

Tomography workshop

Login instructions

Each participant will be getting a public IP address and a public URL besides their name in the excel sheet.

Go to the browser of your choice (Chrome and Firefox preferred) and copy-paste the URL from excel sheet

URL format:

`https://your-public-ip:8443#workshop`

It will give a certificate warning that the site can be deceptive or cannot be trusted.

For Chrome, Advanced -> Proceed to IP ADDRESS (unsafe)

For Safari, Show details -> Visit website

For Firefox, Advanced -> Accept risk and continue

Login: ec2-user

Password: workshop2021

Disclaimer: Users can face network latency depending on their location and network connectivity. Some commands will take a while to execute and it can get slower

Try to avoid full screen. And if the screen froze for some reason, login to the instance using the same URL and credentials.

VNC

Download a **VNC viewer** for your computer. RealVNC or TigerVNC are good options:

<https://www.realvnc.com>

<https://tigervnc.org>

Appion-Protomo (<https://github.com/nysbc/appion-protomo#example-1->)

You can directly browse myamiweb over the browser by entering the following URL:

`http://your-public-ip/myamiweb`

(**Note:** this is *http*, not *https*.)

Datasets: `/home/ec2-user/appion-protomo/emg/data/tiltseries`

It is also pre-loaded inside the docker container.

`/emg/data/tiltseries`

Since the datasets are pre-uploaded, **you should skip the step from the tutorial:**

“Upload first SerialEM-formatted tilt-series to a new session”

▼ **1** Upload first SerialEM-formatted tilt-series to a new session

Make sure your container is running via the `./run.sh` script.

- From inside the `appion-protomo` directory (on the host machine, not inside the container), do the following:

```
Download the following hemagglutinin SerialEM tilt-series (collected on an F20 with a DE-20; from [EM
https://drive.google.com/open?id=1remm05G-R7w_6GLjW1R_jmV6Qzg0fcMx
tar -zxvf HASlow1.tar.gz <your appion-protomo/emg/data/tiltseries/ directory>
```

To execute commands from the command line, open your VNC viewer and connect to:

`your-public-ip:5901`

(password: `appion-protomo`)

And now execute commands.

Dynamo (<http://dynamo-em.org>)

To begin using Dynamo, do the following:

```
cd ~/dynamo/
source dynamo_activate_linux_shipped_MCR.sh
cd ~/tomogram/
dynamo gui
```

We will be going through the template picking, filament picking, and membrane modelling tutorials here:

https://wiki.dynamo.biozentrum.unibas.ch/w/index.php/Walkthrough_for_template_matching

<https://wiki.dynamo.biozentrum.unibas.ch/w/doc/misc/modelFilament.pdf>

<https://wiki.dynamo.biozentrum.unibas.ch/w/doc/misc/modelMembrane.pdf>

EMAN

Login into the instance by referring to the login instructions mentioned above

Open terminal and activate your conda environment

```
conda activate
```

Make sure the system works properly

```
e2speedtest.py
```

Make a new directory and cd into it

```
mkdir workshop
```

```
cd workshop
```

Then start the GUI

```
e2projectmanager.py
```

It takes a couple of minutes to load the GUI

To test the GPU/CUDA installation

```
~/eman2-sphire-sparx/examples/test_tensorflow.py
```

Datasets are preloaded at the following directory path:

/data (when you go to Import tiltseries > Browse, type "/data" into Path:)

Follow the tutorial here:

<https://blake.bcm.edu/emanwiki/EMAN2/e2TomoSmall>

For GPU instances, automatic particle selection can be used following the tutorial here. It also works with the CPU, but will be 10-20x slower.

https://blake.bcm.edu/emanwiki/EMAN2/e2tomo_more#Automated_particle_selection

Semi-automatic tomogram segmentation tutorial can be found here. It also uses the GPU and will be much slower for CPU only instances.

https://blake.bcm.edu/emanwiki/EMAN2/e2tomo#Tomogram_annotation_.28optional.29

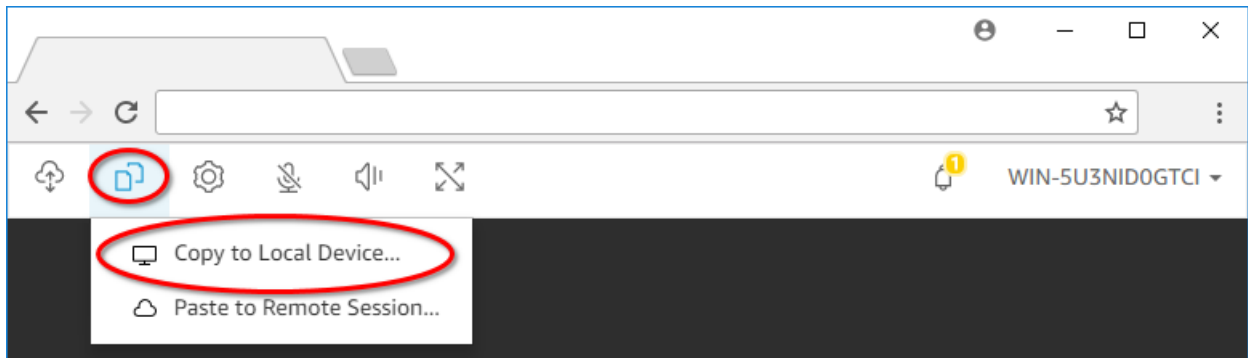
To download data to local machine

http://blake.bcm.edu/dl/tutorial_tomo_mini.zip

Common instructions

To copy text from the instance to your local computer

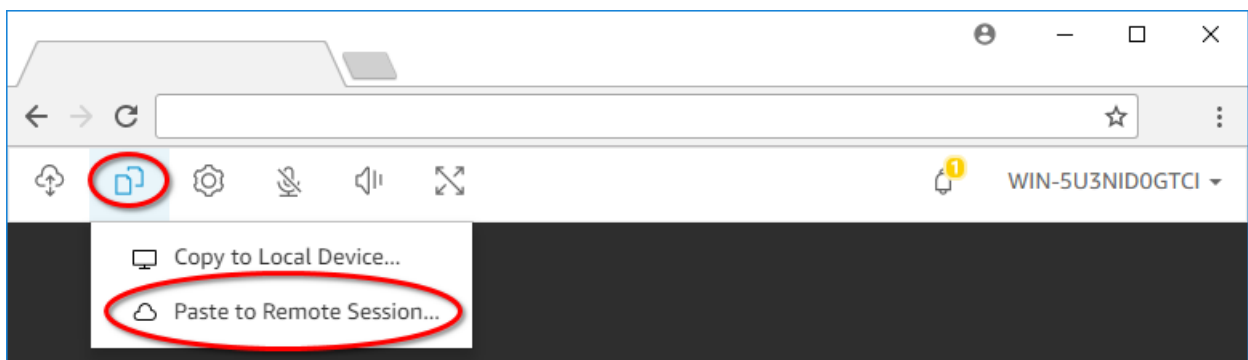
In the web browser, highlight the text to copy and choose Clipboard, Copy to Local Device located in the top-left corner of the interface.



The text is now placed in your computer's clipboard. You can paste it using the paste keyboard shortcut

To copy text from your local computer into the instance

On your local computer, copy the text using the copy keyboard shortcut or right click to copy text. In the web browser, choose Clipboard, Paste to Remote Session located in the top-left corner of the interface.



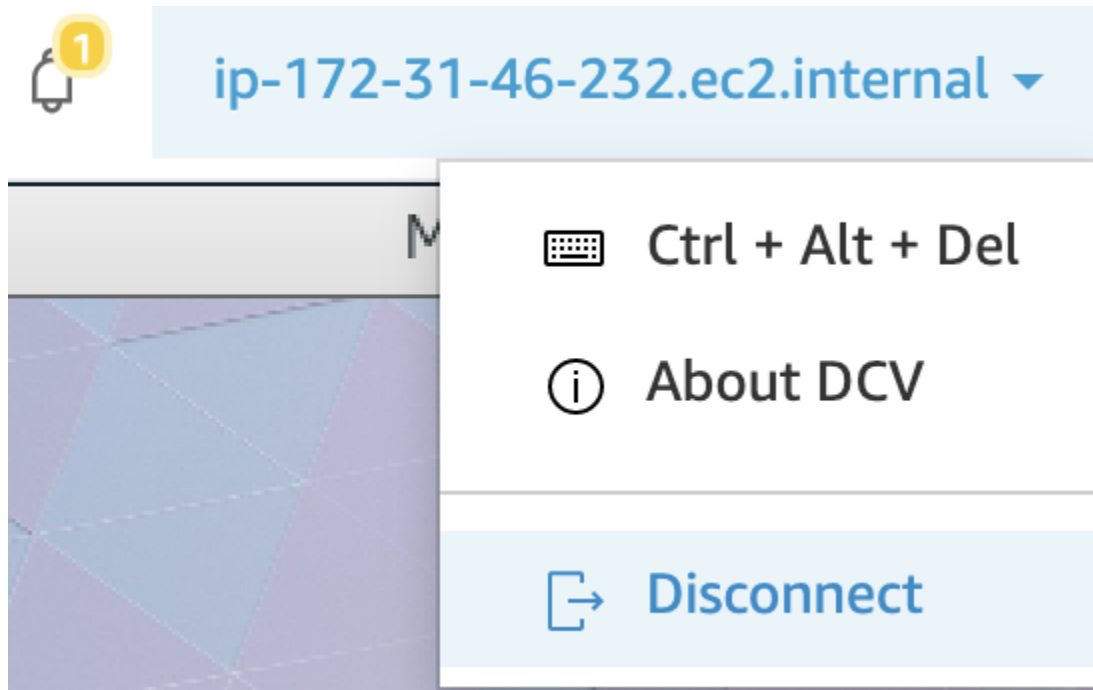
The text is now placed in the NICE DCV session clipboard. You can paste it using the host operating system's paste shortcuts.

Screen layout

Adjust the screen layout command as per your machine by entering the command below:
`dcv set-display-layout --session workshop 1920x1080+0+0`

Session Disconnect issue

Please don't disconnect the session. You will lose connection to the instance.



Instead simply close the browser tab when you're done or not actively using the instance