

Towards Serial Computed Tomography

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Synchrotron-based X-ray microtomography has become an indispensable technique for non-invasive 3D morphological analysis of materials, tissues, small devices and organisms. The growing demand for high-throughput measurements of large specimen collections, e.g., for applications in paleontology (1), linking ecology and morphology (2, 3), genotype-phenotype correlations (4), and even the large-scale digitization of morphological biodiversity (5), is driving the development of increasingly automated X-ray imaging workflows for large comparative morphological studies. However, current high-throughput experiments remain technically demanding and labor-intensive, with existing robotic systems typically limited to scanning only around 50 specimens in a single unattended run.

Future workflows will require substantially increased automation beyond the scanning process itself to encompass the entire pipeline, including sample preparation, data acquisition, image reconstruction, data analysis, and comprehensive data management for measuring campaigns with hundreds and thousands of specimens. We summarize this integrated workflow under the term “Serial CT”. This presentation highlights major recent advances and key technological developments needed for fully automated Serial CT workflows for large-scale morphological research.

We report about two Serial CT systems: one at the HIKA experimental station at the P23 beamline of PETRA III and another at the IMAGE beamline of the KIT Light Source. They are both capable of processing more than 1000 samples at a time. The UFO-II system at IMAGE presently allows Serial CT scanning of such large sample series with a throughput of 60 samples/hour in the filtered white-beam mode. At HIKA, the system can measure 15 samples/hour in the holographic imaging mode with monochromatic beam. Our workflow includes automated CT scanning based on AI sample detection, parallelized data streams, GPU-accelerated 3D reconstruction for quality assurance, automatic metadata collection and compression. First examples studying the morphology of large series of vertebrate model organisms and arthropods demonstrate the potential of Serial CT for life science applications and beyond.

References

- van de Kamp, T., et al. (2018): Parasitoid biology preserved in mineralized fossils. *Nature Communications* 9: 3325.
- Rühr, P.T., et al. (2021): Juvenile ecology drives adult morphology in two insect orders. *Proceedings of the Royal Society B* 288: 20210616.
- Edel, C., et al. (2024): Bite force transmission and mandible shape in grasshoppers, crickets, and allies is not driven by dietary niches. *Evolution* 78: 1958-1968.
- van de Kamp, T., et al. (2022): Evolution of flexible biting in hyperdiverse parasitoid wasps. *Proceedings of the Royal Society B* 289: 20212086.
- Katzke, J., et al. (2026): High-throughput phenomics of global ant biodiversity. *Nature Methods* 23: 663-672.