1	X-ray tomography as a tool for detailed				
2	anatomical analysis				
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38 Abstract

39 40 * Wood identification, anatomical examination and retrieval of quantitative information are important aspects of many research disciplines. 41 Conventional light microscopy with a camera and (semi-)automatic image 42 43 analysis software is an often used methodology for these purposes. More 44 advanced as fluorescence, techniques such scanning electron. 45 transmission electron, confocal laser scanning and atomic force 46 microscopy are also part of the toolset answering to the need for detailed 47 imaging.

* Fast, non-destructive visualization in three dimensions with high
 resolution combined with a broad field of view is sought-after, especially in
 combination with flexible software.

51 * A highly advanced supplement to the existing techniques, namely X-ray 52 sub-micron tomography, meets these requirements. It enables the researcher to visualize the material with a voxel size approaching < 1 μ m 53 54 for small samples (< 1 mm). Furthermore, with tailor-made processing software quantitative data about the wood in two and three dimensions 55 can be obtained. Examples of visualization and analysis of four wood 56 species are given in this paper, focusing on the opportunities of 57 58 tomography at micron and sub-micron resolution.

* X-ray computed tomography offers many possibilities for material
 research in general and wood science in specific, as a qualitative as well
 as a quantitative technique.

63 **1. Introduction**

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65 Wood identification as well as quantification of anatomical features is important for many disciplines such as tree physiology (Fonti et al., 2007), 66 wood technology (Makinen et al., 2008), archaeology (Philippe and 67 68 Bamford, 2008), forensics (Coyle et al., 2001), etc. Identification relies on 69 the macroscopic appearance and the characteristics revealed under a 70 microscope. Mainly, examining axial, tangential and radial microtome 71 sections is necessary for correct determination. Semi-automated image 72 analysis of these sections leads to quantitative data such as porosity, fibre 73 length, vessel diameter, cell wall thickness etc. The conventional approach 74 consists of a microtome, a light microscope with a camera mounted on top 75 and image analysis software. Modern techniques can assist in 76 determination and characterization of wood species: SEM (Scanning 77 Electron Microscopy), TEM (Transmission Electron Microscopy), AFM 78 (Atomic Force Microscopy), CSLM (Confocal Scanning Laser Microscopy) 79 etc. Yet most of the time, obtaining quantitative information is labour- and 80 intensive. In addition to aforementioned techniques, X-ray time 81 tomography is explored in this paper as a tool for detailed anatomical research. It is a technique used in several research disciplines such as 82 medicine (Fu and Kuduvalli, 2008), soil science (Taina et al., 2008), 83 84 hydrology (Wildenschild et al., 2002), entomology (Fuchs et al., 2004), 85 plant physiology (Lee and Kim, 2008) and material science (Cnudde and Jacobs, 2004) to name only a few. Even in wood science, its possibilities 86 are employed. In its two dimensional form, X-ray analysis is already used 87 88 for densitometry (Knapic et al., 2007; Macchioni et al., 2007; Tomazello et 89 al., 2008). X-ray computed tomography in three dimensions is utilized for 90 the analysis of low-density fibreboard under compression (Badel et al., 91 2008), study of wood-plastic composites (Wang et al., 2007), detection of 92 organosilicon compounds (De Vetter et al., 2006), microstructure analysis 93 of spruce wood (Trtik et al., 2007) and quantitative wood anatomy (Steppe 94 et al., 2004).

The purpose of this article is to illustrate the power of X-ray computed 95 tomography as a tool for both descriptive and quantitative wood 96 97 identification and anatomy to resolve details on three-dimensional 98 reconstructions with near sub-micron scale without destruction or labour-99 intensive sample preparation. This non-destructiveness has the advantage 100 to visualize the object's original structure, without cell damage or artefacts 101 during sample preparation. What is more, the flexible set-up allows scanning of objects of diverse dimensions with a sufficient field of view 102 resulting in large high detailed volumes. As such, the sample can be 103 104 examined in all possible directions, making fast evaluation possible. 105 Parallax effects as explained by Park and Telewski (1993) cause no problems and any manipulation of the virtual object is possible. The 106 107 technique is illustrated for four wood species using several selfexplanatory images and calculations of cell wall thickness and cell lumen 108

size on 2D slices with standard MATLAB® algorithms. To highlight the
possibility of 3D quantitative wood anatomy, a subvolume of a data stack
is processed. Special software (Morpho+; Vlassenbroeck et al., 2007) for
handling of large datasets is demonstrated as well.

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114 **2. Materials and methods**

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The four wood species used for X-ray analysis are Scots pine (Pinus 116 silvestris L. - earlywood and latewood), beech (Fagus sylvatica L.), 117 118 movingui (Disthemonanthus benthamianus Baill.) and afzelia (Afzelia 119 bipindensis Harms). These species represent hard- and softwood as well as temperate and tropical wood species. Pine sapwood and beech are 120 often used in European standards whereas movingui and afzelia are 121 122 durable tropical species on the market (e.g. in Belgium). Five samples, two for pine (early- and latewood) and one per other wood species, were 123 prepared by slicing a thin wood section of a larger block and subdividing it 124 125 with a microtome or scalpel in needle-shaped specimens (Fig. 1).

126

127 Fig. 1.

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The tip of this needle-shaped wood sample, measuring approximately one 129 130 mm³ was scanned using the X-ray equipment built at the Centre for X-ray 131 Tomography at Ghent University (UGCT, http://www.ugct.ugent.be). This 132 is a state-of-the-art scanner (Masschaele et al., 2007), highly flexible, with in-house developed software for scanner control, sample reconstruction, 133 134 analysis and visualization. The X-ray source, a nano-focus tube, can reach a focal spot size down to one μ m. All samples were scanned at an 135 136 average voltage of 50 kV and a current of 40 µA with a total scan time of approximately 2 hours. A rotation step size of 0.36° was used. 137 138 Reconstruction took 20 min with Octopus, a server/client tomography 139 reconstruction package for parallel and cone beam aeometrv 140 (Vlassenbroeck et al., 2007). With the described set-up submicron 141 resolution can be reached, resulting in scans with voxels sizing 142 approximately 0.7 x 0.7 x 0.7 µm. The small voxel size gave a clear view 143 on anatomical features. Subvolumes of these reconstructed slices were 144 further manipulated with MATLAB® and Morpho+ (Vlassenbroeck et al., 145 2007). First, the slices were pre-processed aiming at noise removal and 146 image enhancement. This included histogram equalization to transform 147 the values of the greyscale images such that contrast was improved. 148 Subsequently the images were binarized using the topological derivative of Larrabide (2008). Finally, slices were despeckled by removal of small 149 150 isolated pixel islands. For the pine early- and latewood specimen, better results were obtained when images were denoised using the non-linear 151 diifusion technique as outlined by D'Almeida (non-linear diffusion toolbox 152 153 by Frederico D'Almeida). Subsequently, once denoised images were 154 available, wood parameters such as cell wall thickness and cell lumen size 155 could be calculated on 2D slices and labelling of a subvolume of pine (Van den Bulcke et al., 2008) could be performed in three dimensions. Cell 156 157 lumen sizes were determined via marker-based segmentation. This procedure starts with determination of the local maxima of the distance 158 159 transform of the image, as such representing the centres of the cell lumens. Application of the watershed algorithm with these local maxima as 160 161 markers correctly separated cells formerly connected though open pits. In 162 fact, this is an automatic version of the technique described in Reme and 163 Helle (2002) for pit removal. Manual editing was necessary to remove ray cells from analysis and to undo incorrect segmentation, but analysis is 164 165 quite fast, naturally depending on the quality of segmentation. Calculation of cell wall thickness was accomplished by using the distance transform of 166 167 the skeletonised image. The cell wall thickness (CW) then equals (1): 168

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$$CW = \frac{2 \times r \times \sum_{i=1}^{m} \sum_{j=1}^{p} (skel(i, j) \times dist(i, j))}{\sum_{i=1}^{m} \sum_{j=1}^{p} skel(i, j)}$$
(1)

171	with	r	= resolution (μm)
172		skel	= skeletonised cell walls
173		dist	= distance transformed cell walls
174		i, j	= row and column indices
175		<i>m</i> , p	= row and column size of matrix

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In addition, to exemplify the practical use of X-ray computed tomography in wood research, six pine latewood volumes, sampled from pith to bark, were scanned. A modified bronnikov algorithm (Boone et al., 2009) was employed for phase-contrast imaging. Figure 2 shows a slice through one of the two scanned stacks consisting of three of samples separated by an adhesive tape. The voxel size was 1.68 μ m and samples measured approximately 1.6 x 1.8 x 1.1 mm.

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185

Fig. 2.

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For correct analysis, rotation of the samples was obligatory. Once rotated, preprocessing included smoothing, noise removal and automated greyscale thresholding. Analysis of several 2D sections per sample resulted in mean values for cell perimeter and cell wall thickness and a profile in function of age.

- All images were rendered with VGStudio MAX®, MATLAB®, Octopus 3D
 Viewer and Drishti (Limaye, 2006).
- 194

195 **3. Results and discussion**

197 For each wood species, several images will illustrate the anatomy. A 3D 198 reconstruction gives an overview of the scan, cross-sectional views in axial, radial and tangential direction are given similar to conventional 199 cross-sectional views by Wagenführ and Schreiber (1989), IAWA list of 200 microscopic features for hardwood identification (IAWA Committee et al., 201 1989), Schweingruber (1990), IAWA list of microscopic features for 202 203 softwood identification (IAWA Committee et al., 2004) and Wagenführ 204 (2007). Characteristics of the wood are calculated on 2D sections and a 3D subvolume is used for 3D analysis. Finally, the brief study of six pine 205 latewood samples further exemplifies the practical use of X-ray 206 207 tomography in wood research.

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209 **3.1. Microscopic features**

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Below follows an overview of the characteristics of the wood species under study.

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214 Pinus silvestris L.

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216 Scots pine, member of the Pinaceae family, is characterized by its 217 homogeneous anatomy with tracheids as the main structural element and with a minor share of resin channels. Early- (EW) and latewood (LW) are 218 219 clearly different in tracheid wall thickness and lumen size. Pitting of radial of tracheids is predominantly uniseriate. Wood 220 walls ravs are heterocellular, composed of ray parenchyma and ray tracheids with 221 dentate thickenings and small pits. Cross-field pitting is fenestriform, on 222 average one pit per cross-field. These microscopic features can be 223 224 visualized on 3D reconstructions of pine given in Fig. 3 and several views 225 through the volume.

- 226
- 227 Fig. 3.

228 229 Fagus sylvatica L.

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Beech, member of the Fagaceae family, is a temperate hardwood species with a typical diffuse porous structure. The vessels are scattered and only reach small diameters. Wood rays can be subdivided in large and small individuals. Fibres have a relatively small lumen and a moderate thick wall. Vessel ray pitting is horizontal and have much reduced borders (predominantly scalariform). The compilation of images in Fig. 4 illustrates several of these characteristics.

- 238
- 239

Fig. 4.

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241 Disthemonanthus benthamianus Baill.

243 Movingui, member of the Leguminosae-Caesalpinioideae family, is a 244 diffuse-porous tropical hardwood, with little but large vessels and fibres. 245 Parenchyma apotracheal-terminal or paratracheal-aliform. is 246 Heterogeneous wood rays are small and not very high. The presence of silicon in heartwood is not unusual. Fig. 5 illustrates the different 247 248 anatomical aspects of movingui.

249

253

250 Fig. 5.

251252 Afzelia bipindensis Harms

Afzelia, also a member of the Leguminosae-Caesalpinioideae family, is a diffuse-porous tropical hardwood, with little but large vessels and thick fibres. Parenchyma is paratracheal aliform. Wood rays are small and not very high. Vessel perforation is simple. Crystals are abundantly present. The rendered volumes in Fig. 6 exemplify the wood anatomy.

259

260 Fig. 6.

261262 **3.2. Quantitative analysis**

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264 Image processing of large anisotropic volumes is a difficult task. Yet, wood 265 consists of a 3D structure that can be described effectively with 2D sections. Therefore, for the determination of parameters such as cell 266 267 (lumen) size and cell wall thickness, a 2D section is sufficient. The 268 procedure is very straightforward once a noise-free image is obtained. Pre-processing included selection of the tissue of interest, histogram 269 270 equalization, standard noise filtering and image binarization. As an example, Fig. 7 illustrates the difference between the original images with 271 272 noise, the noise-free (MATLAB®) and segmented (Morpho+) images for the four wood species. The segmented image can be used for measuring 273 cell properties; in fact, the segmented images in Figure 6a are colour-274 coded according to their lumen size. 275

276

277

Fig. 7.

Via marker-based watershed image segmentation cell lumen size was
determined. Cell lumen size frequencies are given in the line plots in Fig. 8
for the four wood species. The vessel sizes of afzelia and movingui are not
displayed because of their large size and low frequency. It should be
mentioned that, considering the natural variability of wood anatomy, these
results are not representative of the four species.

- 285
- 286 Fig. 8.

288 The difference in lumen size between early- and latewood tracheids is clear. Larger structures such as rays were labelled as well and manually 289 removed from the analysis, but could be filtered (semi-)automatically using 290 291 shape descriptors, e.g. by their elongated form. Dimensions can be used to split up vessels and fibres. It is clear that by proper demarcation of the 292 293 different zones, the different tissue sizes can be determined. Once such a 294 segmented and labelled dataset is available, calculations of a whole set of 295 properties is straightforward. Cell wall thickness is calculated from these 296 segmented images by skeletonization (Fig. 9). Results for pine are in agreement with the data in literature (Reme and Helle, 2002) while for the 297 other species the reader is referred to Wagenführ and Schreiber (1989) 298 299 and Wagenführ (2007).

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Fig. 9.

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As an example of 3D analysis performed in MATLAB®, the pine earlywood data stack is used. Optimal preprocessing of the stack of the original 2D sections included histogram equalization, noise removal by nonlinear image diffusion and image binarization using the topological derivative. The resulting noise-free, segmented subvolume is given in Fig. 10a. Figure 10b and 10c show the limits of resolution by displaying a three dimensional rendering and a 2D slice of pitting.

310

311 Fig. 10.

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313 Three-dimensional reconstruction of a reduced region of interest based on 314 watershed segmentation of the noise-free volume gives a view on the 315 labelling of the different colour-shuffled tracheid lumens. The original 316 binarized cell wall is visible as the greyish substance in-between in Figure 317 11a. This labelled volume can serve as the basis for calculation of length 318 and shape of single elements. The limits of resolution permit to visualize 319 individual pits as illustrated by Figure 11b. If 3D cell characteristics are desired, subtracting the skeletonised cell walls from the cell wall volume 320 321 leads to the separated structures for volumetric analysis. However, 322 whereas 2D analysis is fast, easy to correct and accurate 3D analysis of 323 large volumes is much more difficult. Especially for hardwood species 324 such analysis will pose problems and should be performed on isolated 325 anatomical regions.

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328

327 3.3 Analysis from pith to bark

A pith to bark analysis was performed for six pine latewood samples. Figure 11 illustrates the rendered volumes and the results of cell wall thickness and total cell perimeter measurements. These data are roughly in agreement with the data presented by Reme and Helle (2002). Obviously, juvenile wood has thinner walls and smaller cells in contrast with mature wood. It should be stressed that these data are not an indepth study of the changing latewood characteristics of Scots pine yet a proof of concept of the use of the X-ray computed modality presented in this paper.

339 Fig. 11.

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341 **4. Conclusions**

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343 X-ray sub-micron tomography has been shown here to be a powerful 344 image acquisition technique for wood research. The level of detail suffices 345 for descriptive and quantitative anatomical analysis as exemplified in this paper. Very small samples can be scanned at very high resolution, making 346 it appropriate for forensics and analysis of cultural heritage. Its non-347 348 destructiveness is an advantage when dealing with valuable material compared to classical methods, entailing the absence of preparation 349 artefacts as well. Furthermore, volume mosaicing will enable the 350 351 reconstruction of larger samples at a high level of detail, only limited by 352 data handling and storage. In addition, a factor not to be neglected is the educational value of 3D images, which could complete the online 353 354 databases such as InsideWood (http://insidewood.lib.ncsu.edu/search) of 355 wood anatomv Central European and species (http://www.wsl.ch/land/products/dendro). At last, once the substrate is 356 357 virtualized, all kinds of manipulation are feasible. The X-ray sub-micron tomography equipment presented in this paper will be a valuable tool in 358 359 material and life sciences in general.

360

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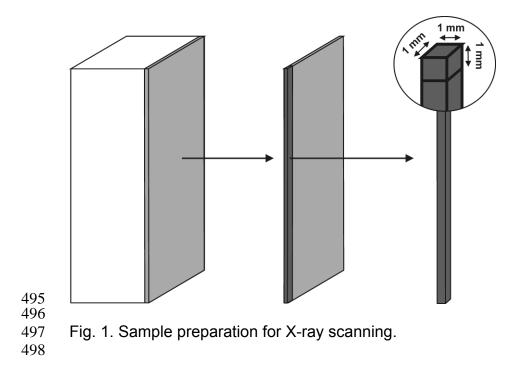
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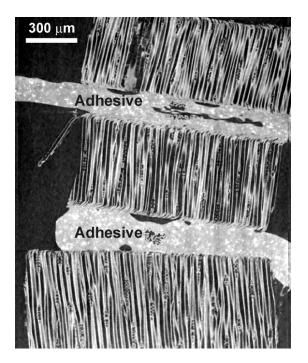
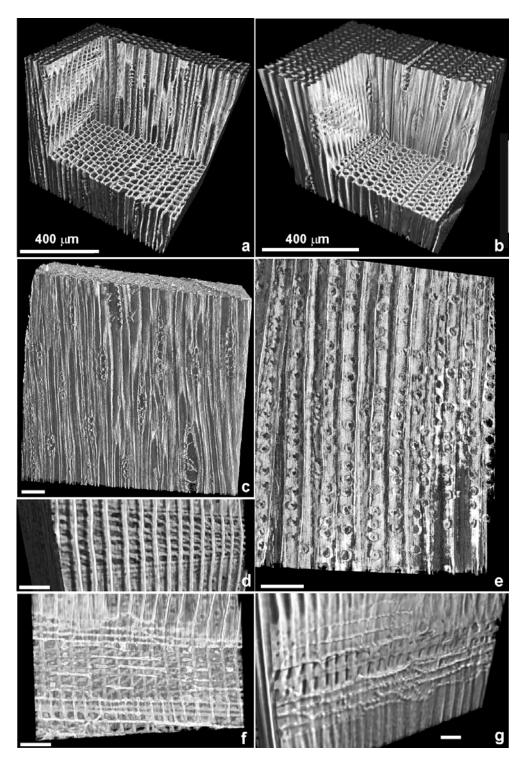


Fig. 2. Cross-sectional view through a stack of three pine latewood samples.



506 Fig. 3. Overview with cut out giving a clear view on the internal anatomy of 507 *Pinus silvestris* L. (a) earlywood and (b) latewood; (c) rays in latewood 508 with limited height; (d) fenestriform cross-field pitting; (e) uniseriate pitting 509 of cell walls of tracheids; (f+g) dentation of cell walls adjacent to ray 510 parenchyma. White bar = 100 μ m.

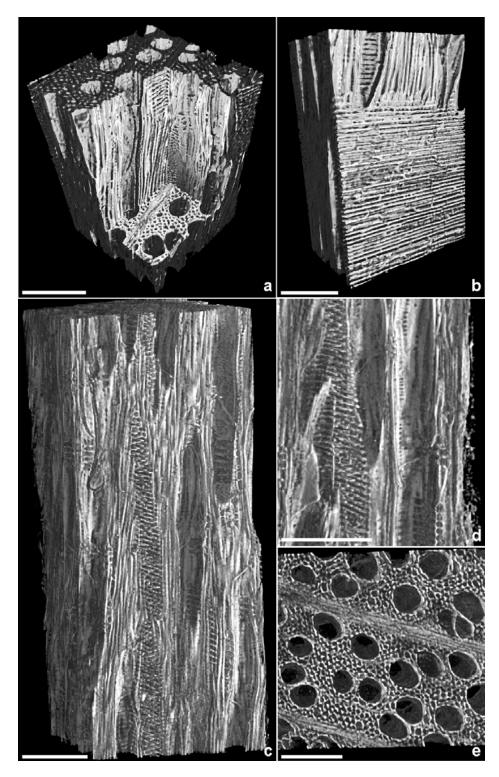




Fig. 4. Overview with cut out (a) giving a clear view on the internal anatomy of *Fagus sylvatica* L.; (b) rays and scalariform vessel-ray pitting; (c) large rays with several vessel cross-sections; (d) perforations of the vessel wall and view on the ray frame; (e) top view. White bar = $200 \mu m$.

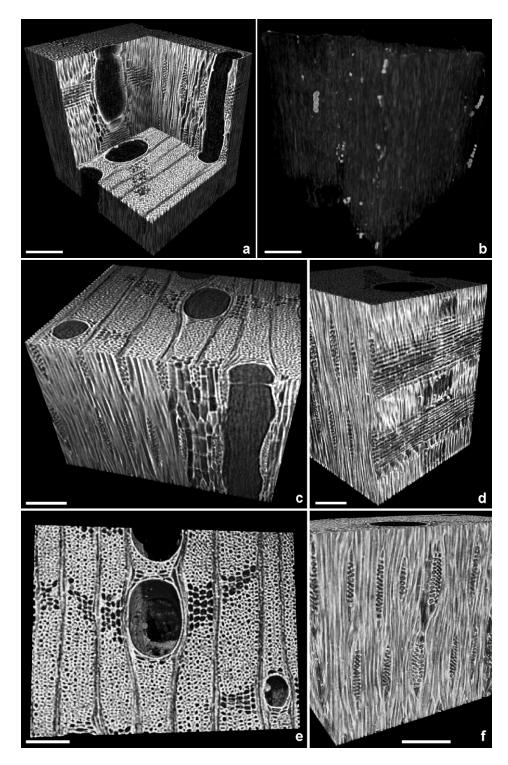
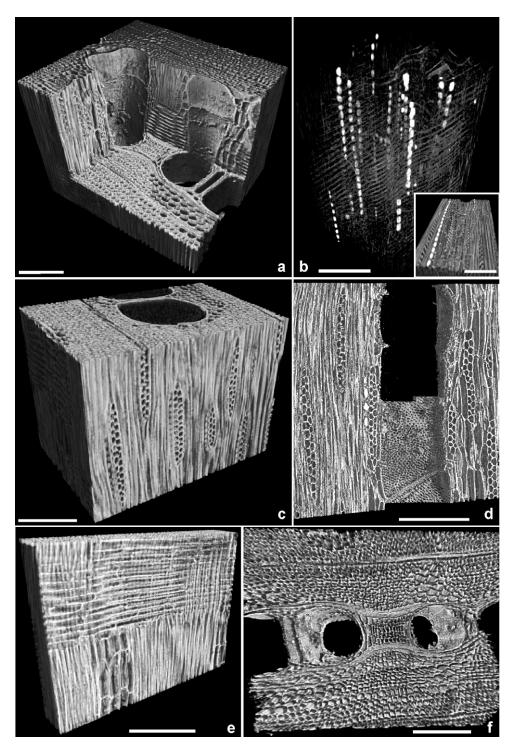
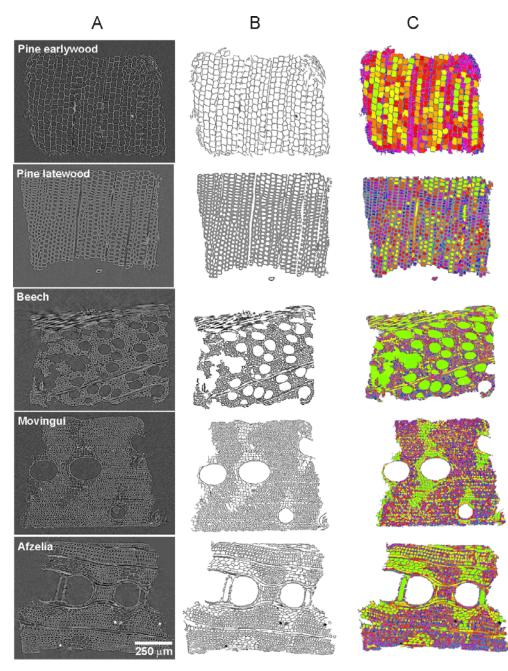


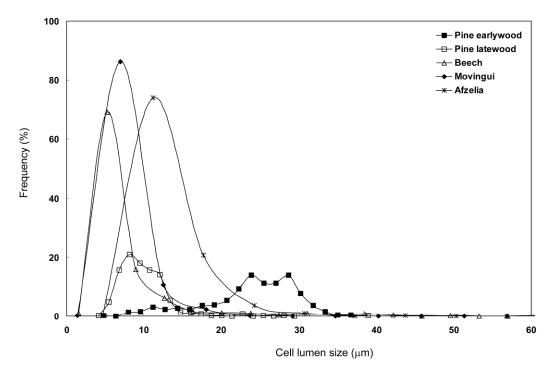
Fig. 5. Overview with cut out (a) giving a clear view on the internal anatomy of *Disthemonanthus benthamianus* Baill.; (b) prismatic crystals; (c) parenchyma, rays and slice through vessel; (d) longitudinal slice through rays; (e) top view; (f) tangential view on rays. White bar = $200 \mu m$.



529 Fig. 6. Overview with cut out (a) giving a clear view on the internal 530 anatomy of *Afzelia bipindensis* Harms; (b) prismatic crystals; (c) rays; (d) 531 simple vessel perforation; (e) view through ray and parenchyma; (f) top 532 view. White bar = $200 \mu m$.

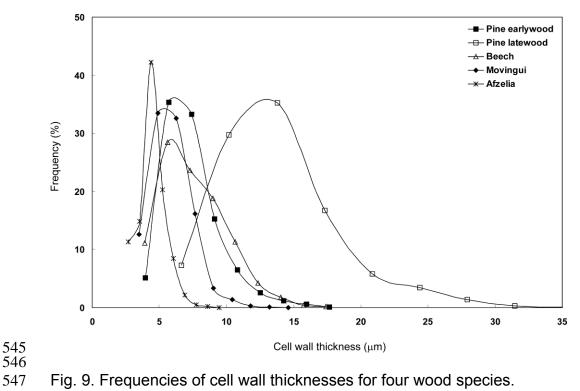








540 Fig. 8. Frequencies of the equivalent diameter of the cell lumen sizes for 541 four wood species.



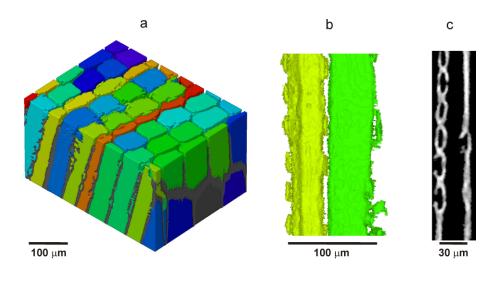
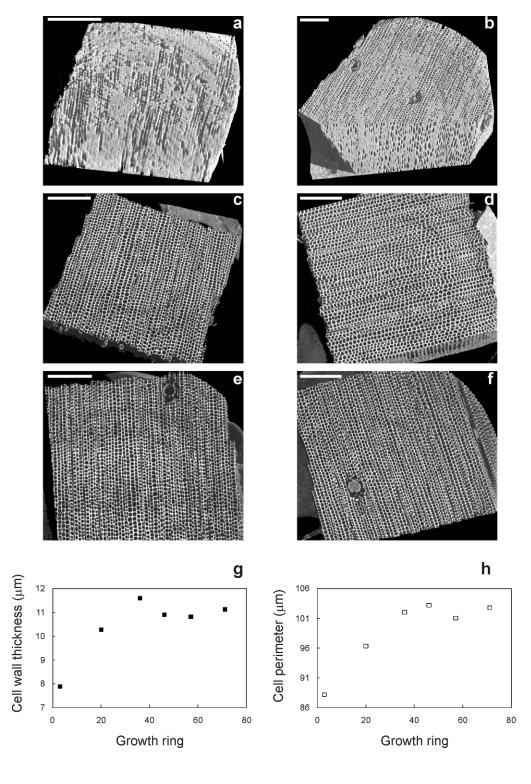


Fig. 10. Labelled cell lumens of the noise-free pine earlywood sample with greyish cell wall (a), detailed rendering of pitting between two cells (b) and 2D slice as an example of the limits of resolution for pit visualization.



559 Fig. 11. Six reconstructed pine latewood volumes sampled from pith to 560 bark (a-f) and their cell wall thickness (g) and cell perimeter (h) in function 561 of the growth ring they were sampled from. White bar = 400 μ m.