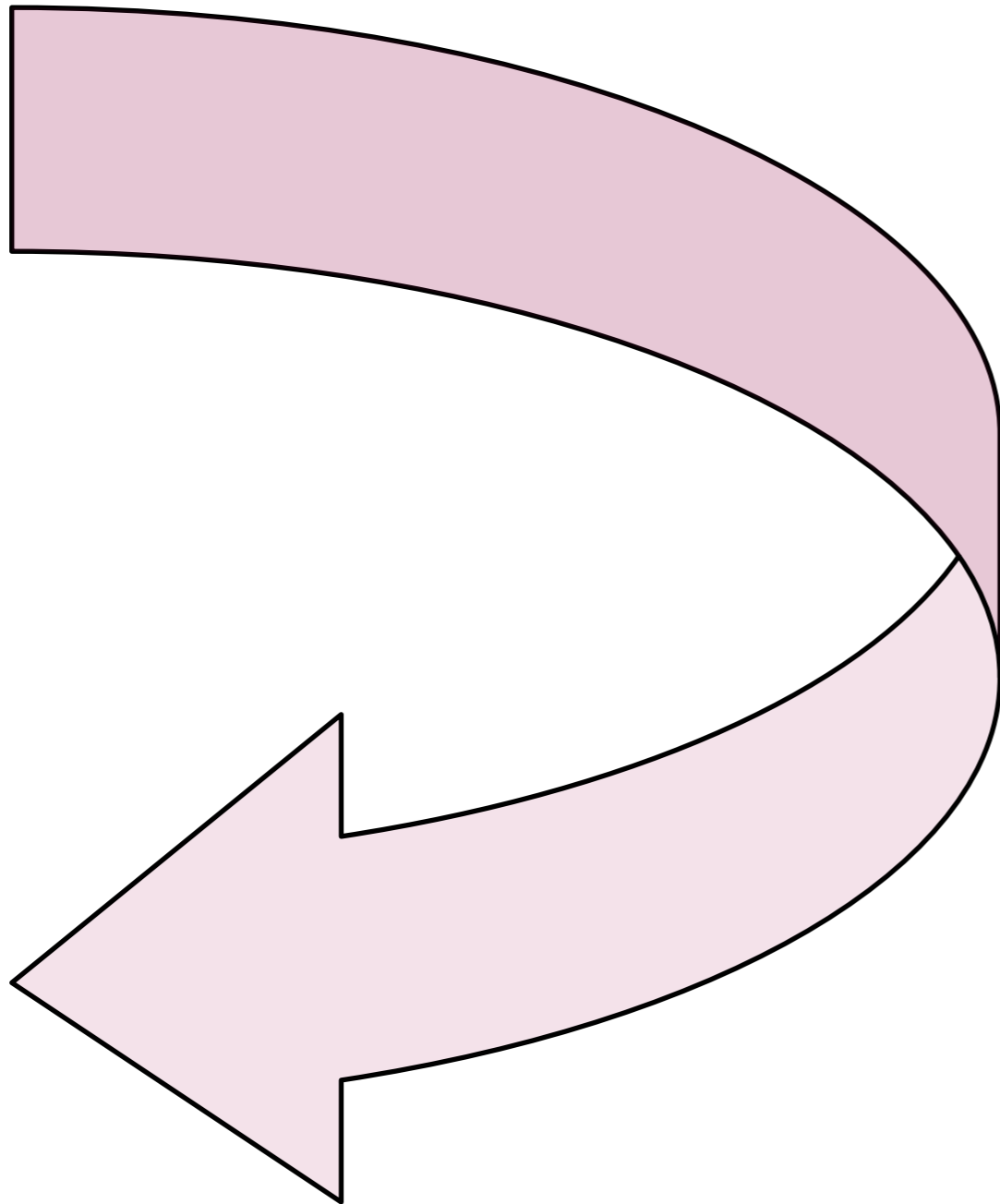


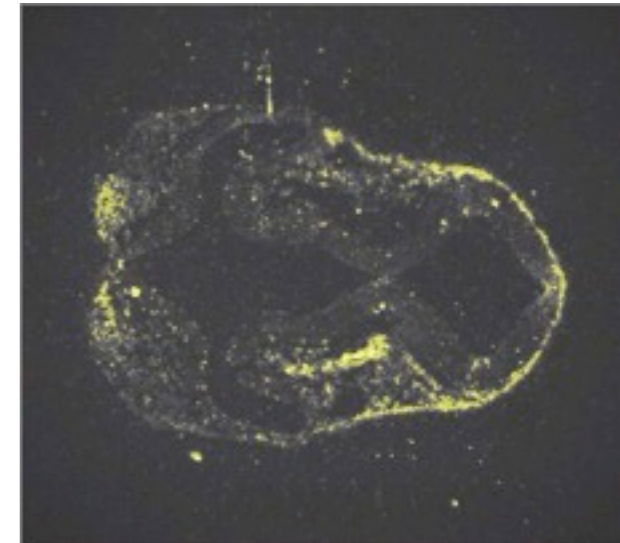
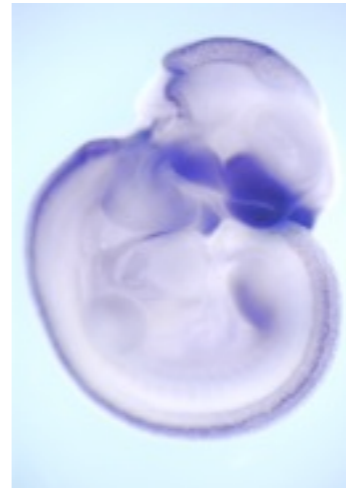
Atlas-Based Bioinformatics

Richard Baldock

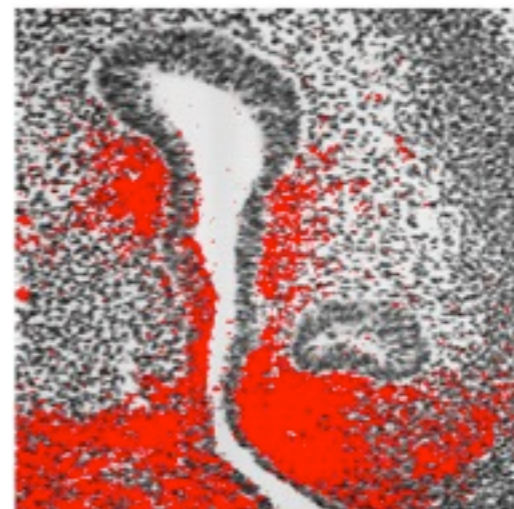
*MRC Human Genetics Unit
Institute of Genetics and Molecular Medicine
Edinburgh, UK*

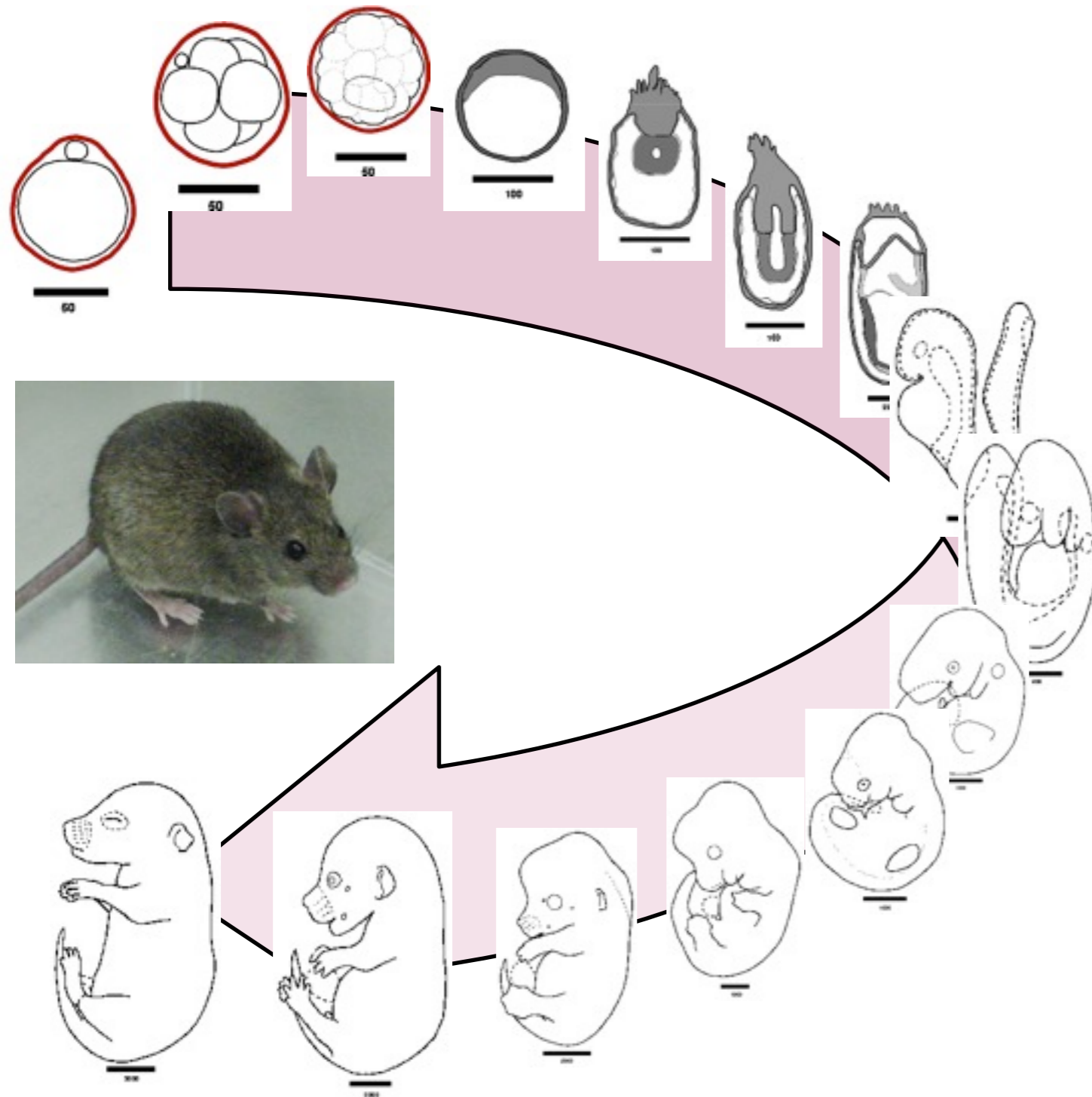


GENE EXPRESSION

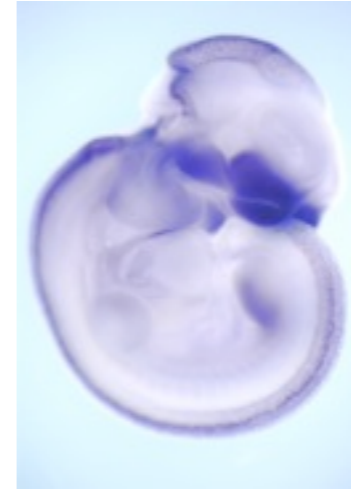


Carol Wicking, University of Queensland

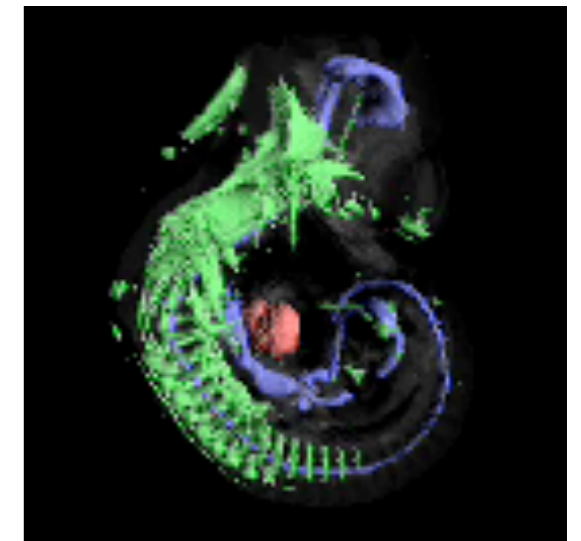
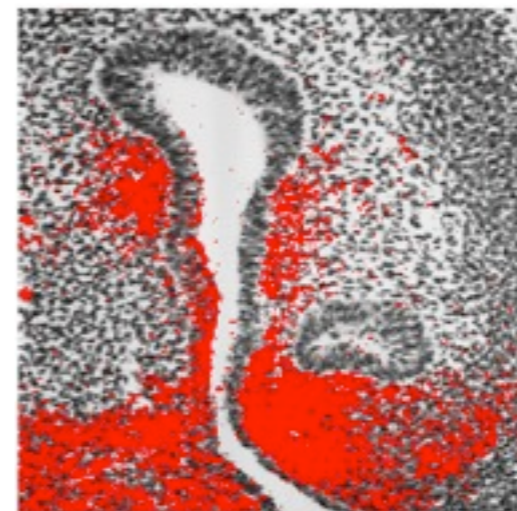
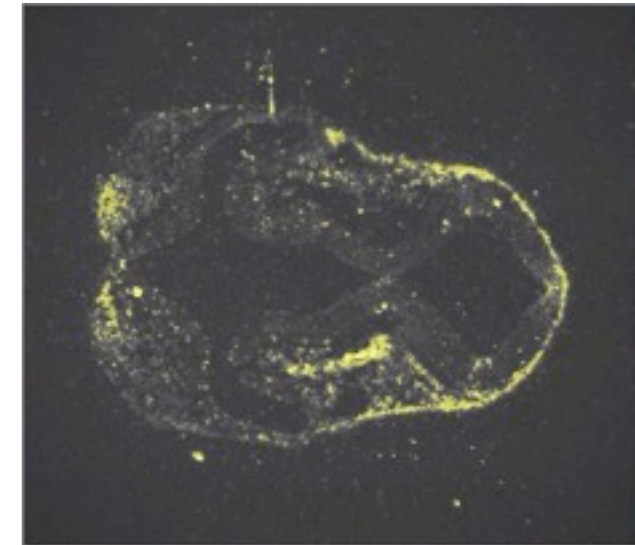


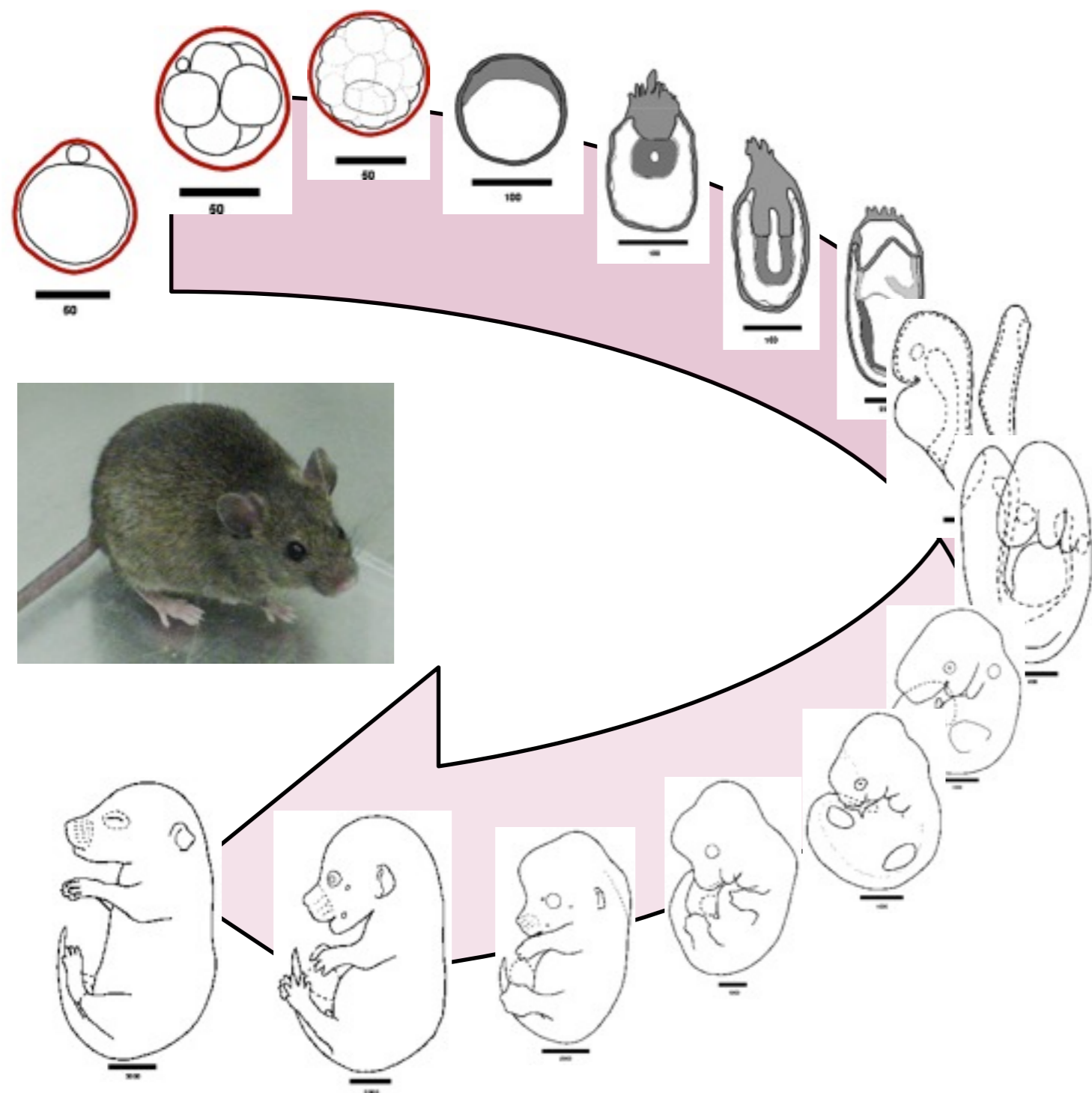


GENE EXPRESSION

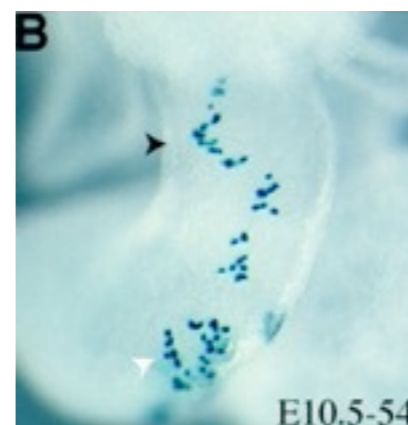


Carol Wicking, University of Queensland





CELL LINEAGE



Sigolène Meilhac
Institut Pasteur

CELL DIVISION



anti-BrdU staining
J. McDermid
McGill University

APOPTOSIS

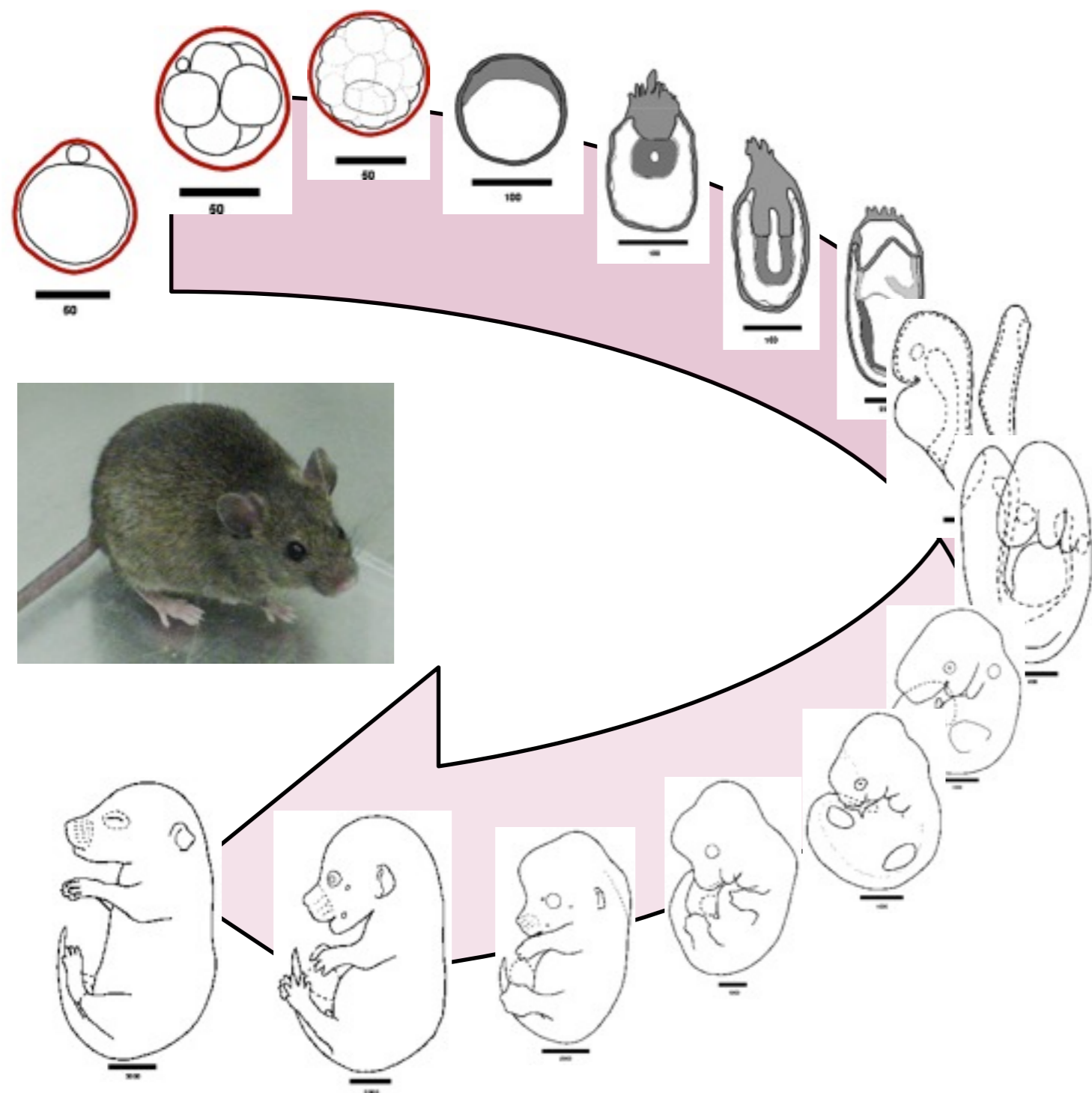


Igf2^{+/m/+p}
Acridine Orange
J. Burns
University of Bristol

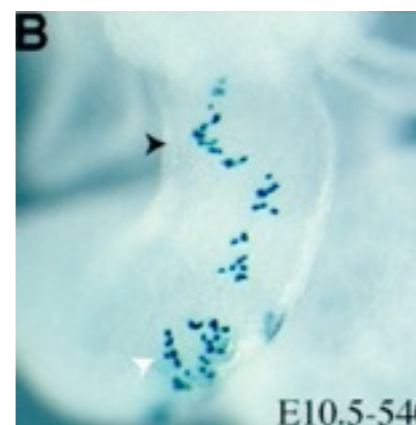
TRANSGENICS



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

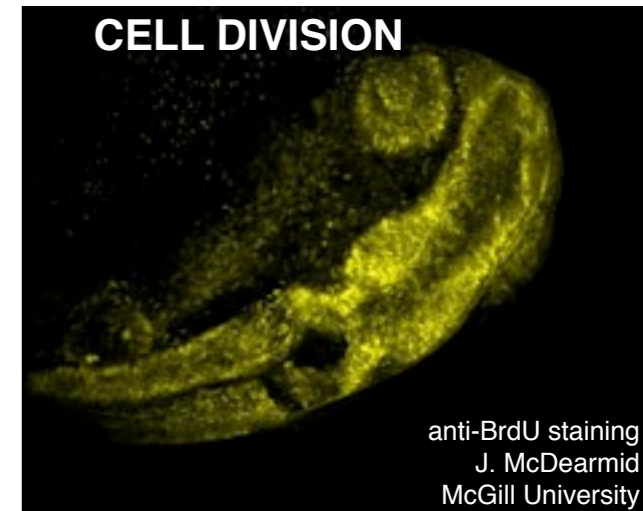


CELL LINEAGE



Sigolène Meilhac
Institut Pasteur

CELL DIVISION



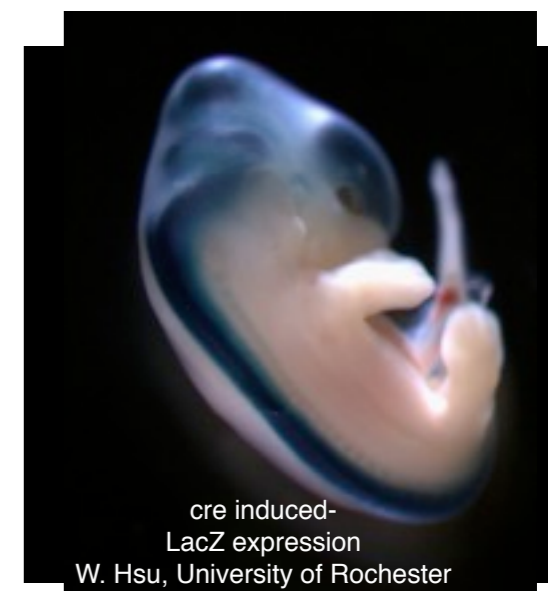
anti-BrdU staining
J. McDermid
McGill University

APOPTOSIS



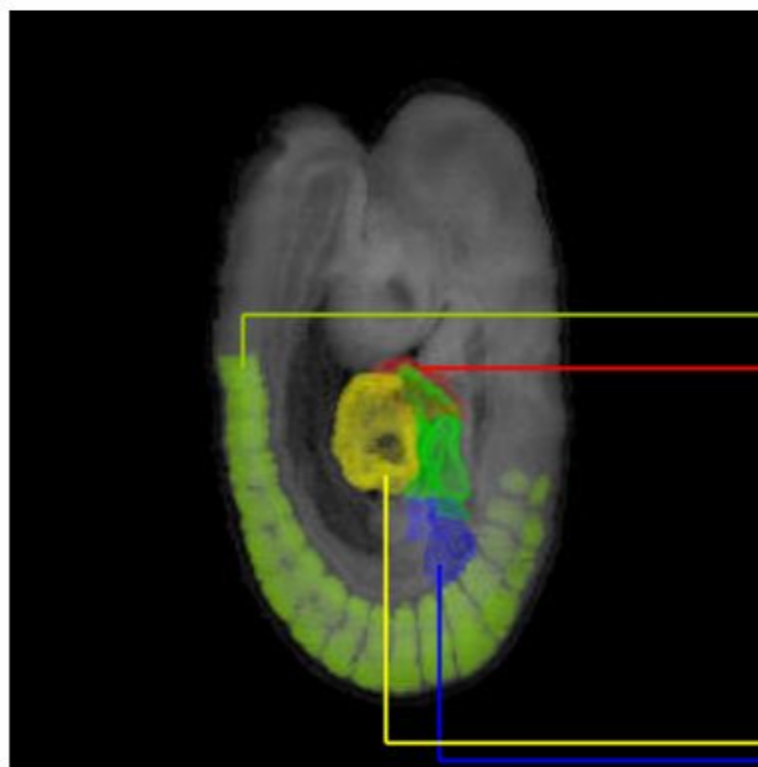
Igf2^{+/m/+p}
Acridine Orange
J. Burns
University of Bristol

TRANSGENICS



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

eMouseAtlas Framework



Stage Browser

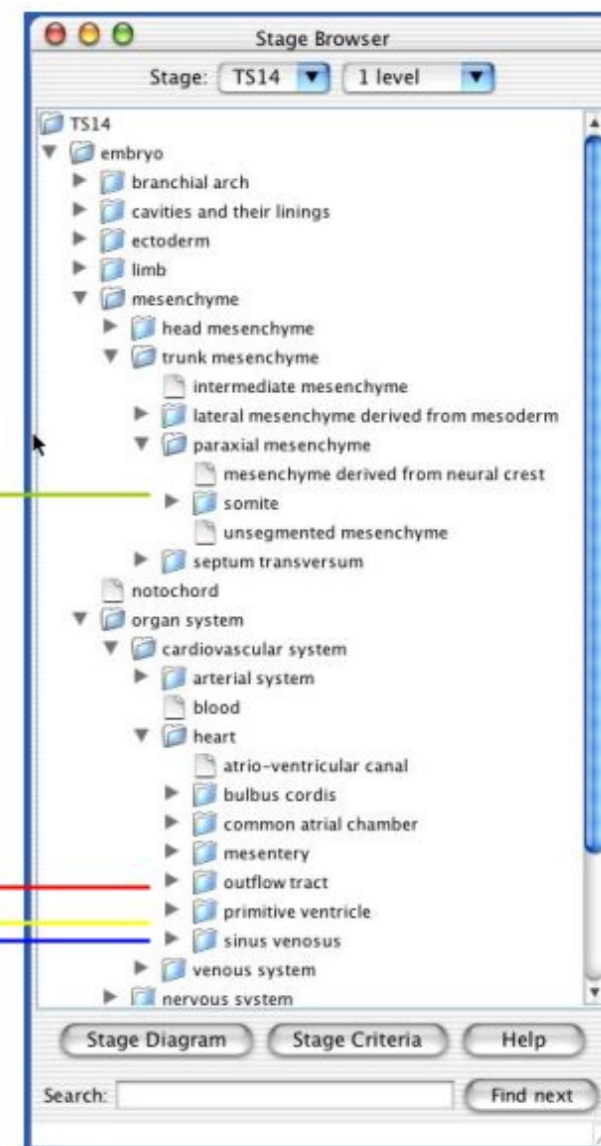
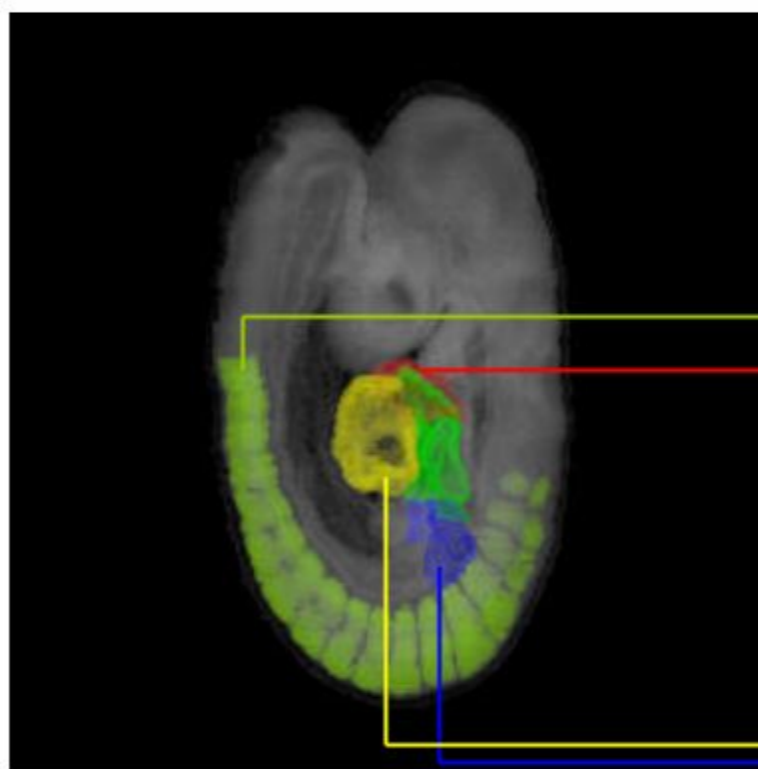
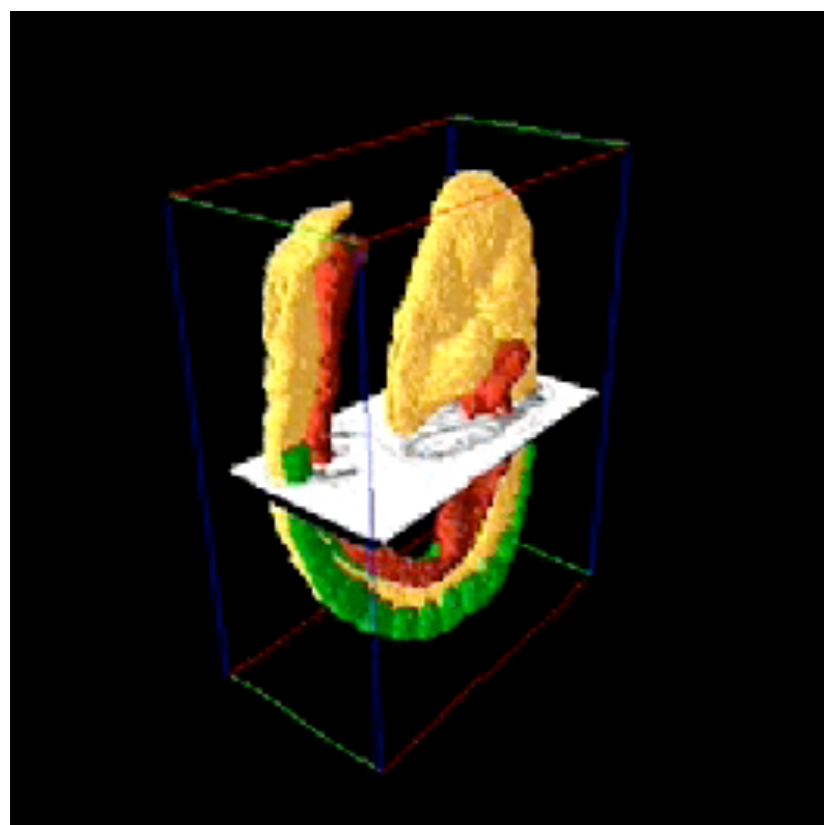
Stage: TS14 1 level

- TS14
 - embryo
 - branchial arch
 - cavities and their linings
 - ectoderm
 - limb
 - mesenchyme
 - head mesenchyme
 - trunk mesenchyme
 - intermediate mesenchyme
 - lateral mesenchyme derived from mesoderm
 - paraxial mesenchyme
 - mesenchyme derived from neural crest
 - somite
 - unsegmented mesenchyme
 - septum transversum
 - notochord
 - organ system
 - cardiovascular system
 - arterial system
 - blood
 - heart
 - atrio-ventricular canal
 - bulbus cordis
 - common atrial chamber
 - mesentery
 - outflow tract
 - primitive ventricle
 - sinus venosus
 - venous system
 - nervous svstem

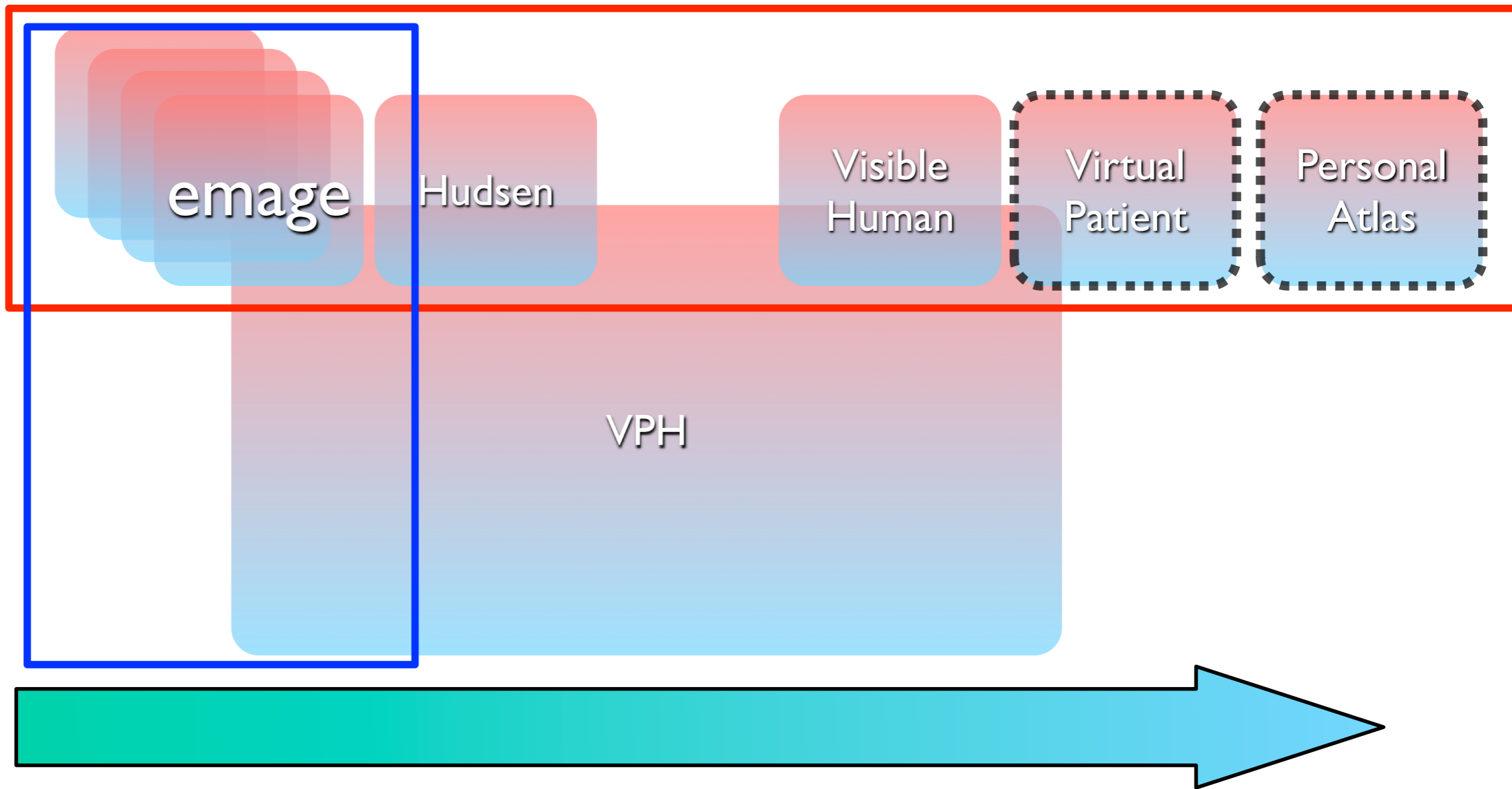
Stage Diagram Stage Criteria Help

Search: Find next

eMouseAtlas Framework



Population
Organism
Tissue
Cell
Organelle
Molecule



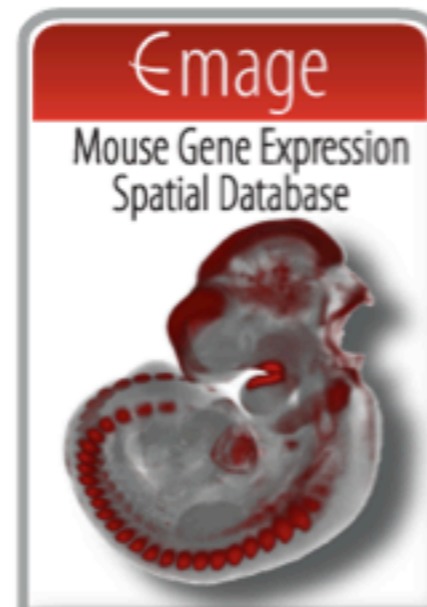
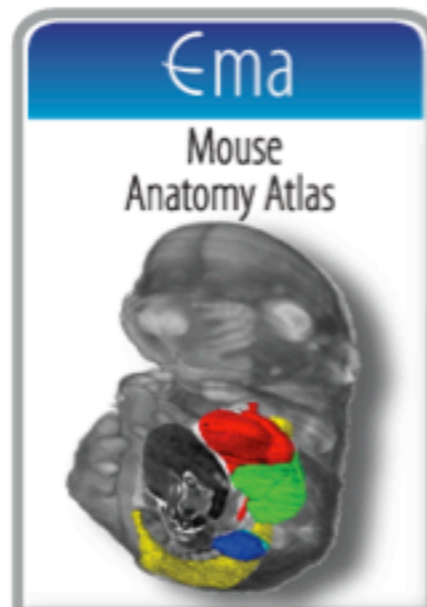
Basic research


Clinical practice

[▲](#) [▼](#)
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](#)



[▲](#) [▼](#)


[All gallery images](#)

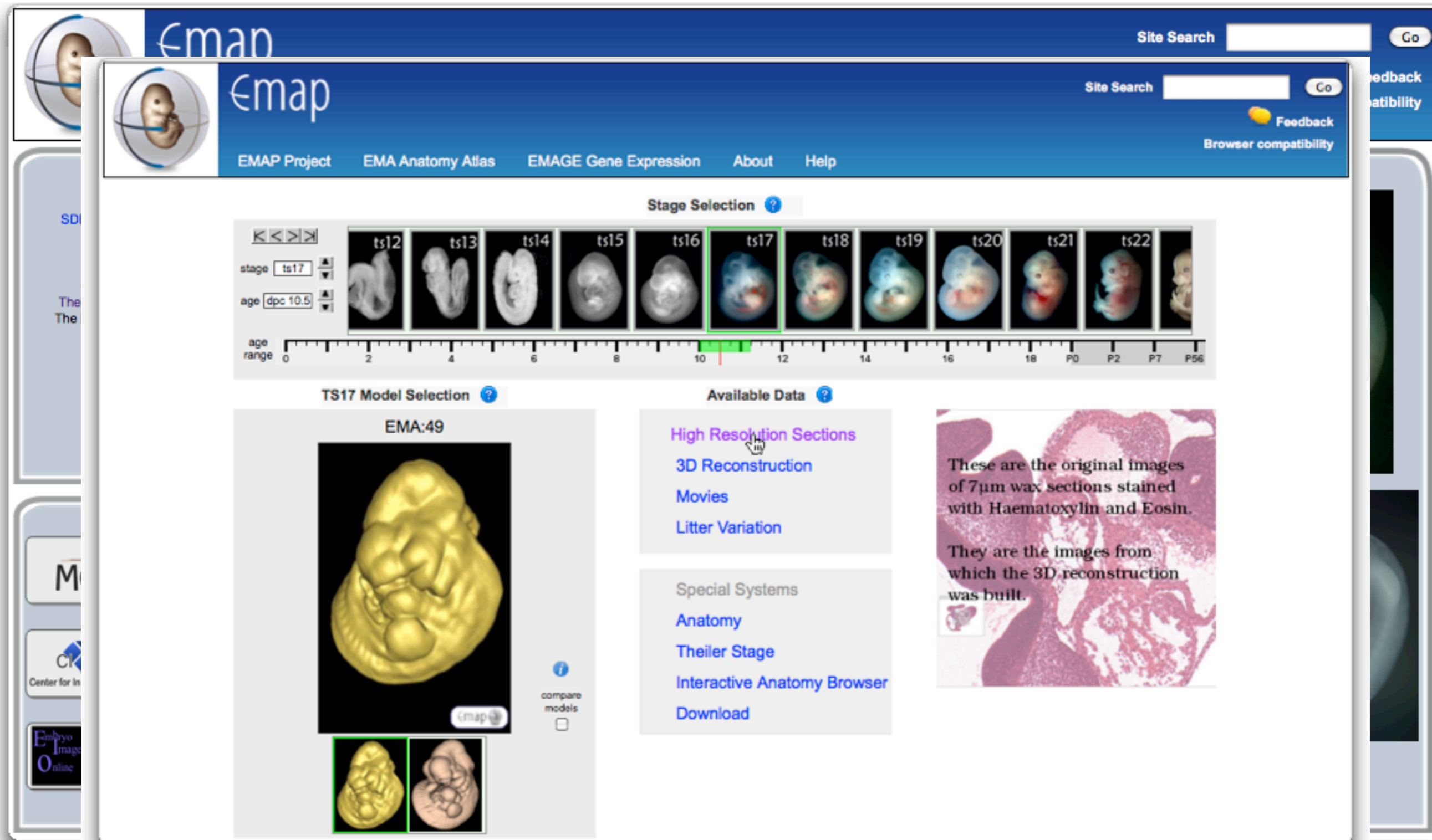
[▲](#) [▼](#)

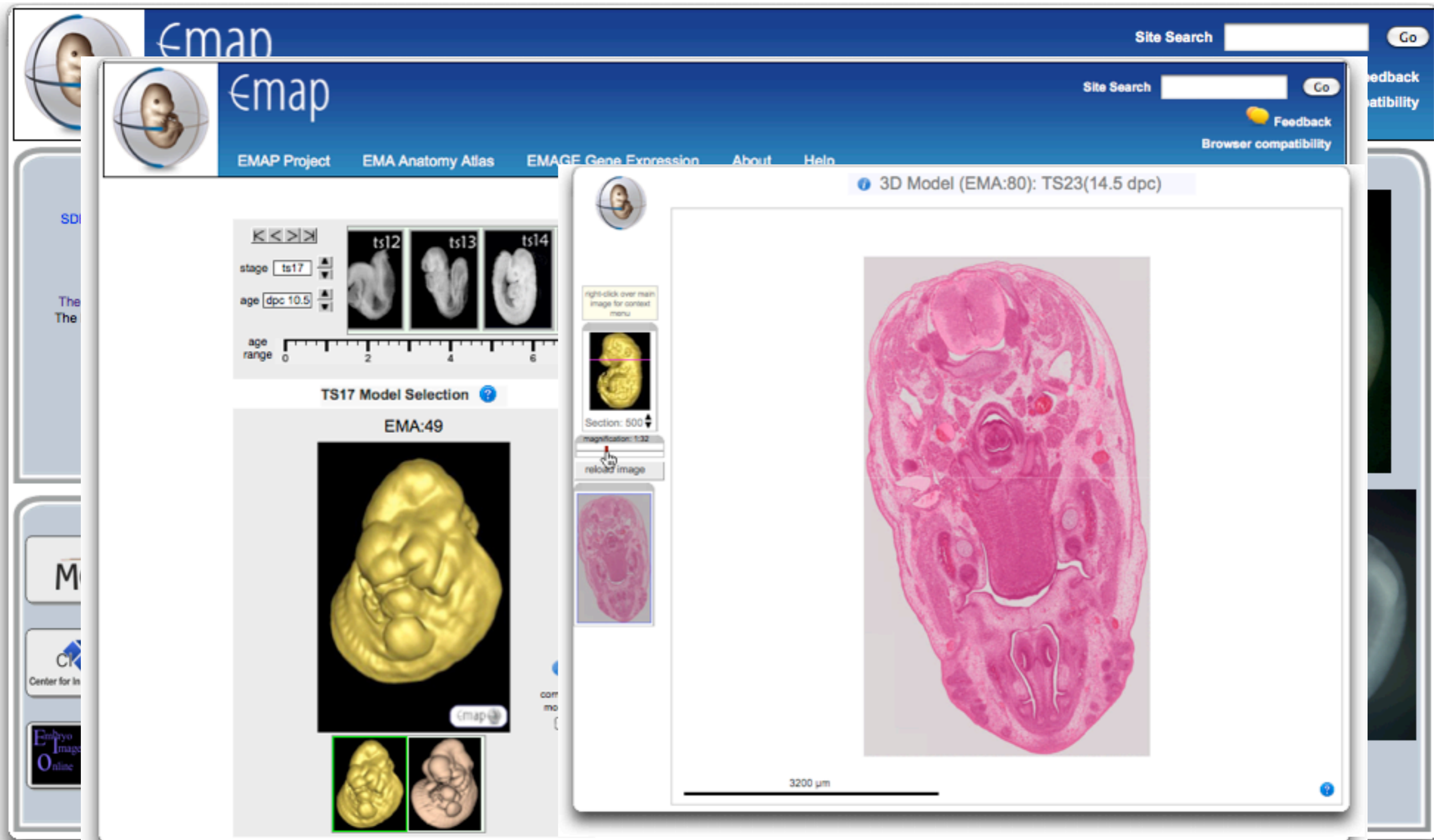
[All atlas links](#)

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.](#)



The screenshot displays the eMouseAtlas web application interface. At the top, there is a navigation bar with the 'Emap' logo and a search bar. Below this is a secondary navigation bar with links for 'EMAP Project', 'EMA Anatomy Atlas', 'EMAGE Gene Expression', 'About', and 'Help'. The main content area is titled 'Stage Selection' and features a timeline of mouse development stages from ts12 to ts22. The 'ts17' stage is currently selected, with a corresponding 3D model shown below. To the right of the 3D model, there is a list of 'Available Data' options: 'High Resolution Sections', '3D Reconstruction', 'Movies', 'Litter Variation', 'Special Systems', 'Anatomy', 'Theiler Stage', 'Interactive Anatomy Browser', and 'Download'. A large histological image of a wax section is also visible on the right side of the interface.

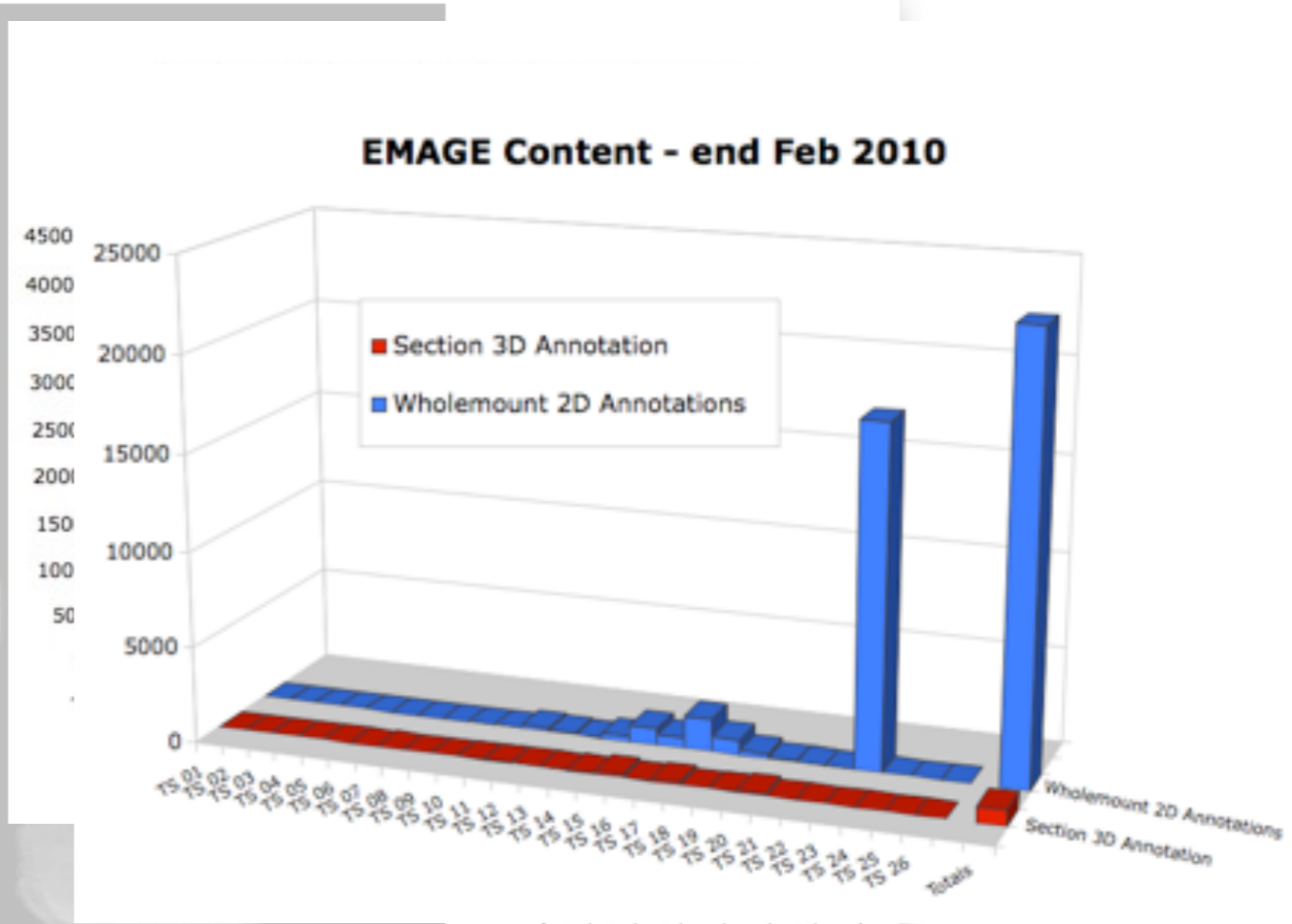
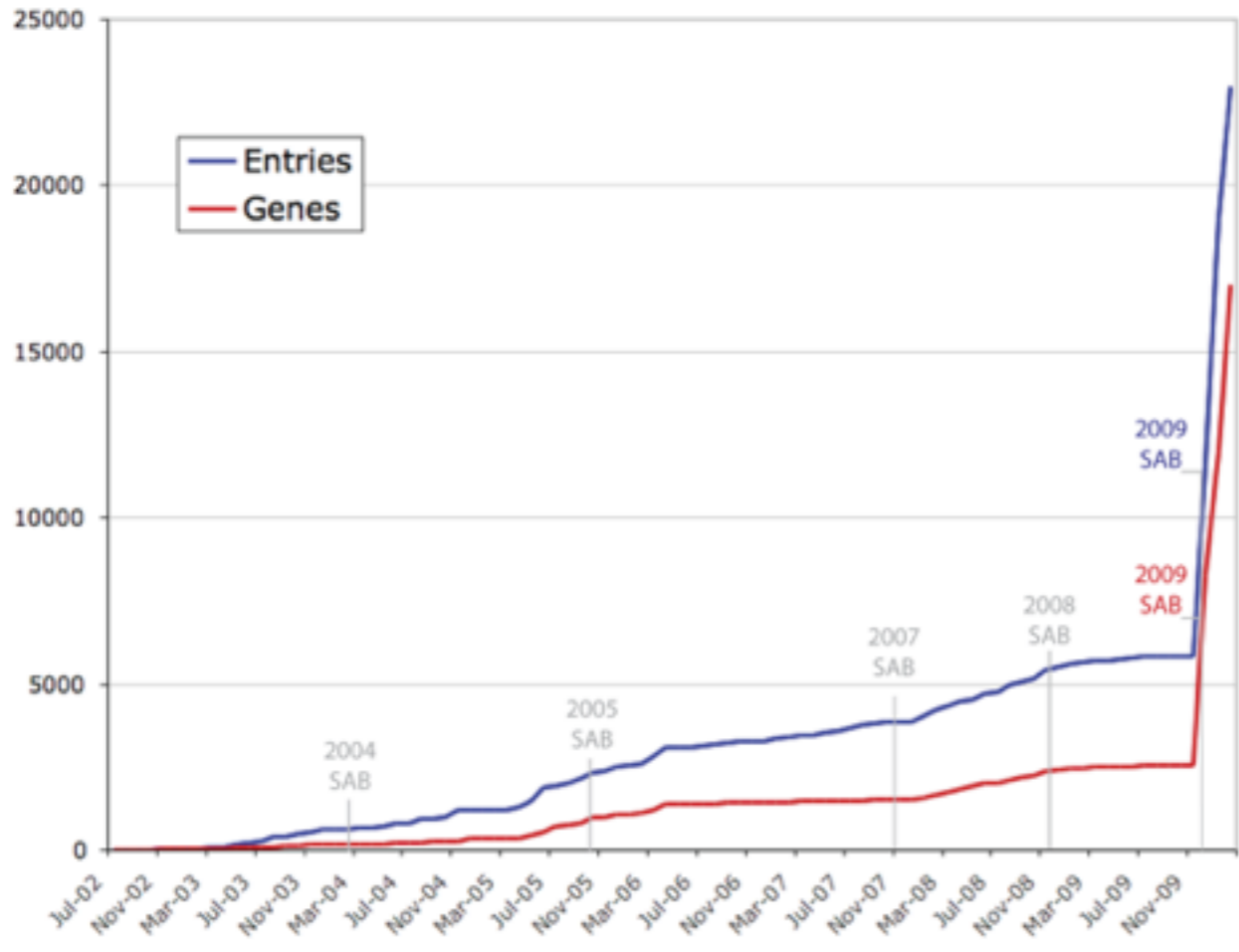


The screenshot displays the eMouseAtlas web application interface. At the top, there is a navigation bar with the Emap logo and site search functionality. Below this, a secondary navigation bar lists various project components: EMAP Project, EMA Anatomy Atlas, EMAGE Gene Expression, About, and Help. The main content area is divided into several panels. On the left, there is a 'TS17 Model Selection' panel with a 3D model of a mouse embryo (EMA:49) and a timeline showing stages ts12, ts13, and ts14. The central panel features a large 3D model of a mouse embryo (EMA:80) at TS23(14.5 dpc). To the right of this model is a histological section image of the same stage, showing internal organs in pink. A scale bar at the bottom of the histological section indicates 3200 μm. The interface includes various interactive elements such as dropdown menus for stage and age, a magnification slider, and a 'reloaded image' button.



The screenshot displays the eMouseAtlas web application interface. At the top, there is a navigation bar with the Emap logo and site search functionality. Below this, a secondary navigation bar lists menu items: EMAP Project, EMA Anatomy Atlas, EMAGE Gene Expression, About, and Help. The main content area is divided into several panels. On the left, there is a 'TS17 Model Selection' panel featuring a 3D model of an embryo (EMA:49) and a timeline of stages (ts12, ts13, ts14) with a stage selector set to 'ts17' and an age selector set to 'dpc 10.5'. The central panel shows a large histological image of a tissue section, identified as '3D Model (EMA:80): TS23(14.5 dpc)'. This panel includes a vertical toolbar with options for 'right-click over main image for context menu', 'Section: 500', 'magnification: 1:1', and 'reload image'. A scale bar at the bottom of the histological image indicates '100 μm'. The right side of the interface contains a sidebar with additional navigation options and a 'Feedback' button.

EMAGE - current status



~22K submissions

Range Theiler 7-25

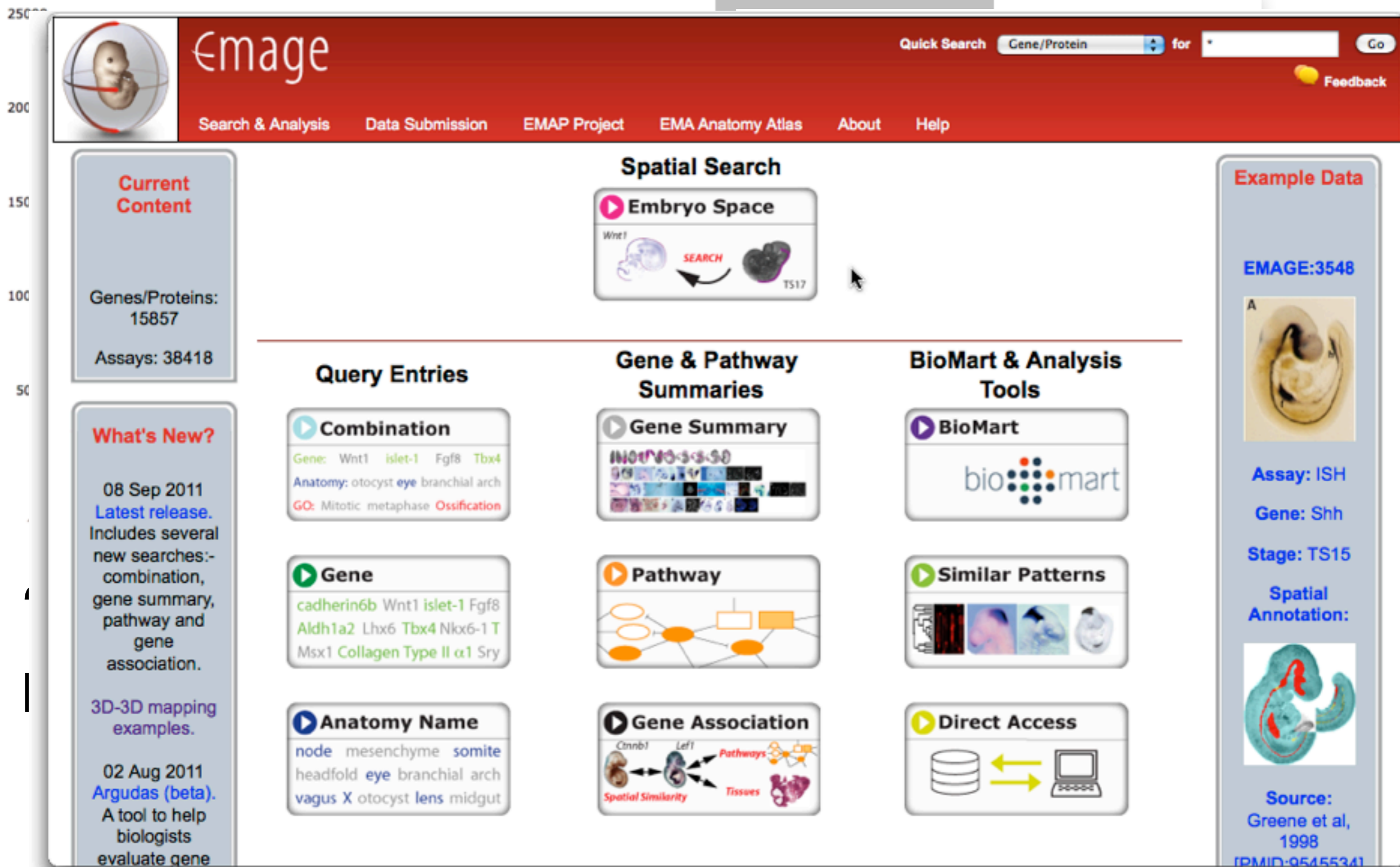
Repository DB: 38.4K entries
submissions

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



Navigation menu:

- [15 16 17 18 19 20 21](#)
- [22 23 24 25 26 27 28](#)
- [Staging wallchart](#)
- [Text anatomy index](#)
- [Anatomy Database](#)
- [FAQs](#)

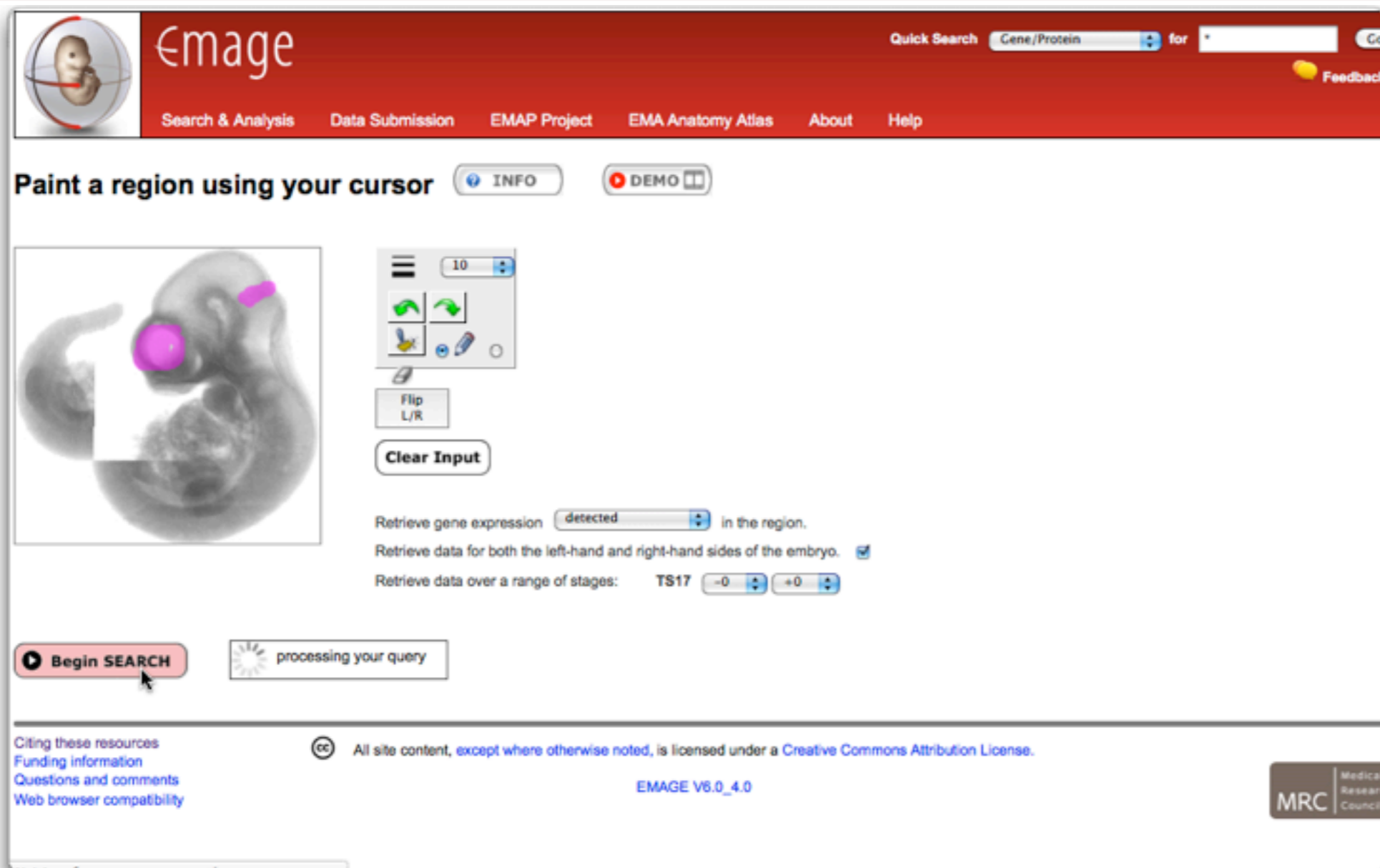


The screenshot shows the EMAGE website interface. At the top, there is a navigation bar with the EMAGE logo and a search bar. Below the navigation bar, there are several main sections:

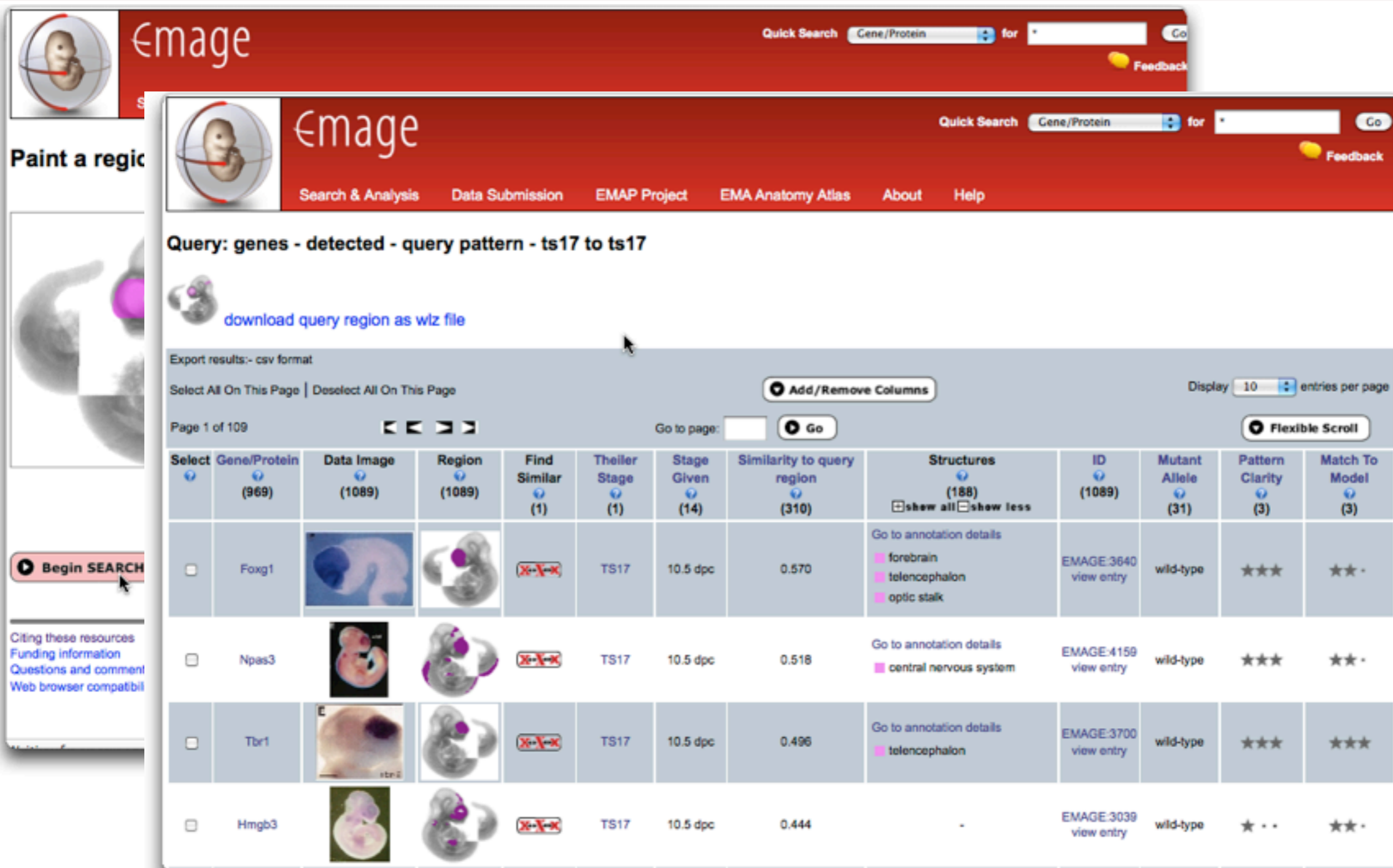
- Current Content:** Genes/Proteins: 15857, Assays: 38418.
- What's New?:**
 - 08 Sep 2011 Latest release. Includes several new searches: combination, gene summary, pathway and gene association.
 - 02 Aug 2011 Argudas (beta). A tool to help biologists evaluate gene
- Spatial Search:** Embryo Space. Includes a search bar and a "SEARCH" button.
- Query Entries:**
 - Combination:** Gene: Wnt1 islet-1 Fgf8 Tbx4; Anatomy: otocyst eye branchial arch; GO: Mitotic metaphase Ossification.
 - Gene:** cadherin6b Wnt1 islet-1 Fgf8 Aldh1a2 Lhx6 Tbx4 Nkx6-1 T Msx1 Collagen Type II α 1 Sry.
 - Anatomy Name:** node mesenchyme somite headfold eye branchial arch vagus X otocyst lens midgut.
- Gene & Pathway Summaries:**
 - Gene Summary:** Shows a gene summary for Wnt1.
 - Pathway:** Shows a pathway diagram.
 - Gene Association:** Shows gene association for Ctnnb1 and Lef1, with links to Pathways and Tissues.
- BioMart & Analysis Tools:**
 - BioMart:** bio::mart logo.
 - Similar Patterns:** Shows similar patterns in gene expression.
 - Direct Access:** Shows direct access to data.
- Example Data:** EMAGE:3548. Assay: ISH. Gene: Shh. Stage: TS15. Spatial Annotation: [Image]. Source: Greene et al, 1998 [PMID:9545534].

Annotations
tion

)
(K)



The screenshot shows the EMAGE web application interface. At the top, there is a red navigation bar with the 'Eimage' logo on the left and a 'Quick Search' field with a dropdown menu set to 'Gene/Protein' and a 'Go' button on the right. Below the navigation bar, there are several menu items: '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 includes an 'INFO' button and a 'DEMO' button. A central image shows a 3D embryo model with a pink circular region highlighted. To the right of the image is a control panel with a zoom slider set to 10, a 'Flip L/R' button, and a 'Clear Input' button. Below the image, there are three input fields: 'Retrieve gene expression' with a dropdown menu set to 'detected', 'Retrieve data for both the left-hand and right-hand sides of the embryo.' with a checked checkbox, and 'Retrieve data over a range of stages:' with a dropdown menu set to 'TS17' and two range adjustment buttons labeled '-0' and '+0'. At the bottom left, there is a 'Begin SEARCH' button and a 'processing your query' status indicator. The footer contains links for 'Citing these resources', 'Funding information', 'Questions and comments', and 'Web browser compatibility', a Creative Commons Attribution License notice, the version number 'EMAGE V6.0_4.0', and the MRC Medical Research Council logo.



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

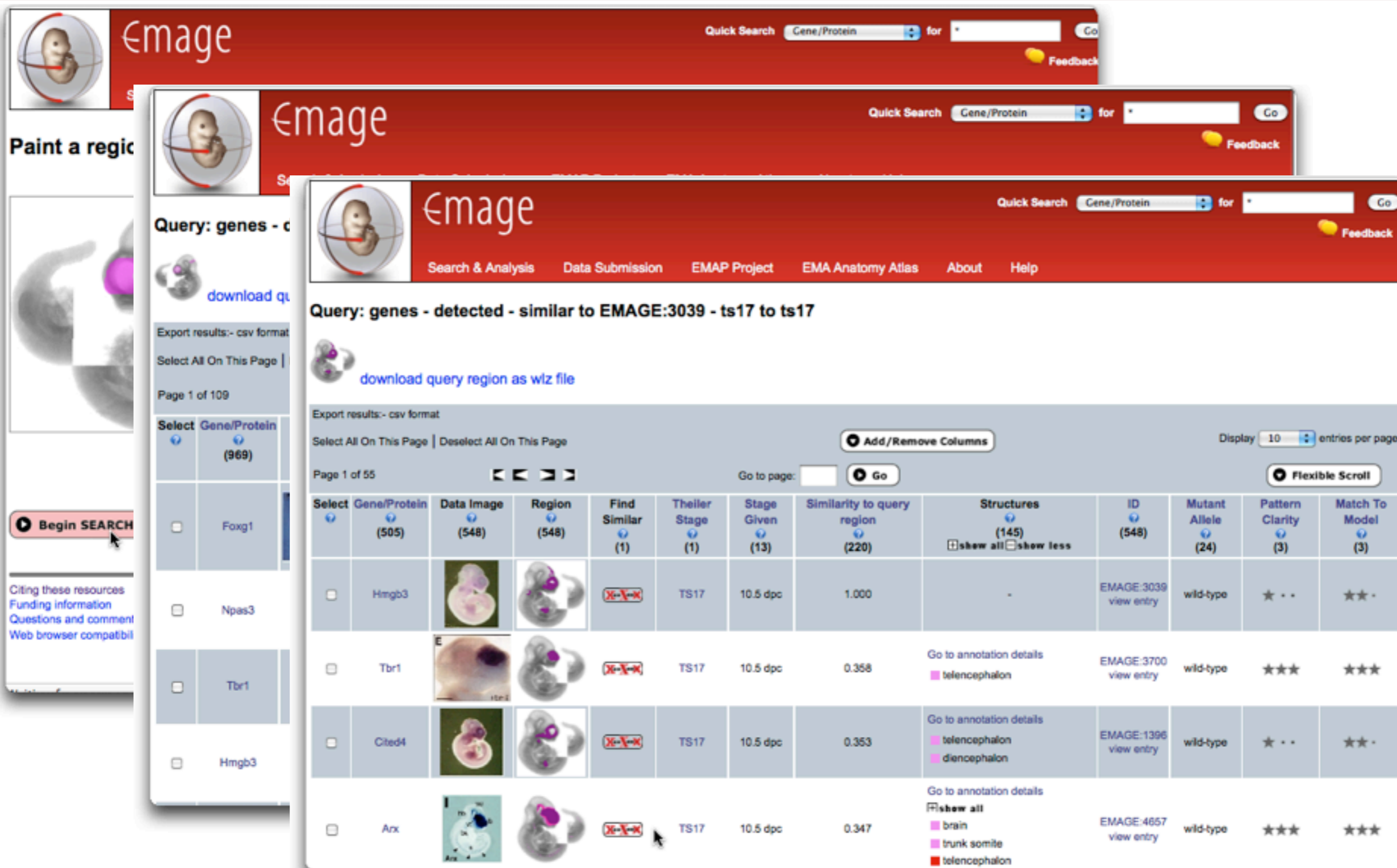
[download query region as wiz file](#)

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)	Theiler Stage (1)	Stage Given (14)	Similarity to query region (310)	Structures (188) <input type="checkbox"/> show all <input type="checkbox"/> 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 Quick Search Gene/Protein for * Go Feedback

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 - similar to EMAGE:3039 - ts17 to ts17

download query region as wiz file

Export results:- csv format







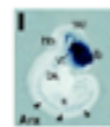

Select All On This Page | Deselect All On This Page

Page 1 of 55

Go to page: Go

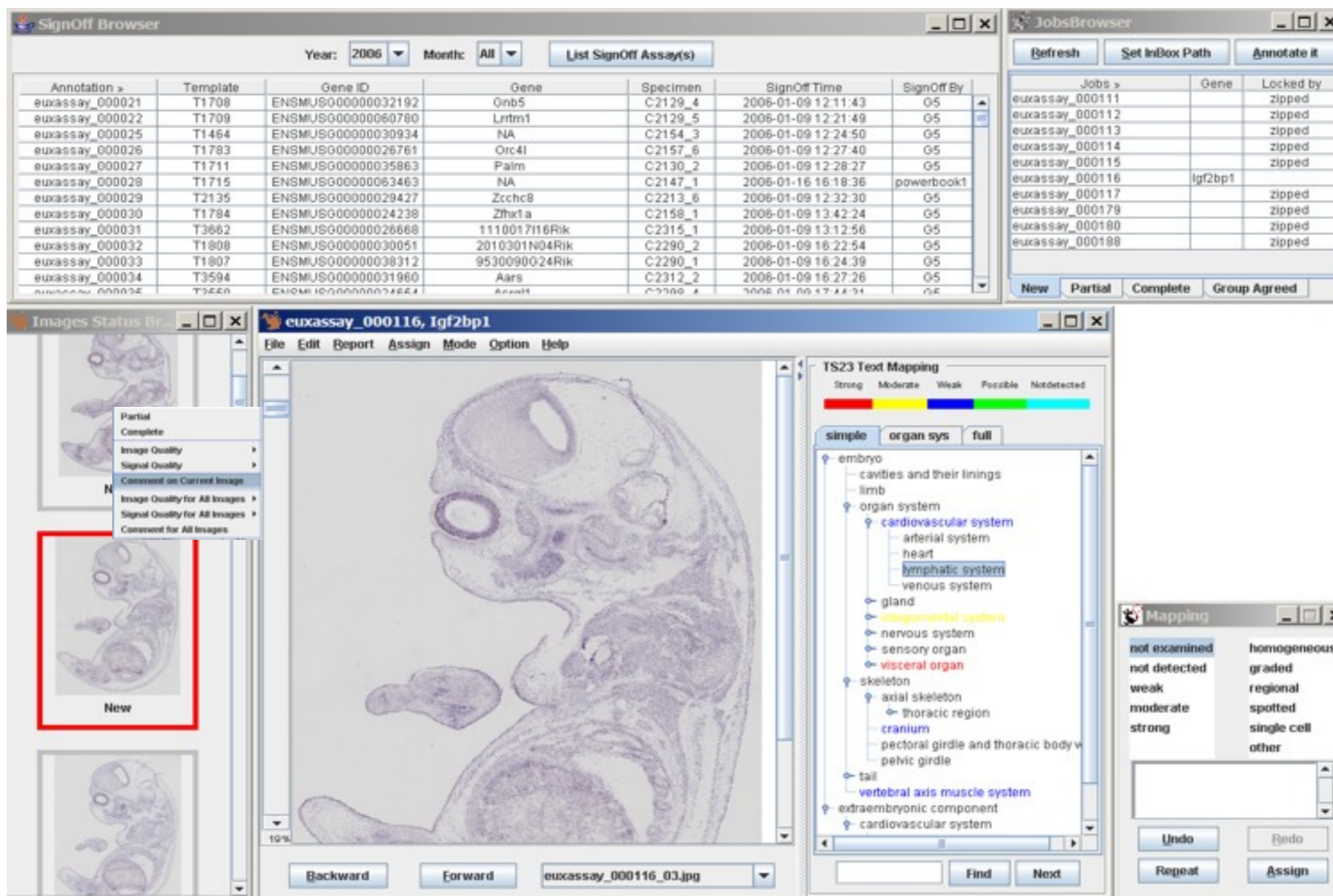
Display 10 entries per page

Flexible Scroll

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) show all show less	(548)	(24)	(3)	(3)
<input type="checkbox"/>	Hmgb3 (505)			X-X-X	TS17 (1)	10.5 dpc (13)	1.000 (220)		EMAGE:3039 view entry	wild-type	★ - -	★★ -
<input type="checkbox"/>	Npas3											
<input type="checkbox"/>	Tbr1			X-X-X	TS17 (1)	10.5 dpc (13)	0.358	Go to annotation details telencephalon	EMAGE:3700 view entry	wild-type	★★★	★★★
<input type="checkbox"/>	Cited4			X-X-X	TS17 (1)	10.5 dpc (13)	0.353	Go to annotation details telencephalon diencephalon	EMAGE:1396 view entry	wild-type	★ - -	★★ -
<input type="checkbox"/>	Arx			X-X-X	TS17 (1)	10.5 dpc (13)	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.

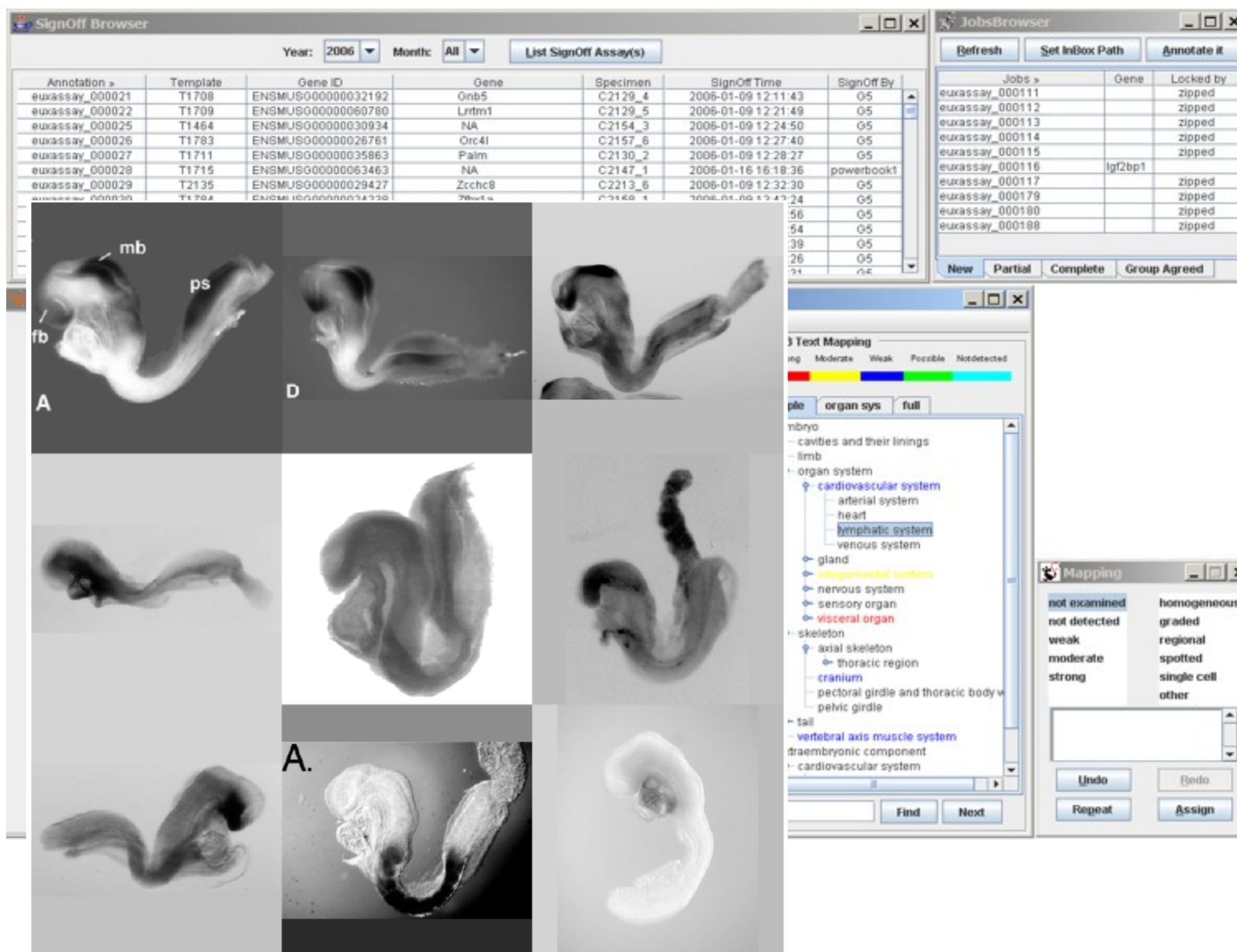
BioAtlas - data mapping



The screenshot displays the BioAtlas software interface, which is used for data mapping and image analysis. It consists of several windows:

- 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 from 2006, including those for genes like *Onb5*, *Lrrtm1*, and *Igf2bp1*.
- JobsBrowser:** A table showing the status of jobs, including columns for Jobs, Gene, and Locked by. It lists assays like *euxassay_000111* through *euxassay_000188*, with some marked as 'zipped'.
- Images Status Browser:** A window showing a grid of images. One image is highlighted with a red box and labeled 'New'. A context menu is visible over the images, offering options like 'Partial', 'Complete', and 'Image Quality'.
- euxassay_000116, Igf2bp1:** The main image analysis window. It displays a histological image of an embryo. On the right, there is a 'TS23 Text Mapping' panel with a color-coded legend (Strong, Moderate, Weak, Possible, Notdetected) and a hierarchical tree of anatomical structures. The 'lymphatic system' is highlighted in blue. Below the image are 'Backward' and 'Forward' navigation buttons.
- Mapping:** A small window showing a list of mapping terms such as 'not examined', 'not detected', 'weak', 'moderate', 'strong', 'homogeneous', 'graded', 'regional', 'spotted', 'single cell', and 'other'. It includes 'Undo', 'Redo', 'Repeat', and 'Assign' buttons.

BioAtlas - data mapping



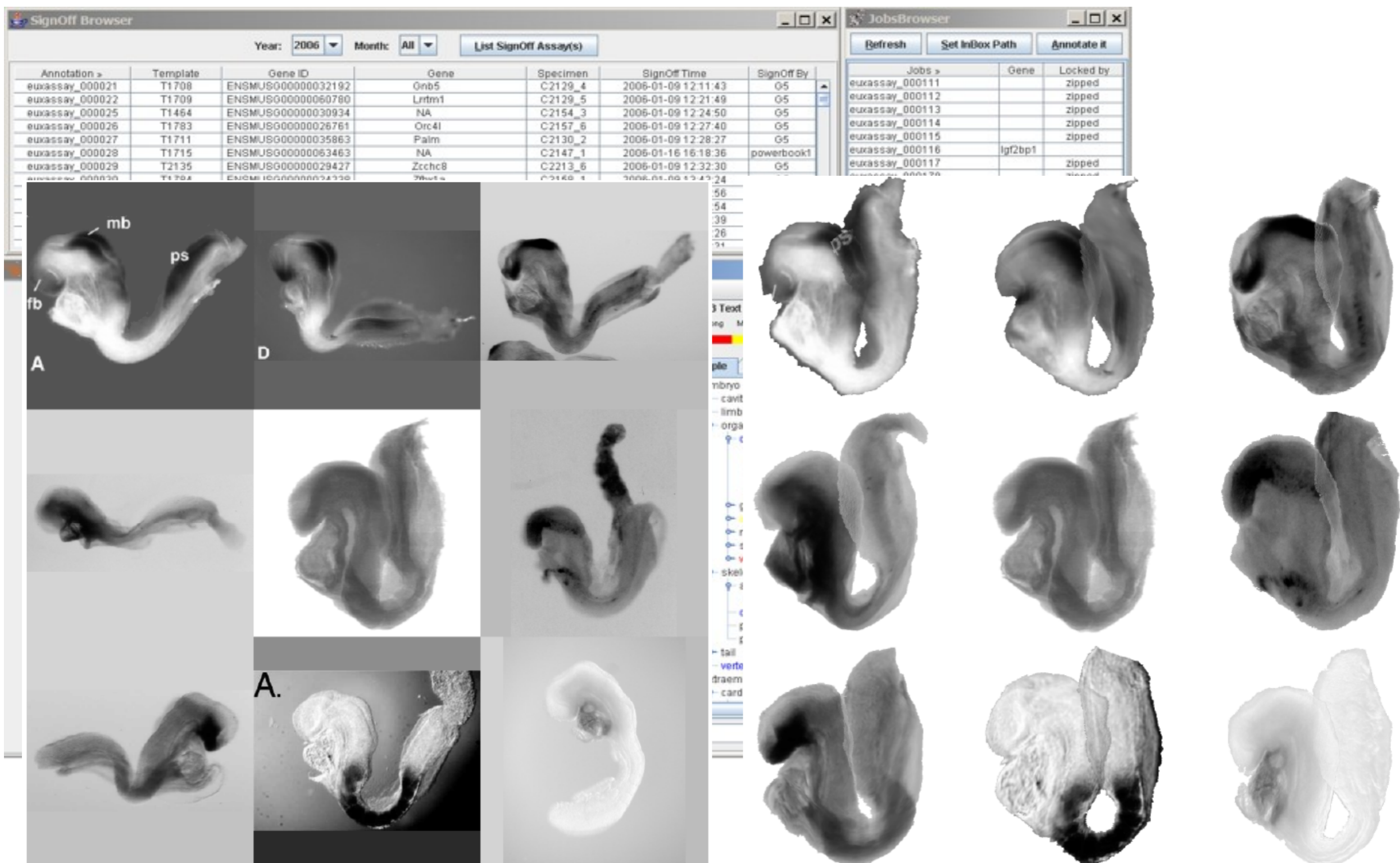
The screenshot displays two main software windows: **SignOff Browser** and **JobsBrowser**.

SignOff Browser shows a table of assay data with columns for Annotation, Template, Gene ID, Gene, Specimen, SignOff Time, and SignOff By. Below the table is a grid of grayscale images of embryos, with some labeled 'mb', 'ps', 'fb', and 'A'.

JobsBrowser shows a table of jobs with columns for Jobs, Gene, and Locked by. Below the table are buttons for 'New', 'Partial', 'Complete', and 'Group Agreed'.

Overlaid on the bottom right is a **Text Mapping** window with a color scale legend and a tree view of anatomical systems. The tree view includes categories like 'organ system', 'skeleton', and 'tail', with sub-items like 'cardiovascular system', 'arterial system', 'heart', 'lymphatic system', 'venous system', 'gland', 'abdominal system', 'nervous system', 'sensory organ', 'visceral organ', 'axial skeleton', 'thoracic region', 'cranium', 'pectoral girdle and thoracic body wall', 'pelvic girdle', 'vertebral axis muscle system', and 'draembryonic component'.

Below the tree view is a **Mapping** window with a list of mapping terms (not examined, not detected, weak, moderate, strong, homogeneous, graded, regional, spotted, single cell, other) and buttons for 'Undo', 'Redo', 'Repeat', and 'Assign'.

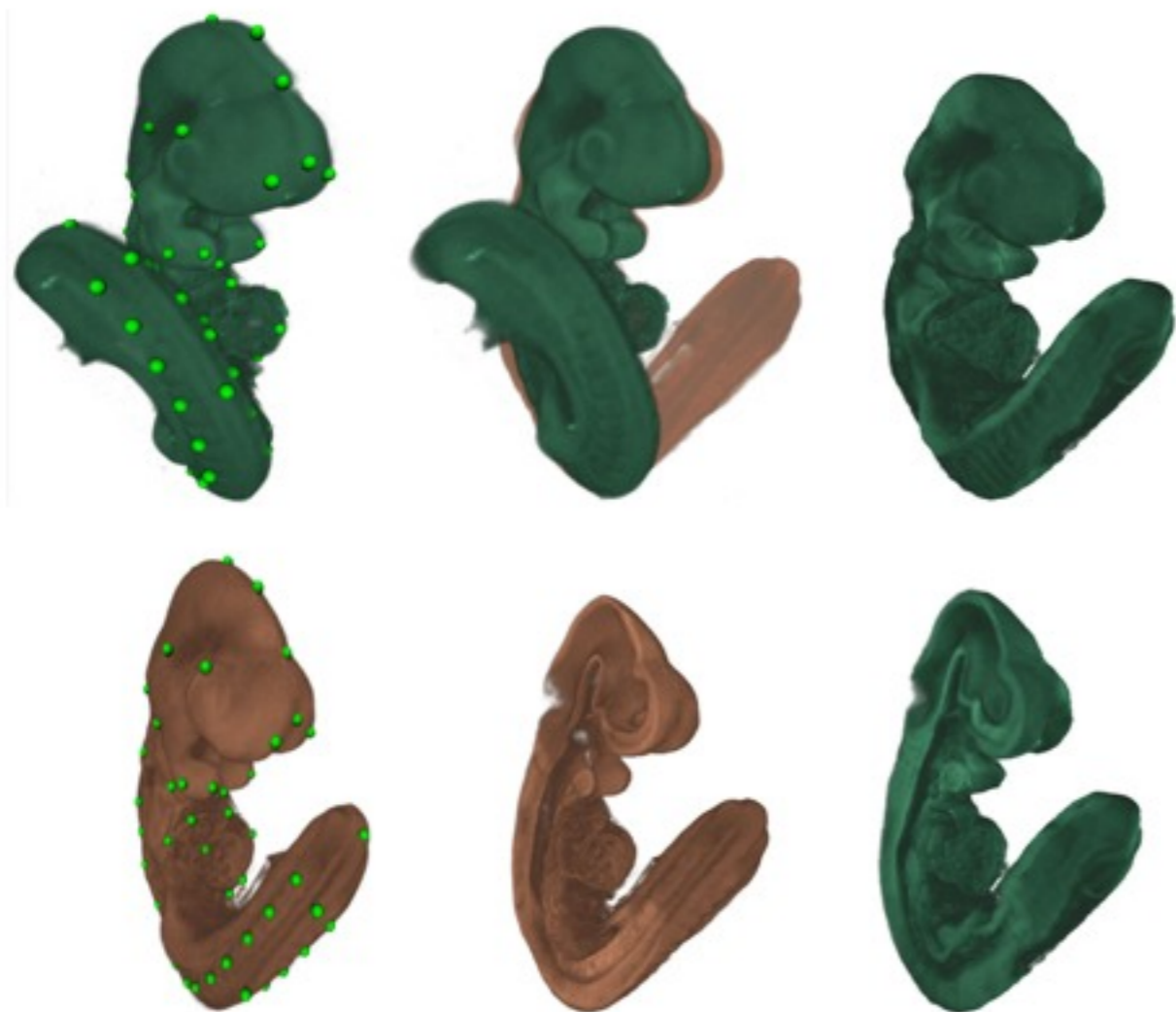




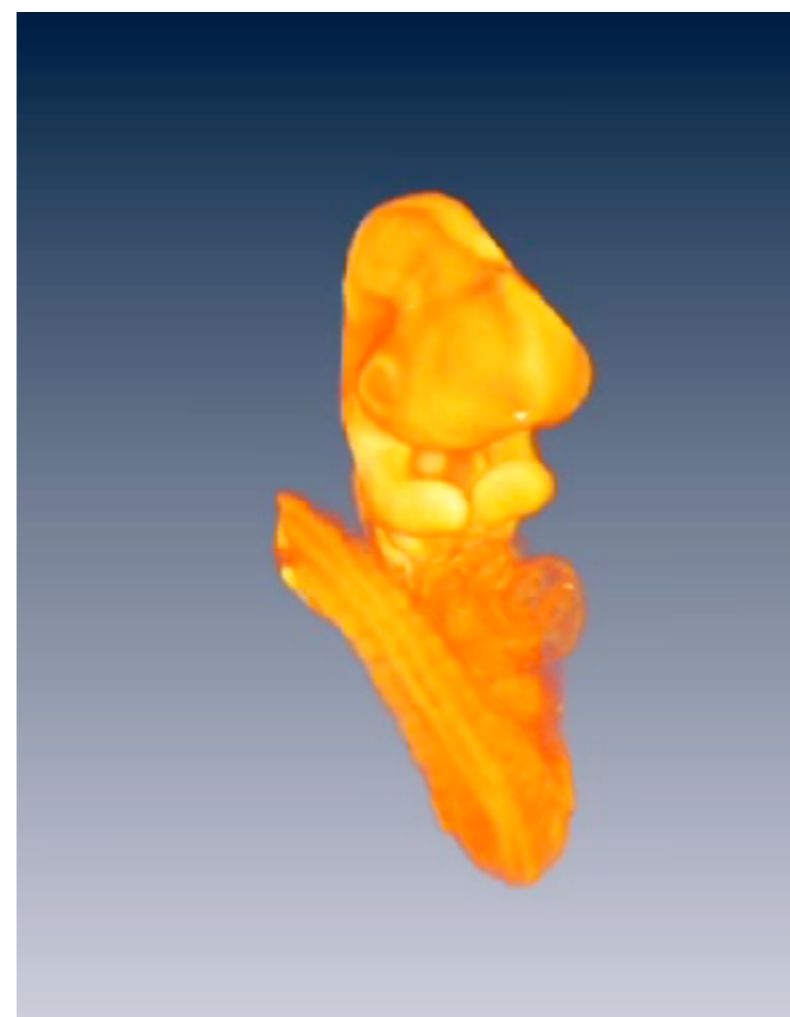
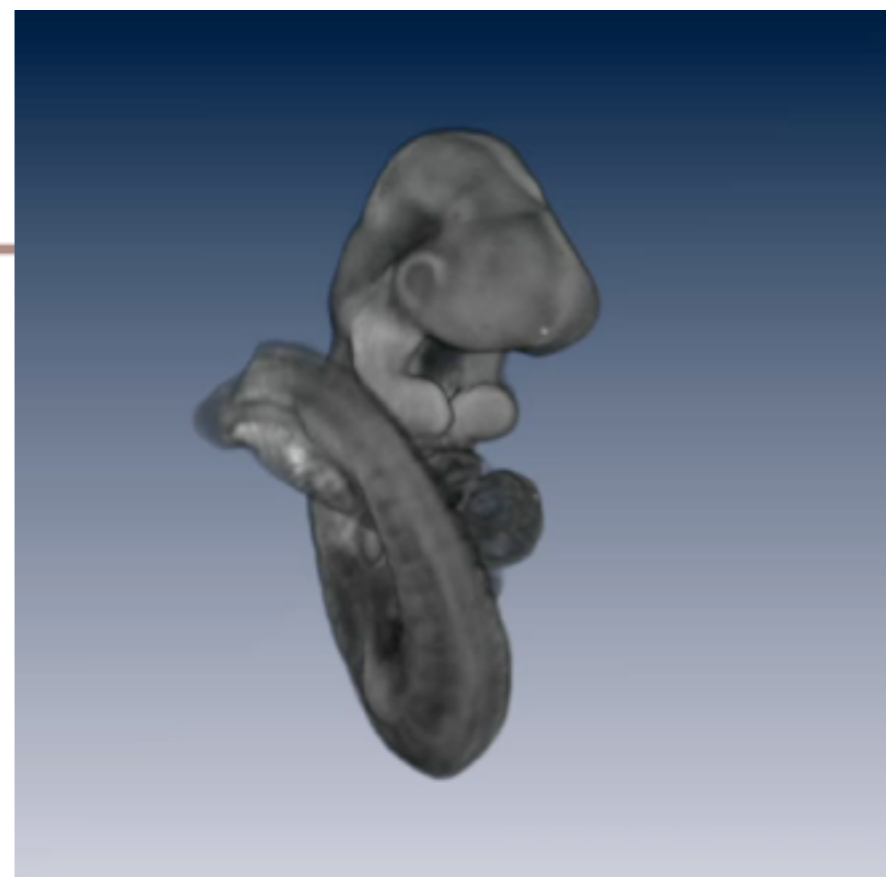
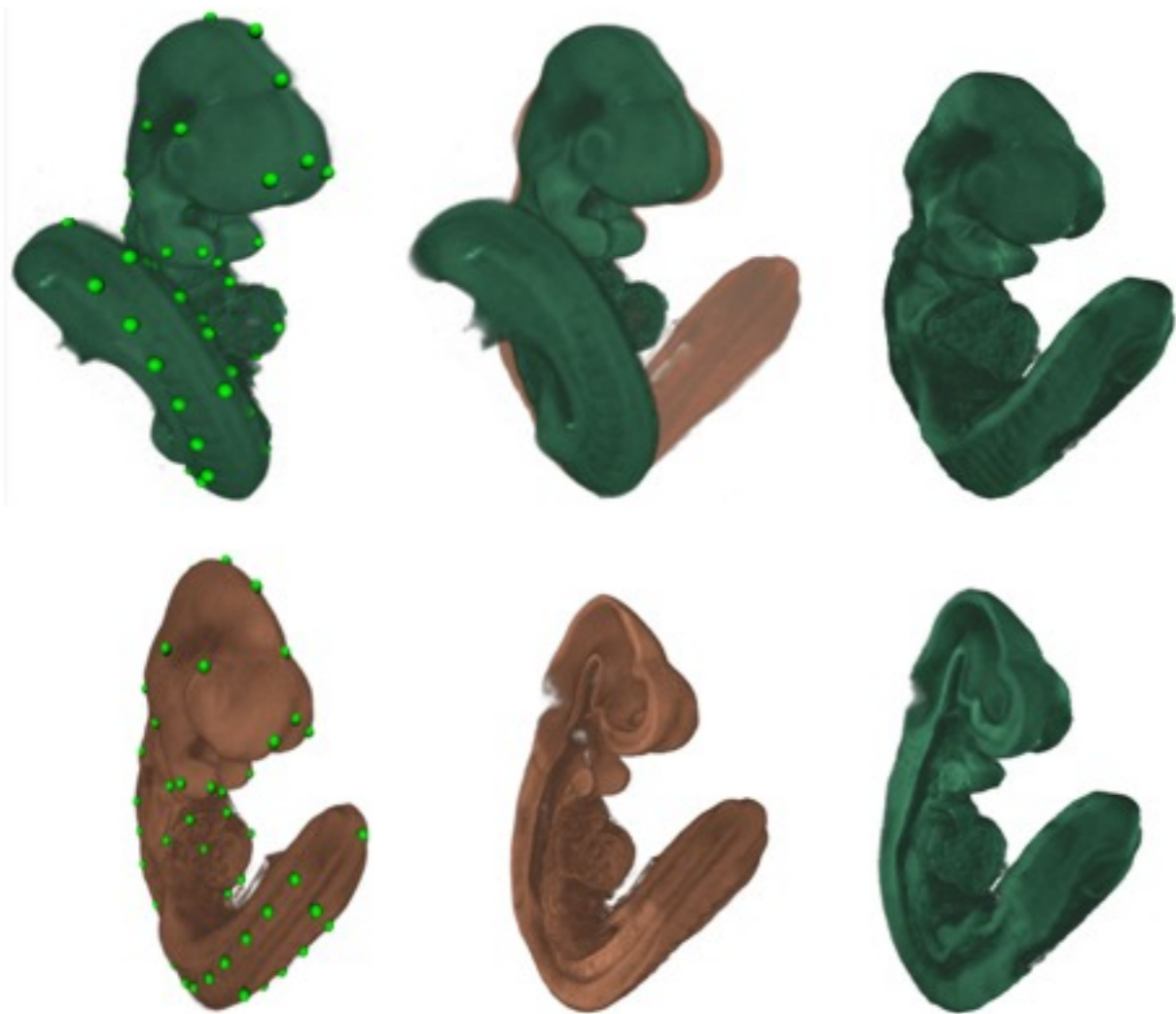
Spatial Data Mapping

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

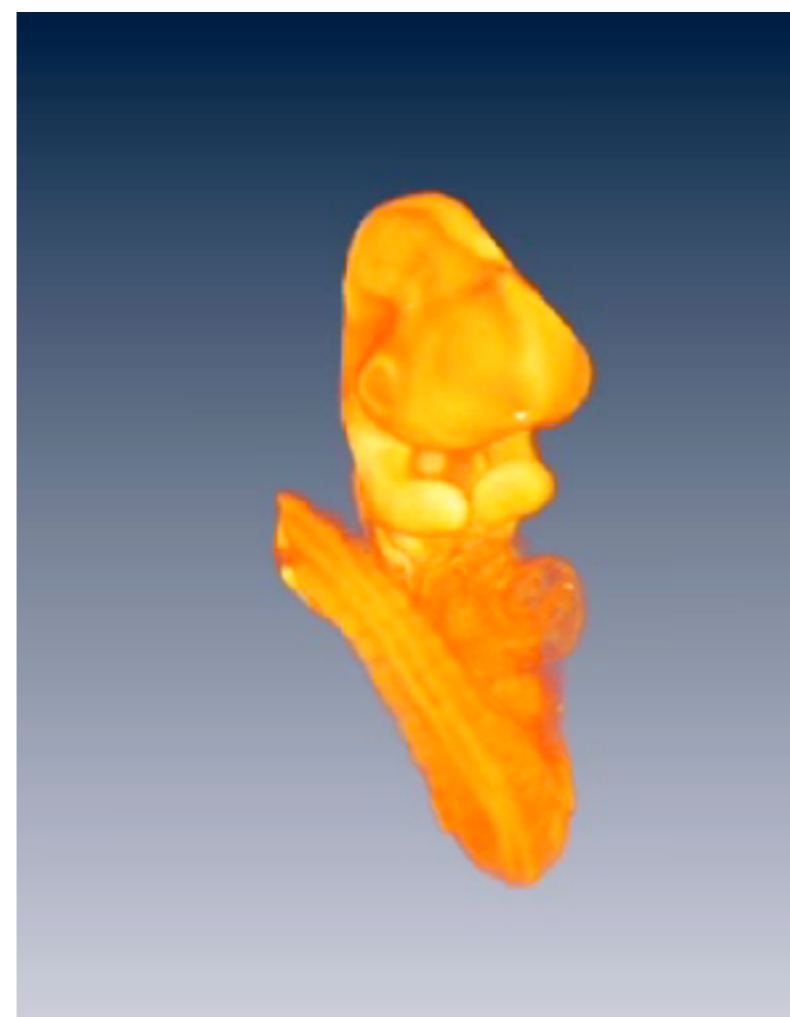
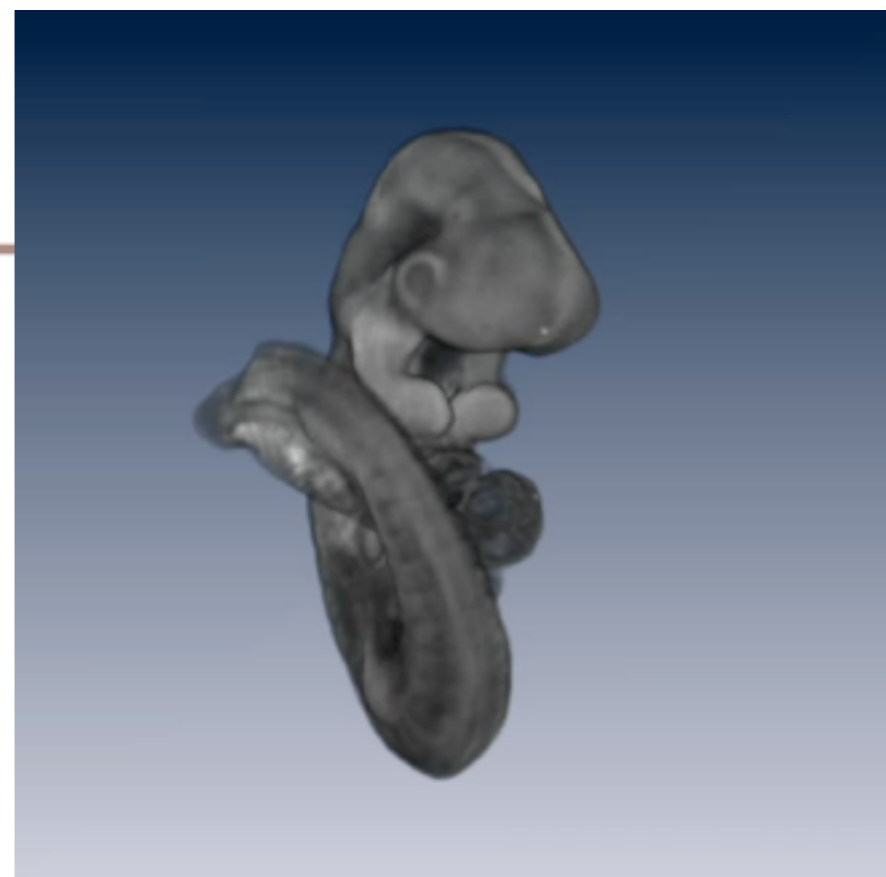
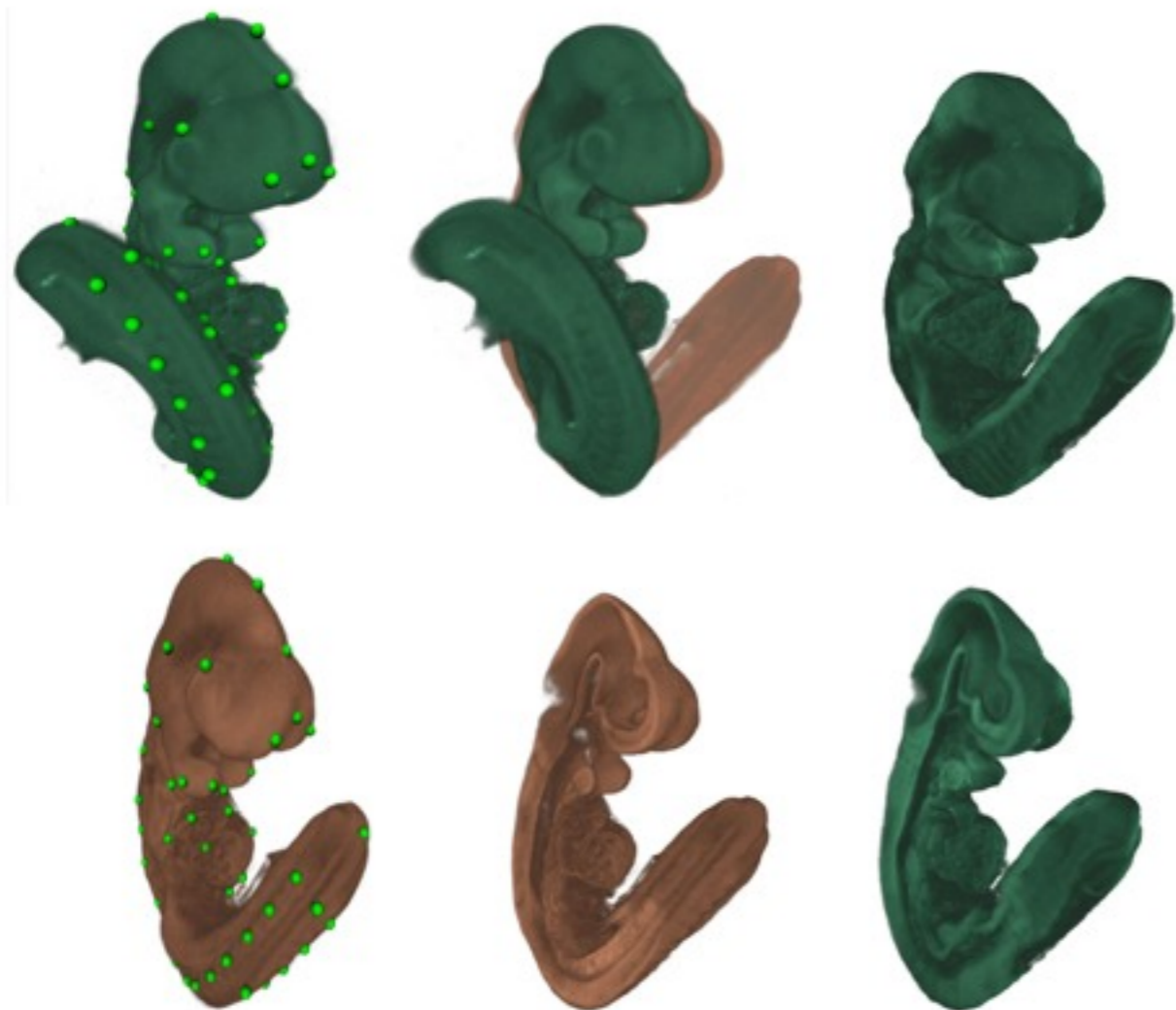
3D Data Mapping - WlzWarp











3D Data Mapping - WlzWarp



3D Data Mapping - WlzWarp



3D Mapping - Wnt signalling pathway

Wnt1		TS17	10.5dpc	3D View	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

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.

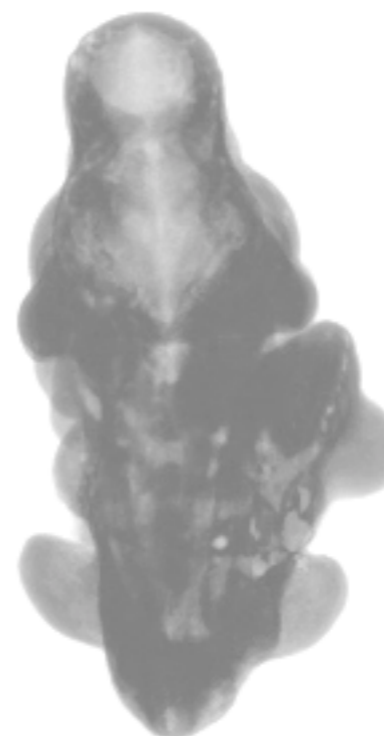
Photograph prior to 3D imaging.

[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



OME Project Objectives

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

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



Emap

Woolz images

A fast interval processor

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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[☆]

Jim Piper^a and Denis Rutovitz^a

^aMRC 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

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Abstract

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Keywords: Ir
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☆ This work

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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domain volume = 5M



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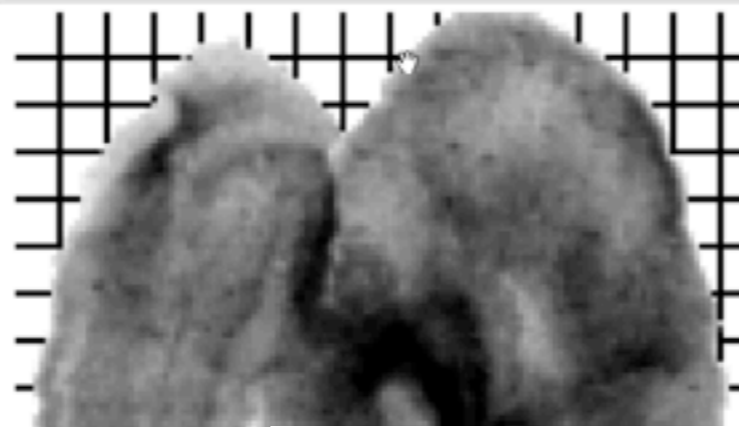
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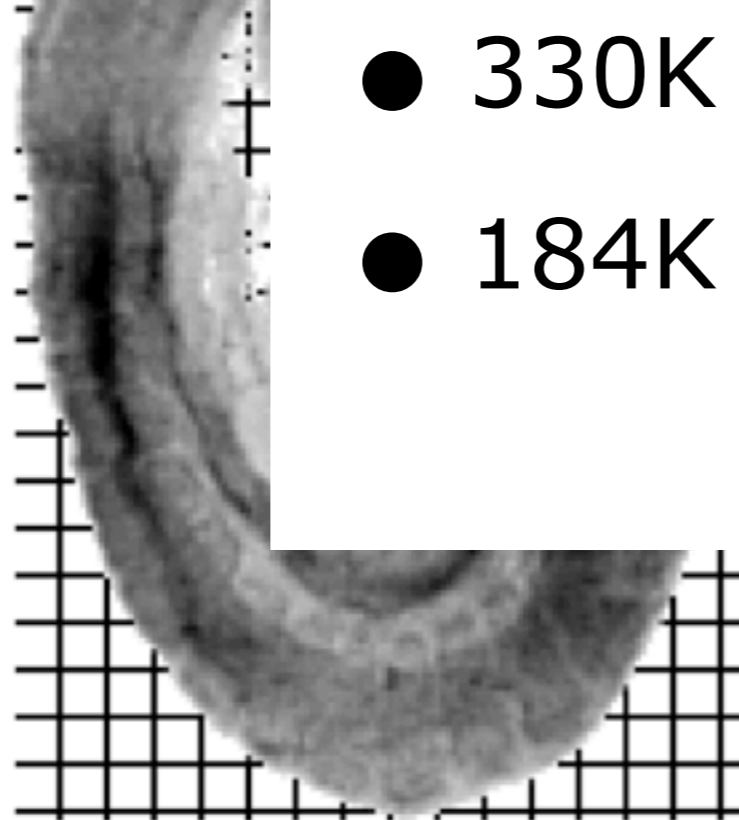
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- 330K lines Ansi C code
- 184K lines application code



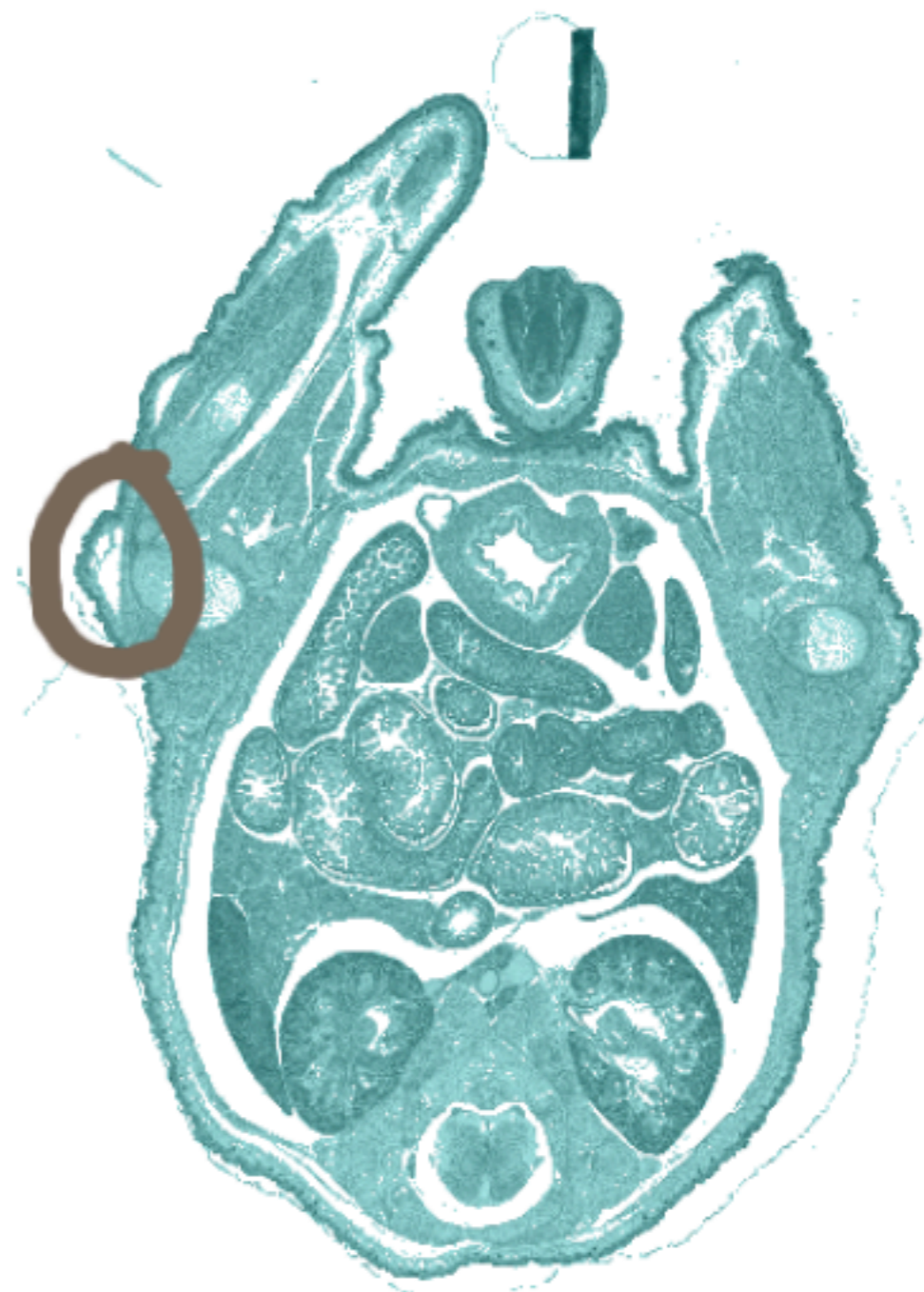
- Domain
 - Rectangle based
 - Interval based
 - 3D planewise domains
- Values
 - Rectangle based
 - Raged and interval based
 - Tiled



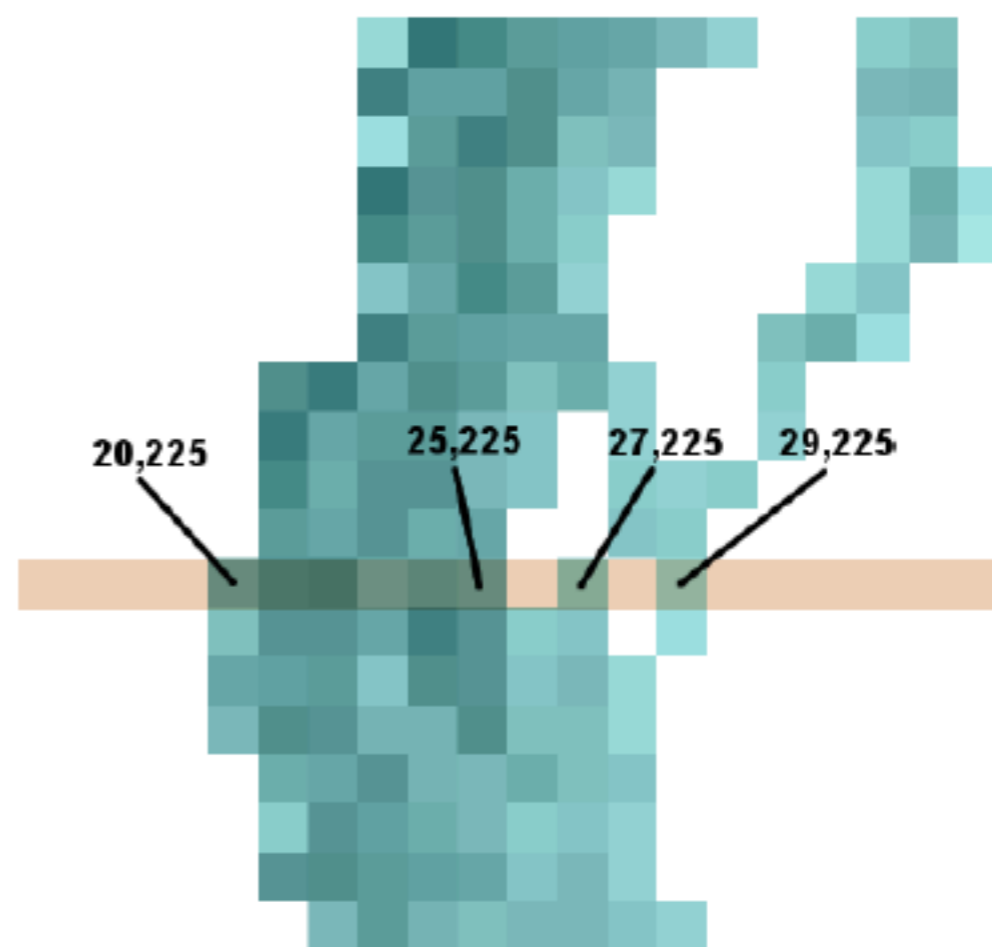
- Domain
 - Rectangle based
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 - Raged and interval based
 - Tiled



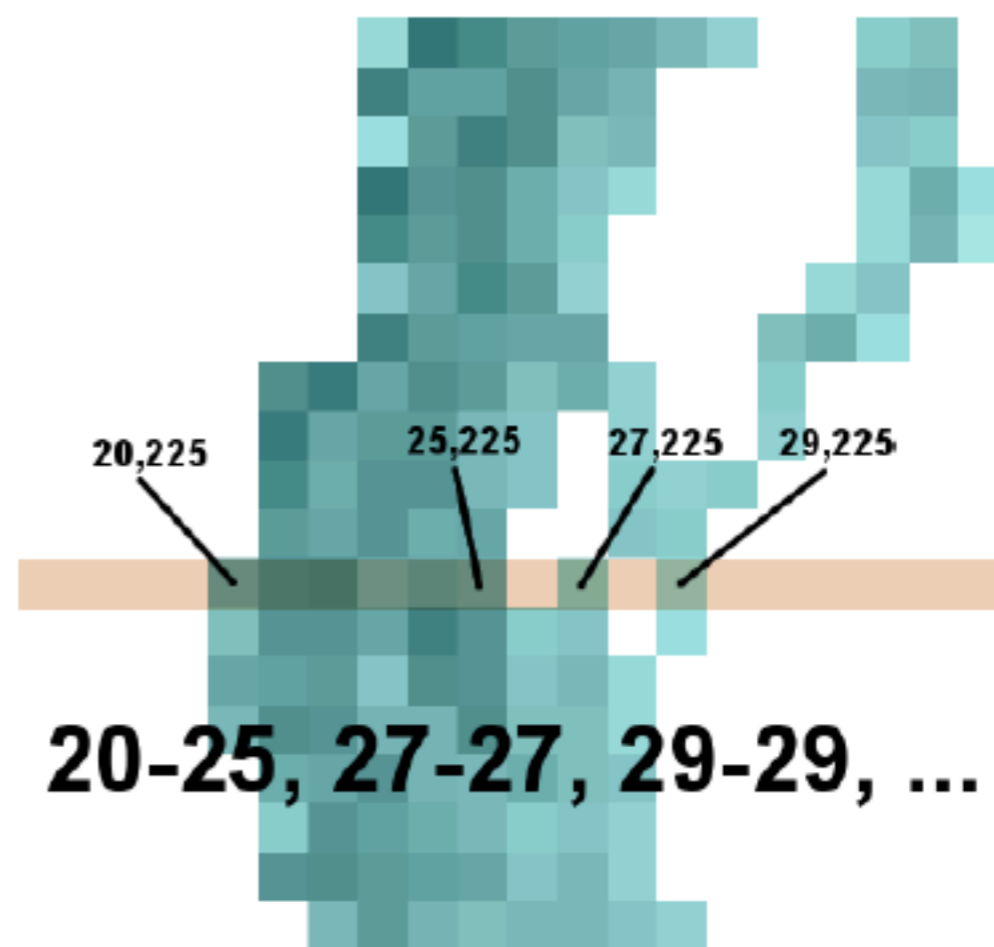
- Domain
 - Rectangle based
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- Domain
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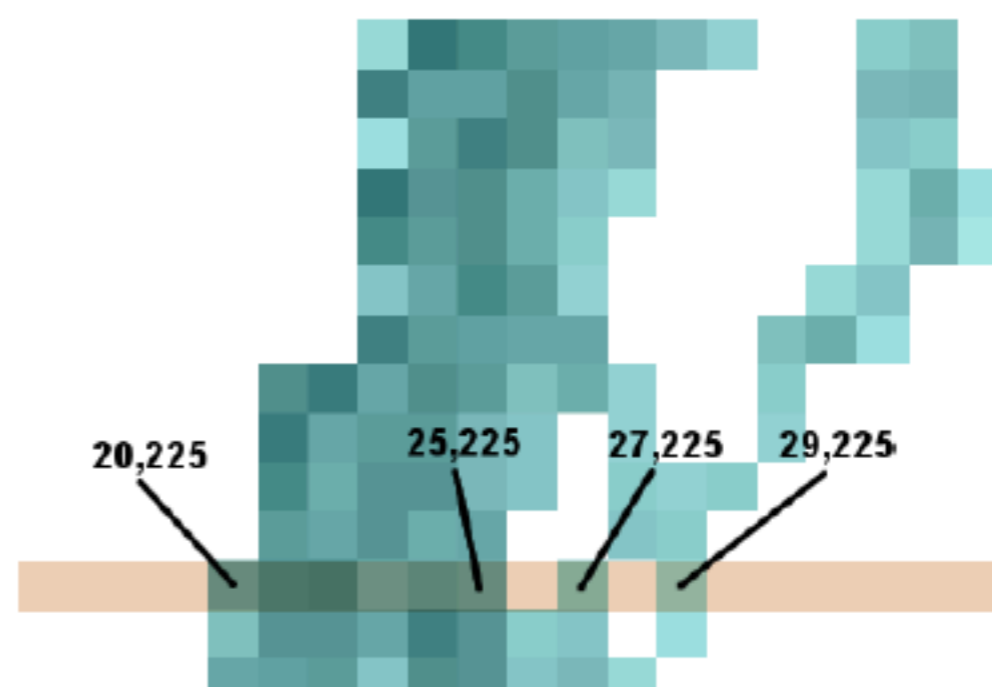


- Domain

- Rectangle based
- Interval based
- 3D planewise domains

- Values

- Rectangle based
- Raged a based
- Tiled



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





Woolz Images



- Domain

- Rect
- Inter
- 3D p

- 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



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

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

- Polylines, boundary lists
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 - ▶ conforming mesh

$$\Delta u = u - x$$

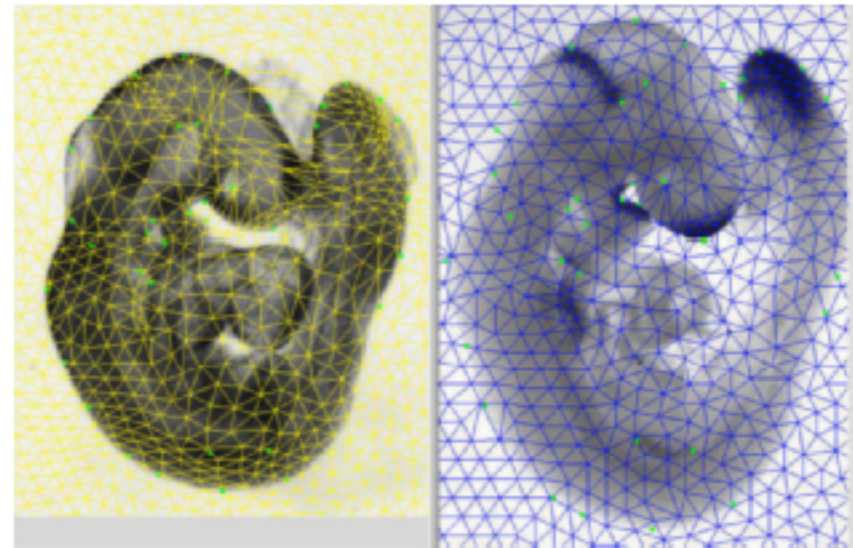
$$\Delta u = P_u(x, y) + \sum_{i=1}^{i=N} \lambda_i b(r_i)$$

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

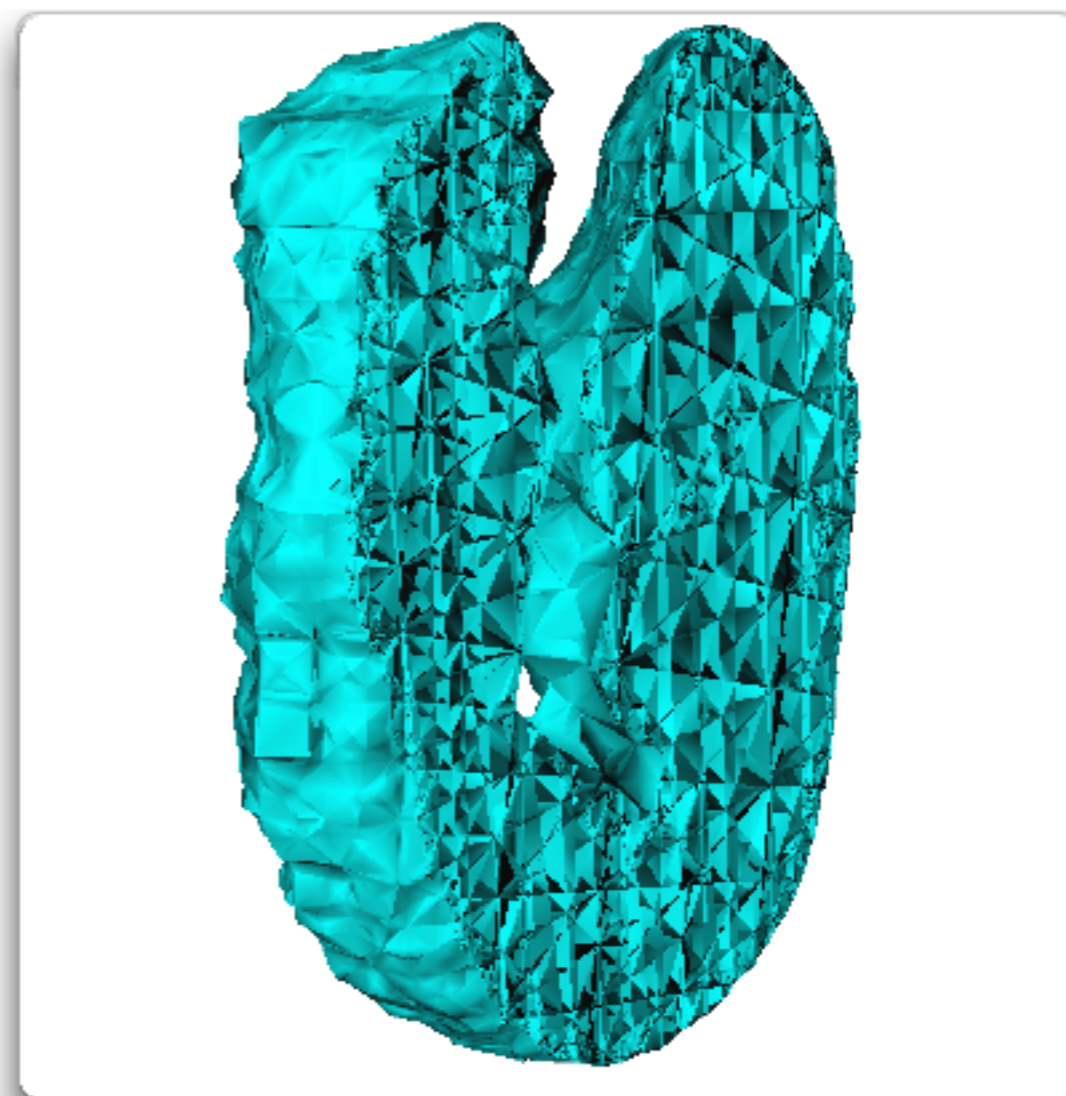
$$b_{MQ}(r) = \sqrt{r^2 + \delta^2}$$

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

- Polylines, boundary lists
- histograms
- meshes - 2D & 3D
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- Polylines, boundary lists
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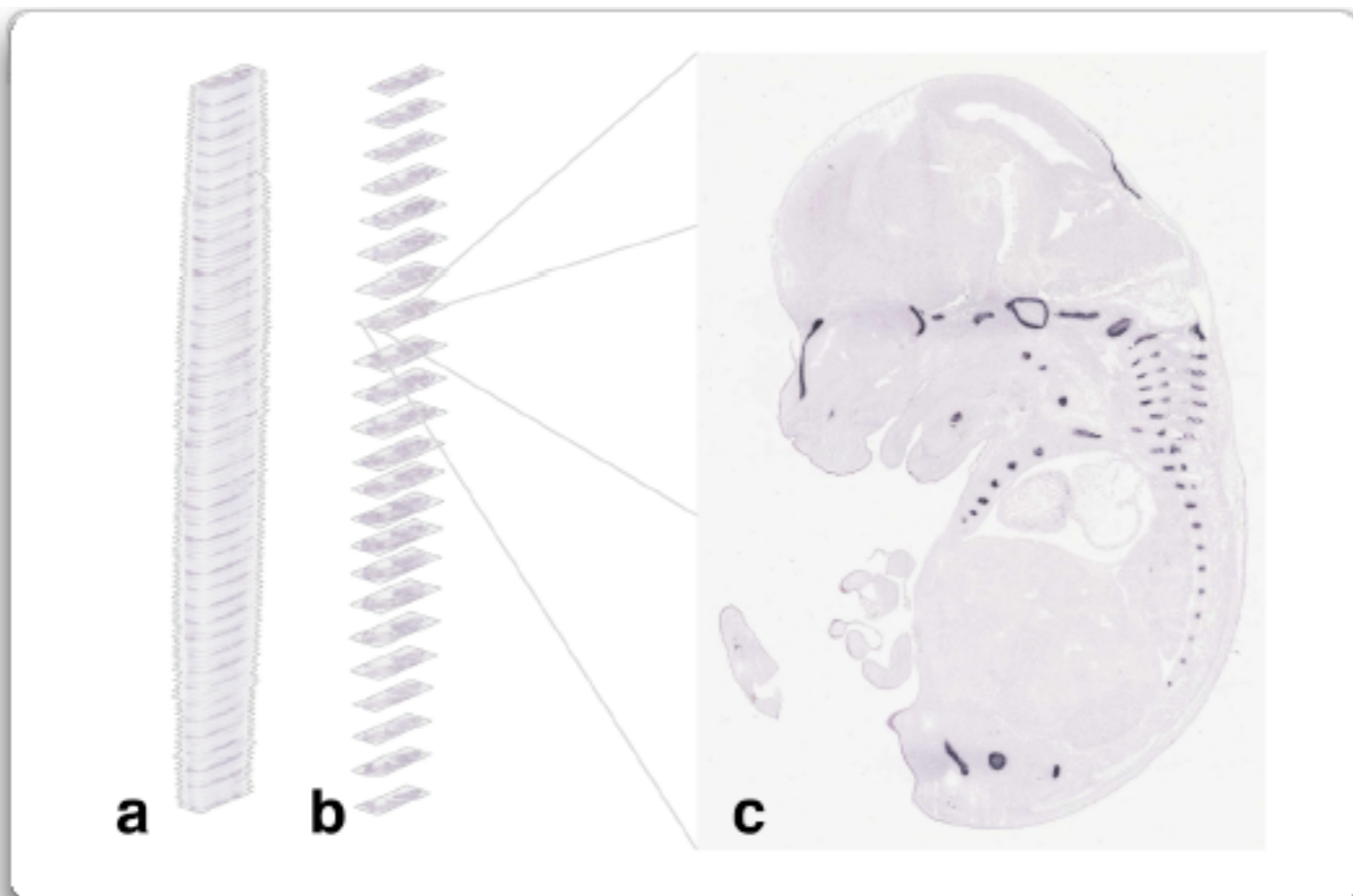
- EurExpress project
 - ▶ 19.5K in situ probes, 350K images
 - ▶ ~24 images per in situ probe
 - ▶ ~0.5 micron resolution in plane
 - ▶ 150 micron plane separation
- EmbryoExpress - 20K images
- Allen Brain Atlas - 200K images
- Require automation - Advanced Normalisation Tool (ANTs)
 - ▶ sparse image, matching mask
 - ▶ Full 3D affine then non-linear warping.



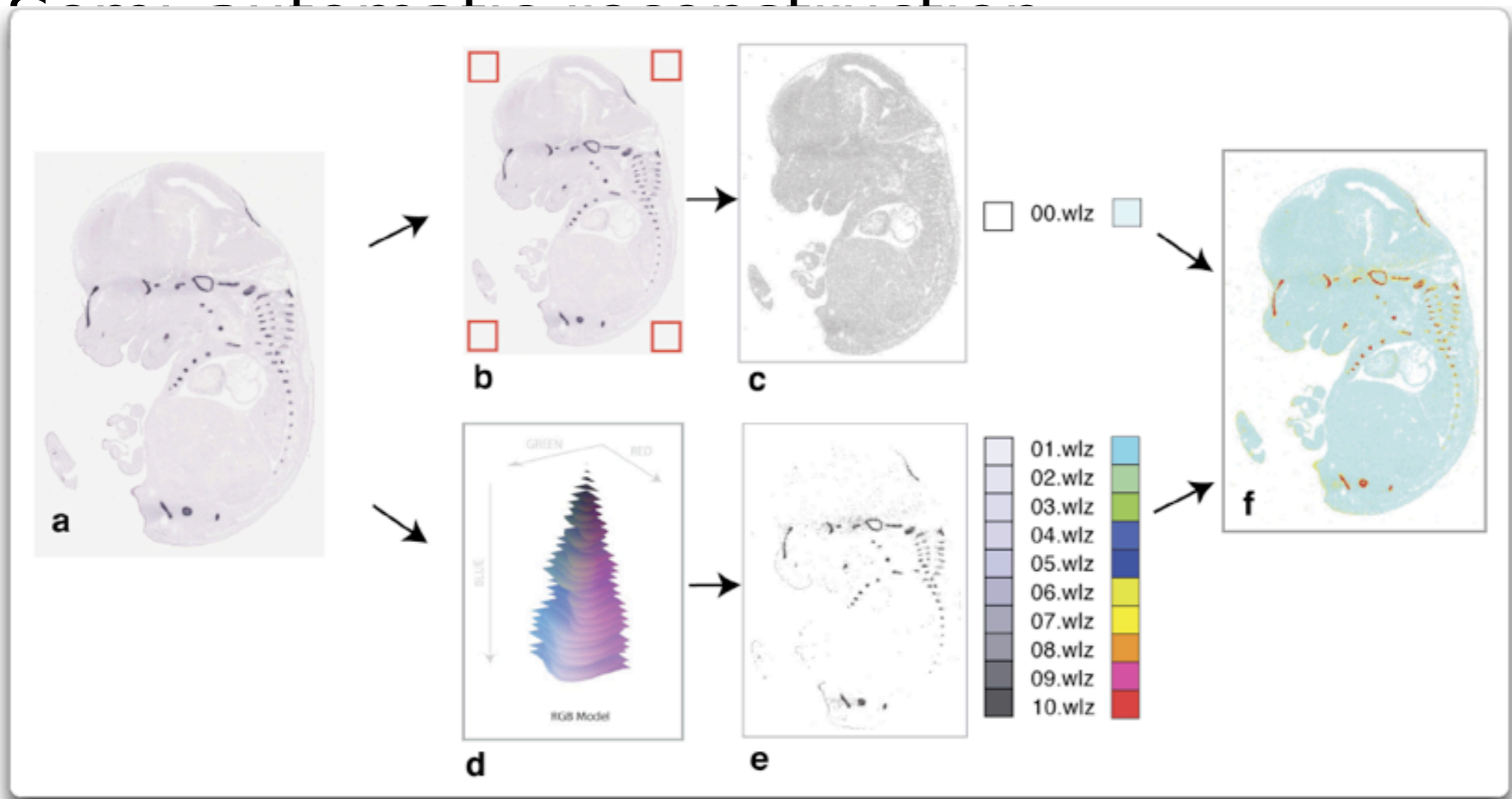
Pseudo Wholemout Mapping to Emap - done

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

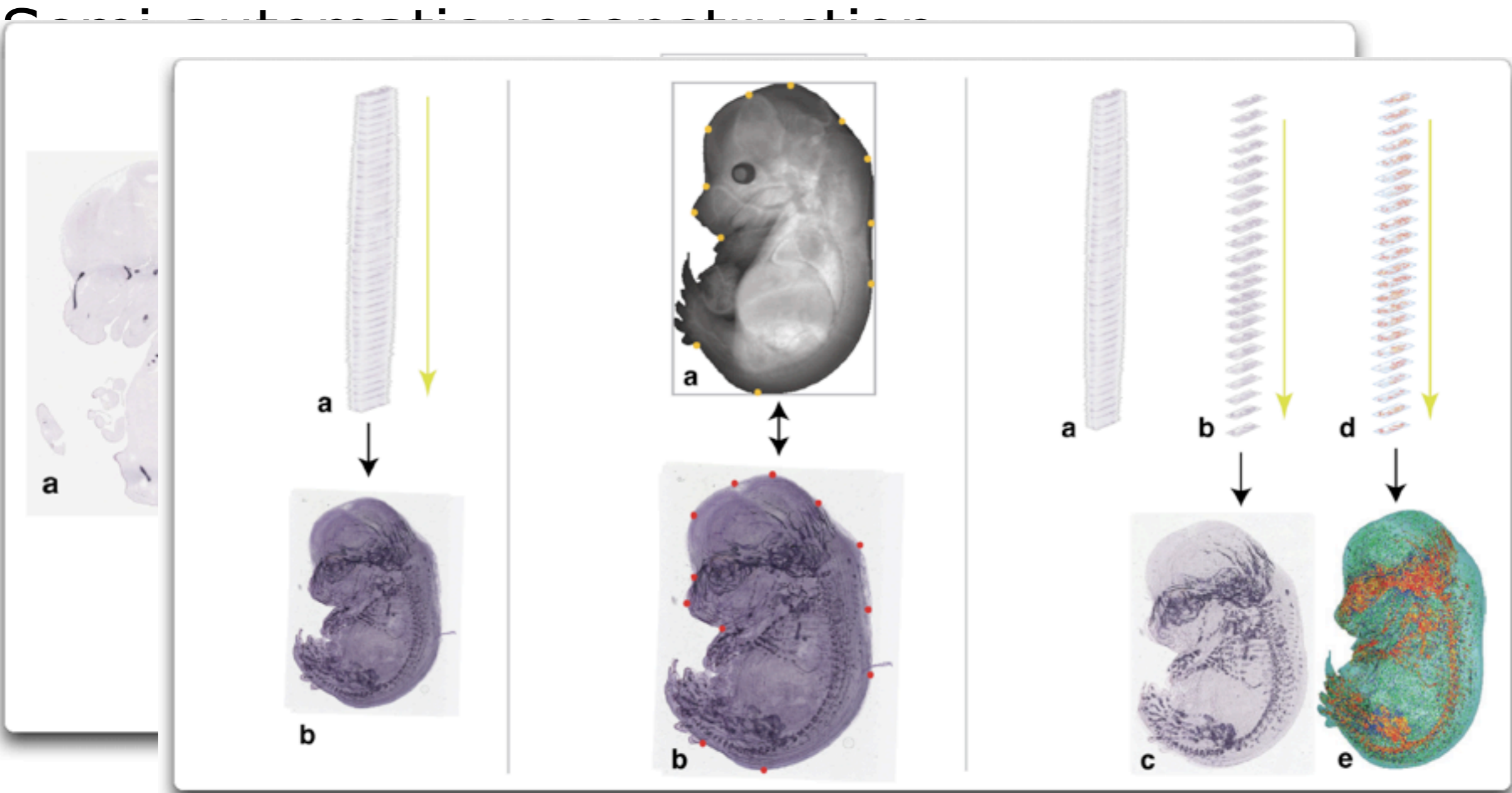
- Semi-automatic reconstruction



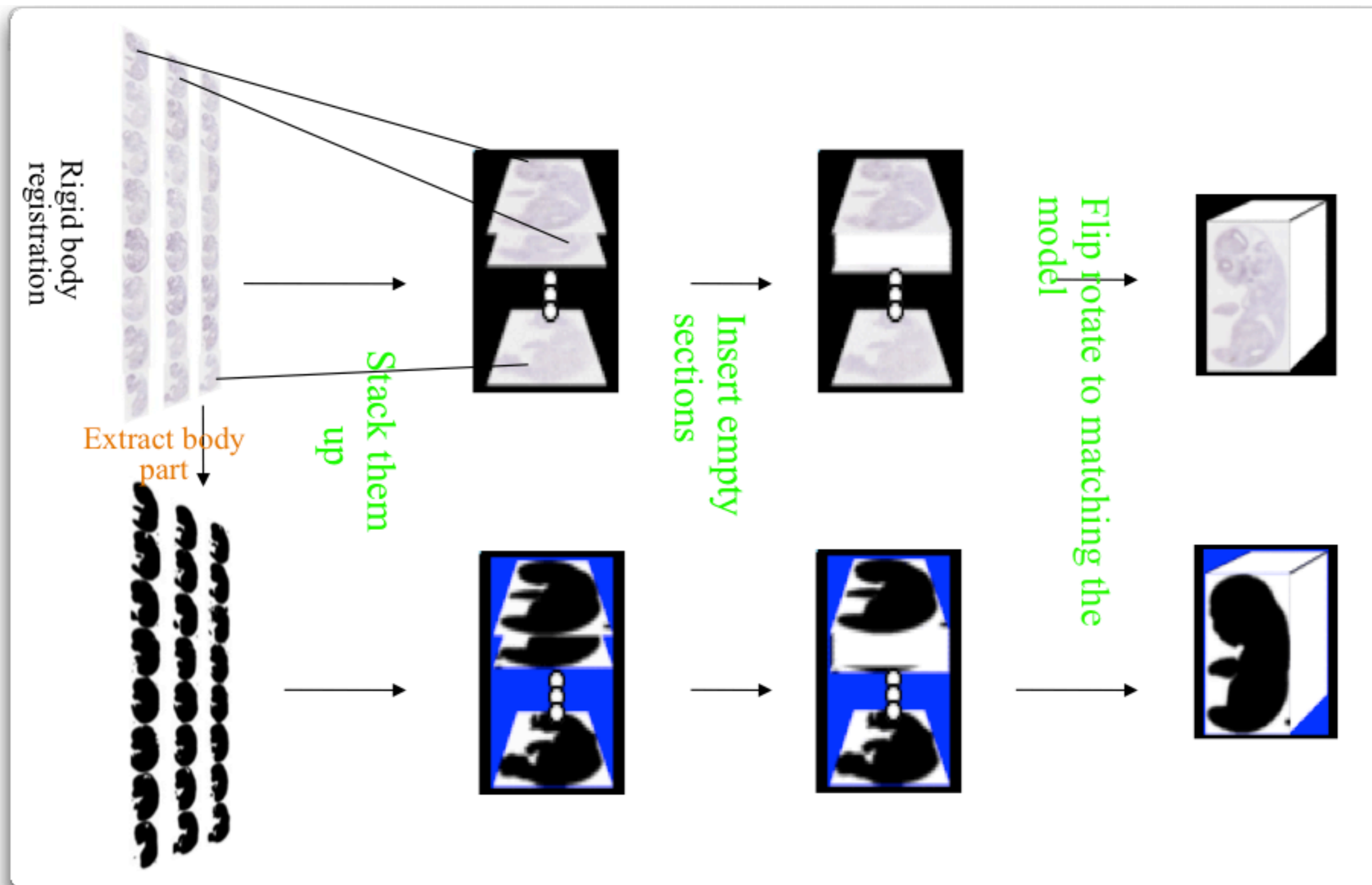
Pseudo Wholemount Mapping to Emap - done



Pseudo Wholemount Mapping to Emap - done



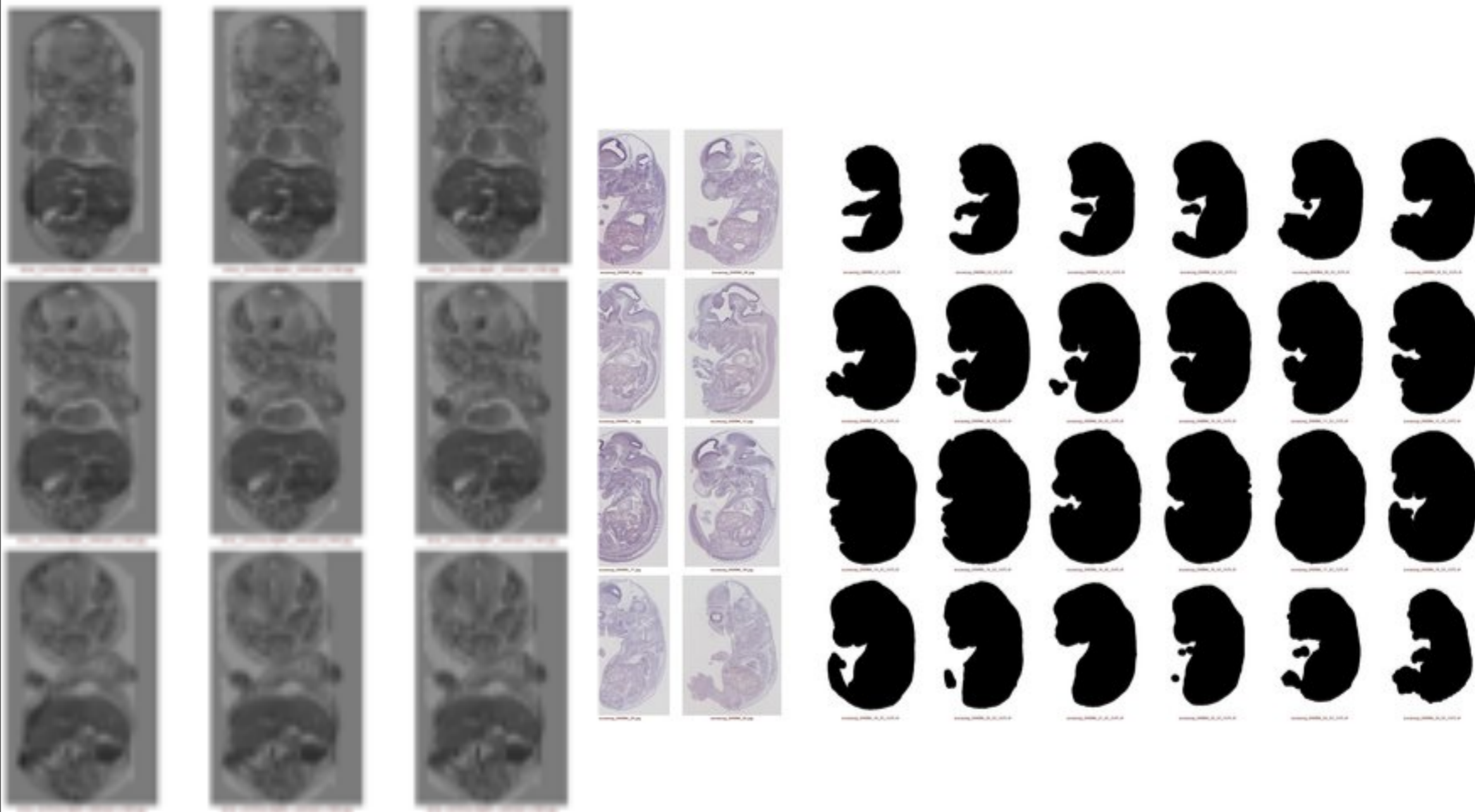
3D Mapping to emap



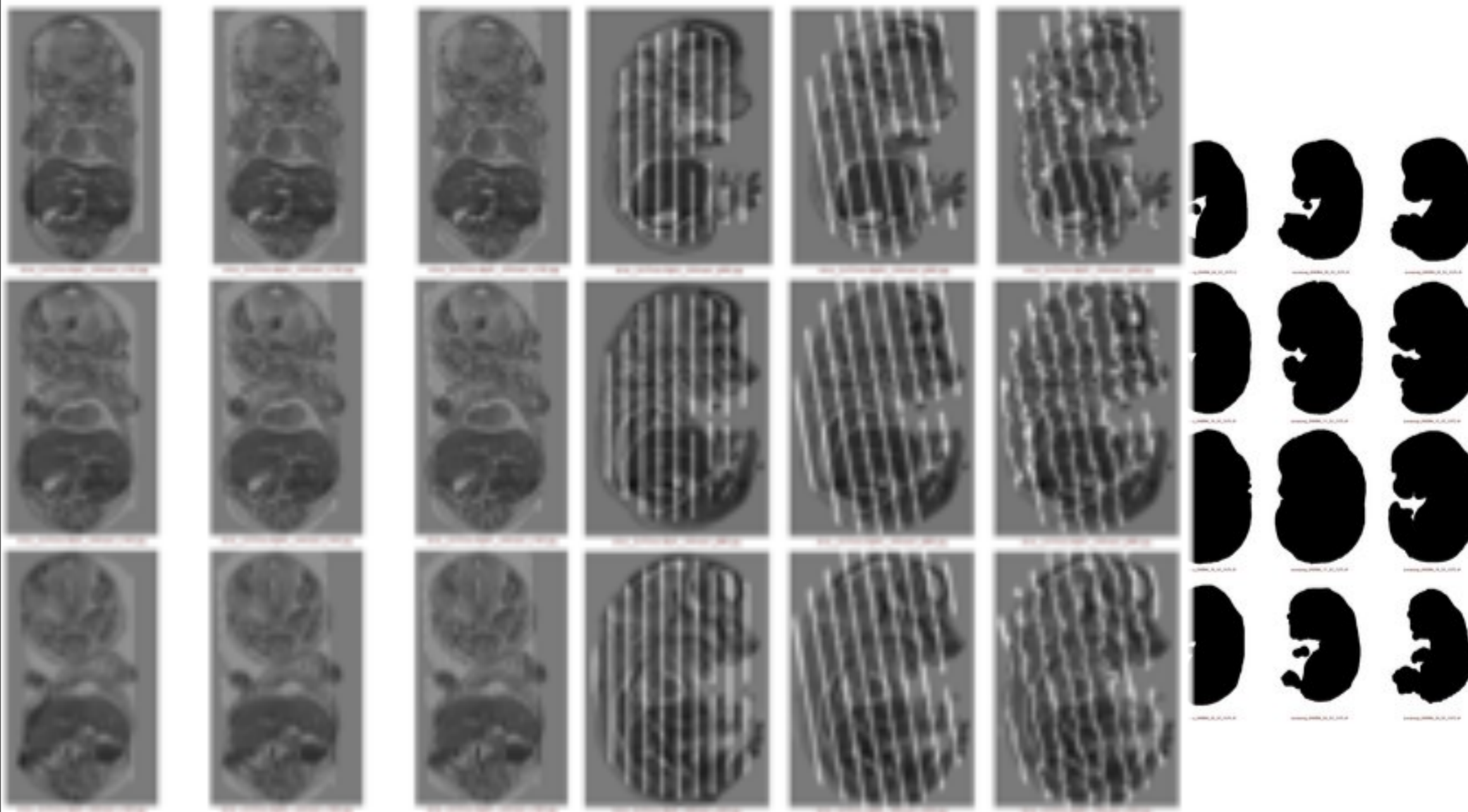
3D Mapping to emap



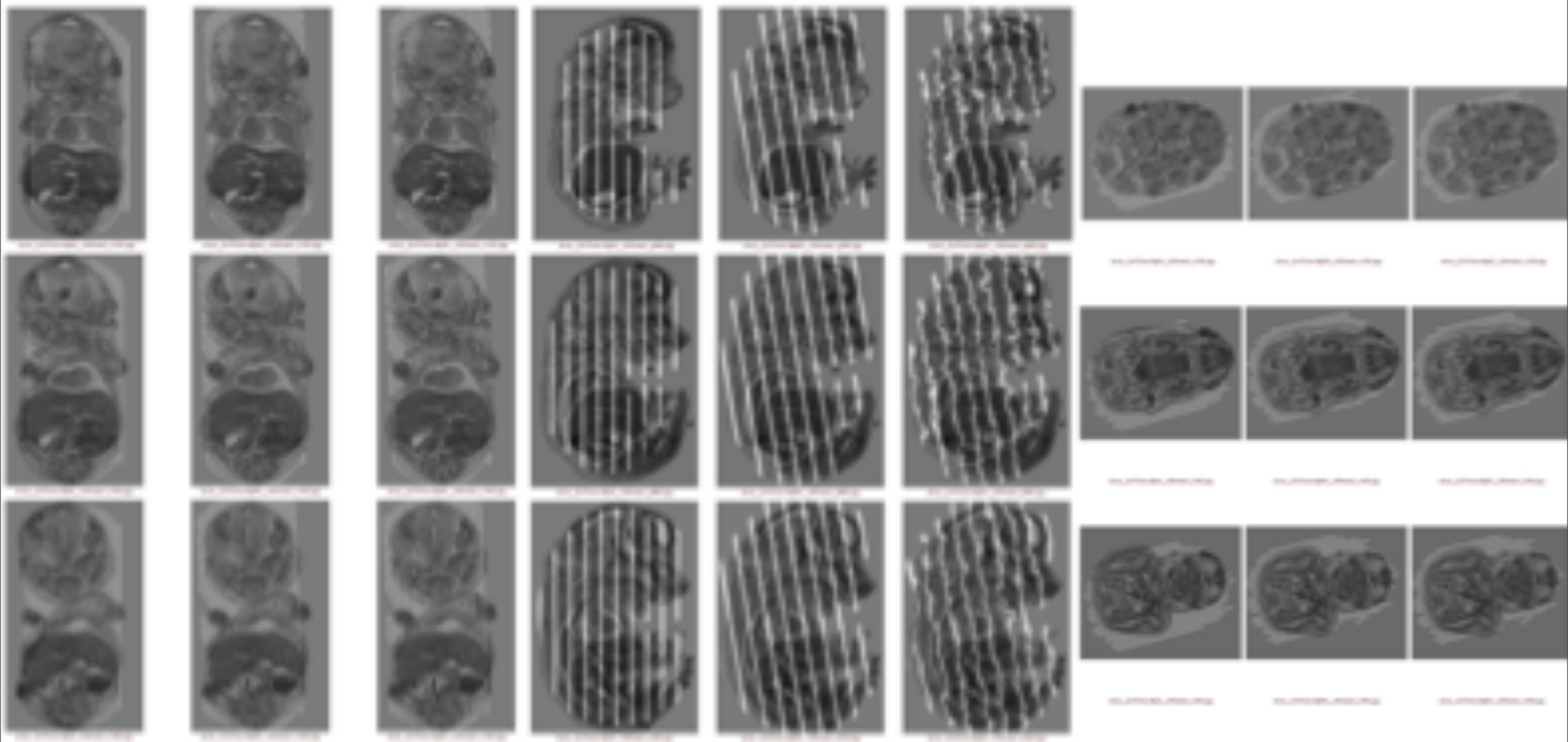
3D Mapping to emap



3D Mapping to emap



3D Mapping to emap



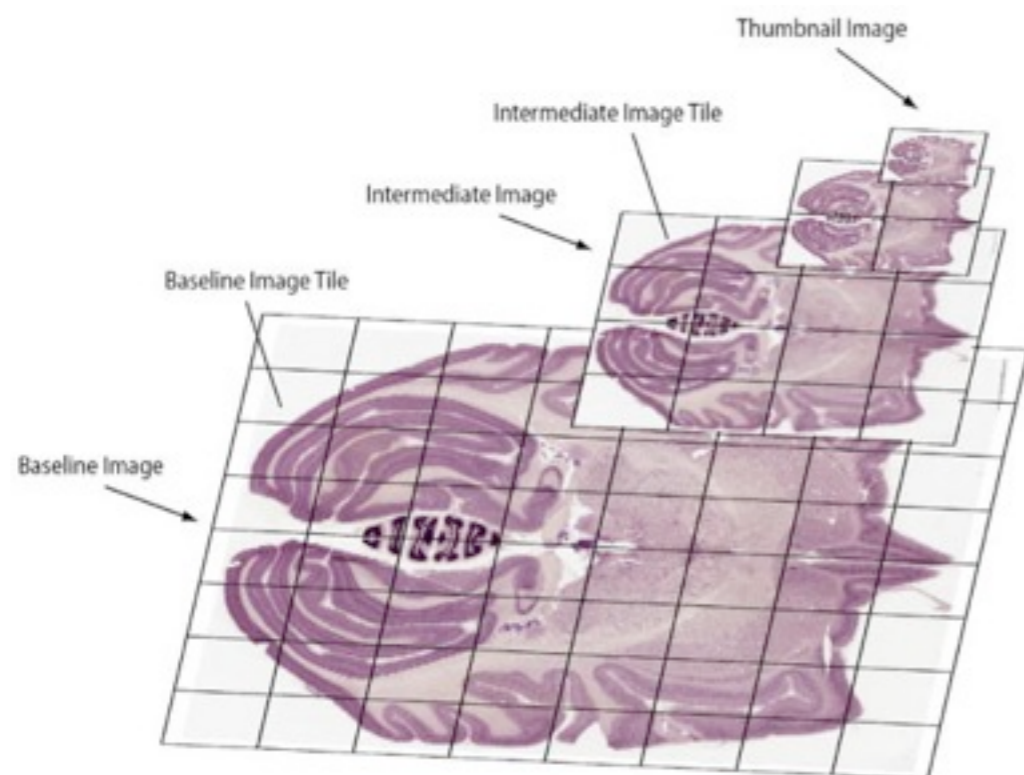


Large Image Data

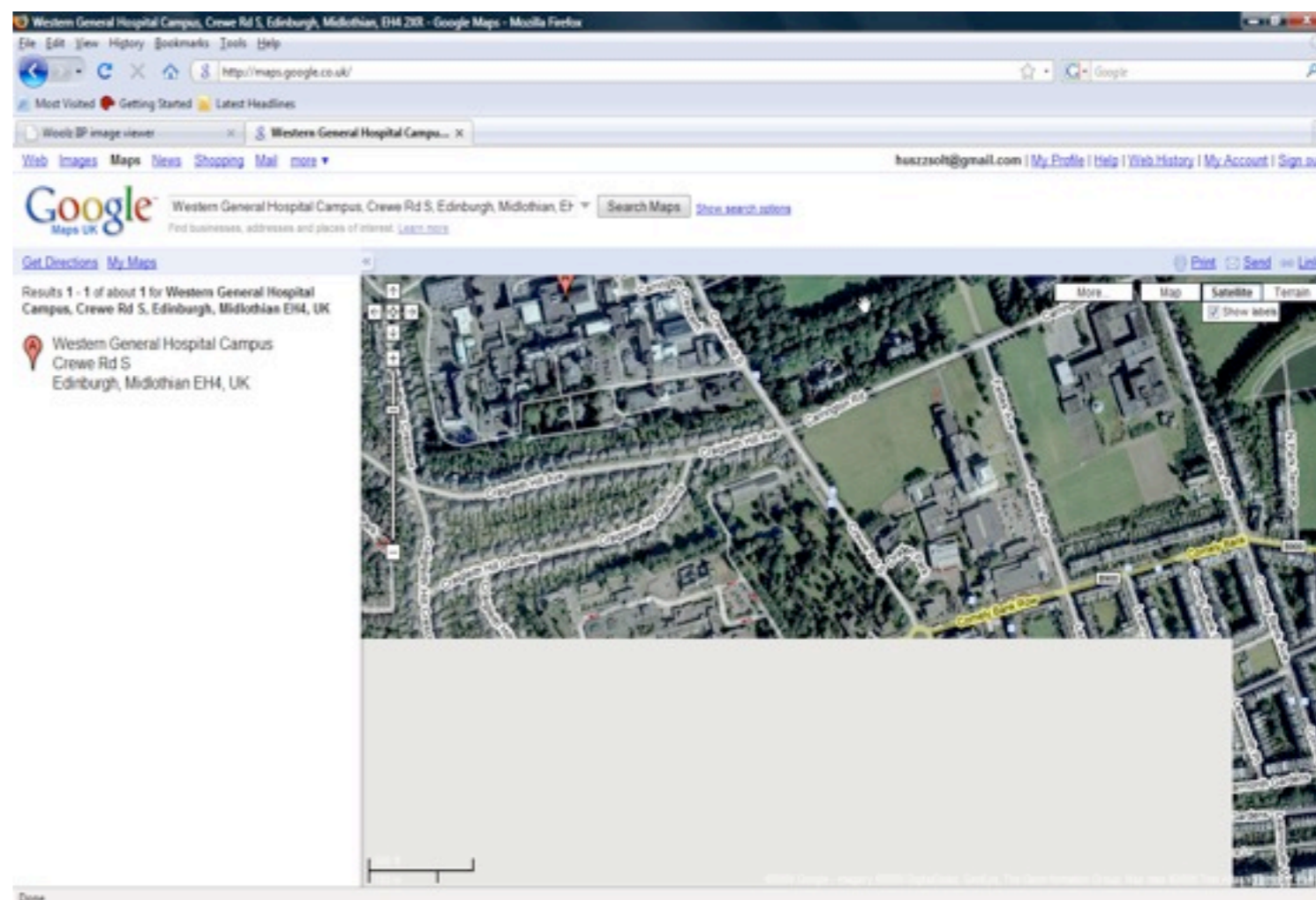
- Single reconstructions already 30+GB
- New EM embryo data ~ 0.5 TB
- OPT data - small (200MB) but many - 5K
- Typical requirement to browse as sections
- Require arbitrary angle re-sectioning

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

Tiled Image Servers



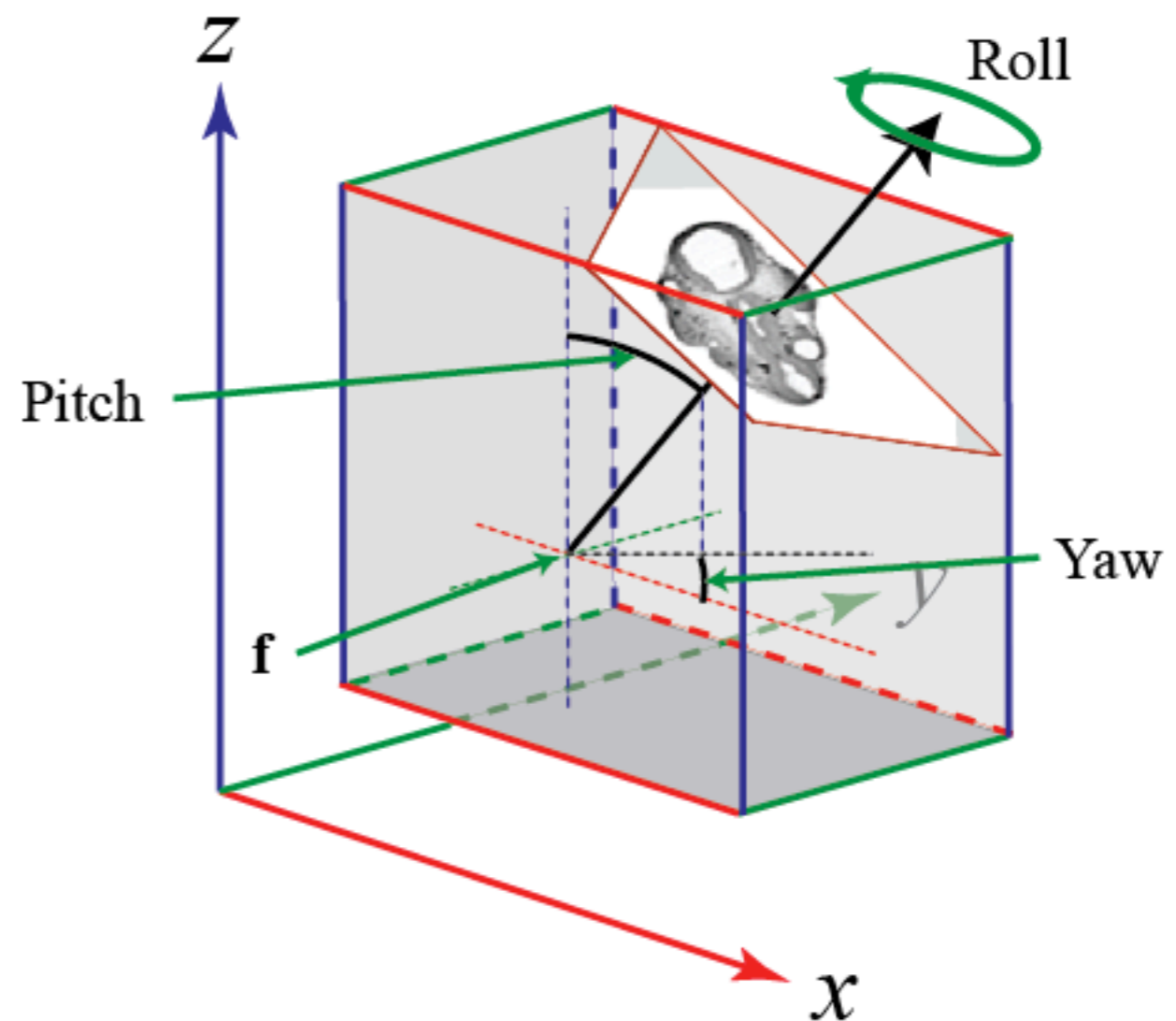
[Shawn Mikula, Issac Trotts, James M. Stone, and Edward G. Jones, Internet-Enabled High-Resolution Brain Mapping and Virtual Microscopy, Neuroimage, vol 35(1), p. 11, 2007]



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

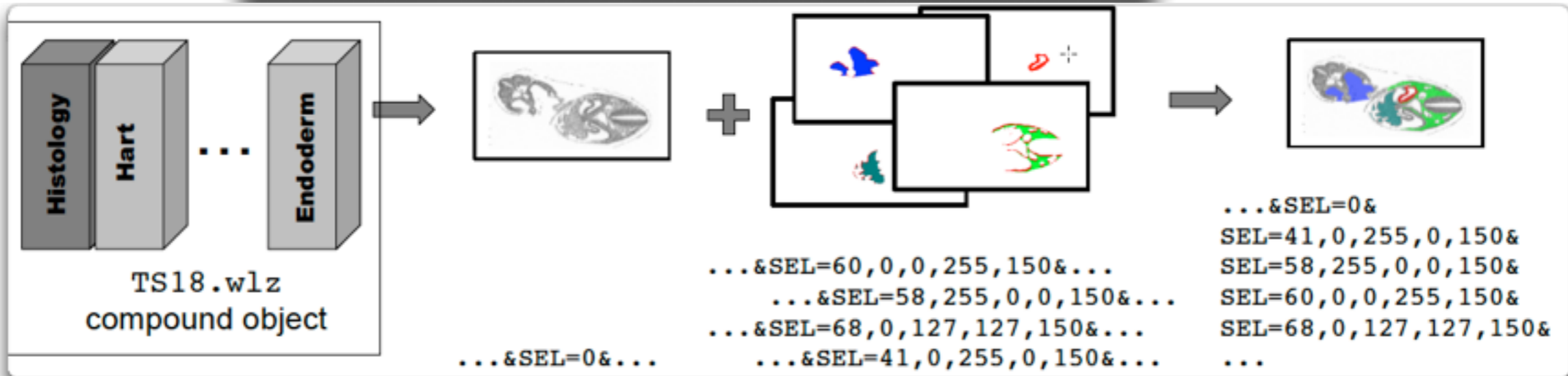
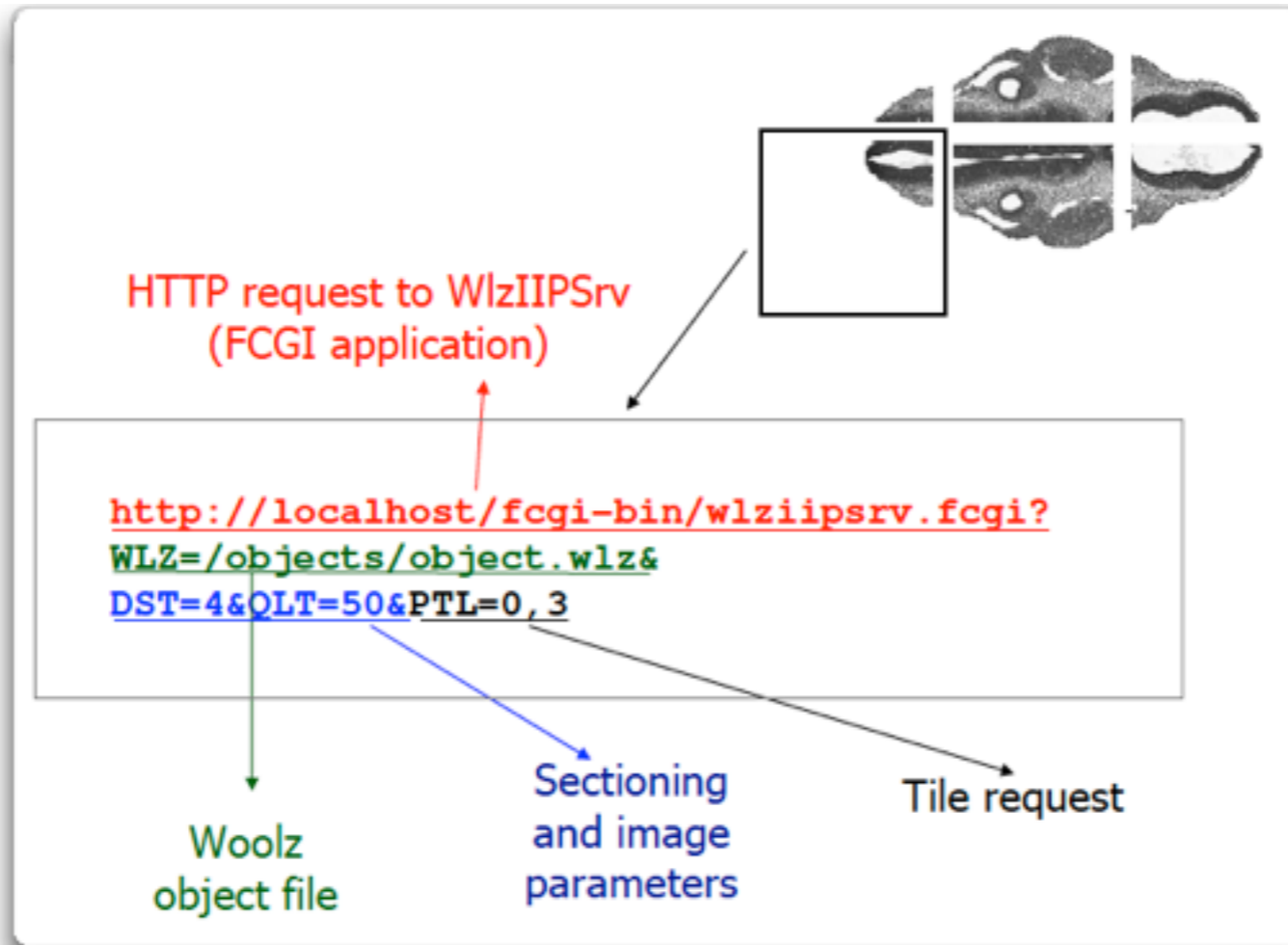
Table 1: Extended command overview

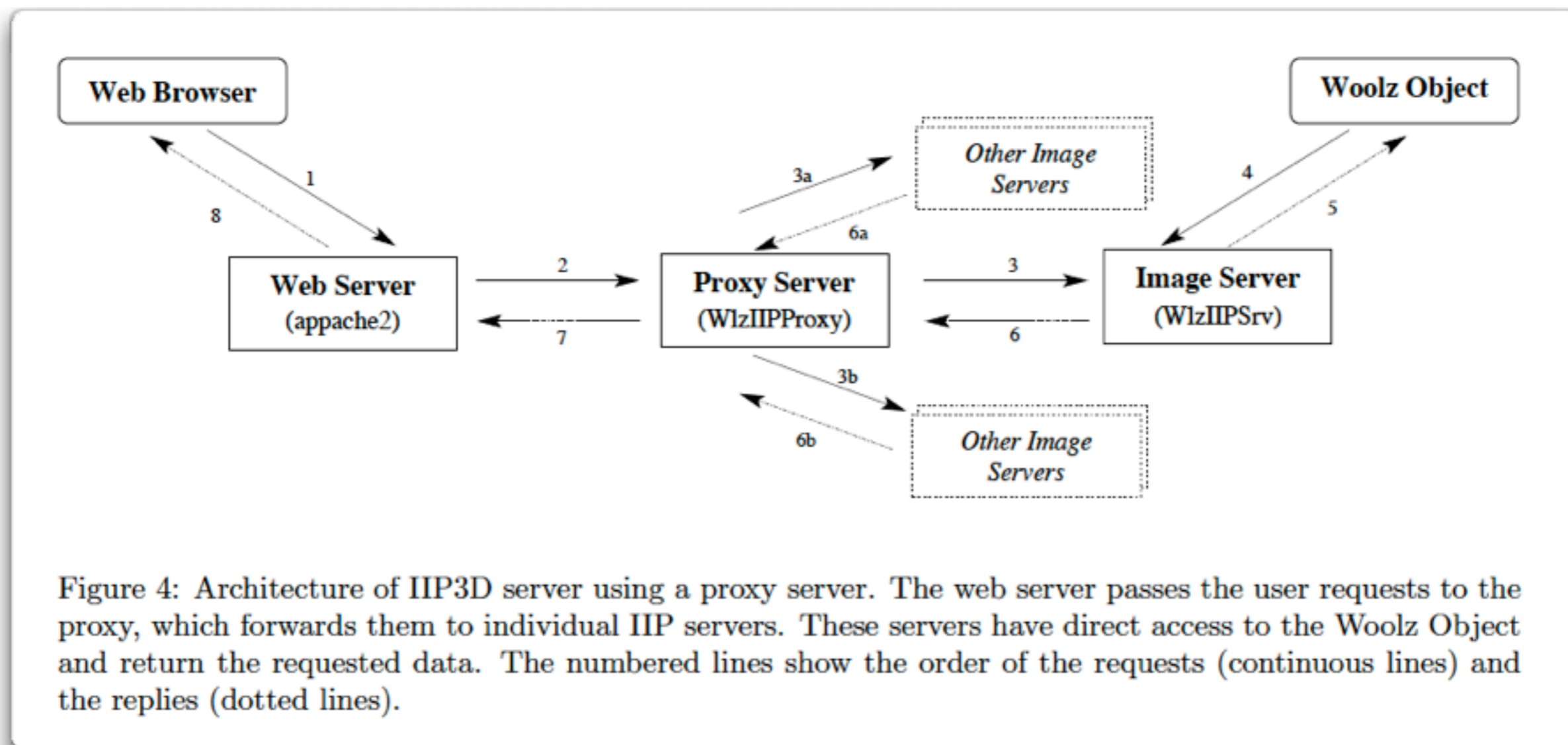
Object	Purpose
IIP-server	Identify if WLZ-IIP is running
Max-size	The size of the section
Tile-size	The size of a tile
Wlz-true-voxel-size	The voxel size of the object
Wlz-volume	The volume of the object
Wlz-distance-range	The range of the sectioning plane distance
Wlz-sectioning-angles	The pitch, yaw 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

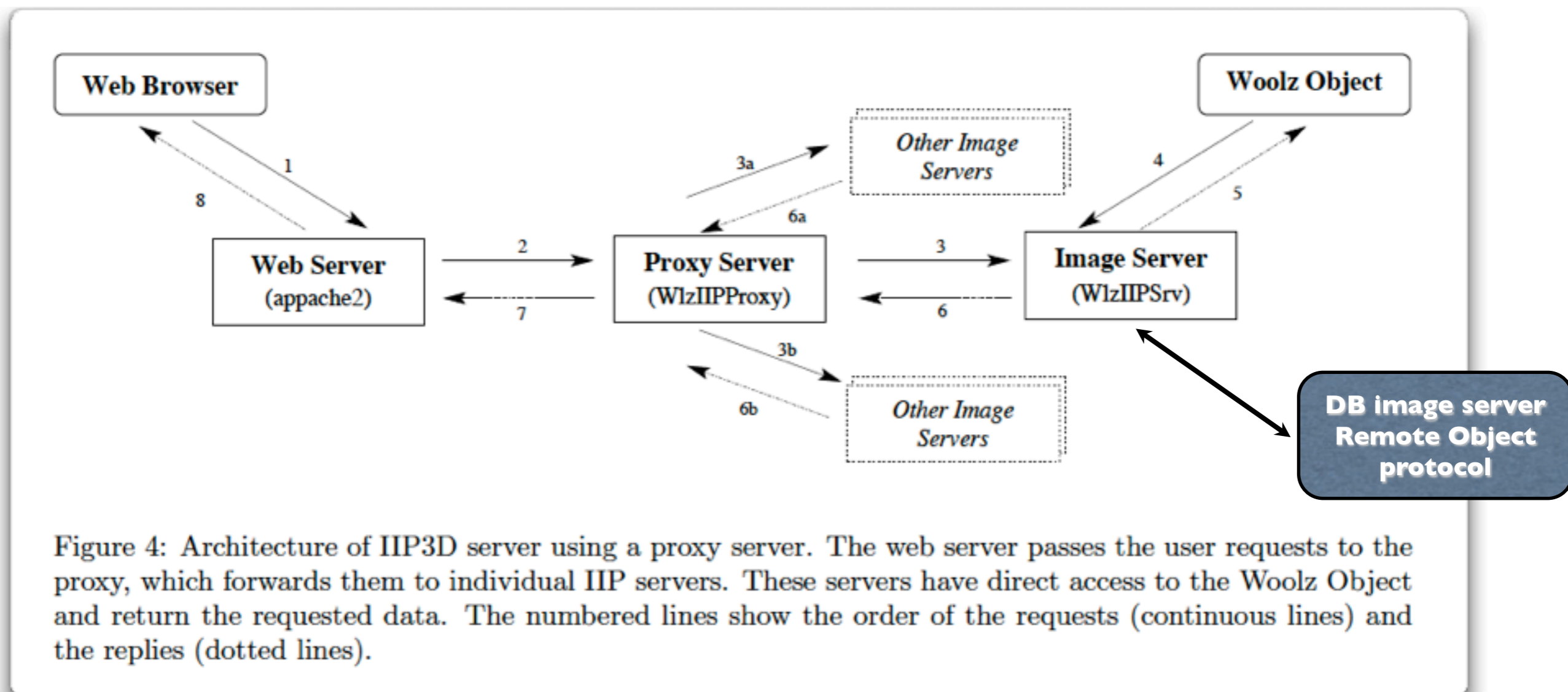
Table 2: Extended object overview



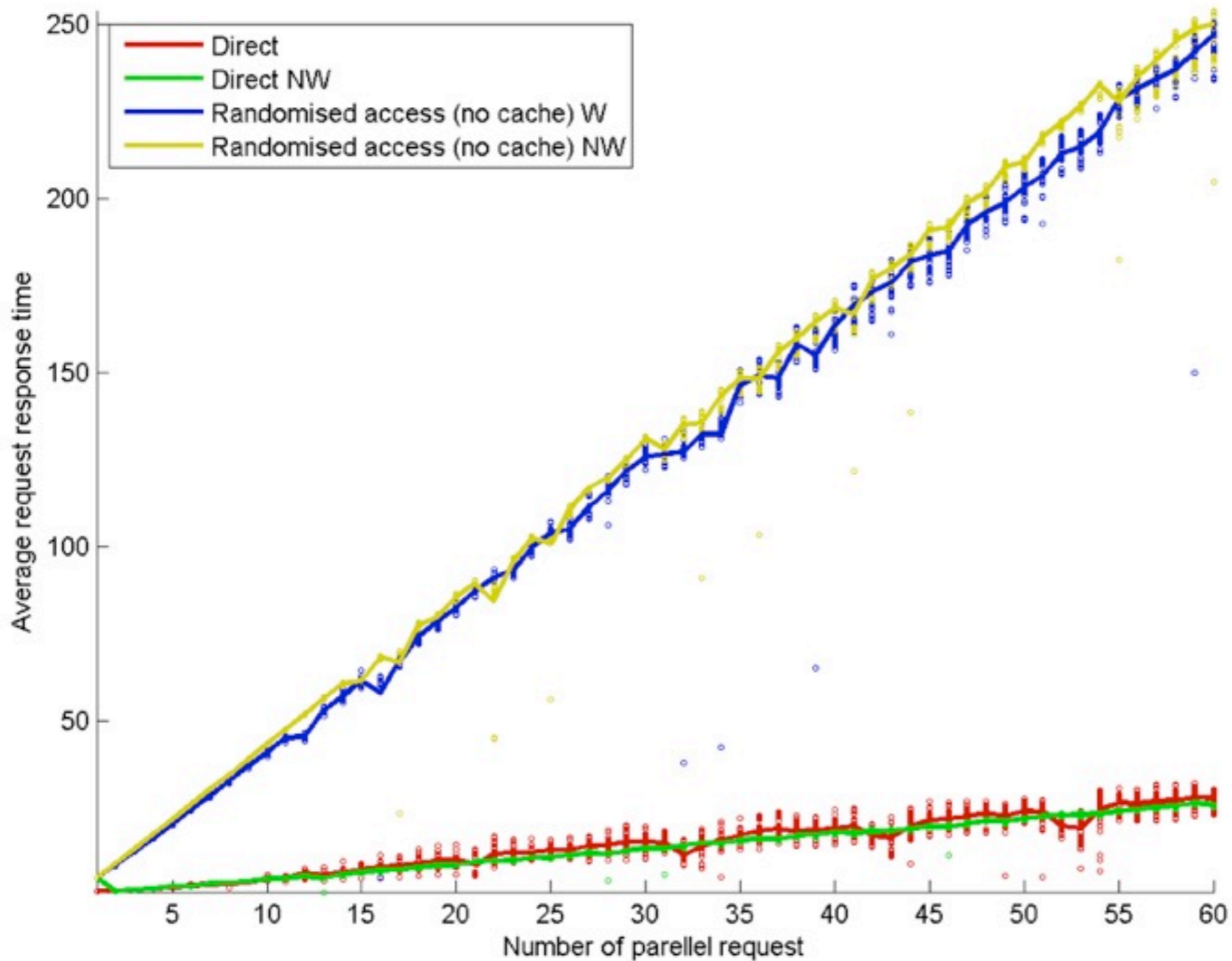
IIP3D



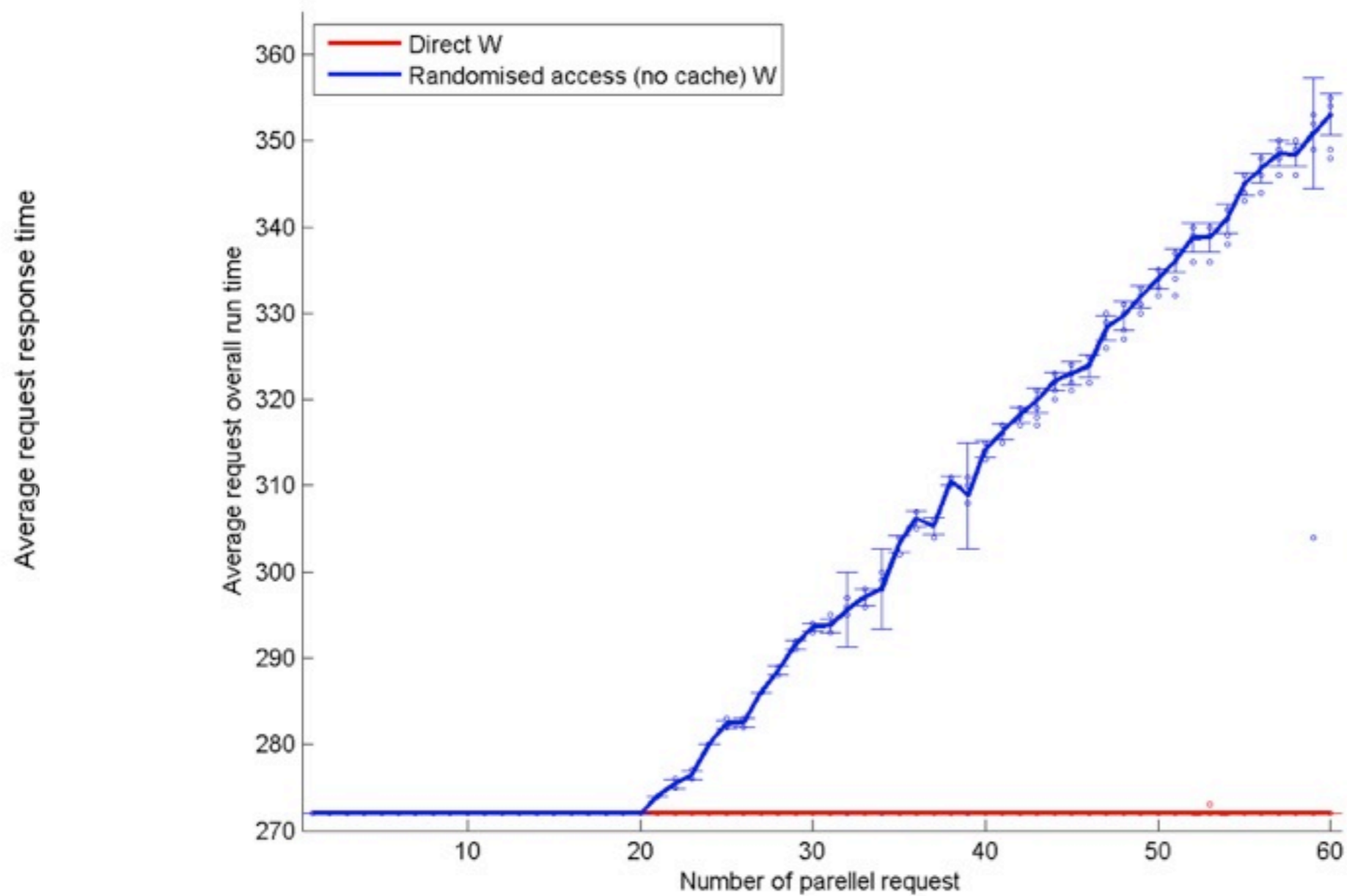




Performance



Performance



- 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
 - ▶

- Atlas models include ontology and domains - image regions for anatomical terms. Typically exclusive
- Gene-expression data, open ended, multiple overlapping patterns

Layers, Overlays & Indexed Objects

- Multiple layers via html image overlay including opacity
 - ▶ currently layers constrained to identical domains
- Regional overlays using an indexed object
 - ▶ currently using "compound object" - regions can overlap
 - ▶ TBD - standard indexed volume - regions spatially exclusive

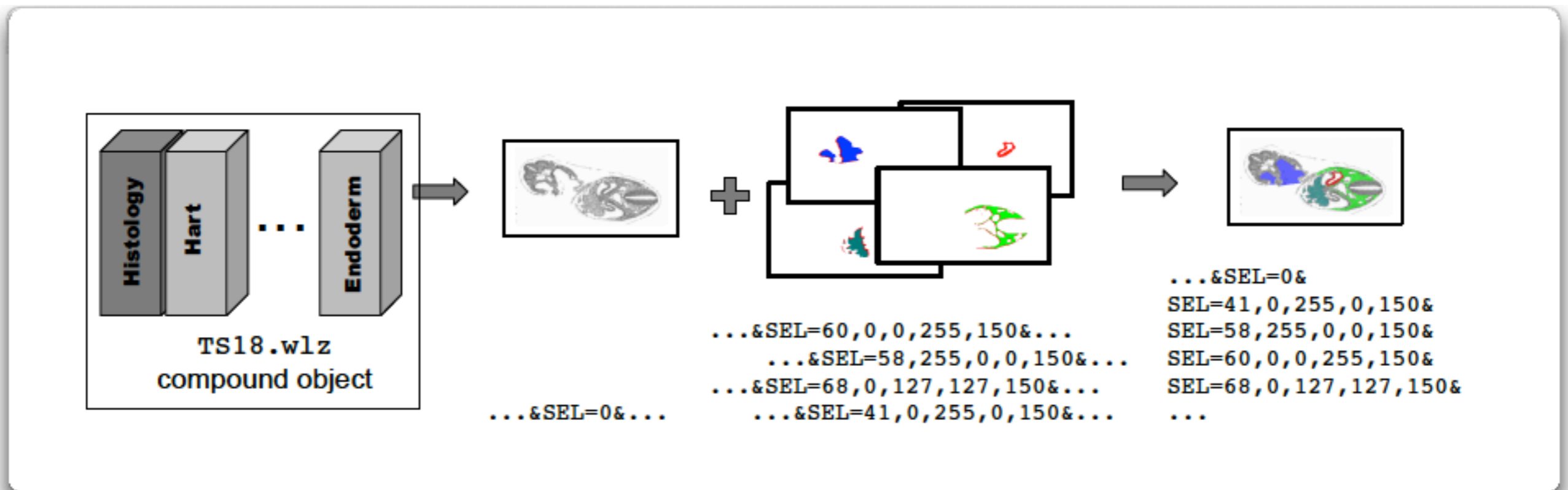


Image Processing IP3D extensions

Operator	Description
<code>diff(<i>exp,exp</i>)</code>	The difference between the two given domains.
<code>dilation(<i>exp,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,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,value,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 lt (less than), le (less than or equal), eq (equal), ge (greater than or equal) and gt (greater than).
<code>union(<i>exp list</i>)</code>	The union of the domains in the given lists.

Table 4: Descriptions of morphological operators

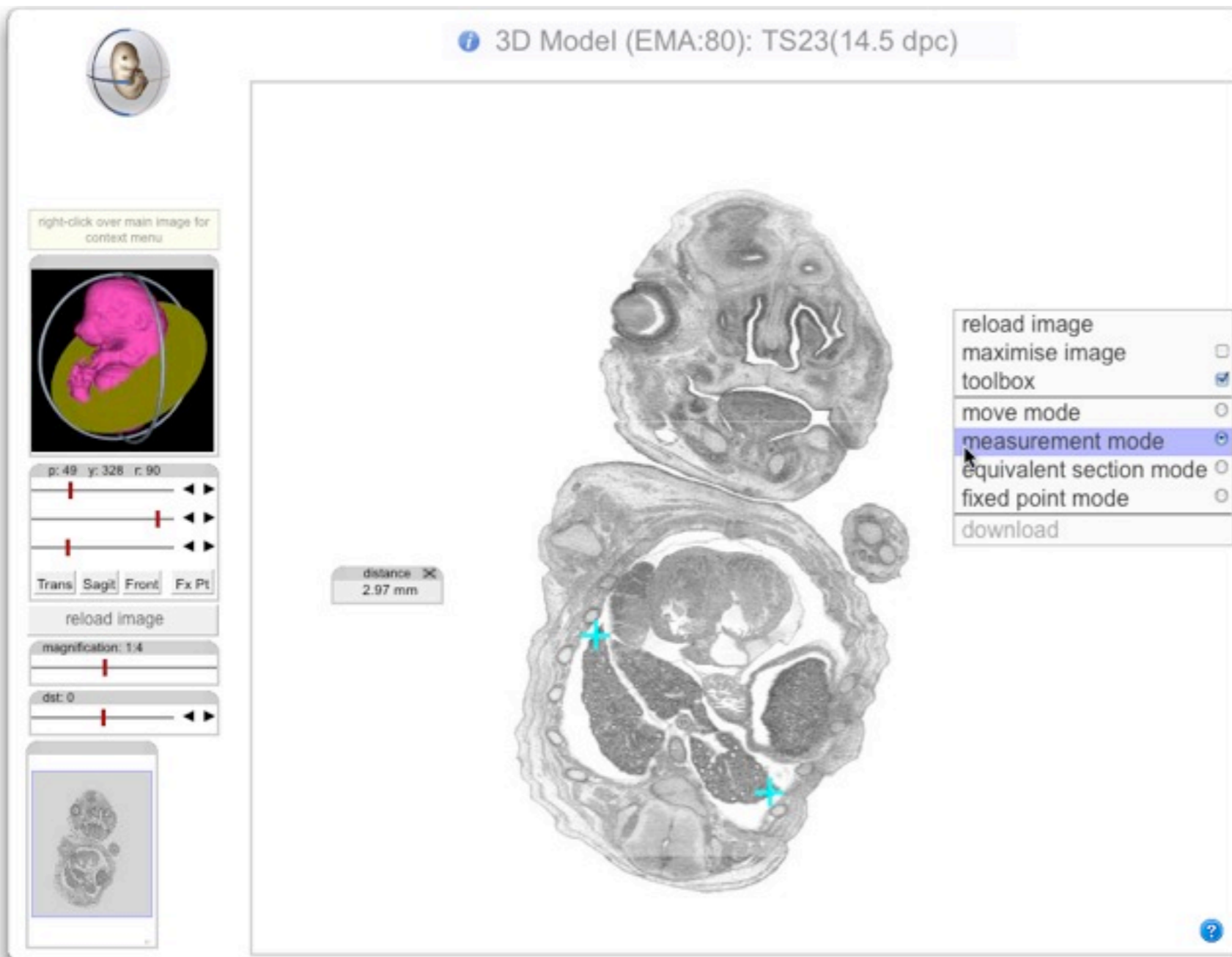
```

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.

IIP3D Examples

3D Model (EMA:80): TS23(14.5 dpc)



right-click over main image for context menu

p: 49 y: 328 r: 90

Trans Sagit Front Fx Pt

reload image

magnification: 1.4

dst: 0

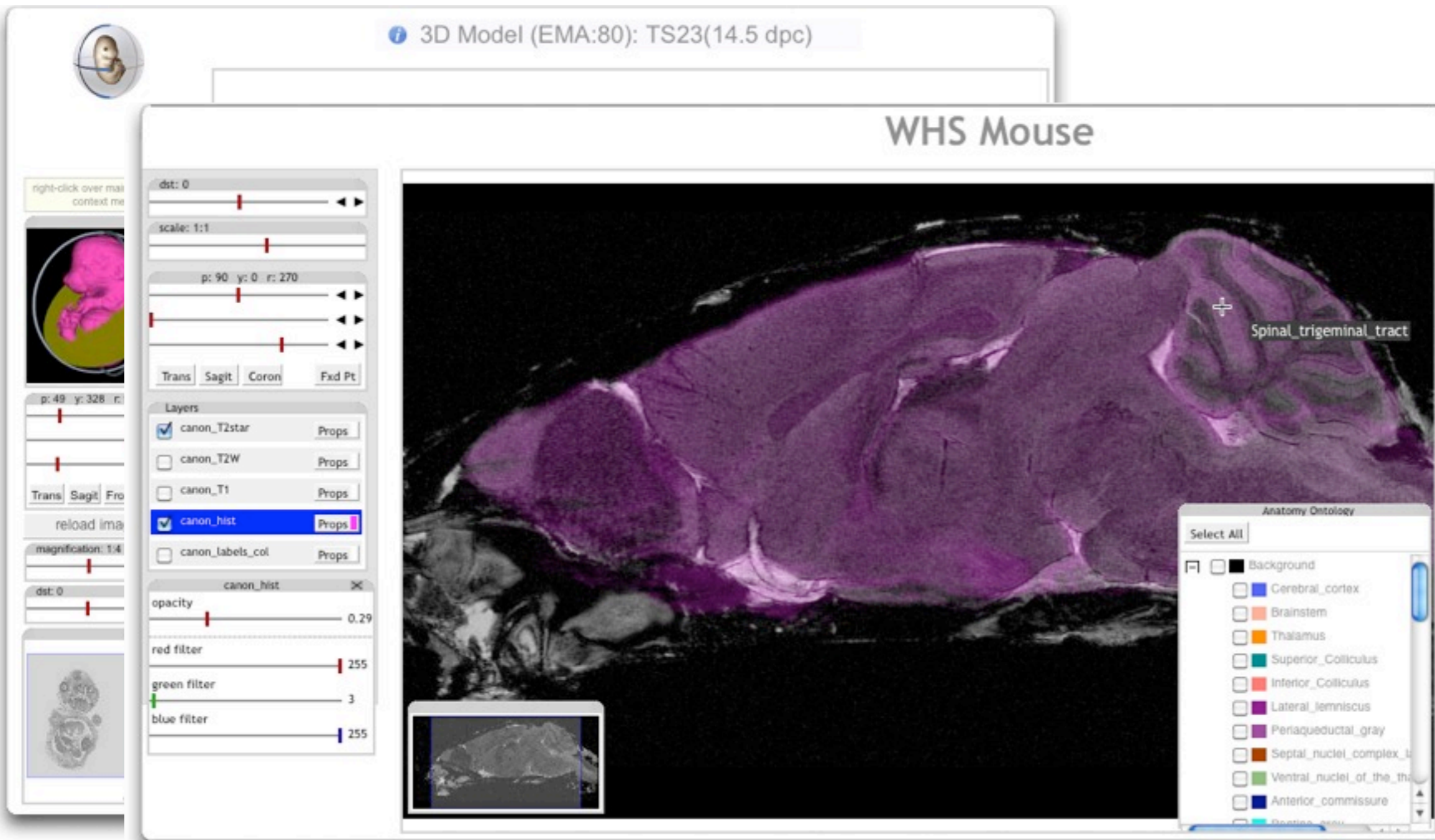
distance 2.97 mm

- reload image
- maximise image
- toolbox
- move mode
- measurement mode
- equivalent section mode
- fixed point mode
- download

IIP3D Examples

3D Model (EMA:80): TS23(14.5 dpc)

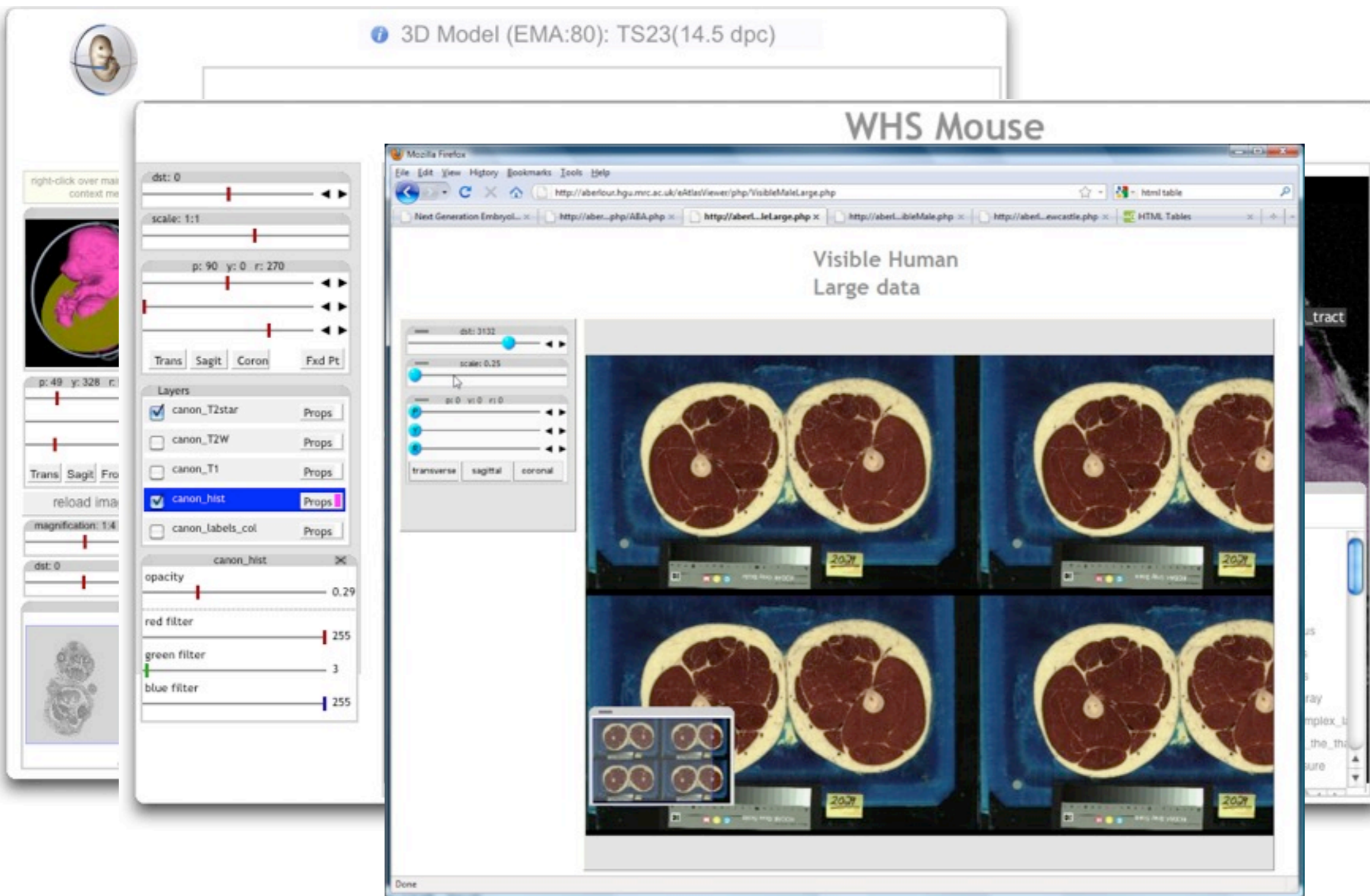
WHS Mouse



The screenshot displays the IIP3D software interface for a 3D model of a mouse brain. The main window shows a purple-colored brain slice with a label 'Spinal_trigeminal_tract' pointing to a specific region. The interface includes several control panels:

- Navigation and View Controls:** Sliders for 'dst: 0', 'scale: 1:1', and coordinates 'p: 90 y: 0 r: 270'. View mode buttons for 'Trans', 'Sagit', 'Coron', and 'Fxd Pt' are present.
- Layers Panel:** A list of layers with checkboxes and 'Props' buttons:
 - canon_T2star
 - canon_T2W
 - canon_T1
 - canon_hist
 - canon_labels_col
- Filtering Panel:** Controls for the 'canon_hist' layer, including 'opacity' (0.29), 'red filter' (255), 'green filter' (3), and 'blue filter' (255).
- Anatomy Ontology Panel:** A list of anatomical structures with checkboxes:
 - Background
 - Cerebral_cortex
 - Brainstem
 - Thalamus
 - Superior_Colliculus
 - Inferior_Colliculus
 - Laterallemniscus
 - Periaqueductal_gray
 - Septal_nuclei_complex
 - Ventral_nuclei_of_the_thalamus
 - Anterior_commissure


IIP3D Examples



The screenshot displays the Emap 3D Model viewer interface. At the top, a tab shows "3D Model (EMA:80): TS23(14.5 dpc)". The main window is titled "WHS Mouse" and contains a browser window with the URL "http://aberfour.hgu.mrc.ac.uk/eAtlasViewer/php/VisibleMaleLarge.php". The browser window displays "Visible Human Large data" and shows four MRI slices of a mouse brain in a 2x2 grid. The interface includes various controls: a "Layers" panel on the left with checkboxes for "canon_T2star", "canon_T2W", "canon_T1", "canon_hist" (checked), and "canon_labels_col"; a "Trans Sagit Coronal" view selector; and a "Filters" panel with sliders for "opacity", "red filter", "green filter", and "blue filter". The browser window also has its own control panel with sliders for "dst: 3132", "scale: 0.25", and "p: 0 y: 0 r: 0", along with "transverse", "sagittal", and "coronal" view options.

IIP3D Examples

3D Model (EMA:80): TS23(14.5 dpc)



right-click over main image for context menu


p: 49 y: 328 r: 0

Trans Sagit Fro

reload ima

magnification: 1:4

dst: 0



dst: 0

scale: 1:1

p: 90 y: 0 r: 270

Trans Sagit Coron Fxd Pt

Layers

- canon_T2star Props
- canon_T2W Props
- canon_T1 Props
- canon_hist Props
- canon_labels_col Props

opacity 0.29


red filter 255

green filter 3

blue filter 255

WHS Mouse

Electronic Atlas of the Developing Human Brain CS17



Right-click over main image for context menu & more options

dst: 0

magnification: 1:1

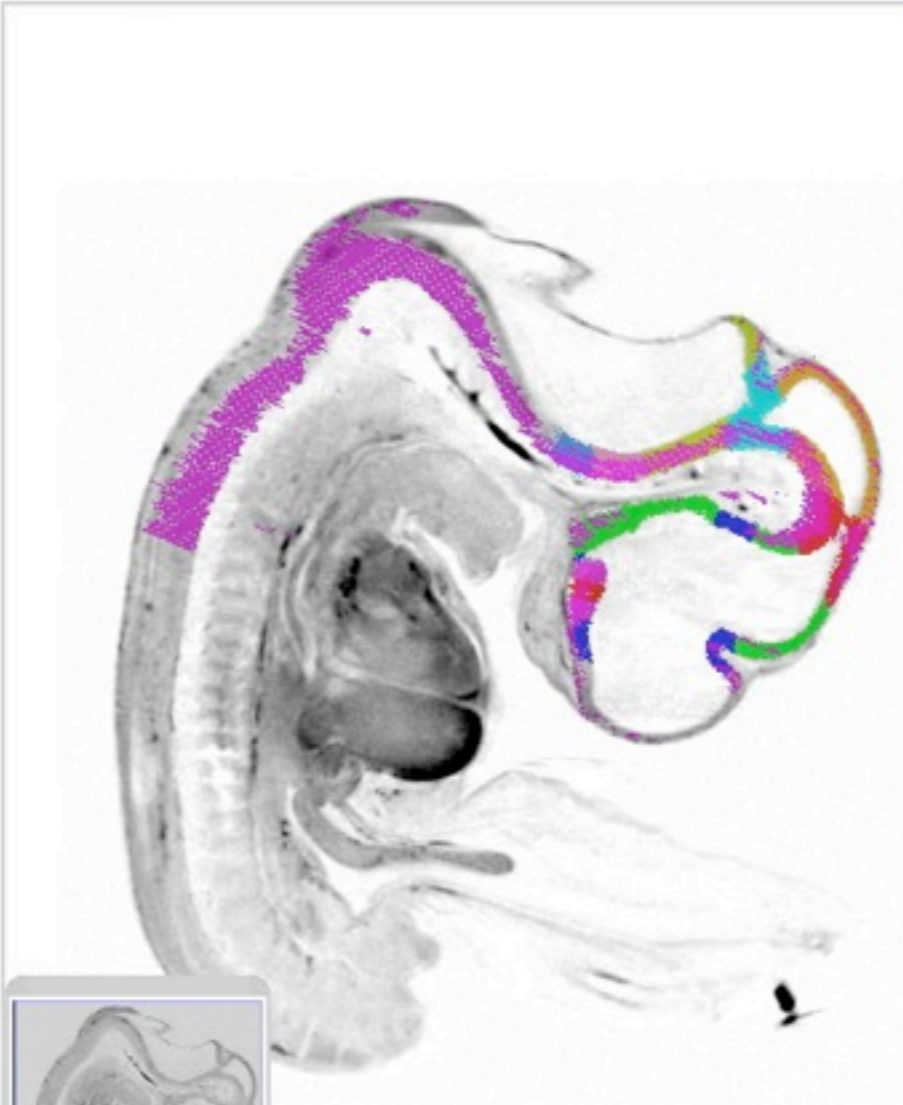
p: 90 y: 90 r: 90

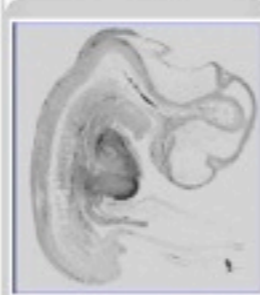
Trans Sagit Front Fx Pt

reload image

Layers

- reference Props
- overlay Props





Anatomy Ontology

Select All

- LGE
- Mesencephalon
- MGE
- DRG
- ear
- eye
- heart
- liver
- p1
- p2
- p3
- Pallium
- POA
- r0
- r1
- r2
- r3
- r4
- r5
- r6
- r7-r11
- spinal_cord
- genes
 - BT_strong
 - BT_weak
 - GAP43_strong
 - GAP43_weak
 - MAP2_strong
 - MAP2_weak
 - PAX6

- IIP3D viewer extension to 3D visualisation
 - ▶ Use X3Dom - Javascript binding to X3D
- navigation feedback
- Anatomy visualisation
 - ▶ see demo

- Extend to 4D

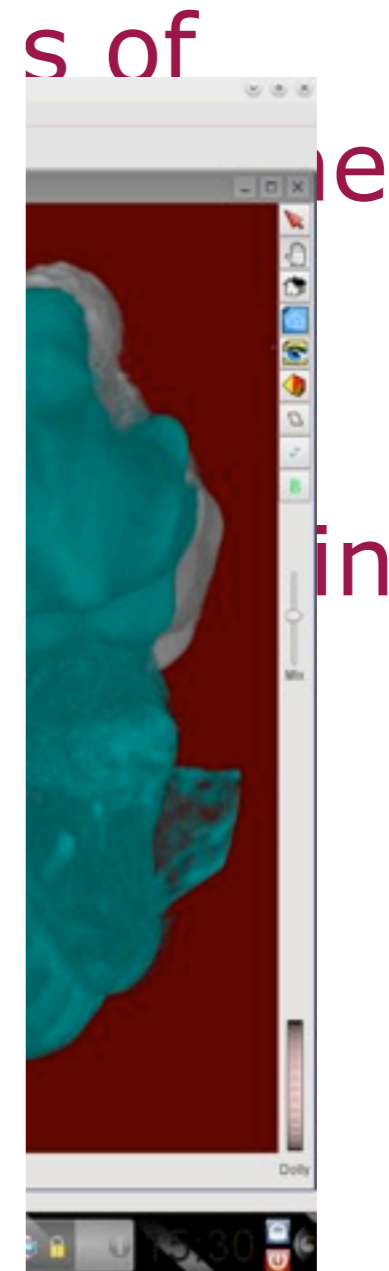
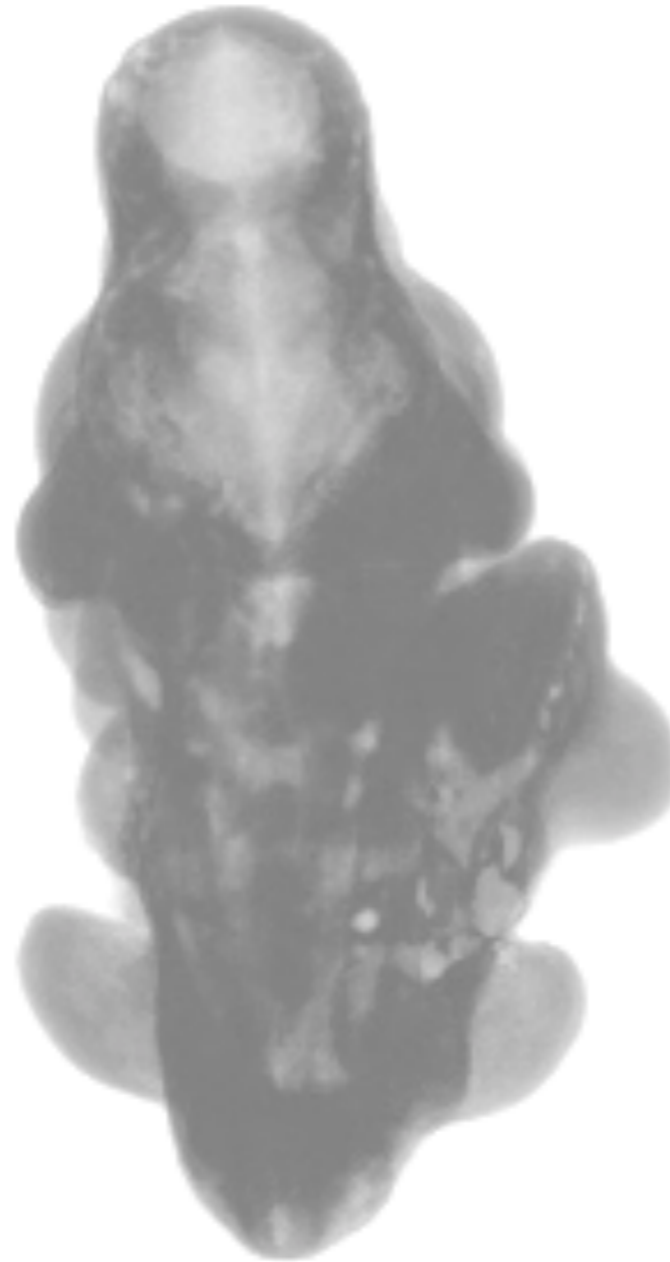
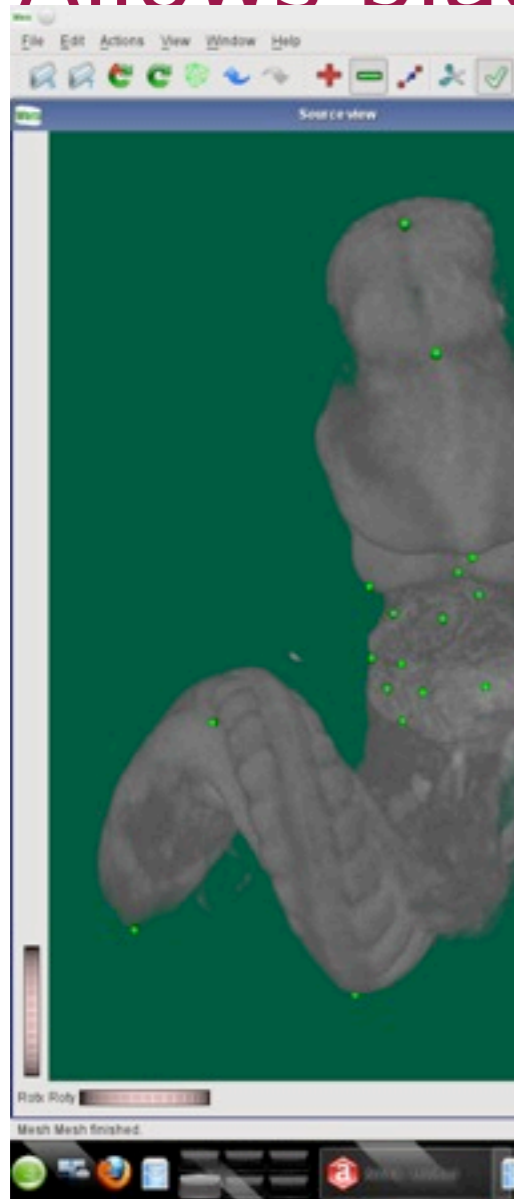


3D mapping - WizWarp

- 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!)

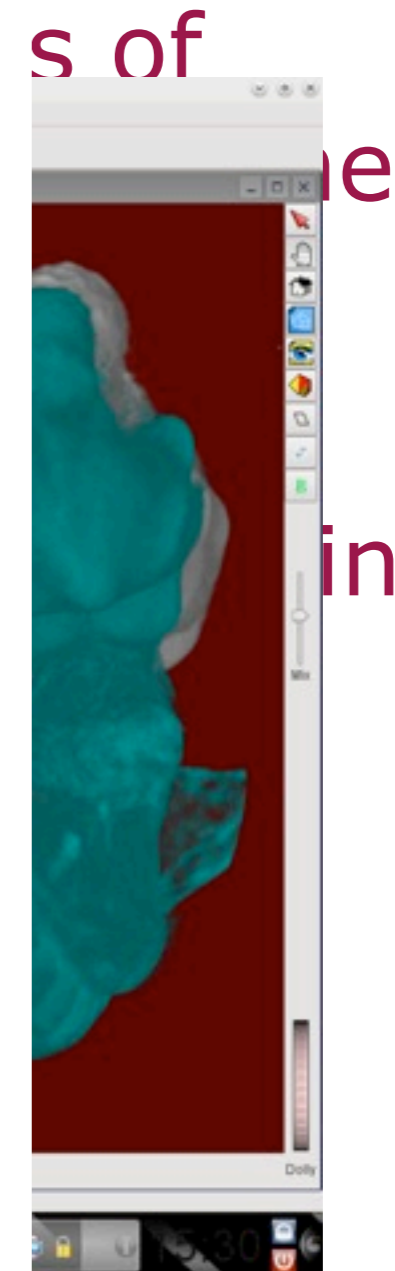
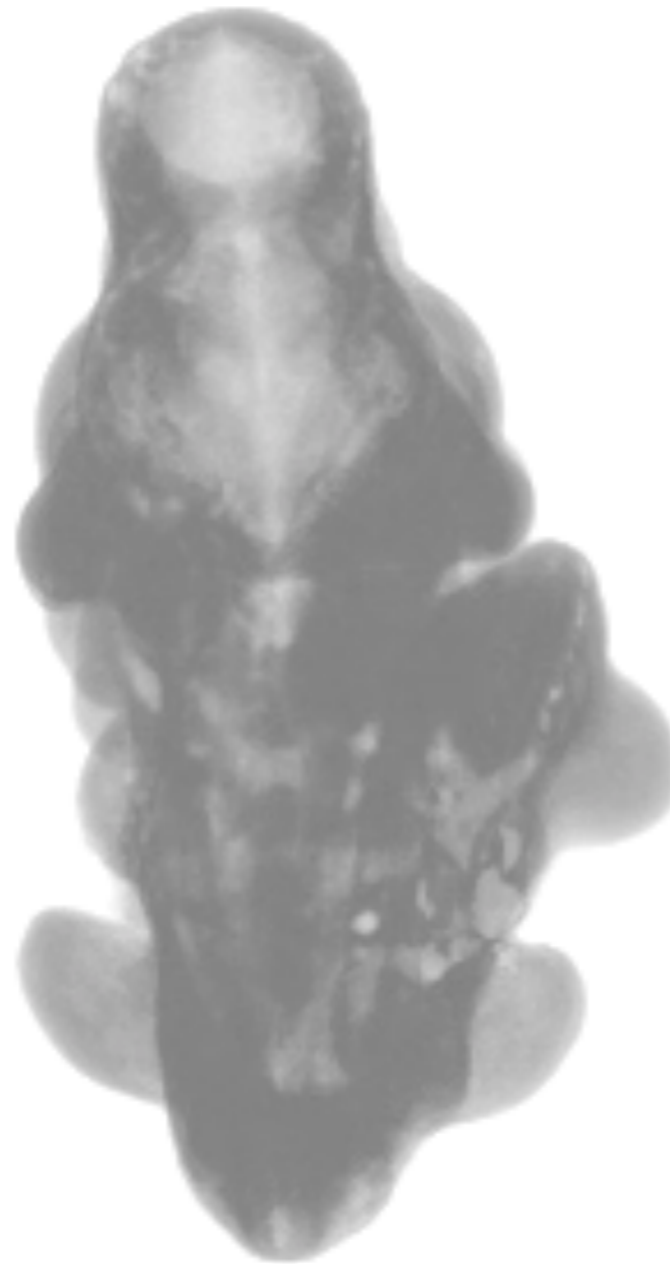
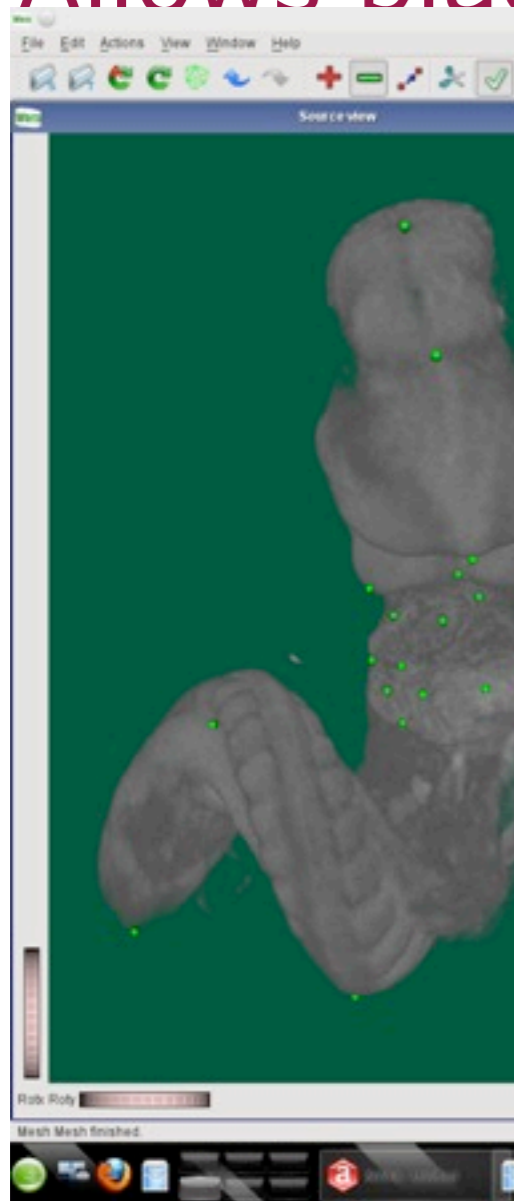
3D mapping - WlzWarp

- Allows placement of **Wnt1**



3D mapping - WlzWarp

- Allows placement of **Wnt1**



- Embryo development 7-5-8.5 dpc
- 11-fold growth of ectoderm cell layer
- complex folding
- lineage clones via HRP cell labelling (iontophoresis)
- pattern recognition very difficult
- conformal transform of ectodermal surface to “flat-map”



Lineage & the Brain

A Camus, K Lawson, W Hill et al
Development 2011



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Development 2011



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