

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

**Richard Baldock**

*MRC Human Genetics Unit*

*Institute of Genetics and Molecular Medicine*

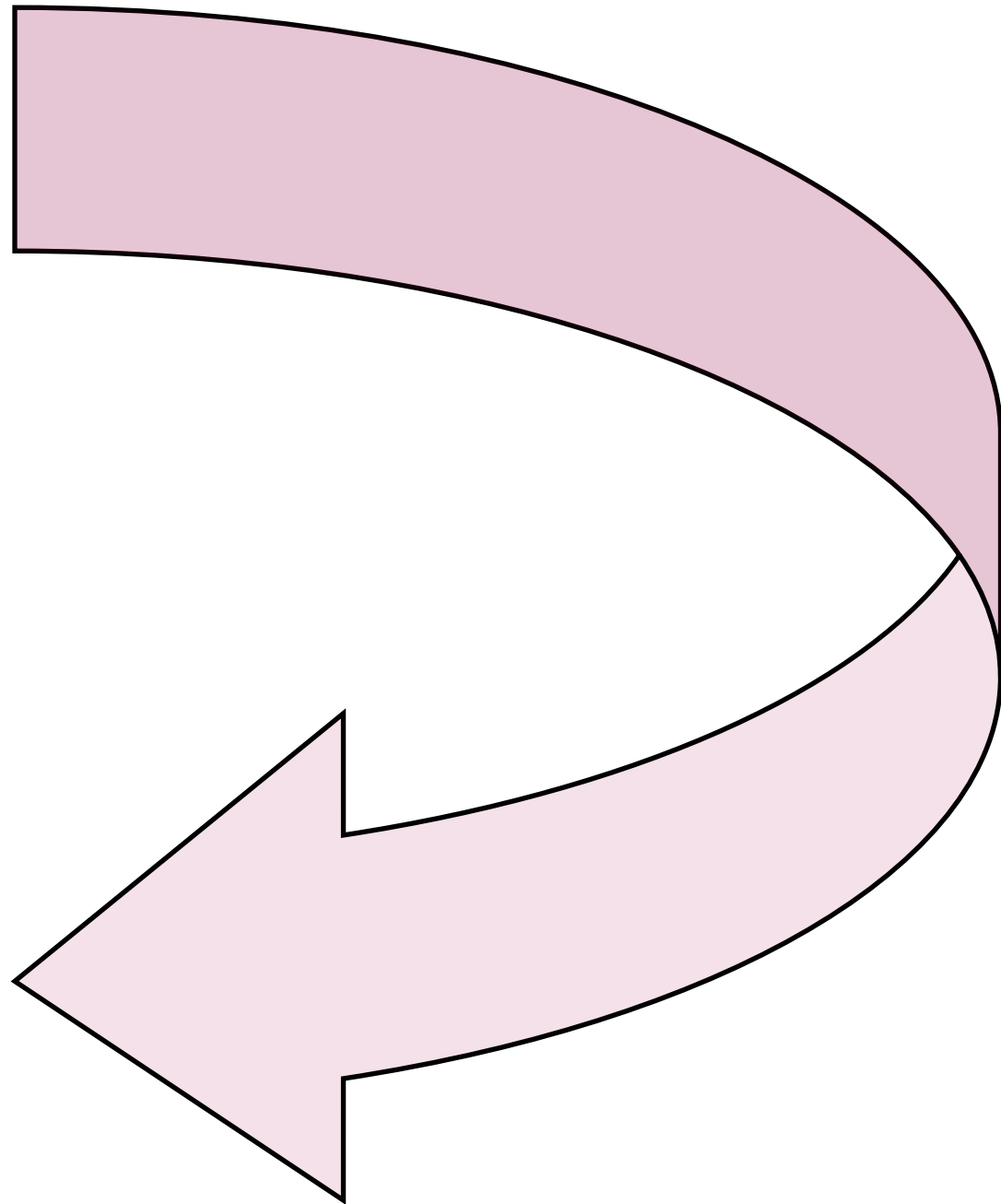
*Edinburgh, UK*



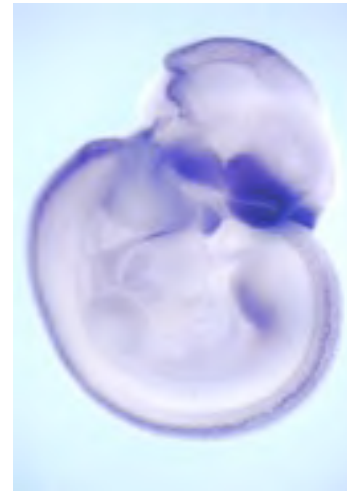
# Credits

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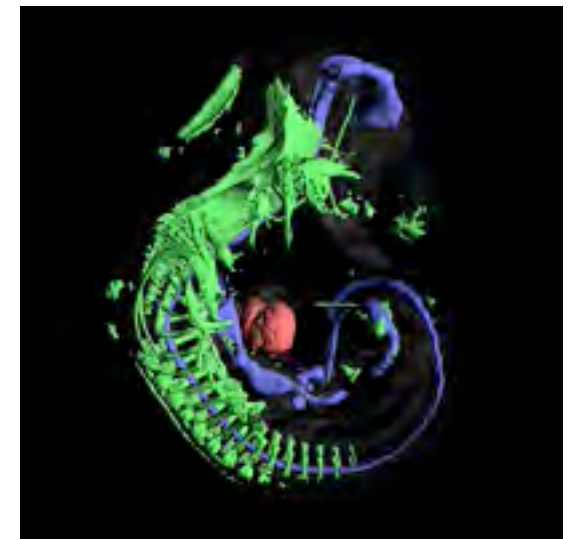
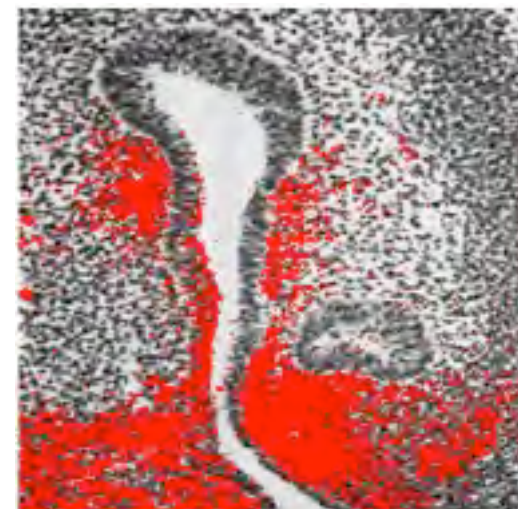
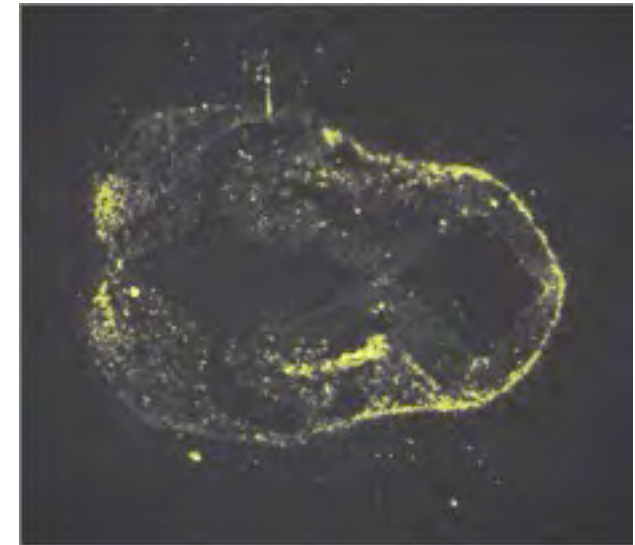
- Bill Hill
- Jianguo Rao



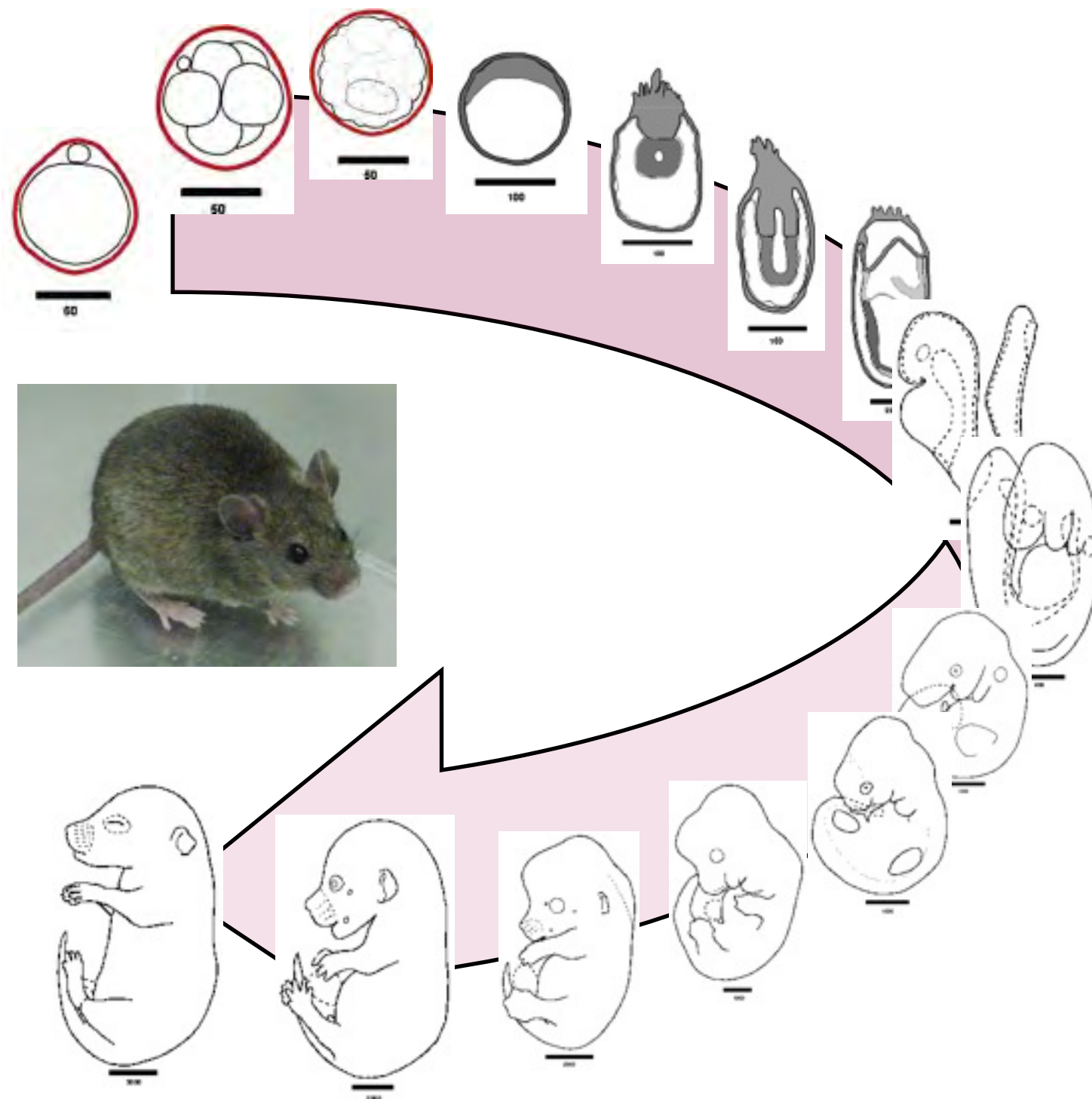
## GENE EXPRESSION



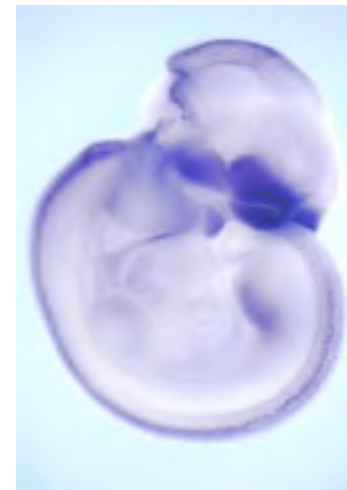
Carol Wicking, University of Queensland



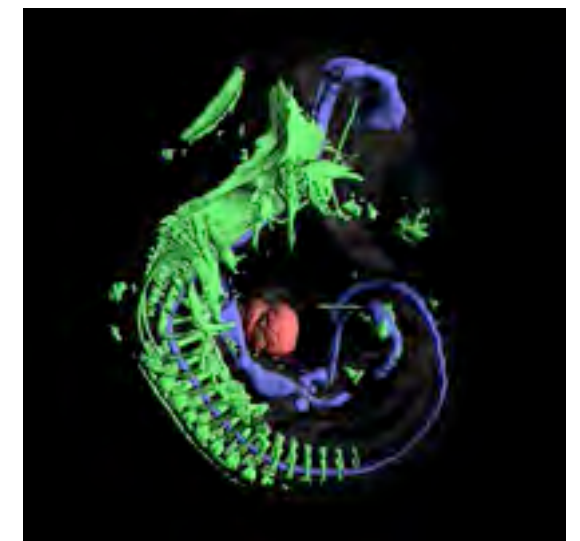
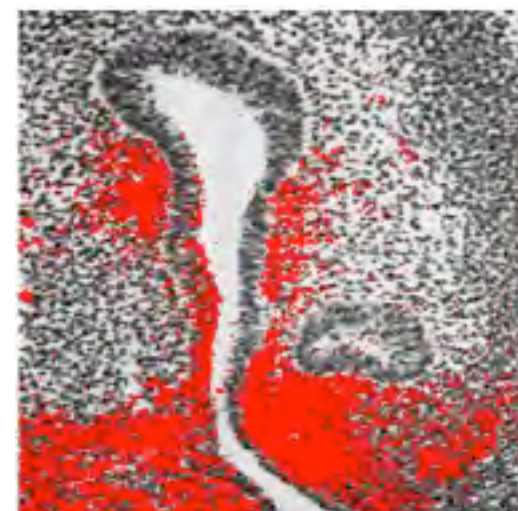
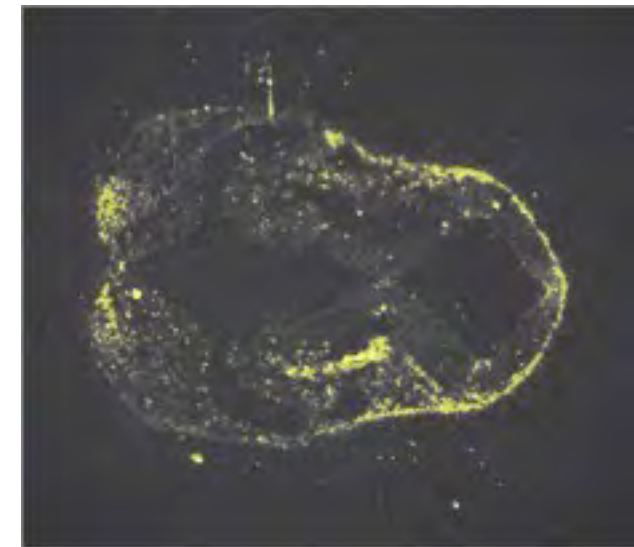
# eMouseAtlas - Development and Gene-Expression



## GENE EXPRESSION



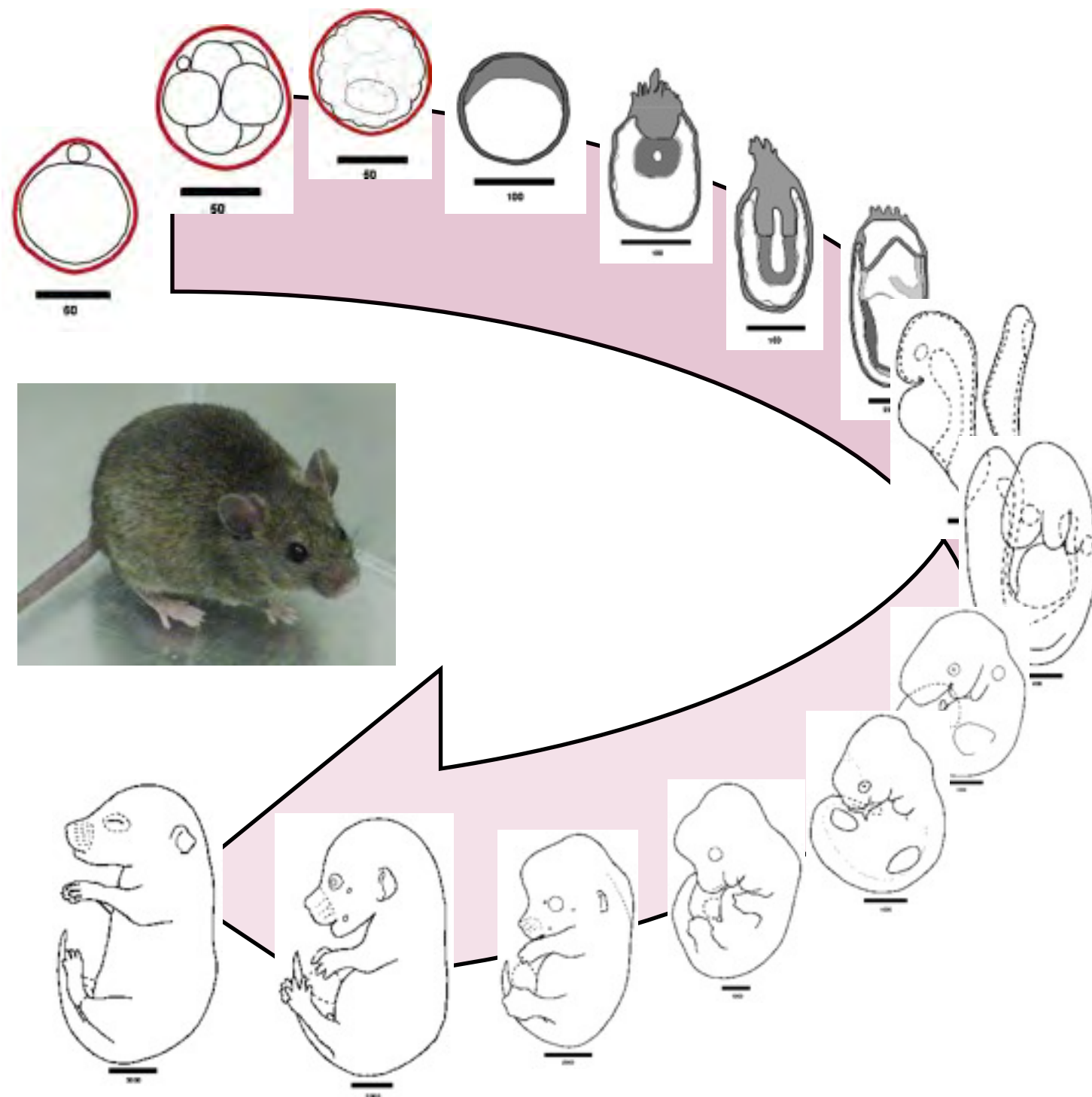
Carol Wicking, University of Queensland



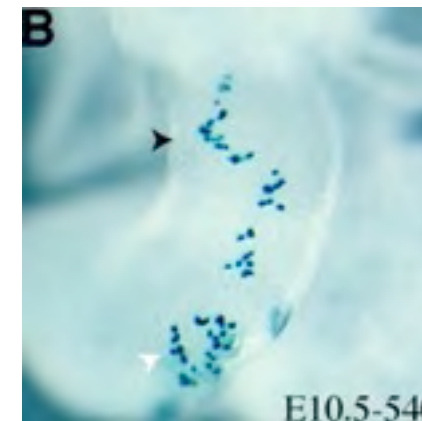




# eMouseAtlas - Development and Gene-Expression



## CELL LINEAGE



Sigolène Meilhac  
Institut Pasteur

## CELL DIVISION



anti-BrdU staining  
J. McDearmid  
McGill University

## APOPTOSIS

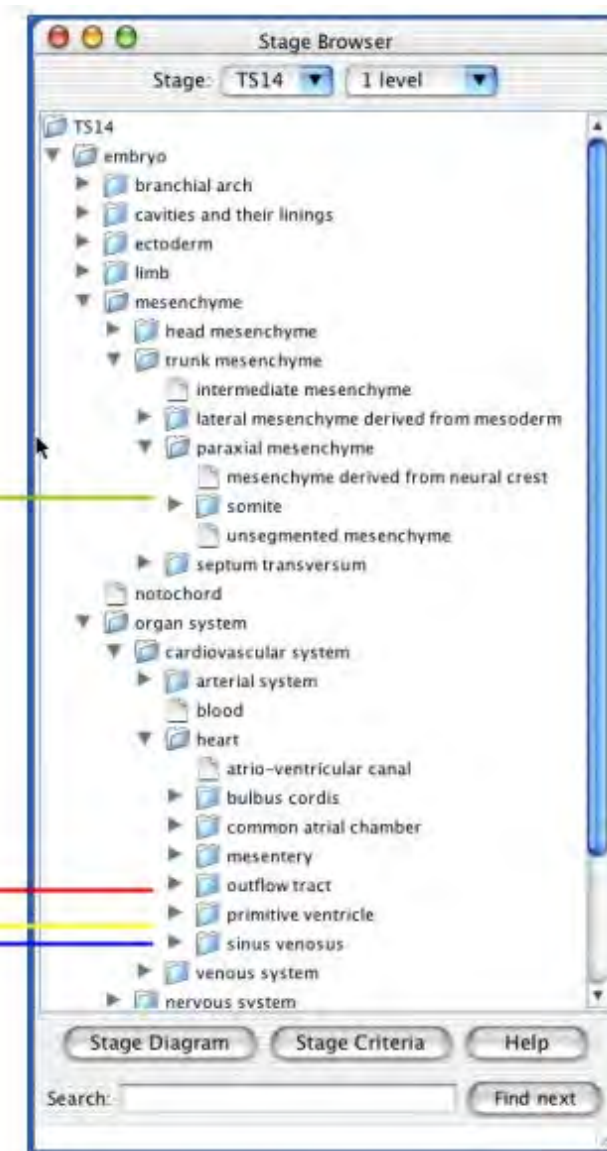
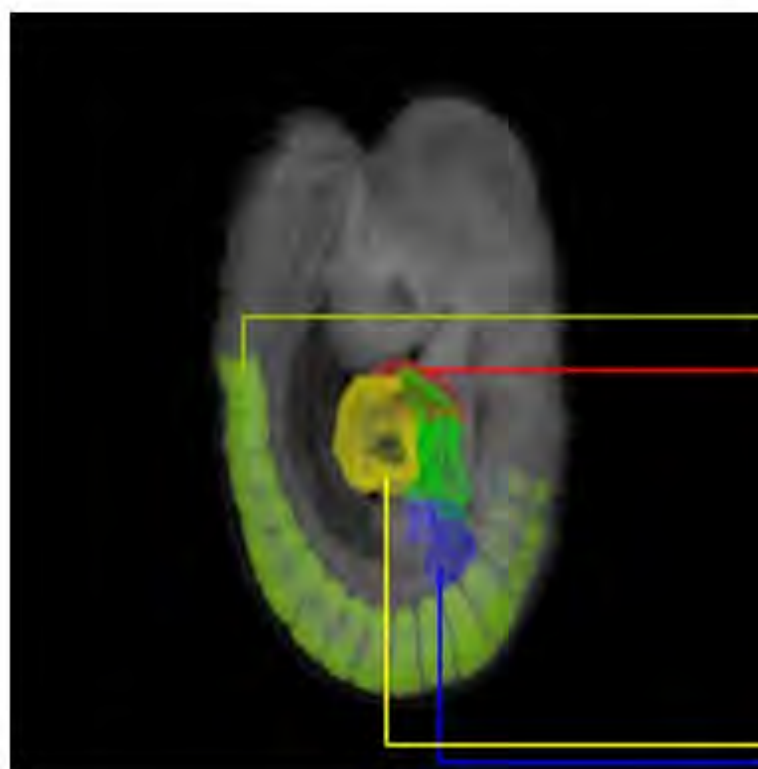
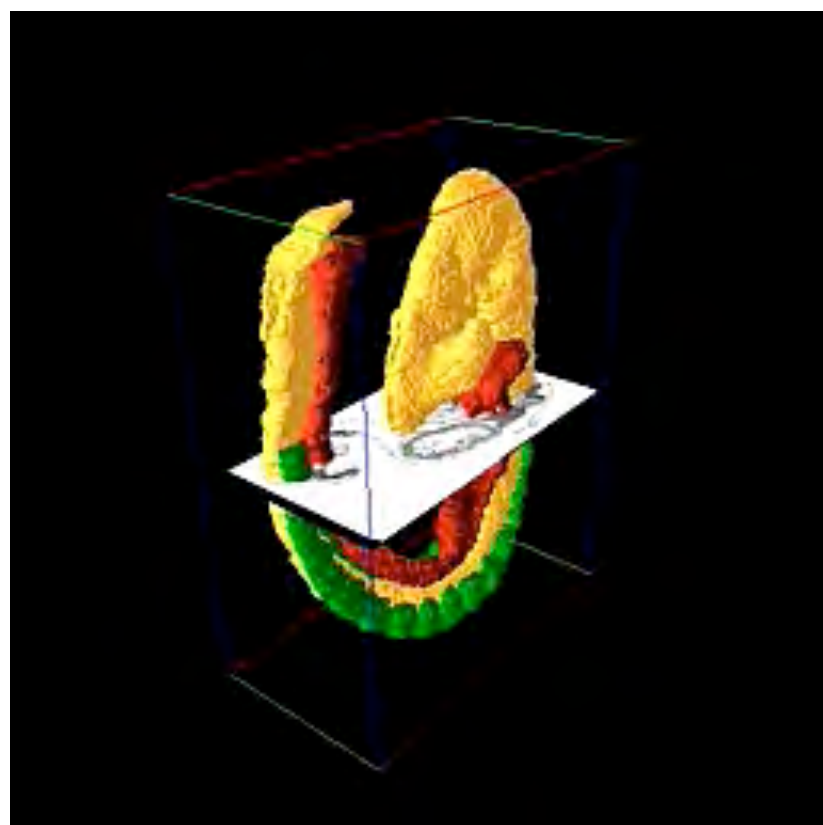


Acridine Orange  
J. Burns  
University of Bristol

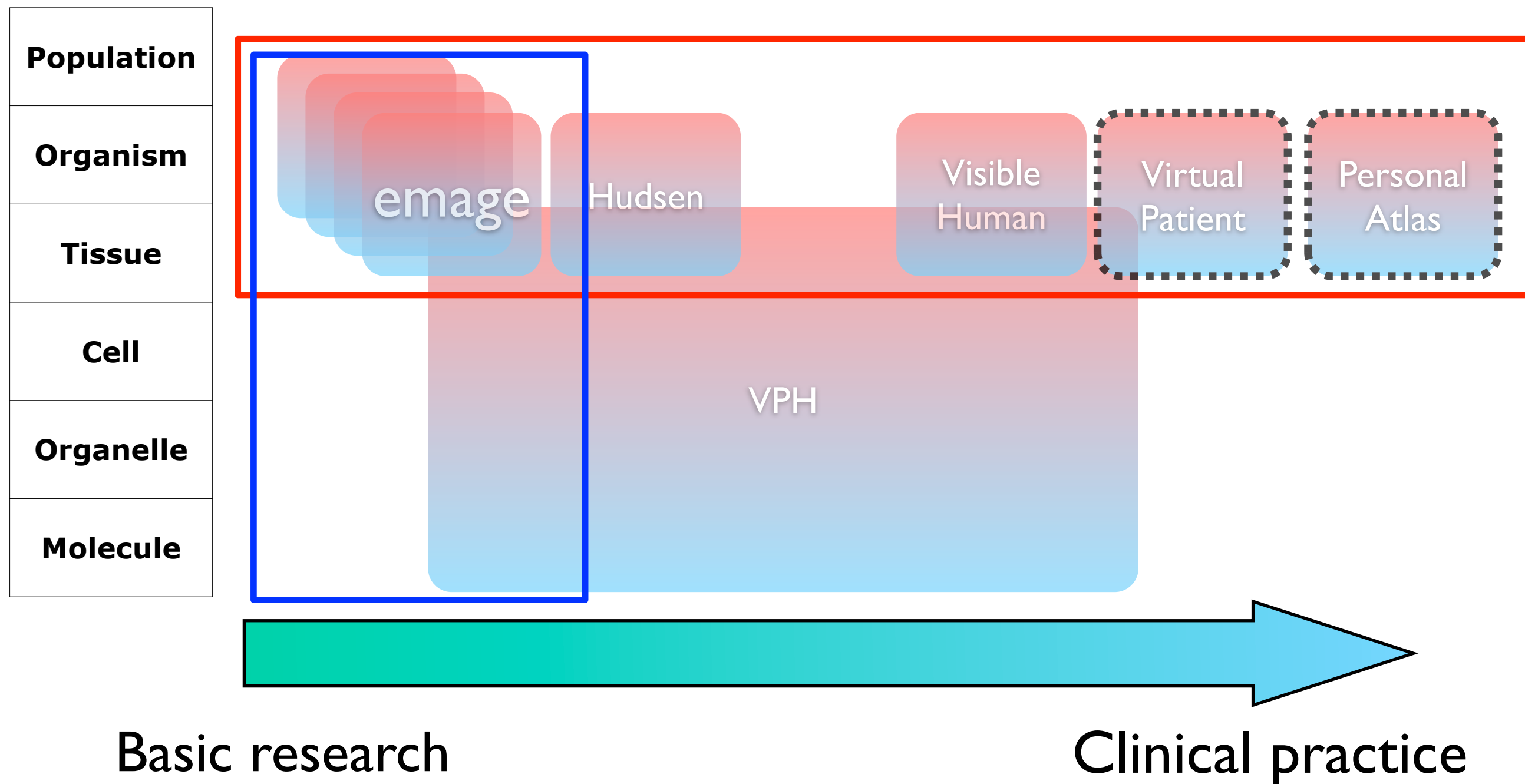
## TRANSGENICS



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



# Atlas-Based Infrastructures








# eMouseAtlas



emap

EMAP Project    EMA Anatomy Atlas    EMAGE Gene Expression    About    Help

Site Search

 Feedback

Browser compatibility

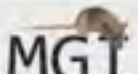
21st-25th July 2011  
Visit our stand at the  
SDB 70th Annual Meeting Chicago


17th-20th September 2011  
The 6th International Chick Meeting  
The Roslin Institute in Edinburgh, UK


All news items


ema  
Mouse  
Anatomy Atlas


image  
Mouse Gene Expression  
Spatial Database

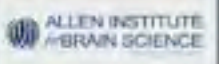
MG1

CALTECH

CI-M  
Center for In Vivo Microscopy

3D Mouse Limb Anatomy Atlas


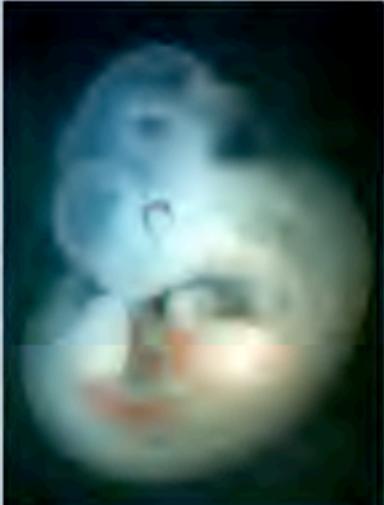
E-Mouse Atlas

ALLEN INSTITUTE  
FOR BRAIN SCIENCE

All atlas links

WELCOME to EMAP  
The e-Mouse Atlas Project

- EMA, the e-Mouse Atlas. A 3-D anatomical atlas of mouse embryo development including detailed histology. EMA includes the EMAP ontology of anatomical structure.  
[More about EMAP](#)
- EMAGE, the e-Mouse Atlas of Gene Expression. A database of mouse gene expression where, uniquely, the gene expression is mapped into the EMA 3-D space and can be queried spatially.  
[More about EMAGE](#).

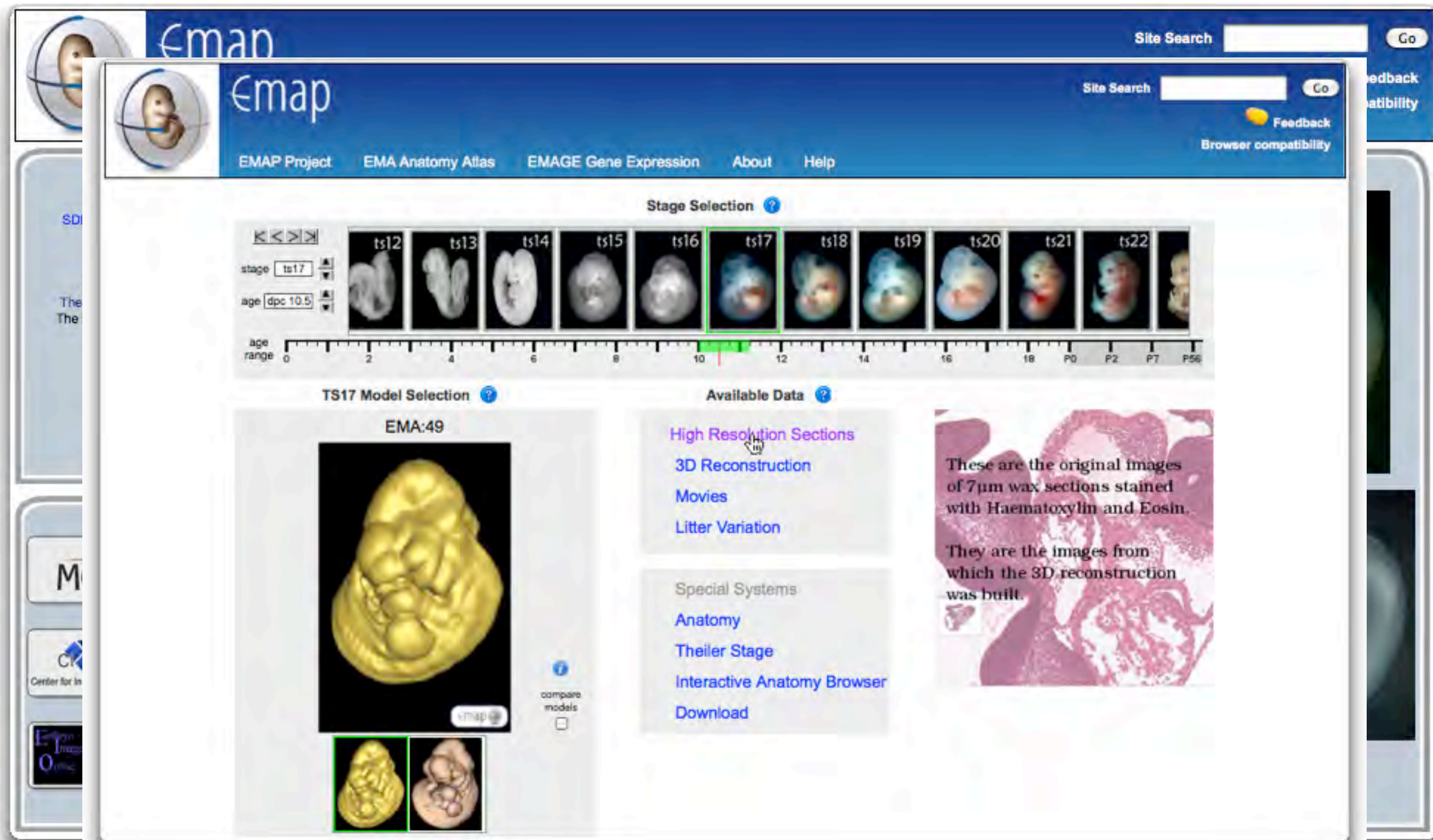


All gallery images

MRC

Human  
Genetics  
Unit

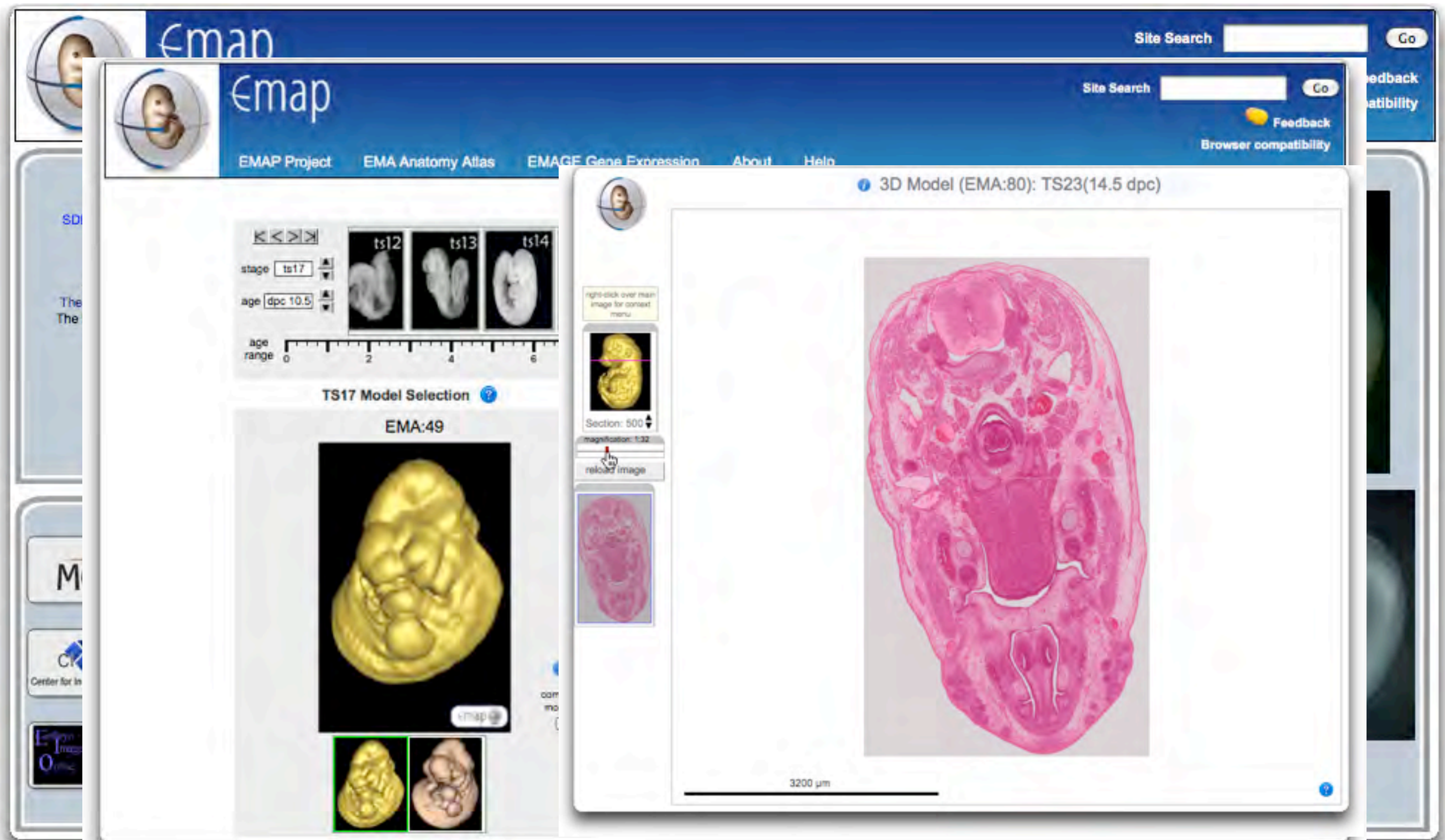




The screenshot displays the eMouseAtlas web application interface. At the top, there is a navigation bar with the 'Emap' logo and links for 'EMAP Project', 'EMA Anatomy Atlas', 'EMAGE Gene Expression', 'About', and 'Help'. A 'Site Search' box is located on the right. Below the navigation bar, the 'Stage Selection' section features a timeline of mouse development stages from ts12 to ts22, with ts17 highlighted. A 'TS17 Model Selection' section shows a 3D model of a mouse embryo (EMA:49) and a 'compare models' button. An 'Available Data' section lists various data types: High Resolution Sections, 3D Reconstruction, Movies, Litter Variation, Special Systems, Anatomy, Theiler Stage, Interactive Anatomy Browser, and Download. A text box on the right explains that the images are original 7µm wax sections stained with Haematoxylin and Eosin, used for 3D reconstruction.



# eMouseAtlas





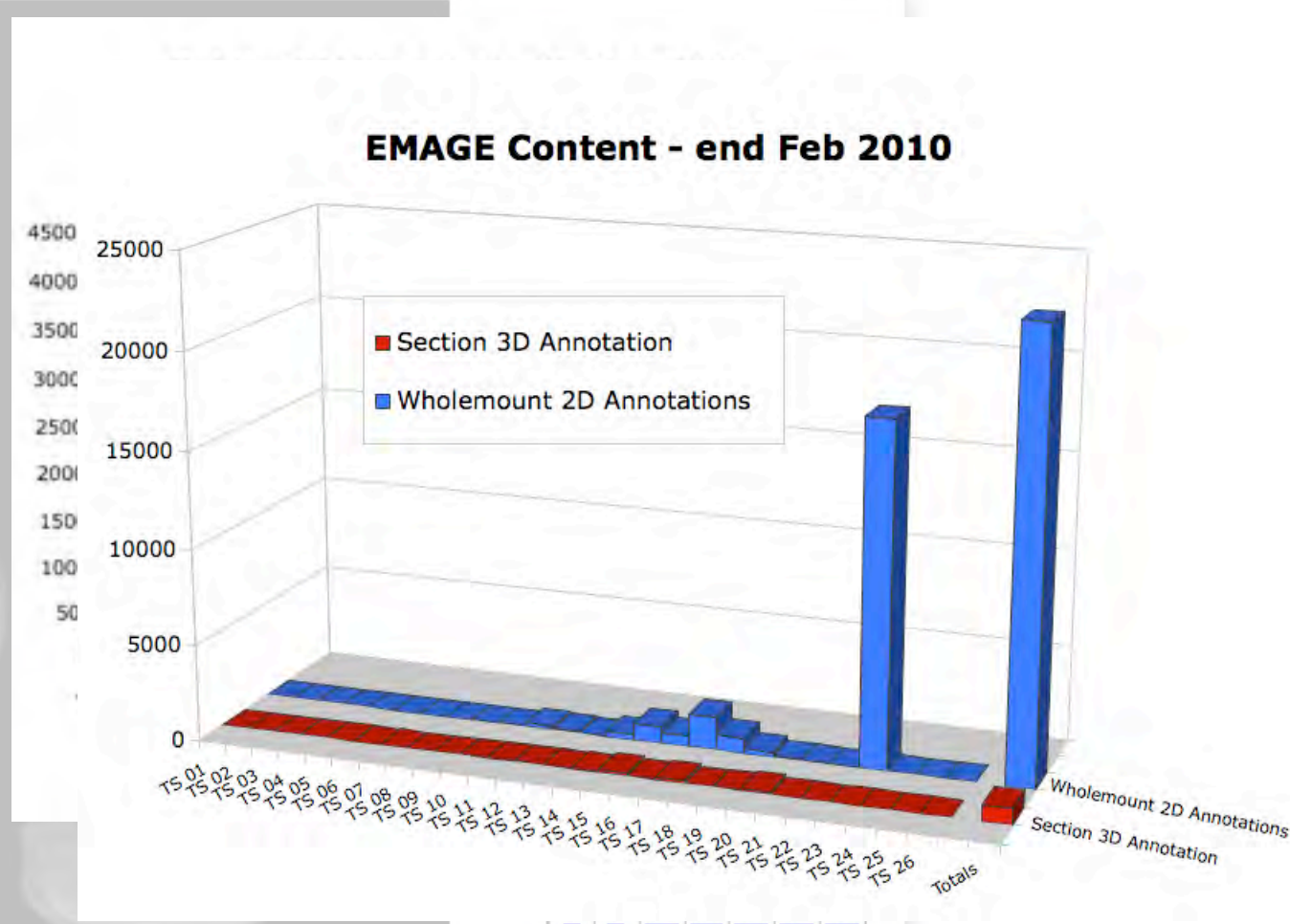
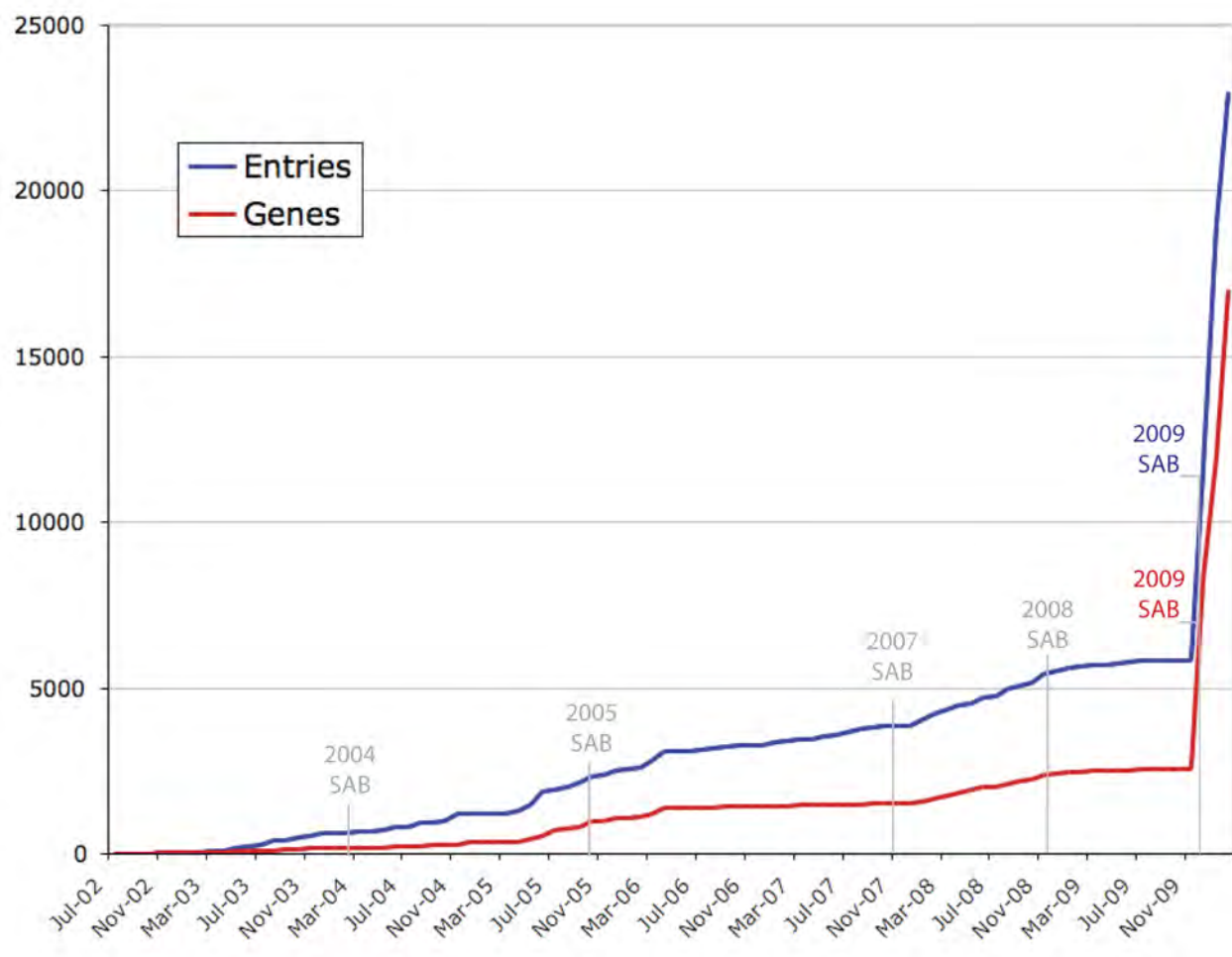


# eMouseAtlas





# EMAGE - current status



~22K submissions  
Range Theiler 7-25

Repository DB: 38.4K entries

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

Plus

TS26 ~18dpc  
not to scale

TS22 ~14dpc

TS20 ~12dpc

15	16	17	18	19	20	21
22	23	24	25	26	27	28

<a href="#">Criteria Summary table</a>
<a href="#">Staging wallchart</a>
<a href="#">Text anatomy index</a>
<a href="#">Anatomy Database</a>

[FAQs](#)



# EMAGE - current status

The screenshot displays the EMAGE website interface. At the top, there is a navigation bar with the EMAGE logo, a search bar, and links for Search & Analysis, Data Submission, EMAP Project, EMA Anatomy Atlas, About, and Help. The main content area is divided into several sections:

- Current Content:** Genes/Proteins: 15857, Assays: 38418.
- What's New?:** 08 Sep 2011 Latest release. Includes several new searches:- combination, gene summary, pathway and gene association. 3D-3D mapping examples. 02 Aug 2011 Argudas (beta). A tool to help biologists evaluate gene
- Spatial Search:** Embryo Space. A diagram shows a search for Wnt1 and TS17.
- Query Entries:** Combination (Genes: Wnt1, islet-1, Fgf8, Tbx4; Anatomy: otocyst, eye, branchial arch; GO: Mitotic, metaphase, Ossification), Gene (cadherinob, Wnt1, islet-1, Fgf8, Aldh1a2, Lhx6, Tbx4, Nkx6-1, T, Msx1, Collagen Type II, α1, Sry), Anatomy Name (node, mesenchyme, somite, headfold, eye, branchial arch, vagus X, otocyst, lens, midgut).
- Gene & Pathway Summaries:** Gene Summary (a diagram showing gene expression patterns), Pathway (a diagram showing a signaling pathway), Gene Association (a diagram showing gene associations).
- BioMart & Analysis Tools:** BioMart, Similar Patterns, Direct Access.
- Example Data:** EMAGE:3548. Assay: ISH, Gene: Shh, Stage: TS15, Spatial Annotation: (a diagram showing spatial expression patterns), Source: Greene et al, 1998, PMID:95455341.

Annotations  
ition

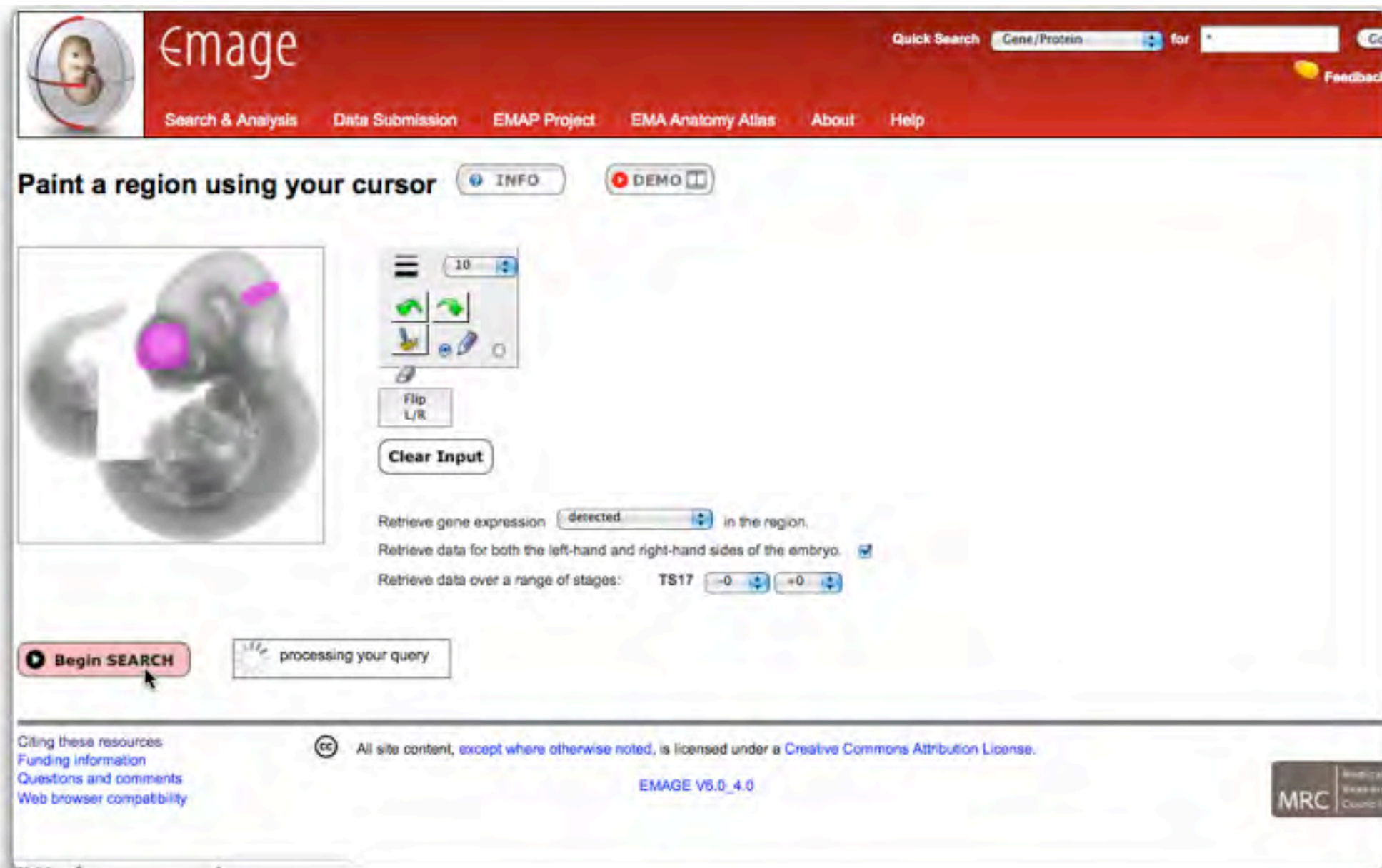
5K)

Human  
Genetics  
Unit

MRC



# EMAGE Embryo Space



The screenshot shows the EMAGE web application interface. At the top, there is a red header bar with the 'Eimage' logo on the left and a 'Quick Search' bar on the right. Below the header, a navigation menu includes links for 'Search & Analysis', 'Data Submission', 'EMAP Project', 'EMA Anatomy Atlas', 'About', and 'Help'. The main content area is titled 'Paint a region using your cursor' and features a 3D embryo model with a pink region highlighted. To the right of the model is a toolbar with various icons for interaction, including a 'Flip L/R' button and a 'Clear Input' button. Below the toolbar, there are input fields for 'Retrieve gene expression' (set to 'detected'), 'Retrieve data for both the left-hand and right-hand sides of the embryo' (checked), and 'Retrieve data over a range of stages' (set to 'TS17'). A 'Begin SEARCH' button is prominently displayed. At the bottom, there is a footer section with links for 'Citing these resources', 'Funding information', 'Questions and comments', and 'Web browser compatibility'. The footer also includes a Creative Commons Attribution License notice, the version 'EMAGE V6.0\_4.0', and the MRC logo.





# EMAGE Embryo Space

**Emage** Quick Search Gene/Protein for \* Go Feedback

**Emage** Quick Search Gene/Protein for \* Go Feedback

Search & Analysis Data Submission EMAP Project EMA Anatomy Atlas About Help

Query: genes - detected - query pattern - ts17 to ts17

download query region as wiz file

Export results:- csv format

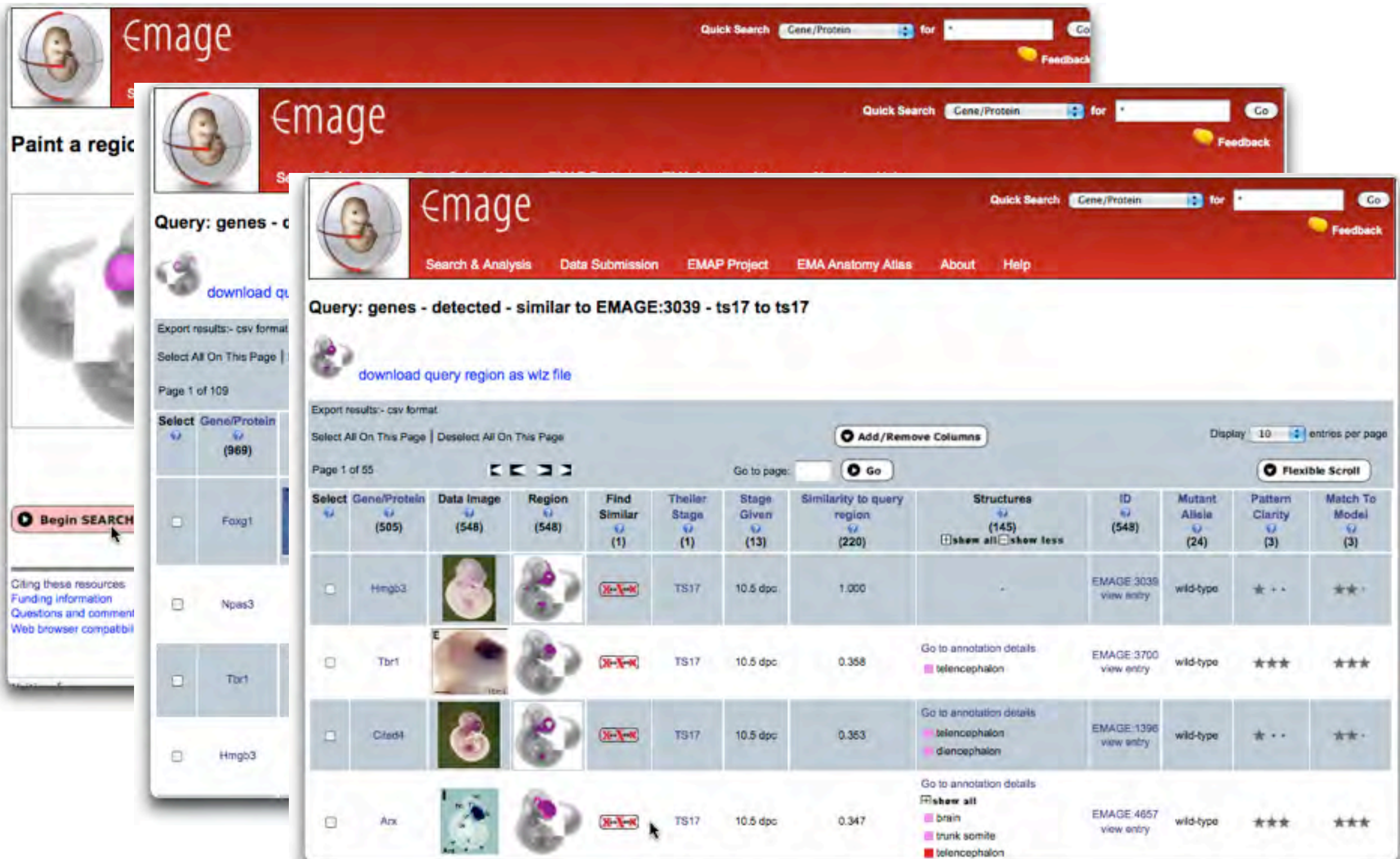
Select All On This Page | Deselect All On This Page Add/Remove Columns Display 10 entries per page

Page 1 of 109 Go to page: Go Flexible Scroll

Select	Gene/Protein (969)	Data Image (1089)	Region (1089)	Find Similar (1)	Thailer Stage (1)	Stage Given (14)	Similarity to query region (310)	Structures (188) show all show less	ID (1089)	Mutant Allele (31)	Pattern Clarity (3)	Match To Model (3)
<input type="checkbox"/>	Foxg1				TS17	10.5 dpc	0.570	Go to annotation details forebrain telencephalon optic stalk	EMAGE:3640 view entry	wild-type	☆☆☆	☆☆
<input type="checkbox"/>	Npas3				TS17	10.5 dpc	0.518	Go to annotation details central nervous system	EMAGE:4159 view entry	wild-type	☆☆☆	☆☆
<input type="checkbox"/>	Tbr1				TS17	10.5 dpc	0.496	Go to annotation details telencephalon	EMAGE:3700 view entry	wild-type	☆☆☆	☆☆☆
<input type="checkbox"/>	Hmgb3				TS17	10.5 dpc	0.444	-	EMAGE:3039 view entry	wild-type	☆☆	☆☆



# EMAGE Embryo Space

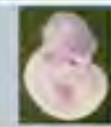













**EMAGE** Quick Search Gene/Protein for \* Go Feedback

**Query: genes - detected - similar to EMAGE:3039 - ts17 to ts17**

download query region as wiz file

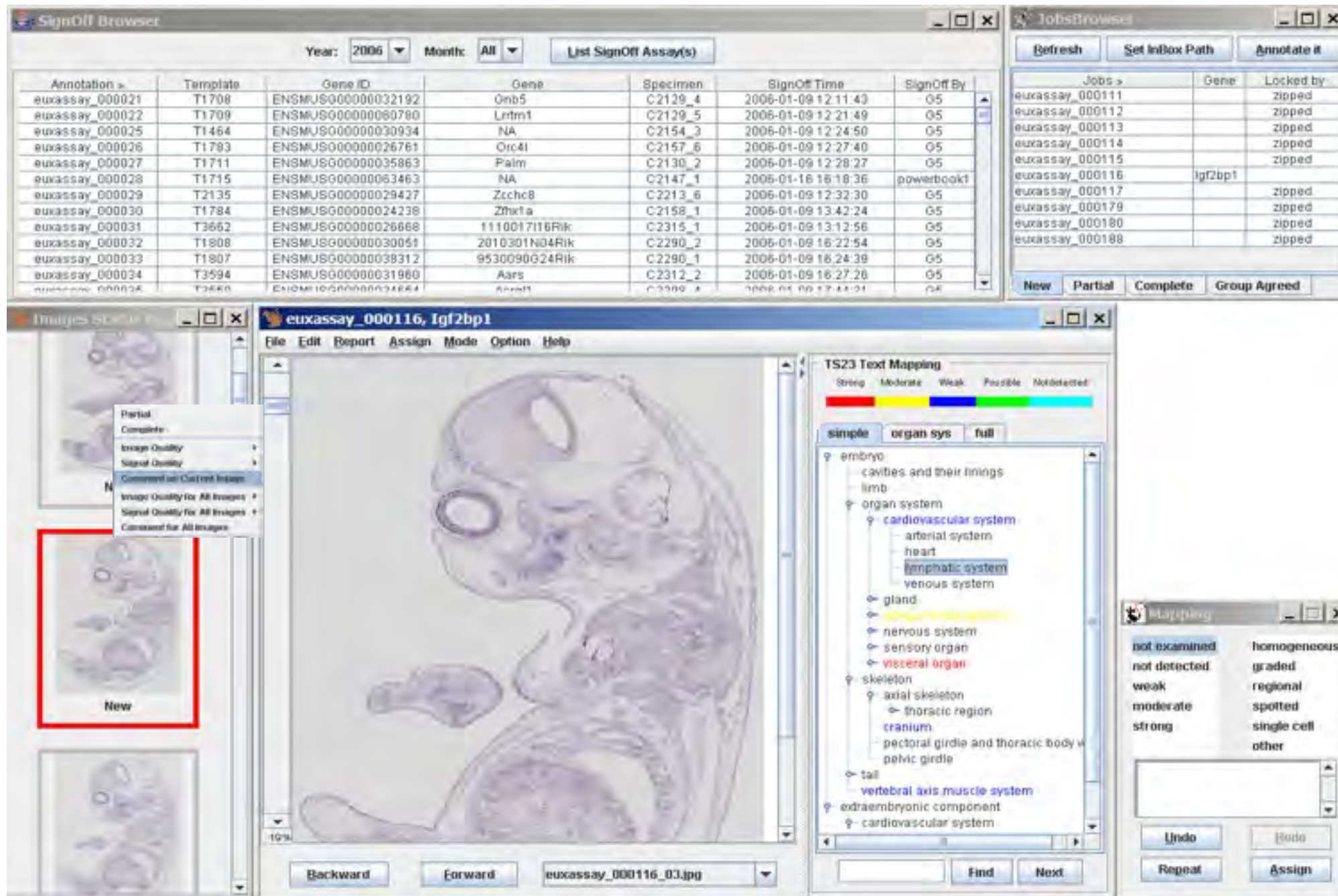
Export results:- csv format  
Select All On This Page | Deselect All On This Page  
Page 1 of 55  
Go to page:  Go

Select	Gene/Protein	Data Image	Region	Find Similar	Theiler Stage	Stage Given	Similarity to query region	Structures	ID	Mutant Allele	Pattern Clarity	Match To Model
<input type="checkbox"/>	Foxg1 (969)							(145)	(548)	(24)	(3)	(3)
<input type="checkbox"/>	Hmgb3 (505)				TS17 (1)	10.5 dpc (13)	1.000 (220)	show all show less	EMAGE 3039 view entry	wild-type	★ + +	★ ★ +
<input type="checkbox"/>	Tbr1				TS17	10.5 dpc	0.358	Go to annotation details telencephalon	EMAGE 3700 view entry	wild-type	★ ★ ★	★ ★ ★
<input type="checkbox"/>	Cited1				TS17	10.5 dpc	0.353	Go to annotation details telencephalon dienecephalon	EMAGE 1396 view entry	wild-type	★ + +	★ ★ +
<input type="checkbox"/>	Arx				TS17	10.5 dpc	0.347	Go to annotation details show all brain trunk somite telencephalon	EMAGE 4657 view entry	wild-type	★ ★ ★	★ ★ ★

- 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.



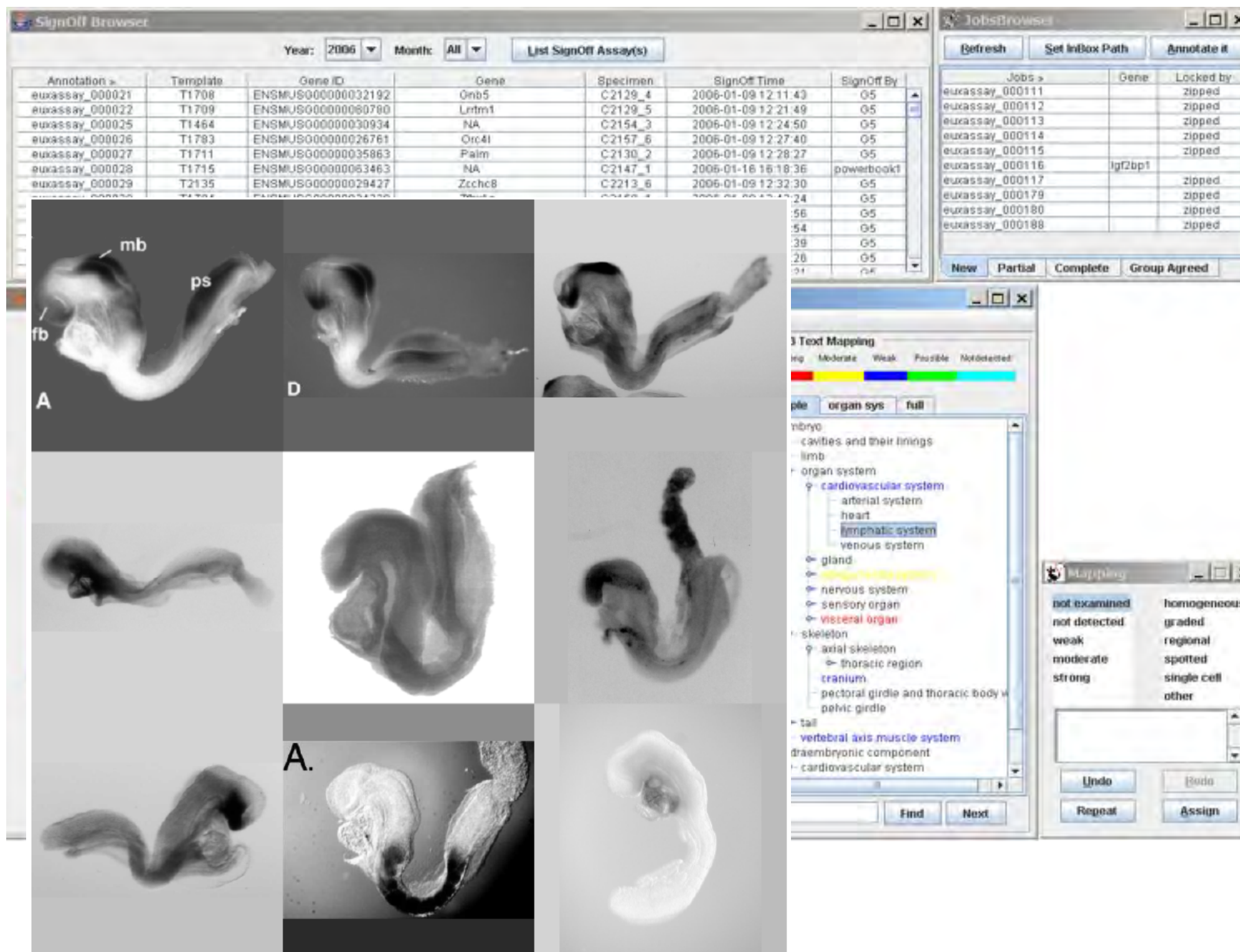
# BioAtlas - data mapping



The screenshot displays the BioAtlas data mapping interface, which includes several key components:

- SignOff Browser:** A table listing assay data with columns for Annotation, Template, Gene ID, Gene, Specimen, SignOff Time, and SignOff By. The table shows various assays like eucassay\_000021 through eucassay\_000034.
- Jobs Browser:** A table showing job status with columns for Jobs, Gene, and Locked by. It lists jobs like eucassay\_000111 through eucassay\_000188, with status 'zipped'.
- Images Browser:** A panel on the left showing a list of images, with a 'New' image highlighted in a red box.
- Main Image Viewer:** Displays a large histological image of a tissue section. Below the image are 'Backward' and 'Forward' navigation buttons and a file name 'eucassay\_000116\_03.jpg'.
- TS23 Text Mapping:** A panel on the right showing a hierarchical tree of anatomical structures. The tree includes categories like 'embryo', 'organ system', 'cardiovascular system', 'gland', 'nervous system', 'sensory organ', 'visceral organ', 'skeleton', 'axial skeleton', 'tail', 'vertebral axis muscle system', 'extraembryonic component', and 'cardiovascular system'. A color-coded legend at the top indicates mapping strength: Strong (red), Moderate (yellow), Weak (blue), Possible (green), and Not detected (cyan).
- Mapping Panel:** A small panel at the bottom right with buttons for 'Undo', 'Redo', 'Repeat', and 'Assign', along with a text input field.

# BioAtlas - data mapping



The screenshot displays the SignOff Browser and Jobs Browser interfaces. The SignOff Browser shows a table of gene expression data with columns for Annotation, Template, Gene ID, Gene, Specimen, SignOff Time, and SignOff By. The Jobs Browser shows a table of jobs with columns for Jobs, Gene, and Locked by. The SignOff Browser also includes a section for embryo images, showing various views of embryos with labels like mb, ps, fb, and A.

**SignOff Browser Table:**

Annotation	Template	Gene ID	Gene	Specimen	SignOff Time	SignOff By
euxassay_000021	T1708	ENSMUSG000000032192	Omb5	C2129_4	2006-01-09 12:11:43	G5
euxassay_000022	T1709	ENSMUSG000000060780	Lrtm1	C2129_5	2006-01-09 12:21:49	G5
euxassay_000025	T1464	ENSMUSG000000030934	NA	C2154_3	2006-01-09 12:24:50	G5
euxassay_000026	T1783	ENSMUSG000000026761	Orc4l	C2157_6	2006-01-09 12:27:40	G5
euxassay_000027	T1711	ENSMUSG000000035863	Palm	C2130_2	2006-01-09 12:28:27	G5
euxassay_000028	T1715	ENSMUSG000000063463	NA	C2147_1	2006-01-16 16:18:36	powerbook1
euxassay_000029	T2135	ENSMUSG000000029427	Zcchc8	C2213_6	2006-01-09 12:32:30	G5

**Jobs Browser Table:**

Jobs	Gene	Locked by
euxassay_000111		zipped
euxassay_000112		zipped
euxassay_000113		zipped
euxassay_000114		zipped
euxassay_000115		zipped
euxassay_000116	Igf2bp1	zipped
euxassay_000117		zipped
euxassay_000179		zipped
euxassay_000180		zipped
euxassay_000188		zipped

**Text Mapping Interface:**

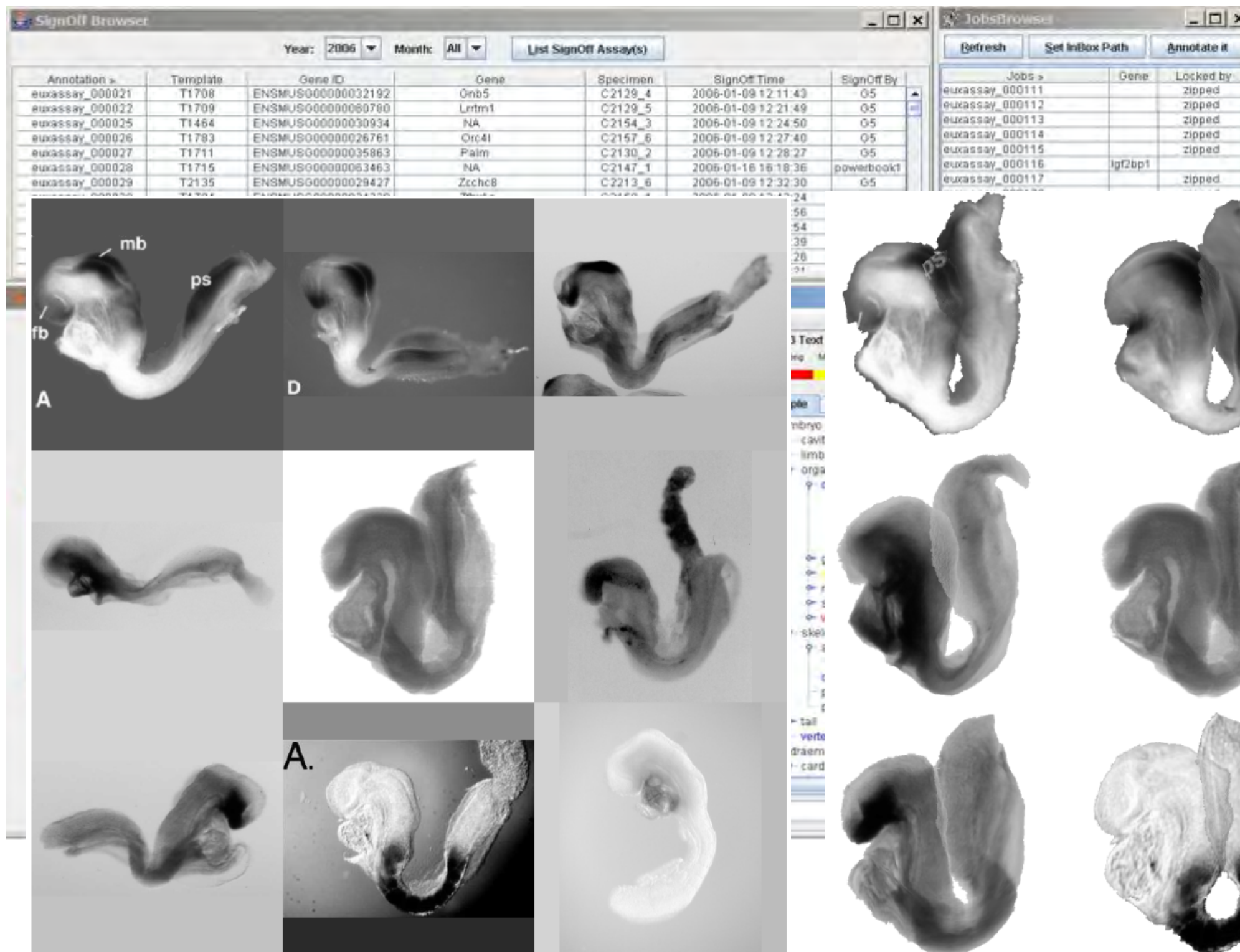
The Text Mapping interface shows a hierarchical tree of biological structures. The tree is organized into categories: embryo, organ system, gland, nervous system, sensory organ, visceral organ, skeleton, tail, and cardiovascular system. The 'organ system' category is expanded, showing sub-categories like cardiovascular system, arterial system, heart, lymphatic system, and venous system. The 'skeleton' category is also expanded, showing sub-categories like axial skeleton, thoracic region, cranium, pectoral girdle and thoracic body wall, and pelvic girdle. The 'tail' category is expanded, showing sub-categories like vertebral axis muscle system, draembryonic component, and cardiovascular system.

**Mapping Interface:**

The Mapping interface shows a table of mapping results. The table has two columns: 'not examined' and 'homogeneous'. The rows are: 'not detected', 'graded', 'weak', 'regional', 'moderate', 'spotted', 'strong', 'single cell', and 'other'. The 'not examined' column is highlighted in blue. The 'homogeneous' column is highlighted in green. The 'not detected' row is highlighted in red. The 'graded' row is highlighted in yellow. The 'weak' row is highlighted in orange. The 'regional' row is highlighted in light green. The 'moderate' row is highlighted in light blue. The 'spotted' row is highlighted in light yellow. The 'strong' row is highlighted in light green. The 'single cell' row is highlighted in light blue. The 'other' row is highlighted in light yellow.



# BioAtlas - data mapping







# Spatial Data Mapping

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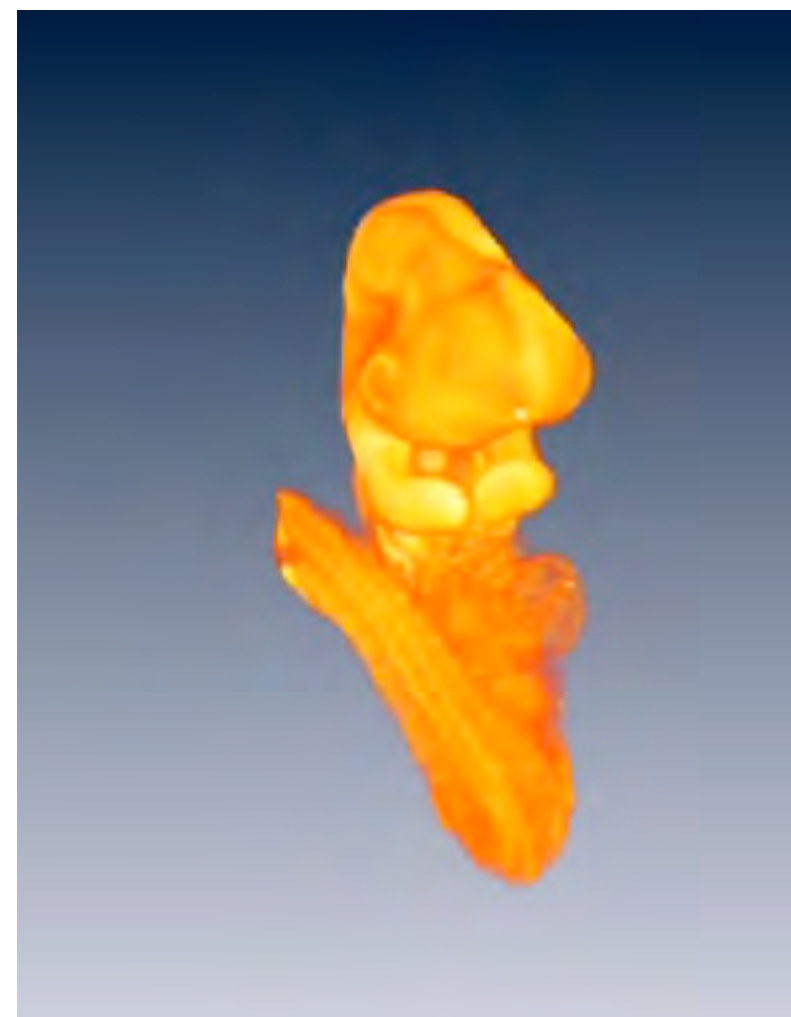
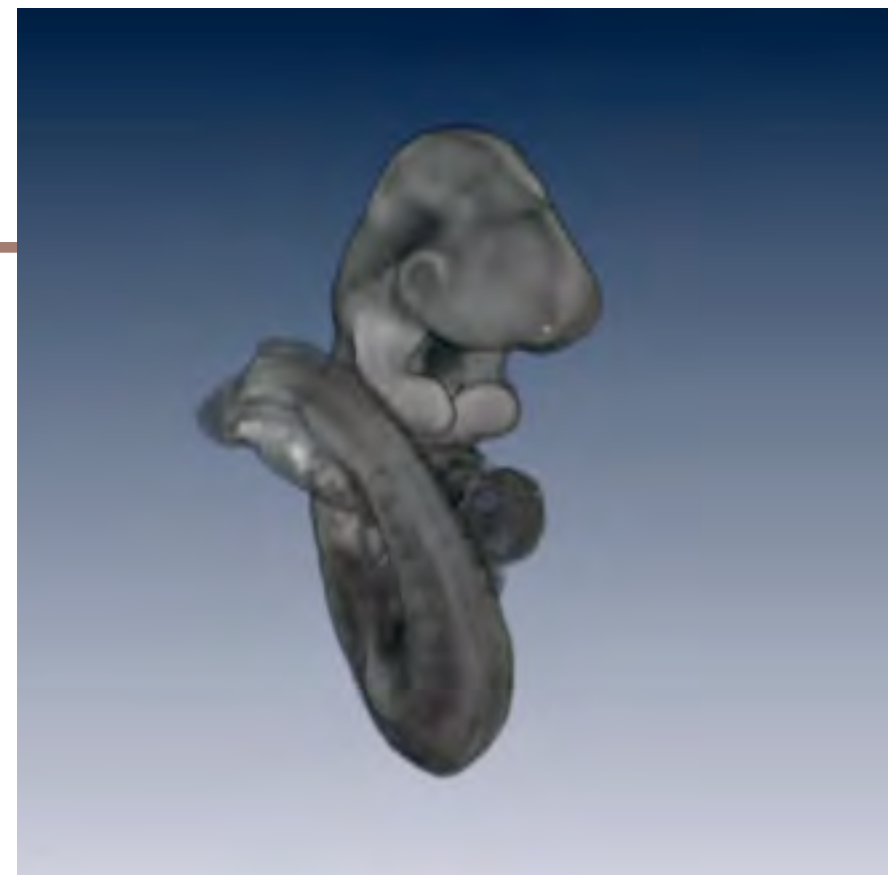
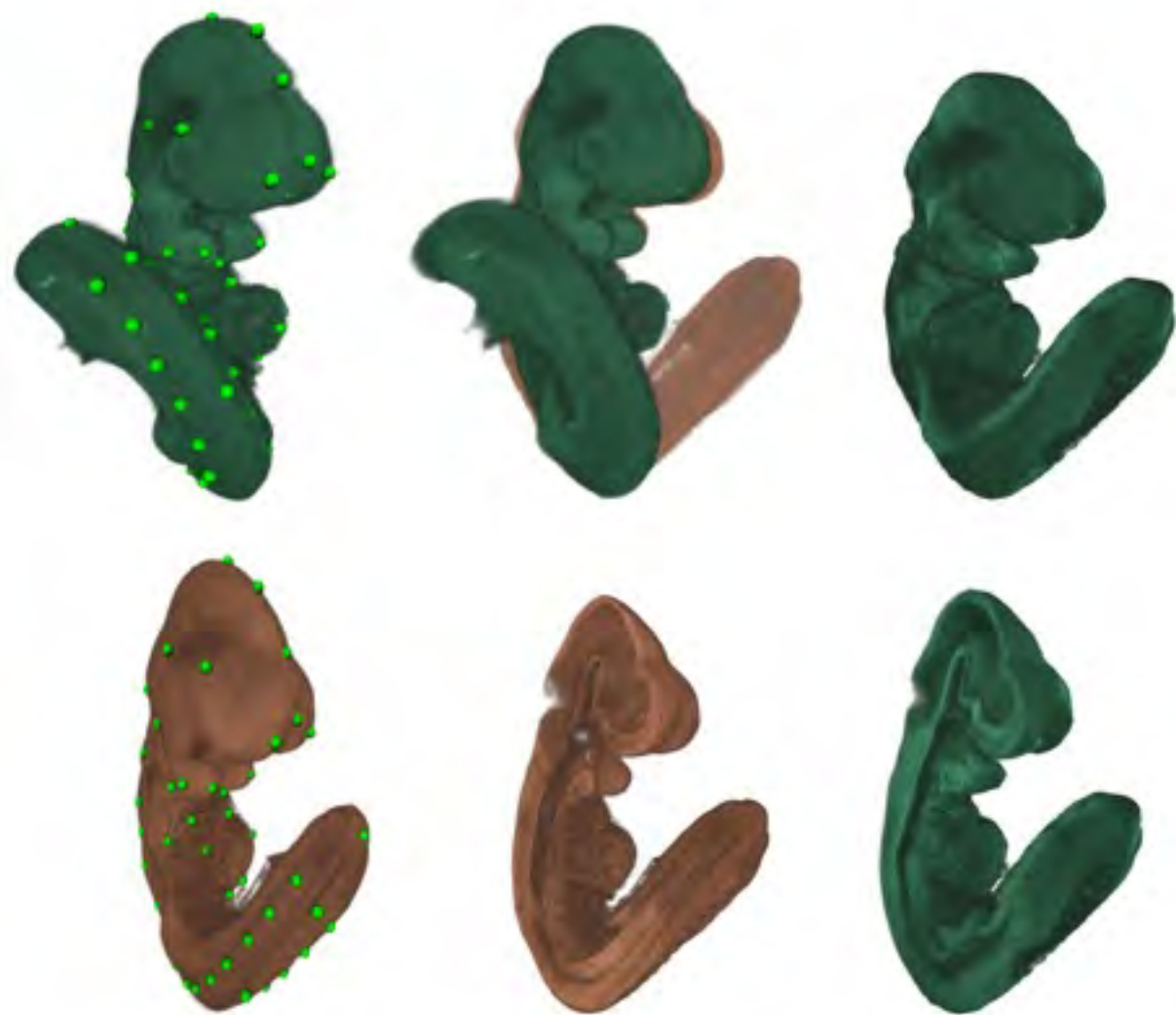
- Manual tie-point alignment (Wlzwarp)
  - ▶ mesh-based constrained distance transform
  - ▶ interactive
  - ▶ arbitrary complexity
- Automated fine tuning (ITK/ANTs)
- Editor review



# 3D Data Mapping - WlzWarp

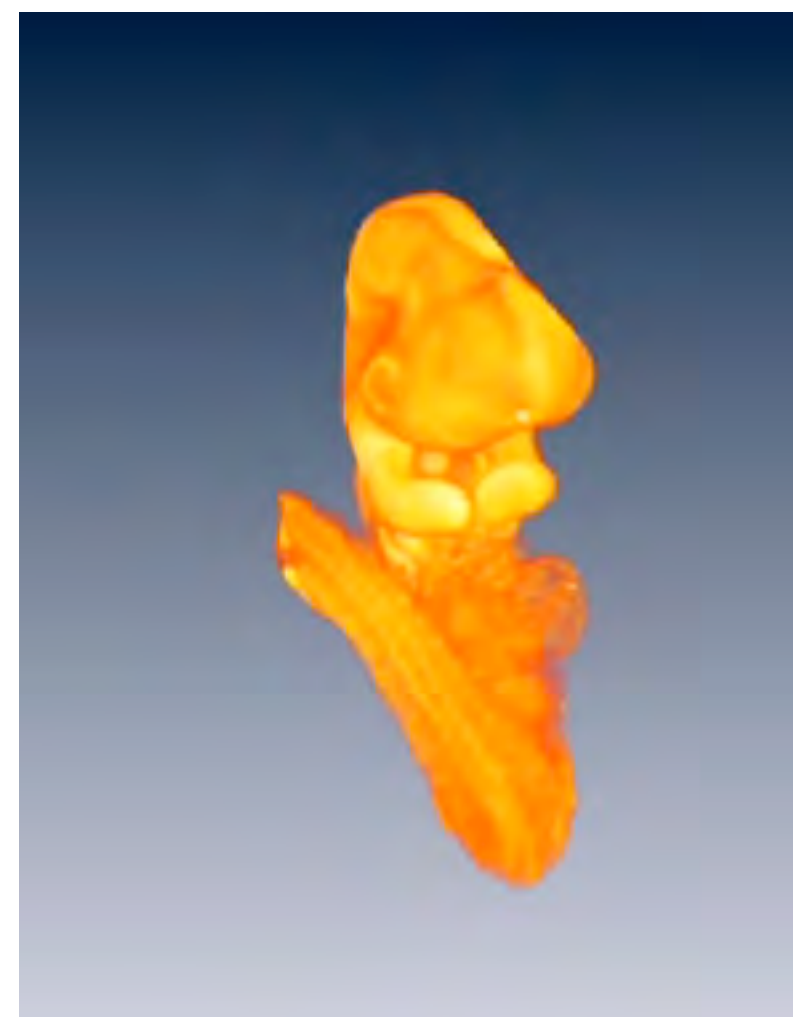
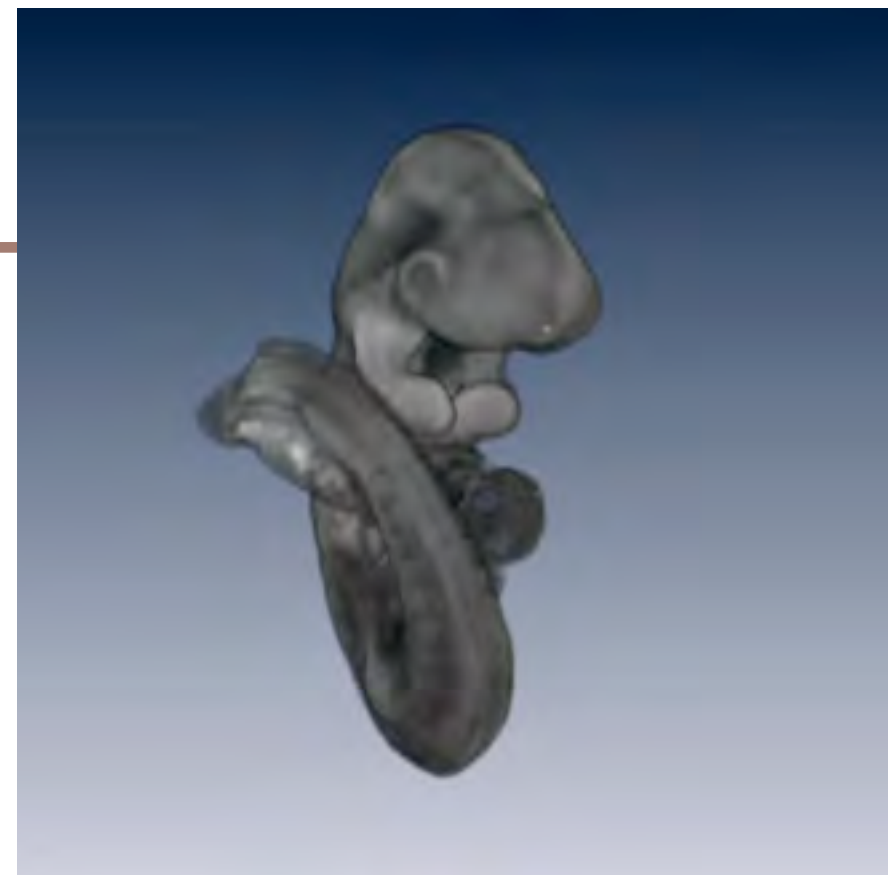
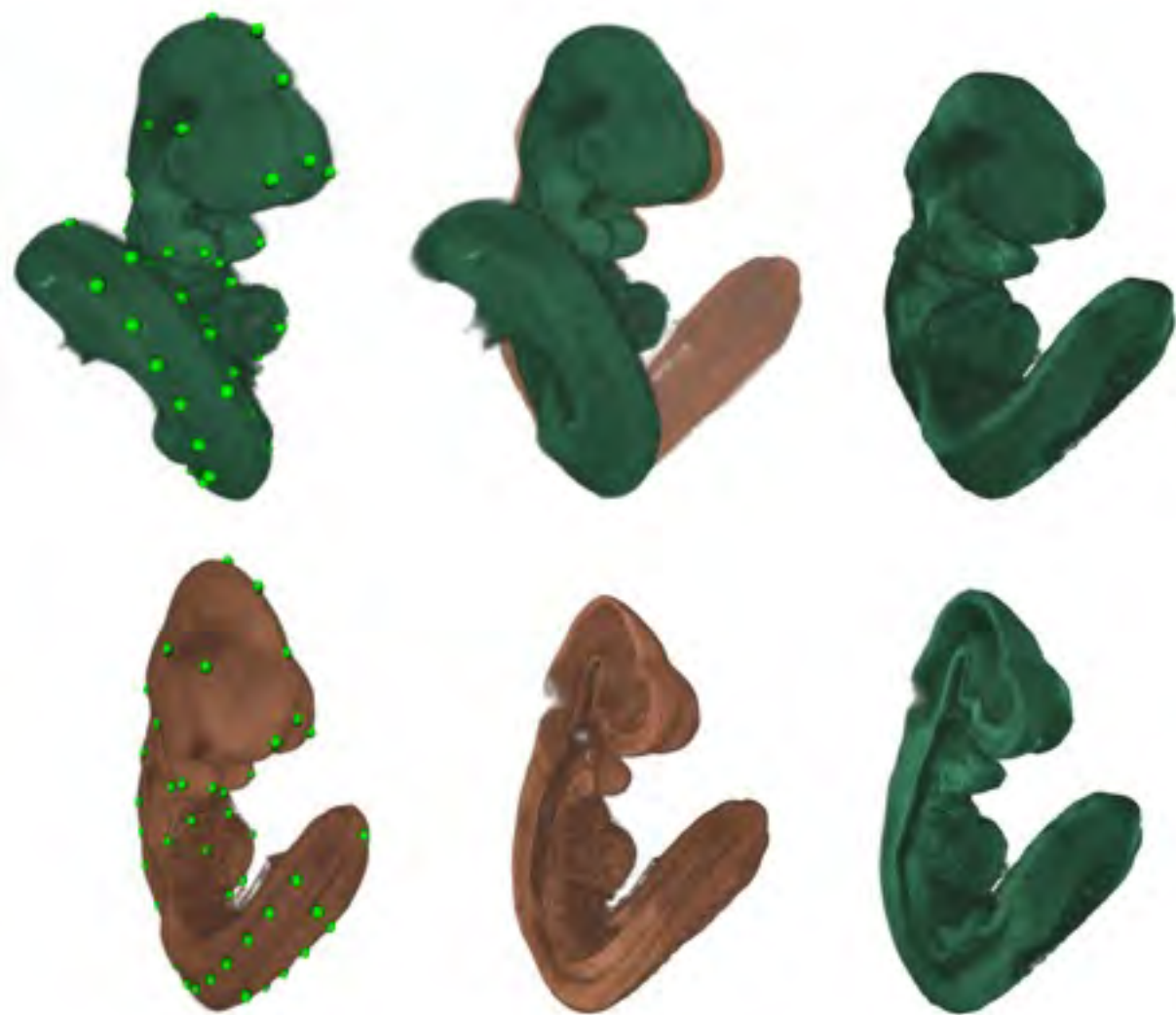


# 3D Data Mapping - WlzWarp






# 3D Data Mapping - WlzWarp



# 3D Mapping - Wnt signalling pathway

Wnt1		TS17	10.5dpc	3D View	<a href="#">EMAGE:6132</a>
Wnt2		TS17	10.5dpc	3D View	<a href="#">EMAGE:6134</a>
Wnt3		TS17	10.5dpc	<a href="#">3D View</a>	<a href="#">EMAGE:6138</a>
Wnt3A		TS17	10.5dpc	<a href="#">3D View</a>	<a href="#">EMAGE:6141</a>
Wnt4		TS17	10.5dpc	3D View	<a href="#">EMAGE:6142</a>
Wnt5A		TS17	10.5dpc	<a href="#">3D View</a>	<a href="#">EMAGE:6144</a>
Wnt6		TS17	10.5dpc	<a href="#">3D View</a>	<a href="#">EMAGE:6148</a>
Wnt7A		TS17	10.5dpc	<a href="#">3D View</a>	<a href="#">EMAGE:6150</a>

**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	<a href="#">EMAGE:6132</a>
Wnt2		TS17	10.5dpc	3D View	<a href="#">EMAGE:6134</a>
Wnt3		TS17	10.5dpc	<a href="#">3D View</a>	<a href="#">EMAGE:6138</a>
Wnt3A		TS17	10.5dpc	<a href="#">3D View</a>	<a href="#">EMAGE:6141</a>
Wnt4		TS17	10.5dpc	3D View	<a href="#">EMAGE:6142</a>
Wnt5A		TS17	10.5dpc	<a href="#">3D View</a>	<a href="#">EMAGE:6144</a>
Wnt6		TS17	10.5dpc	<a href="#">3D View</a>	<a href="#">EMAGE:6148</a>
Wnt7A		TS17	10.5dpc	<a href="#">3D View</a>	<a href="#">EMAGE:6150</a>

**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.

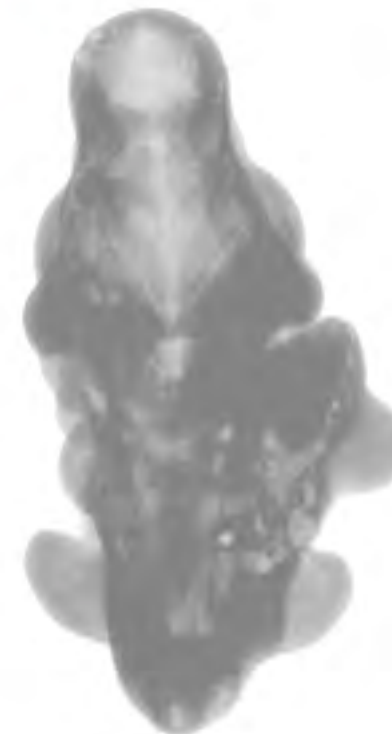
Photograph prior to 3D imaging.

[View 3D opt image](#) 

[Download 3D images in woolz format.](#)

Expression pattern clarity: ★★ -

Wnt1





- 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

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





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

A first internal processing

G.A. I

<sup>a</sup>MRC

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Pattern Recognition Letters

Volume 3, Issue 2, March 1985, Pages 119-129

## Data structures for image processing in a C language and Unix environment<sup>☆</sup>

Jim Piper<sup>a</sup> and Denis Rutovitz<sup>a</sup>

<sup>a</sup>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

<sup>☆</sup>This work was supported entirely by the UK Medical Research Council.



## A fast internal process

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## Data st and Un

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<sup>a</sup>MRC Clinic  
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### Abstract

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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.

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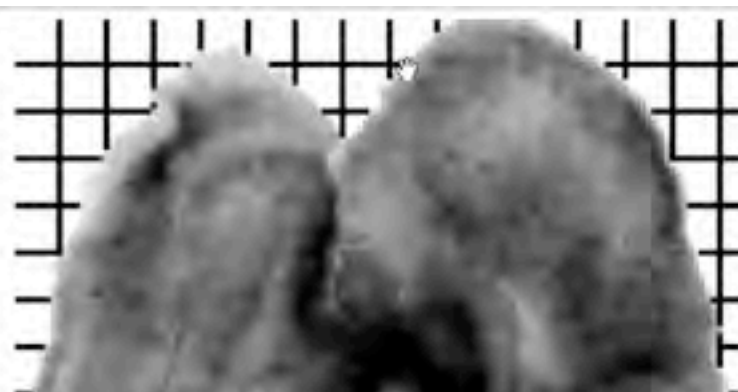
Cytometry. 1994 May 1;16(1):7-16.

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

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### Abstra

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

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

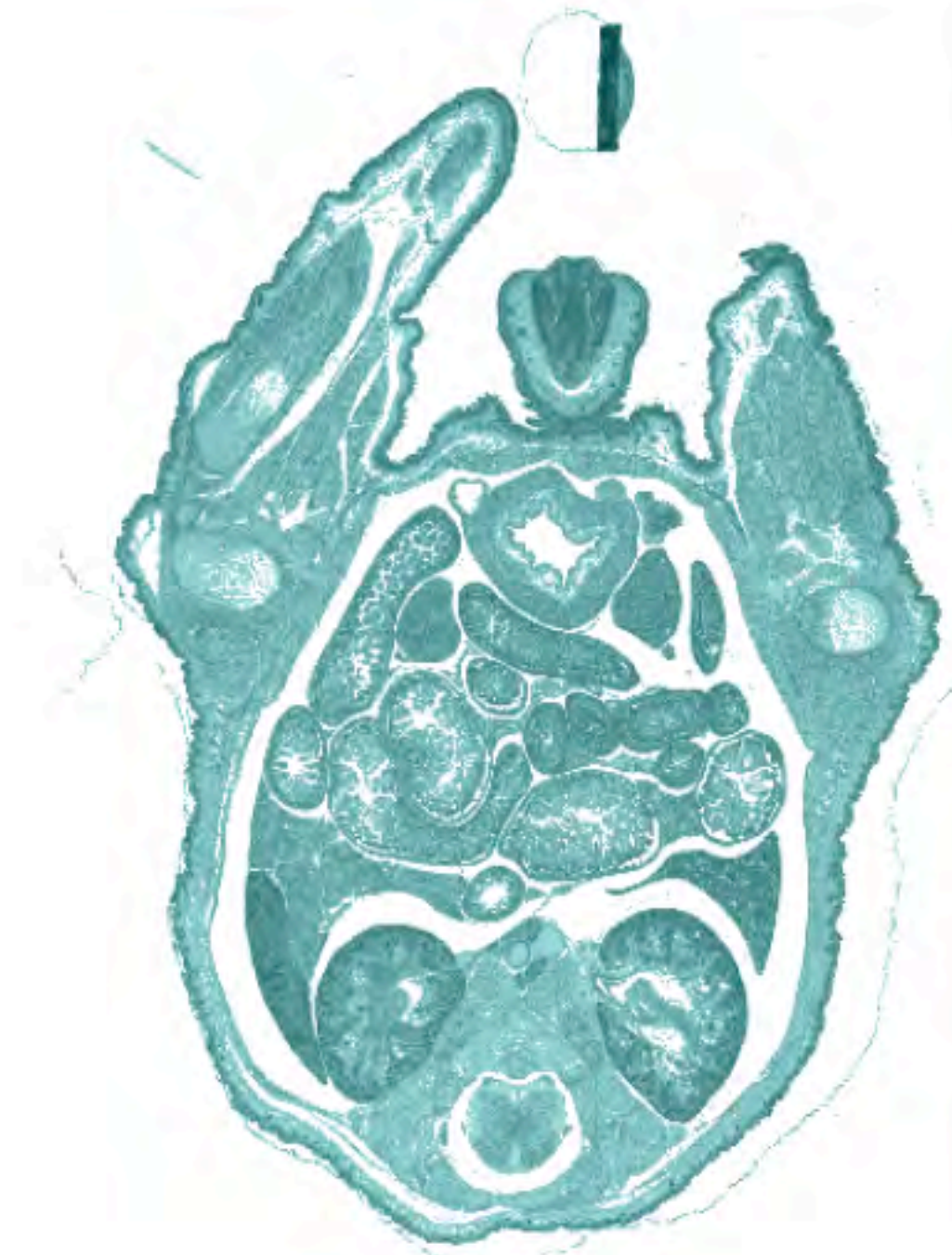




- Domain
  - Rectangle based
  - Interval based
  - 3D planewise domains

## Values

- Rectangle based
- Raged and interval based
- Tiled



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

## Values

- Rectangle based
- Raged and interval based
- Tiled

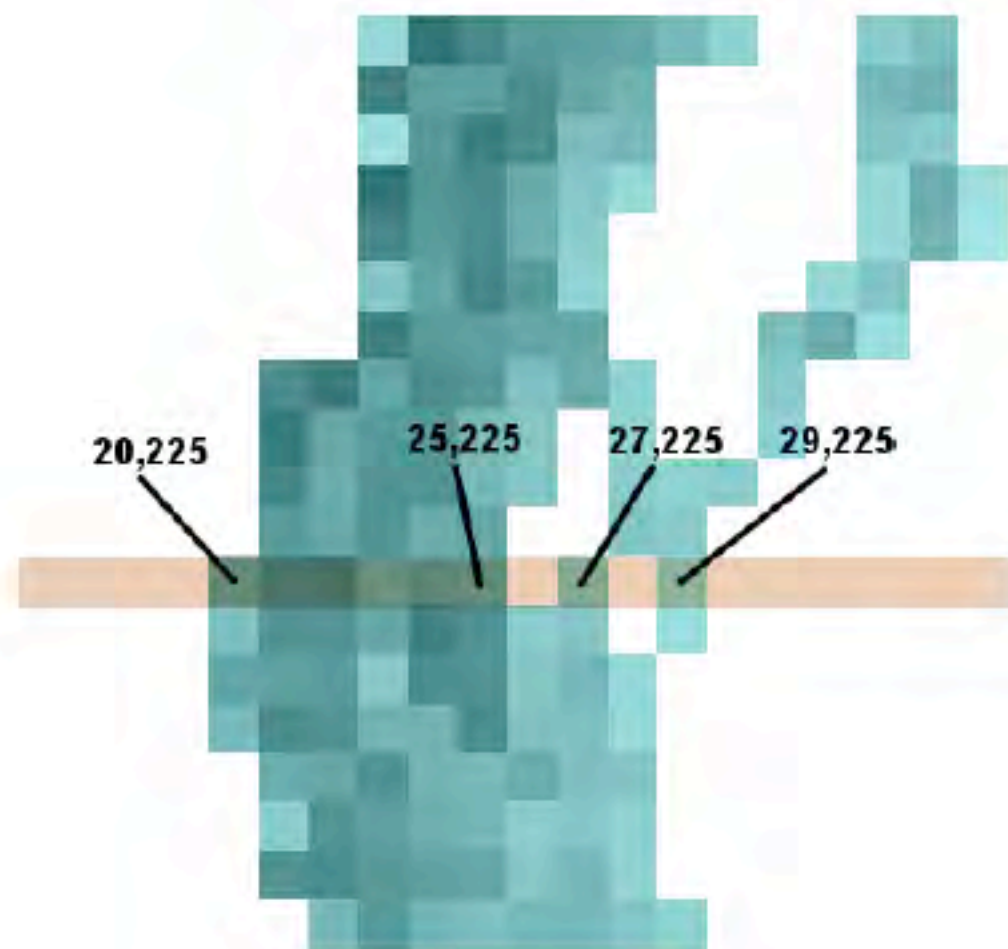




- Domain
  - Rectangle based
  - Interval based
  - 3D planewise domains

## Values

- Rectangle based
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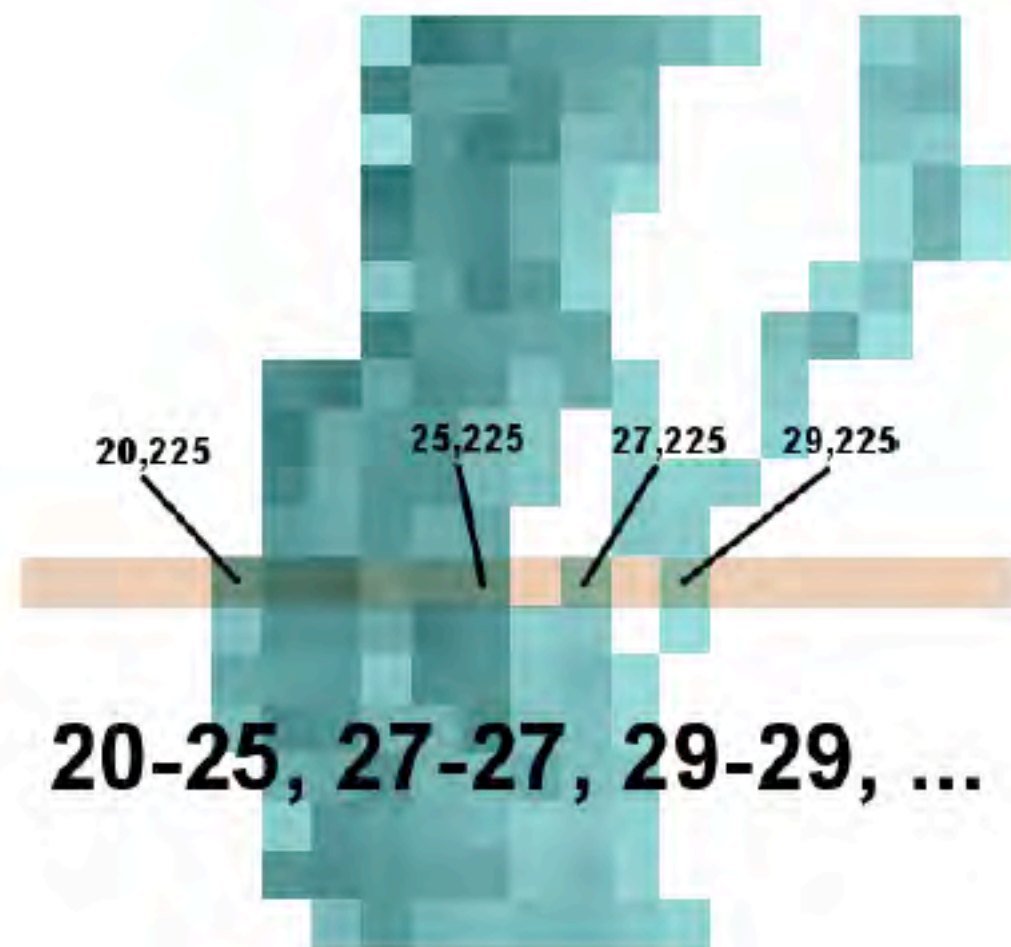




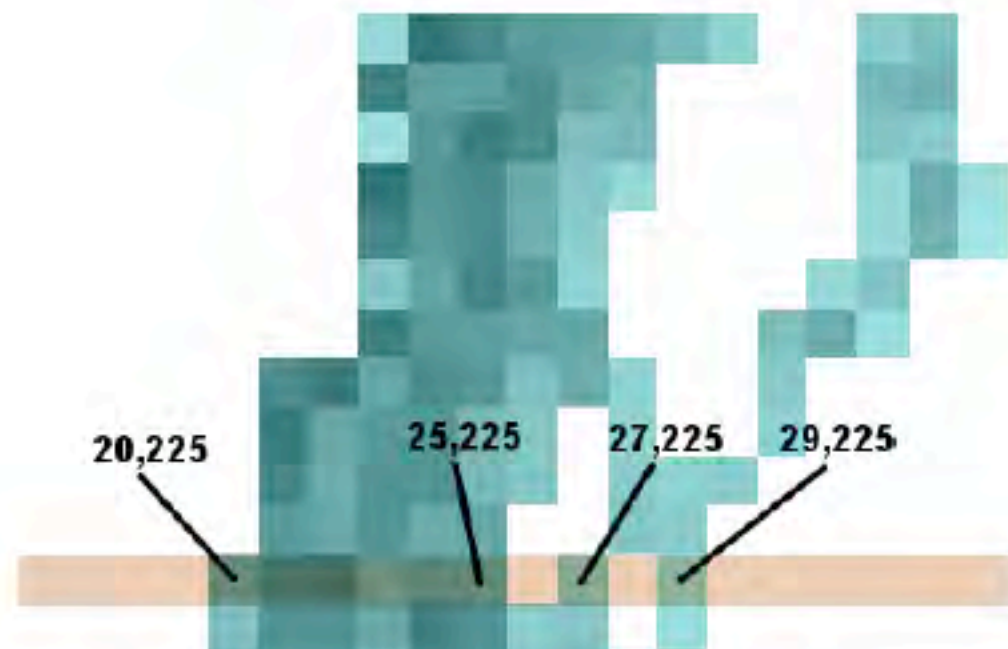
- Domain
  - Rectangle based
  - Interval based
  - 3D planewise domains

- Values

- Rectangle based
- Ranged and interval based
- Tiled



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



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

## Domain

- Rectangle based
- Interval based
- 3D plane-wise domain

- **Values**

- Rectangle based
- Raged and interval based
- Tiled





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





- Values
  - Rect
  - Range
  - 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

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



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

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

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

$$\Delta u = u - x$$

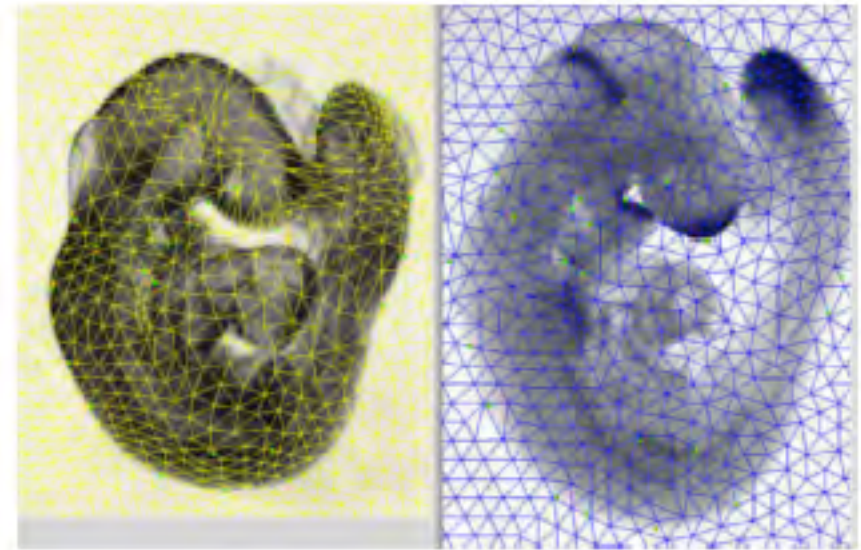
$$\Delta u = P_u(x, y) + \sum_{i=1}^{i=N} \lambda_i b(r_i)$$

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

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

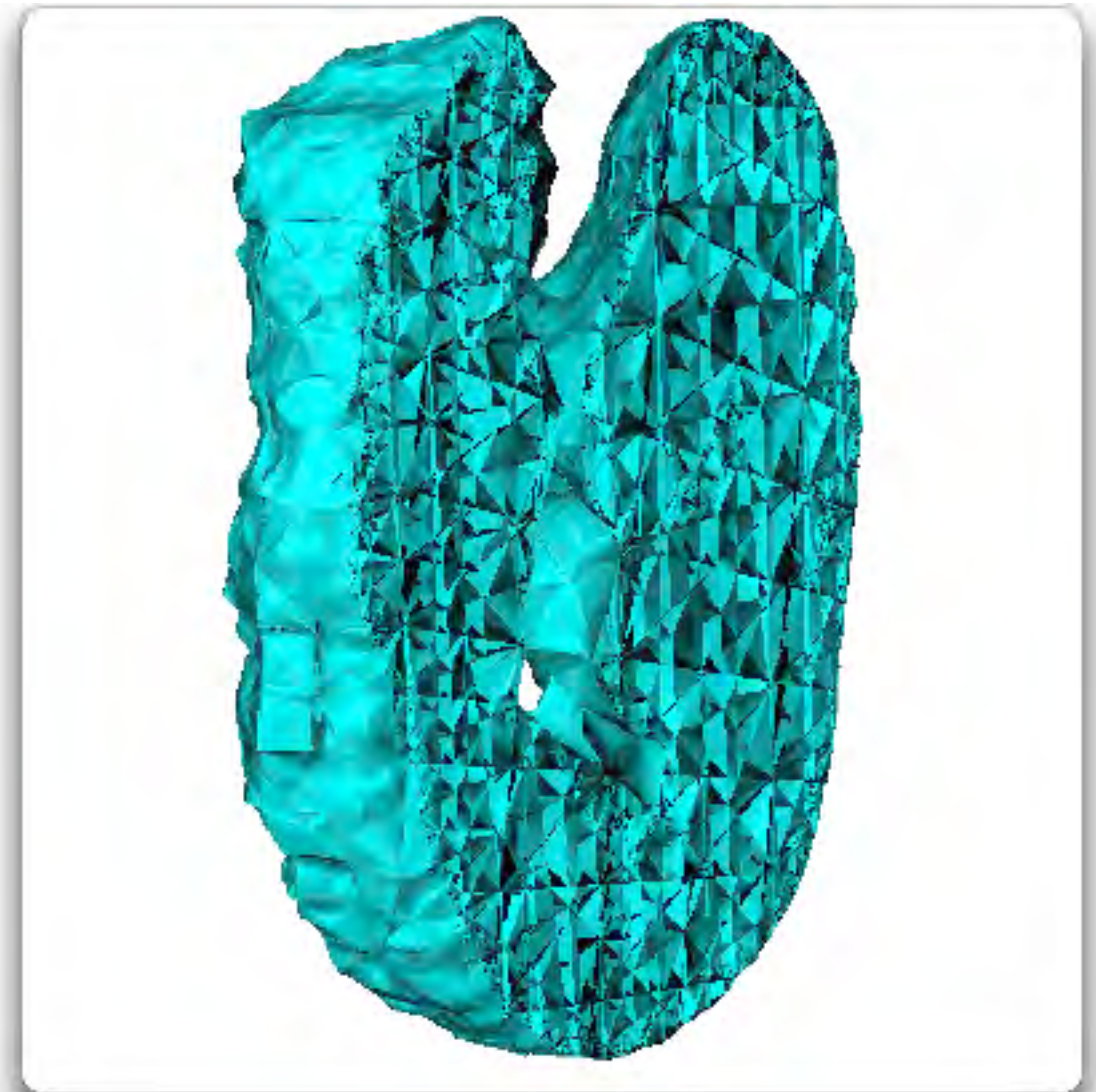
$$b_{IMQ}(r) = \frac{1}{\sqrt{r^2 + \delta^2}}$$

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





- Polylines, boundary lists
- histograms
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- transforms
  - ▶ affine
  - ▶ basis function
  - ▶ mesh
  - ▶ conforming mesh



- 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....

- 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.



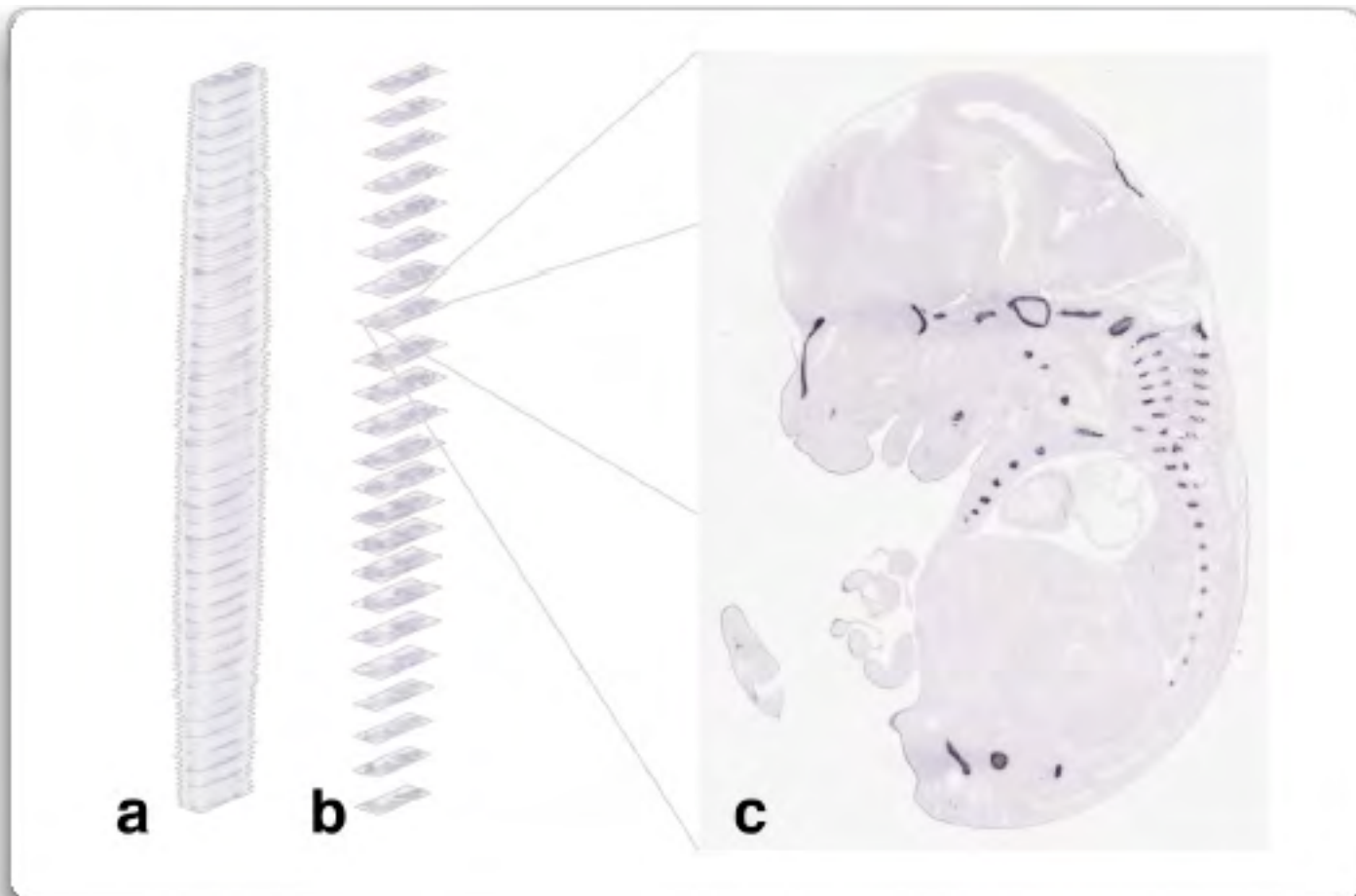


# Pseudo Wholemount Mapping to Emap - done

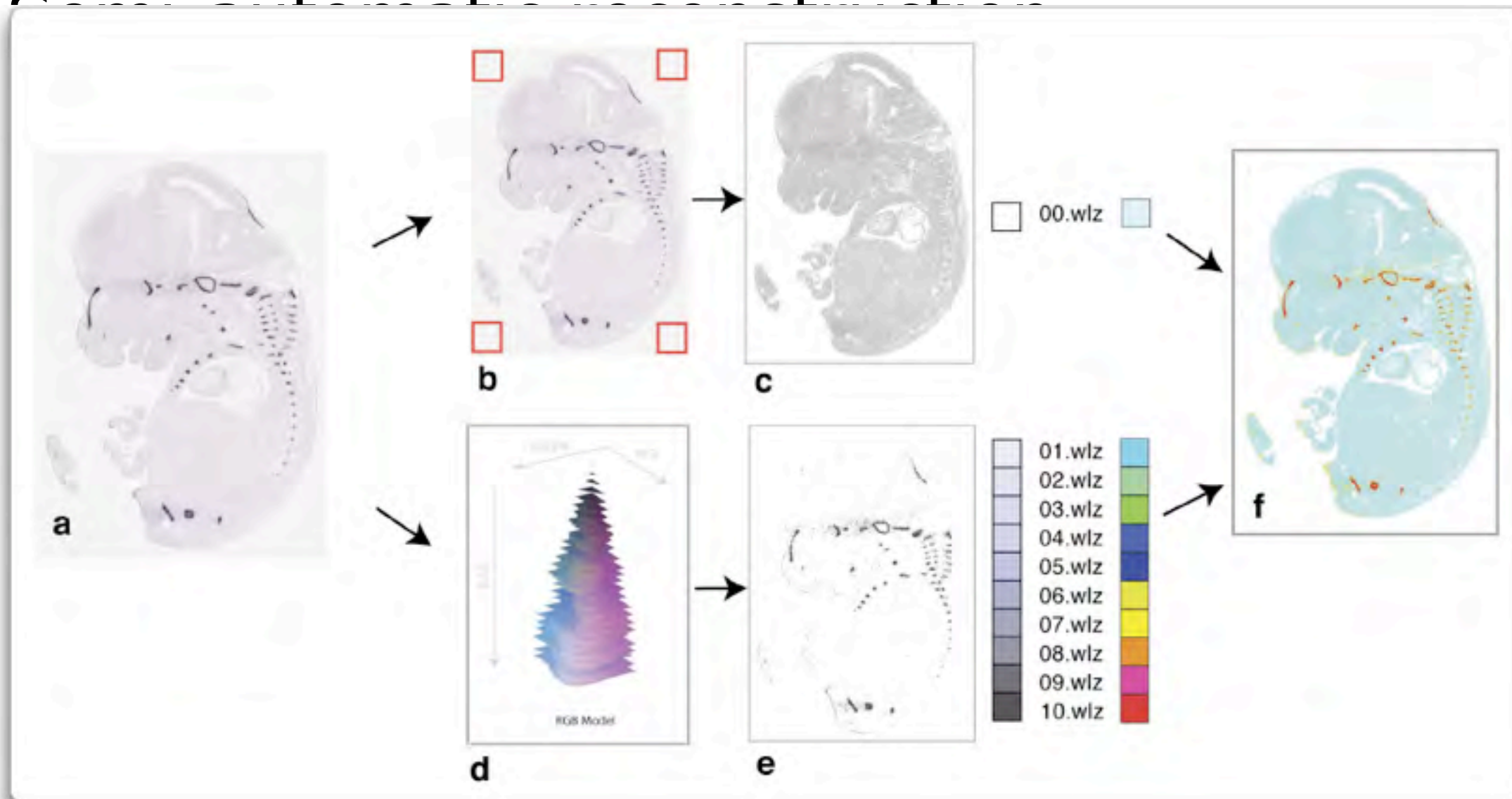
---

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

- Semi-automatic reconstruction

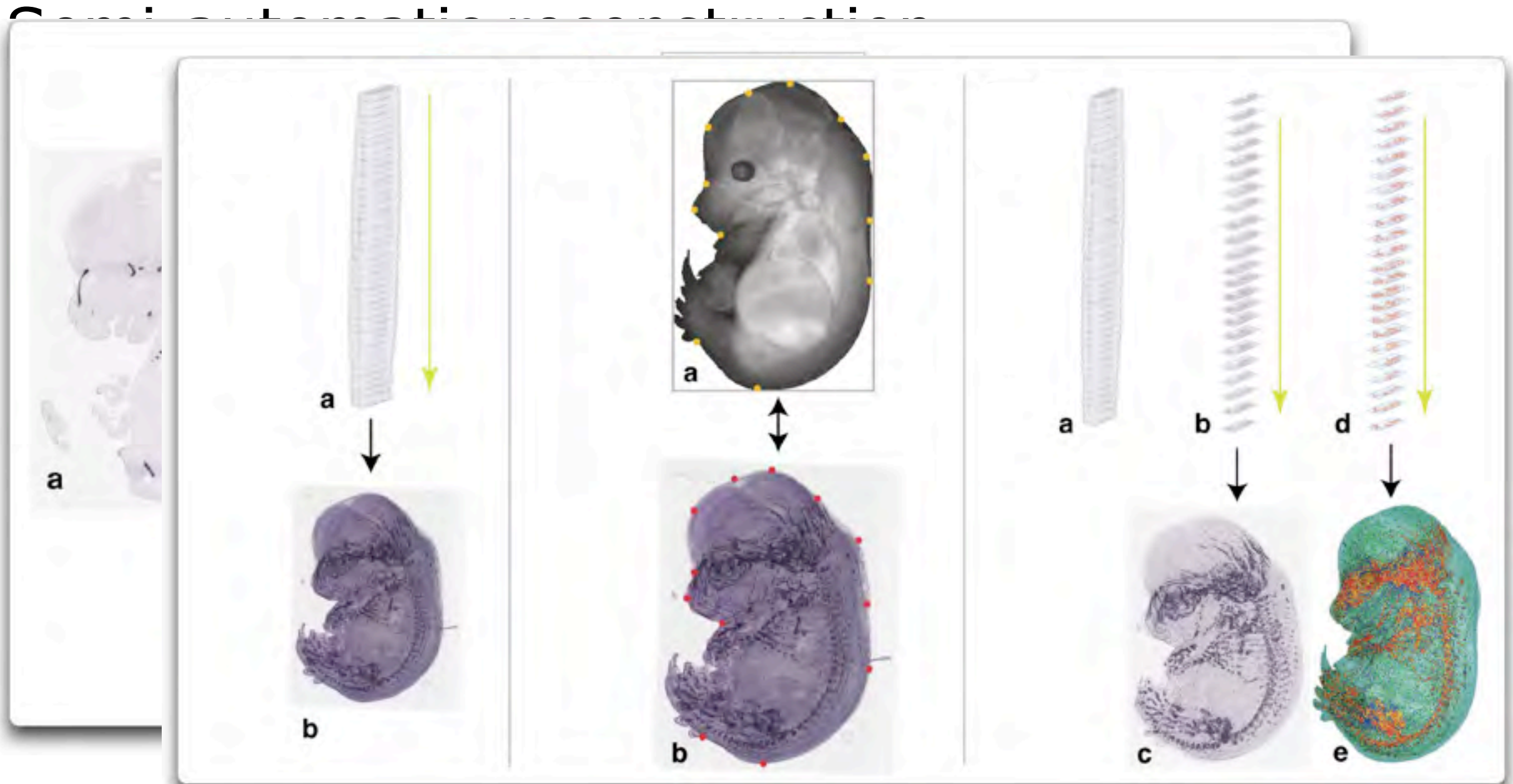


# Pseudo Wholemount Mapping to Emap - done

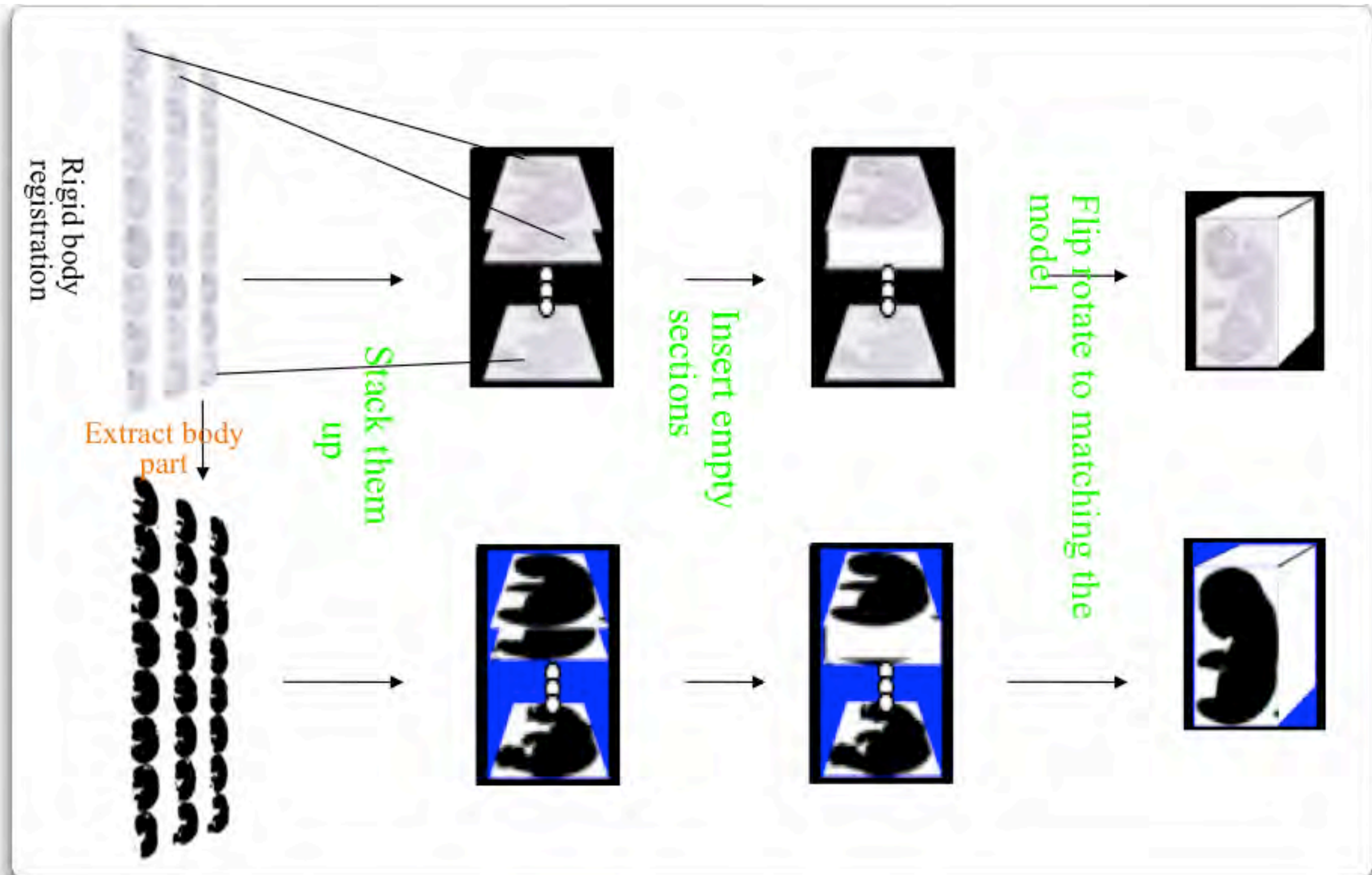




# Pseudo Wholemount Mapping to Emap - done



# 3D Mapping to emap



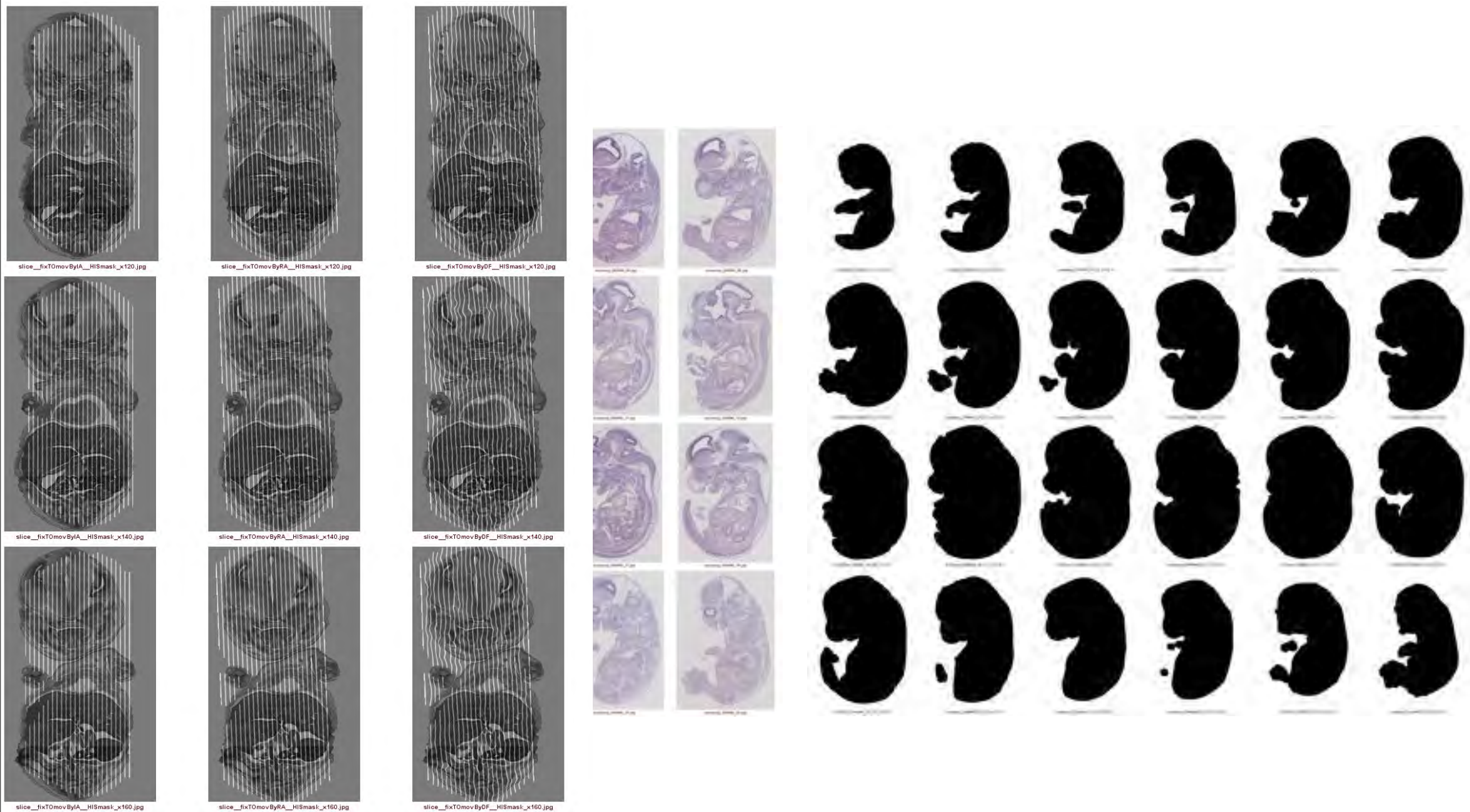
# 3D Mapping to emap







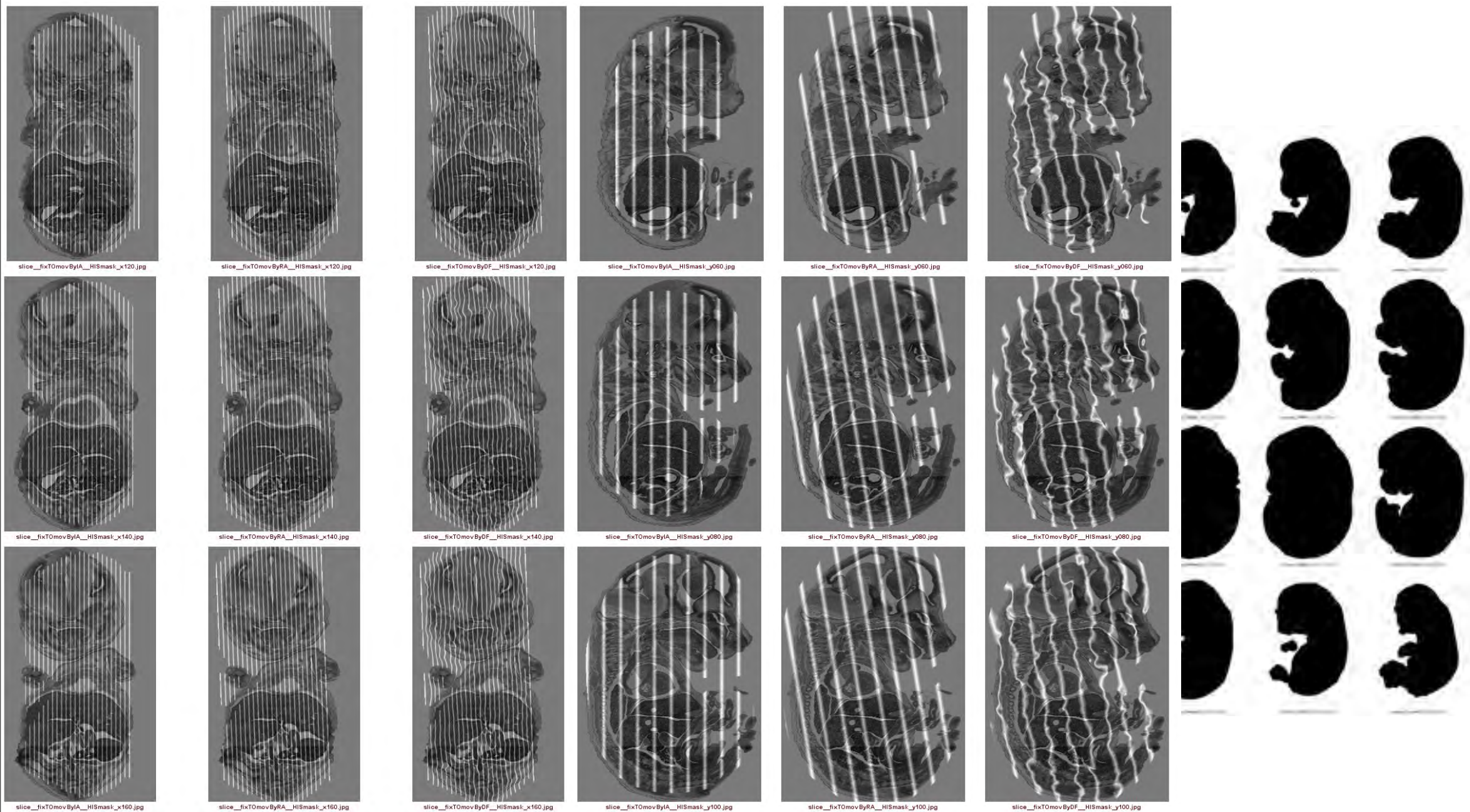
# 3D Mapping to emap







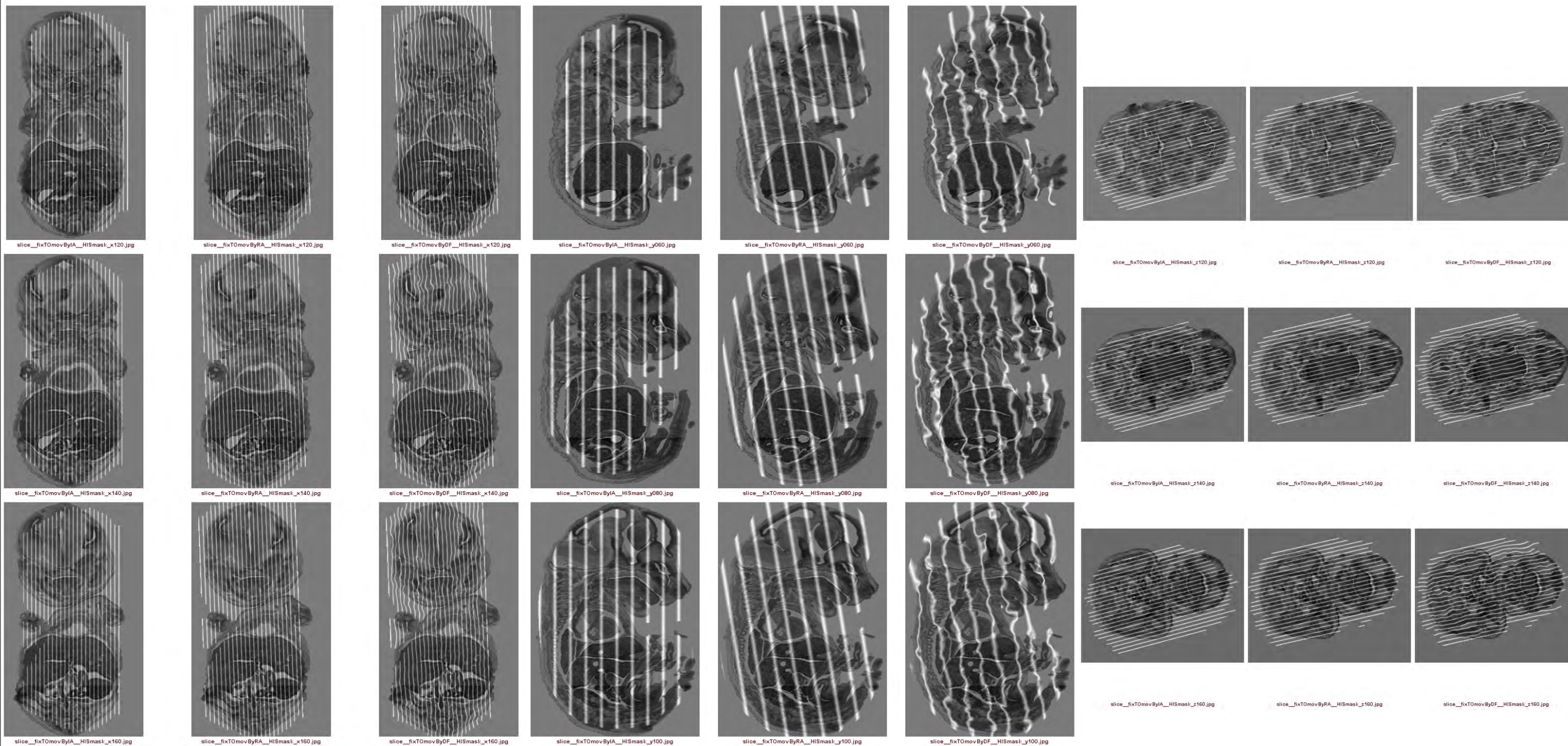
# 3D Mapping to emap







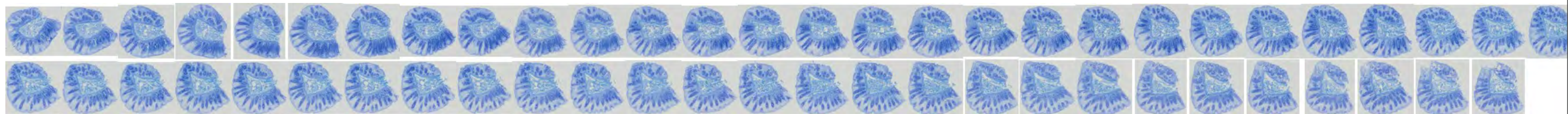
# 3D Mapping to emap





- 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

- Typical task:
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  - ▶ serial sections (1-2 micron)
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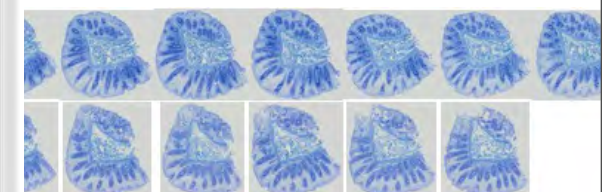
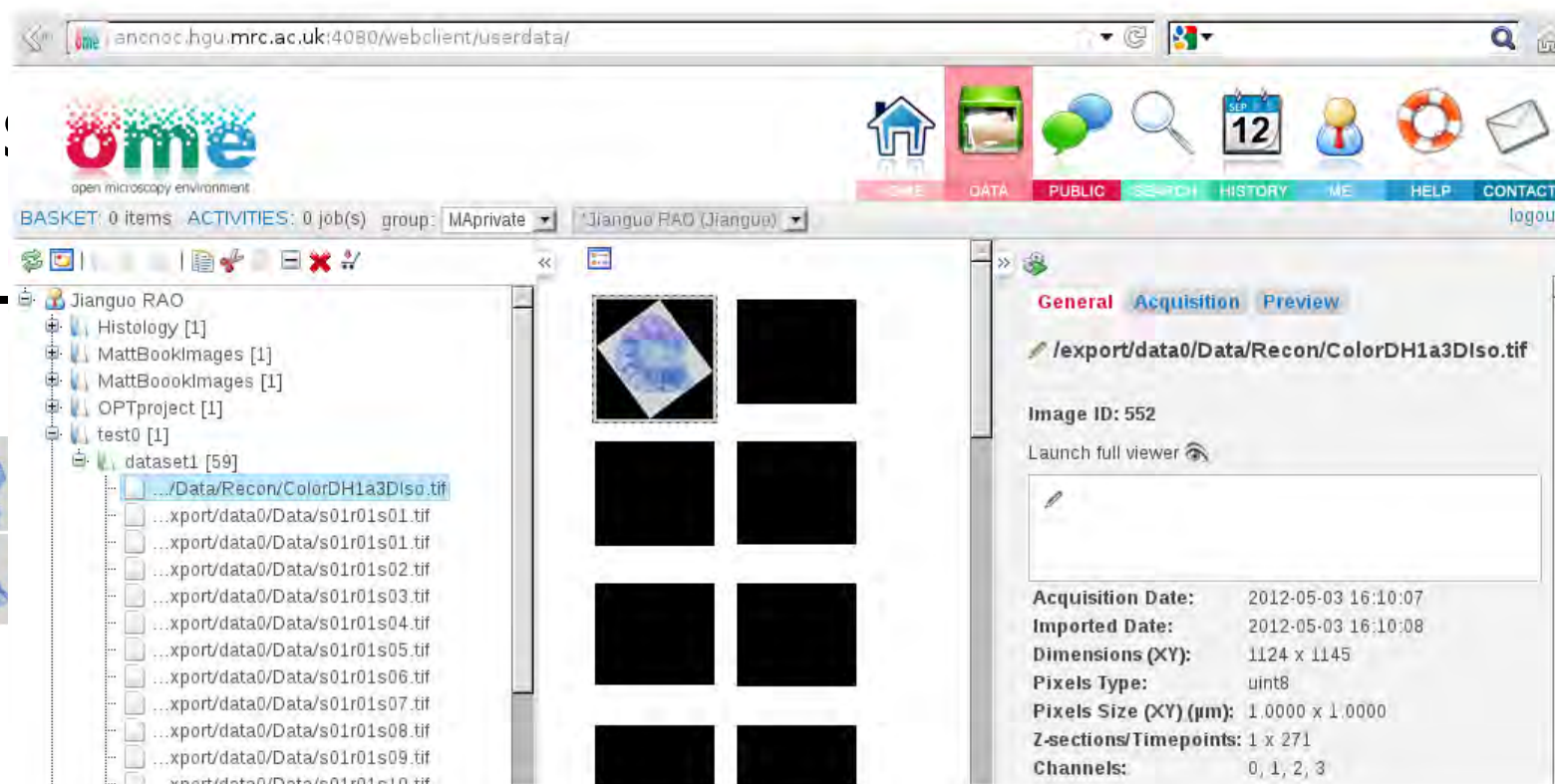
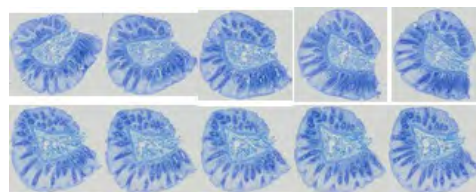
# Serial Section Reconstruction

## ● Typical task:

- ▶ 2D high-res (.3 micron) histology
- ▶ serial sections (1-2 micron)
- ▶ 3D image for tissue module geometry and stats

▶ recon

▶ "user-





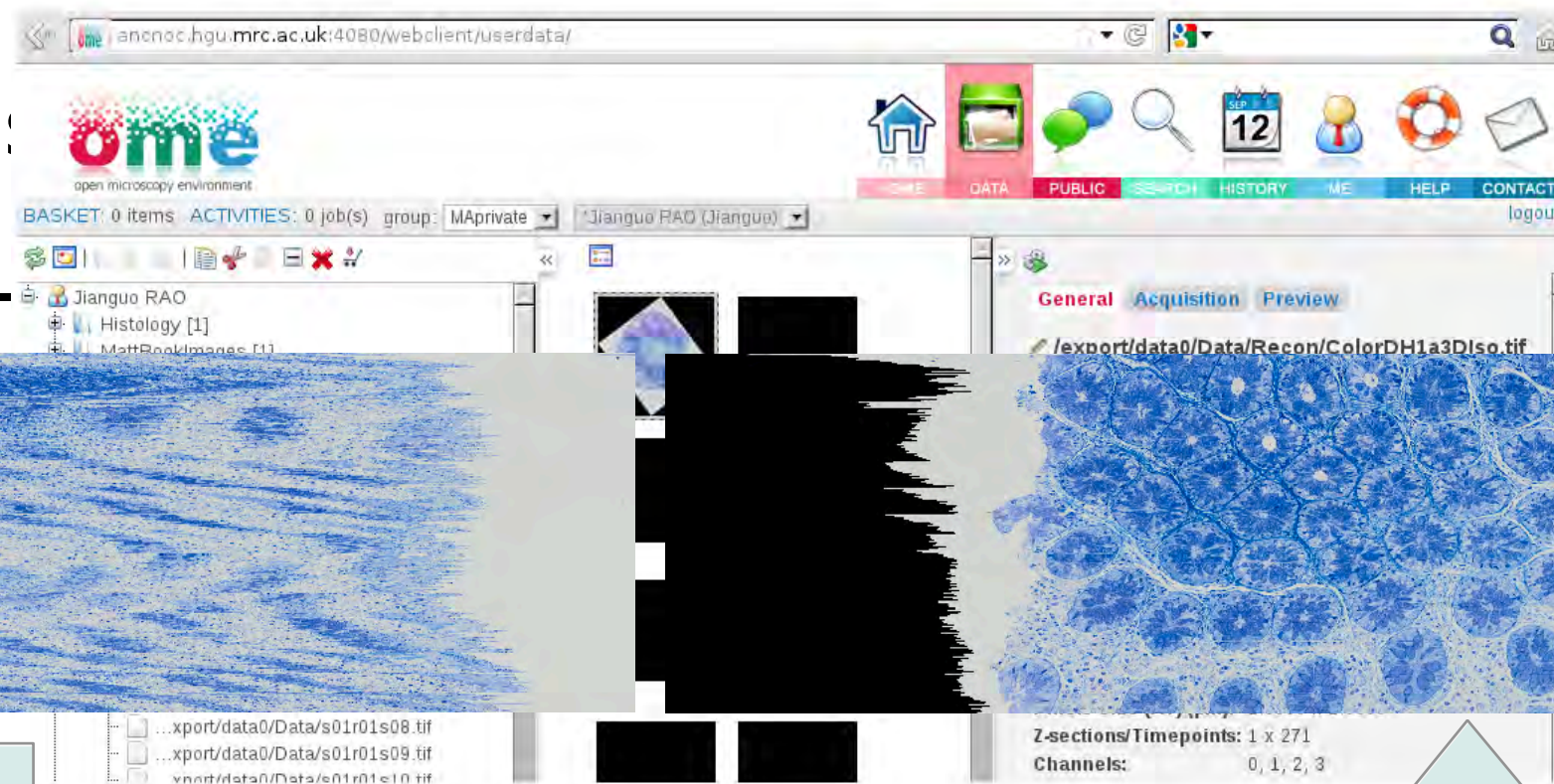
# Serial Section Reconstruction

## ● Typical task:

- ▶ 2D high-res (.3 micron) histology
- ▶ serial sections (1-2 micron)
- ▶ 3D image for tissue module geometry and stats

▶ recon

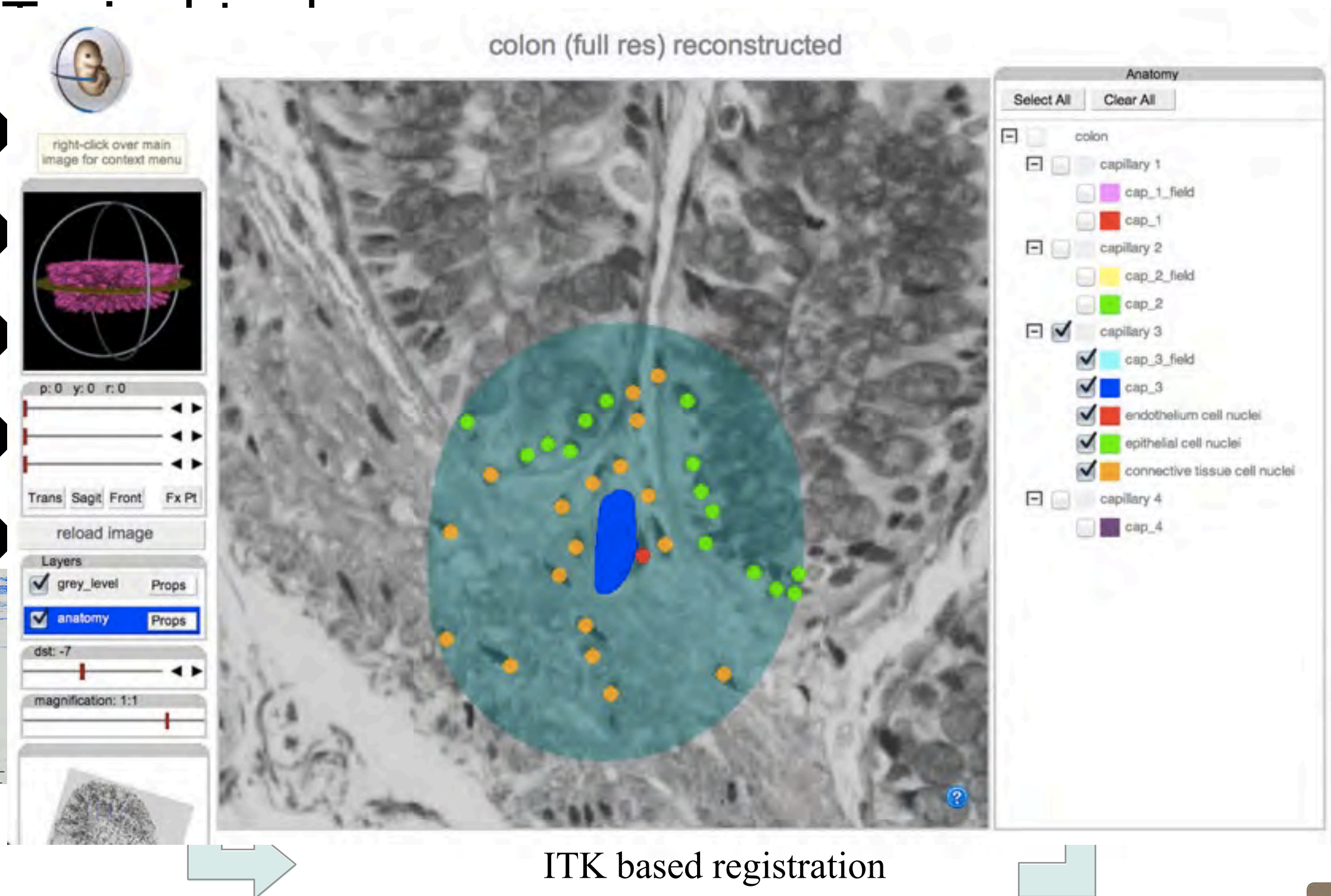
▶ "user-



ITK based registration



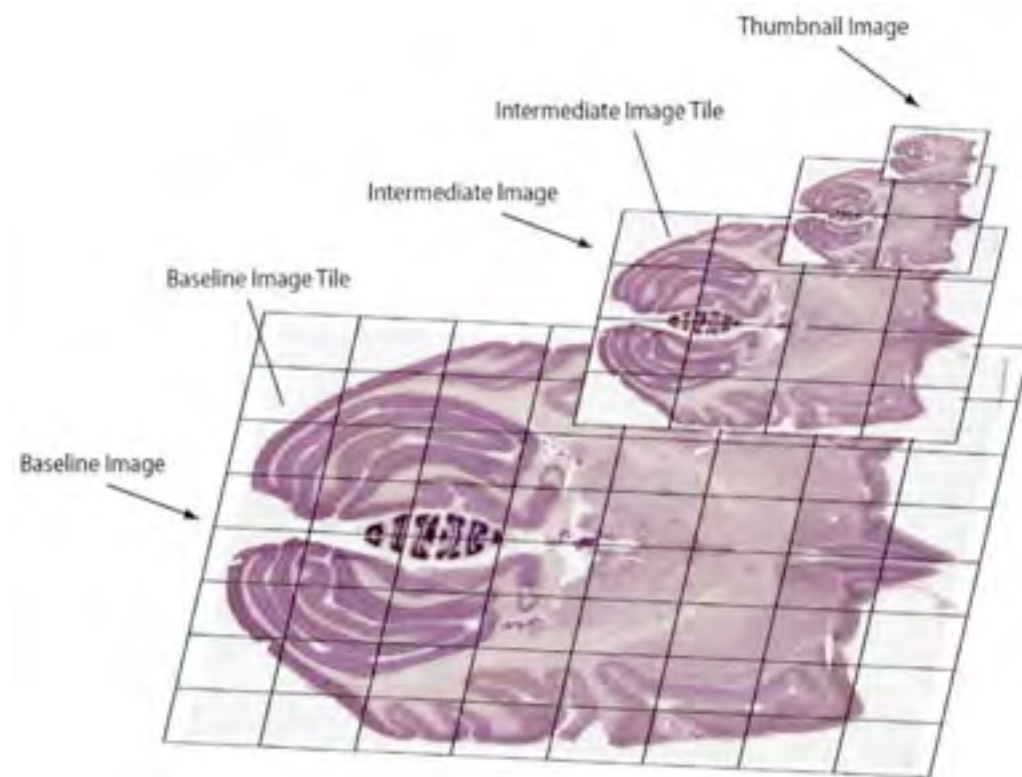
# Serial Section Reconstruction



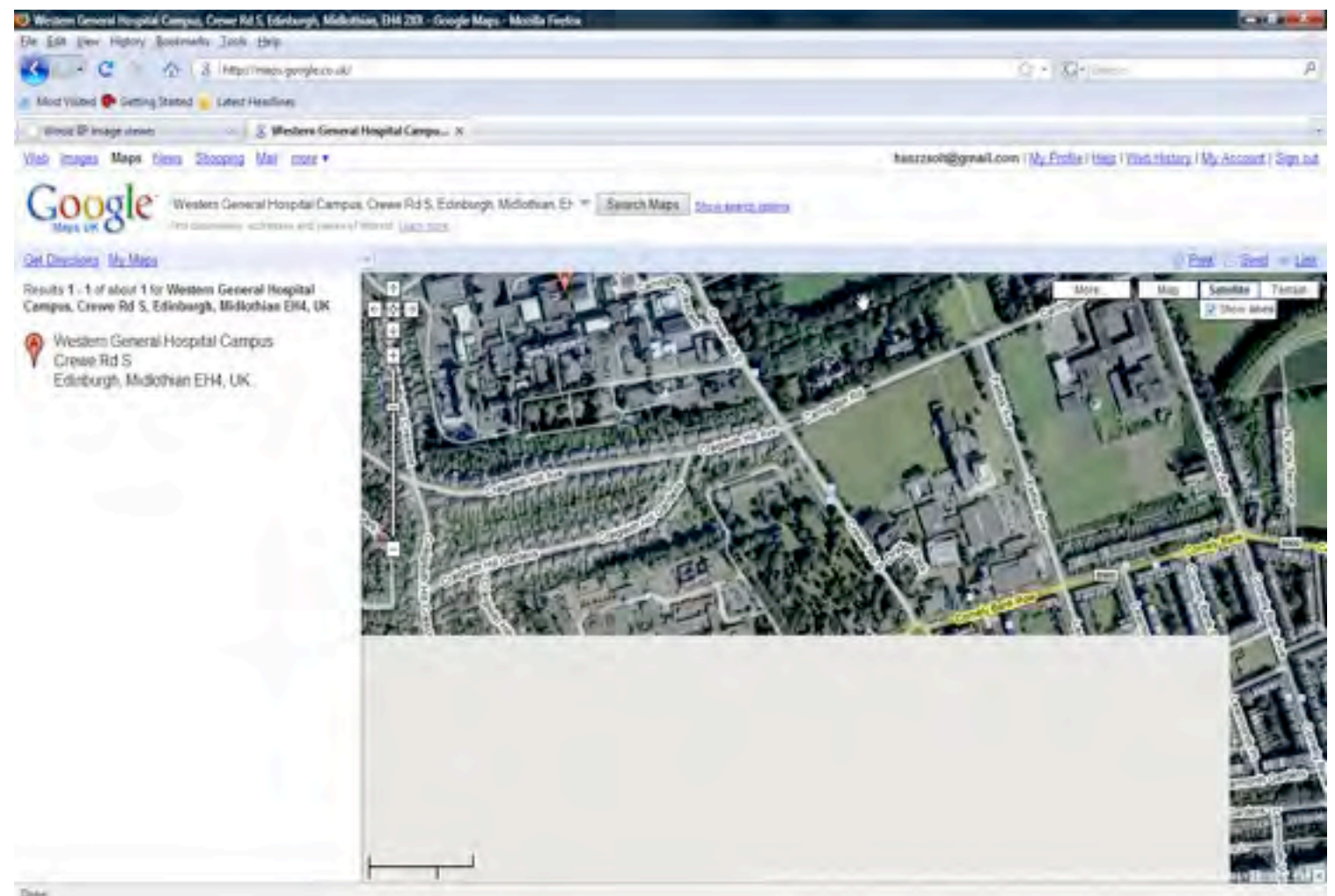
- Single light microscopy reconstructions already 30+GB, microCT sets ~200GB
- New EM embryo data ~0.5TB
- OPT data - small (200MB) but many - 5K
- Typical requirement to browse as sections
- Require arbitrary angle re-sectioning
- BLB - want to browse online using no more than a web-browser



# Tiled Image Servers



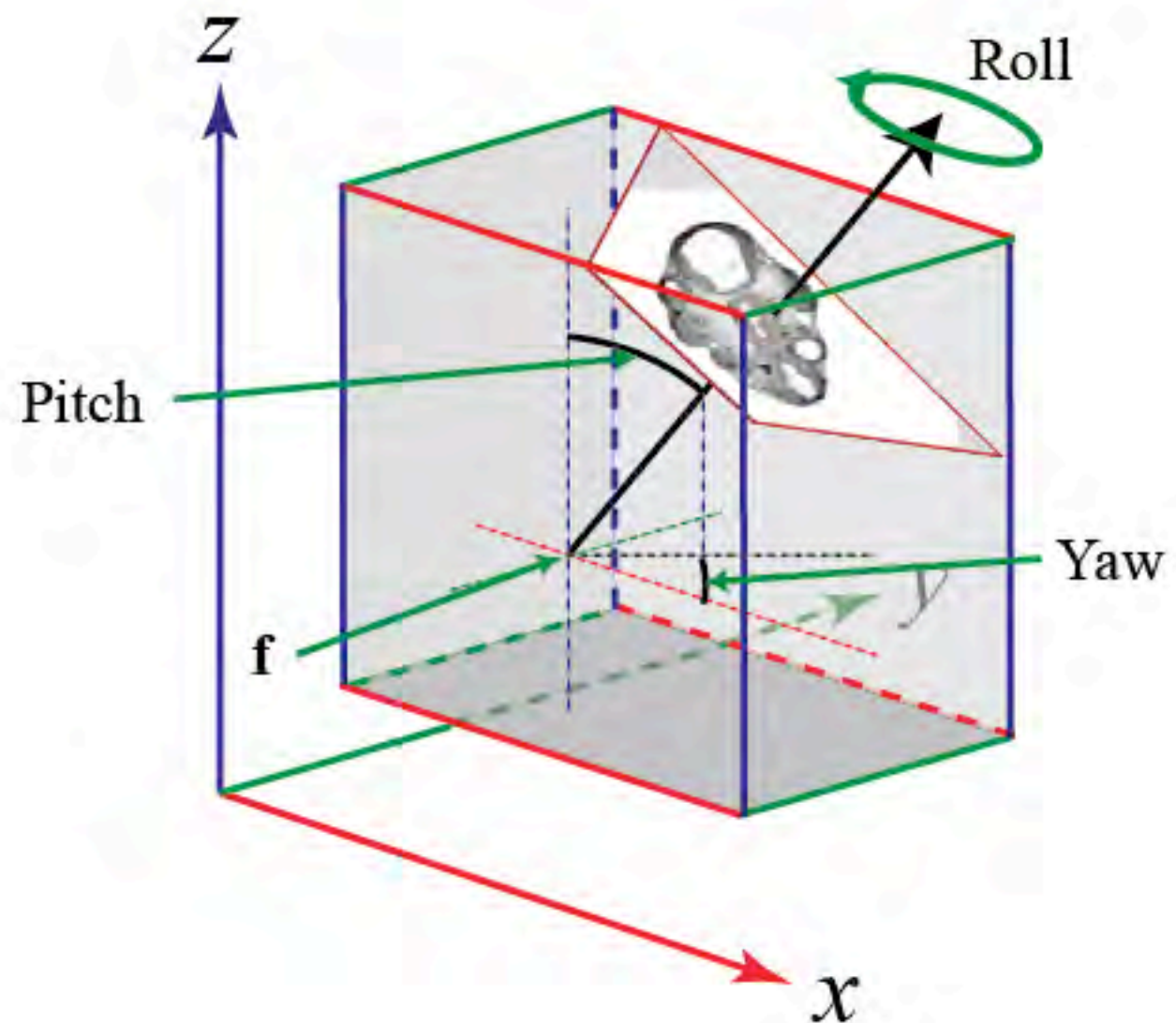
[Shawn Mikula, Issac Trotts, James M. Stone, and Edward G. Jones, Internet-Enabled High-Resolution Brain Mapping and Virtual Microscopy, Neuroimage, vol 35(1), p. 11, 2007]



[maps.google.com]

# Sectioning Parameters

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





# IIP3D - Extensions

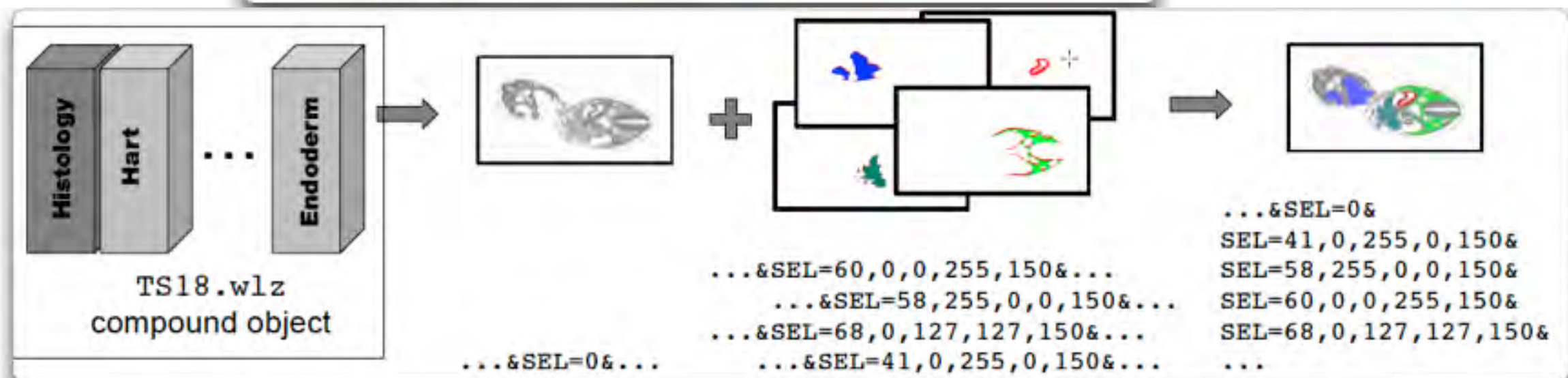
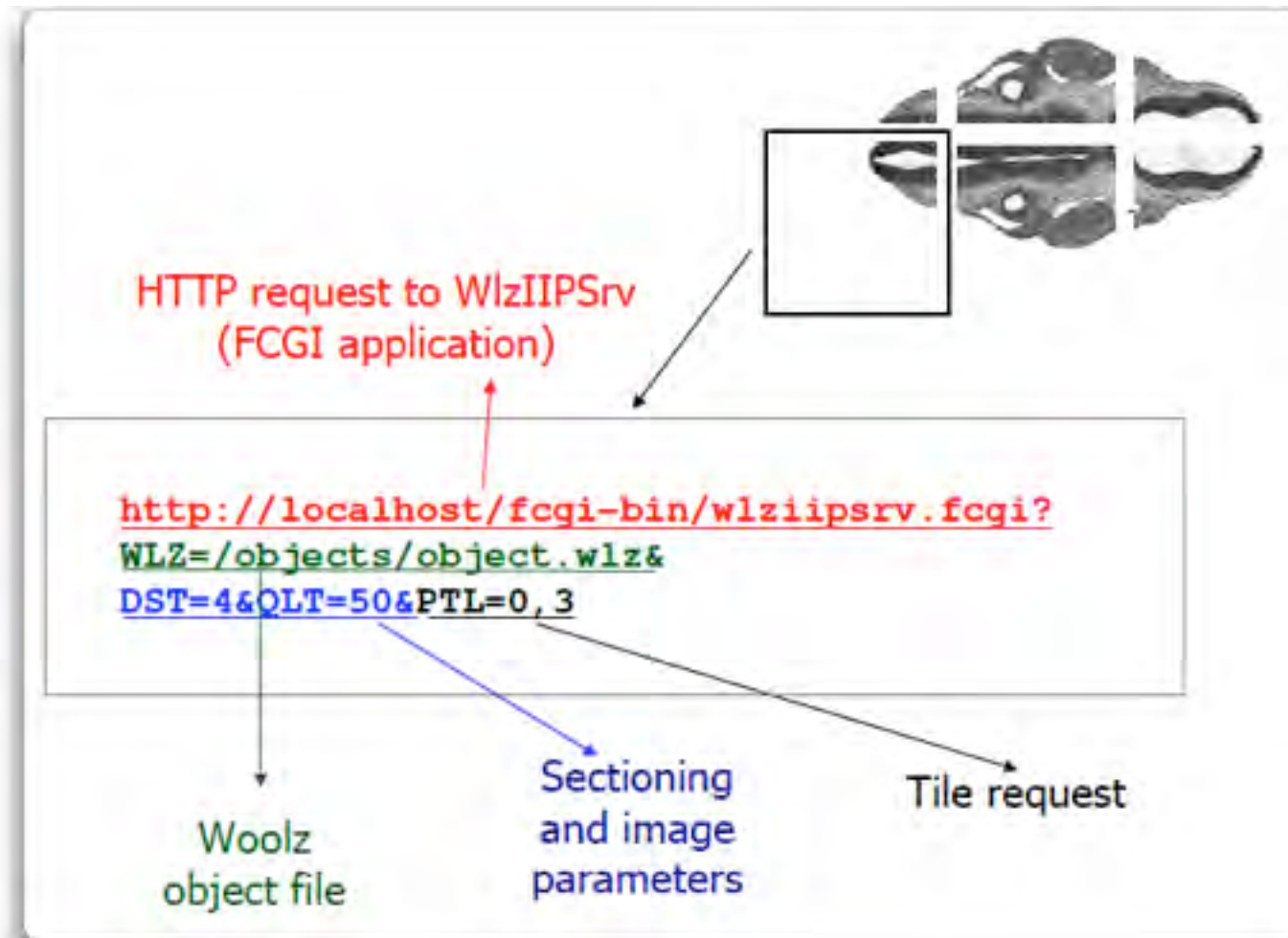
Command	Purpose	Syntax
<b>WLZ</b>	Specify the Woolz object	<b>WLZ=</b> <i>path</i>
<b>DST</b>	Specify the distance of the sectioning plane	<b>DST=</b> <i>dis</i>
<b>FXP</b>	Specify the fixed point of the viewing section rotation	<b>FXP=</b> <i>X,Y,Z</i>
<b>FXT</b>	Specify the second fixed point of the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

Table 1: Extended command overview

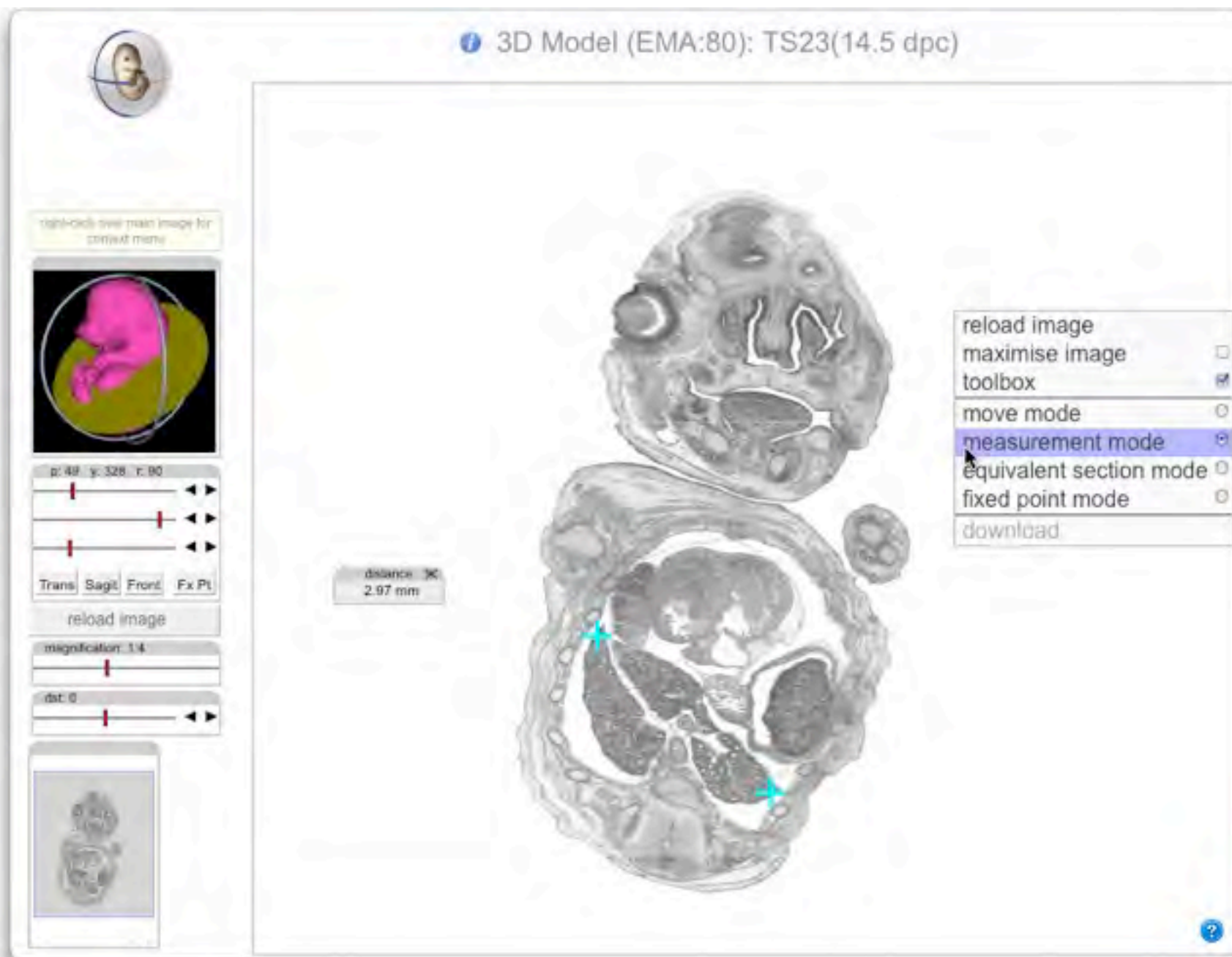
Object	Purpose
<b>IIP-server</b>	Identify if WLZ-IIP is running
<b>Max-size</b>	The size of the section
<b>Tile-size</b>	The size of a tile
<b>Wlz-true-voxel-size</b>	The voxel size of the object
<b>Wlz-volume</b>	The volume of the object
<b>Wlz-distance-range</b>	The range of the sectioning plane distance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

Table 2: Extended object overview



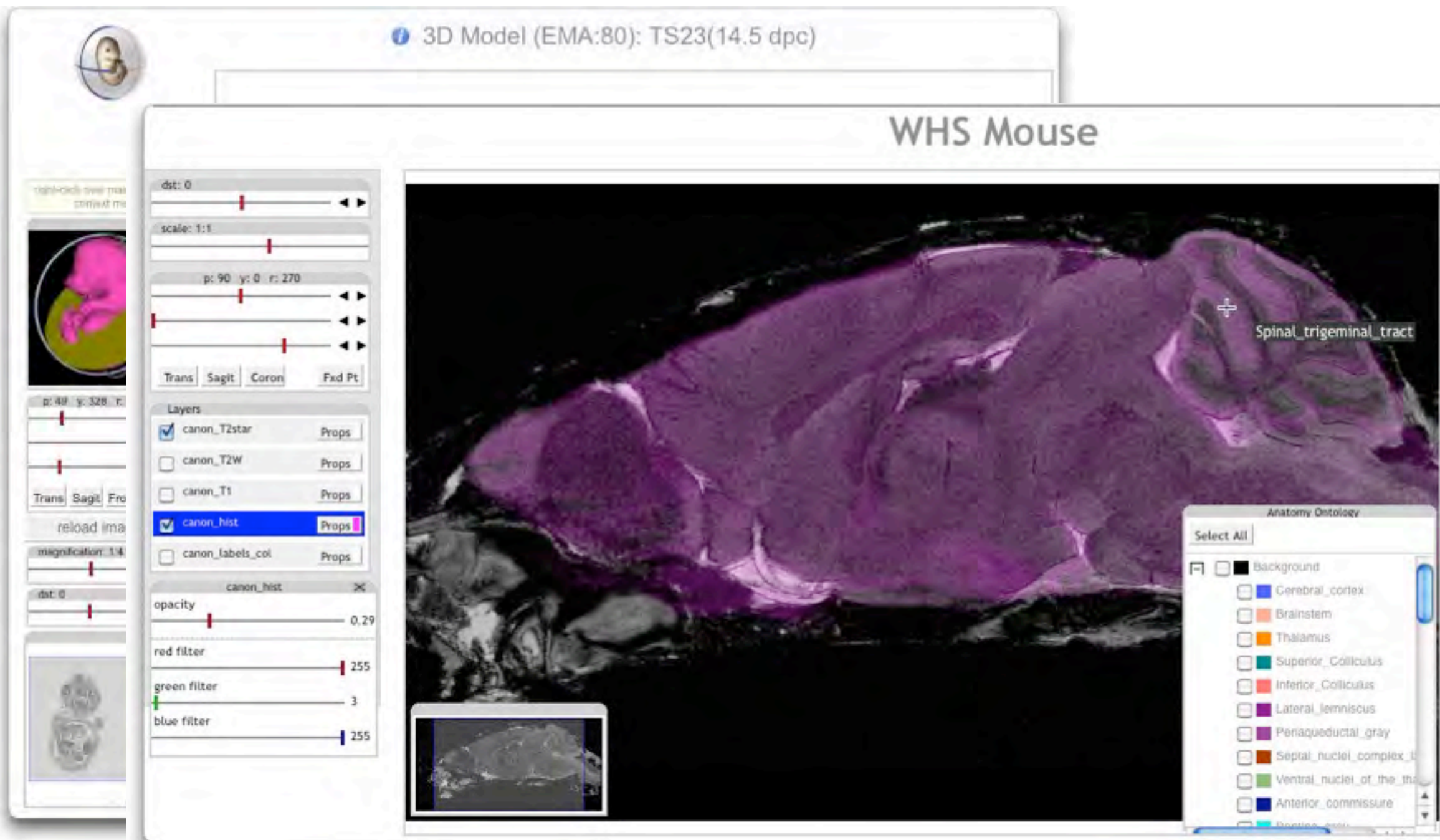


# IIP3D Examples





# IIP3D Examples



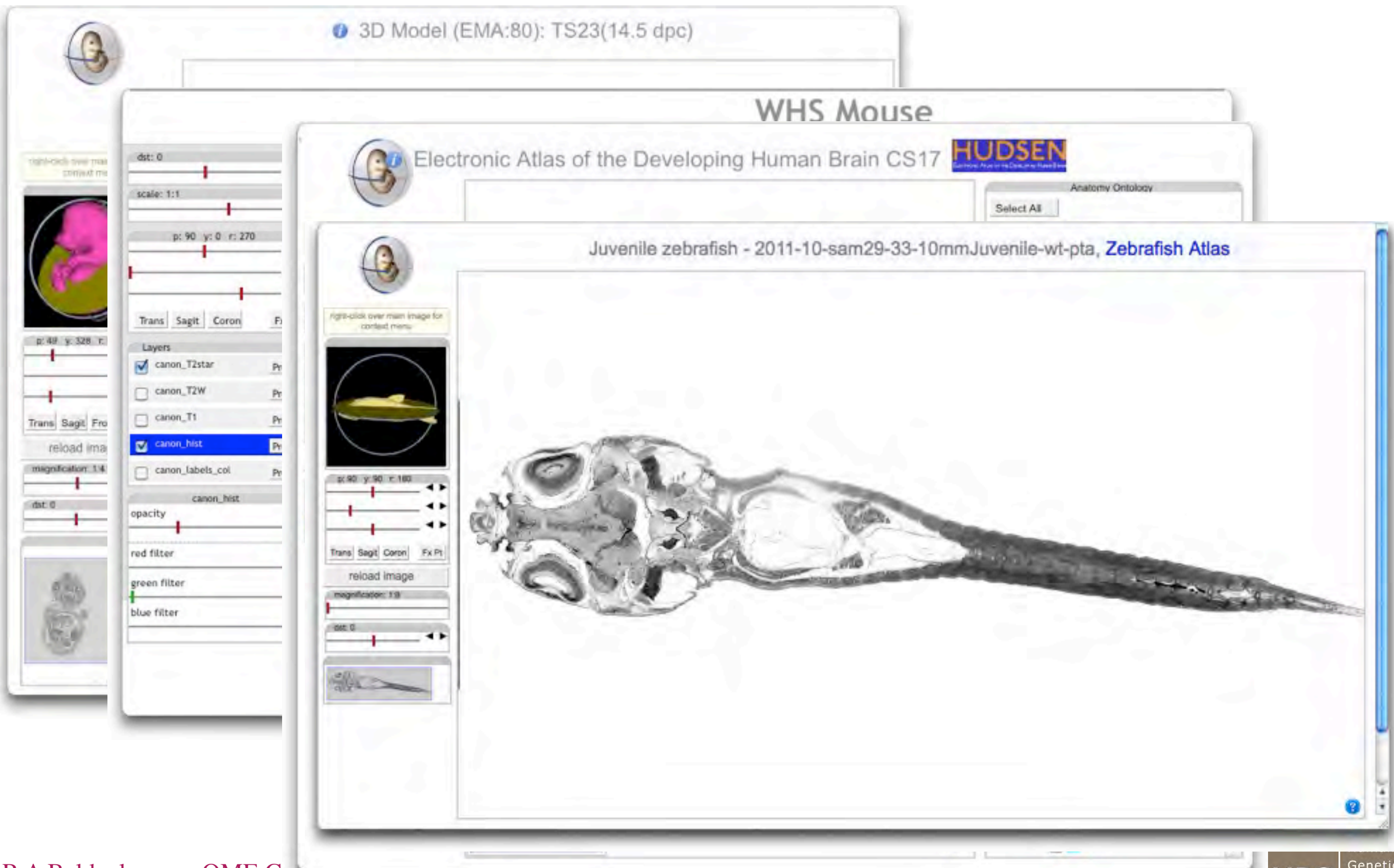


# IIP3D Examples





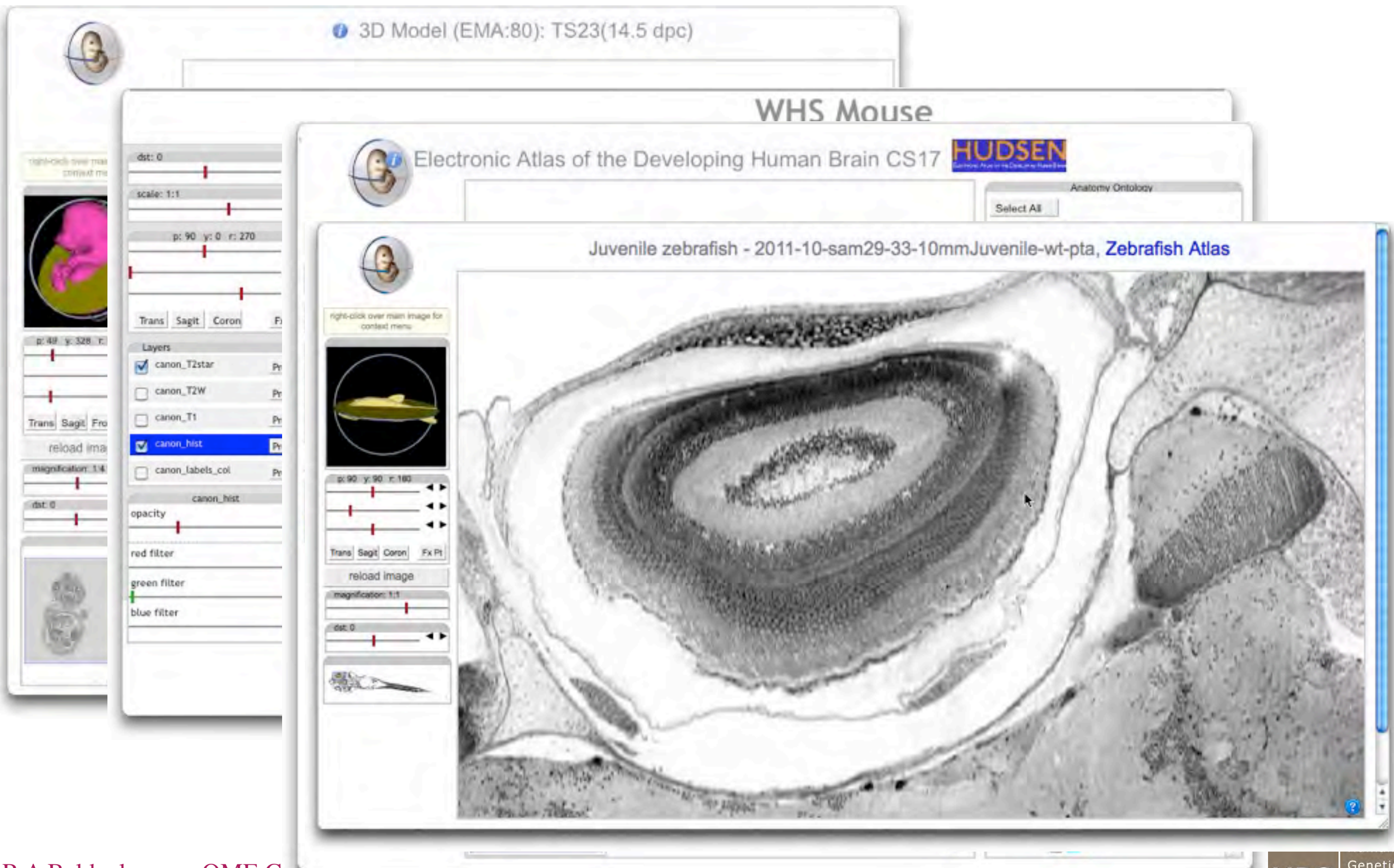
# IIP3D Examples







# IIP3D Examples





# Image Processing IIP3D extensions

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

Table 4: Descriptions of morphological operators

```

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

```

Table 3: Syntax for morphological expressions.

# Image Processing IIP3D extensions

Operator	Description
<code>diff(<i>exp,exp</i>)</code>	The difference between the two given domains.
<code>dilation(<i>exp,radius</i>)</code>	voxels.
<code>domain(<i>exp</i>)</code>	voxels.
<code>erosion(<i>exp,radius</i>)</code>	given lists.
<code>intersect(<i>exp list</i>)</code>	values sat-
<code>threshold(<i>exp,value</i>)</code>	Here the
	arisons are
	eq (equal),
	reater than).
	lists.
<code>union(<i>exp list</i>)</code>	

<b>MAP</b>	<b>Purpose</b>	Defines a colour or grey value mapping. Grey values outside the mapped region are clamped to the minimum and maximum output colour component or 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.
	<b>Syntax</b>	MAP=mspec[,mspec[,mspec[,mspec]]] where mspec=t, l1, l1u, o1, ou, p0, p1
	<b>Input Parameters</b>	t $\in$ IDENTITY   LINEAR   GAMMA   SIGMOID The mapping function FLOAT l1 Input lower grey value FLOAT l1 Input upper grey value FLOAT o1 Output lower colour component or grey value FLOAT o1 Output upper colour component or grey value FLOAT p0 Gamma ( $\gamma$ ) or first sigmoid parameter ( $\mu$ ) FLOAT p1 Second sigmoid parameter ( $\sigma$ )
	<b>Response Example</b>	none $\Rightarrow$ MAP=LINEAR, 0, 4095, 0, 255 Input grey values in the range 0-4095 are mapped to output values with the range 0-255
	<b>Default value</b>	IDENTITY

Table 3: Syntax for morphological expressions.



# Image Processing IIP3D extensions

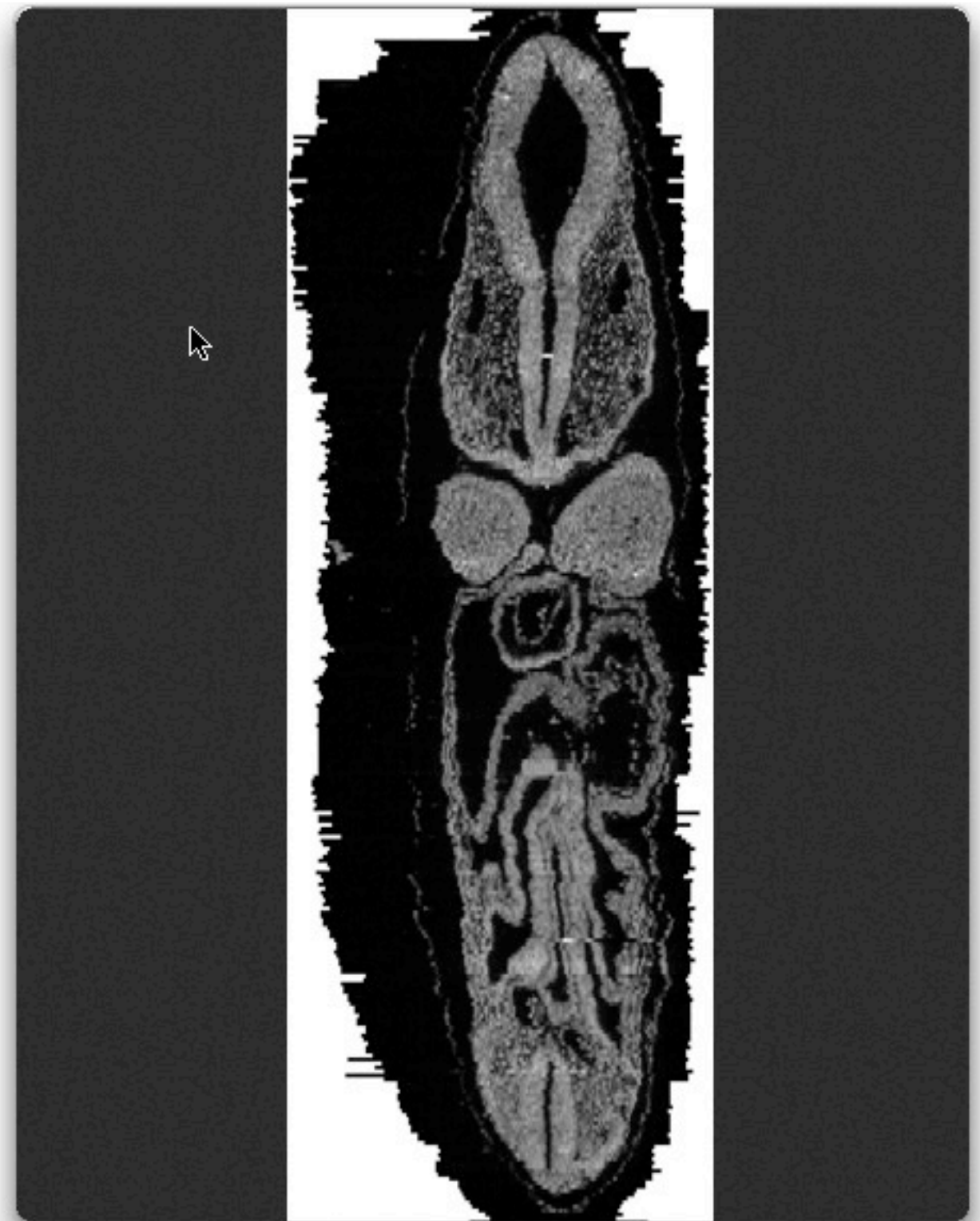
---

`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`

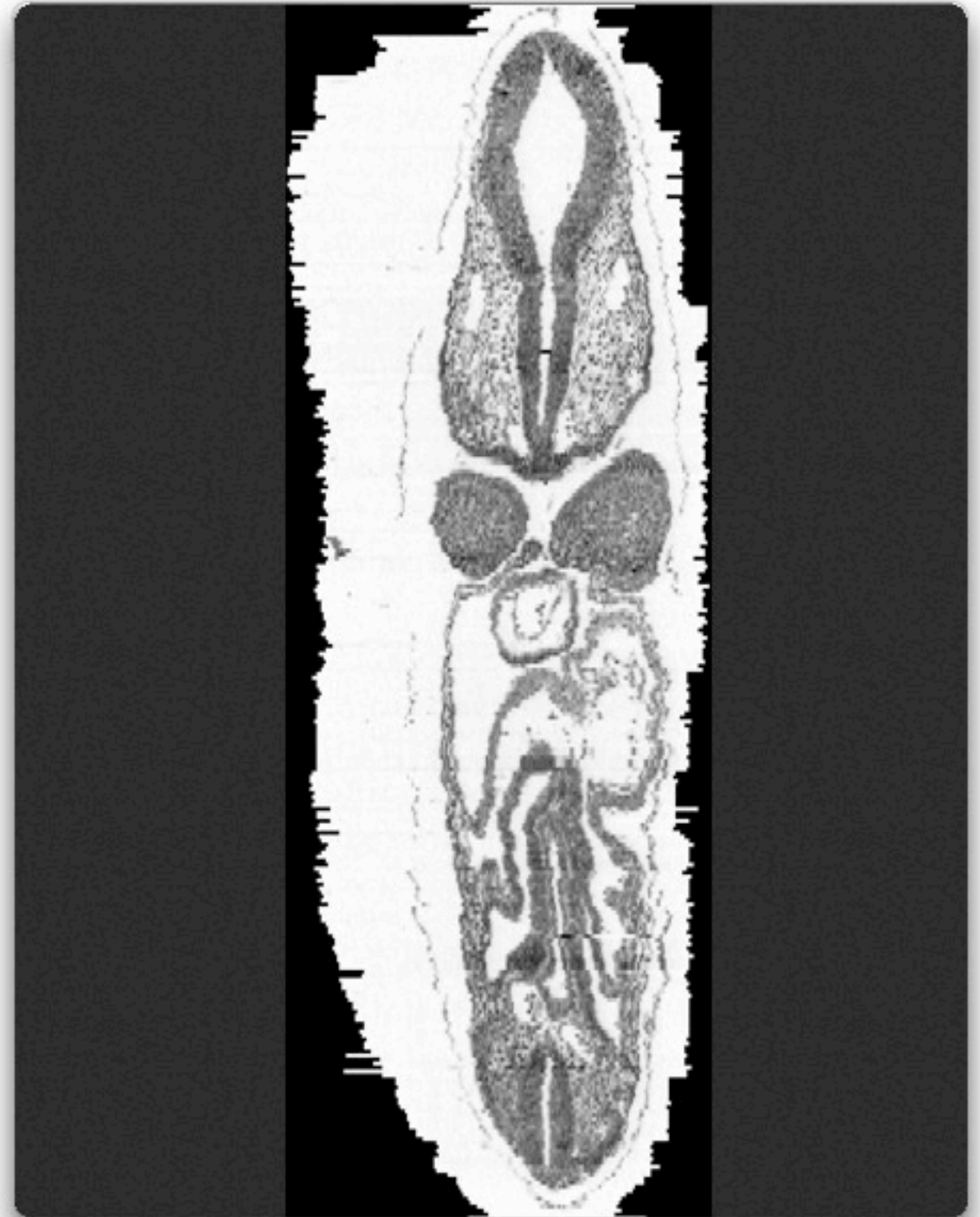
`SEL=0&MAP=GAMMA,0,255,0,255,1.6&QLT=50&CVT=jpeg`

# 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=5

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



=jpeg



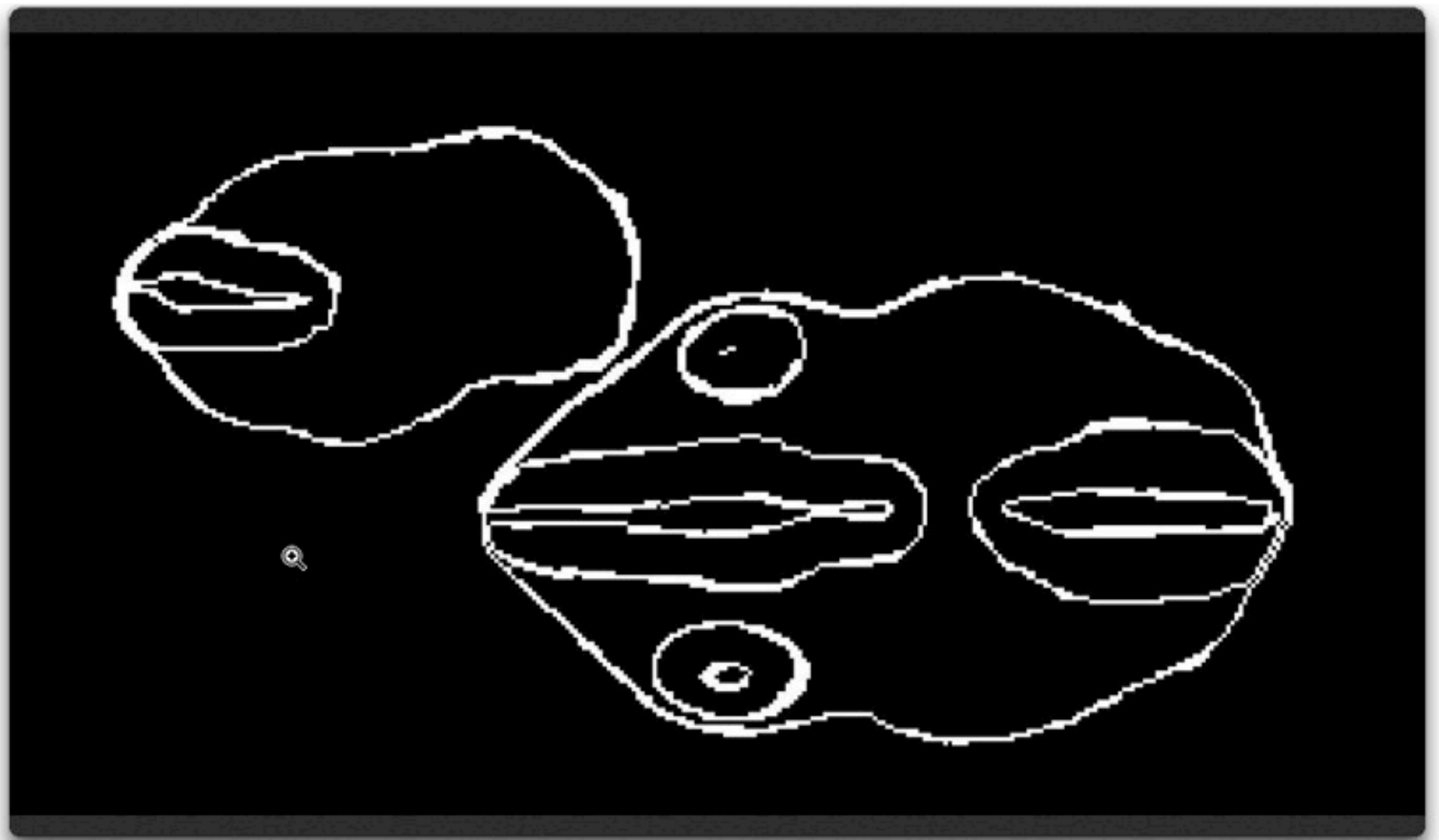
# Image Processing IIP3D extensions

---

`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

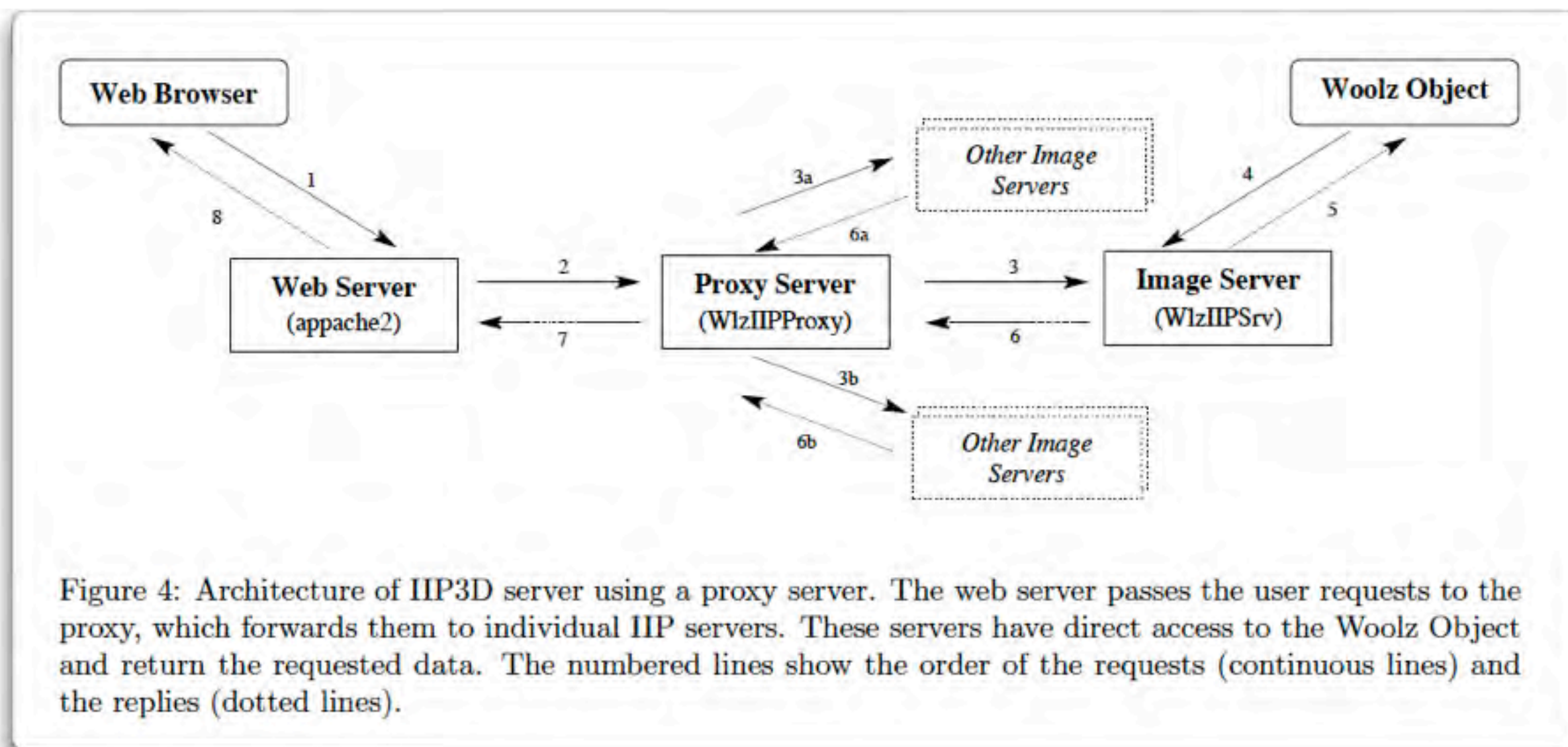
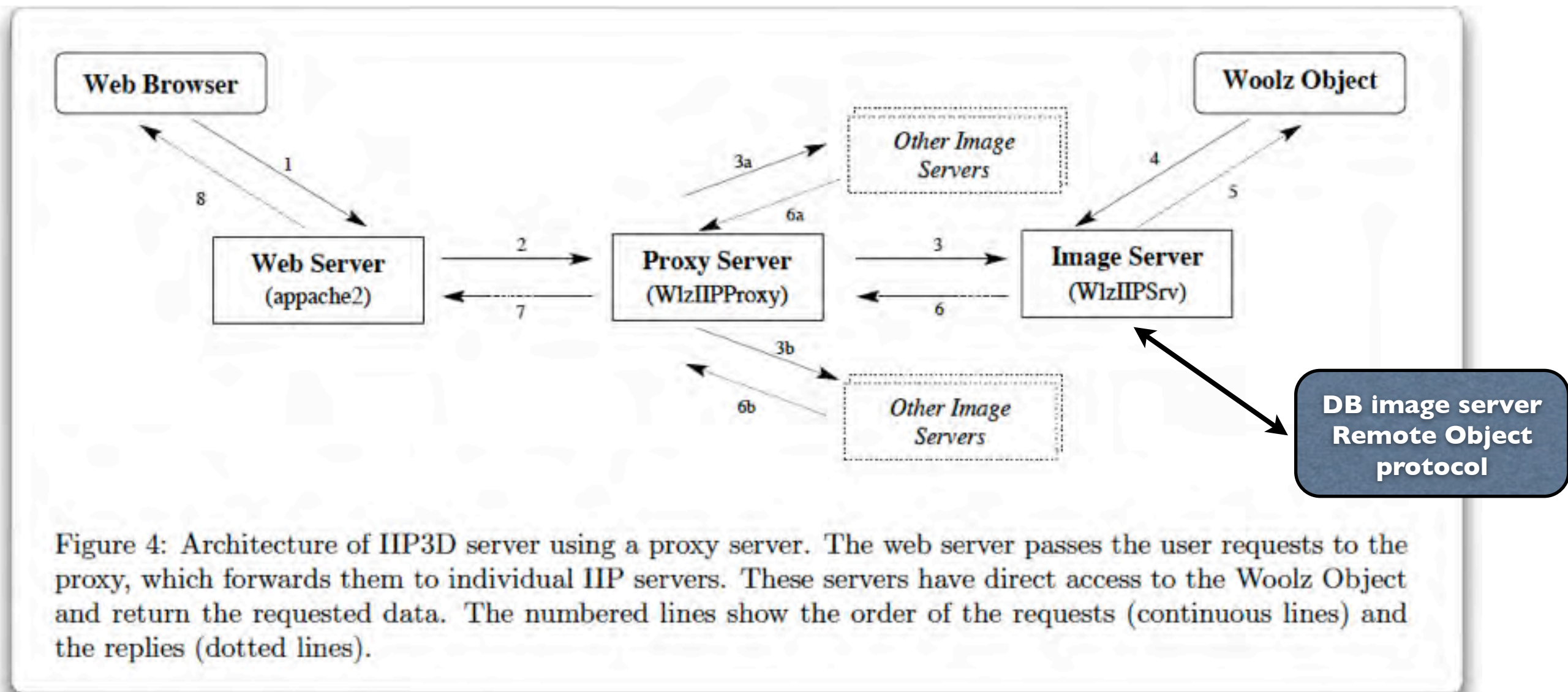


Figure 4: Architecture of IIP3D server using a proxy server. The web server passes the user requests to the proxy, which forwards them to individual IIP servers. These servers have direct access to the Woolz Object and return the requested data. The numbered lines show the order of the requests (continuous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



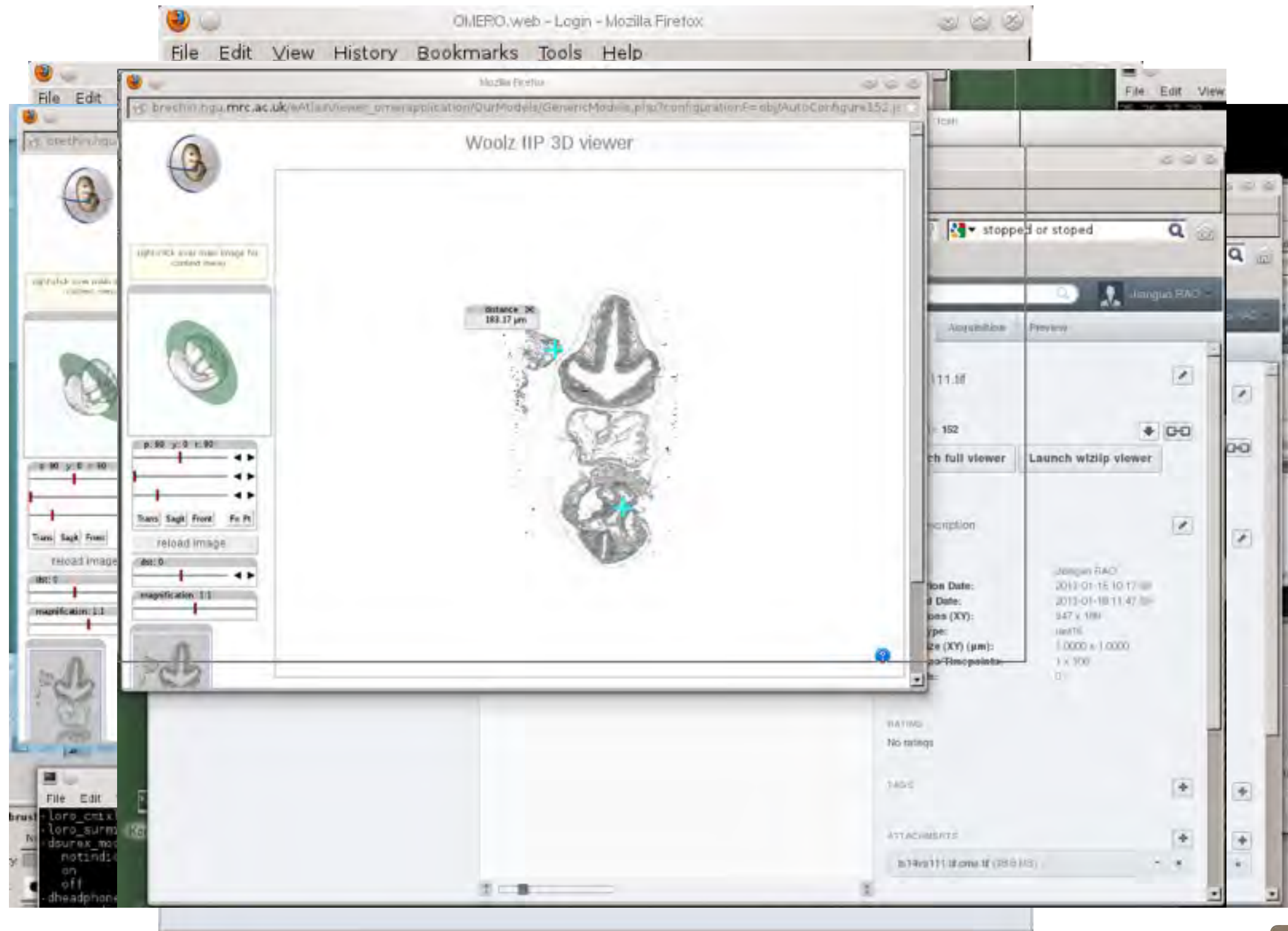
# IIP3D Web-App Architecture



- 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







## 3D mapping - WlzWarp

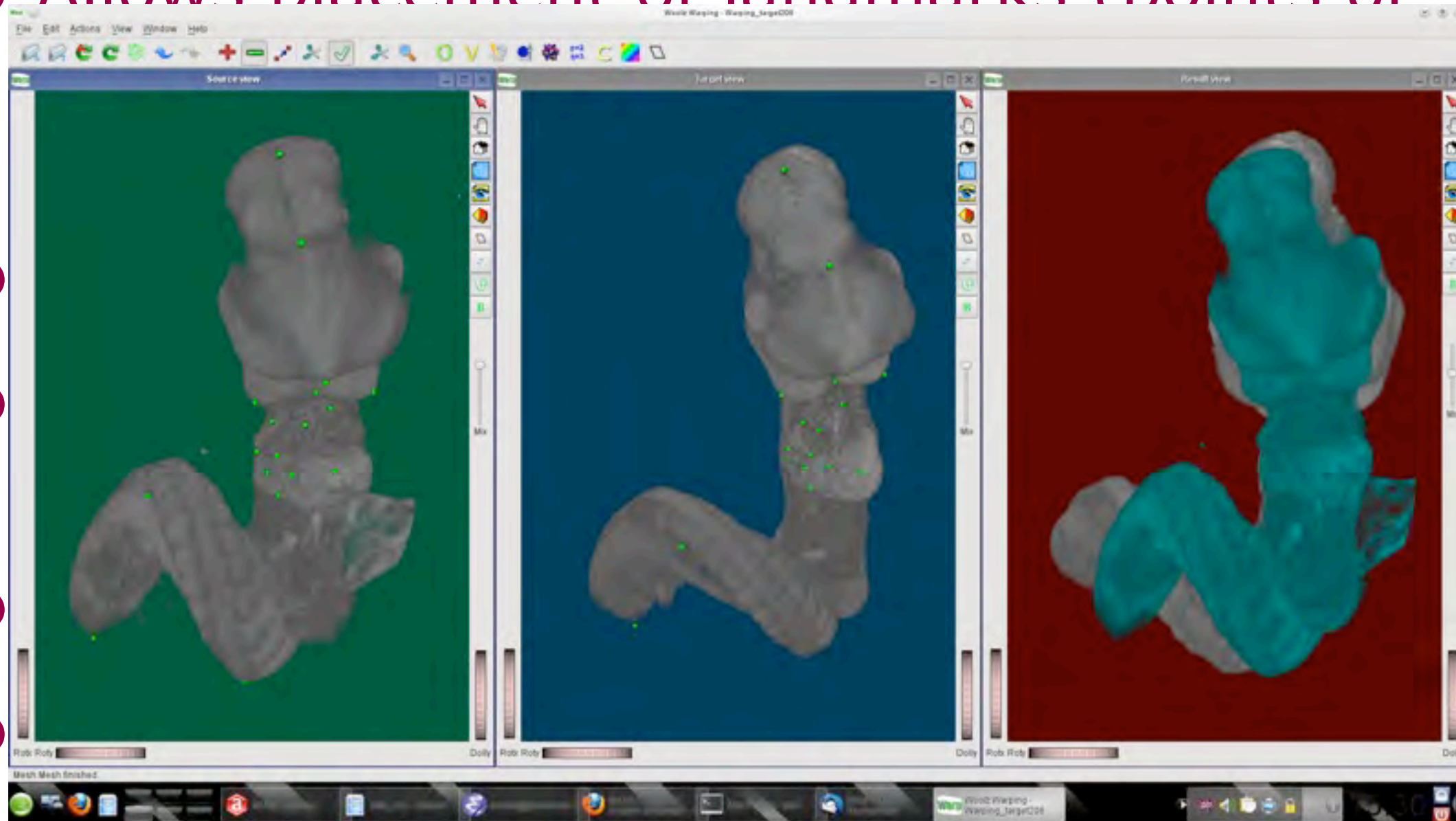
---

- 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, Windows
- Open Source (Free!)



# 3D mapping - WlzWarp

- Allows placement of landmarks (points of interest)

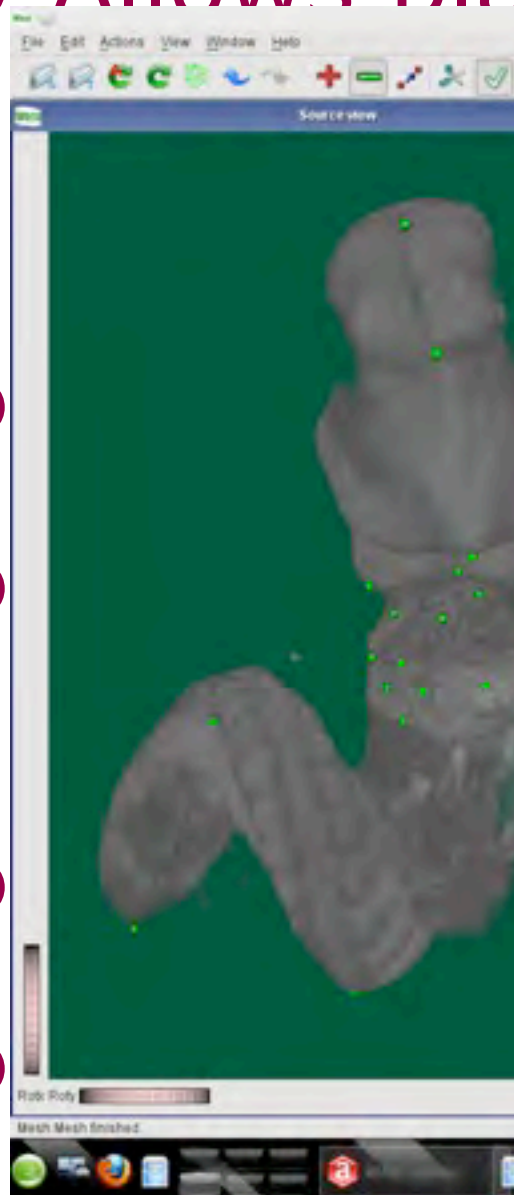


- Open Source (Free!)



# 3D mapping - WlzWarp

- Allows planar



Wnt1



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- Open Source (Free!)





# eMouseAtlas



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