

Northeastern Collaborative Access Team

# EDNA at NE-CAT

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# **NE-CAT Beamlines**

#### 24ID-C

- Variable energy beamline: 6-21keV
- Focused beam flux: 10<sup>14</sup> photons/s
- Focal spot: 20 microns (v) x 60 microns (h)
- MD2 micro-diffractometer with apertures down to 5 microns and SC3 Minikappa

#### • 24ID-E

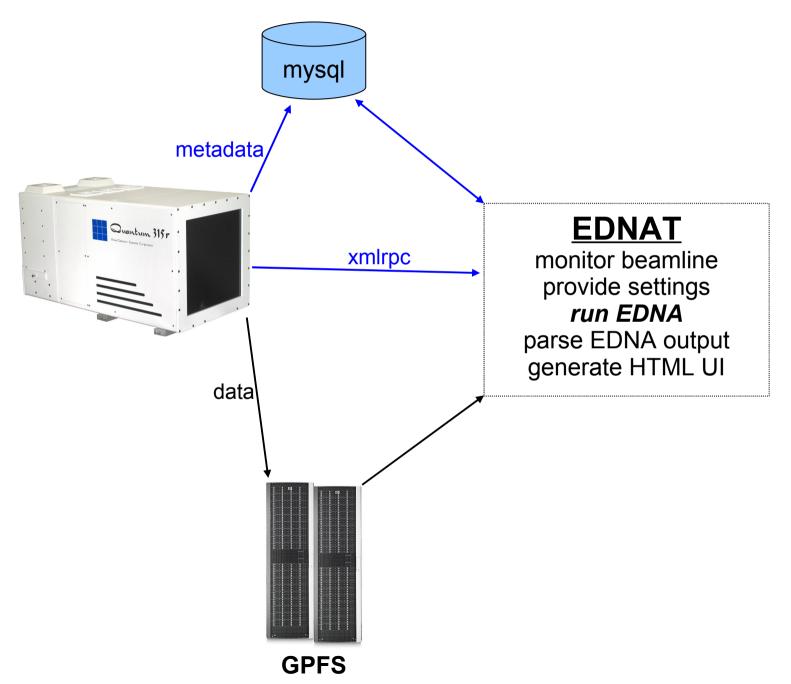
- Fixed energy beamline: 12662eV (Se Peak)
- Focused beam flux: 10<sup>13</sup> photons/s
- Focal spot: 20 microns (v) x 1000 microns (h)
- MD2 micro-diffractometer with apertures down to 5 microns

# How Is EDNA Used?

 Currently EDNA is the data-processing core for our automated data collection strategy generation

- Every snap that is recorded is processed.
- Each distinct "trip" has its own html GUI with all the snaps processed.
- Currently all files are on the local filesystem & copied to users' directory for transport home.

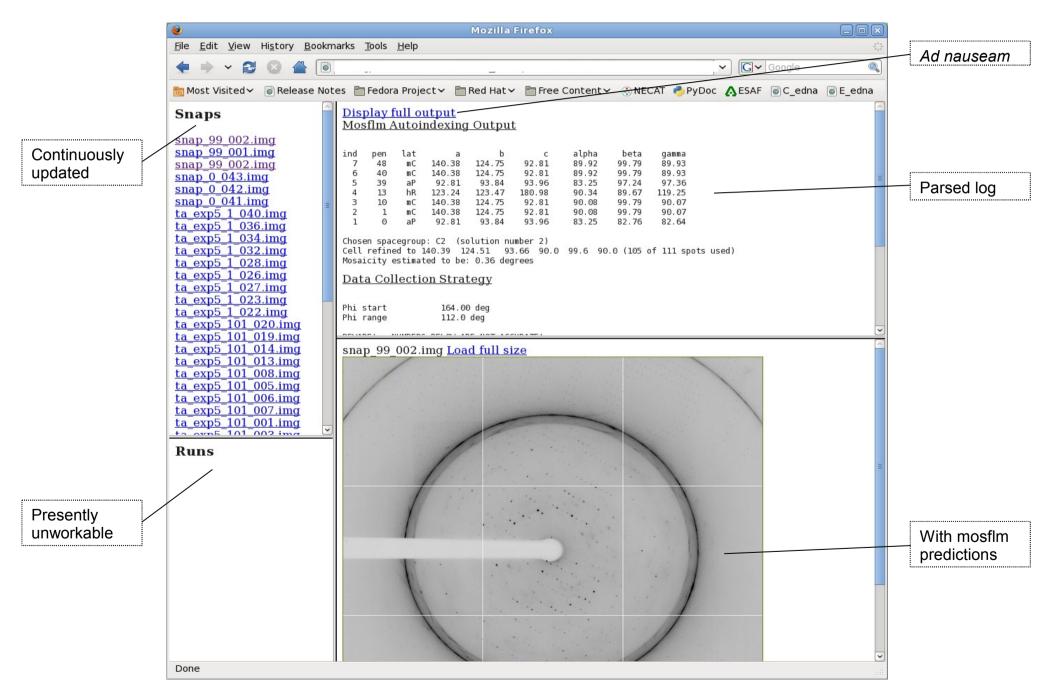
### **NECAT Data Flow**



### **NECAT EDNA Control UI**

	Preferences 🗙			
,		Anomalous	False 🗘	
Controls		Spacegroup Override	None	Autoindexing
remote connections		Hi Res Cutoff (A)	3.5	options
		Transmission (%)	AUTO	From
		Aperture Size (um)	AUTO 💲	beamline
Start		Crystal Size (x,y,z um)	100 100 100	
<u>Stop</u>		Ratio crystal:beam	2.0	
Preferences		Sample Type	protein 🗘	
Quit		Molecules in unit cell	1 🗘	
		Residues per Molecule	250	
		Susceptbility	1.0	BEST options
		BEST complexity	none 🗘	I
EDNAT wraps EDNA and provides:	$\mathbf{i}$	Max Total Exposure (s)	120	
Control UI (wxPython)		Minimum Exposure per Image (s	5) 1	
Beamline monitoring Image collection monitoring	$\backslash$	Override user directory	False 🗘 None	
EDNA calling & monitoring		Override working directory	True 🗘 /gpfs1/users/necat/fmurphy/	
Output parsing Output UI (HTML)			<mark>⊗ c</mark> ancel 🧶 <u>O</u> K	

### **NECAT EDNA Results UI**



## **EDNA Implementation**

 GUI is actually parsed logfile, xml was explored, but parsing logfile was easier

 RADDOSE is calibrated to a test crystal experimentally

 Modules, input.xml and command line modified to take a range of keywords

## Additional Keywords

- crystal size x, y, z
- beam size x, y, gauss
- susceptibility
- # monomers, residues, heavy atoms, copies in ASU
- shape
- anomalous
- indexing high resolution
- changed default solvent content 47% -> 55%

## **Problems in Implementing**

Program versions mismatching – mosflm, Best

Prototype fails due to results being too precise
– if result off by 0.0001 = Failure

 Default settings are too buried – being in one top level module would make more accessible

Running time dependent on directory tree size
– seems to be a python module search issue

### EDNA Weaknesses (an end user's view)

No GUI

Not enough "intelligence" at decision points

e.g. autoindexing resolution setting

Logging and directory structure is overly burdensome

Integration does not work

Defaults are inaccessible