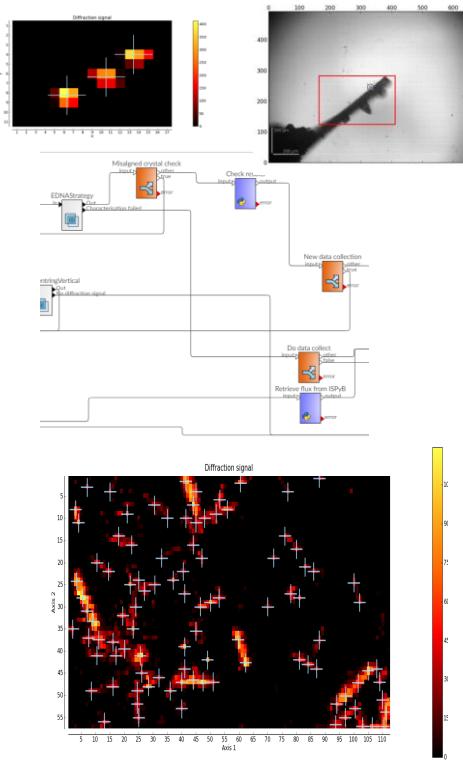
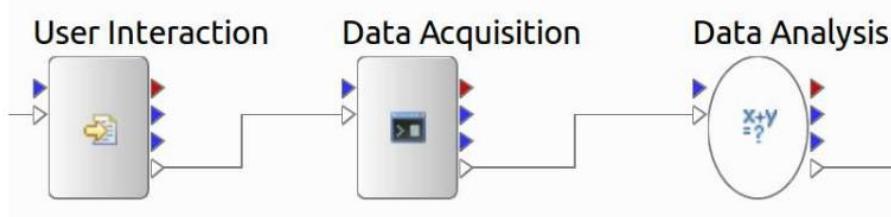


Multi-crystal data collection capabilities at the ESRF

Olof Svensson
Data Analysis Unit / ISDD

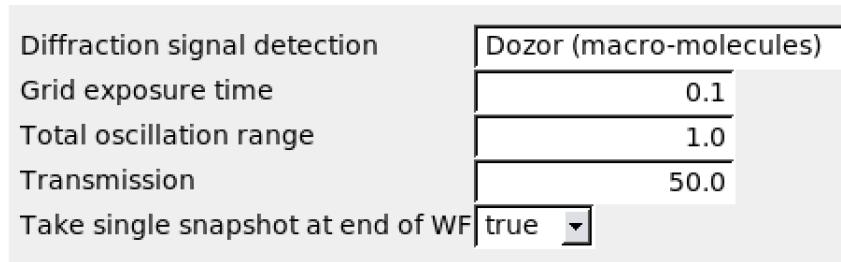


- **Multi-crystal data collections implemented as workflows**

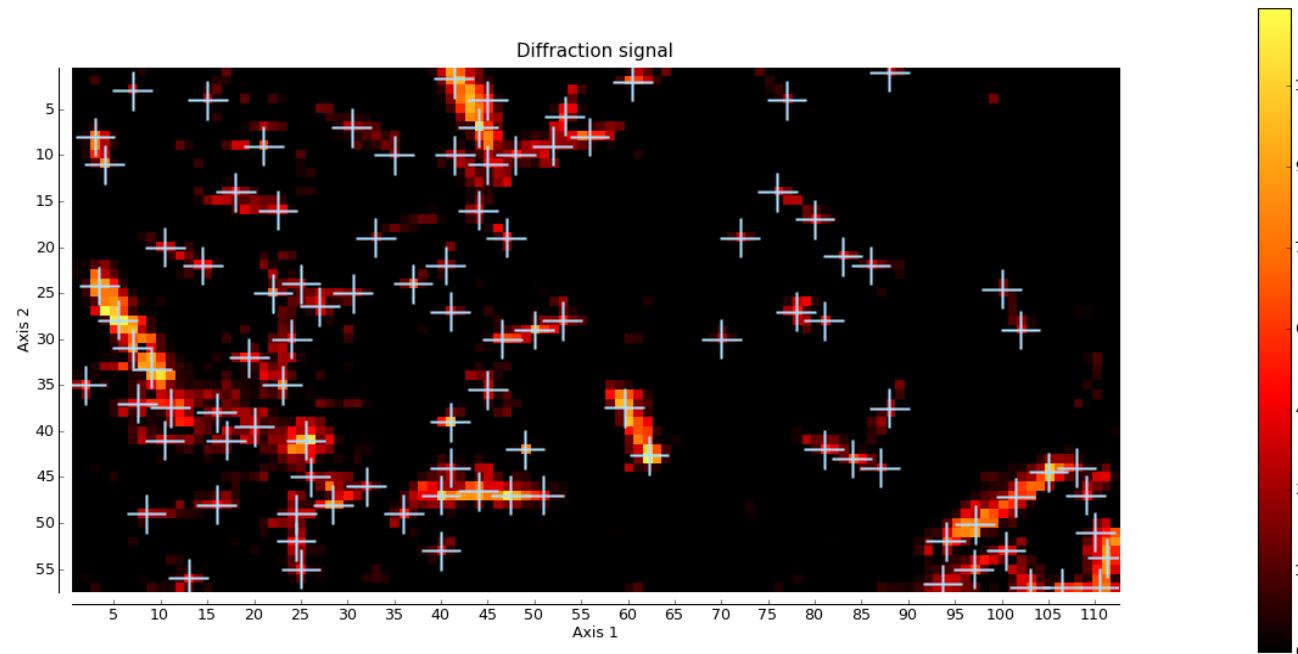


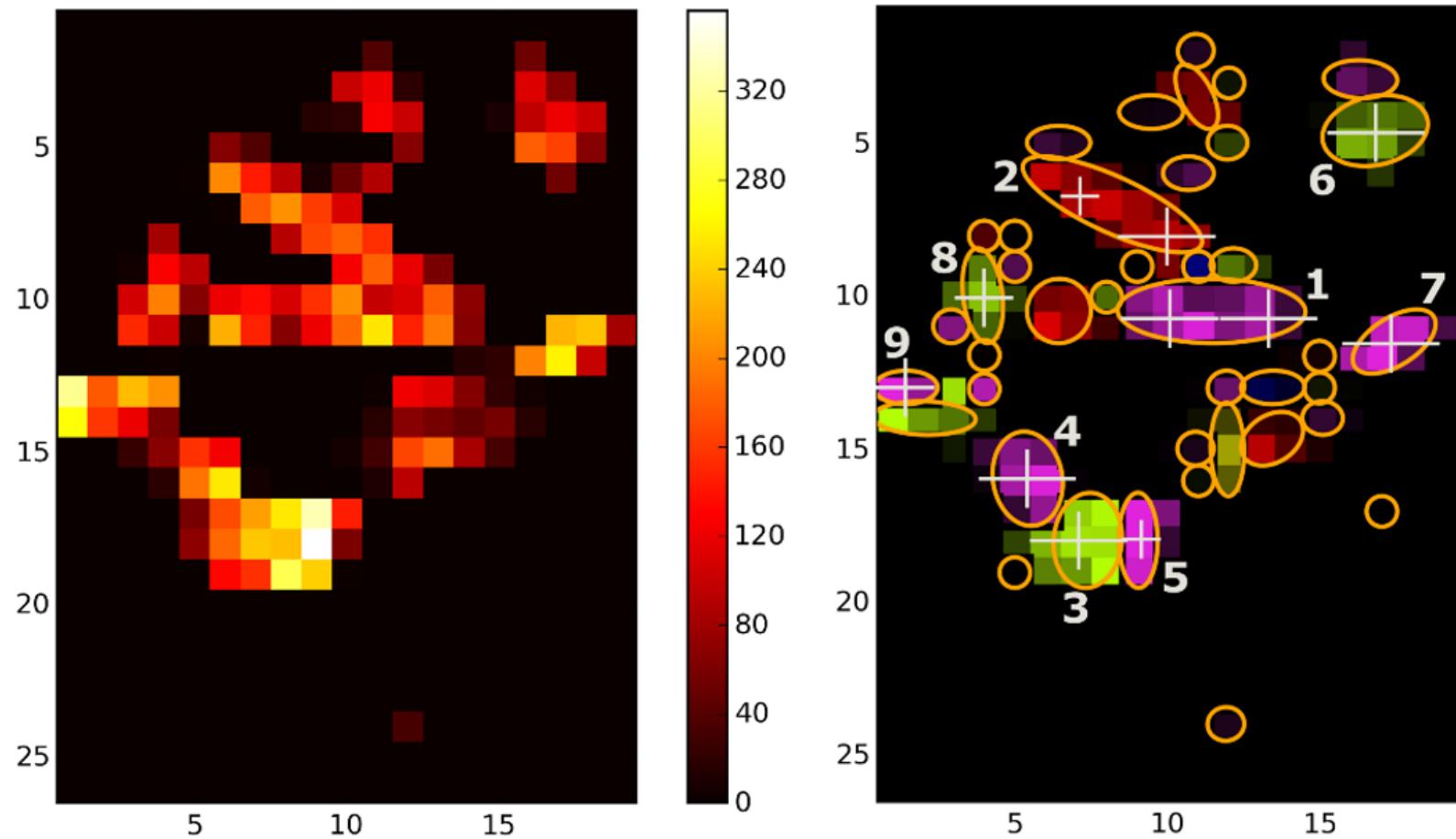
- **Mesh and collect – interactive**
- **Fully automatic workflows :**
 - MXPressE : Auto-mesh, X-ray centring, characterisation, data collection
 - MXPressO : Auto-mesh, X-ray centring, data collection 180 degrees
 - MXPressI : Auto-mesh, X-ray centring, characterisation, data collection 180 degrees with resolution from characterisation

- Manual grid selection in mxCuBE + initial parameters:



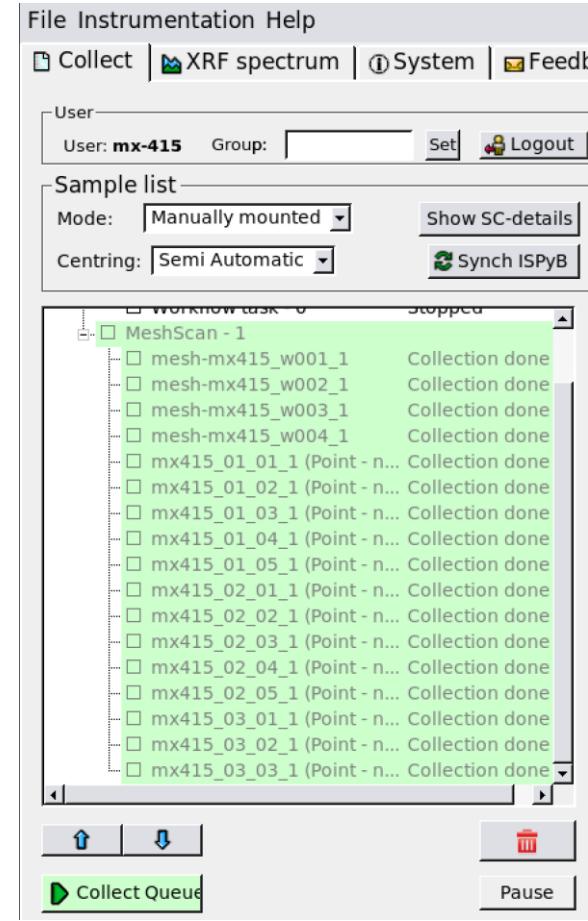
- 2D X-ray grid :





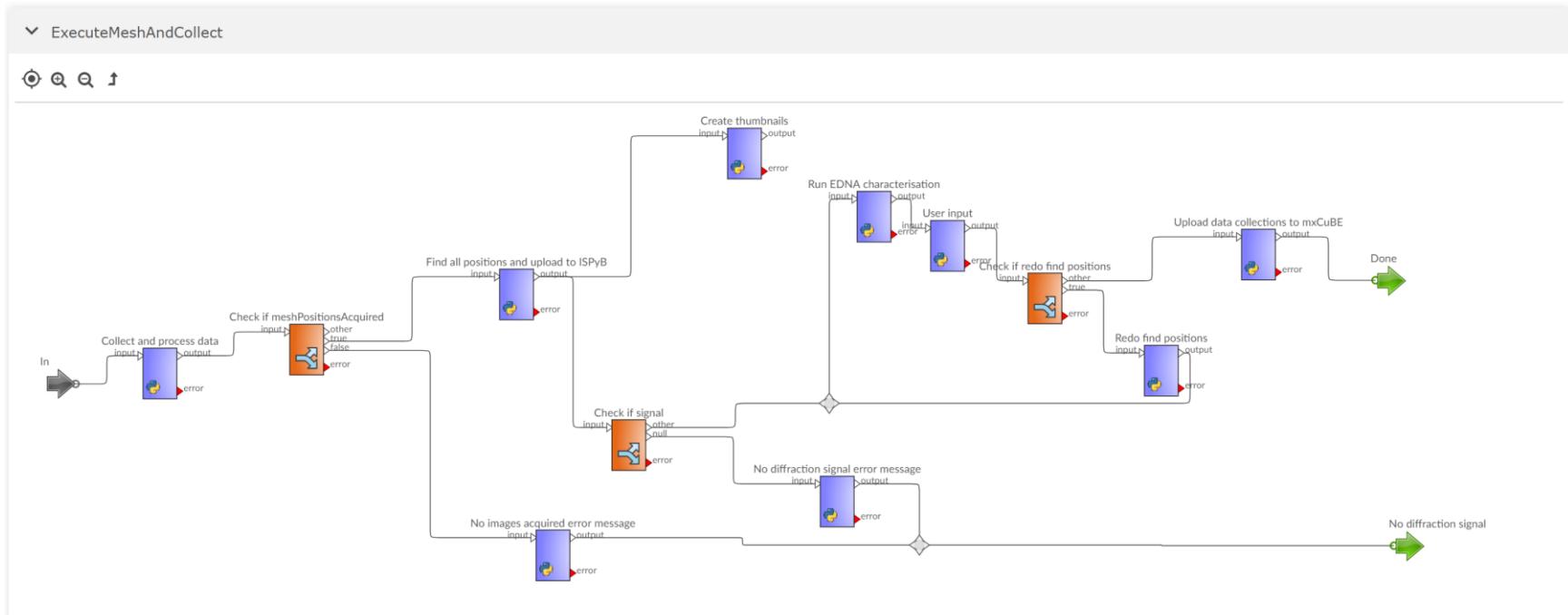
- Characterisation on strongest grid image(s)
- User input :

Diffraction signal detection	Dozor (macro-molecules)
Resolution	2.93
Data threshold	100000.0
Redo find positions?	false
Exposure time	5.41463414634
Transmission	50.0
Total oscillation range	10.0
No images	100
Max no data collection positions	5
Number of data collection iterations	1
Radius	3.0
Aimed I/Sigma at highest resolution	1.0
Inverse beam data collection	false
Flux	1e+12
Time to reach Henderson limit	541.5
XDSAPP auto-processing	true
Grenades_fastproc auto-processing	true
Grenades_parallelproc auto-processing	false
EDNA_proc auto-processing	false
XIA2_DIALS auto-processing	false
autoPROC auto-processing	false



- Data collection on found positions :

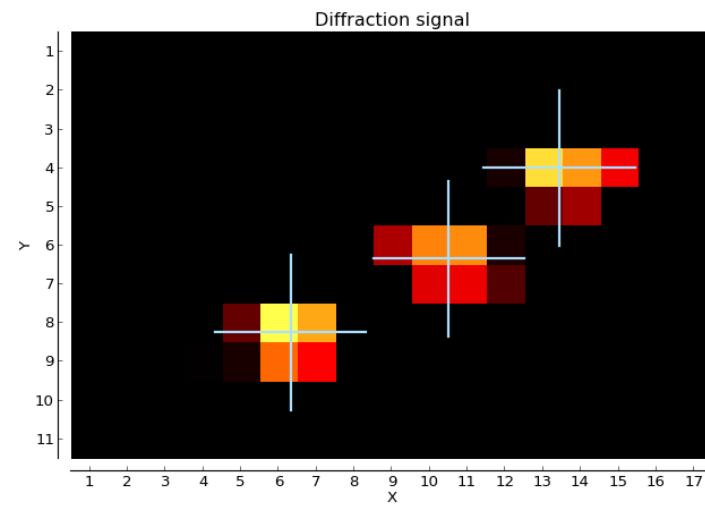
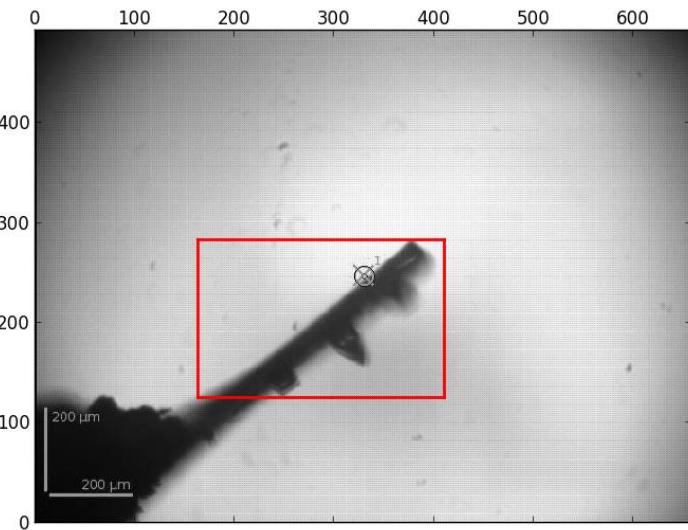
BEAMLINE EXPERT SYSTEM – PASSERELLE EDM



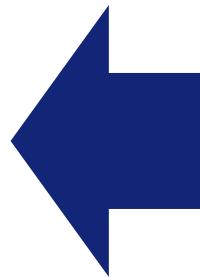
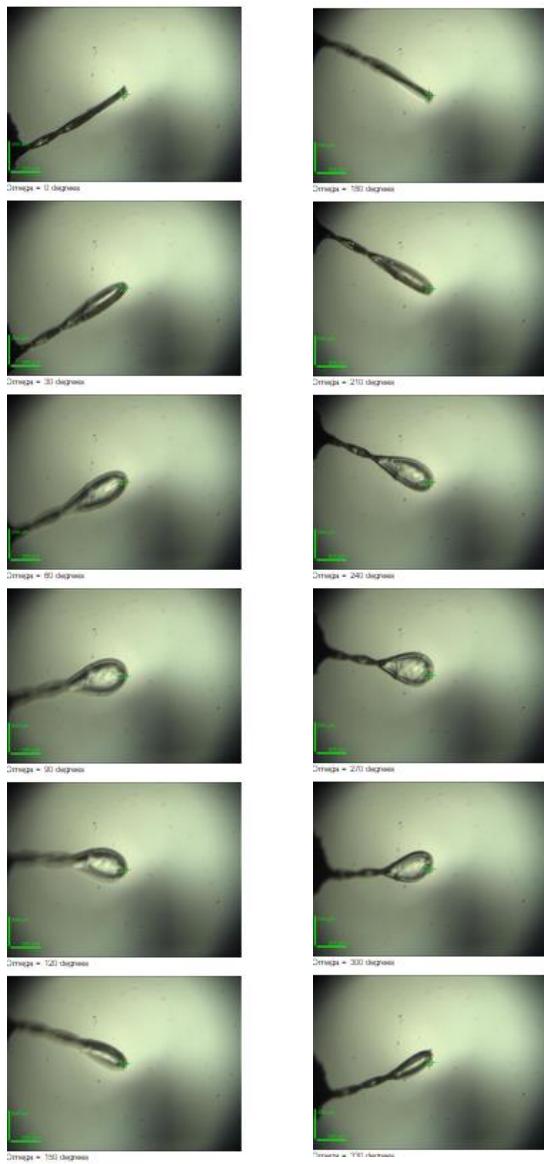
MXPress diffraction plan choices:

- Type of experiment:
 - MXPressE: automesh, X-ray centring, (EDNA) characterization, data collection
 - MXPressO : automesh, X-ray centring, 180 degree standard data collection
 - MXPressI : automesh, X-ray centring, characterization, 180 degree data collection at resolution given by characterization (ranking resolution), data collection
 - MXPressM : Loop screening; automesh, 2D mesh
 - MXPressP : Pseudo helical; automesh, X-ray centring with many point detection, characterization on strongest position, full data collection on strongest position, partial data collections on remaining positions
- Common choices:
 - SAD / no SAD
 - No positions
 - Beam size
 - Crystal space group and cell dimensions
 - Crystal susceptibility to radiation damage

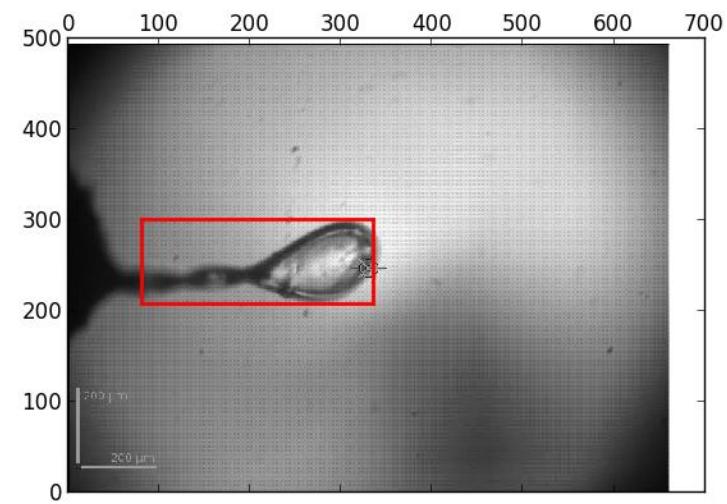
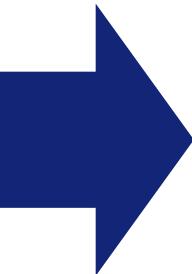
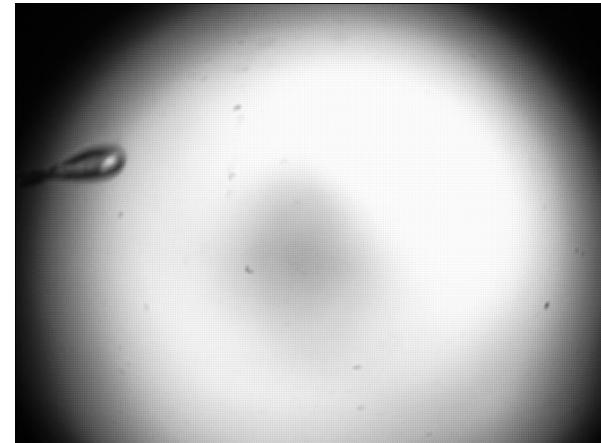
- Number of positions taken from ISPyB diffraction plan
- Auto mesh, max loop size
- 2D X-ray grid
- For every position :
 - Vertical centring 90 degrees apart from 2D mesh
 - Characterisation
 - Data collection



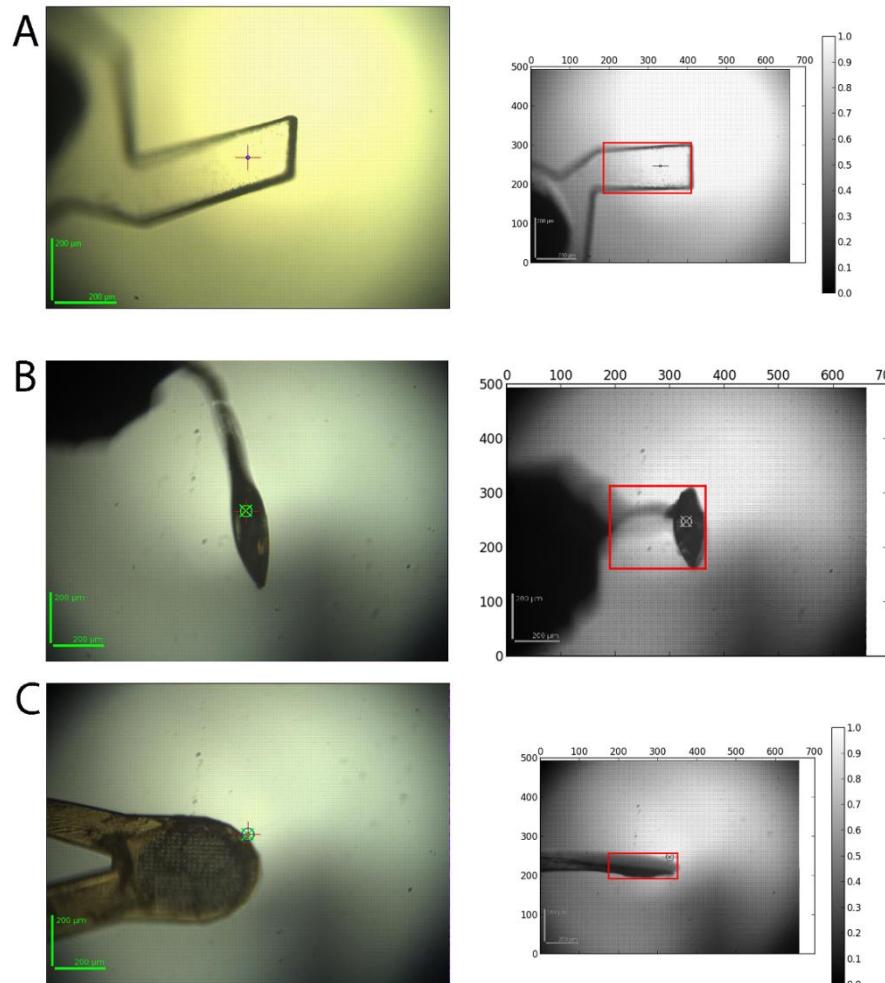
AUTO MESH



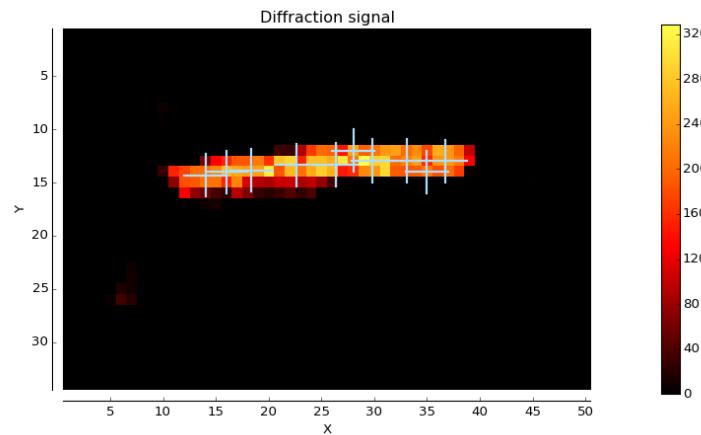
Auto loop centring with Lucid 2



Code on github: <https://github.com/olofsvensson/AutoMesh> (\rightarrow mxCuBE?)

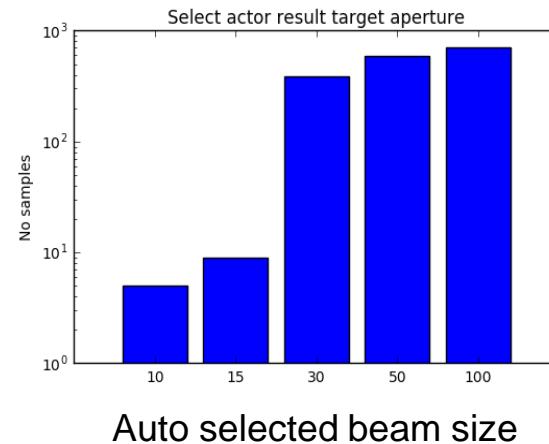


- Number of positions taken from ISPyB diffraction plan, default 5
- Initial 2D mesh on max loop size
- Normal characterization and full data collection on first position
- Pseudo-helical characterization for remaining points
- For remaining positions :
 - Vertical centring 90 degrees apart from 2D mesh
 - Partial data collection from pseudo-helical characterisation



Dynamic aperture adjustment

- Aperture automatically set to match crystal size determined from X-ray centring
- Can be overridden by aperture desired by user



Improved error handling

- Automatic recovery in case of detection of non-centred crystal

ACKNOWLEDGEMENTS

- David von Stetten, Max Nanao, Sasha Popov, Daniele de Sanctis, Stéphanie Monaco, Didier Nurizzo, Matias Guijarro, Solange Delageneire, Alejandro de Maria, Marcus Oskarsson, Pascal Theveneau, Christoph Mueller-Dieckmann, Gordon Leonard, David Flot, Igor Melnikov and Antonia Beteva (ESRF)
- Matthew Bowler, Andrew McCarthy and Michael Hons (EMBL Grenoble)
- Erwin de Ley and Koen Heunick (Isencia, Belgium)
- The ESRF Data Analysis Unit, Beamline Control Unit and Structural Biology group

Further reading:

- **Fully automatic characterization and data collection from crystals of biological macromolecules**, Svensson, O., Malbet-Monaco, S., Popov, A., Nurizzo, D., & Bowler, M. W. (2015). Acta Crystallographica Section D: Biological Crystallography, 71(Pt 8), 1757–1767. <http://doi.org/10.1107/S1399004715011918>
- **MeshAndCollect: an automated multi-crystal data-collection workflow for synchrotron macromolecular crystallography beamlines**, Ulrich Zander · Gleb Bourenkov · Alexander N Popov · Daniele De Sanctis · Olof Svensson · Andrew A Mccarthy · Ekaterina Round · Valentin Gordeliy · Christoph Mueller-Dieckmann · Gordon A Leonard, ACTA CRYSTALLOGRAPHICA SECTION D BIOLOGICAL CRYSTALLOGRAPHY 71(11):2328-2343 · NOVEMBER 2015