EDNA at Diamond





Why is Diamond developing software

- To help users maximise their beamtime by helping users get as much from their data and samples.
- Because of this:
 - Software must be fast to allow feedback within a reasonable timescale.
 - Software must be as automated as possible as users are otherwise occupied (or at best tired ⊗!).
 - Data collection is only a part of the process so the scientific software presented to the users at Diamond must be all encompassing.
- 'Remote' beamtime.



EDNA activities (Active/deployed)

- EDNA Kernel
- EDNA MX Characterisation V1, (Alun session 2)
 Deployed and investigating best way to use it
- DArc EDNA Archiving pipeline
 - Actively developed, prone to system failures
- EDNA Tomography Pipeline, (Mark)
 - Used but bespoke
- DIMPLE, EDNA Difference Map Pipeline, (Ronan)
 - Non EDNA prototype available to users
 - SAXS automated ab initio low resolution shape determination (GNOM/DAMMIN)
 - Early stages



Future (not started) EDNA applications

• Spectroscopy

XIA2

- Further SAS pipelines
- Data reduction manager
 - (we run many data reduction packages and the tasks need managing)

MX structure Solution



Current resources

- Out of a scientific software team of 8 developers supporting all diamond science beamlines, 6 are capable of developing/have developed EDNA applications, 5 are actively developing a range of applications.
- ~2.5 FTE developing EDNA Kernel, MXCharaterisation, DIMPLE, DArc, Tomography and SAXS.



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Automated ab initio low resolution shape determination

XSDataInputSolutionScattering experimentalDataQ : XSDataFloat [0*] experimentalDataValues : XSDataFloat [0*]	XSDataResultSolutionScattering corelationFitValues : XSDataFloat [0*] fitFile : XSDataFile lineProfileFitQuality : XSDataFloat logFile : XSDataFile pdbMoleculeFile : XSDataFile pdbSolventFile : XSDataFile scatteringFitQ : XSDataFloat [0*] scatteringFitValues : XSDataFloat [0*]	Control Plugin for the whole process. It should estimate optimal rMax value for GNOM and run multiple instances of DAMMIN/ DAMMIF for different particle shapes in parallel.	SolutionScattering control plugin will automate small angle scattering data processing by running GNOM and DAMMIN/DAMMIF programs for optimal reconstruction of the shape of the sample. Control plugin will iterate
EXSDataInputGnom experimentalDataQ : XSDataFloat [0*] experimentalDataValues : XSDataFloat [0*] rMax : XSDataFloat	XSDataResultGnom fitQuality: XSDataFloat output: XSDataFle scatteringFitQ: XSDataFloat [0*] scatteringFitValues: XSDataFloat [0*] radiusOfCrossSection: XSDataFloat radiusOfCrossSection: XSDataFloat	Execution plugin which launches and runs GNOM. This plugin is likely to be run multiple times to refine rMax value.	
SSDataInputDammin expectedParticalShape : XSDataInteger gnomOutputFile : XSDataFile initialDummyAtomModel : XSDataInteger pdbInputFile : XSDataFile symmetry : XSDataString	radiusOfGyration : XSDataFloat XSDataResultDammin fitFile : XSDataFile logFile : XSDataFile pdbMoleculeFile : XSDataFile pdbSolventFile : XSDataFile XSDataResultDammif	Execution plugins for launching DAMMIN and DAMMIF.	GNOM runs to obtain optimal value for rMax parameter and run several instances of DAMMIN/DAMMIF with different particle shapes in parallel.
expectedParticalShape : XSDataInteger gnomOutputFile : XSDataFile initialDummyAtomModel : XSDataInteger pdbInputFile : XSDataFile symmetry : XSDataString	fitFile : XSDataFile logFile : XSDataFile pdbMoleculeFile : XSDataFile pdbSolventFile : XSDataFile		diamond

SolutionScattering plugin: Current status

- Execution tests for all plugins are implemented using Lysosyme test data supplied with GNOM/DAMMIN/DAMMIF.
- Input/Output data is referenced in the corresponding .xml configuration files.
- Execution plugin tests can be run independently.
- Pipeline test makes single run of GNOM with the default rMax value (50). The output data is processed using DAMMIF with the spherical particle model.

