

X-RAY CT-BASED HIGH-THROUGHPUT INCREMENT CORE ANALYSIS

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X-ray CT scanning is a powerful tool for non-destructive three dimensional visualization and analysis of the interior of an object. This tool has proven valuable in many different research fields and has also significant potential in tree ring research on increment cores. Not only does it minimize sample preparation, it also allows to screen, archive and study cores at different resolutions. Tree ring width measurements – on species with density-related growth ring boundaries –, density profiling as well as quantification of certain wood anatomical features can be derived from the virtual 3D core volumes.



We will exemplify the use of such a multi-resolution approach on increment cores of Central Africa, more specifically from the Mayombe forest in the Democratic Republic of Congo. Therefore, we will use the Nanowood facility of Woodlab-UGent, part of the Ghent University Centre for X-ray Tomography (UGCT). Standard cone-beam scanning at 110 µm resolution for high-throughput screening and archiving of 33 cores up to 60 cm can be accomplished in a single run (step 1) and with related software density profiling – and in some cases tree ring analysis – is within reach (De Mil et al. 2016). When more detail is required based on the analyses of screening step 1, helical cone-beam scanning at 35 µm resolution can be accomplished on 6 intact cores of 30 cm length in a single run (step 2) and analysis can be performed with the same software allowing tree ring boundary demarcation, density profiling (De Ridder et al. 2011, Van den Bulcke et al. 2014) and for certain species quantification of specific wood anatomical features. For resolving anatomical features at higher resolution, single growth rings of interest derived from step 1 or 2 can be scanned and analysed at resolutions between 5-10 µm (step 3). Multi-resolution guided scanning of increment cores is as such a valuable tool for building a virtual increment core database without sample destruction.

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