Lecture 10

EMAN2

Chimera

Chimera

Run chimera, and open a MRC model and a PDB model

Tools->General Controls->IDLE (may be on a different menu in other vers.)

```
>>> om=chimera.openModels
>>> om.list()
[<_surface.Surface_Model object at 0xf4ebf9c8>,
<_chimera.Molecule object at 0xf46e16b0>]

>>> a=om.list()[0]
>>> dir(a)
...
>>> a.display=False
>>> a.display=True
```

Chimera

```
>>> xf=a.openState.xform
>>> dir(xf)
...
>>> xf.yRotate(25.0)
>>> a.openState.xform=xf
```

Modify EMANimator:

chimeraext/Animator/ModelParms_chimera.py

chimeraext/Animator/Animator.py

EMAN2

```
>>> from EMAN2 import *
>>> img=test_image()

>>> imgs=EMData.read_images(“imgs.hed”)              <-- reads all images
>>> imgs[0].get_attr_dict()
...
>>> for i in imgs: print i.get_attr(“maximum”)
...
>>> img=EMData()
>>> img.read_image(“file.mrc”)
>>> print img.get_xsize(),img.get_ysize,img.get_zsize()
...
>>> for i in imgs[1:]: imgs[0]+=i
>>> imgs[0]/=len(imgs)
>>> display(imgs[0])
>>> imgs[0].write_image(“out.mrc”)
```

Using a Processor

- dump_processors()
- dump_processors_list() – introspection

```
a=EMData()
...
b=a.process(“name”,{“m”:2.0,”b”:1.0})
```

– or –

```
a.process_inplace(“name”,{key:value,key:value})
```

– or –

```
# if initialization is expensive
p=Processor.get(“name”,{k:v,k:v})
for i in imgs:
    p.process_inplace(i)
```

Other Modular classes

- dump_aligners()
  - newimg=img.align(“name”,img2,{k:v},”cmpname”,{k,v})

- dump_cmps()
  - img.cmp(“name”,img2,{k:v})

- dump_projectors()
  - prj=vol.project(“name”,{k:v,k:v})

Other Modular classes

- dump_reconstructors()

```
r=Reconstructors.get(“name”,{k:v,k:v})
r.setup()
r.insert_slice(img,Transform3D)
...
vol=r.finish()
```

- dump_averagers()

```
r=Averagers.get(“name”,{k:v,k:v})
r.add_image(img)
...
avg=r.finish()
```