Principles of Signal Whitening Fourier Transform (SWIFT) Image Registration

Art Wetzel
Aug 2014 MMBioS Meeting

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
  - 1.3x10^6 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
Scanning EM will be the first to capture petascale datasets
Recent description of automated sectioning and SEM methods

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.
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 \(\sim 250,000\) hours = 1.1K/sec
  - AlignTK Bock/Reid 10TB \(\sim 100,000\) 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

A multi band filter includes more signal power but some also more noise

A matched filter includes signal components weighted according to their size

http://www.bores.com/courses/advanced/matched/11_mat.htm
FFT-based correlation algorithm

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

\[ g_1(i,j) \xrightarrow{FFT} \hat{g}_1(u,v) \]

\[ g_2(i,j) \xrightarrow{FFT} \hat{g}_2(u,v) \]

Complex conjugate

Changing the sign of the image part

\[ \hat{\Phi}(u,v) = \hat{g}_1(u,v) \cdot \hat{g}_2^*(u,v) \]

Cross-correlation

Auto-correlation

Lecture 5 on Fundam
$N \log(N)$ 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

APODIZING MASKS (H.R. SUITER)

PSF

CLEAR

APODIZED

CLEAR NORMALIZED

MTF

CLEAR

APODIZED

0.47

1.0

0.70

0.49

0.24

1.0

0.70

0.49

0.24

0.2

0.1

0.0

Window Functions in Time domain - w(n)

0

10

20

30

40

50

60

Rectangular

Hanning

Hamming

Bartlett

Blackman

Kaiser

Gaussian

Flat-top

IMAGE RADIUS (r)

0.0

0.2

0.4

0.6

0.8

1.0

NORMALIZED SPATIAL FREQUENCY

0.0

0.2

0.4

0.6

0.8

1.0

MMBioS National Center for Multiscale Modeling of Biological Systems
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
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

\[
\begin{bmatrix}
  x' \\
  y'
\end{bmatrix} = \begin{bmatrix}
  a_0 & a_1 \\
  b_0 & b_1
\end{bmatrix} \begin{bmatrix}
  x \\
  y
\end{bmatrix} + \begin{bmatrix}
  a_2 \\
  b_2
\end{bmatrix}
\]

\[
\begin{bmatrix}
  x' \\
  y' \\
  1
\end{bmatrix} = \begin{bmatrix}
  a_0 & a_1 & a_2 \\
  b_0 & b_1 & b_2 \\
  0 & 0 & 1
\end{bmatrix} \begin{bmatrix}
  x \\
  y \\
  1
\end{bmatrix}
\]

affine transformation in homogeneous coordinates
Affine scale rotation & shear

Beziers 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 incorporated into the VVFS
Stop for today.
More questions or discussion?