Principles of Signal Whitening Fourier Transform (SWIFT) Image Registration

Art Wetzel

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SEM image sets from connectomics collaborators…

Jeff Lichtman and Josh Morgan
The Center for Brain Science, Harvard

Florian Engert and David Hildebrand
Molecular and Cellular Biology, Harvard

Contents:

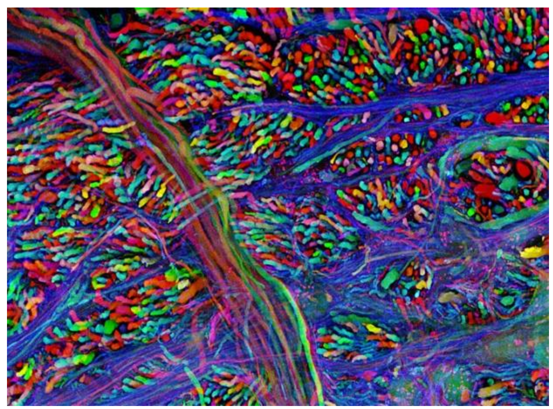
- Background on connectomics, SEM & collaborations
- Approaches to the EM registration problem
- Signal whitening & fourier transform concepts
- Main software components
- Examples
- Future

Sebastian Seung and Jeff Lichtman definition of Connectomics

"an emerging field defined by high-throughput generation of data about neural connectivity, and subsequent mining of that data for knowledge about the brain. A *connectome* is a summary of the structure of a neural network, an annotated list of all synaptic connections between the neurons inside a brain or brain region."

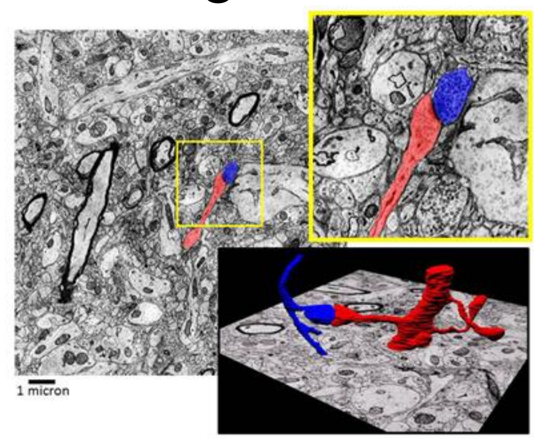
DTI "tractography" Human Connectome Project at MRI 2 mm resolution

~10 MB/volume
1.3×10^6 mm^3



"Brainbow" stained neuropil at 300 nm optical resolution

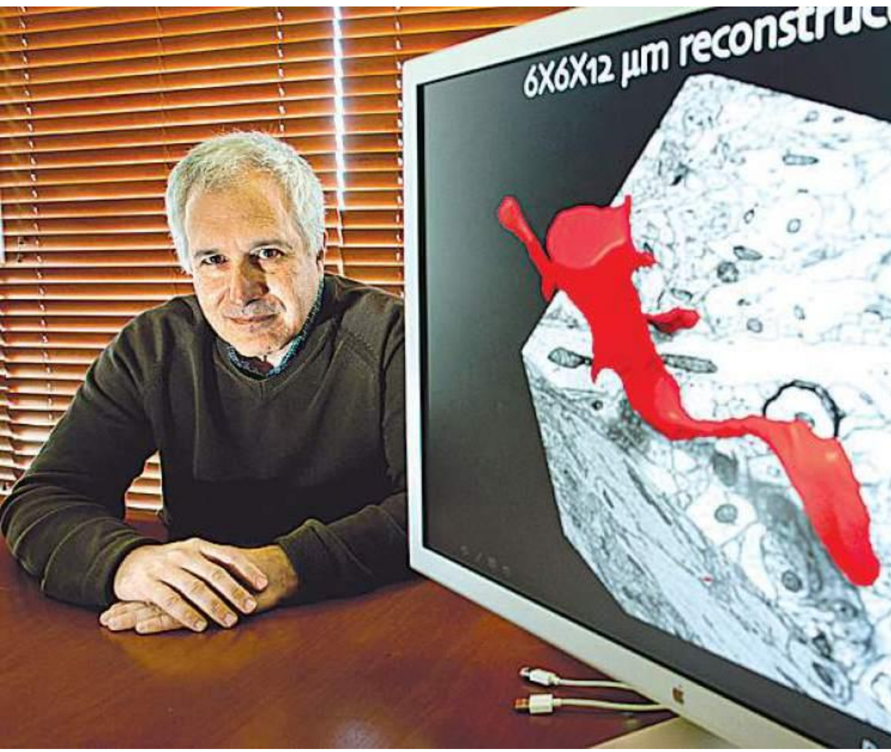
~10 GB/mm^3



Serial section electron microscopy reconstruction at 3-4 nm resolution

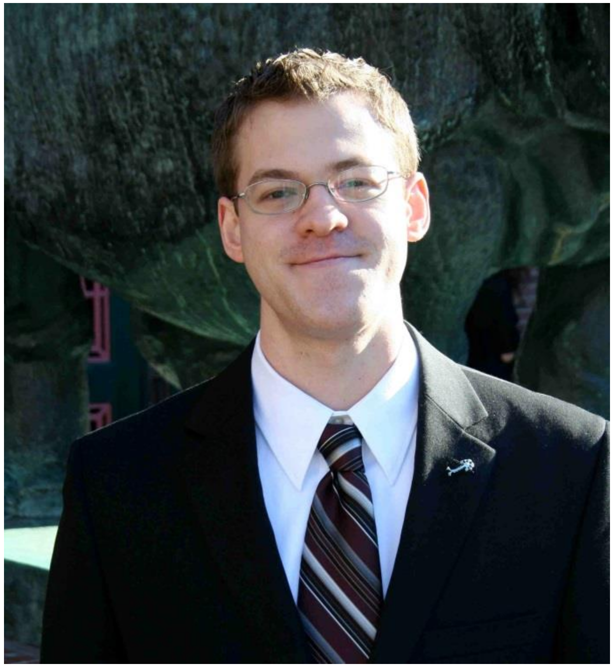
~1 PB/mm^3

Mouse brain studies with Jeff Lictman and Josh Morgan



zebrafish studies with Florian Engert and David Hildebrand

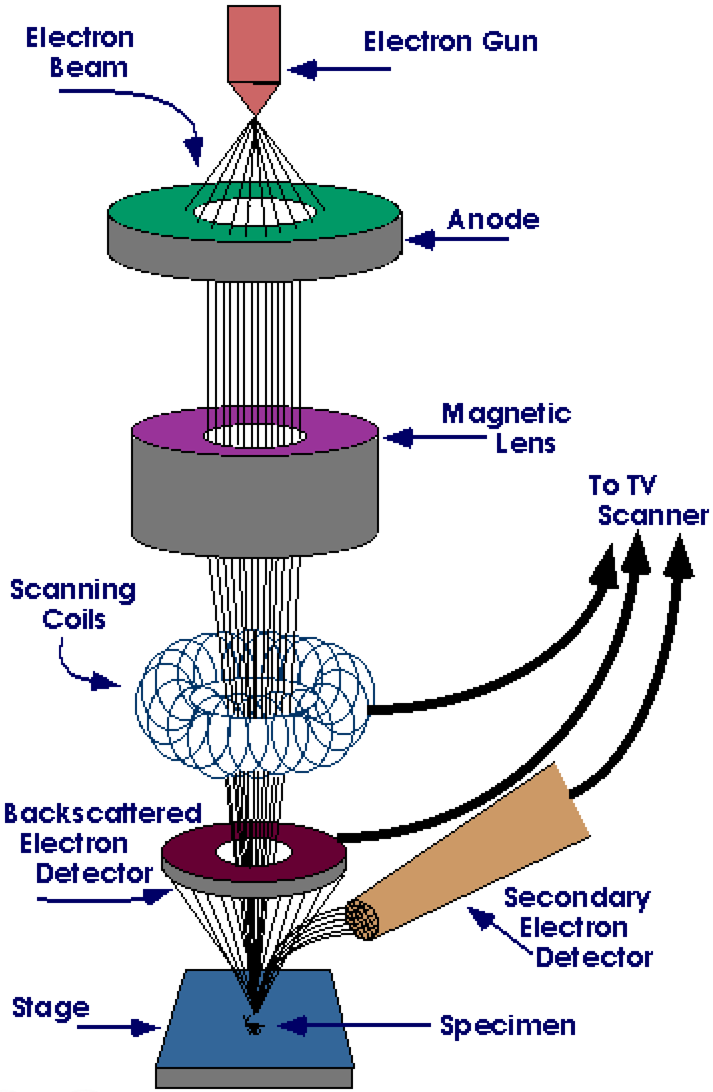
The picture shows a micrograph of a transgenic larval zebrafish with pan-neuronal GCaMP2 expression. *(potential cover art)*



ENGERT LAB

Harvard University | Department of Molecular and Cellular Biology

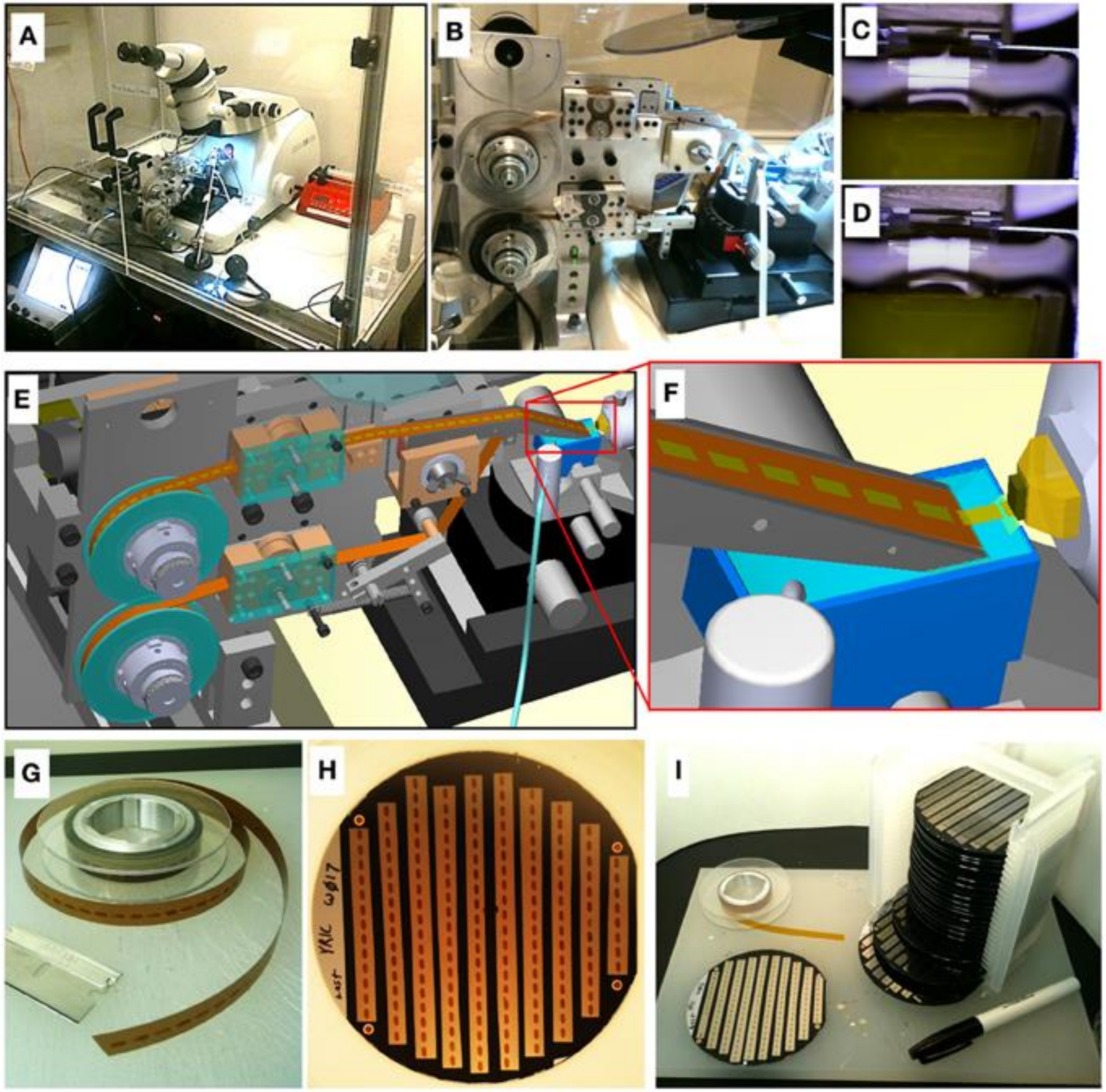
Scanning EM will be the first to capture petascale datasets



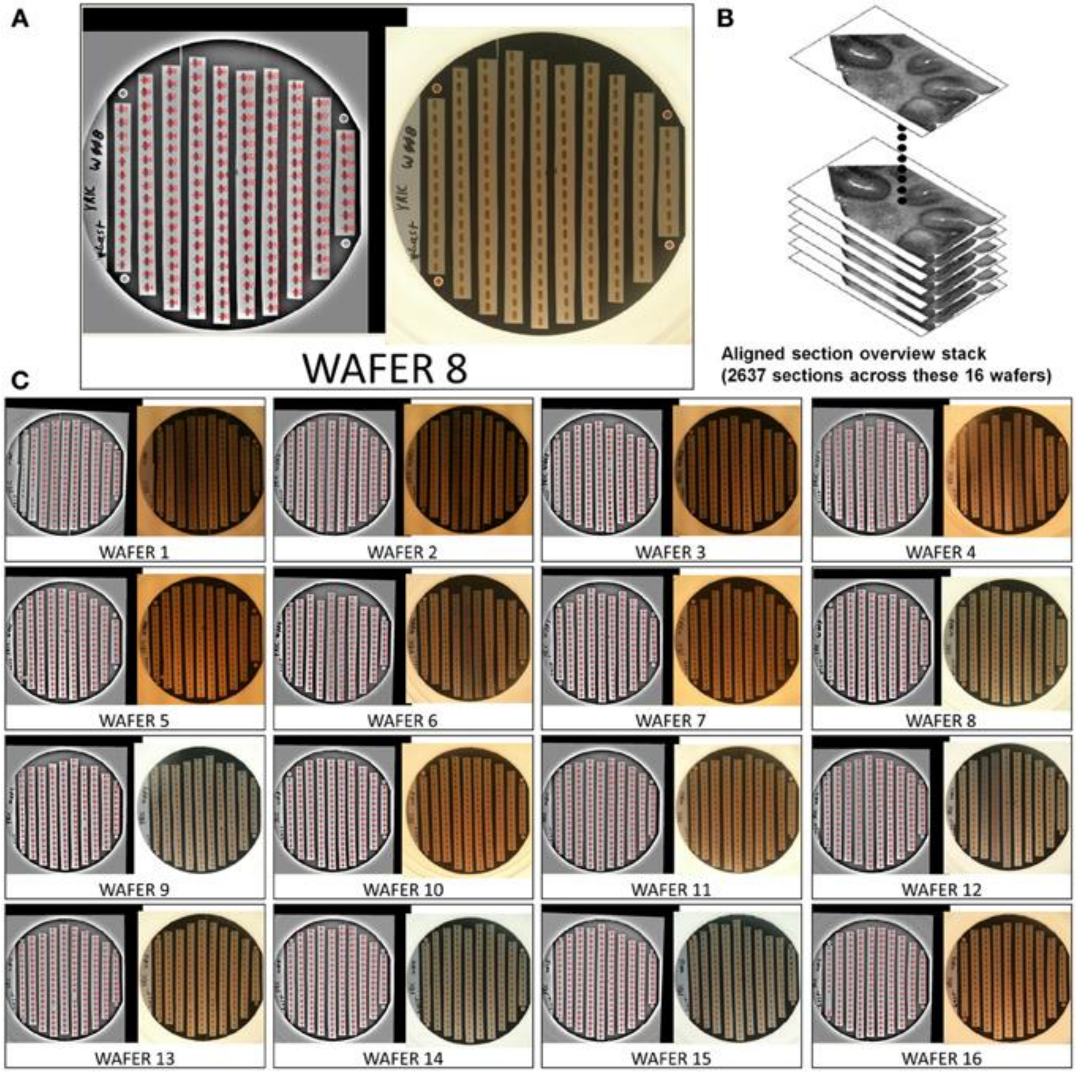
Recent description of automated sectioning and SEM methods

- Hayworth K.J., Morgan J.L., Schalek R., Berger D.R., Hildebrand D.G.C. and Lichtman J.W. (2014) Imaging ATUM ultrathin section libraries with WaferMapper: a multi-scale approach to EM reconstruction of neural circuits. *Front. Neural Circuits* **8**:68. doi: 10.3389/fncir.2014.00068

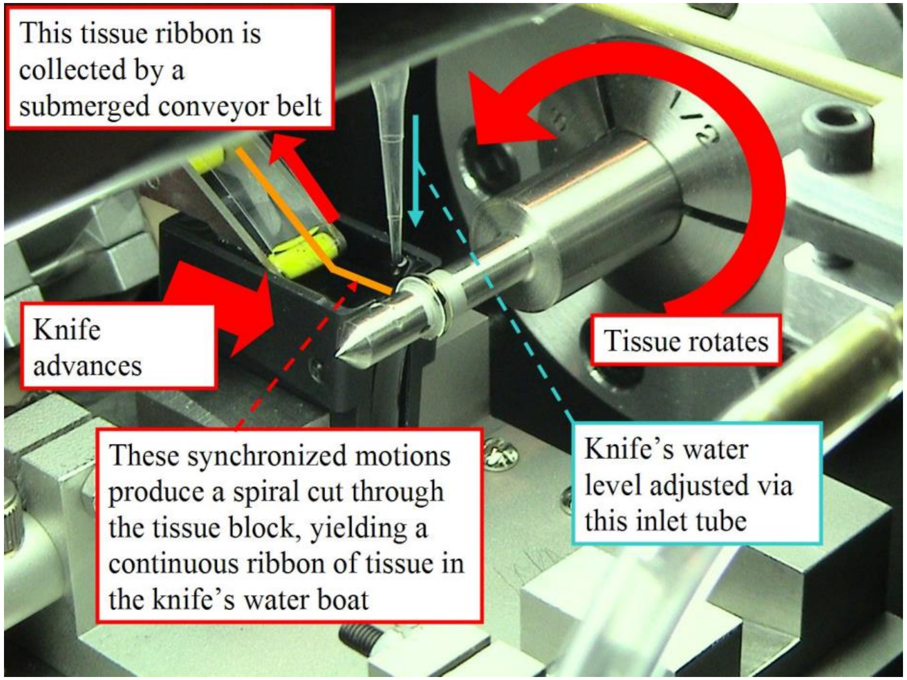
From: Imaging ATUM ultrathin section libraries with WaferMapper



Hundreds of sections per wafer with many wafers in large datasets



Petascale connectomics will need accelerated sectioning, imaging, registration, analysis and simplified world-wide data sharing



Lichtman's team at Harvard has developed the automated tape collecting Ultramicrotome (ATLUM) and will deploy a 61-beam 1 Gpixel/sec SEM in 2014.

Quote from: Imaging ATUM ultrathin section libraries with WaferMapper: a multi-scale approach to EM reconstruction of neural circuits by Kenneth J. Hayworth, Josh L. Morgan, Richard Schalek, Daniel R. Berger, David G. C. Hildebrand and Jeff W. Lichtman

Stitching and Alignment

Small EM volumes (<1 terabyte) can be aligned on a powerful desktop computer using publicly available alignment software such as the registration plugins for Fiji (Schindelin et al.,2012). However, the stitching and alignment of high resolution images becomes increasingly difficult as data sets become larger. The computational power required to manipulate and process terabytes of images requires hardware that is not standard in most labs and, while most steps in alignment are amenable to parallelization, running these steps in parallel often requires changes in code and expertise in managing clusters. Because of these problems, aligning multi-terabyte datasets is currently being done by only a few groups. However, the recent production of many multi-terabyte EM volumes has spurred efforts to scale up alignment tools to make it easier for the broader research community to turn hundreds of terabytes of EM images into usable 3D tissue maps.

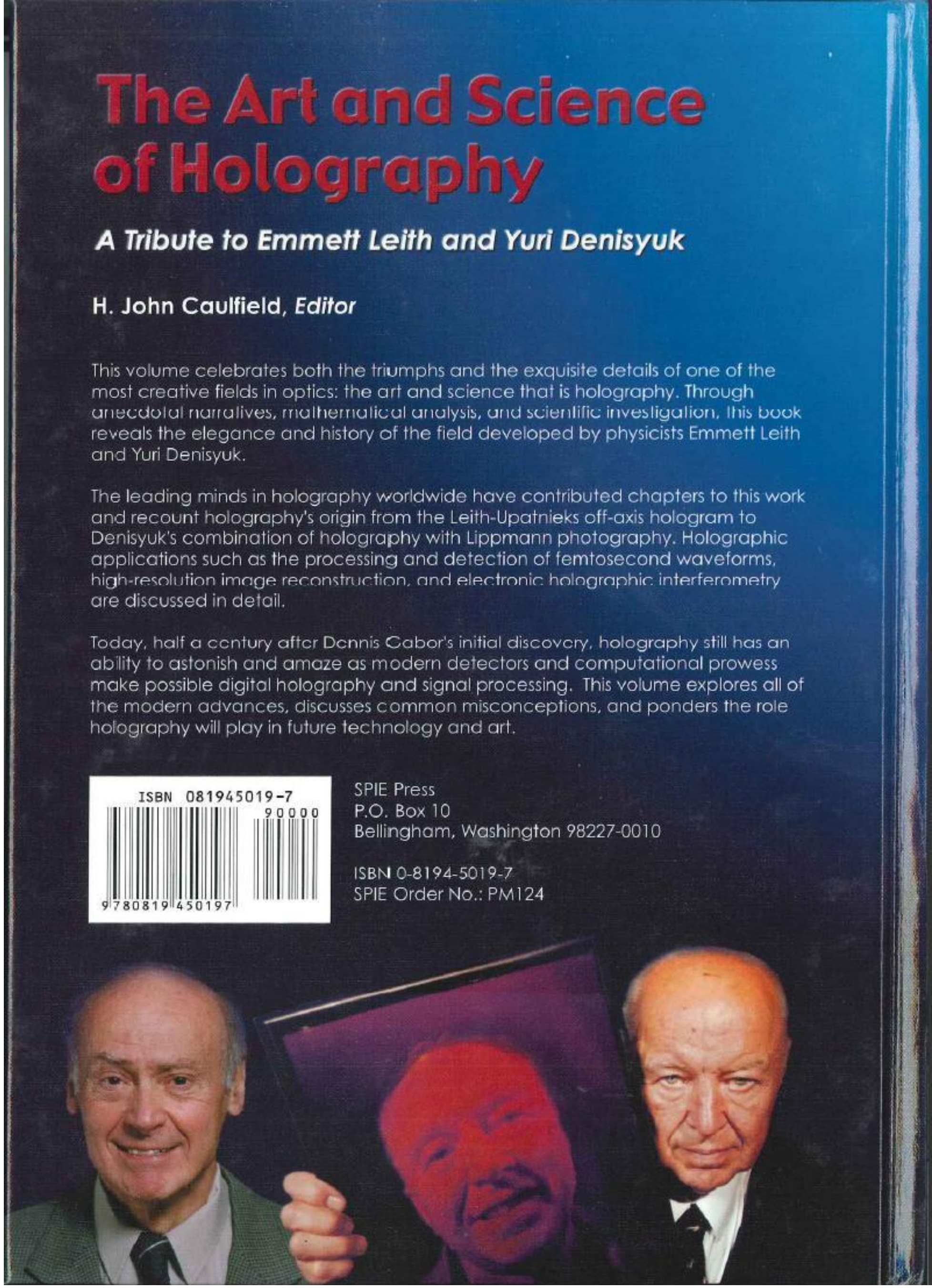
Why do we need yet another registration method?

- Need a "differential diagnosis" of the problem
- Higher speed (GPU and parallel cores are not enough)
  - 1TB BigBrain ~250,000 hours = 1.1K/sec
  - AlignTK Bock/Reid 10TB ~100,000 hours = 30K/sec
  - SWIFT goal > 1M/sec per core
- More robust with less human intervention
  - BigBrain 1000 hr
- Better accuracy (both global and local)
- Pipeline operation over regions of large image sets
- Feed directly to analysis tools via VVFS

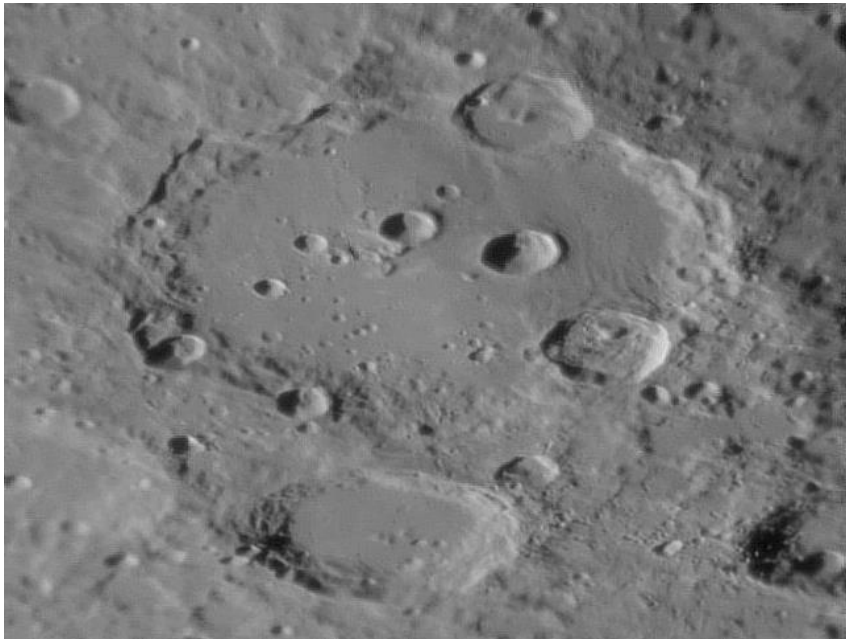
Approaches to EM registration

- AlignTK – based primarily on Pearson correlation and spring model relaxation to iteratively converge on the global shape
- SWIFT – uses spatial frequency scaling heuristics to obtain very high confidence image matching and applies Z direction averaging and Kalman smoothing to fit a global shape model

SWIFT inspiration from fourier optics & signal processing

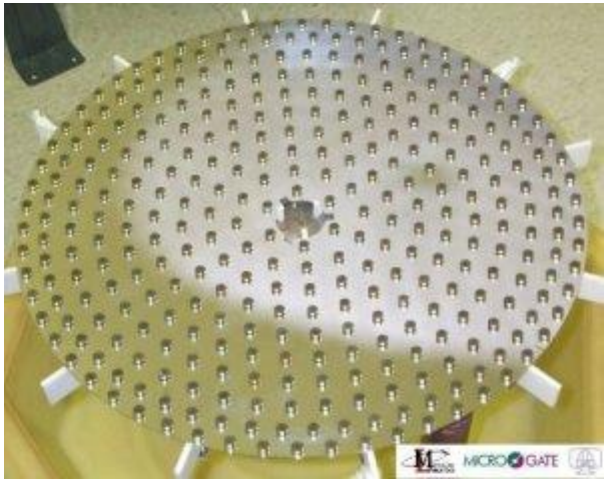


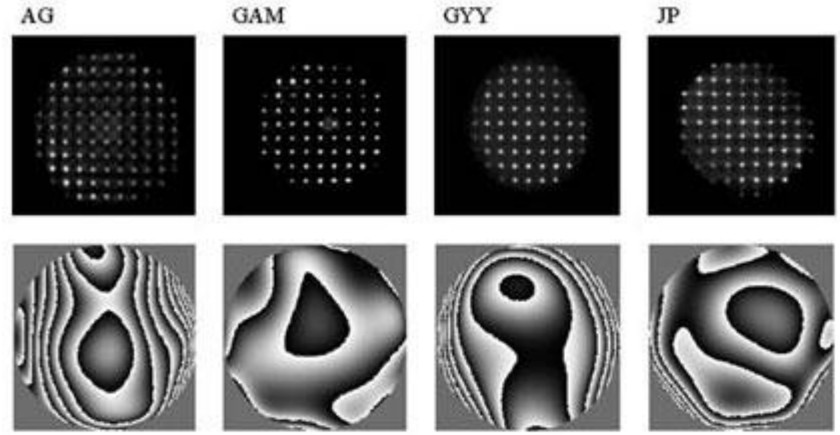
Similarities to Lucky Imaging

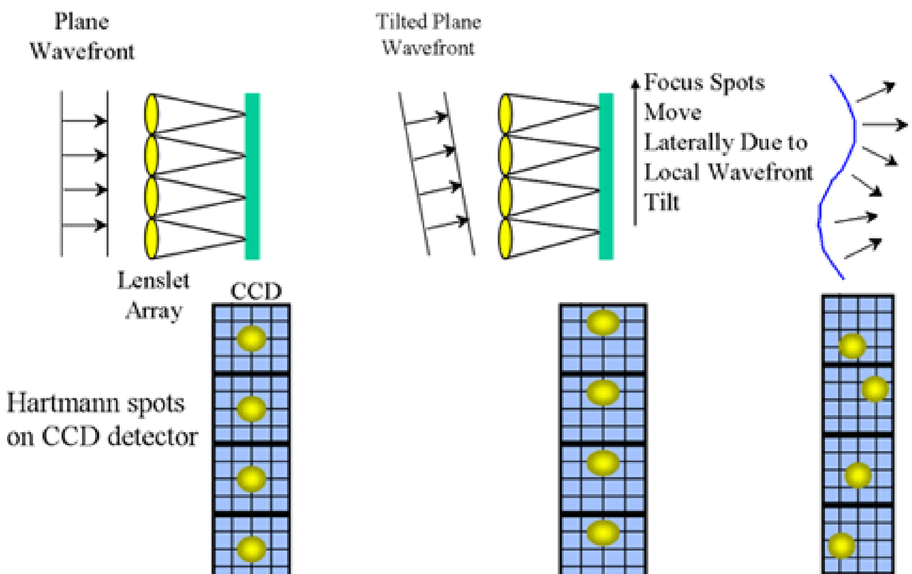


http://www.ast.cam.ac.uk/research/instrumentation.surveys.and.projects/

Similarity to adaptive optics





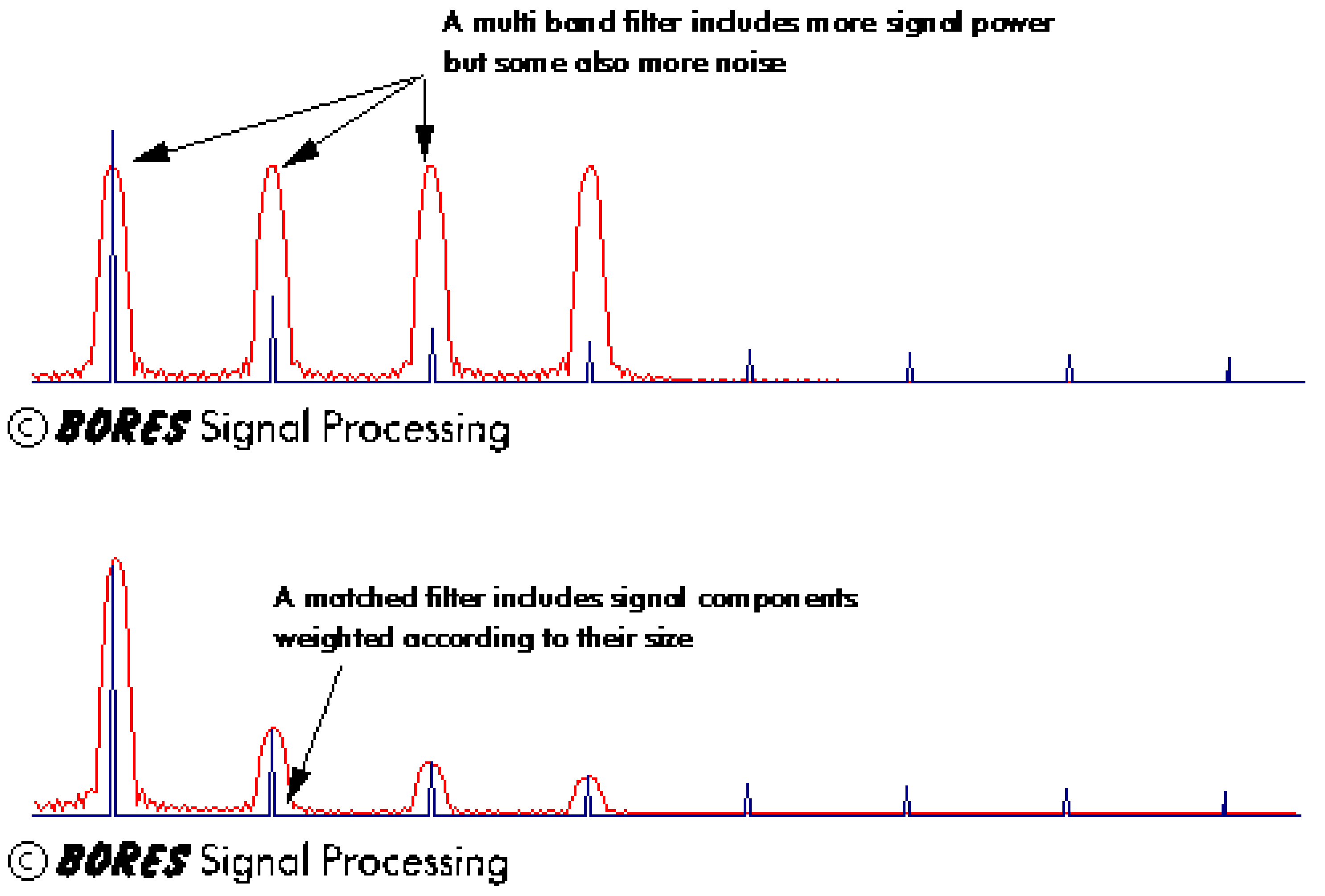


From http://www.astro.virginia.edu/class/majewski/astr511/lectures/seeingcomp/seeingcomp.html

Importance of signal whitening

- Conventional correlation is highly multimodal
- Phase only correlation is intolerant of deformation
- Adaptive whitening is typically unimodal & robust
  - Differential weighing of frequencies by useful content
  - Approaches the SNR of optimal matched filtering
  - Runs at speed similar to normal FFT correlation
  - Allows arrays of smaller FFT patch sizes
  - Can test different whitening levels with low added cost
  - Provides useful basis for further content analysis

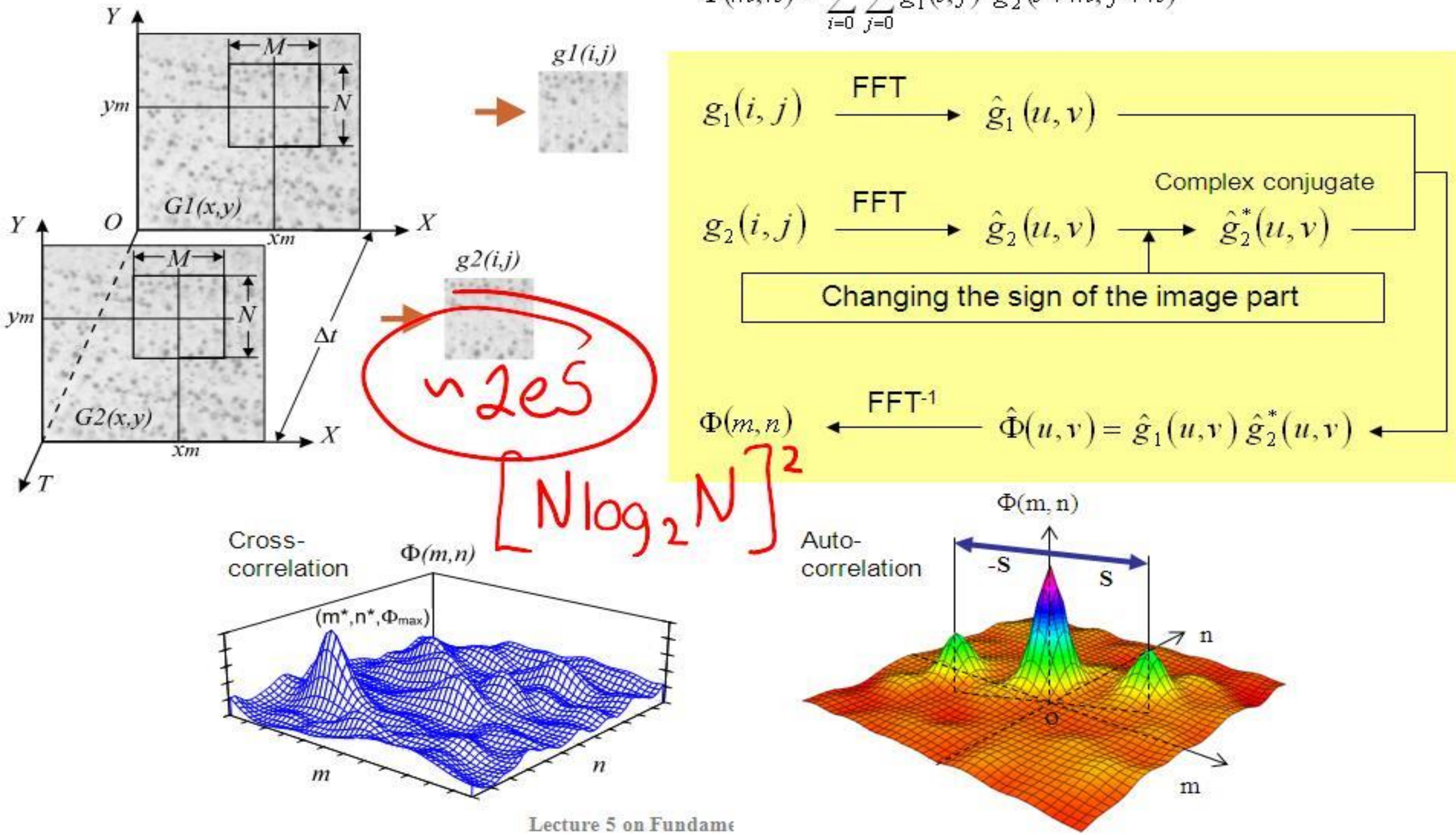
Graphical view of whitening



http://www.bores.com/courses/advanced/matched/11_mat.htm

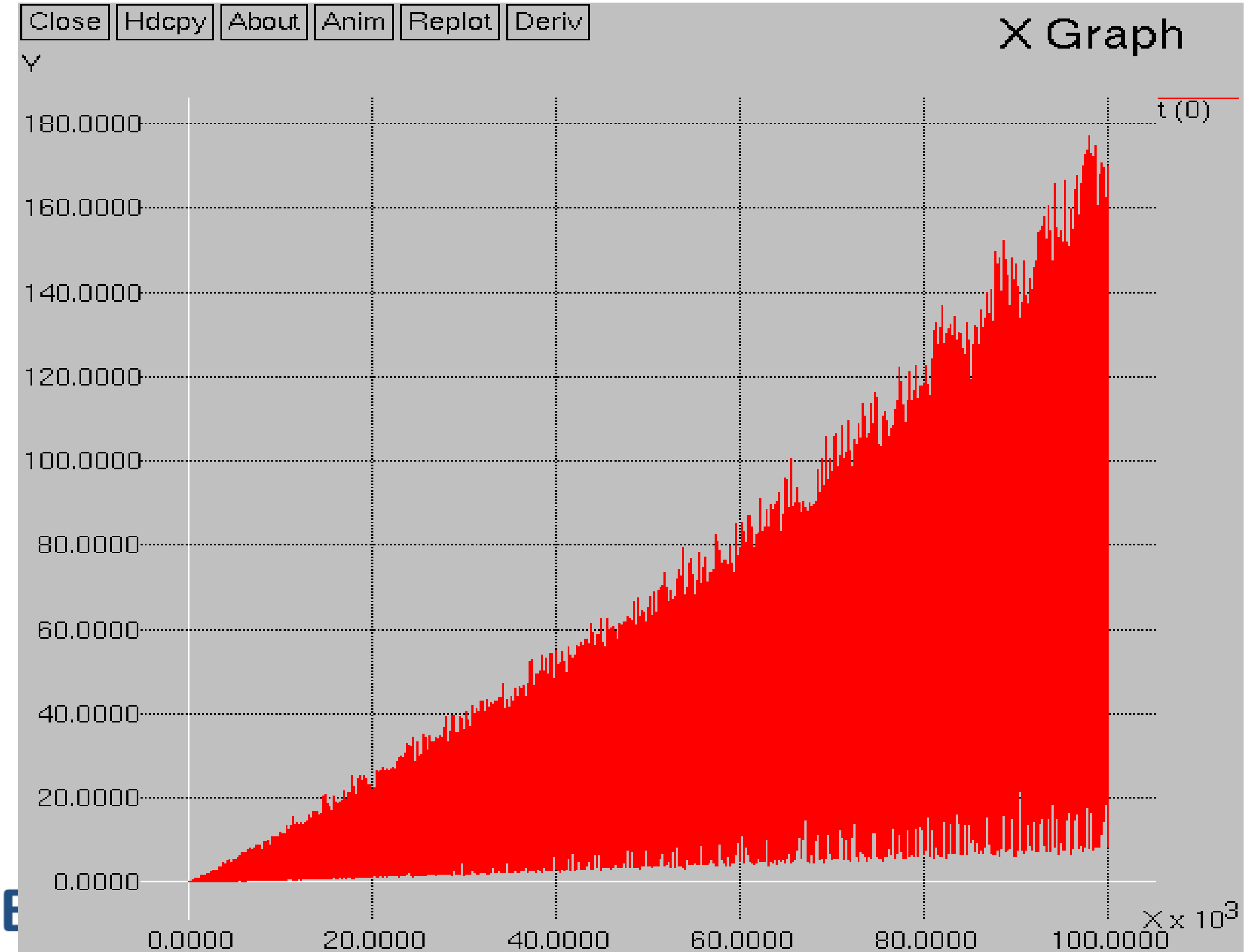
FFT-based correlation algorithm

$$\Phi(m,n)=\sum_{i=0}^{M-1}\sum_{j=0}^{N-1} g_1(i,j)\cdot g_2(i+m,j+n)$$

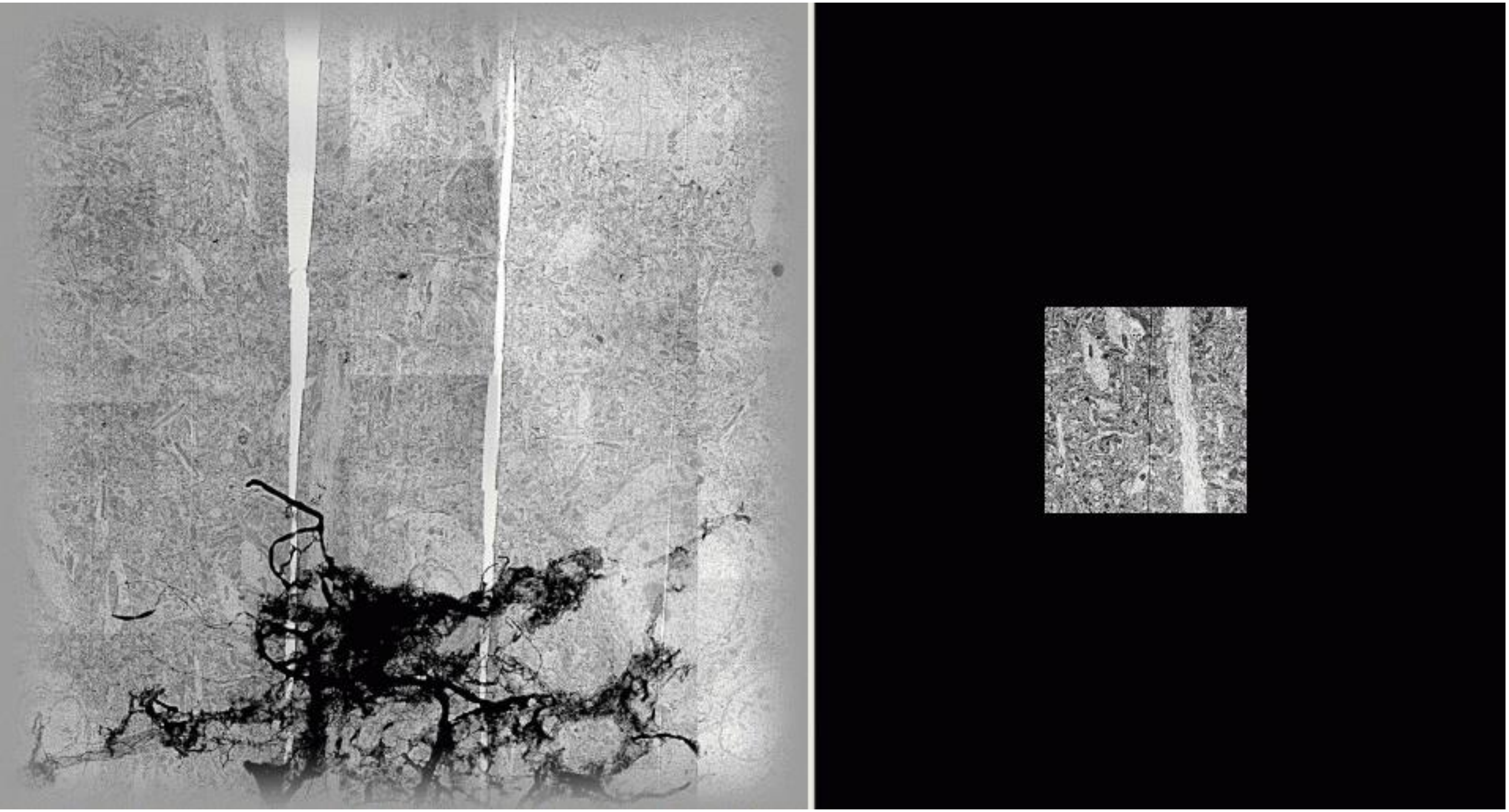


https://nanohub.org/site/resources/2014/03/20569/slides/009.03.jpg

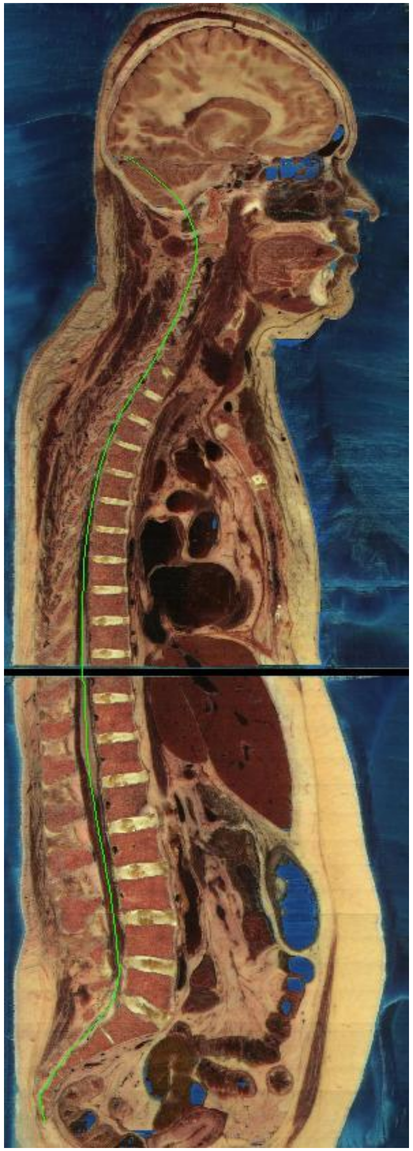
N*log(N) complexity FFTW Mega CPU ticks vs size



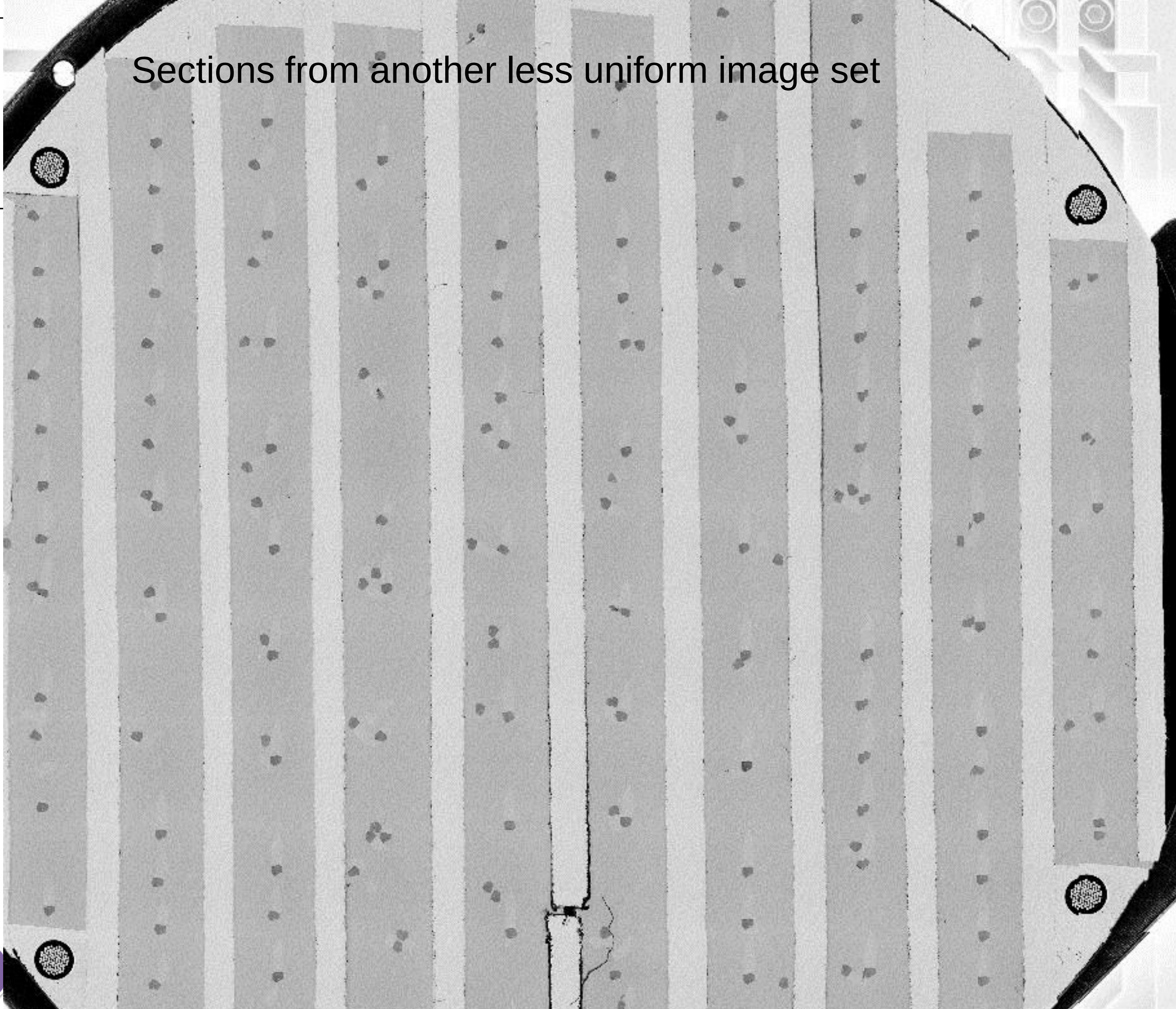
Signal whitening in the SWiFT approach matches difficult cases



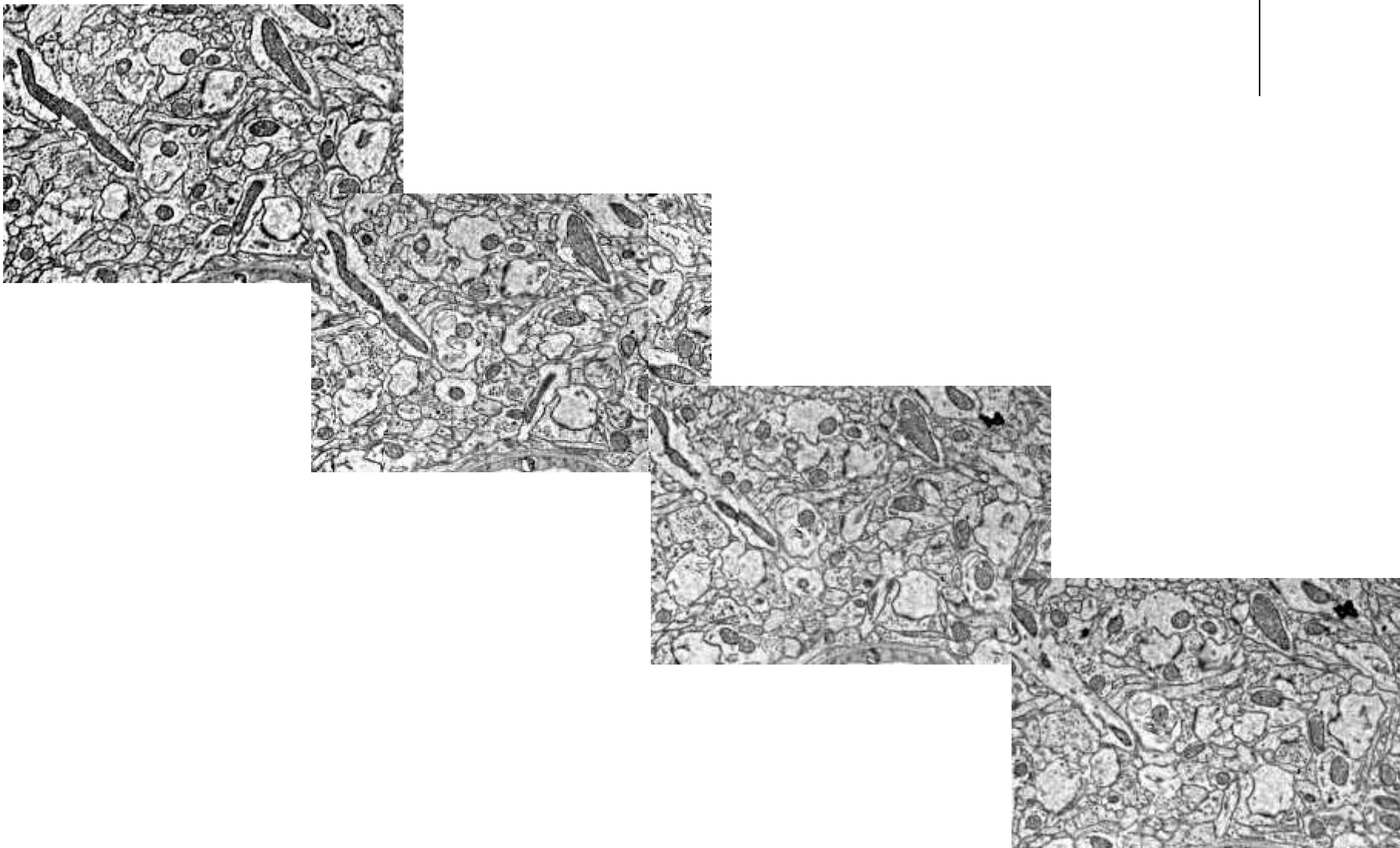
Global alignment will often need additional anatomical information



Sections from another less uniform image set



Out of order sections must be resolved by detailed content



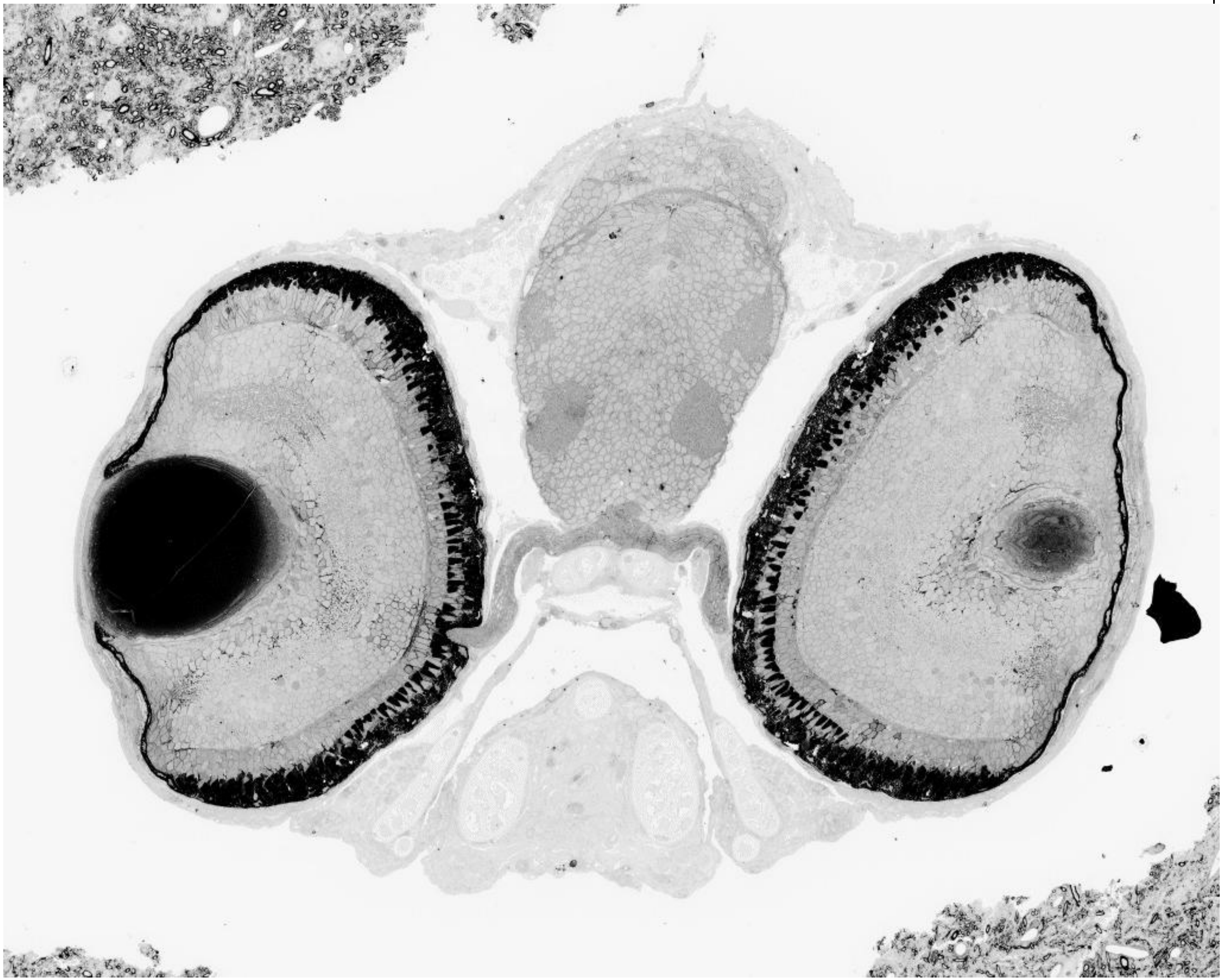
The main SWIFT components

- iscale – produces pre-scaled image hierarchies
- SWIM – Signal Whitening Image Matching
- PSC-VB for 3D cut-plane viewing
- iavg – average image sets and make VB stacks
- MIR – Multi Image Rendering generates output
- remod – produce a “model” from an image set
- “qiv” and modified “xv” for image review

Examples using David Hildebrand’s zebrafish dataset

- Imaged by the WaferMapper SEM method
- Nominally 18200 sections at overview scale
- 16000 reimaged 60nm/pixel 16-bit 10Kx8K
- 12546 imaged 20nm/pixel ROI 14Kx15K
- Also 2-photon optical

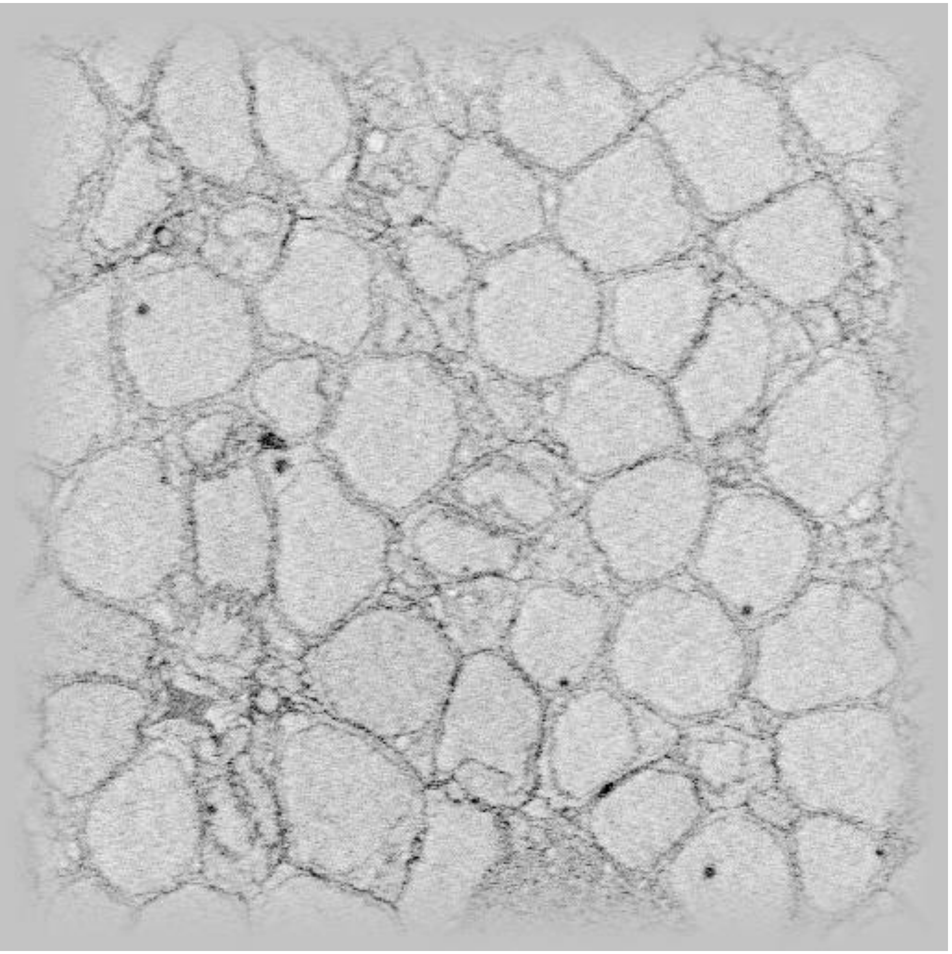
Example SWIM operation 13460-13480

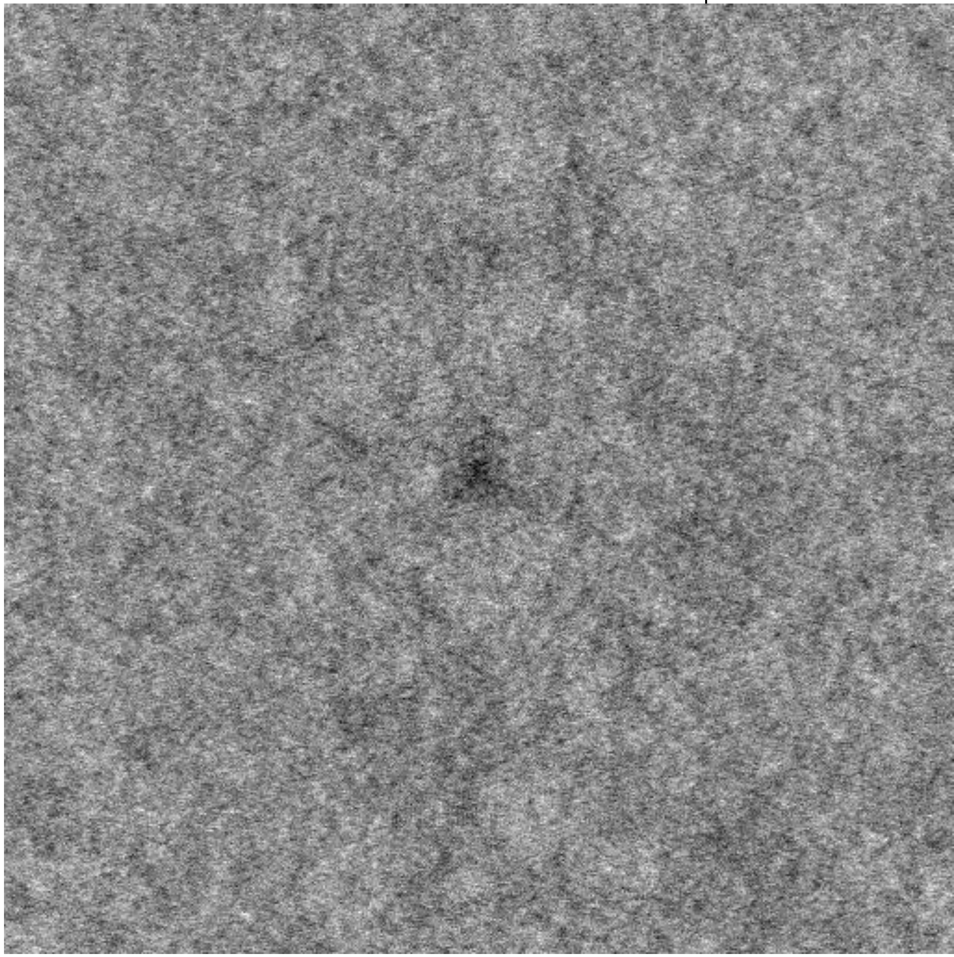


Example SWIM operation 13460-13480

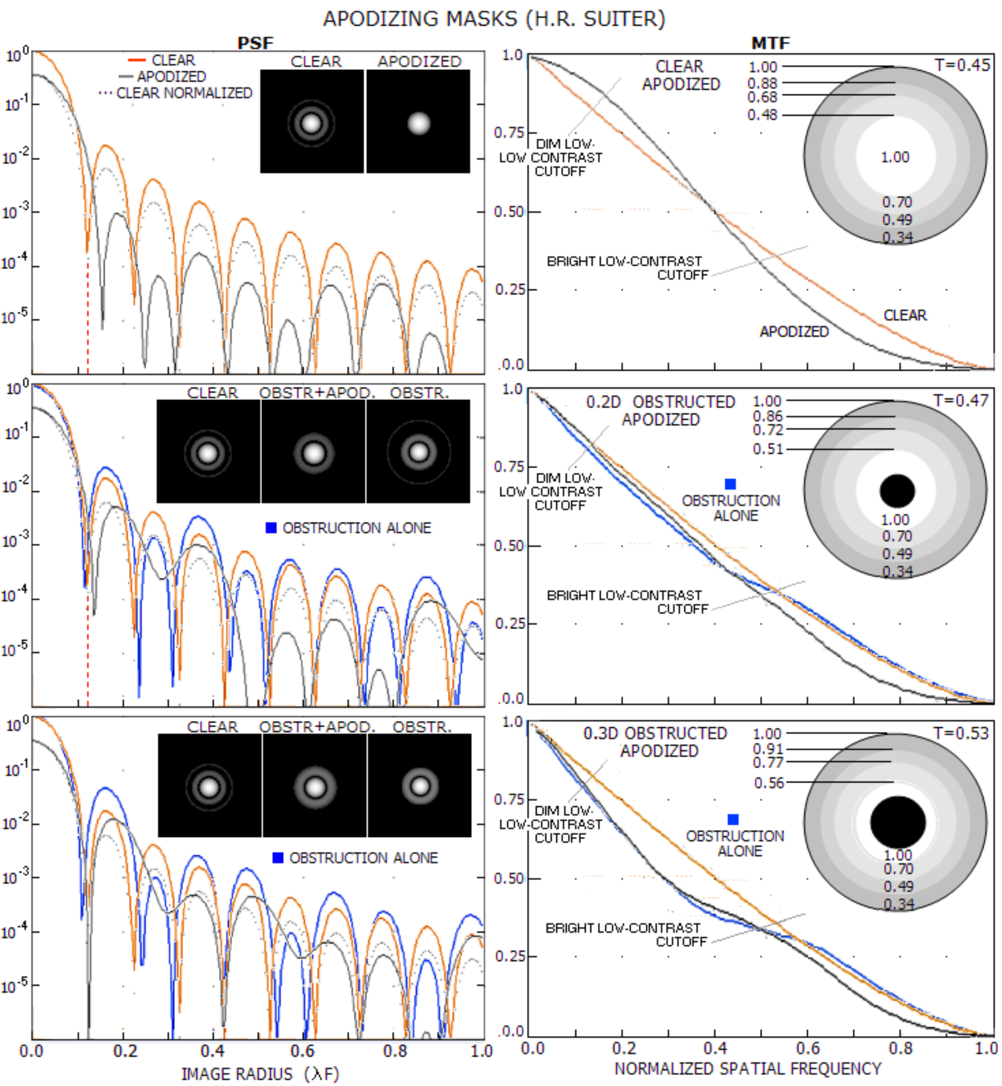
```
swim512 -i 3 S1pgms/13460.pgm 5820 2960 S1pgms/13480.pgm 5820 2960
5.18008: S1pgms/13460.pgm 5820 2960 S1pgms/13480.pgm 5848.06 2955.12
 -4.87524 28.4756)
elapsed_sec 0.364596
tickrate 2.99239e+09
targs        57195
tinit     53953755
tread    663131153 =    348443745 +    314687408
tprep     44142008 =     11551065 +     32590943
tffts    128881777 =     18853778 +     53670569 +     56357430
tmult    143644439
tpost     56839868
total   1091013615
nread 1 1
nft 1 3 ncalls 1
ticks/pixel 4161.89
pixels 262144
pixels/sec 718999
loopquit 1  threshquit 0
niter 1: 1 1.45853
niter 2: 1 4.26346
niter 3: 1 25.5223
```

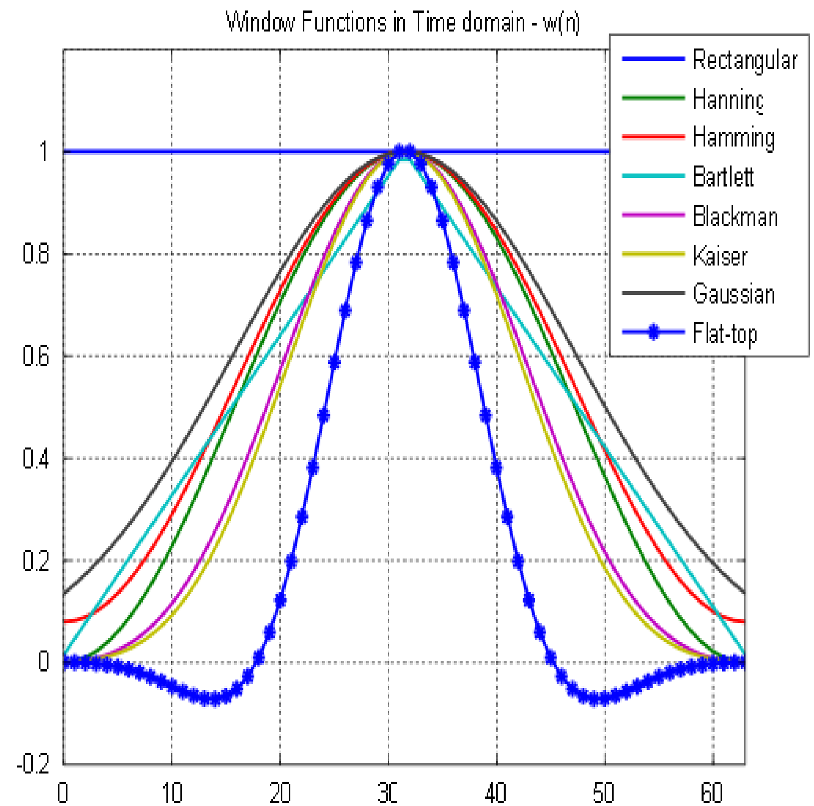
Example SWIM operation 13460-13480



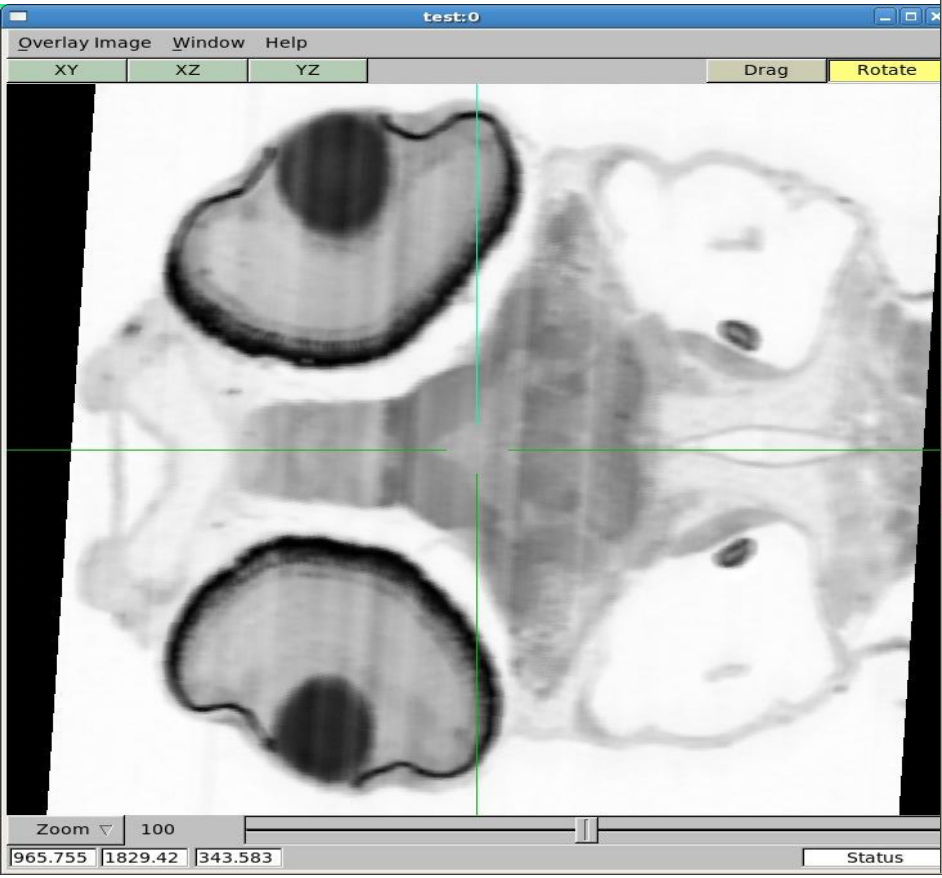


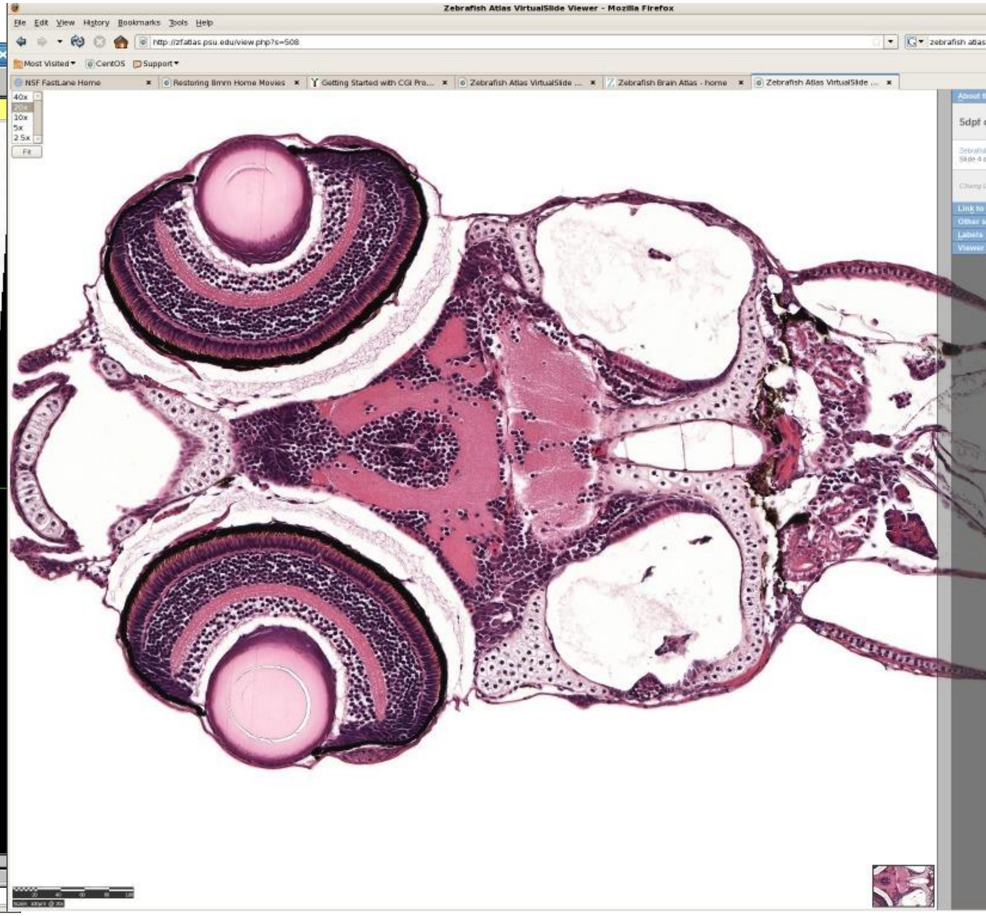
Apodization vs window functions



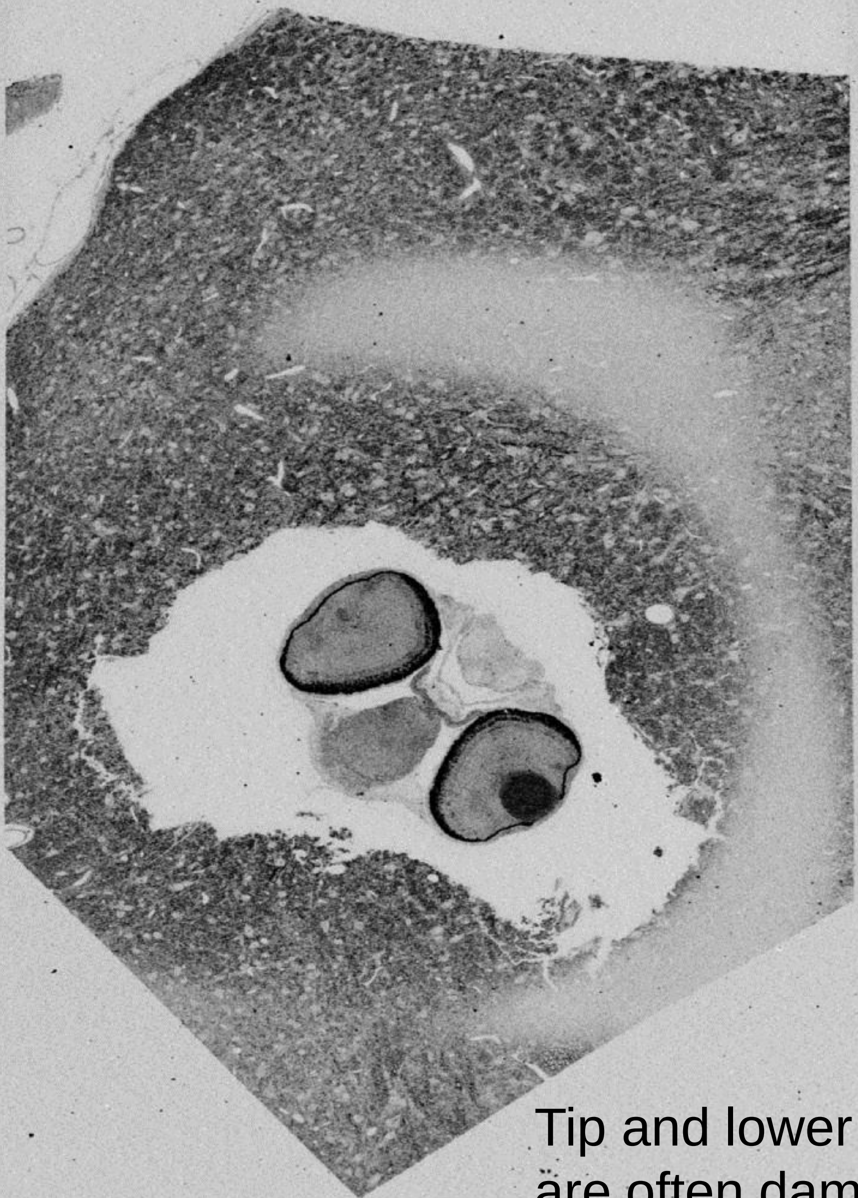


Need to produce anatomically correct renditions to compare with other specimens and Atlas data





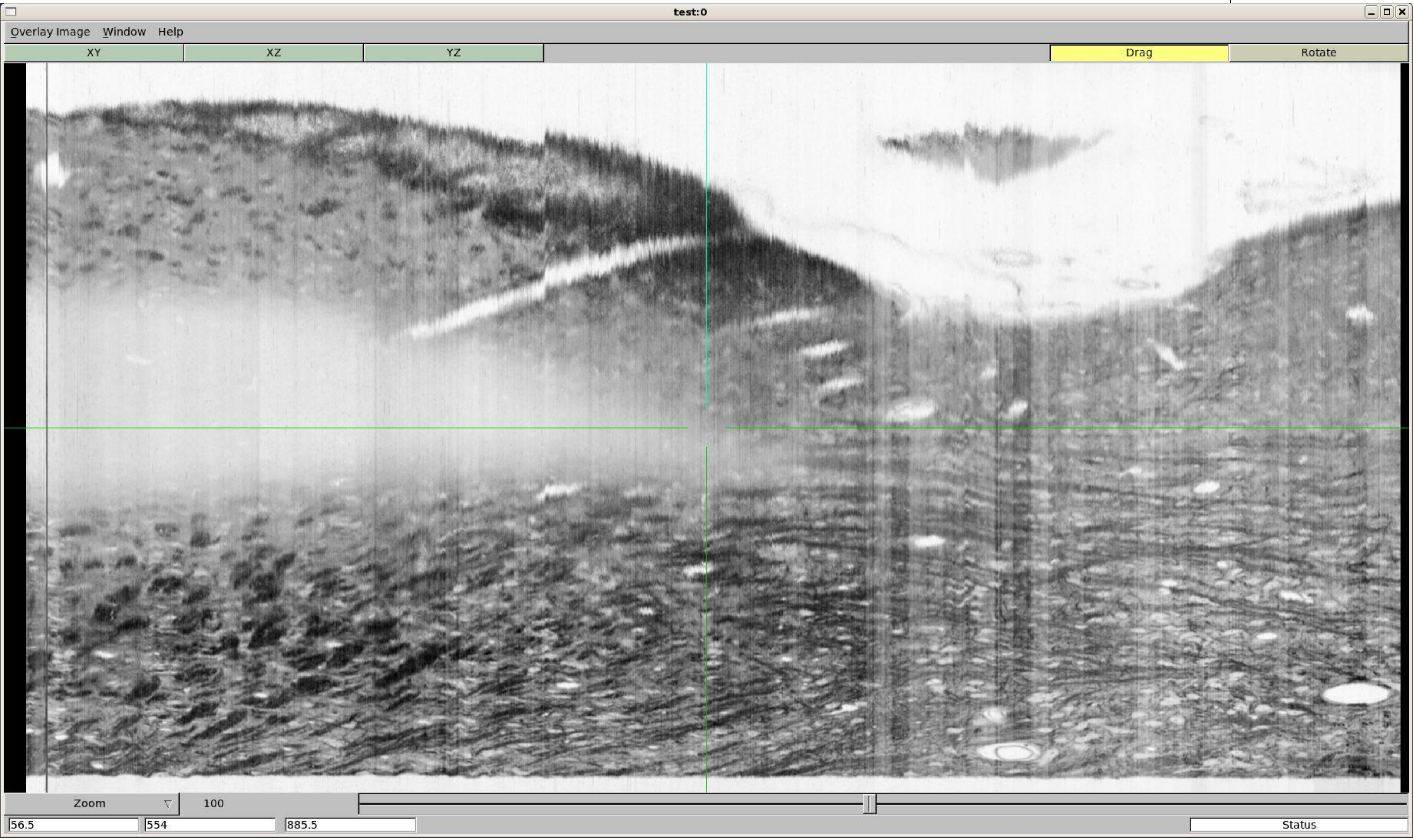
Top surface is highly variable



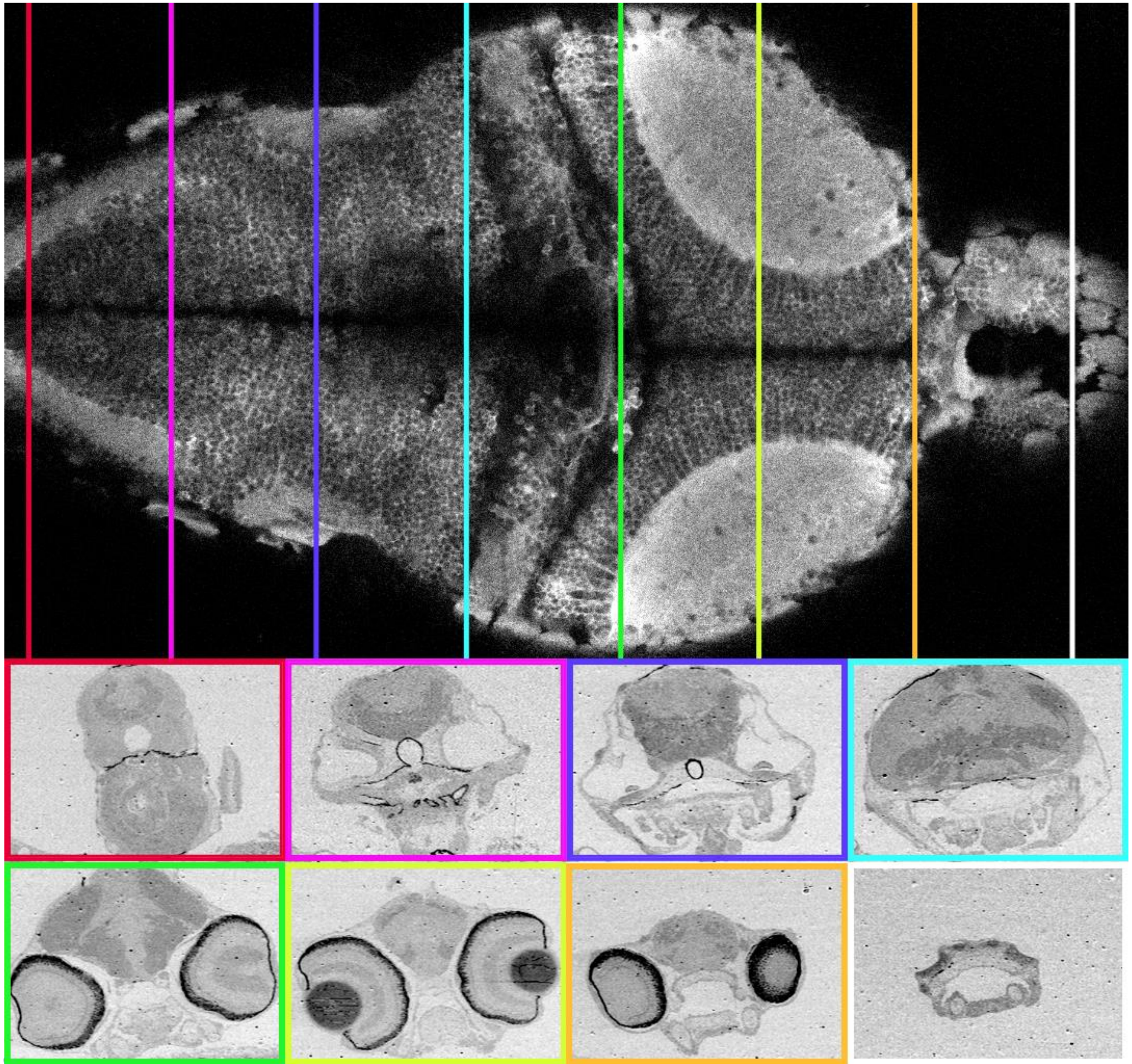
Lower left is
a particularly
stable point

Tip and lower right
are often damaged

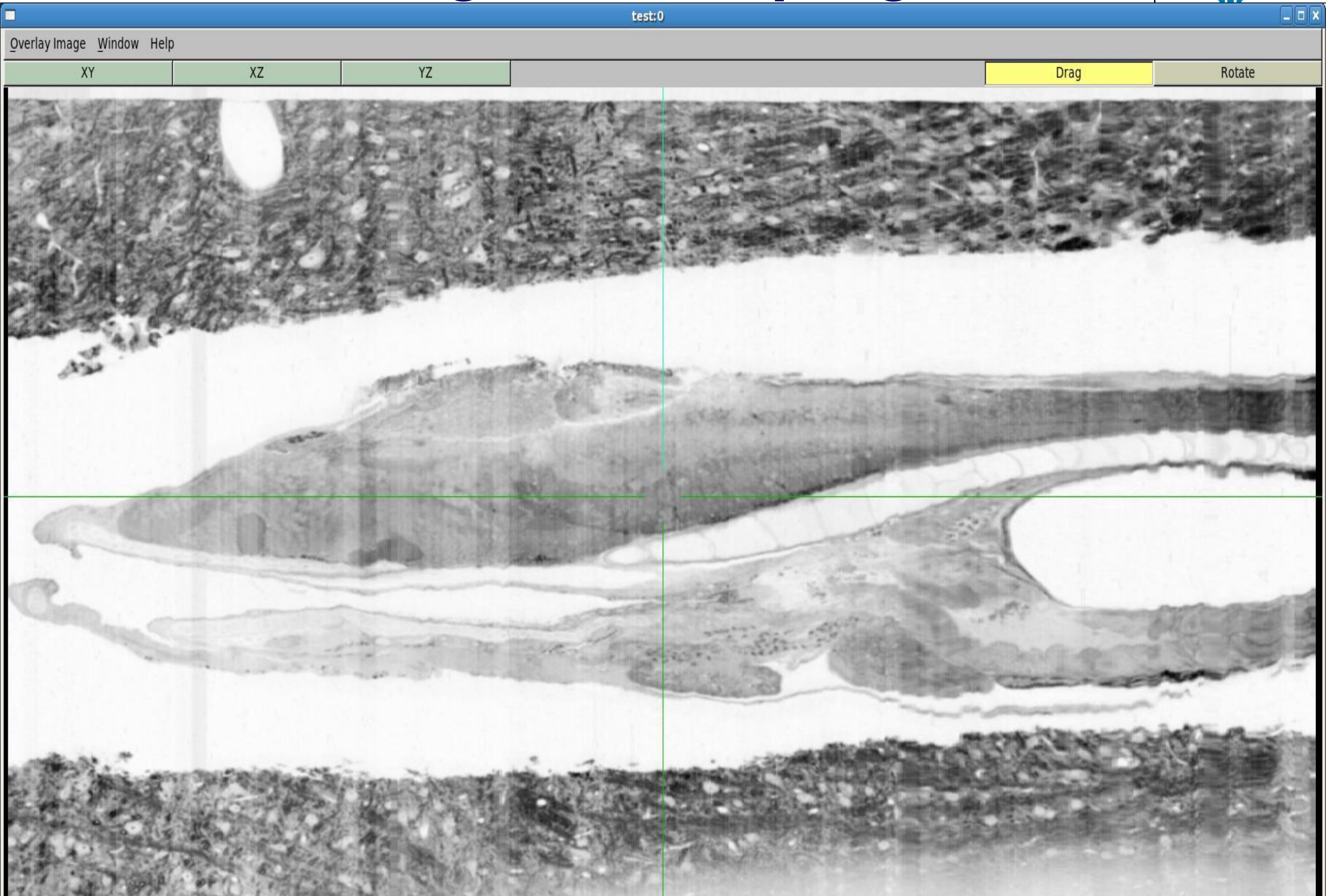
Difficult compression variations



6) The goal is to correspond the same nuclei across the two modalities (optical and EM) to preserve cell identity.



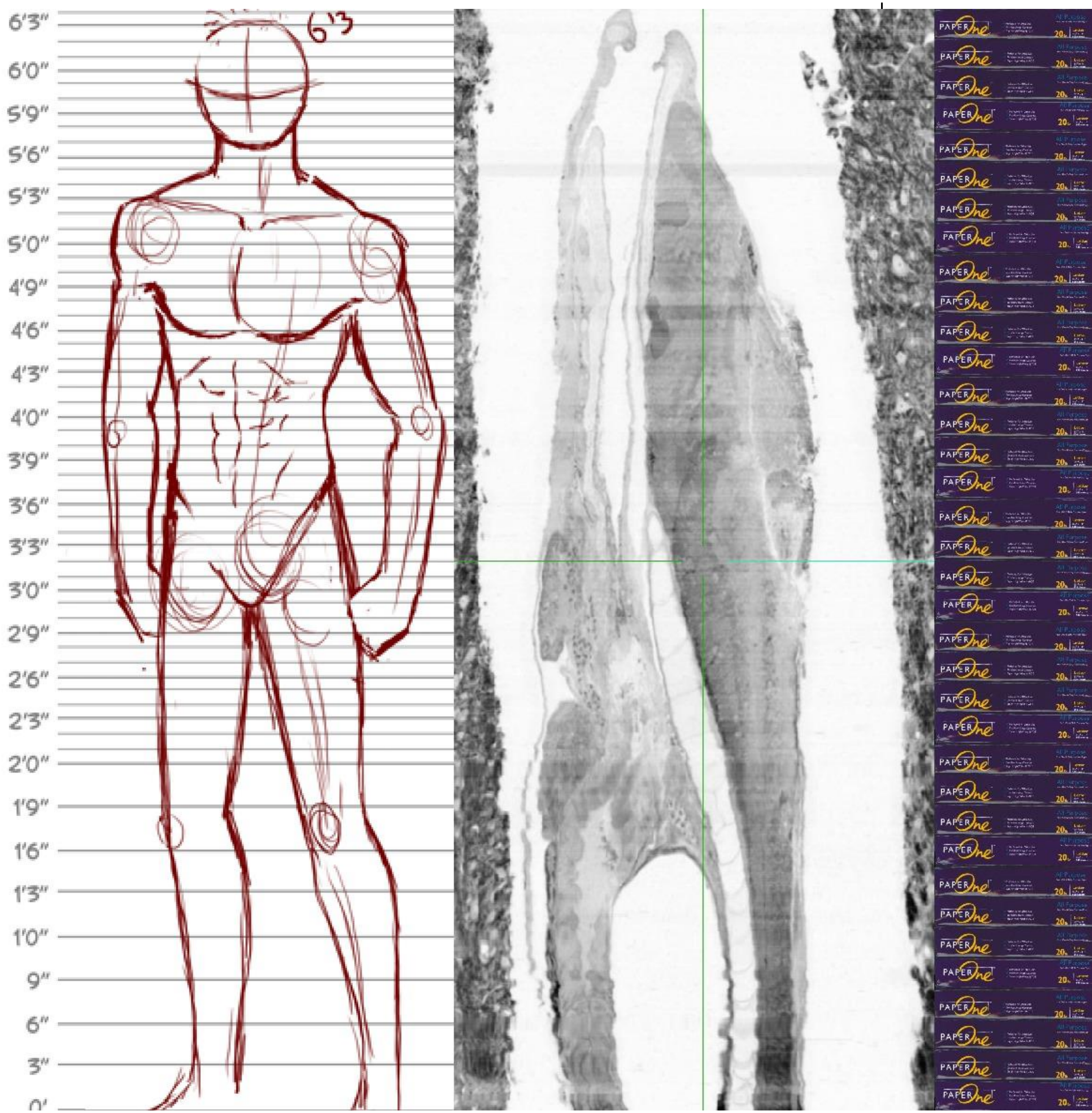
zebrafish alignment in progress



“remod” averages out defects and random shifts

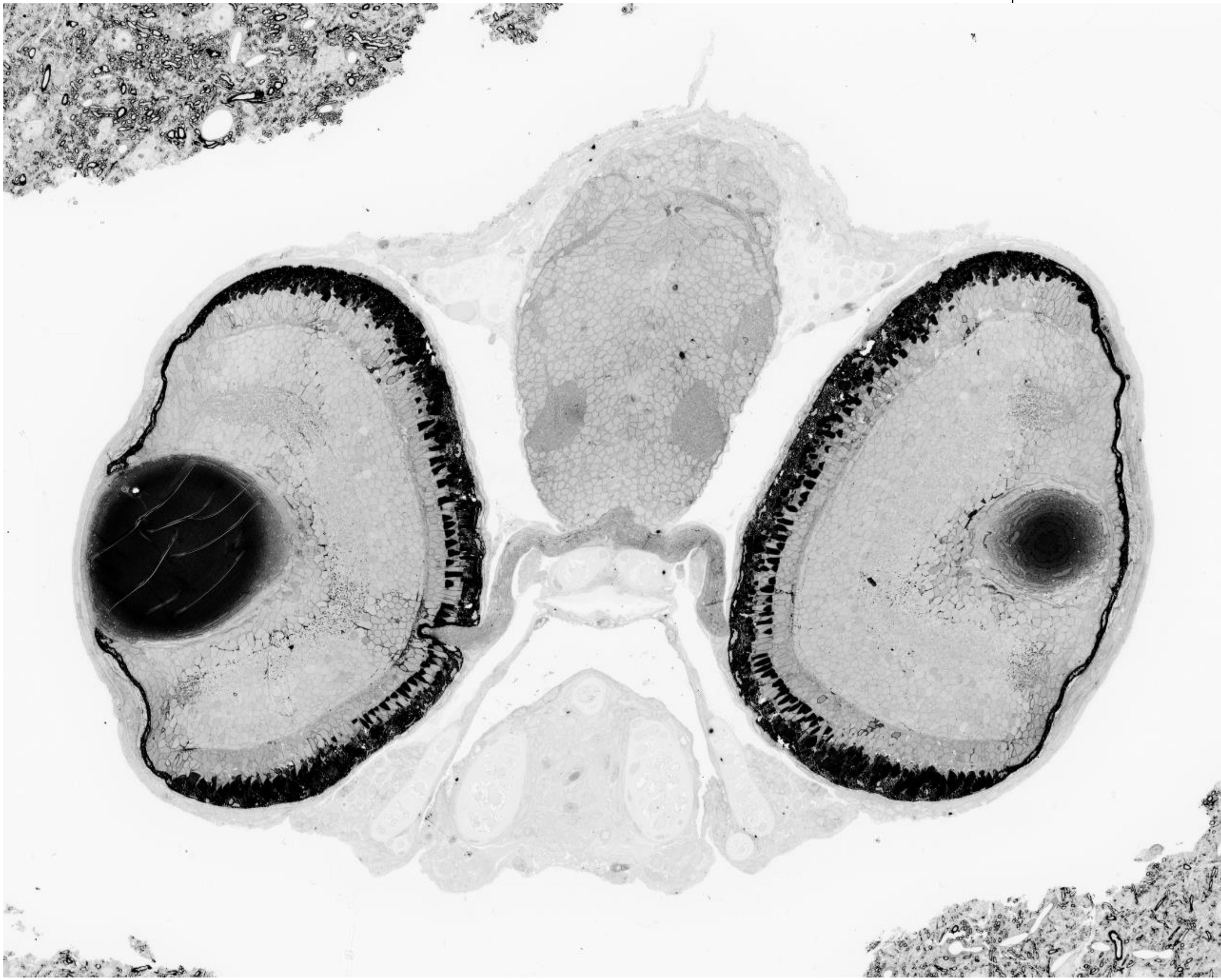
Example MIR image assembly

```
[awetzel@za tmp]$ cat tall-
B 1170 1174 3
RF ht-scale.ppm
0 0 0 0
0 1177 0 588
RF wide-sag-ZF.jpg
490 0 11 740
1000 0 11 200
490 1174 1801 740
RF human6-3.ppm
98 0 0 6
98 1163 0 587
RF paper18000sheets.ppm
1002 0 0 0
1002 1174 0 4153
RW tall-fish-composite.ppm
```



MIR transform by triangle mesh

```
B 1280 1024
F 13500.pgm
Z 250
636 569 636 569
636 25 724 25
210 180 292 180
0 630 0 630
400 1020 300 1020
653 1013 562 1000
1033 919 953 954
1277 558 1277 558
1053 86 1155 91
T
0 1 2
0 2 3
0 3 4
0 4 5
0 5 6
0 6 7
0 7 8
0 8 1
W new13500.pgm
```

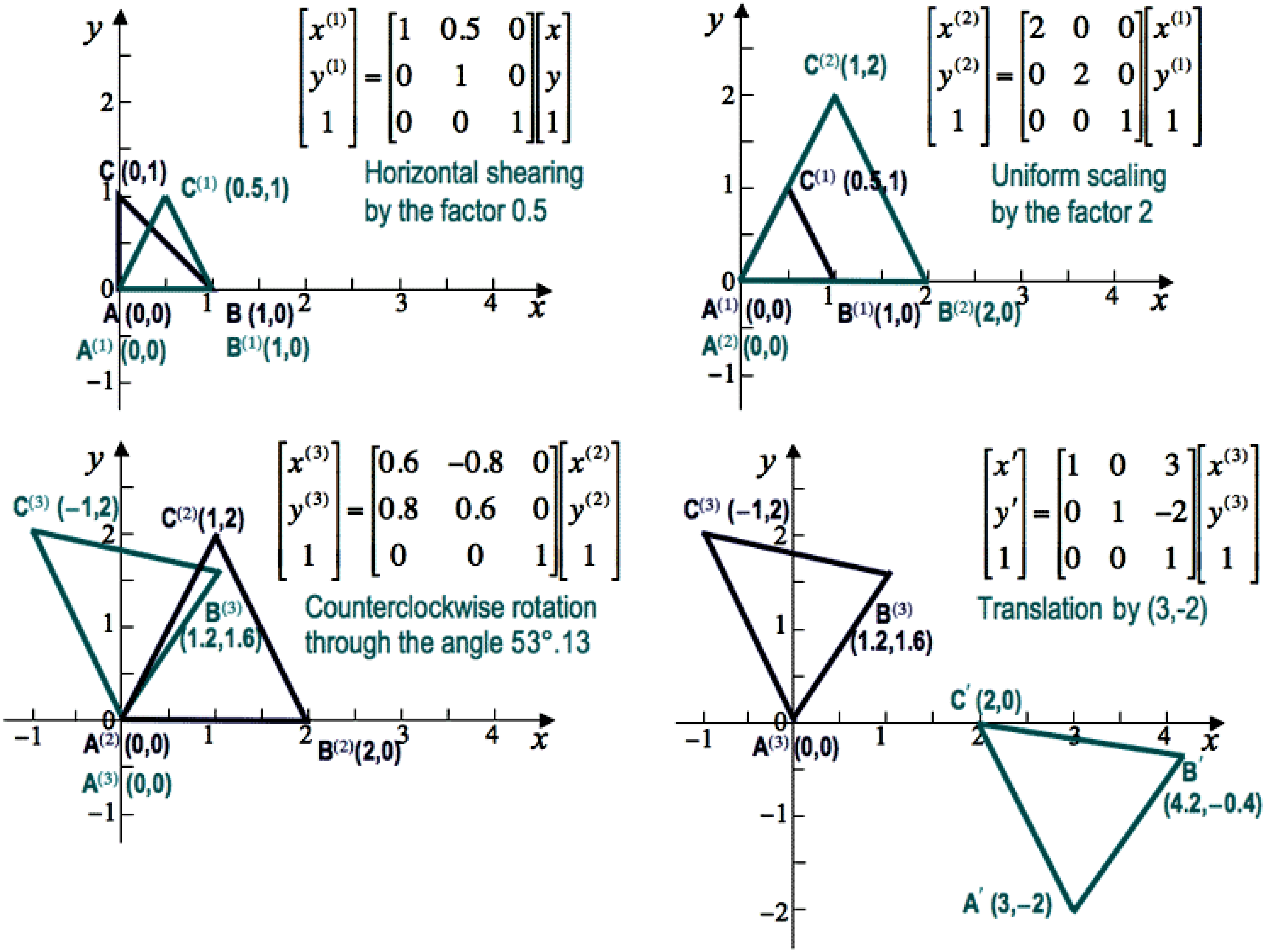


Why triangles?

- Supported as a standard graphics primitive
- GPU triangles are highly optimized
- Any mapping of 3 points to 3 points is affine
- Over determined sets give least squares affine
- Affine transforms are simple matrix multiplies
- Affine of affine is affine
- Affine of Bezier is Bezier
- Local affine triangles blend into Bezier triangles allowing long range quadratic and cubic curves

$$\begin{bmatrix} x' \\ y' \end{bmatrix} = \begin{bmatrix} a_0 & a_1 \\ b_0 & b_1 \end{bmatrix} \begin{bmatrix} x \\ y \end{bmatrix} + \begin{bmatrix} a_2 \\ b_2 \end{bmatrix} \quad \Leftrightarrow \quad \underbrace{\begin{bmatrix} x' \\ y' \\ 1 \end{bmatrix} = \begin{bmatrix} a_0 & a_1 & a_2 \\ b_0 & b_1 & b_2 \\ 0 & 0 & 1 \end{bmatrix} \begin{bmatrix} x \\ x \\ 1 \end{bmatrix}}_{\text{affine transformation in homogeneous coordinates}}$$

Affine scale rotation & shear



$$\begin{bmatrix} x^{(1)} \\ y^{(1)} \\ 1 \end{bmatrix} = \begin{bmatrix} 1 & 0.5 & 0 \\ 0 & 1 & 0 \\ 0 & 0 & 1 \end{bmatrix} \begin{bmatrix} x \\ y \\ 1 \end{bmatrix}$$

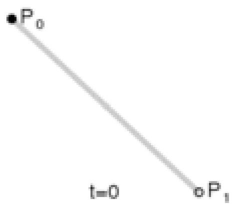
$$\begin{bmatrix} x^{(2)} \\ y^{(2)} \\ 1 \end{bmatrix} = \begin{bmatrix} 2 & 0 & 0 \\ 0 & 2 & 0 \\ 0 & 0 & 1 \end{bmatrix} \begin{bmatrix} x^{(1)} \\ y^{(1)} \\ 1 \end{bmatrix}$$

$$\begin{bmatrix} x^{(3)} \\ y^{(3)} \\ 1 \end{bmatrix} = \begin{bmatrix} 0.6 & -0.8 & 0 \\ 0.8 & 0.6 & 0 \\ 0 & 0 & 1 \end{bmatrix} \begin{bmatrix} x^{(2)} \\ y^{(2)} \\ 1 \end{bmatrix}$$

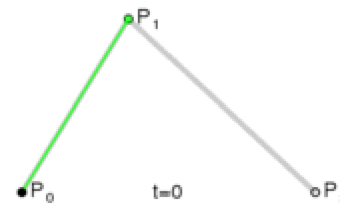
$$\begin{bmatrix} x' \\ y' \\ 1 \end{bmatrix} = \begin{bmatrix} 1 & 0 & 3 \\ 0 & 1 & -2 \\ 0 & 0 & 1 \end{bmatrix} \begin{bmatrix} x^{(3)} \\ y^{(3)} \\ 1 \end{bmatrix}$$

https://www.cs.auckland.ac.nz/courses/compsci773s1c/lectures/ImageProcessing-html/topic2.htm

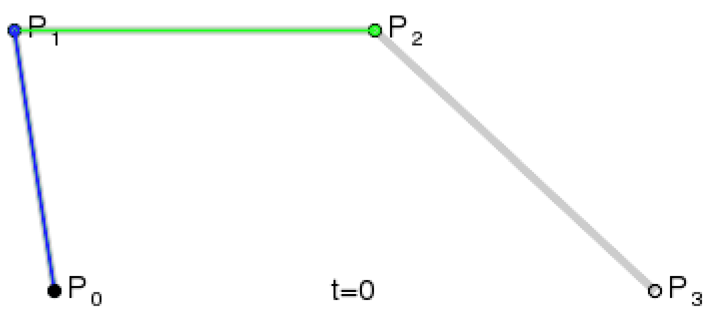
Bezier curves



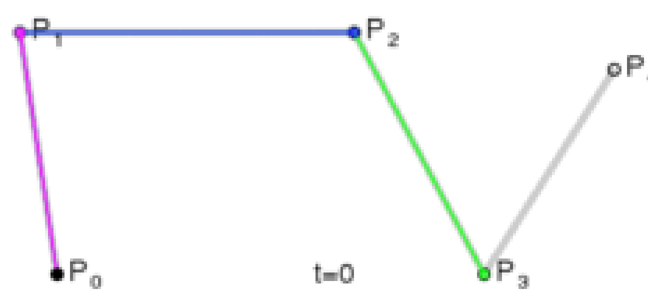
Linear interpolation



Quadratic = parabolic arc



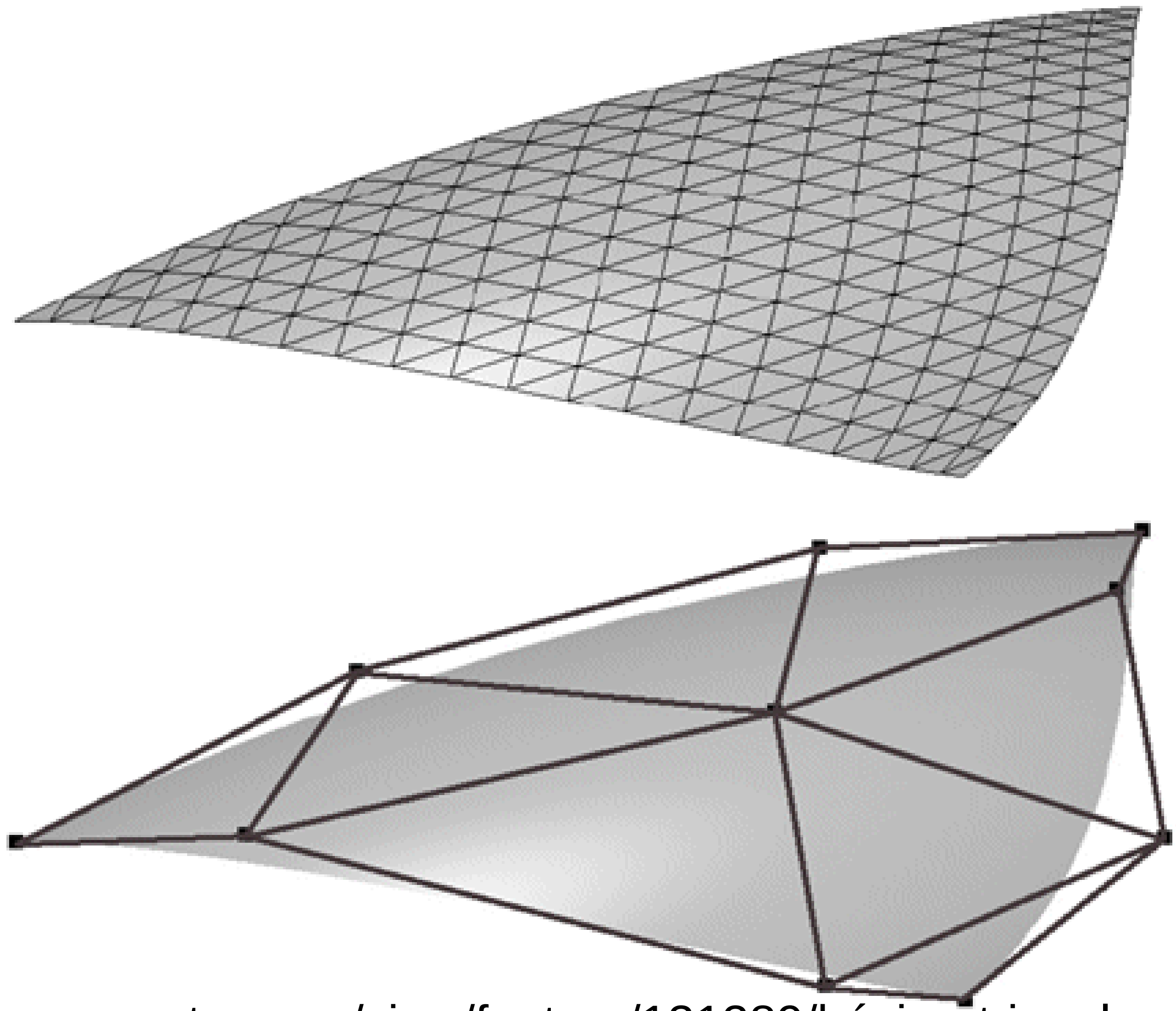
Cubic



Fourth order

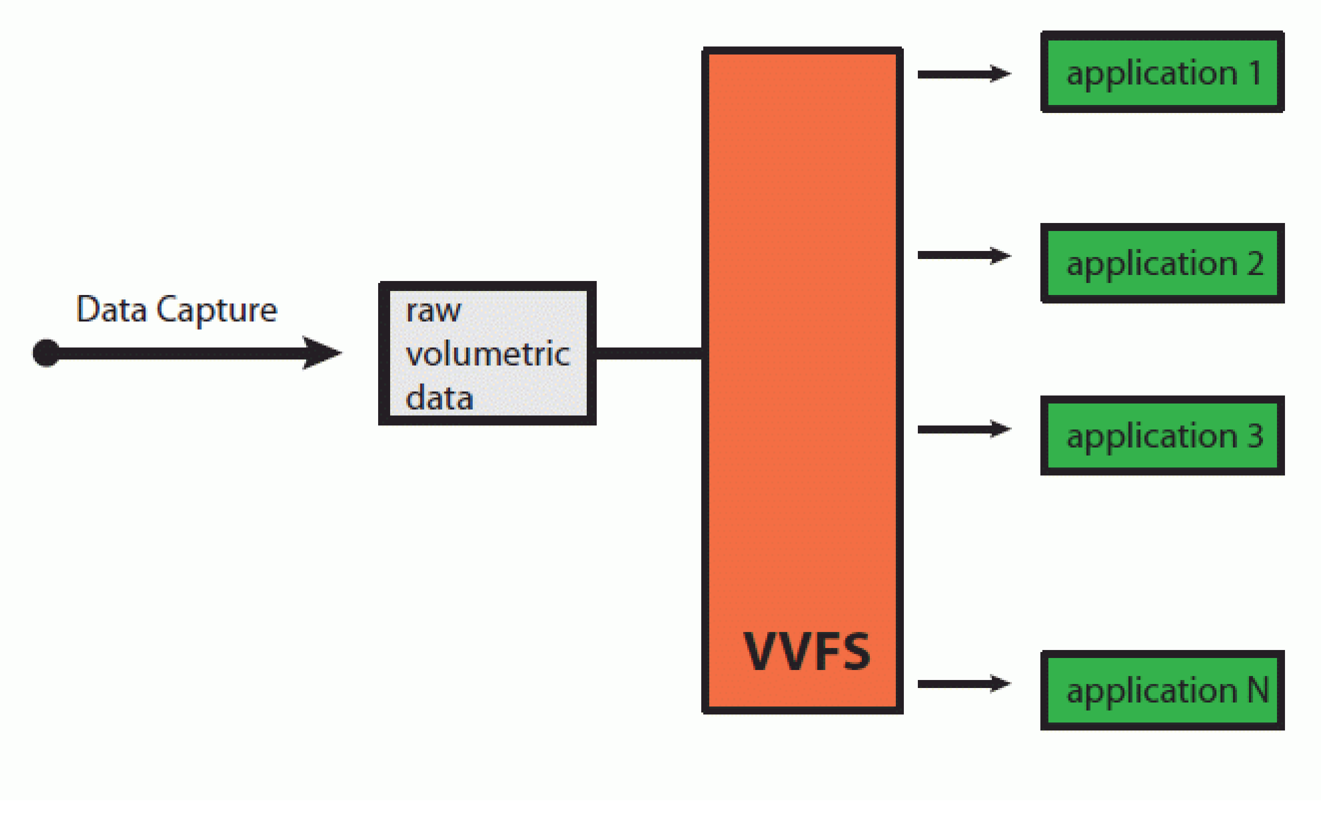
http://en.wikipedia.org/wiki/Bezier_curve

Curves extend to Bezier triangles



http://www.gamasutra.com/view/feature/131389/bézier_triangles_and_npatches

Functions similar to MIR will be incorproated into the VVFS



Stop for today.
More questions or discussion?