

Installation

- Continuous build
<https://blake.bcm.edu/emanwiki/EMAN2/Install/BinaryInstallAnaconda>
- Build from source
https://blake.bcm.edu/emanwiki/EMAN2/COMPILE_EMAN2_ANACONDA

Mini tutorial

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

Download

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

Other tools

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

https://blake.bcm.edu/emanwiki/EMAN2/e2tomo_new

Basic usage and visualization

[e2projectmanager.py](#)

- Browser
- Help

Import tilt series

- Import tilt series stack
[Raw data - Import tilt series](#)
- Micrographs with angle in file name
[Raw data - Generate tilt series](#)

Reconstruct tomogram

[3D reconstruction - Reconstruct tomograms](#)

- Landmark based alignment
- Patch tracking

CTF estimation

[3D reconstruction - CTF estimation](#)

- Handedness testing

Reconstruct all tomogram

All CTF estimation

Evaluate tomograms

[Analysis and Visualization - Evaluate tomograms](#)

Particle selection

- Manual boxing
[Subtomogram averaging - Manual boxing](#)

- Template matching
[Subtomogram averaging - Reference-based boxing](#)
- Import from segmentation
[Segmentation - Find particles from segmentation](#)
- Deep learning boxing
[Subtomogram averaging - Convnet based auto-boxing](#)

Extract particles

[Subtomogram averaging - Extract particles](#)

Initial model generation

[Subtomogram averaging - New initial model generation](#)

Subtomogram refinement

[Subtomogram averaging - New 3D refinement](#)

Heterogeneity analysis

- Mask crafting
[e2display browser - filter tool](#)
- Multimodel refinement
[e2spt_refinemulti_new.py](#)
- Continuous movement
[e2spt_trajfromrefine.py](#)