Contrast enhancement for visualizing neuronal cytoarchitecture by propagation-based x-ray phase-contrast tomography

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ARTICLE INFO

Keywords:
3d neuronal cytoarchitecture
Phase-contrast x-ray tomography
Synchrotron-based x-ray imaging
Laboratory-based x-ray imaging
Embedding media for contrast enhancement

ABSTRACT

Knowledge of the three-dimensional (3d) neuronal cytoarchitecture is an important factor in order to understand the connection between tissue structure and function or to visualize pathological changes in neurodegenerative diseases or tumor development. The gold standard in neuropathology is histology, a technique which provides insights into the cellular organization based on sectioning of the sample. Conventional histology, however, misses the complete 3d information as only individual two-dimensional slices through the object are available. In this work, we use propagation-based phase-contrast x-ray tomography to perform 3d virtual histology on cerebellar tissue from mice. This technique enables us to non-invasively visualize the entire 3d density distribution of the examined samples at isotropic (sub-)cellular resolution. One central challenge, however, of the technique is the fact that contrast for important structural features can be easily lost due to small electron density differences, notably between the cells and surrounding tissue. Here, we evaluate the influence of different embedding media, which are intermediate steps in sample preparation for classical histology, on contrast formation and examine the applicability of the different sample preparations both at a synchrotron-based holotomography setup as well as a laboratory source.

1. Introduction

The gold standard to decipher the cytoarchitecture of neuronal tissue on the (sub-)cellular scale is histology, based on slicing the sample into thin sections in order to gain insights into the three-dimensional (3d) cellular distribution (Li et al., 2010). It is a time consuming technique which consists of several steps of tissue preparation and processing, including, e.g., fixation, dehydra
tion and embedding of the tissue, followed by the mechanical slicing procedure, staining of features of interest and observation of the individual sections under a light microscope. While it provides excellent results in 2d, the resolution in the third dimension is limited by the slice thickness, leading to an anisotropic reconstruction of the 3d cytoarchitecture, and the sample is destroyed afterwards. Furthermore, artifacts can easily occur due to the mechanical slicing procedure. Computed tomography (CT) offers a high potential for non-destructive 3d virtual histology, without any need for slicing due to the high penetration depth of x-rays through tissue. It provides isotropic reconstruction of the 3d cytoarchitecture based on differences in absorption coefficient (absorption contrast) or electron density (phase contrast). As the entire 3d information is available, virtual slices can be generated in any direction, which is one of the many advantages of virtual histology. In this way, slice orientation can be selected a posteriori to visualize specific features of the sample. In order to achieve sufficient contrast to resolve single cells within the tissue, the phase shift induced by the sample can be exploited for image formation instead of the absorption contrast, on which clinical CT is based. As this phase shift cannot be measured directly, it has to be made visible in the intensity images, e.g., via Talbot interferometry (Momose et al., 1996; Weitkamp et al., 2005; Pfeiffer et al., 2008), edge illumination (Munro et al., 2012; Hagen et al., 2014) or speckle-based imaging (Morgan et al., 2012; Zdora et al., 2017).

In this work, we use free space propagation between the object and the detector (Nugent et al., 1996; Paganin and Nugent, 1998; Cloetens et al., 1999; Bartels et al., 2015a), as this form of phase contrast imaging
provides the high resolution needed to visualize single cells within the reconstructed volume (Zanette et al., 2013; Lang et al., 2014; Töpperwien et al., 2018). Depending on the Fresnel number $F = \frac{n}{\lambda}$, where $p$ is the pixel size, $\lambda$ the wave length and $n$ the distance between the object and the detector, image formation can be classified to be in the direct-contrast regime ($F < 1$), in which phase contrast is visible as edge enhancement, or in the holographic regime ($F > 1$), in which contrast transfer is higher and multiple interference fringes can be observed. In both cases, phase retrieval has to be performed in order to retrieve quantitative information about the object’s phase distribution (Cloetens et al., 1999; Paganin et al., 2002; Witte et al., 2009; Hagemann et al., 2018).

The potential of propagation-based x-ray phase-contrast tomography as a novel large-scale, label-free, 3d neuroimaging technique, has been tested in a number of recent studies. The cerebral angio-architecture was visualized within large brain regions of rats in Zhang et al. (2015). Ex vivo whole brain scans of small animal models were evaluated in view of brain tissue morphology for both normal and cancerous tissue, and the treatment effects of X-Ray Microbeam Radiation Therapy on nervous tissue were investigated (Barbone et al., 2018). Importantly, resolution and contrast was demonstrated to be sufficient for single cell identification in larger volumes both for rodents (Fratini et al., 2015; Bukreeva et al., 2017), as well as for human tissues (Hieber et al., 2016; Khimchenko et al., 2018; Töpperwien et al., 2018). The density and spatial distribution of neurons, for example, is of interest as a structural marker in physiology and pathology. To this end, it is particularly important that automated segmentation can be achieved for unstained tissue, as shown in Hieber et al. (2016), Bukreeva et al. (2017), Töpperwien et al. (2018). 3d resolution beyond the optical limit was first demonstrated by Khimchenko and co-workers (Khimchenko et al., 2018). Tissue alterations in different disease states, for example vascular alterations and neuronal loss in a multiple sclerosis model (Cedola et al., 2017), or plaque formation in Alzheimer’s disease models (Astolfo et al., 2016; Massimi et al., 2019) have also been addressed. Finally, in view of a broader accessibility, it is important to note that phase-contrast tomography of neuronal tissues with sub-micron resolution has also been translated to compact laboratory x-ray sources (Töpperwien et al., 2017, 2018).

In all of the recent studies mentioned above, sufficient contrast for small soft tissue features was the key advantage of the technique with respect to conventional CT. Phase-contrast CT is capable to exploit the small signals of electron density differences between cells and the surrounding tissue, but in the case of hydrated samples this can easily fall below the detection threshold. Optimization of the sample preparation becomes crucial in view of maintaining or increasing the contrast levels. One possibility is to use radiocontrast agents such as metals in order to stain specific features of interest within the sample (Bartels et al., 2015b; Krenkel et al., 2015; Töpperwien et al., 2016a; Strotton et al., 2018). Another possibility is to embed the sample in a medium with an electron density differing from the main tissue components, resulting in a more global contrast increase (Hieber et al., 2016; Bukreeva et al., 2017; Khimchenko et al., 2018; Töpperwien et al., 2018). In Strotton et al. (2018), different mounting, staining and experimental parameters were evaluated in terms of stability, contrast and image quality for imaging of spinal cord tissue at a synchrotron-based microtomography setup.

In this work, we study the effect of the embedding media on contrast formation on the cellular and sub-cellular level in unstained tissue. To this end, we focus on cerebellar tissue from mice. The cerebellum represents a perfect natural test object, as it exhibits features of different length scales (the large Purkinje cells with a soma size of 20–40 μm and the small cells in the granular layer with sizes of 5–8 μm in humans (Shepherd, 2004)) and of different densities, e.g. the low-cell molecular layer as opposed to the cell-dense granular layer. In earlier work, we have demonstrated that drying of tissue according to the evaporation-of-solvent method leads to reconstructions with a high contrast, allowing for the unambiguous identification of single cells within the volume (Töpperwien et al., 2017). The applicability of this preparation to human tissue, however, still needs experimental validation. Further, it is accompanied by considerable shrinkage. Here, we concentrate on less invasive embedding media, which are furthermore all well established as intermediate steps in a paraffin-embedding sequence and are therefore of standard use in the preparation of human brain samples in pathology, namely PBS (electron density: ~337 nm$^{-3}$), ethanol (~269 nm$^{-3}$) and the wax itself (~311 nm$^{-3}$) (Khimchenko et al., 2016, 2018; Töpperwien et al., 2018). This offers the additional advantage that the tissue is also well suited for a subsequent histological examination without the need for rehydration and stain removal and reembedding of the samples (Holme et al., 2014; Hieber et al., 2016; Khimchenko et al., 2018). The experiments were performed both at a high-resolution synchrotron-based holo-tomography endstation (Salidtt et al., 2015; Töpperwien et al., 2018) and at a home-built laboratory setup (Töpperwien et al., 2017, 2018). This enables imaging of the sample on multiple length scales and fields of view.

2. Materials and methods

2.1. Sample preparation

Wild type mice were either perfused with 10% sucrose solution for 10 min, followed by the dissection of the brain and fixation overnight in a solution containing 1% paraformaldehyde and 1% glutaraldehyde, or sacrificed with CO$_2$, followed by the dissection of the brain and fixation in 10% formalin for 24 h.

Hydrated samples. In a first step, the fixed brain was cut into 500 μm or 1 mm thick slices. A liquid chamber was built with two aluminum rings with a diameter of 5 cm and a width of 500 μm which were covered with polypropylene foil on one side. Placing the brain slice together with additional PBS onto one of the foils and gluing a second ring on top of it results in a closed chamber around the sample (cf. Fig. 1 (a)). The orientation of the aluminum rings determines the width of the chamber, as they can act as spacers between the polypropylene foils. In order to mount the sample stably in the setup, the width of the chamber equalled the width of the brain slice so that it was kept in place by the pressure of the polypropylene foils. In a last step, the resulting liquid chamber was clamped into a brass sample holder for mounting in the setup. As the measurements at the laboratory required a smaller sample-to-detector distance, the sample size was restricted and the aluminum rings could not be used. In this case, the sample was prepared similar to the ethanol-embedded case, as described in the following.

Ethanol-embedded samples. The fixed brain was sliced into 500 μm or 1 mm thick sections. For the exchange of water content, an ascending ethanol series was performed (70%: 1 × 15 min, 90%: 1 × 15 min, 100%: 2 × 15 min, 100%: 1 × 30 min, 100%: 1 × 45 min). Subsequently, a 1 mm punch was taken from the brain slice in order to reduce absorption of parts of the sample which lie outside the field of view and squeezed into a Kapton tube with 1 mm diameter, which was glued to a sample holder. The punch was positioned based on visual inspection such that all layers of the cerebellum were included in the respective volume. In order to maintain experimental conditions and prevent the sample from drying, the tube was filled with additional ethanol and sealed with 2-component glue (cf. Fig. 1 (b)). For long measurements, as necessary at the laboratory, an additional layer of haematocrit sealing compound (Brand, Germany) was inserted between the ethanol and glue, since this proved to be more stable with regard to evaporation of the solvent.

Paraffin-embedded samples. After fixation, the entire mouse brain was embedded in paraffin. To this end, water content was removed via an ascending ethanol series (60%: 1 × 1.5 h, 75%: 2 × 1.5 h, 96%: 2 × 1.5 h, 100%: 2 × 1.5 h). Subsequently the ethanol was exchanged by xylene (2 × 1.5 h) and the sample was transferred to molten paraffin wax (~60° C). After complete infiltration (2 × 1.5 h), the tissue was embedded in a fresh batch of paraffin, which was subsequently hardened. For the experiments, a 1 mm biopsy punch was taken and squeezed into a 1 mm
Kapton tube glued to a sample holder (cf. Fig. 1(c)). As the wax is hard at room temperature, no additional sealing of the Kapton tube was necessary as opposed to the preparations in ethanol or PBS.

2.2. Experimental setups

Synchrotron setup. The experiments were performed at the Göttingen Instrument for Nano-Imaging with X-Rays (GINIX) which is installed at the P10 beamline of the storage ring PETRA III at DESY in Hamburg (Salditt et al., 2015; Töpperwien et al., 2018). The photons were monochromatized by a Si(111) channelcut-monochromator to an energy of 8 keV and prefocused by a set of Kirkpatrick-Baez mirrors to a focal spot of approximately 300 × 300 nm². To reduce high-frequency artifacts caused by inhomogeneities on the mirror surfaces, as well as to decrease the focus size and to obtain a higher degree of spatial coherence, a waveguide was placed into the focal plane of the mirrors (Neubauer et al., 2014; Chen et al., 2015; Hoffmann-Urlaub et al., 2016). At a distance z₀₀ behind the waveguide, the sample was positioned on a fully motorized sample stage, allowing for a precise alignment of both the rotation axis with respect to the beam as well as the sample with respect to the field of view. Approximately 5 mm behind the sample, a scintillator-based fiber-coupled scMOS detector with a Gadox scintillator and a pixel size p = 6.5 μm (Photonic Science, UK) was located. Image formation by free space propagation for these experimental parameters results in the so-called holographic regime. Note that the divergent beam geometry leads to a selectable geometrical magnification M = s₀₀/z₀₀, with the source-to-detector distance z₀₀ resulting in an image with effective pixel size pₑₚ = p/M. In this way, propagation imaging is enabled at the nanoscale. The parameters used for the experiments are listed in Table 1.

Laboratory setup. In the laboratory setup (Töpperwien et al., 2017, 2018), x-rays were generated by a liquid-metal jet microfocus source (Excillum, Sweden), consisting of Galinstan with the main energy peak at the Ga-Kα line at 9.25 keV. The liquid-metal anode enabled sufficient spatial coherence while providing a comparably large photon flux. As in the synchrotron setup, the sample was placed on a fully motorized sample stage and the photons were detected further downstream. Due to lower magnification and smaller propagation distance compared to the synchrotron setup, image formation is now in the so-called direct-contrast regime. This is well suited for laboratory measurements, since this regime is more robust with respect to low spatial and temporal coherence. In order to reach (sub-)cellular resolution, the setup was operated in the ‘inverse’ geometry, i.e., the sample was placed close to the detector, leading to a magnification M ≈ 1, and a high-resolution detector with a pixel size of 0.54 μm (XSi80m micron, Rigaku, Czech Republic) was used (Töpperwien et al., 2017, 2018). A detailed list of the experimental parameters is given in Table 1.

2.3. Data analysis

Synchrotron measurements. Phase retrieval was performed with the contrast transfer function (CTF)-based reconstruction algorithm introduced by Cloetens et al. (Cloetens et al., 1999; Turner et al., 2004; Zabler et al., 2005) on all empty-beam corrected projections (cf. Fig. 2(a) and b), 3(a,b) and 4(a,b). In the experiments on the ethanol- and paraffin-embedded samples, projections were recorded at several propagation distances to avoid artifacts due to the zero crossings of the CTF. In this case, the cone-beam geometry of the setup leads to a varying magnification and field of view in the single projections. To account for this, the corresponding projections were scaled to the pixel size with the highest magnification, aligned via a cross-correlation in Fourier space (Guizar-Sicairos et al., 2008) and cropped to the same field of view. An additional high-pass filter was applied on the empty-beam corrected projections to reduce low-frequency artifacts caused by an unstable illumination during the measurement. Ring removal was performed on the individual sinograms prior to tomographic reconstruction, either with a wavelet-based technique (Münch et al., 2009) (hydrated) or a simpler approach based on integration of the sinogram along the angle and subsequent filtering (Ketcham, 2006) (ethanol/paraffin). Tomographic reconstruction was carried out with the Matlab implementation of the filtered backprojection with a standard Ram-Lak filter. In order to obtain a higher signal-to-noise ratio (SNR), all slices were filtered with a Gaussian function with a standard deviation of 0.7 pixels (hydrated) or 1 pixel (ethanol/paraffin), leading to a denoising of the images at the cost of a slight image blur. Segmentation of the large Purkinje cells was performed in Avizo 9 (Thermo Fisher Scientific, USA), using a gray-value based region growing tool with manually defined seeding points. In order to also segment smaller features with a low signal-to-noise ratio (SNR), the segmentation was subsequently manually refined.

Laboratory measurements. Phase reconstruction was performed on the

<table>
<thead>
<tr>
<th>Table 1</th>
<th>Parameters for the experiments at the synchrotron as well as laboratory setup.</th>
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<tbody>
<tr>
<td>synchrotron</td>
<td>laboratory hydrated ethanol/paraffin all samples</td>
</tr>
<tr>
<td>energy (keV)</td>
<td>8</td>
</tr>
<tr>
<td>s₀₀ (mm)</td>
<td>141</td>
</tr>
<tr>
<td>s₁₁ (m)</td>
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<tr>
<td>pₑₚ (nm)</td>
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<tr>
<td>field of view (mm²)</td>
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<tr>
<td>number of distances</td>
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</tr>
<tr>
<td>number of projections</td>
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</tr>
<tr>
<td>angular range (°)</td>
<td>[0,180]</td>
</tr>
<tr>
<td>exposure time (s)</td>
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empty-beam corrected projections using the Bronnikov-aided correction (BAC) algorithm (Witte et al., 2009; Topperwien et al., 2016b). In order to increase the SNR, all projections were resampled by a factor 2. Tomographic reconstruction was carried out with the cone-beam implementation of the ASTRA toolbox (Palenstijn et al., 2011; van Aarle et al., 2015, 2016). Prior to the tomographic reconstruction, the simple ring removal approach was performed on the individual sinograms. By applying a Gaussian filter with a standard deviation of 1 pixel on the reconstructed slices, the SNR was further increased, though at the cost of a slight blurring of sample features.

3. Results

3.1. Synchrotron setup

Hydrated sample. Two exemplary slices through the reconstructed density distribution of the hydrated brain slice are depicted in Fig. 2(c). Note that the orientation of these virtual slices was chosen such that they lie parallel to the Purkinje cell layer. The typical layers of the cerebellar cortex, namely the cell-rich granular layer (GL), the low-cell molecular layer (ML) and the mono-cellular Purkinje cell layer (PCL), as well as the white matter (WM) consisting of large axon bundles, can be clearly distinguished. Within these layers, single cells can be resolved, especially the large Purkinje cells comprising a high contrast with respect to the surrounding tissue. Even sub-cellular details are to some extent visible as, e.g., inner structure of the granule cell nuclei or the nucleolus of the Purkinje cells (cf. Fig. 2(c), inset on the right) as well as large branches of their dendritic trees. However, overall contrast is relatively low and a clear separation between single cells, especially in the cell-dense granular layer, is challenging. The contrast obtained for different features within the cerebellum can be quantified via the Weber contrast, defined as (Peli, 1990)

\[ C = \frac{I_{\text{target}} - I_{\text{background}}}{I_{\text{background}}} \quad (1) \]

which is a measure for the contrast of specific targets compared to their background. In order to reveal the 3d cytoarchitecture of neuronal tissue, the exact localization of cells is necessary and hence, their contrast against the surrounding tissue is the main challenge. Due to the difference in cell types, contrast was determined for both the Purkinje cells as well as the granular layer. To this end, several cells with comparatively high contrast based on visual inspection were manually selected and their resulting contrast against the surrounding tissue was averaged, yielding \( C_{\text{PCL}} \approx 0.5 \) and \( C_{\text{GL}} \approx 0.19 \), respectively. Note that for better comparability, the gray values of the reconstructed volume were shifted so that the minimum is given by 0, as different offsets, e.g., caused by region-of-interest tomography, influence the absolute values for the Weber contrast. In order to visualize the 3d structure of the high-contrast Purkinje cell layer, selected cells were segmented, including the large cell body and the parts of the dendritic tree which could be well distinguished from background. The result is depicted in Fig. 2(d), with two individual Purkinje cells shown at the bottom. The typical shape of the Purkinje cells with a large and nearly two-dimensional dendritic tree, as well as their parallel arrangement within the entire layer can be well recognized. However, when considering the single cells it becomes clear that due to a lack of contrast, only the main part of the dendritic tree, close to the cell body where branches are thickest, is resolved. An estimate of the resolution can be either achieved by considering the Fourier shell correlation (FSC) (van Heel, 1987; Harauz and van Heel, 1986), yielding the overall quality of the experiment, or via an error function fit to the edge of a highly contrasted feature within the slices, measuring the system blur for the given experimental parameters. To generate two independent datasets for the calculation of the FSC, the tomographic scan was divided into two subsets, consisting of every second projection and starting with the first or second, respectively. The intersection point between the FSC of the central 1000 voxels of these reconstructions and the 1/2-bit threshold curve determines the spatial frequency of the smallest feature for which enough data was collected for interpretation (van Heel and Schatz, 2005), resulting in a half-period resolution of 809 nm. The resolution estimate via an error function fit to the profiles along manually selected edges between Purkinje cell bodies, exhibiting a comparably large contrast, and the surrounding tissue, yielded a FWHM of ~1.11 μm and hence a half-period resolution of ~555 nm. The large difference between the two values indicates that noise and a weak contrast of the sample features, which have a large influence on the result obtained via
...the FSC, significantly limit the (globally defined) resolution, notwithstanding higher resolution of local features with stronger contrast.

**Ethanol-embedded sample.** Two orthogonal virtual slices through the obtained 3d density distribution are shown in Fig. 3(c). The layers of the cerebellar cortex, including the single cells within these layers as well as the white matter are clearly resolved. Additionally, sub-cellular details as, e.g., the inner structure of the granule cell nuclei or the thick branches of the dendritic tree as well as to some extent the nucleus of the Purkinje cells can be recognized. The contrast of single cells against surrounding tissue was again determined via eqn. (1), yielding $C_{PCL} \approx 0.99$ for the Purkinje cell and $C_{GL} \approx 0.34$ for the granular layer. The 3d shape of the Purkinje cell layer is depicted in Fig. 3(d), showing the typical flat dendritic tree and the parallel orientation of the cells to each other. Although they exhibit a higher contrast compared to the hydrated tissue, the amount of detail within this segmentation is approximately the same, which is probably due to the shrinking of the sample upon dehydration which is further quantified below.

An estimate for the achieved resolution was gained both via the FSC criterion, and an error function fit to an edge between a high-contrast feature and surrounding tissue in the reconstructed slices. The FSC curve of the central 1000$^3$ voxels intersected the 1/2-bit threshold curve at 0.092 cycles/pixel, corresponding to a half period resolution of 1.02 $\mu$m. The fit of an error function to the edge between selected Purkinje cells and surrounding tissue yielded a FWHM of ~800 nm and hence a half-period resolution of ~400 nm. This again shows that the dataset has a relatively high noise level and low contrast in the bulk of the reconstructed density distribution, which significantly limit the (global) resolution.

**Paraffin-embedded sample.** Two orthogonal slices through the reconstructed density distribution are depicted in Fig. 4(c). Again, the typical layers of the cerebellum are resolved down to the (sub-)cellular level. Within the cells, especially the large Purkinje cells, details as the nucleus and also the surrounding nuclei can be unambiguously distinguished whereas structures as the soma or dendritic tree of the Purkinje cells exhibit a relatively low contrast and can only be roughly visualized. This can be further quantified via the corresponding Weber contrast values, yielding $C_{PCL} \approx 0.2$ for the Purkinje cell layer and $C_{GL} \approx 0.56$ for the granular layer, respectively.

A segmentation of the Purkinje cell layer was performed on a selected number of cells, leading to the result depicted in Fig. 4(d). As in the case of the hydrated and ethanol-embedded sample, the typical flat shape and parallel orientation of the cells can be well recognized, though at lower detail due to the weak contrast of the dendritic tree in this preparation. The superior contrast of the cell nuclei, however, allows for an automatic segmentation of the small cells in the molecular and granular layer based on the Spherical Hough transform, as described in Topperwien et al. (2018) for human tissue. In Fig. 4(e) the result of this segmentation is shown both overlaid on a 2d slice and in 3d. The overlay of the segmentation on the corresponding virtual slice through the volume on the left shows that despite the larger cell density and hence denser packing of cells in mouse tissue, an automatic segmentation can be performed at high precision. This allows for a subsequent analysis of cellular distributions in 3d based on the exact locations of the cells within in the reconstructed volume.

Analogous to the hydrated and ethanol-embedded brain slices, the resolution of the scan was both estimated via the FSC criterion as well as an error function fit. The intersection between the FSC of the central 1000$^3$ voxels and the 1/2 threshold curve yielded a half-period resolution of 930 nm. For the determination of resolution via an error function fit, the edge between the high-contrast nucleolus of the large Purkinje cells and surrounding tissue was chosen, since the contrast of the previously considered cell bodies is comparatively low. This leads to a half-period resolution of ~310 nm, again indicating the large influence of noise and contrast on the estimated values.

**Comparison.** A comparison between the reconstructed densities for hydrated, ethanol-embedded and paraffin-embedded tissue is depicted in Fig. 5 and the obtained values for the Weber contrast as well as resolution are listed in Table 2. Embedding in ethanol leads to an overall increase in...
Fig. 4. Paraffin-embedded mouse cerebellum at the synchrotron setup. (a) Exemplary empty-beam corrected projection, in which cracks within the paraffin can be recognized as bright features. Note that in order to reduce low-frequency artifacts due to a changing illumination, a high-pass filter was applied. (b) Reconstructed phase map obtained via the CTF-based algorithm for homogeneous objects using four propagation distances. (c) Orthogonal slices through the reconstructed density distribution, showing the layers of the cerebellar cortex (granular layer (GL), molecular layer (ML) and Purkinje cell layer (PCL)) as well as white matter (WM). Especially the nucleoli can be visualized at high contrast. (d) Segmentation of the Purkinje cell layer. The Purkinje cells show the expected two-dimensional shape and parallel arrangement. However, due to the relatively low contrast of sub-cellular details as the cell body or the dendritic tree, only a small part of these large cells can be visualized in 3d. (e) The high contrast of the nuclei in the granular and molecular layer, however, allows for their automatic detection (left), enabling the visualization of the cellular cytoarchitecture in 3d (right). Scale bars: 50 μm.

Fig. 5. Comparison between the different embedding media used for experiments at the synchrotron setup. Tissue contrast within the hydrated brain slice (a) is relatively low when regarding the small cells in the granular as well as molecular layer, and single cells cannot be unambiguously identified. The cell bodies and to some extent even the dendritic tree of the large Purkinje cells can, however, be visualized at comparably high contrast. The exchange of water content by ethanol (b) leads to an overall increase in tissue contrast, allowing for the identification of single cells in all layers of the cerebellum. In the paraffin-embedded tissue (c), contrast within sub-cellular details of the Purkinje cells, as, e.g., the cell bodies or the dendritic tree, is low with respect to the surrounding tissue. For the cell nuclei/nucleoli of the GL and ML, contrast is, however, much higher than in the other preparations. Scale bars: 50 μm (top) and 25 μm (bottom).
Table 2
Comparison of the achieved resolutions as well as contrast values and cell sizes in the synchrotron measurements for the Purkinje cell as well as granular layer.

<table>
<thead>
<tr>
<th></th>
<th>half-period res. (PSC/edge)</th>
<th>contrast in PCL</th>
<th>contrast in GL</th>
<th>cell size PCL</th>
<th>cell size GL</th>
</tr>
</thead>
<tbody>
<tr>
<td>hydrated</td>
<td>809 nm/555 nm</td>
<td>−0.60</td>
<td>−0.19</td>
<td>−15.8 μm</td>
<td>−6.3 μm</td>
</tr>
<tr>
<td>ethanol</td>
<td>1.02 μm/400 nm</td>
<td>−0.99</td>
<td>−0.34</td>
<td>−14.7 μm</td>
<td>−4.4 μm</td>
</tr>
<tr>
<td>paraffin</td>
<td>930 nm/310 nm</td>
<td>−0.20</td>
<td>−0.56</td>
<td>−14.7 μm</td>
<td>−4 μm</td>
</tr>
</tbody>
</table>

The tissue contrast compared to a hydrated brain slice which can be recognized by visual inspection and by regarding the Weber contrast values. Note, however, that unwanted experimental factors due to varying waveguide performance, sample motion in liquid, as well as small differences in data processing are not accounted for in this estimation. Hence, absolute values are only approximative and should better be regarded as a lower bound representing the current state of the art. The liquid embedding, in particular, may have been penalized in the comparison by motion artifacts. Within the reconstructed volume, subcellular structures as the dendritic tree and nucleolus of the Purkinje cells or the inner structure of the granule cell nucleus can be resolved at higher detail, when comparing hydrated to ethanol embedding. The latter also leads to an increase in resolution when comparing hydrated to ethanol embedding. The latter also leads to an increase in resolution when regarding the fit of an error function to the edge between Purkinje cells and the surrounding tissue, which can be explained by the higher contrast of the considered features. Already by visual inspection it is evident that the embedding in paraffin does not increase overall tissue contrast but rather emphasizes the cell nucleoli and nuclei, whereas features as the soma or the dendritic tree of the Purkinje cells are depicted at lower contrast compared to the ethanol-embedded and even the hydrated tissue (cf. Table 2). Hence, paraffin is especially well-suited for the visualization and localization of the individual cell nuclei. One further advantage is the increased stability of the sample, both with respect to internal changes during the measurement, as, e.g., bubble formation, as well as sample mounting, which could also explain the higher resolution for this dataset determined via edge steepness.

Finally, we consider the amount of tissue shrinkage due to the dehydration process involved both in ethanol as well as paraffin embedding. This shrinkage can already be observed in Fig. 5 in comparison to the hydrated brain slice, especially when regarding the small cells within the granular layer. The size of the Purkinje cell bodies was estimated by manually determining their diameters for a few selected cells, yielding ~15.8 μm for the hydrated, ~14.7 μm for the ethanol-embedded and ~14.7 μm for the paraffin-embedded tissue. For the granular layer, cell diameters of ~6.3 μm, ~4.4 μm and ~4 μm were determined. Hence, especially in the granular layer, a significant shrinking due to the dehydration process can be observed. Note, however, that this size determination obviously depends on the selected cells as well as the manual definition of the cell borders, which is challenging in some cases due to the lack of contrast. Hence, the absolute values should again be considered as estimates.

3.2. Laboratory setup

Exemplary slices through the tomographic reconstructions obtained at the laboratory setup are depicted in Fig. 6. Note that the results from the hydrated brain slice in (a) show the same slice, which was either filtered with a Gaussian function with a standard deviation of 1 pixel (top) or 2 pixels (bottom) to account for the low SNR, whereas for the other two preparation technique, orthogonal slices are shown.

Despite the relatively low contrast achieved for the hydrated brain slice, all layers of the cerebellar cortex can be unambiguously identified, including the mono-cellular layer of the Purkinje cells and partly even sub-cellular details as their nucleolus (cf. Fig. 7(a) and (b)). To some extent, also the small cells within the molecular and granular layer can be recognized, especially in the slice which was filtered with a larger standard deviation. Due to myelin sheaths around the axons in the white matter, containing a high amount of fat, this layer is especially well visible in this preparation technique. The Weber contrast values were estimated as C\textsubscript{GL} ~ 0.10 for the Purkinje cell layer and C\textsubscript{PCL} ~ 0.06 for the granular layer, respectively. Compared to the hydrated brain slice, ethanol embedding leads to an increase in overall tissue contrast, similar to the experiments at the synchrotron setup. All layers of the cerebellar cortex as well as the cells contained within them are well visible. Especially the cells in the molecular layer as well as the large Purkinje cells show a high contrast and within their cell bodies, the nucleolus and to some extent even the nucleus in which the nucleolus is contained are resolved (cf. Fig. 7(c)). The Weber contrast values were estimated based on manually selected cells, yielding C\textsubscript{PCL} ~ 0.34 for the Purkinje cell layer and C\textsubscript{PCL} ~ 0.23 for the granular layer, respectively. This confirms the global increase of tissue contrast with respect to the hydrated brain slice.

In the paraffin-embedded tissue, the different layers of the cerebellar cortex, including the single cells within them, as well as the white matter can also be unambiguously identified due to a higher contrast of the cells against surrounding tissue. Similar to the synchrotron results, this increase is not global but the cell nuclei show a superior contrast compared to surrounding tissue, which can be recognized in Fig. 6(c), where the cell-dense granular layer is the dominating structure. In Fig. 7(d) this superior contrast is also visible on the (sub-)cellular scale, leading to a high visibility of single cells within the granular layer and the enclosed nucleolus and nucleus of the large Purkinje cells. This visual impression can be confirmed by the estimated Weber contrast values, yielding C\textsubscript{PCL} ~ 0.19 for the Purkinje cell layer and C\textsubscript{PCL} ~ 0.36 for the granular layer (see Table 3 for an overview of all contrast values).

The 3D cytoarchitecture can be visualized by volume renderings of the reconstructed volumes, as depicted in Fig. 8 for the ethanol- and paraffin-embedded samples. In both cases, the layers of the cerebellum are well distinguishable and single cells can be visualized in 3D. The differences in contrast, however, lead to a higher visibility of the cells in the molecular layer and the Purkinje cells in the case of the ethanol-embedded sample, whereas in the paraffin-embedded sample, the cells in the molecular and also the dense granular layer can be better visualized. Moreover, blood vessels can be recognized as well, which also allows for an examination of the vasculature in 3D.

The resolution achieved at the laboratory setup for the different sample preparations was estimated via the FSC criterion. In this case the experimental conditions were identical for all measurements. The intersection between the FSC for the central 1000\textsuperscript{3} voxels of the reconstructed volumes and the 1/2-bit threshold curve yielded half-period resolutions of 3.0 μm for the hydrated, 1.57 μm for the ethanol-embedded and 1.55 μm for the paraffin-embedded tissue. This proves the stability of the laboratory setup as well as the sample mounting, since a resolution of ~1.5 × the (resampled) pixel size was achieved despite the long exposure times. At the same time, this shows the negative influence of a low-contrast sample preparation (as in PBS), resulting in a significant loss of resolution.

4. Summary, conclusions and discussion

In summary, propagation-based phase-contrast tomography was performed both at the synchrotron and at a laboratory setup on mouse cerebellar tissue to visualize the underlying 3D cytoarchitecture and to evaluate the evolution of contrast when using different embedding media. At both setups, the typical layers of the cerebellum were visualized at a resolution high enough to identify individual cells and to some extent also sub-cellular details in all three preparations, hydrated as well as ethanol and paraffin embedding. The synchrotron setup provided results with a higher resolution in which details as the inner structure of the...
granule cell nuclei or the thicker branches of the Purkinje cell dendrites could be resolved. The laboratory setup, on the other hand, allowed for a larger volume to be probed and offers higher accessibility. All preparation techniques provided results in which the overall cytoarchitecture of the cerebellum was well represented, contrast of individual features varied between the different embedding media. In hydrated tissue, white matter, containing a large amount of myelinated axon bundles, showed a comparably high contrast, most notably in the results of the laboratory setup, whereas cells within the cerebellar cortex were less visible. However, single cells could still be recognized both at the synchrotron and even at the laboratory, especially the large Purkinje cells. One major advantage of this preparation is that, apart from and even at the laboratory, especially the large Purkinje cells. One major advantage of this preparation is that, apart from and even at the laboratory, especially the large Purkinje cells. One major advantage of this preparation is that, apart from and even at the laboratory, especially the large Purkinje cells. One major advantage of this preparation is that, apart from and even at the laboratory, especially the large Purkinje cells. One major advantage of this preparation is that, apart from and even at the laboratory, especially the large Purkinje cells. One major advantage of this preparation is that, apr...
that by variation of photon energy and geometric parameters, the FOV is easily scalable, and the FOV can be increased up to the entire brain at the price of correspondingly smaller resolution. Since the technique is non-destructive large FOVs can be scanned first to identify regions-of-interest (ROI), which are then scanned at higher resolution. This will be especially important in the future, for example for studies of neurological diseases that affect specific brain regions and cellular morphologies within different regions. Controlled biopsy punches based on prior scans of large tissues scanned in overview CT has for example already been demonstrated in Töpperwien et al. (2019). Furthermore, the entire cellular cytoarchitecture could be probed by subsequent and densely sampled biopsy punches. A second important issue is the capability to reconstruct single neurons in 3d. In this work, we have demonstrated this only for the relatively easy task of segmenting the Purkinje cells (PC). In future, it will be important to extend this to other cell types. For this purpose, the larger volumes of neurons in human brain compared to mouse will certainly help. Regarding synchrotron radiation, we can anticipate that contrast can be increased and noise can be decreased by reducing the photon energy and increasing flux density. Already at present, different neuronal shapes can be identified visually, but automated segmentation often remains a challenge. To this end contrast variation based on different embedding media, as introduced here, will provide a valuable tool to highlight different neuron types. Potentially, one could even vary contrast in the same sample by exchange of solvent (e.g. ethanol-water mixtures), resulting in several gray values for the same voxel. This would significantly facilitate segmentation and classifications based on gray-value distributions in a higher dimensional space. Third, we must address the fact, that the current reconstructions fail to reveal the complete dendritic trees of the PCs. The main branches of the dendrites can be segmented, but contrast is not sufficient to visualize the entire elaborate structure, which may be limiting in studies of PC degeneration or development. By additionally increasing the contrast via metal staining of the features of interest, this could be significantly improved. Based on the rapid improvements in x-ray optics and source brilliance, however, we expect that these limits will also shift for unstained tissue, for which the physically limiting factor is a minimum of density difference between dendrite and environment. It is precisely this variable which can be controlled based on the embedding medium. Further, we want to briefly comment on the accessibility of the technique. The laboratory setup, in particular, offers permanent accessibility as no application for beamtime is necessary. This makes this setup useful for applications requiring a high throughout as well as short term availability. In this respect, it is important to stress that the laboratory setup used is a home-built instrument optimized for the purpose, but by no means restricted to groups with exclusive technical skills. All components, source, positioning units and detector are commercial, and the setup used is a home-built instrument optimized for the purpose, but by no means restricted to groups with exclusive technical skills. All components, source, positioning units and detector are commercial, and the selection of geometry and parameters has been described in detail in Töpperwien (2018). We expect that commercial providers will soon offer a similar set of components and parameters. For the image quality obtained, the reconstruction algorithms are at least as important as the hardware. We have worked with our own numerical implementations

Table 3
Comparison of the achieved resolutions as well as contrast values in the laboratory measurements for the Purkinje cell as well as granular layer.

<table>
<thead>
<tr>
<th>Embedding Medium</th>
<th>half-period res. (PSC)</th>
<th>contrast in PCL</th>
<th>contrast in GL</th>
</tr>
</thead>
<tbody>
<tr>
<td>hydrated</td>
<td>3.0 µm</td>
<td>-0.10</td>
<td>-0.06</td>
</tr>
<tr>
<td>ethanol</td>
<td>1.57 µm</td>
<td>-0.34</td>
<td>-0.23</td>
</tr>
<tr>
<td>paraffin</td>
<td>1.55 µm</td>
<td>-0.19</td>
<td>-0.36</td>
</tr>
</tbody>
</table>
Acknowledgments

We thank Julia Scherber and Bärbel Heidrich for help in sample preparation and Michael Sprung for excellent support during the beamtime at DESY beamline P10. Financial support by the collaborative research center 755 Nanoscale Photonic Imaging as well as the Clusters of Excellence 171 Nanoscale Microscopy and Molecular Physiology of the Brain and 2067 Multiscale Bioimaging: From Molecular Machines to Networks of Excitable Cells of the German research foundation (DFG) is gratefully acknowledged.

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