

Intro



CANCER PREVENTION & RESEARCH INSTITUTE OF TEXAS

*Gulf
Coast
Consortia* *for* Quantitative Biomedical Sciences

Pre-Filtering of Cancer Platelets

- Problem: post-reconstruction filtering enhances artifacts
- Sources of artifacts:
 - interpolation
 - inaccuracy in alignment
 - missing data
- Goals: improve contrast and feature identification

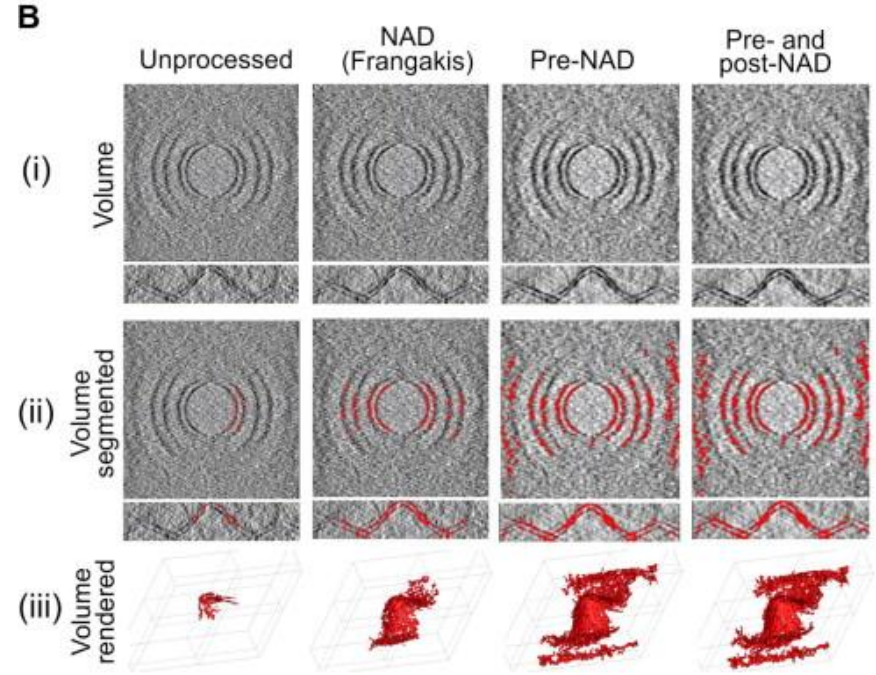


Prefiltering Pipeline

- Filters
 - Highpass
 - Lowpass
 - preNAD (preNID)
- Align filtered tiltseries -> apply to (CTF corrected) unfiltered tiltseries
- Identify features in filtered tomogram
- Extract particles from unfiltered tomogram

PreNAD vs. (post)NAD

- Maiorca et al. 2012 demonstrated more significant improvement from preNAD vs. NAD.
- Possible to do pre- and post filtering.



Pipeline Testing

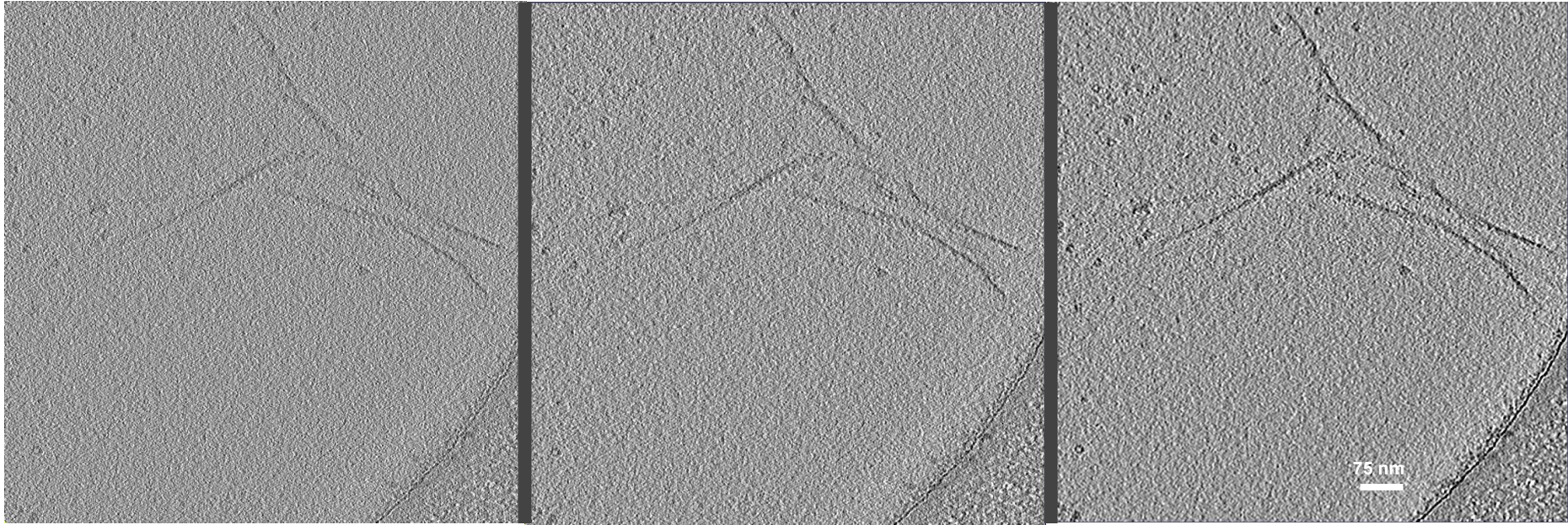
- Epsilon 15
 - High contrast
 - Large particles
- Isolated TRiC
 - Lower contrast
 - Small particles
- mHTT/TRiC
 - Lowest contrast
 - Heterogeneous
- Cellular tomograms (Jessica)

mHTT/TRiC Pre vs. Post Filtering

Unfiltered

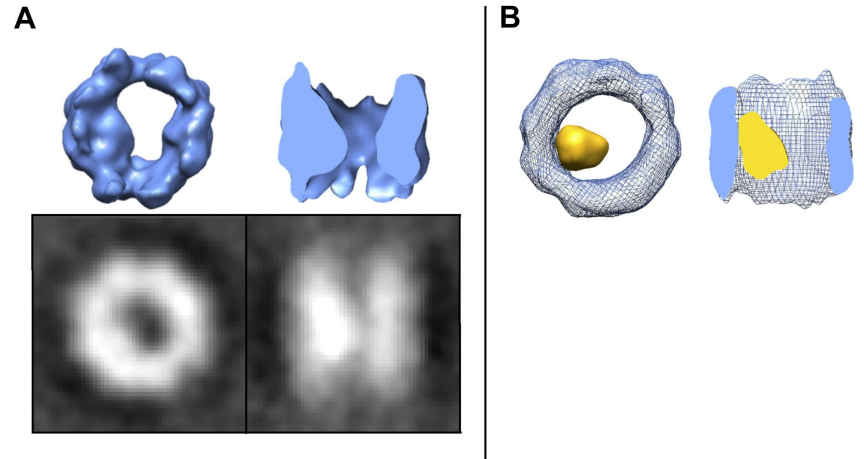
Post-reconstruction NAD

preNAD



TRiC/Huntingtin Data

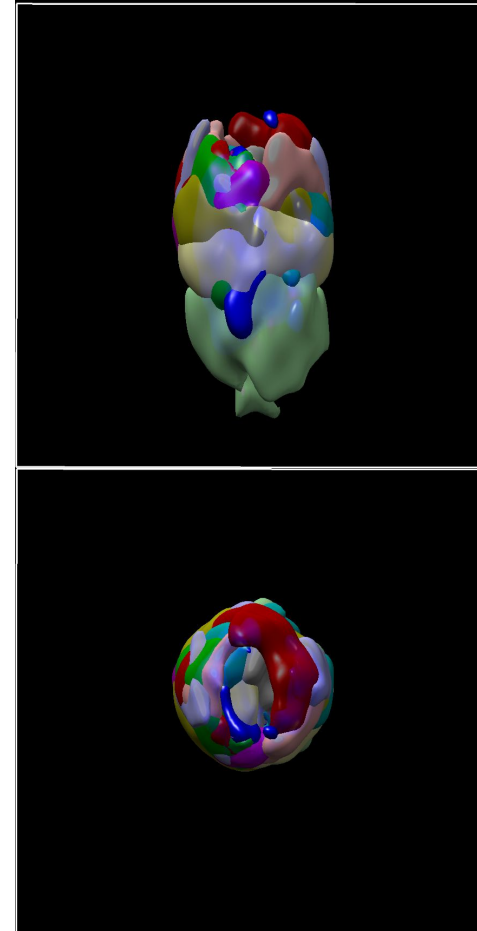
- Shahmoradian et al. 2013 showed TRiC inhibition of mutant huntingtin aggregation
- Wanted to process previously unused tiltseries to increase particle number
- Seeking to improve structure



New Boxing

- Using this pipeline, boxed ~1300 TRiC particles from ten tomograms. (vs. ~700)
- Some overlap with previously processed tiltseries, but still ~1000 particles from unused tiltseries
- Might allow for testing picking consistency

Unpublished results

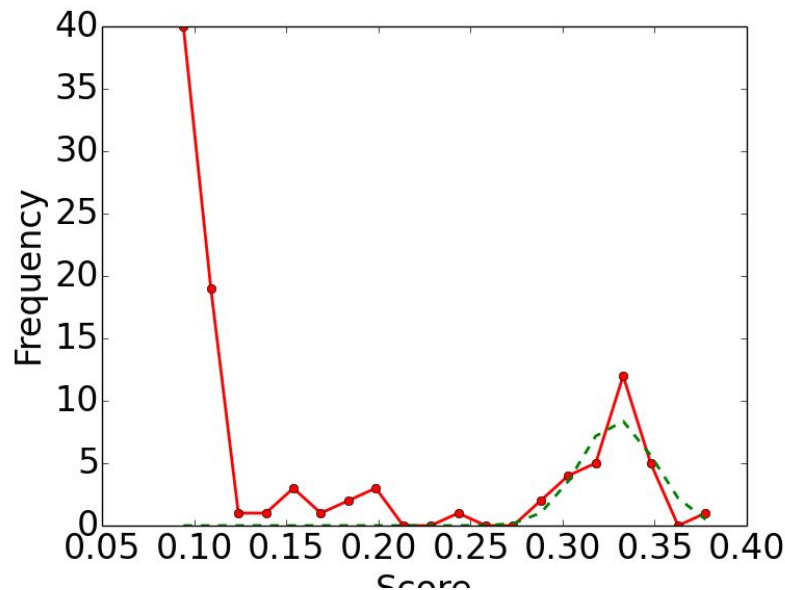


Template Matching

- Tested capabilities of existing template matching methods for incorporation into EMAN2 (improve e2spt_autoboxer)
- Template matching tools
 - Omnimatch
 - MOLMATCH
 - PyTom

PyTom

- Compilation problems
- Simplified Web Server
- No translation mode
- No symmetry mode
- Unwieldy output files
- Mathematically shaky particle number estimation
- Not GPU enabled



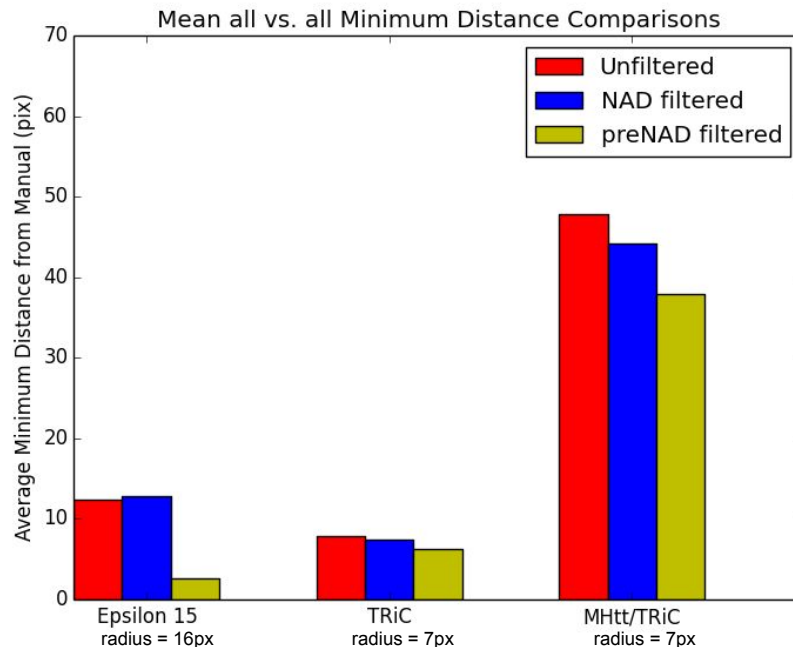
```
Activities Terminal
jgalaz@prism:~/pytom/pytomc
File Edit View Search Terminal Help
Good luck!
jgalaz@prism pytomc]$ ./compile.py --libDir ~/ /usr/lib64/ /usr/lib64/openmpi/lib --includeDir ~/ /usr/i
nclude/ /usr/include/python2.6 /usr/lib64/python2.6/site-packages/numpy/core/include/numpy/ /usr/include/
openmpi-x86_64/ ~/boost-1.30.1/boost --exeDir ~/ /usr/lib64/openmpi/bin --pythonVersion 2.6 --target all
Searching : mpicc Found : True
Searching : mpicxx Found : True
Searching : openmpicxx Found : False
Searching : mpicxx-openmpi-gcc45 Found : False
Searching : libmpi.so Found : True
Searching : mpi.h Found : True
Searching : Python.h Found : True
Searching : libpython2.6.so Found : True
Searching : fftw3.h Found : True
Searching : libfftw3.so Found : True
Searching : type_traits.hpp Found : True
Searching : ndarrayobject.h Found : True
Check compiling prerequisites:
```

Implement in EMAN2

- Improvements over PyTom
 - ease of installation/use
 - greater configurability
 - better parallelization (not forced to use MPI)
 - able to apply symmetry
 - further automation

Autoboxing with preNAD

- All vs. all particle minimum distance comparison.
- Improved automated picking with preNAD over postNAD.
- Further testing needed (more tomograms, more manual boxing to compare).



Coding Contribution

- Wrote `e2spt_pytom2eman.py`
- Wrote `e2spt_particledist.py`
- Fixed various bugs in `e2spt_boxer.py`
- Expanded `e2spt_coordsrefactor.py`

Future

- Jesus still processing TRiC data
- Using prefiltering pipeline for more accurate particle picking, allowing for higher resolution structures.
- Applying PyTom and filtering pipeline to TRiC data, microplatelets, etc.
- Once EMAN2 autoboxer implemented, running comparisons with PyTom.