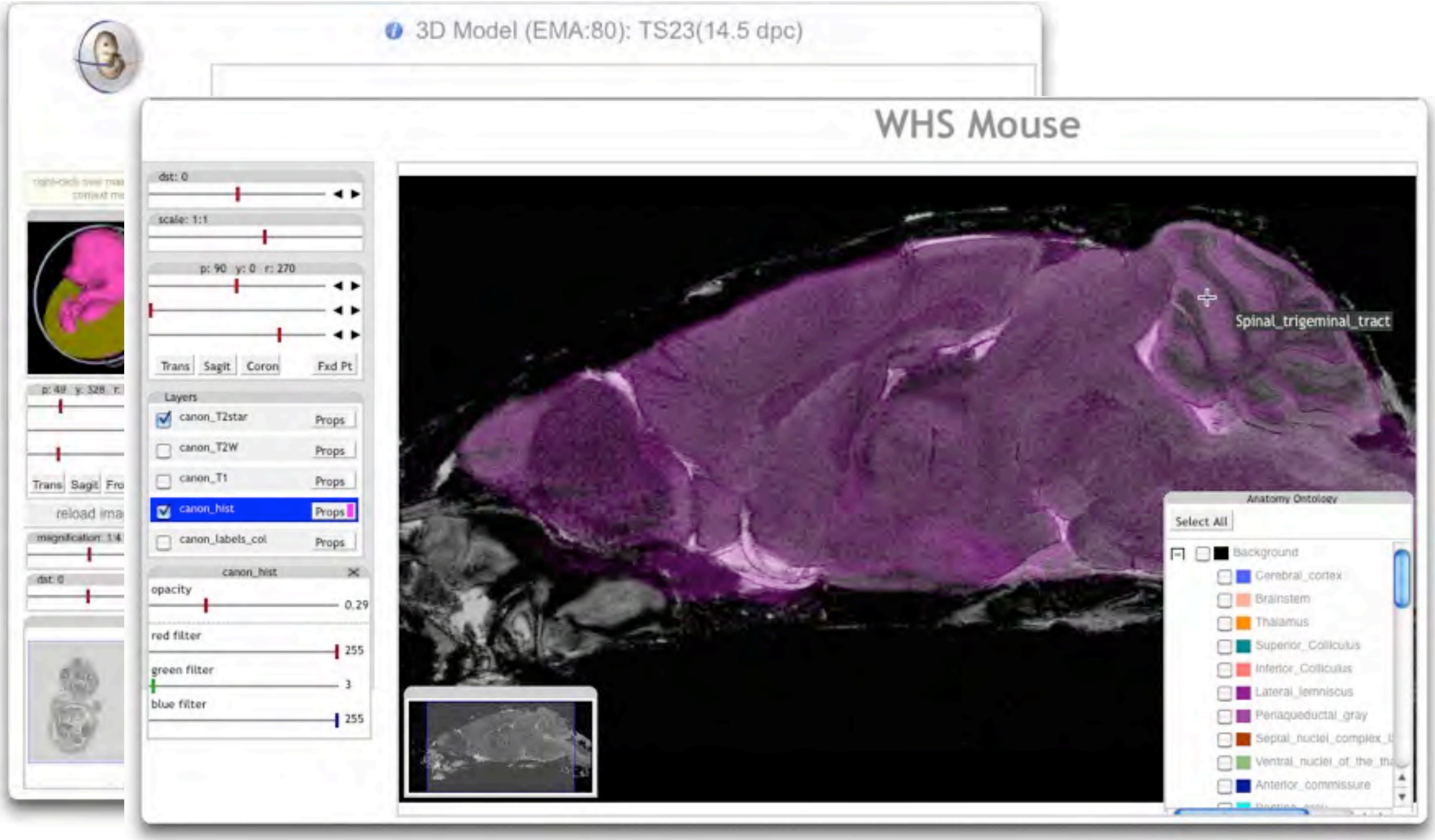


HTTP request to WlzIIPSrv
(FCGI application)
http://localhost/fcgi-bin/wlziipsrv.fcgi?
WLZ=/objects/object.wlz&
DST=4&QLT=50&PTL=0,3
Woolz
object file
Sectioning
and image
parameters
Tile request
Histology
Hart
...
Endoderm
TS18.wlz
compound object
...&SEL=0&...
...&SEL=60,0,0,255,150&...
...&SEL=58,255,0,0,150&...
...&SEL=68,0,127,127,150&...
...&SEL=41,0,255,0,150&...
...&SEL=0&
SEL=41,0,255,0,150&
SEL=58,255,0,0,150&
SEL=60,0,0,255,150&
SEL=68,0,127,127,150&
...

# IIP3D Examples

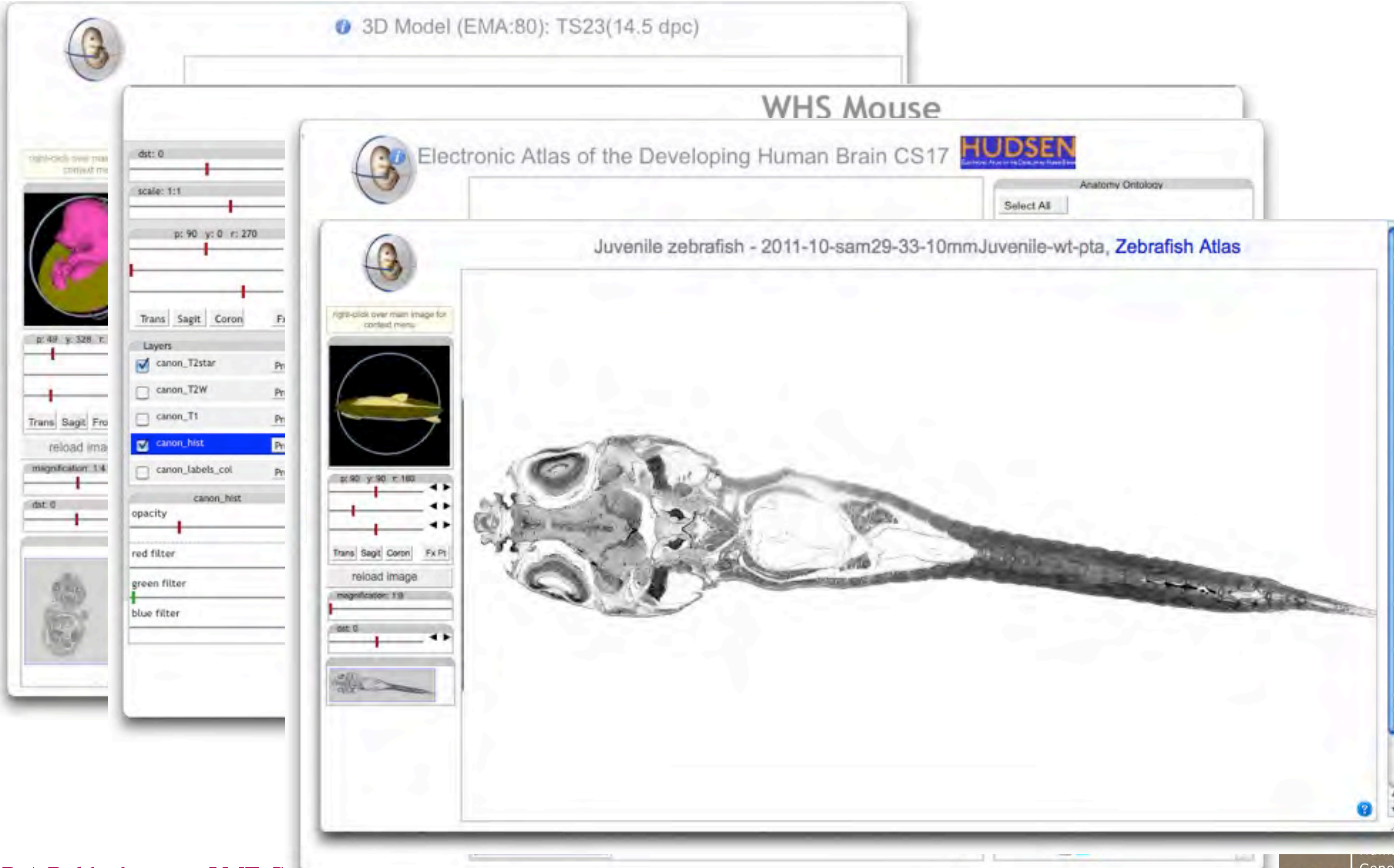


# IIP3D Examples

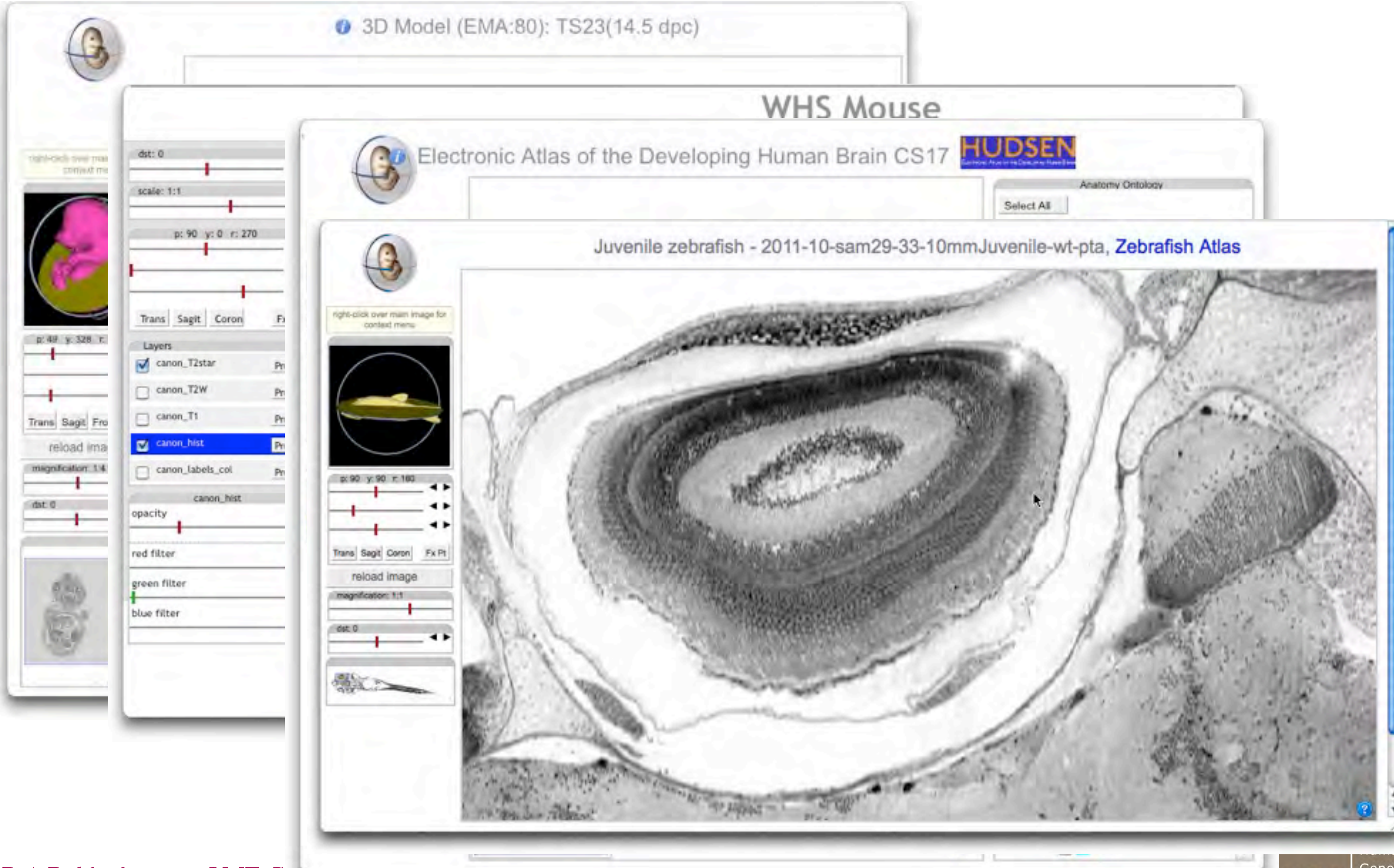


# IIP3D Examples

# IIP3D Examples



# IIP3D Examples






Thursday, 28 February 2013

# Image Processing IIP3D extensions

| Operator | Description |
|---|---|
| diff(*exp*,*exp*) | The difference between the two given domains. |
| dilation(*exp*,*radius*) | The dilation of the domain by *radius* voxels. |
| domain(*exp*) | The domain of an object. |
| erosion(*exp*,*radius*) | The erosion of the domain by *radius* voxels. |
| intersect(*exp list*) | The intersection of the domains in the given lists. |
| threshold(*exp*,*value*,*comparison*) | Creates an object where the image values satisfy the given *value* and *comparison*. Here the value is floating point and valid comparisons are `lt` (less than), `le` (less than or equal), `eq` (equal), `ge` (greater than or equal) and `gt)` (greater than). |
| union(*exp list*) | The union of the domains in the given lists. |

Table 4: Descriptions of morphological operators

<table>
<tr><td>exp list</td><td>:=</td><td>(exp | idx list)(,exp list)</td></tr>
<tr><td>idx list</td><td>:=</td><td>(idx | (idx-) | (idx-idx) | (-idx))(,idx list)</td></tr>
<tr><td>exp</td><td>:=</td><td>idx) |</td></tr>
<tr><td></td><td></td><td>diff(exp,exp) |</td></tr>
<tr><td></td><td></td><td>dilation(exp,uint) |</td></tr>
<tr><td></td><td></td><td>domain(exp) |</td></tr>
<tr><td></td><td></td><td>erosion(exp,uint) |</td></tr>
<tr><td></td><td></td><td>intersect(exp list,exp list) |</td></tr>
<tr><td></td><td></td><td>threshold(exp,val,cmp)</td></tr>
<tr><td></td><td></td><td>union(exp list,exp list) |</td></tr>
<tr><td>idx</td><td>:=</td><td><code>[0-9]+</code></td></tr>
<tr><td>uint</td><td>:=</td><td><code>[1-9][0-9]*</code></td></tr>
<tr><td>val</td><td>:=</td><td><code>[-+]?[0-9]*.?[0-9]+([eE][-+]?[0-9]+)?</code></td></tr>
<tr><td>cmp</td><td>:=</td><td><code>(lt)|(le)|(eq)|(ge)|(gt)</code></td></tr>
</table>

Table 3: Syntax for morphological expressions.

# Image Processing IIP3D extensions

| Operator | Description |
| --- | --- |
| diff(*exp*,*exp*) | The difference between the two given domains. |
| dilation(*exp*,*radi* | voxels. |
| domain(*exp*) | |
| erosion(*exp*,*radiu* | oxels. |
| intersect(*exp list* | given lists. |
| threshold(*exp*,*val* | values sat- Here the arisons are **eq** (equal), eater than). |
| union(*exp list*) | lists. |

| MAP | | |
| --- | --- | --- |
| | **Purpose** | Defines a colour or grey value mapping. Grey values outside the mapped region are clamped to the minimum and maximum output colour componentor grey values. There may be 1,2,3 or 4 mapping specifications given; with a single mapping specification meaning a grey value mapping, two specifications a grey with alpha mapping, three an RGB mapping and four an RGB$\alpha$ mapping. |
| | **Syntax** | `MAP=`*mspec*`[,`*mspec*`[,`*mspec*`[,`*mspec*`]]]`<br>where *mspec*=*t*,*il*,*iu*,*ol*,*ou*,*p0*,*p1* |
| | **Input Parameters** | $t \in$ *IDENTITY \| LINEAR \| GAMMA \| SIGMOID*<br>The mapping function<br>`FLOAT` *il*<br>Input lower grey value<br>`FLOAT` *il*<br>Input upper grey value<br>`FLOAT` *ol*<br>Output lower colour component or grey value<br>`FLOAT` *ol*<br>Output upper colour component or grey value<br>`FLOAT` *p0*<br>Gamma ($\gamma$)or first sigmoid parameter ($\mu$)<br>`FLOAT` *p1*<br>Second sigmoid parameter ($\sigma$) |
| | **Response** | none |
| | **Example** | ⇒`MAP=LINEAR,0,4095,0,255`<br>Input grey values in the range 0-4095 are mapped to output values with the range 0-255 |
| | **Default value** | `IDENTITY` |

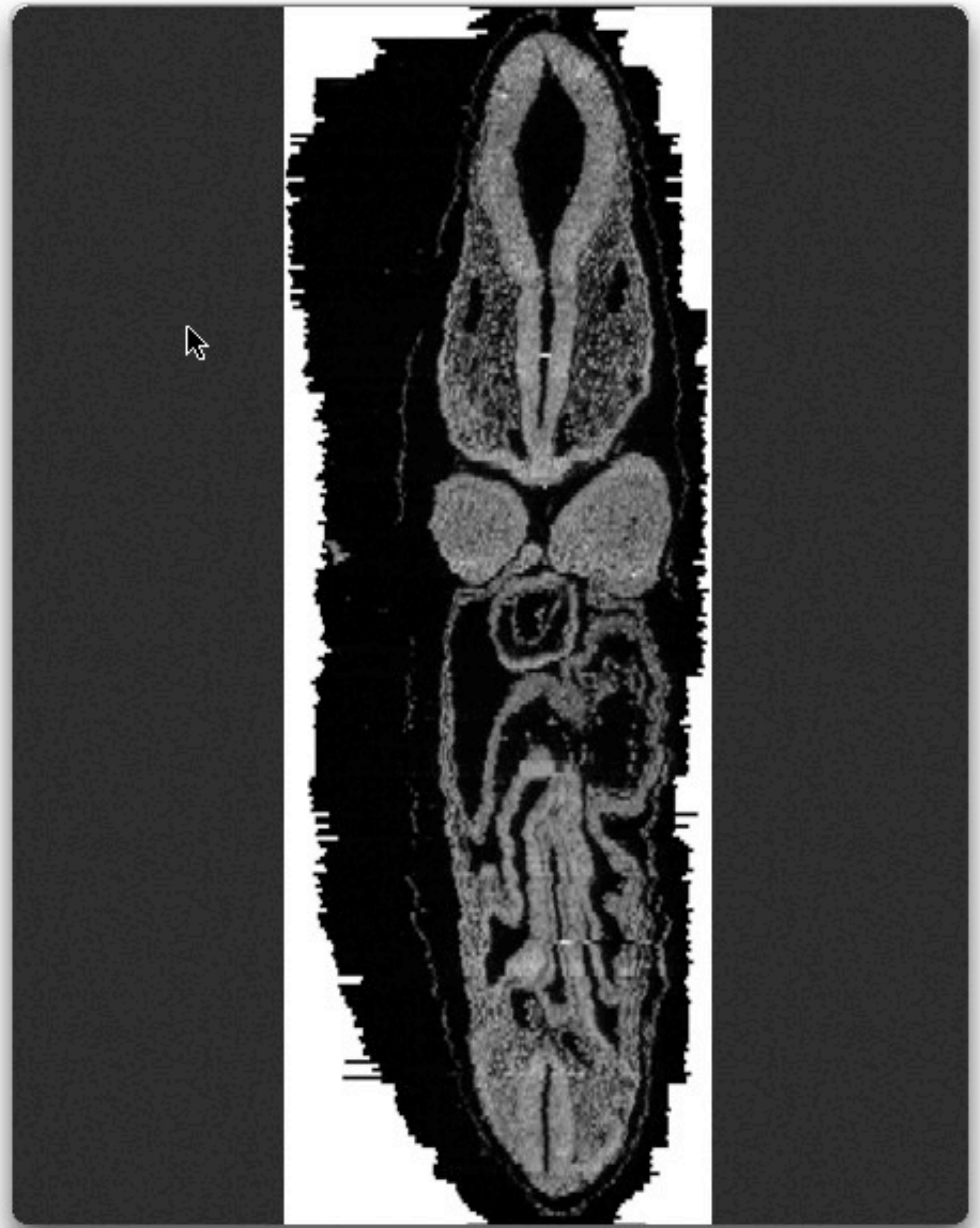
Table 3: Syntax for morphological expressions.

# Image Processing IIP3D extensions

SEL=0&MAP=LINEAR,0,255,255,0&QLT=50&CVT=jpeg

# Image Processing IIP3D extensions

SEL=0&MAP=LINEAR,0,255,255,0&QLT=50



# Image Processing IIP3D extensions

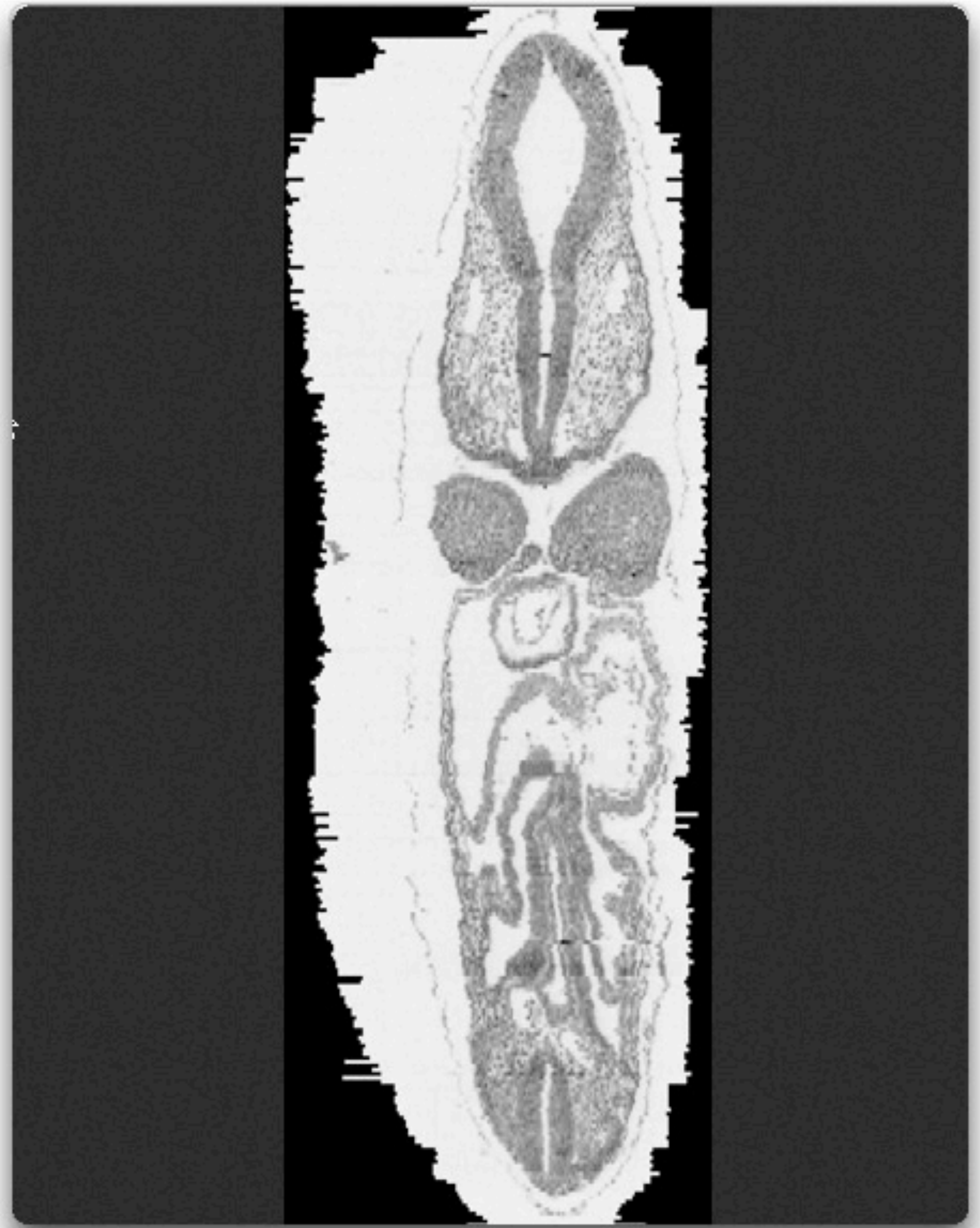
SEL=0&MAP=LINEAR,0,255,255,0&QLT=50&CVT=jpeg

SEL=0&MAP=LINEAR,0,4096,0,255&QLT=50&CVT=jpeg

# Image Processing IIP3D extensions

SEL=0&MAP=LINEAR,0,255,255,0&QLT=50

SEL=0&MAP=LINEAR,0,4096,0,255&QLT=5



# Image Processing IIP3D extensions

SEL=0&MAP=LINEAR,0,255,255,0&QLT=50&CVT=jpeg

SEL=0&MAP=LINEAR,0,4096,0,255&QLT=50&CVT=jpeg

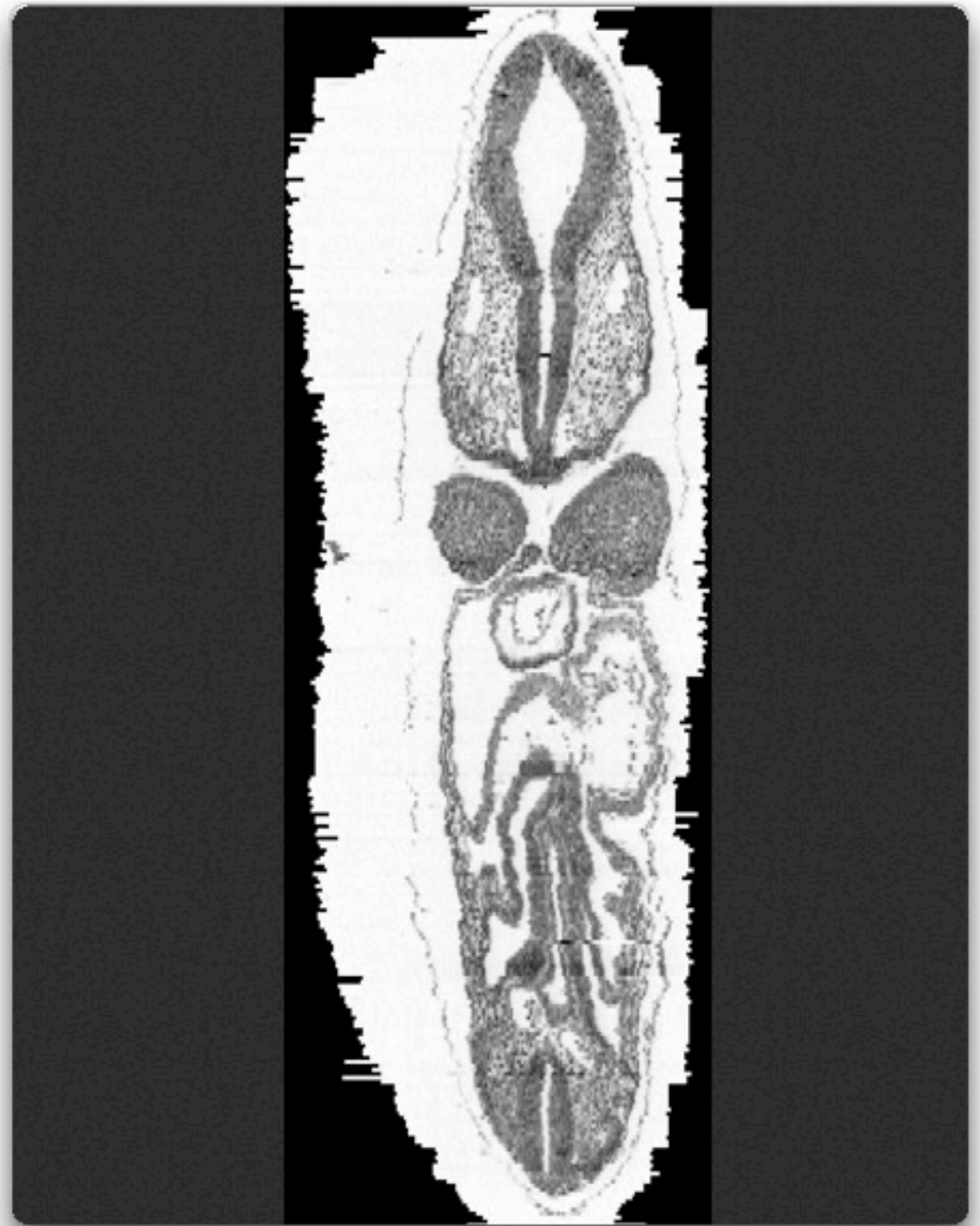
SEL=0&MAP=GAMMA,0,255,0,255,1.6&QLT=50&CVT=jpeg

# Image Processing IIP3D extensions

SEL=0&MAP=LINEAR,0,255,255,0&QLT=50

SEL=0&MAP=LINEAR,0,4096,0,255&QLT=5

SEL=0&MAP=GAMMA,0,255,0,255,1.6&QLT



# Image Processing IIP3D extensions

SEL=0&MAP=LINEAR,0,255,255,0&QLT=50&CVT=jpeg

SEL=0&MAP=LINEAR,0,4096,0,255&QLT=50&CVT=jpeg

SEL=0&MAP=GAMMA,0,255,0,255,1.6&QLT=50&CVT=jpeg

SEL=0&MAP=LINEAR,0,255,0,0,LINEAR,0,255,0,255,LINEAR,0,255,0,255&QLT=50&CVT=jpeg

# Image Processing IIP3D extensions

SEL=0&MAP=LINEAR,0,255,255,0&QLT=50

SEL=0&MAP=LINEAR,0,4096,0,255&QLT=5

SEL=0&MAP=GAMMA,0,255,0,255,1.6&QLT

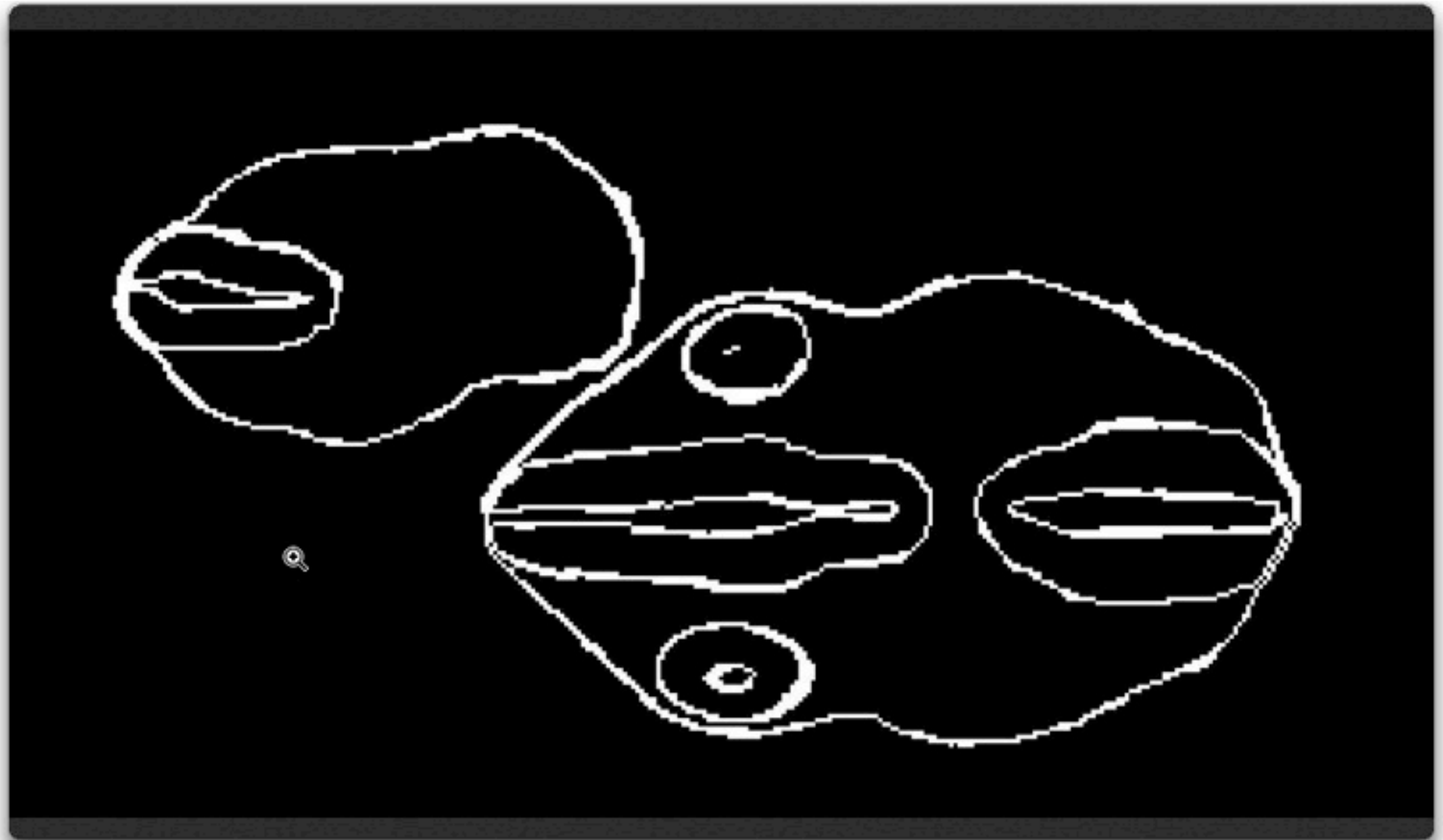
SEL=0&MAP=LINEAR,0,255,0,0,LINEAR,0,2 =jpeg

# Image Processing IIP3D extensions

SEL=union(diff(dilation(2,1),2),diff(dilation(1,1),1))&QLT=50&CVT=jpeg

# Image Processing IIP3D extensions

SEL=union(diff(dilation(2,1),2),diff(dilation(1,1),1))&QLT=50&CVT=jpeg



# Image Processing IIP3D extensions

SEL=union(diff(dilation(2,1),2),diff(dilation(1,1),1))&QLT=50&CVT=jpeg

SEL=diff(dilation(erosion(threshold(0,250,lt),3),3),2),
0,255,0,255&QLT=50&CVT=jpeg

# Image Processing IIP3D extensions

SEL=union(diff(dilation(2,1),2),diff(dilation(1,1),1)

SEL=diff(dilation(erosion(threshold(0,250,lt),3),3),
0,255,0,255&QLT=50&CVT=jpeg

# IIP3D Web-App Architecture

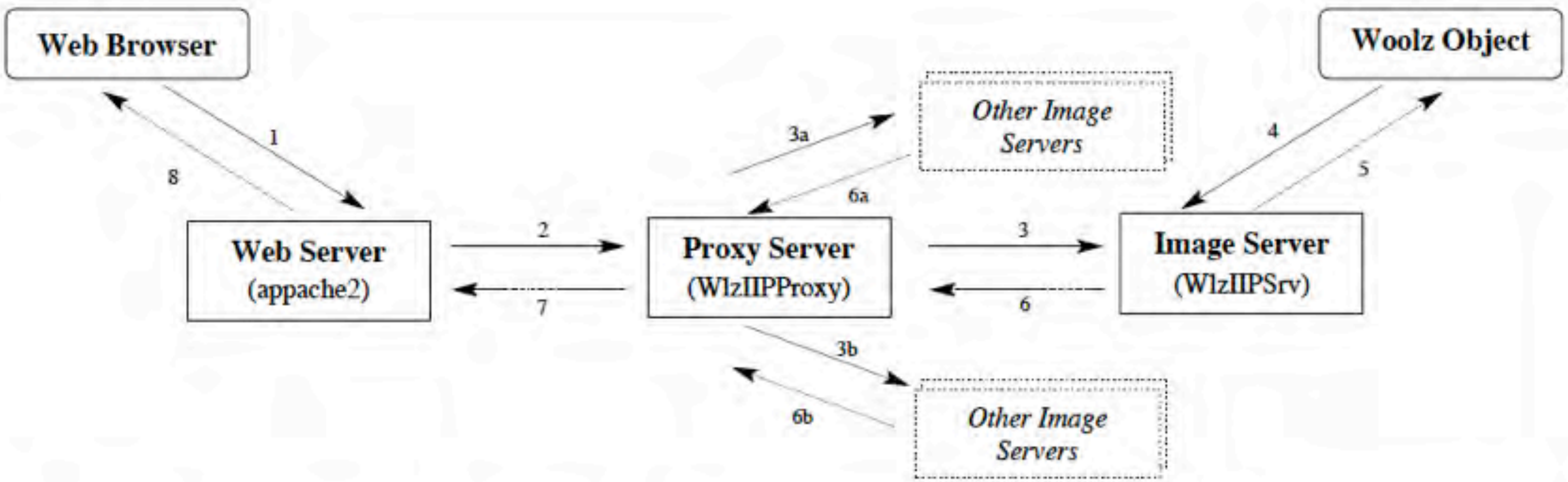



Figure 4: Architecture of IIP3D server using a proxy server. The web server passes the user requests to the proxy, which forwards them to individual IIP servers. These servers have direct access to the Woolz Object and return the requested data. The numbered lines show the order of the requests (continuous lines) and the replies (dotted lines).

# IIP3D Web-App Architecture

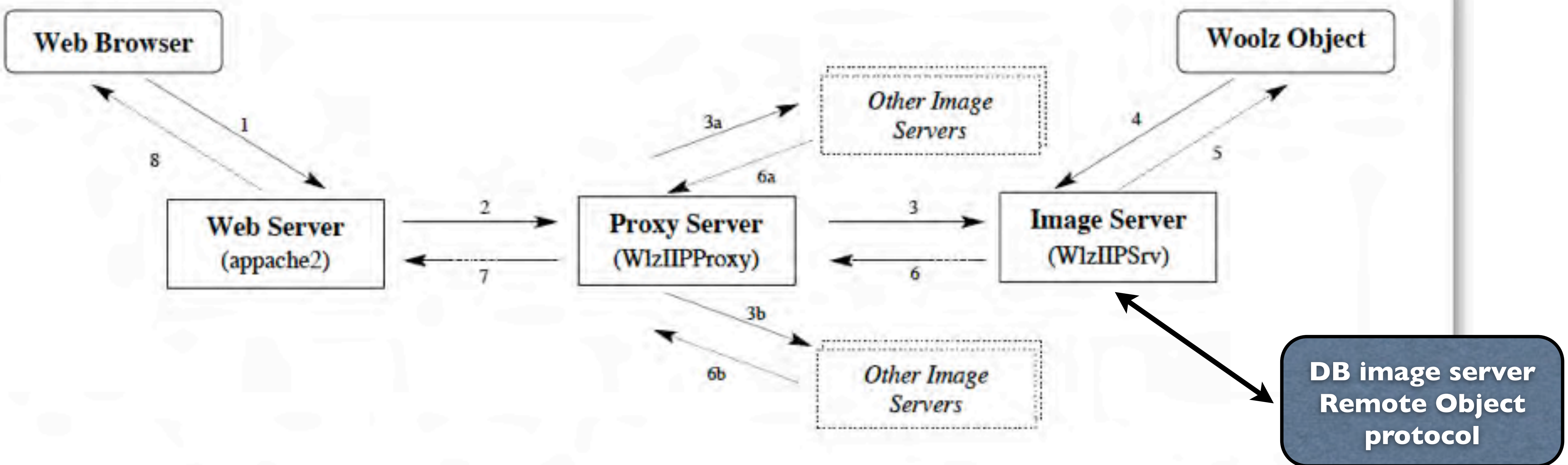
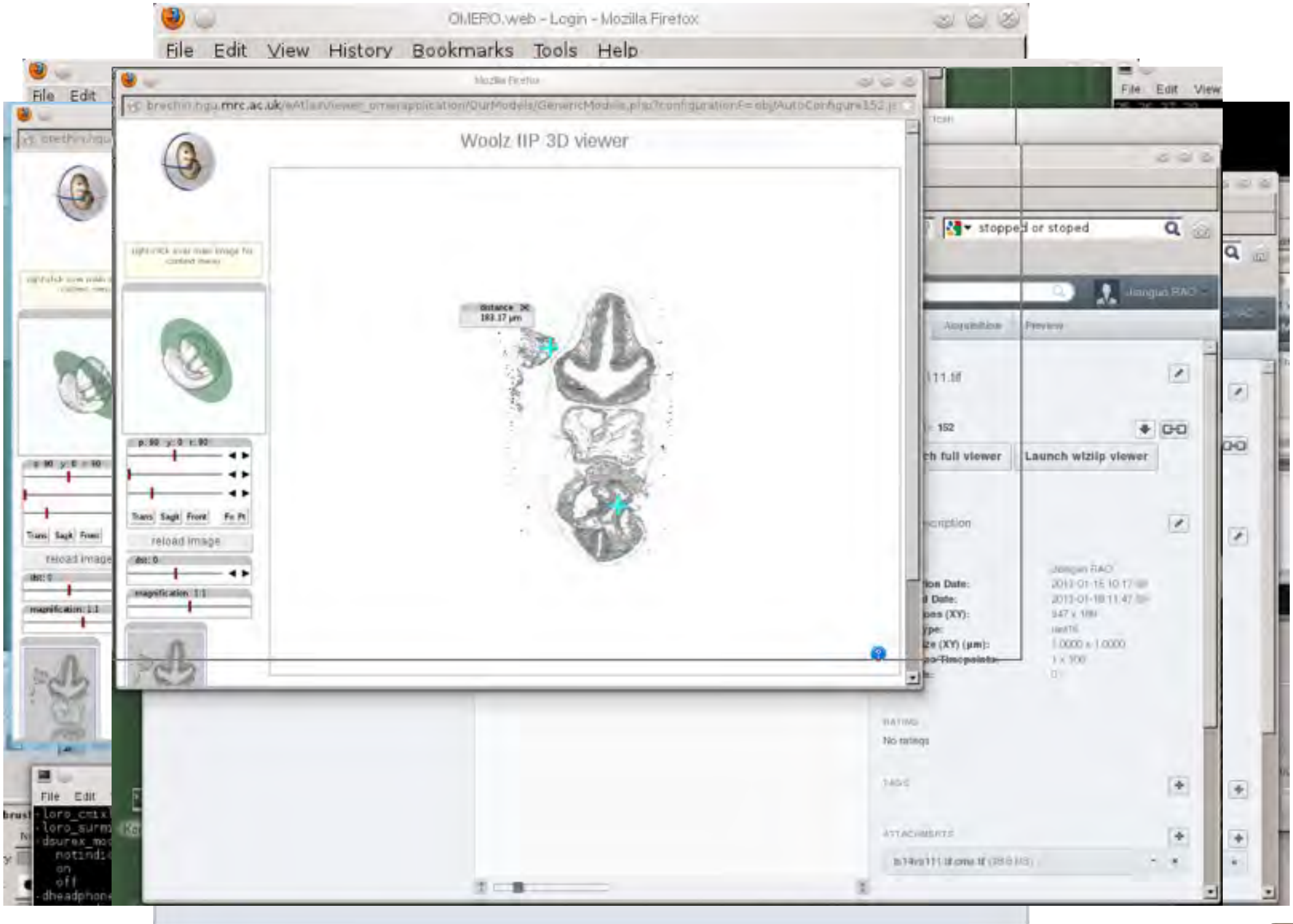



Figure 4: Architecture of IIP3D server using a proxy server. The web server passes the user requests to the proxy, which forwards them to individual IIP servers. These servers have direct access to the Woolz Object and return the requested data. The numbered lines show the order of the requests (continuous lines) and the replies (dotted lines).

# IIP3D Clients

- Javascript
  - Ajax
  - MVC design, uses MooTools & Yahoo Widgets
- Multi-section at high resolution
- Volume overlays
- Anatomy & gene-expression overlays
- Controls
  - viewing angles - virtual sections
  - zoom
  - distance, fixed point
  - section locator & view angle feedback
  - distance measurement, query by image value
  - contrast, grey-slicing and mapping
  - thresholding, domain processing

# IIP3D and OMERO





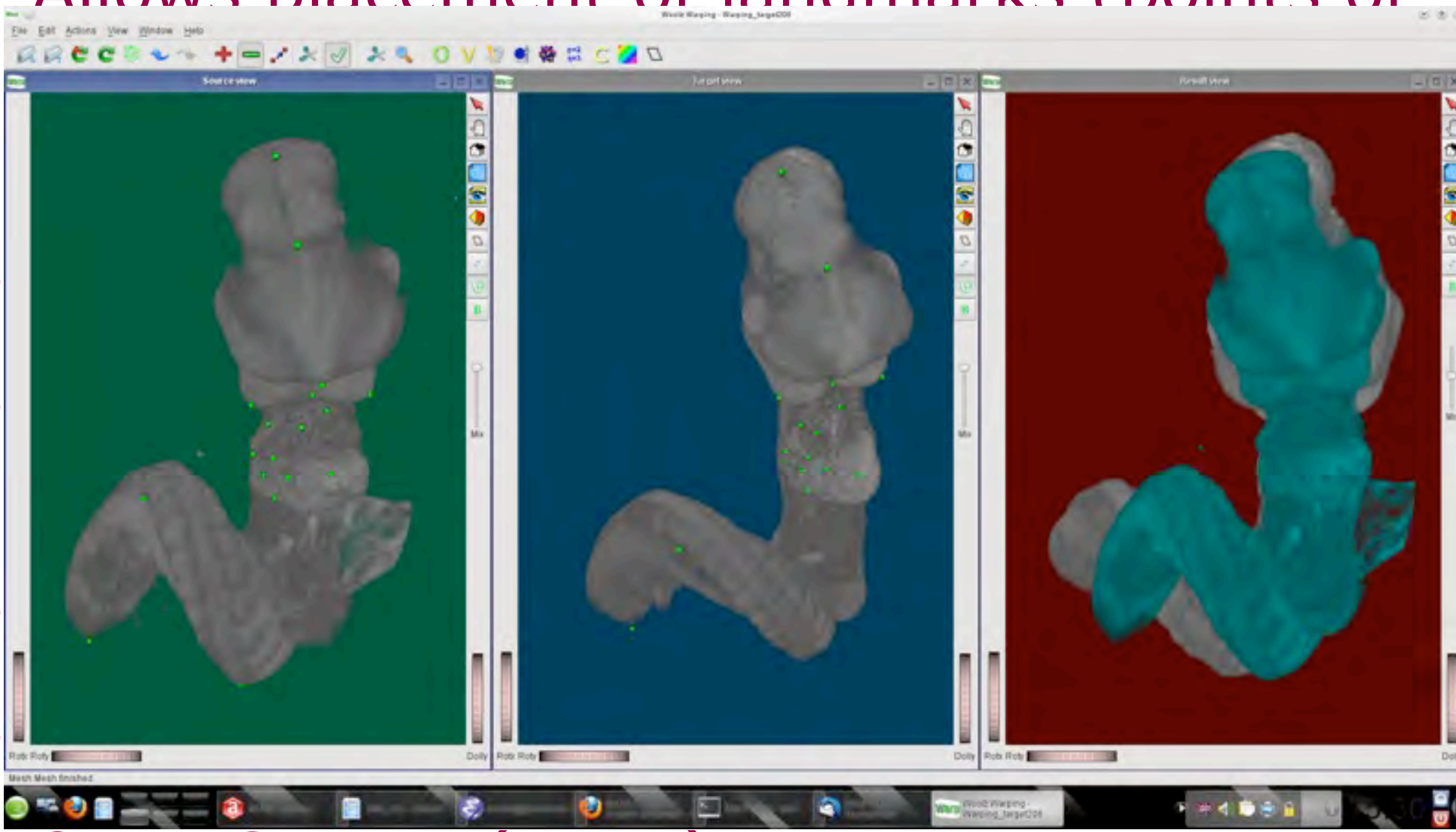

Thursday, 28 February 2013

## 3D mapping - WlzWarp

- Allows placement of landmarks (points of equivalence) on source and target on volume renders instead of isosurfaces
- On-the-fly feedback of warping progress
- Uses constrained distance transform (CDT) in warping
- Woolz, Qt, Coin3D(+SIMVoleon)
- Linux, OS X, Windoes
- Open Source (Free!)

# 3D mapping - WlzWarp

- Allows placement of landmarks (points of

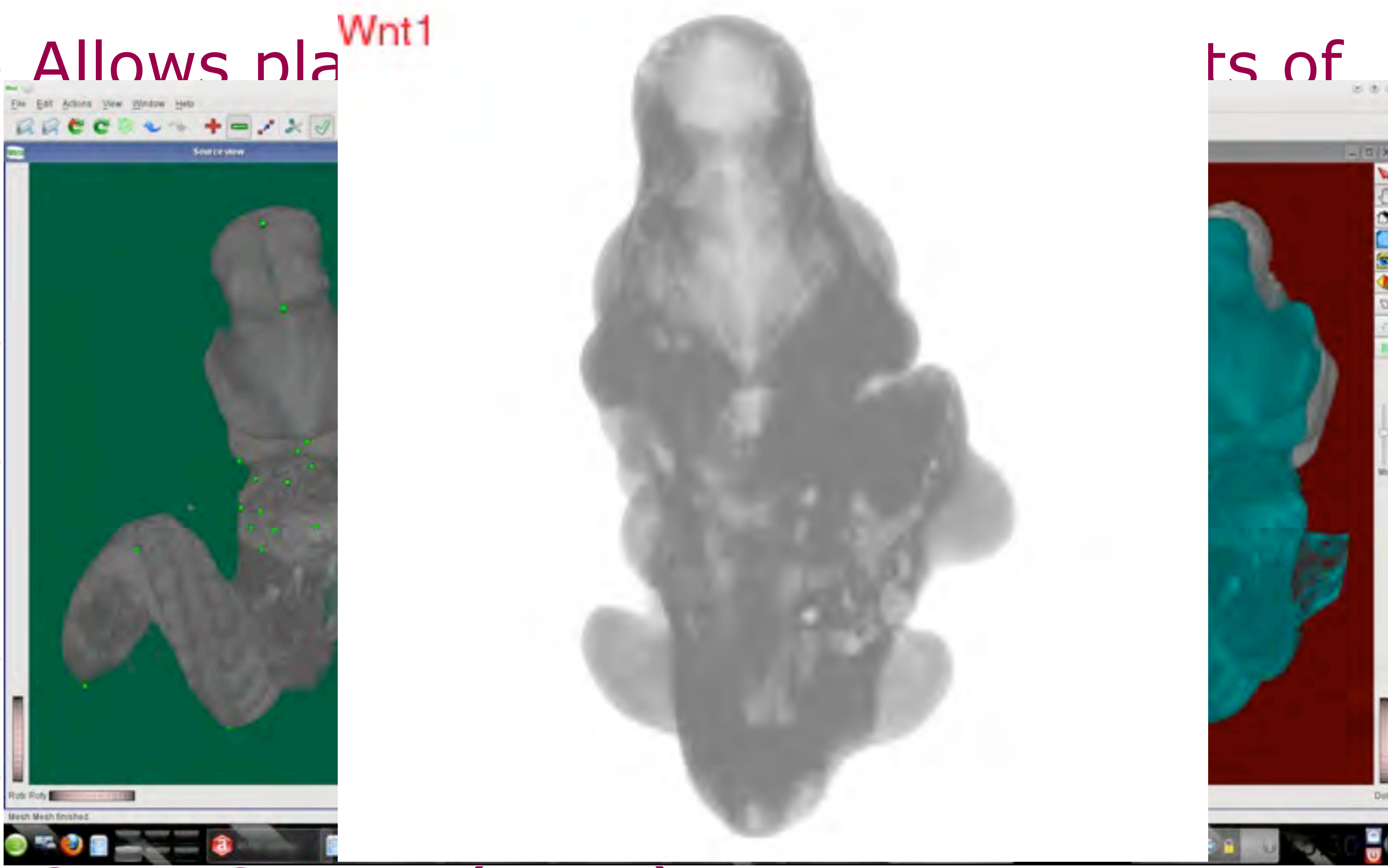


ne

in

- Open Source (Free!)

# 3D mapping - WlzWarp

- Allows pla ts of
  ne
- 
- in
- 
- 



- Open Source (Free!)

# eMouseAtlas

*MRC Human Genetics Unit, Edinburgh*

EMAGE:
Chris Armit
Shanmugasundaram Venkataraman
Lorna Richardson
Peter Stevenson

EMAP:
Albert Burger
Bill Hill
Nick Burton
Yiya Yang
Julie Moss
Liz Graham
Allyson Ross

Duncan Davidson
Richard Baldock

NIH GUDMAP:
Simon Harding
Bernard Haggerty
Koosum Roochum

BBSRC:
Mike Wicks

FP7 RICORDO:
Xu Gu

Wellcome OME:
Jianguo Rao

Colin Semple
Pedro Coutinho
Ian Overton

*Heriot Watt University*

Albert Burger

*Jackson Laboratory*

Martin Ringwald

*Institute of Human Genetics, Newcastle University*

Susan Lindsay
Janet Kerwin

*University of Edinburgh*

Douglas Armstrong
Nestor Milyeav

*University of Dundee*

Jason Swedlow

*Other*

Jonathan Bard
Matt Kaufman

*Funding*

MRC, BBSRC, EU FP5,6,7, NIH, Wellcome Trust