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SIBERIA – Stitcher, Integrated in Beamline Environment, Rigid, Infallible and Alacritous

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Here we present a recent highlight at the high throughput tomography setup at the P14 EMBL beamline on Petra III (Hamburg, Germany) [1,2]: an automatically executed fast stitching of 3D volumes triggered on the completion of the last reconstruction in a series of scans acquired in a raster pattern. SIBERIA has been developed to allow the beamline user to explore the stitched reconstructed data volume shortly after the data collection. Our reconstructions finish as fast as within ~30s after the completion of the scan [3]. Their size ranges from ~10GB to ~125GB depending on the acquisition mode (cropped, standard, extended field of view). A number of reconstructed volumes are needed to accommodate samples larger than the ~1.3mm x 1.3mm FOV that the beamline can illuminate. SIBERIA running on a single cluster node with 512GB RAM, and 176 hyper-threads produces a ready-to-be-viewed stitch in as little as 20s after reconstruction end for 2 volumes. With increasing the number of volumes and overlaps between them its execution time increases correspondingly, but remains within minutes for large datasets (e.g. 12 min for 3x3 volumes, 4096x4096x1016 pixels each, with 28 overlapping pairs). The data is read from, and written onto a 1.7PB BeeGFS storage system. SIBERIA follows a globally optimal stitching algorithm similar to that described in [4]. It is, however, a brand new implementation in C/C++ optimized for speed, and for the already existing computing environment at the beamline.

Footnotes

^{*}[1] Polikarpov, M et al. (2019). Acta Cryst. D75, 947–958.

^{**} [2] Albers J et al. Journal of Synchrotron Radiation (2024). DOI: 10.1107/S160057752300944X

^{***} [3] Nikolova M et al. NOBUGS (2024). <https://indico.esrf.fr/event/114/contributions/747/>

^{****} [4] Preibisch S et al. Bioinformatics 2009, 25(11):1463–1465. 10.1093/bioinformatics/btp184

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