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Towards Serial Computed Tomography of Small Organisms

Synchrotron-based X-ray microtomography has become an indispensable technique for non-invasive morphological analysis of small organisms. Extending its application to large-scale studies—such as genotype–phenotype correlation or the comprehensive digitization of museum collections—requires a paradigm shift in methodology. To meet this demand, we introduce an integrated, highly automated workflow for “serial tomography,”enabling routine high-throughput 3D imaging of extensive sample collections. The workflow combines robotic sample preparation, beamline-specific handling solutions, automated scanning, GPU-accelerated 3D reconstruction, and AI-driven quality assurance. Distributed data acquisition across multiple servers ensures efficient processing, while continuous metadata integration—from initial preparation through reconstruction—supports data traceability and interoperability. Here, we present two customized robotic systems currently being commissioned: one at the IMAGE beamline of the KIT Light Source and another at the HIKA experimental station at the P23 beamline of PETRA III. Demonstrations on diverse insect collections and model organism series illustrate the system’s capacity to deliver large-scale morphological datasets. In the long term, this approach will provide the scientific community with scalable access to synchrotron-based 3D morphological studies, facilitating comparative analyses and addressing fundamental questions across the life sciences.

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