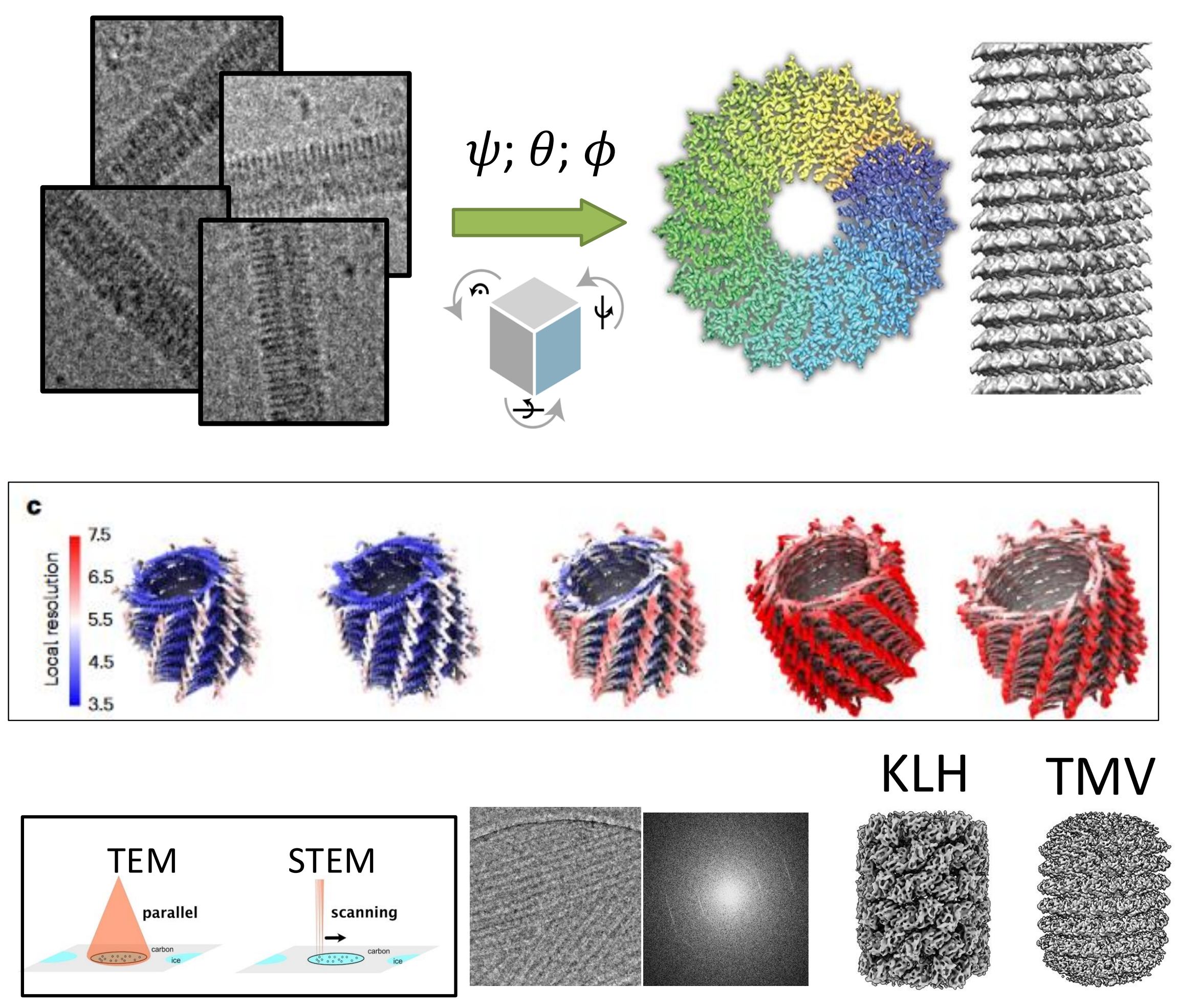
Automating Cryo-EM Metadata Management with ELN

Chaitali Bagwe[1], Thomas Heidler[1], Florian Rhiem[1], Daniel Mann[1] and Carsten Sachse[1,2]
[1]Ernst Ruska Centre / Structure Biology (ER-C-3), Forschungszentrum Jülich, Germany
[2]Heinrich-Heine-Universität Düsseldorf, Department of Biology, Universitätsstraße 1, 40225 Düsseldorf Germany

Abstract

- At the Ernst-Ruska Centre-3/ Structural Biology (ER-C-3), Forschungszentrum Jülich, cryo-electron microscopy (cryo-EM) is used to determine high resolution structures of biological samples.
- Modern cryo-EM experiments generate large amounts of image data together with important metadata, such as microscope settings, acquisition parameters, and experimental conditions.
- At shared facilities, this metadata is often scattered across different vendor-specific tools, file formats, and storage locations, making it incomplete, inconsistent, and difficult to access.
- To address this, ER-C has developed an automated metadata management workflow. Custom Python tools capture metadata directly from microscope acquisition software during data collection.
- The captured metadata is transformed into standardized records and integrated into SampleDB.



Bioimaging and microscopy metadata

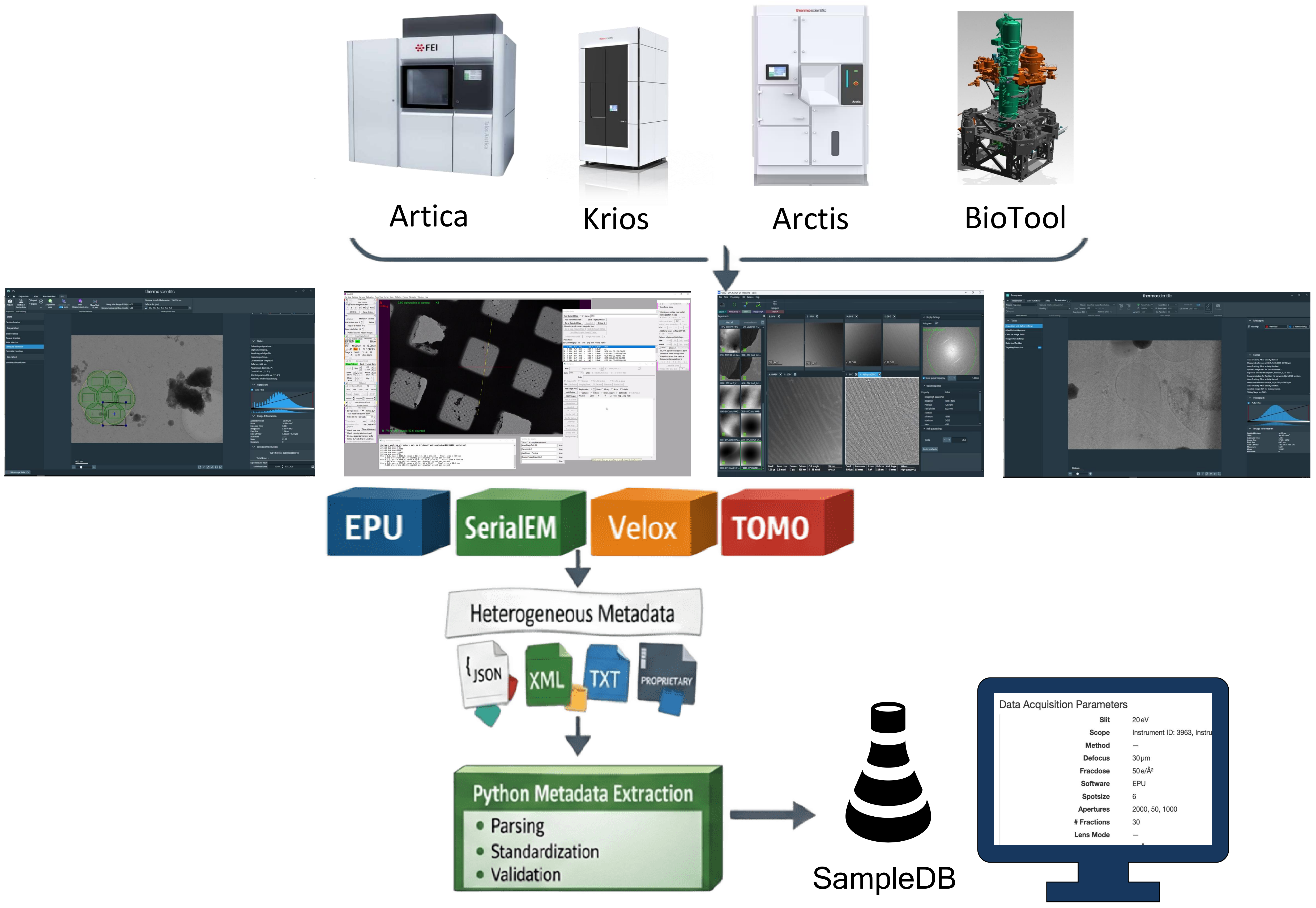
Sample information:
- Sample name
- Sample type
- User info, etc.

Microscope settings:
- Camera used
- Acceleration
- Pixel Size
- Pixel Dose, etc.

Software information:
- Software used
- Software version

Acquistion parameters:
- Acquisition per hole
- No. of images acquired
- Images per hour

Workflow



Data Acquisition Parameters

Slit	20 eV
Scope	Instrument ID: 3963, Instru
Method	—
Defocus	30 µm
Fracdose	50 e/Å²
Software	EPU
Spotsize	6
Apertures	2000, 50, 1000
# Fractions	30
Lens Mode	—

Conclusion

- The project delivers an automated workflow that extracts metadata from Cryo-EM microscopes and stores it in SampleDB.
- Ensuring that datasets generated at the ER-C are FAIR-compliant and traceable.
- Enables accurate reconstruction of microscope settings, facilitating reproducible imaging under identical experimental conditions.
- The project strengthens the reliability of information processing in biological systems research, ensuring that high-quality structural information is supported by equally robust and accessible metadata.

References

- SampleDB – Research Data Management platform developed by PGI-JCNS: https://scientific-it-systems.iffgit.fz-juelich.de/SampleDB/
- ER-C User Facility: https://er-c.org/
- EPU (Thermo Fisher Scientific): https://www.thermofisher.com/de/de/home/electron-microscopy/products/software-em-3d-vis/epu-software.html
- SerialEM: https://bio3d.colorado.edu/SerialEM/
- Velox (Thermo Fisher Scientific): https://www.thermofisher.com/de/de/home/electron-microscopy/products/software-em-3d-vis/velox-software.html
- TOMO (Thermo Fisher Scientific): https://www.thermofisher.com/de/de/home/electron-microscopy/products/software-em-3d-vis/cryotomo-tomography-software-suite.html