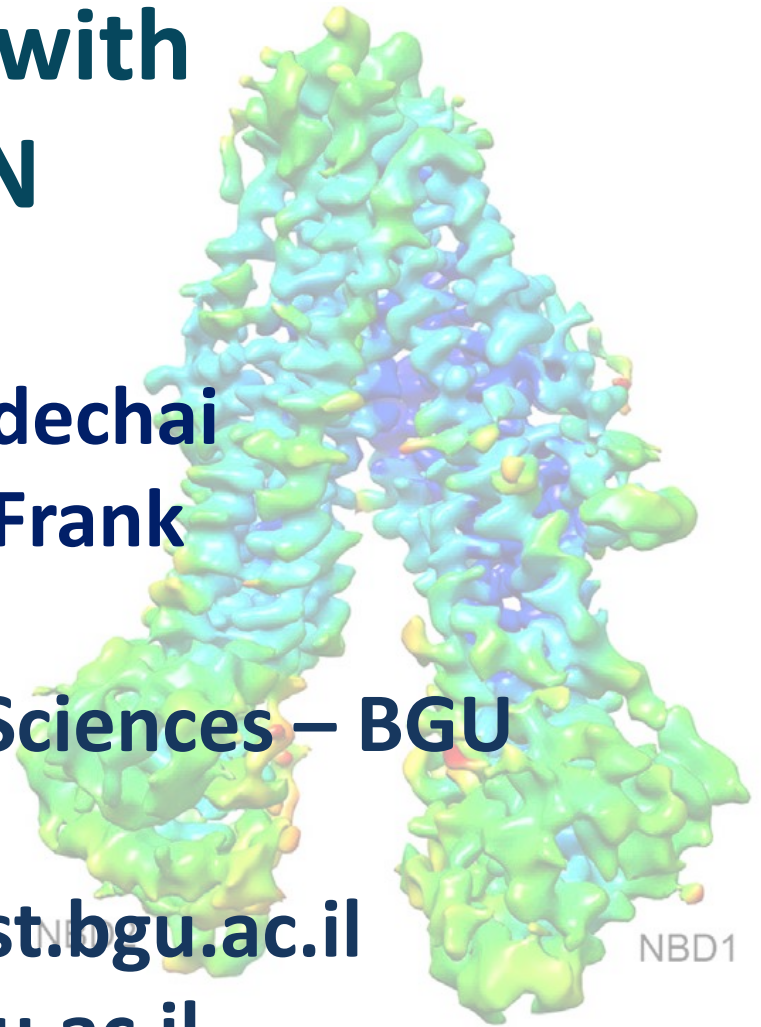


2D classification and initial model building with EMAN

**Amitai Mordechai
Gabriel A. Frank**

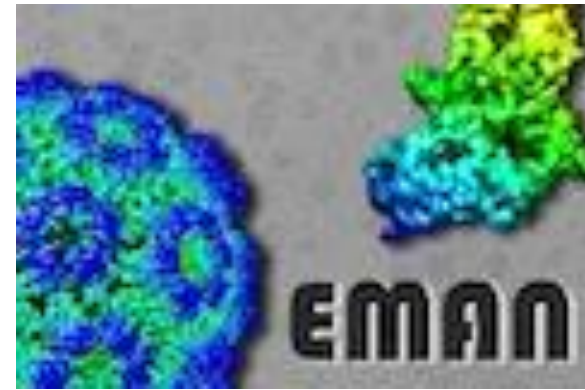
Department of Life Sciences – BGU

**Mordeami@post.bgu.ac.il
frankg@bgu.ac.il**



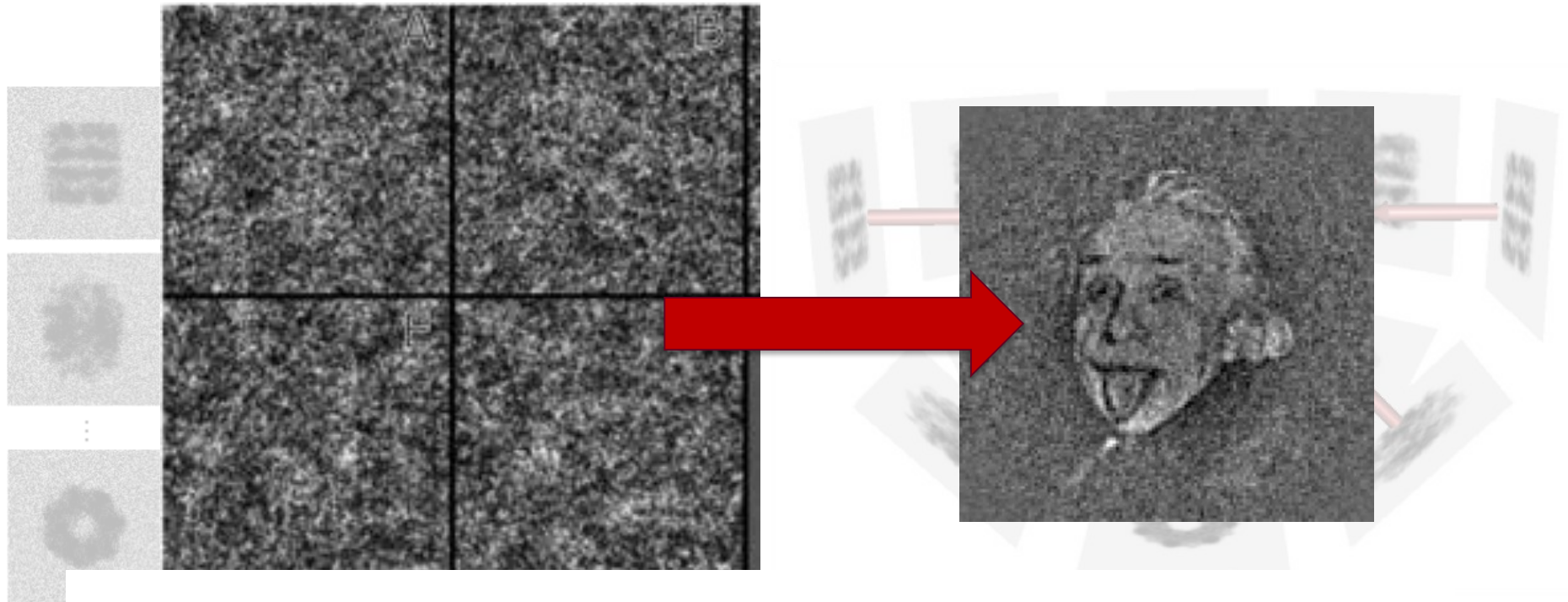
EMAN2

- EMAN2 is a group of programs, utilities and a pipeline for EM image processing
- EMAN excels in several topics:
 - Quick computation on small computers
 - Tweakable 3D initial model building
 - Template based and AI based particle picking



Maintained by S. Ludtke
Baylor College of Medicine
(<https://blake.bcm.edu/emmanwiki/EMAN2>)

Single particle reconstruction

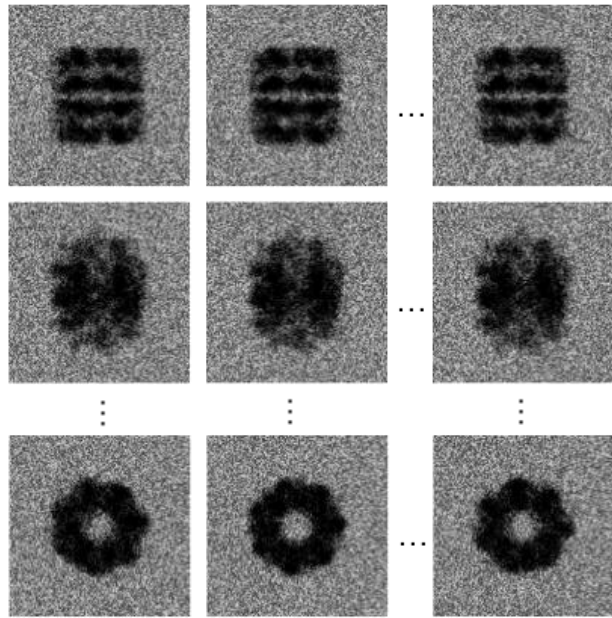


Reconstruction is a type of a fit!!!

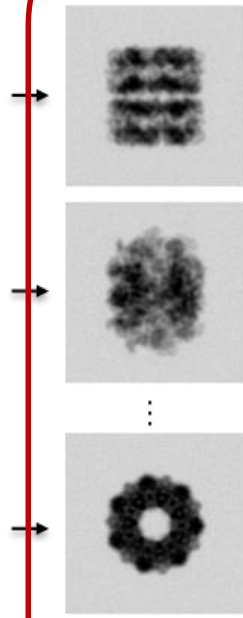
- We determine the shifts and rotation parameters of each particle
 - Very high noise

Clear need for a good initial guess for expectation maximization to succeed

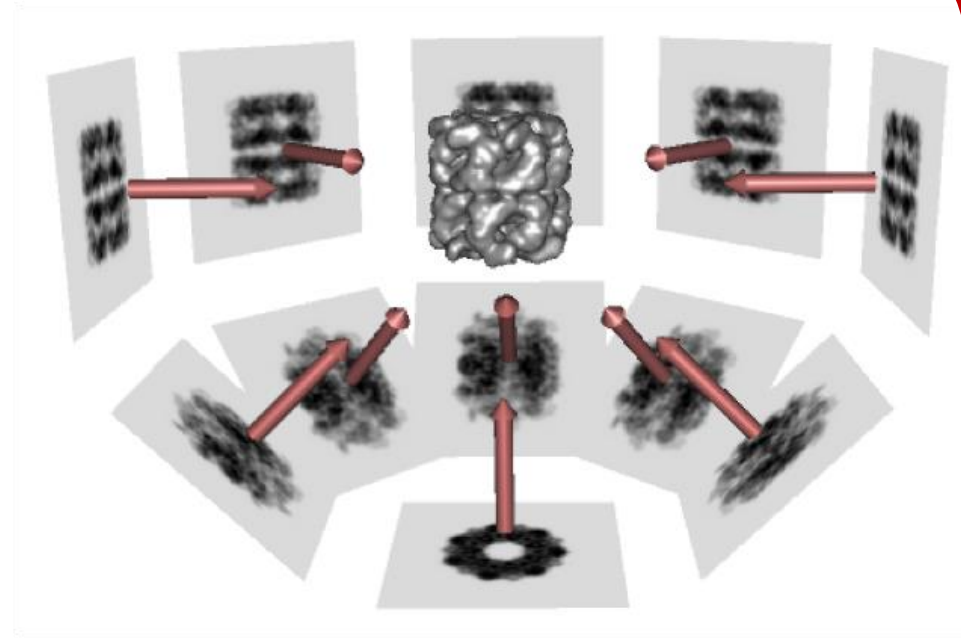
Single particle reconstruction



Particle peaking



Class averages



Reconstruction

**EMANS strategy: 2D Classes averages are less noisy
Used them for generating the initial model**

We can learn from 2D class averages

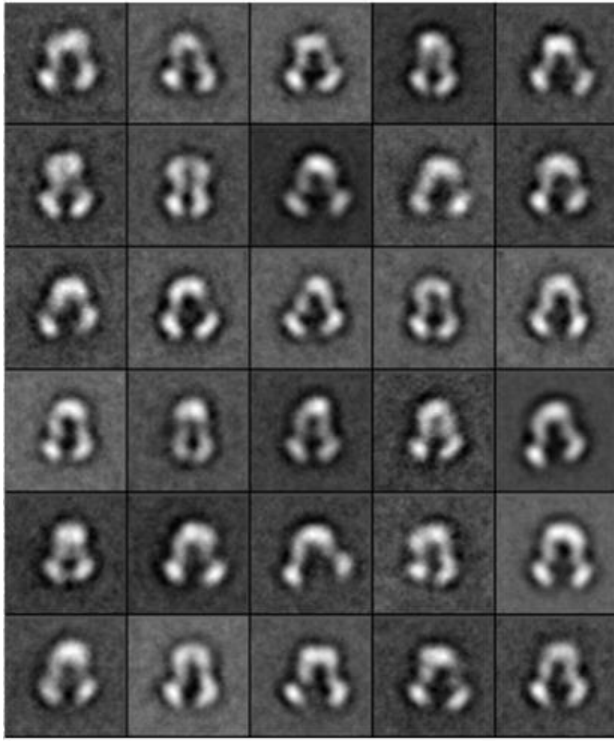
2D class averages is the last unbiased look you have on your data!



Data quality:

Look for secondary structure elements

Flexibility – DDM vs nanodiscs

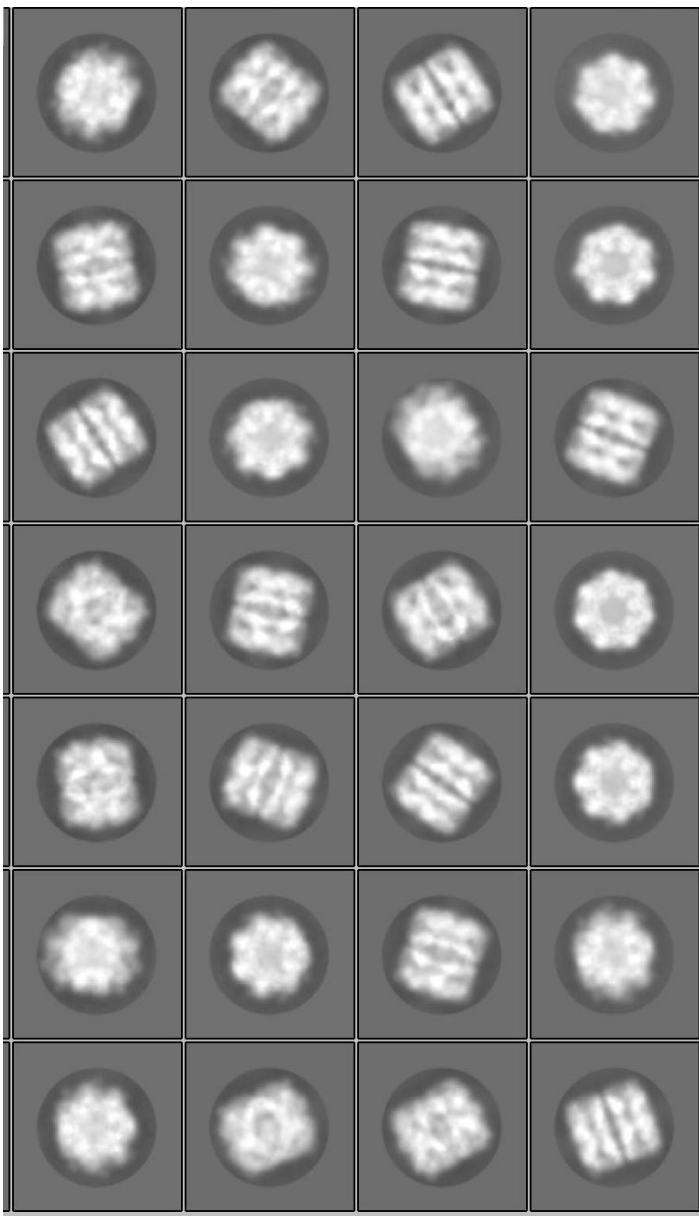


DDM

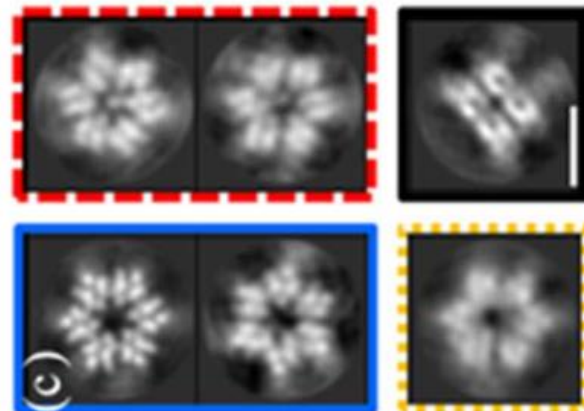


POPG nanodiscs (MSP1D1)

Quality of the biochemistry: (negative stain in this case)



- Preferred orientation
- Integrity of molecular complexes
- Symmetry and number of units
- Class average which are mirror image of each other – **A good sign**
- Compositional and conformational variability



What to look for in your 3D model

- Features with handedness
- Good fit of the projections to the 2D classes

Tricks

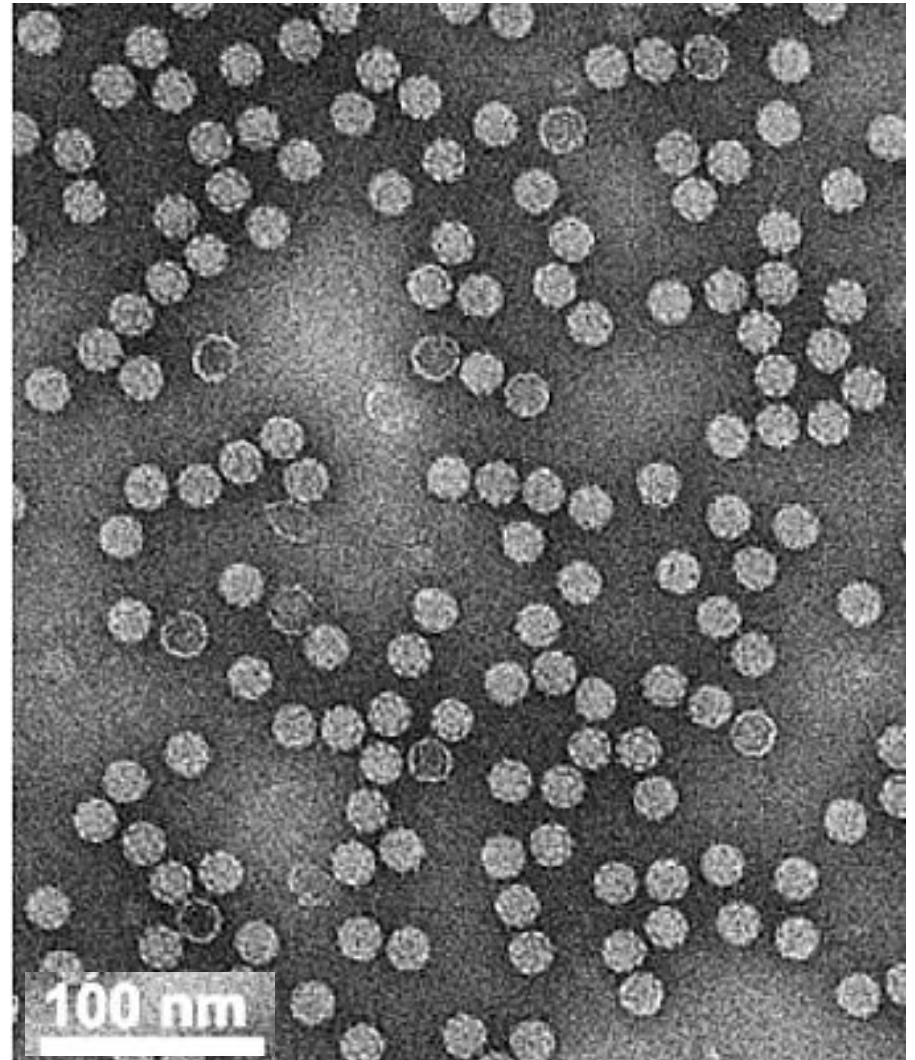
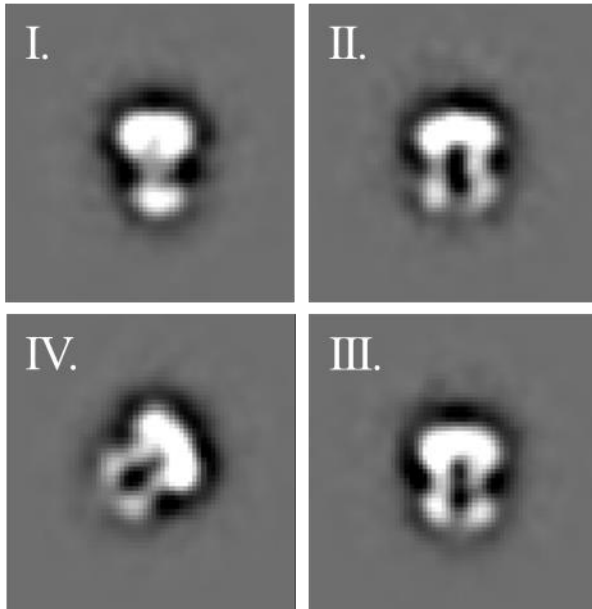
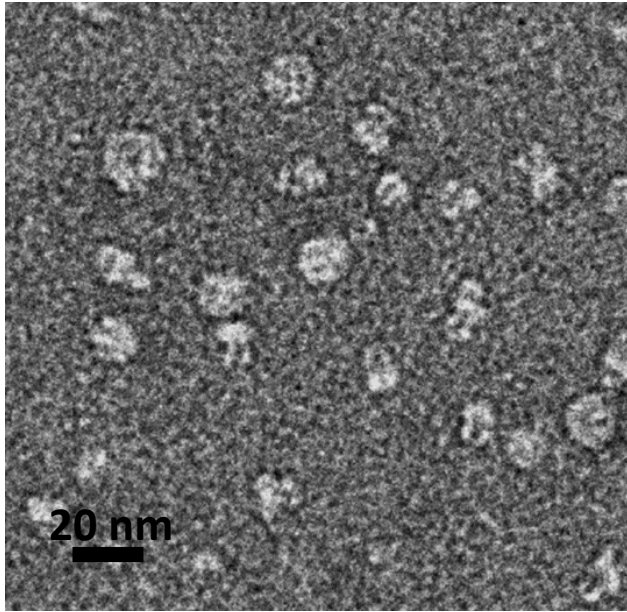
- Automatically deleted classes can be added in a larger number to insure their incorporation
- Class averages can be introduced from any other program
- Reduce box size in case of “long” artificial horns

Thanks

Yehuda Baruch – BGU

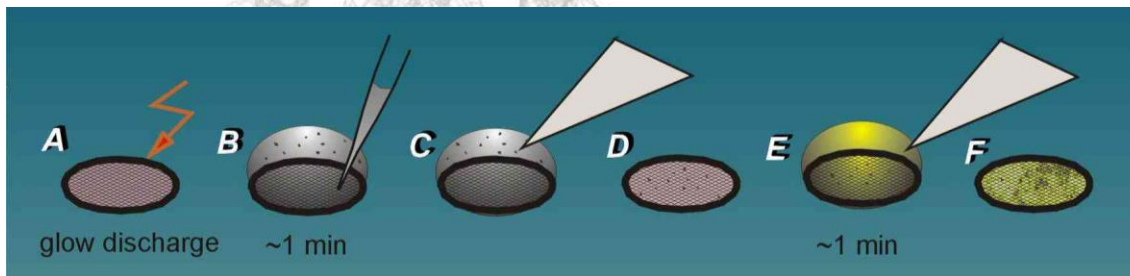
Mario J. Borghia - NIH

Negative staining microscopy



Negative staining microscopy - protocol

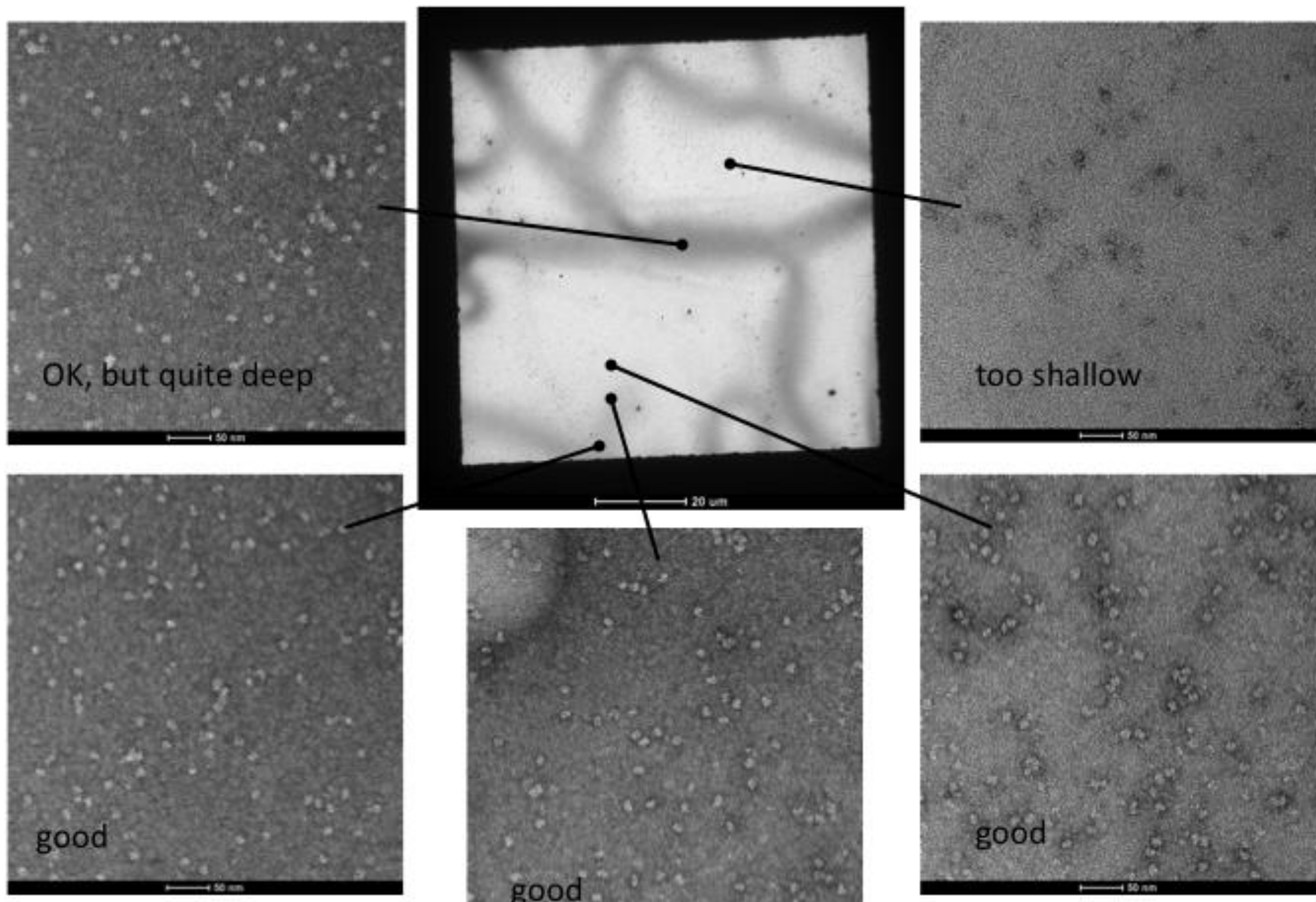
- A sample deposited on a carbon coated grid
- Most of the sample is wicked off
- A drop of staining solution is placed on top of the sample
- Most of the staining solution is wicked off – the rest is allowed to dry
- Staining encloses the structure of interest in a metal salt



- Uranyl Acetate or Formate pH 4-5
- Ammonium Molybdate pH ~7
- Methylamine Vanadate, Methylamine Tungstate



Negative staining microscopy – in the TEM



Negative staining microscopy

- Quick and affordable
- Easy to do and analyze
- Very good for quality control and testing homogeneity of the samples
- Quick low resolution epitope mapping
- Only ~20-25 Å
- Artifacts: Effects of pH, interaction with the carbon, samples are “squashed”

