

Automating reflectometry reduction and analysis at Diamond Light Source

M4 Colloids — 2019/07/12

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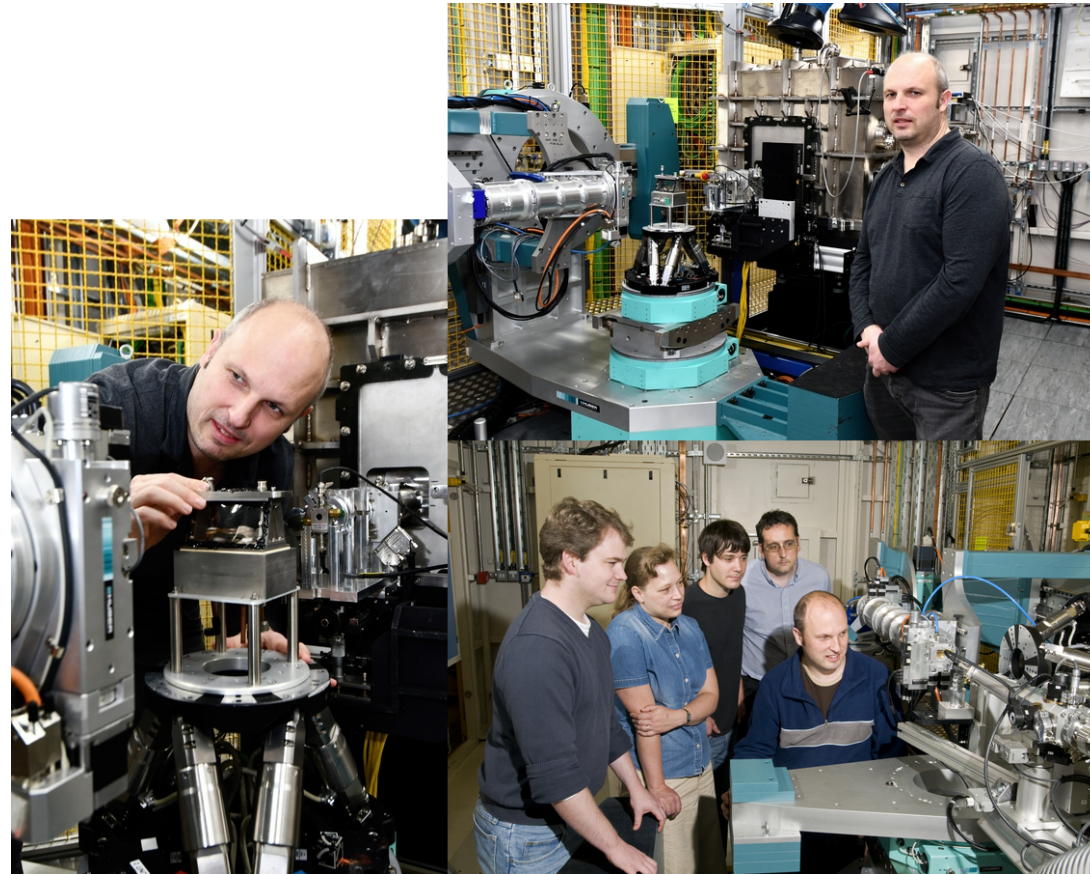
@ andrew.mccluskey@diamond.ac.uk

an_drewmcc

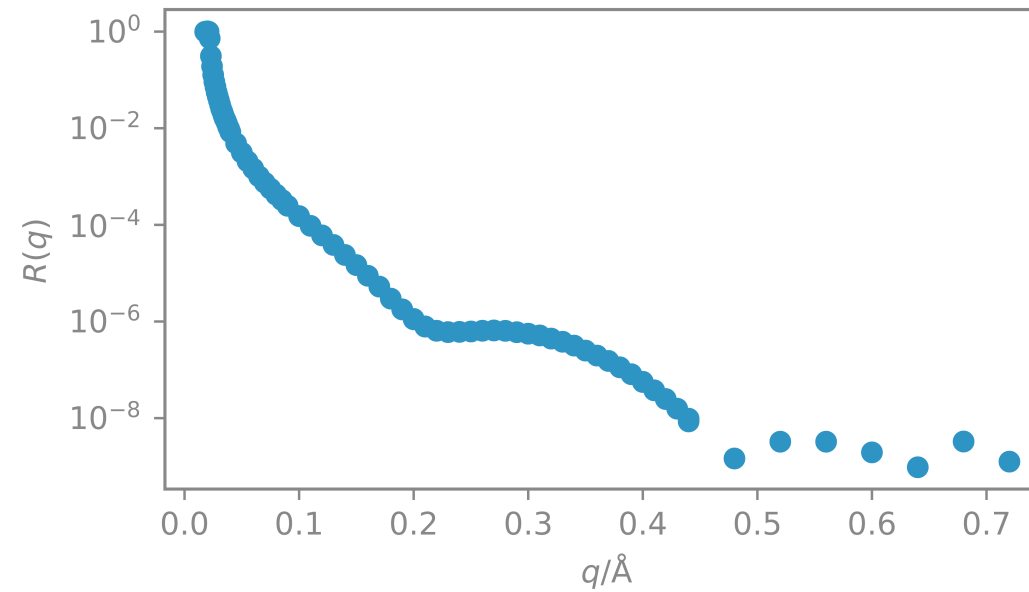
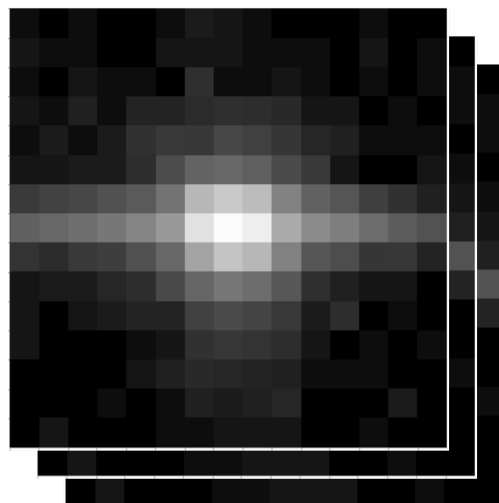
♂ (he/him)

reflectometry is a tool that uses x-rays or neutrons to probe interfaces

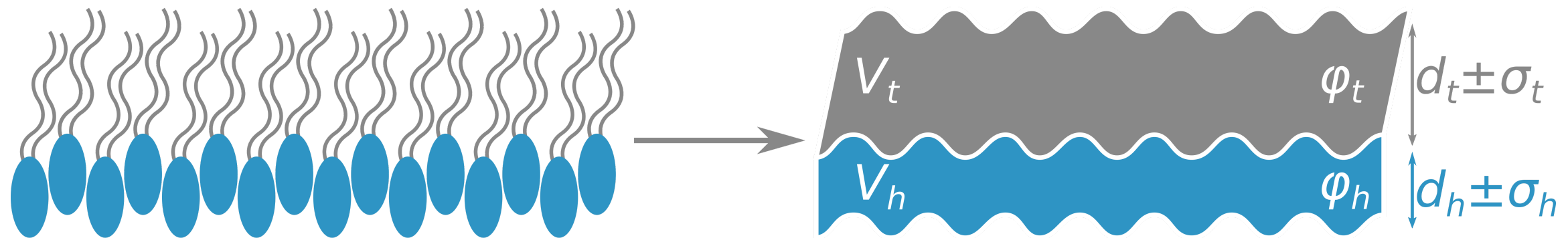
users bring cool science to the beamline



experimental data is reduced



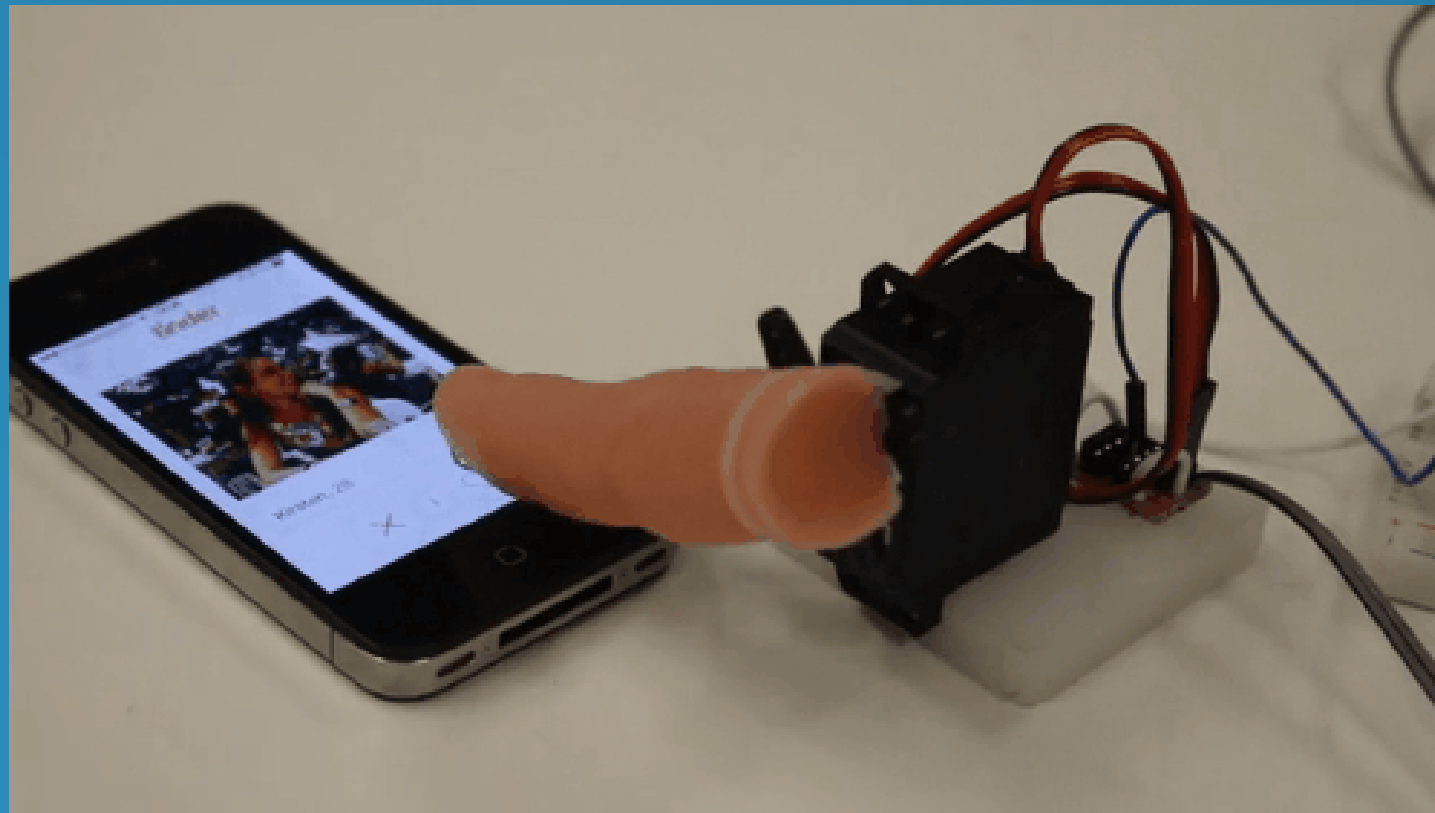
data analysis is performed



nature paper is written and published



greater automation → more science



hopefully good science too

what can we automate?

- Users bringing the cool science: 🧐
 - Data reduction: ✅
 - Data analysis: 🙌
 - Writing papers: 😞

let's automate data reduction

x-ray reflectometry reduction is well studied

Previous literature focuses on point detectors, while modern instruments utilise area detectors

A. Gibaud, G. Vignaud, & S. K. Sinha. *Acta Cryst.*, **A49**, 642-648, 1993

F. Salah, B. Harzallah, & A. van der Lee. *J. Appl. Crystallogr.*, **40**, 813-819, 2007.

not re-inventing the wheel, but re-
building it



Activitiesruntime-uk.ac.diamond.dawn.product - /scratch/Ino76132/runtime-uk.ac.diamond.dawn.product - DAWN S...Mon Jul 8, 12:52:43

runtime-uk.ac.diamond.dawn.product - /scratch/Ino76132/runtime-uk.ac.diamond.dawn.product - DAWN Science

FileToolsWindowHelp

Project ExFile VieweData Slice ViewProcessingModel 'Crop Around Peak [2D]'

data

312332.dat312333.dat312334.dat312335.dat312336.dat

Current slice of data: [0,:195,:487]

Input

file_image[0,:,:]

0150

0450

1e+041e+031e+021e+011e+00

Processing

Crop Around Peak [2D]

Image Integration

Gaussian Background Subtraction [Background Subtraction]

Set Poisson Error [Error]

Normalisation [metadata]

Q-Normalisation for DCD [Reflectivity]

Area Correction [Reflectivity]

Sum

Output

Output

312332_Sum

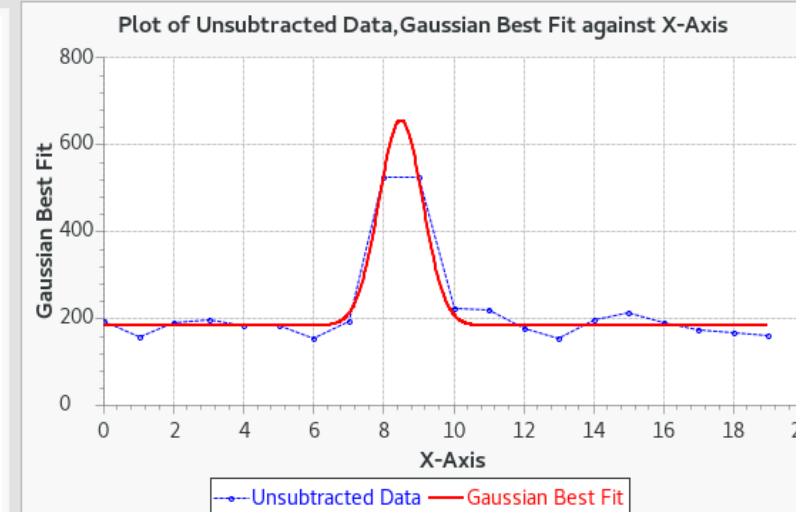
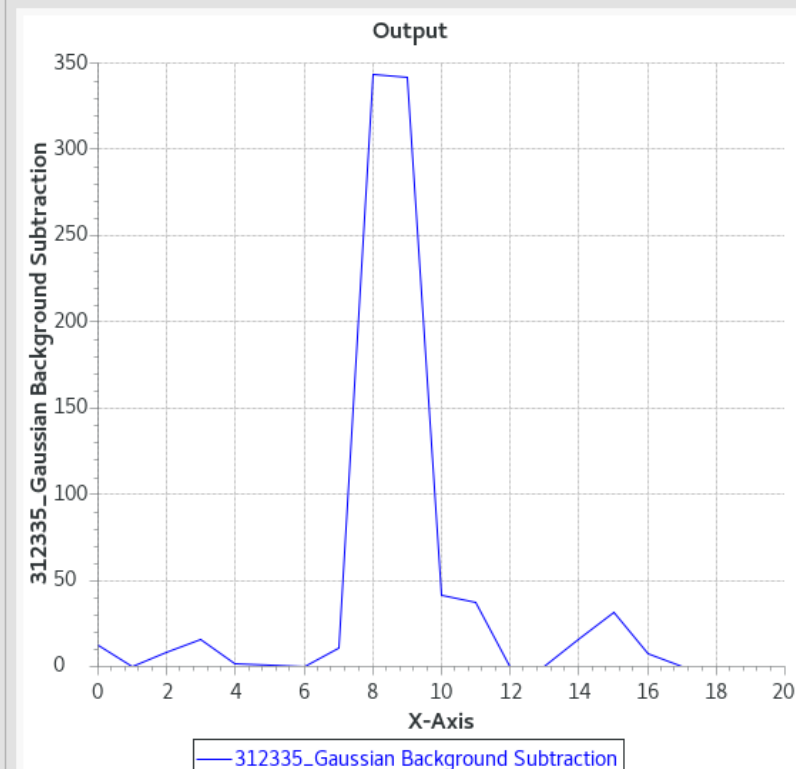
020

014

1e+061e+051e+041e+031e+021e+011e+00

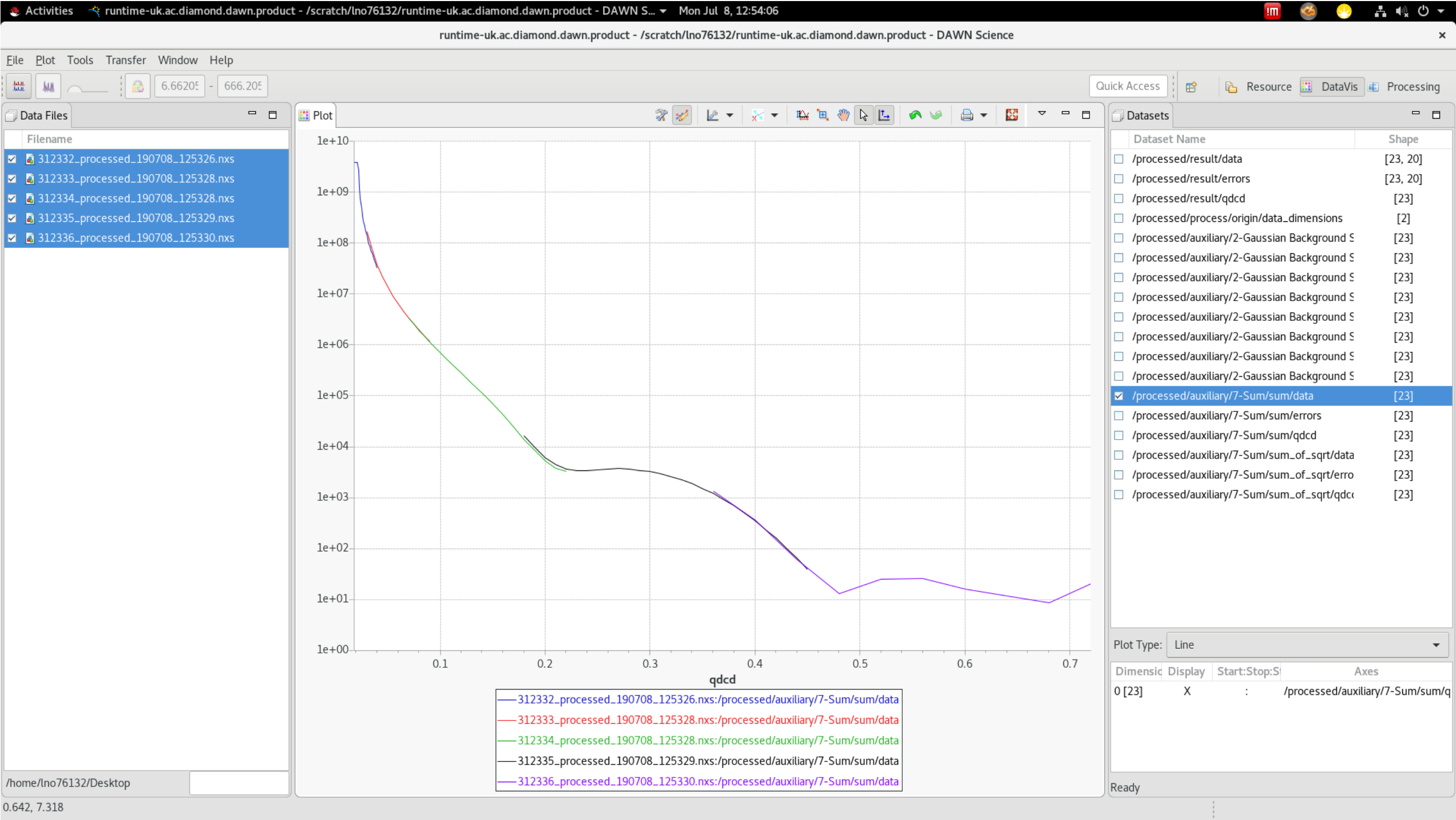
Model 'Crop Around Peak [2D]'

Name	Value
x-Box Length	15.0
y-Box Length	20.0



A 1D Gaussian function with an x-axis offset has been fit to the data.

The parameters are as follows:
Peak position = 8.506005E+00
Full-width half maximum = 1.473161E+00
Peak area = 7.395714E+02
x-Axis offset = 1.824224E+02
This offset has then been subtracted from the data.



File Plot Tools Transfer Window Help

6.6620E - 666.20E

Data Files

- Filename
- ☐

312332_processed_190708_125326.nxs
- ☐

312333_processed_190708_125328.nxs
- ☐

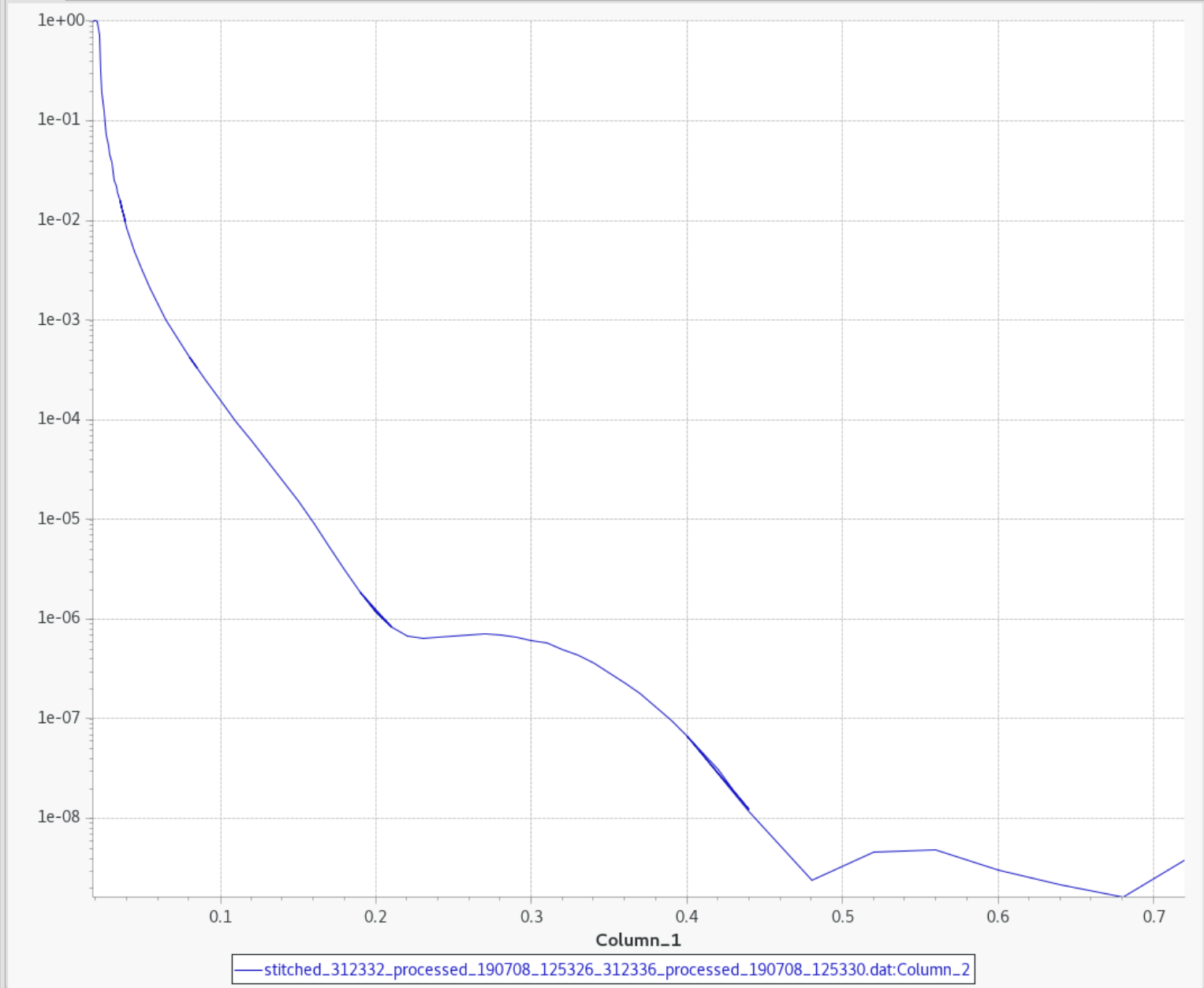
312334_processed_190708_125328.nxs
- ☐

312335_processed_190708_125329.nxs
- ☐

312336_processed_190708_125330.nxs
- ☒

stitched_312332_processed_190708_125326_312336_processed_190708_125330.dat

Plot



Quick Access Resource DataVis Processing

Datasets

Dataset Name	Shape
☐ Column_1	[82]
☒ Column_2	[82]
☐ Column_3	[82]
☐ Column_4	[82]

Plot Type: Line

Dimension	Display	Start:Stop:Step	Axis
0 [82]	X	:	Column_1

/home/Ino76132/Desktop

Ready

this will enable automated reduction

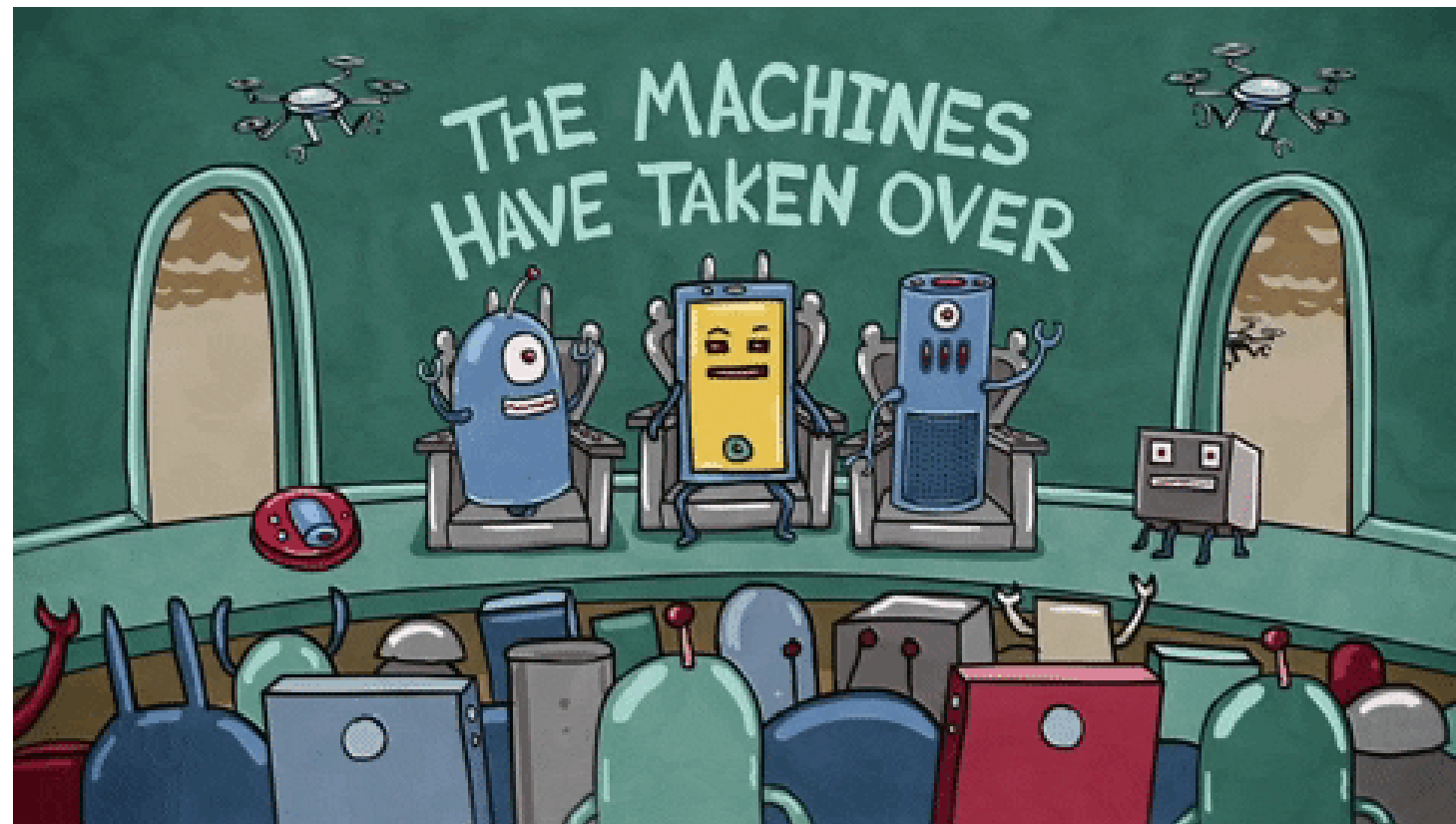
- Only a single processing pipeline for a given experiment
 - The processing is modular
 - Coming to i07 in October 2019

now for data analysis

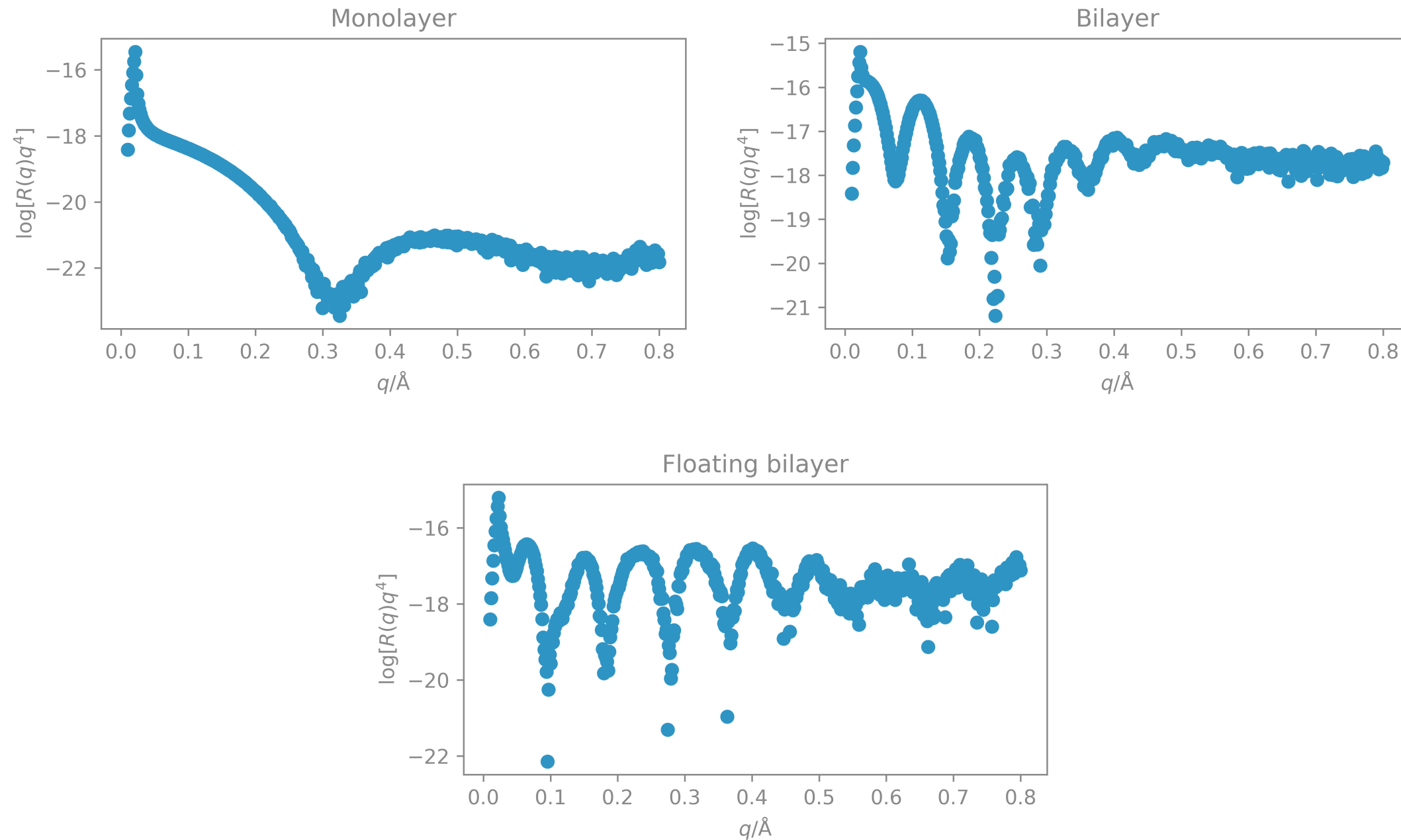
reflectometry analysis is model- dependent

Can we automate the model selection?

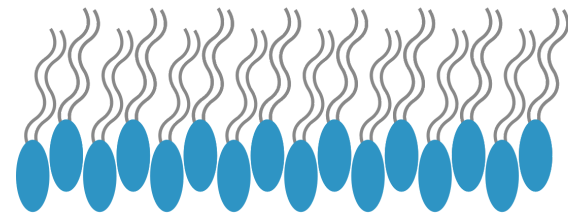
machine learning for model selection



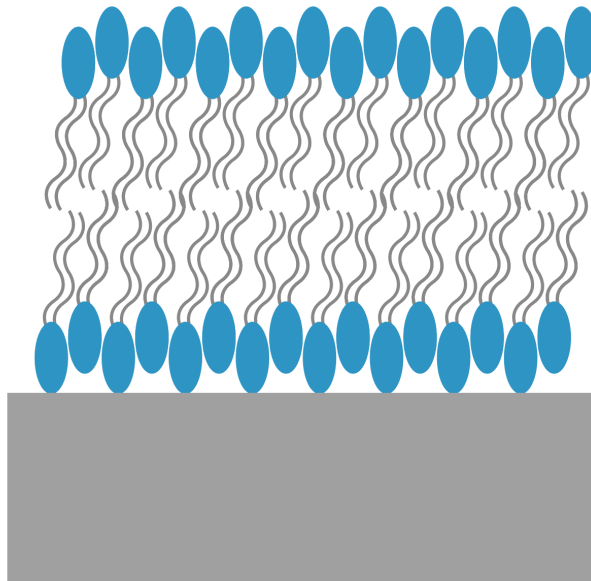
ml-driven classification



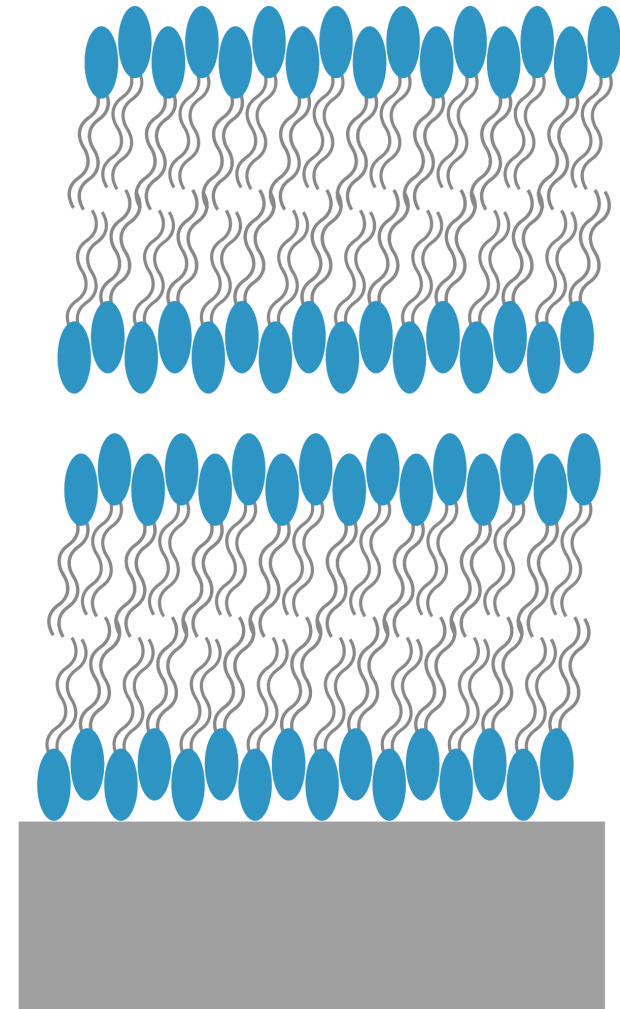
ml-driven classification



1



2



3

1. A. R. McCluskey, *et al.* *Phys. Chem. Chem. Phys.*, **21**, 6133-6141, 2019.

2. Y. Gerelli. *Phys. Rev. Lett.*, **122**, 248101, 2019.

3. V. Rondelli, G. Fragneto, S. Motta, E. Del Favero, L. Cantù, *J. Phys. Conf. Ser.*, **340**, 012083, 2012.

convolutional neural network

Very quick and accurate for "model" data;
2 epochs → 100 % validation accuracy

how robust is our model?

	Monolayer	Bilayer	Floating Bilayer
DPPC Validation	100 %	100 %	100 %
DXPC Validation	100 %	100 %	100 %

why machine learning?

with ml we can advise analysis

We can create *generic* analysis interfaces which the machine learned classification would suggest

jupyter notebook

This could be in the form of a Jupyter Notebook that you could run from your office

Analysis of X-ray reflectometry from a surfactant monolayer

This Jupyter Notebook can facilitate the analysis of your experimental X-ray reflectometry data from a surfactant/lipid monolayer. This will improve the [reproducibility](#) and reliability of your analysis and results.

When writing your publication, please be sure to cite this Jupyter Notebook:

- A. R. McCluskey. (2019, July 12). Analysis of X-ray reflectometry from a surfactant monolayer (Version 1.0.0). Zenodo. DOI: [10.5281/zenodo.xxxxxxx](https://doi.org/10.5281/zenodo.xxxxxxx)

The publication that this model was taken from:

- A. R. McCluskey, A. Sanchez-Fernandez, K. J. Edler, S. C. Parker, A. J. Jackson, R. A. Campbell, and T. Arnold. (2019). *Phys. Chem. Chem. Phys.*, **21**, 6133-6141. DOI: [10.1039/C9CP00203K](https://doi.org/10.1039/C9CP00203K).

And the software that was used to perform the analysis:

- A. R. J. Nelson and S. W. Prescott. (2019). *J. Appl. Crystallogr.*, **52**, 193-200. DOI: [10.1107/S1600576718017296](https://doi.org/10.1107/S1600576718017296).

How to use

To use this analysis methodology, please follow through this notebook and fill in the required fields. Once all of the fields are completed, select "Cell" from the toolbar at the top of the page and choose "Run All". This will run the commands in all of the Python cells throughout the Notebook, generate an analysis output, which will describe the model system that best agrees with the experimental data, and publication quality figures for use in your paper/talk.

If you need any help along the way please contact andrew.mccluskey@diamond.ac.uk or scientificsoftware@diamond.ac.uk.

The model

The model is that of a surfactant or lipid monolayer that has self-assembled at an air-liquid interface. Shown below is a pictorial example of the expected structure, and the associated model that will be used in the analysis.

Figure 1. expected structure of the surfactant monolayer and a graphical description of the model.

Figure 1. expected structure of the surfactant monolayer and a graphical description of the model.

automated script

Or an automated analysis script could be run on well tagged data

```
1 from __future__ import division
2 import refnx
3 from refnx.reflect import ReflectModel, SLD, Structure
4 from refnx.dataset import ReflectDataset
5 from refnx.analysis import (Transform, CurveFitter, Objective, GlobalObjective,
6
7 import numpy as np
8
9 import sys
10 sys.path.insert(0, "models/")
11 sys.path.insert(0, "utils/")
12
13 import two_layer as ol
14 import toolbox as tb
15
16 import json
17
18
19 surface_pressure = sys.argv[1]
20 seed = int(sys.argv[2])
21 contrasts = ['d13acmw', 'd13d2o', 'hd2o', 'd70acmw', 'd70d2o', 'd83acmw', 'd83d2
22 apm = float(sys.argv[3])
23 iden = sys.argv[4]
24 guide = json.load(open('scripts/guide.json', 'r'))
25 free_parameters = guide[iden]
26
27
28 data_dir = 'data/surf_pres_{}'.format(surface_pressure)
29
30 output_dir = 'output/all_data/{}/seed_{}'.format(iden, seed)
31
32 datasets = []
33 for i in range(len(contrasts)):
34     # Create a dataset for each contrast
35     # Create a dataset for each contrast
```

conclusions

- i07 will have automated data reduction by the year end
- We are developing ML-driven approaches to analytical model selection
 - These will enable directed or automated down-stream analysis
 - Stretch goal is users leave with analysed data

acknowledgements

- Tim Snow (DLS)
- Jos Cooper (ISIS)
- Keith Butler (SCD)

funding





Penny and Sadie, good dogs