

S2C2 High Resolution CryoET Image Processing Virtual Workshop

March 1-3, 2022

Agenda

Tuesday, March 1, 2022

Time	Title	Speaker
8:00 AM – 8:15 AM	Welcome Greeting and Introduction	Wah Chiu
8:15 AM – 9:45 AM	EM images: what you want vs. what you get and why	David DeRosier
9:45 AM – 9:55 AM	Break	
9:55 AM – 11:25 AM	Basics of Image Processing: from the data you have to the structures you'd like	Frederick Sigworth
11:25 AM – 11:35 AM	Break	
11:35 AM – 1:05 PM	Visualizing proteasomes in tomograms with ChimeraX	Tom Goddard
1:05 PM	End of Day	

Wednesday, March 2, 2022

Time	Title	Speaker
8:00 AM – 10:00 AM	CryoET processing toward atomic resolution (EMAN2)	Steven Ludtke
10:00 AM – 10:10 AM	Break	
10:10 AM – 12:10 PM	Continued: CryoET processing toward atomic resolution	Steven Ludtke
12:10 PM – 12:20 PM	Break	
12:20 PM – 2:00 PM	Continued: CryoET processing toward atomic resolution	Steven Ludtke
2:00 PM	End of Day	

Thursday, March 3, 2022

Time	Title	Speaker
8:00 AM – 10:00 AM	Using the Warp-RELION-M pipeline to obtain high-resolution structures from tilt series	Dimitry Tegunov
10:00 AM – 10:10 AM	Break	
10:10 AM – 12:10 PM	Continued: Using the Warp-RELION-M pipeline to obtain high-resolution structures from tilt series	Dimitry Tegunov
12:10 PM – 12:20 PM	Break	
12:20 PM – 2:00 PM	Continued: Using the Warp-RELION-M pipeline to obtain high-resolution structures from tilt series	Dimitry Tegunov
2:00 PM	Close of Meeting	

Requirements for the training:

Software & Data & Materials needed for presentations:

Second Monitor for laptop or a 27" monitor (at least) for desktop for running the tutorial and following the Zoom session simultaneously.

The minimum recommended specs for running Steven Ludtke's tutorial are:

- 16 GB RAM (8 GB may be possible if you don't have anything else going on the machine at all)
- 4 cores @ >2 ghz

- 20 gb free disk space
- a high-performance disk (SSD or RAID) will significantly reduce runtimes
- * a 1080P or better display is highly recommended, but not absolutely required

Software:

- **Tom Goddard's tutorial at 11:35 AM on first day**
 - ChimeraX 1.3: <https://www.rbvi.ucsf.edu/chimerax/download.html> – **PLEASE NOTE: THIS NEEDS TO BE DONE BEFORE FEBRUARY 28 AS THE CHIMERAX WEBSITE MAY BE DOWN BETWEEN FEBRUARY 28 – MARCH 2.**
 - Follow-along tutorial (may change): <https://www.rbvi.ucsf.edu/chimerax/data/rml-sep2019/proteasomes.html>
- **Steven Ludtke's tutorial on second day**
 - For the EMAN2 sessions, requirements to participate are:
 - Install a current snapshot version of EMAN2 (not the last 2.91 release): https://cryoem.bcm.edu/cryoem/downloads/view_eman2_version/25 or https://blake.bcm.edu/emanwiki/EMAN2/COMPILE_EMAN2_ANACONDA
 - Download the "small" tutorial data set: http://blake.bcm.edu/dl/tutorial_tomo_mini.zip
 - We will be going through the tutorial here: <https://blake.bcm.edu/emanwiki/EMAN2/e2TomoSmall>
 - Longer instructions for participants for the EMAN2 demo day:
 - General EMAN2 information is available at <https://eman2.org> (also <https://blake.bcm.edu/emanwiki/EMAN2>)
 - If you wish to participate, not just observe, **you MUST have the latest snapshot version of EMAN2 (not the 2.91 release) installed prior to the workshop.** With >200 registrants there is no way we will be able to help individuals debug their specific installations during the session. Clearly you can just observe the tutorial rather than doing it yourself, but you won't learn as much that way.
 - Installing EMAN2 from source isn't much more difficult than installing the binaries, and is the recommended strategy for current snapshots: https://eman2.org/COMPILE_EMAN2_ANACONDA but fairly up to date binaries are also available: <https://eman2.org/Install/BinaryInstallAnaconda>
 - Please download the tutorial data in advance: http://blake.bcm.edu/dl/tutorial_tomo_mini.zip
 - The tutorial itself is here: <https://eman2.org/e2TomoSmall>
- **Dmitry Tegunov's tutorial on third day**
 - Software:
 - Warp 1.0.9 nightly build (www.warpem.com),
 - Cube (www.github.com/dtegunov/cube),
 - RELION 3.2 (www.github.com/3dem/relioln),
 - IMOD 4.8 or newer (bio3d.colorado.edu/imod/)
 - Data:
 - Tilt series from EMPIAR-10491 (<https://www.ebi.ac.uk/empiar/EMPIAR-10491/>).
 - optionally (will be discussed, but not processed) EMPIAR-10499 (<https://www.ebi.ac.uk/empiar/EMPIAR-10499/>)