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# **Abstract**

Abstract in English.



# Tartalmi kivonat

Absztrakt magyarul.



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## **LIST OF TABLES**

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# **Introduction**

Coming soon.

## **INTRODUCTION**

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# Chapter 1

## Live imaging in three dimensions

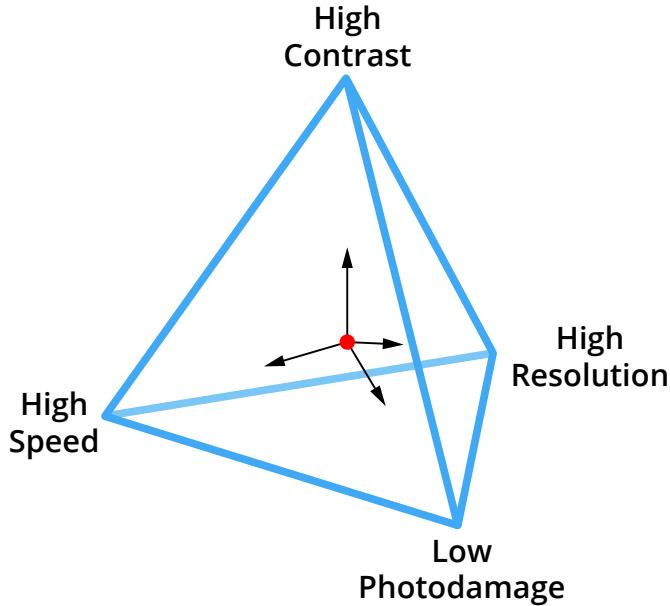
Unraveling the secrets of mammalian development has been a long standing challenge for developmental biologists and medical professionals alike. This phase of early life is an incredibly complex and dynamic process spanning through large scales in space and time. Subcellular processes at the nanoscale are happening in the range of milliseconds or faster, while whole embryo reorganizations and tissue migration events take place over the course of hours [1]. Resolving these processes presents a true challenge, since to also understand the underlying mechanisms molecular specificity is just as crucial as high spatial and temporal resolution.

Light microscopy is one of the oldest methods that is still widely used today to investigate the inner workings of microscopic life. A particularly important branch is fluorescence microscopy [2], that relies on using fluorescent labels to mark specific regions inside the specimens. Light-sheet microscopy is a relatively new addition to the arsenal of tools that comprise light microscopy methods, and is especially suitable for live imaging of embryonic samples over extended periods of time [3, 4]. It is also easily adapted to the sample, allowing to image a large variety of specimens, from entire organs, such as cleared mouse brains [5], to the subcellular processes occurring inside cultured cells [6].

In an ideal setting, the ultimate microscope would be able to record a continuous, 3D, and multicolor dataset of any biological process of interest with the highest possible resolution. Unfortunately this is not possible; due to several limitations in physics and biology, a compromise is necessary. The diffractive nature of light, the lifetime of fluorescent probes and the photosensitivity of biological specimens all require microscopy to be able to adapt to answer the question at hand. In order to acquire useful data one has to choose a tradeoff between spatial and temporal resolution, and signal contrast, while making sure the biology is not affected by the imaging process itself (Fig. 1.1) [7].

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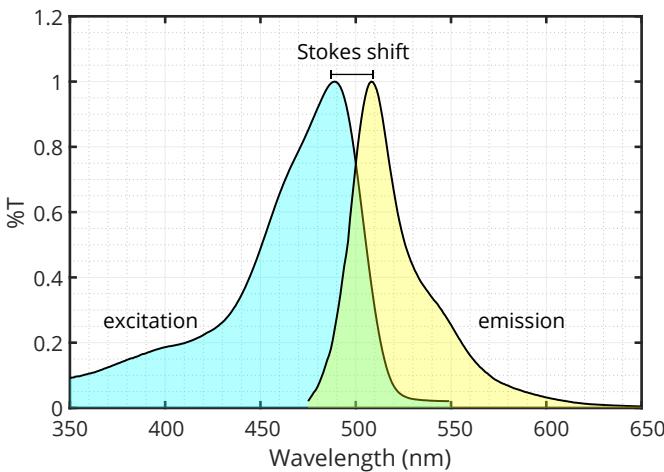


**Figure 1.1: Tradeoffs in fluorescence microscopy for live imaging.** Also called the “pyramid of frustration”. When optimizing the imaging conditions (red dot), a tradeoff has to be made between resolution, contrast, and imaging speed, while avoiding photodamage. One can only be improved at the expense of the others due to the limited photon budget of the fluorescent molecules. Adapted from [7].

### 1.1 Wide-field fluorescence microscopy

Fluorescence microscopy [2, 8], as a subset of light microscopy is one of the few methods that allow subcellular imaging of live specimens. The first use of the term fluorescence is credited to George Gabriel Stokes [9], and it refers to the phenomenon when a molecule emits light after absorbing light or other electromagnetic radiation. As the name of the technique suggests, this method collects fluorescent light from the specimens which has numerous advantages, but also some drawbacks. Since biological tissue is usually not fluorescent, except for some autofluorescence at shorter wavelengths, fluorescent dyes or proteins have to be introduced to the system in order to be able to collect the necessary information. The advantage of this is that the signal of the labeled structures will be of very high ratio compared to the background.

A fluorescent molecule is capable of absorbing photons in a given range (excitation spectrum) and temporarily store its energy by having an electron in a higher energy orbital, *i.e.* in an excited state. This excited state, however is not stable, and the electron quickly jumps back to the ground state while emitting a photon with equal energy to the energy difference between the excited and ground states. The energy of the absorbed and emitted photons are not the same, as energy loss occurs due to internal relaxation events, and the emitted photon has lower energy than the absorbed photon. This phenomenon is called the Stokes shift, or red shift, and can be exploited in microscopy to drastically increase the signal to noise ratio by filtering out the illumination light (Fig. 1.2).



**Figure 1.2: Excitation and emission spectrum of enhanced green fluorescent protein (EGFP).** Excitation spectrum in blue, emission spectrum in yellow. The separation between the two spectra is due to the Stokes shift, which is 19 nm for EGFP. Emitted and excitation light can be separated by a long-pass filter at 500 nm. Data from [10].

### 1.1.1 Fluorescent proteins

Traditionally synthetic fluorescent dyes were used to label certain structures in the specimens. Some of these directly bind to their target, and others can be used when conjugated to an antibody specific to the structure of interest. The drawback of these methods is that the fluorescent label has to be added to the sample from an external source, and, in many cases, this also necessitates sample preparation techniques incompatible with live imaging, such as fixation [11].

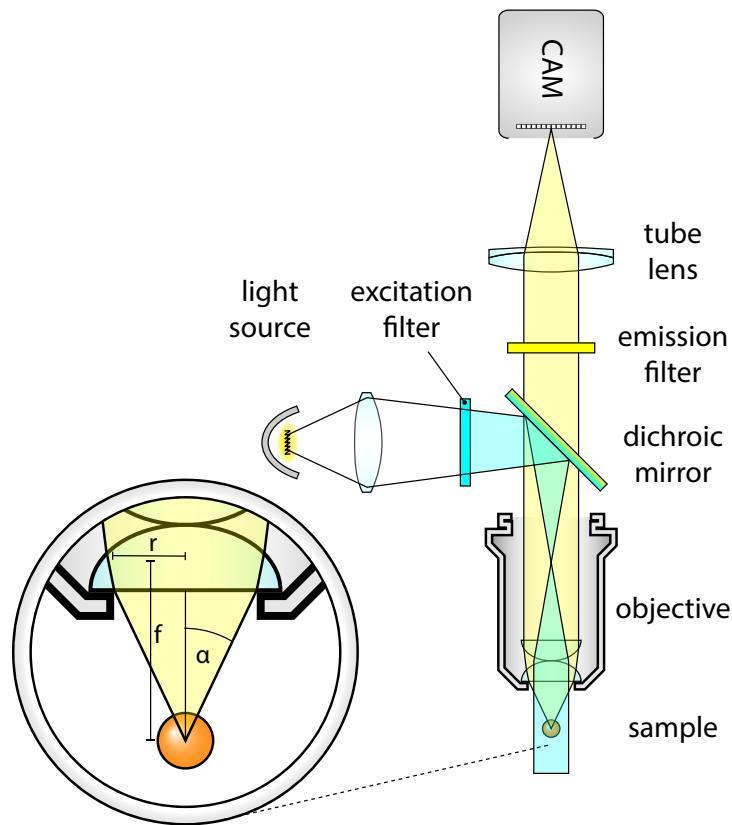
The discovery of fluorescent proteins have revolutionized fluorescence microscopy. Since these molecules are proteins, they can be produced directly by the organism if the proper genetic modifications are performed. Even though this was a hurdle at the time of discovering the green fluorescent protein (GFP) [12], the first of its kind, genetic engineering techniques evolved since then [13], and not only has it been successfully integrated in the genome of nematodes [14], zebrafish [15], and mice [16], but many variants have been also engineered by introducing mutations to increase fluorescence intensity, and to change the fluorescence spectrum to allow multicolor imaging [16–19]. The usefulness and impact of these proteins are so profound, that in 2008 the Nobel Prize in chemistry was awarded to Osamu Shimomura, Martin Chalfie, and Roger Tsien “for the discovery and development of the green fluorescent protein, GFP” [20].

### 1.1.2 Wide-field image formation

By imaging fluorescently labelled specimens, a wide-field fluorescence microscope has the capability of discriminating illumination light from fluorescent light due to the Stokes shift described in the previous section. The microscope’s operating principle is depicted

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**Figure 1.3: Wide-field fluorescence microscope.** (a) The light source is focused on the back focal plane of the objective to provide an even illumination to the sample. Emitted photons are collected by the objective, and are separated from the illumination light by a dichroic mirror. (b),  $\alpha$

in Figure 1.3.

A light source, typically a mercury lamp is focused on the back focal plane of the objective to create even illumination at the sample. Before entering the objective, the light is filtered, so only those wavelengths that correspond to the excitation properties of the observed fluorophores are transmitted. Since the same objective is used for both illumination and detection, a dichroic mirror is utilized to decouple the illumination and detection paths. The emitted light is filtered again to make sure any reflected and scattered light from the illumination source is blocked to increase signal to noise ratio.

Finally, the light is focused by a tube lens to create a magnified image in the camera sensor. This type of imaging is called infinity corrected optics, since the back focal point of the objective is in “infinity”, meaning that the light exiting the back aperture is parallel. This is achieved by placing the sample exactly at the focal point of the objective. Infinity corrected optics has the advantage that it allows placing various additional optical elements in the infinity space (*i.e.* the space between the objective and the tube lens) without affecting the image quality. In this example such elements are the dichroic mirror and the emission filter.

The combination of the objective and tube lens together will determine the magnification of the system, it will be the ratio of the focal lengths of these lenses:

$$M = \frac{f_{TL}}{f_{OBJ}}. \quad (1.1)$$

The final field of view of the microscope will depend on the magnification, and also on the size of the imaging sensor:

$$FOV = \frac{A}{M}, \quad (1.2)$$

where  $A$  is the area of the sensor.

Apart from magnification, the most important property of the objective is the half-angle of the light acceptance cone,  $\alpha$ . This not only determines the amount of collected light, but also the achievable resolution of the system (see next section). This angle depends on the size of the lens relative to its focal length. In other words depends on the aperture of the lens, which is why the expression *numerical aperture* (NA) is more commonly used to express this property of the objective:

$$NA = n \cdot \sin \alpha. \quad (1.3)$$

For small  $\alpha$  angles, the following approximation holds true:  $\sin \alpha \approx \tan \alpha \approx \alpha$ . Thus, the numerical aperture can also be expressed as a ratio of the radius of the lens and the focal length:

$$NA \approx n \frac{r}{f}, \quad \text{when } \alpha \ll 1. \quad (1.4)$$

### 1.1.3 Resolution of a wide-field microscope

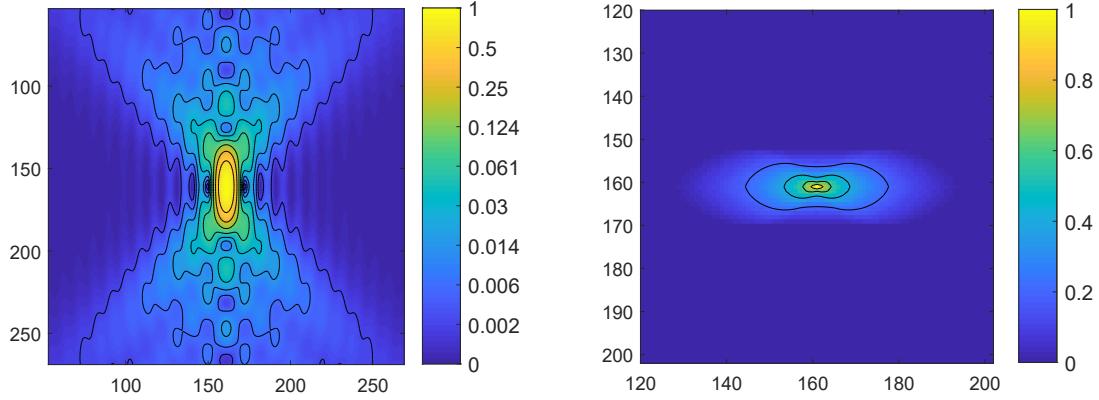
The resolution of an optical systems is defined by the size of the smallest distinguishable feature on the image. Practically this means the minimum distance between two point-like objects so that the two objects can still be resolved. This mainly depends on two factors: the NA of the objective, and the pixel size of the imaging sensor.

Even if the imaging sensor would have infinitely fine resolution, it is not possible to reach arbitrary high resolutions due to the wave nature of light and diffraction effects that occur at the aperture of the objective. This means that depending on the wavelength of the light, any point source will have a finite size on the image, it will be spread out, that will limit the resolution. The shape of this image is called the *point spread function*, or PSF (Fig. 1.4), as this function describes the behavior of the optical system when imaging a point like source. This property of lenses was already discovered by Abbe in 1873 [21], when he constructed his famous formula for resolution:

$$\delta = \frac{\lambda}{2 \cdot NA}. \quad (1.5)$$

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**Figure 1.4: Axial cross section of the PSF and OTF of a wide-field microscope.** Simulated PSF and OTF for a wide-field microscope with a water immersion objective ( $n = 1.33$ ).  $NA = 1.1$ ,  $\lambda = 510\text{ nm}$

where  $d$  is the smallest distance between two distinguishable features.

Another representation of the optical performance, is the *optical transfer function*, or OTF (Fig. 1.4), which is the Fourier transform of the PSF:

$$\text{OTF} = F(\text{PSF}). \quad (1.6)$$

As this function operates in the frequency space, it describes how the different frequencies are affected by the system. The resolution can also be defined as the support of the OTF, since this describes the highest frequency that is still transmitted through the optical system. Any pattern with higher frequency will be lost, thus beyond the resolution limit. For circularly symmetric PSFs, the OTF will be real valued, however if this is not the case, the Fourier transform also introduces complex components.

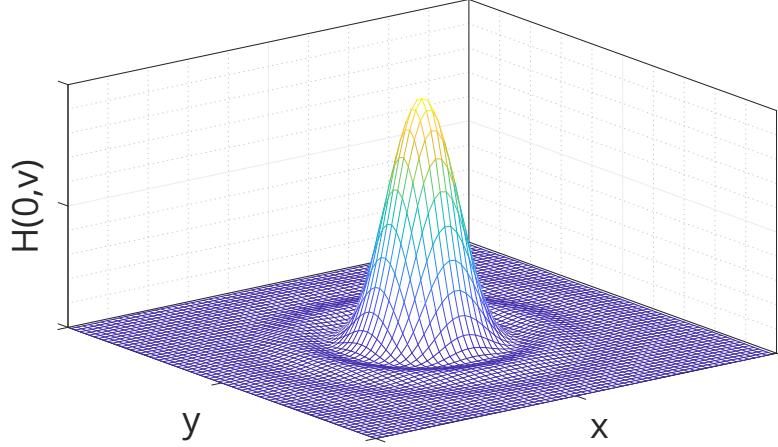
Abbe's formula can be derived from the scalar theory of diffraction using a paraxial approximation (Fraunhofer diffraction, [22]) that describes the intensity of the electric field in the focus of a lens [23]:

$$H(u, v) = C_0 \left| \int_0^1 J_0(vr) e^{-i\frac{1}{2} \cdot ur^2} r dr \right|^2, \quad (1.7)$$

where  $C_0$  is a normalization constant, and  $J_0$  is the zero order Bessel function of the first kind. Furthermore, instead of the commonly used Cartesian coordinates  $x$ ,  $y$  and  $z$ , the following optical coordinates are defined:

$$v = \frac{2\pi nr}{\lambda_0} \sin \alpha, \quad u = \frac{8\pi nz}{\lambda_0} \sin^2 \frac{\alpha}{2} \quad (1.8)$$

where  $r = \sqrt{x^2 + y^2}$  is the distance from the optical axis, and  $\alpha$  is the light collection



**Figure 1.5: Airy pattern.** Airy pattern calculated in Matlab based on Eq. 1.9

angle as shown on Fig. 1.3.

To determine the lateral resolution of the system, let's substitute  $u = 0$  as the axial optical coordinate, and evaluate Eq. 1.7 which will give the intensity distribution inn the focal plane:

$$H(0, v) = C_0 \left| \int_0^1 J_0(vr)rdr \right|^2 = \left( 2 \frac{J_1(v)}{v} \right)^2, \quad (1.9)$$

where  $J_1$  is the first order Bessel function of the first kind. This equation describes the famous Airy pattern (Fig. 1.5) which will be the shape of the PSF in the focal plane. The width of this pattern is the resolution, and although there are multiple definitions for this, the most commonly accepted is the Rayleigh criterion [22, 24] which defines the resolution as the distance between the central peak and the first local minimum. As this lies at  $v = 3.38$ , the resolution can be expressed by substituting this value to Eq. 1.8 and calculating the real distance ( $r$ ):

$$\delta_{xy} = \frac{3.83}{2\pi} \frac{\lambda_0}{n \cdot \sin \alpha} \approx 0.61 \frac{\lambda_0}{NA}, \quad (1.10)$$

which is equivalent to Abbe's original formula (Eq. 1.5). The only difference is the scaling factor which is due to the slightly different interpretations of width of the Airy disk as mentioned earlier.

Similarly, to calculate the intensity distribution along the axial direction, let's substitute  $v = 0$  to Eq. 1.7:

$$H(u, 0) = C_0 \left( \frac{\sin \frac{u}{4}}{\frac{u}{4}} \right)^2. \quad (1.11)$$

For this expression the first minimum lies at  $u = 4\pi$ . Converting back to Cartesian

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coordinates, the axial resolution can be expressed as:

$$\delta_z = \frac{2n\lambda_0}{NA^2}. \quad (1.12)$$

So far we only considered a single, point-like emitter. As the intensity function describes how an optical system “spreads out” the image of a point, it is also called the Point Spread Function (PSF, Fig. 1.4). In a more realistic scenario, however the emitters are neither point-like, nor single. Effectively, however, for every emitter the PSF would be imaged on the sensor, and this creates the final image. In mathematical terms, this can be expressed as a convolution operation between the underlying fluorophore distribution of the object ( $O$ ) and the PSF ( $H$ ):

$$I(u, v) = O(u, v) * H(u, v). \quad (1.13)$$

The effective result of this kind of diffraction limited image formation is a blurred image with a finite resolution of  $\delta_{xy}$  in the lateral direction, and  $\delta_z$  in the axial direction.

The PSF is further affected by the illumination pattern as well. Since the number of emitted fluorescent photons are roughly proportional to the illumination intensity, if the illumination has any structure at the order of the detection resolution, it will have an effect on the overall PSF of the system, which can be expressed as:

$$H_{sys} = H_{ill} \cdot H_{det}, \quad (1.14)$$

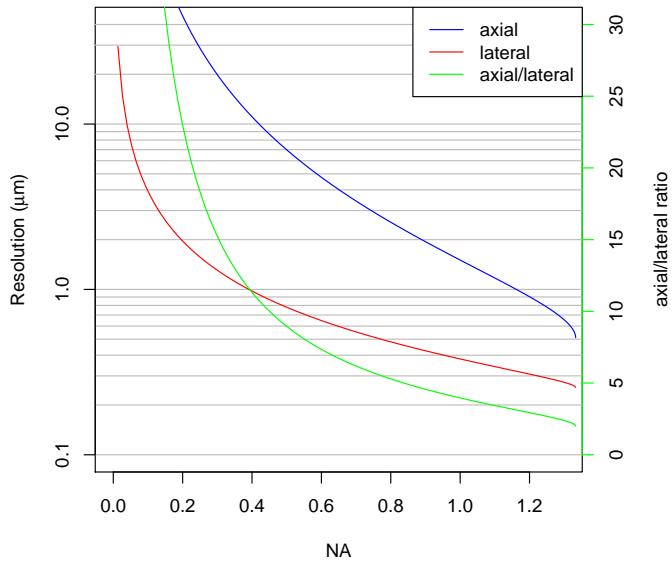
where  $H_{ill}$  is the point spread function of the illumination, and  $H_{det}$  is the point spread function of the detection.

### 1.2 Point scanning methods

In most cases, a wide-field microscope is used to image a section of a tissue, thus axial resolution is not a concern. Imaging live specimens, however is not so straightforward, as these samples are usually much thicker than a typical section. For these samples 3-dimensional (3D) imaging is highly beneficial, which necessitates some kind of optical sectioning technique to be able to discriminate the features at different depths.

Due to the design of the wide-field microscope, any photons emitted from outside the focal plane will also be detected by the sensor, however as these are not originating from the focus, only a blur will be visible. This blur potentially degrades image quality and signal-to-noise ratio to such extent that makes imaging thick sample very difficult if not impossible in a wide-field microscope.

Evaluating Equations 1.10 and 1.12 for a range of possible numerical apertures reveals



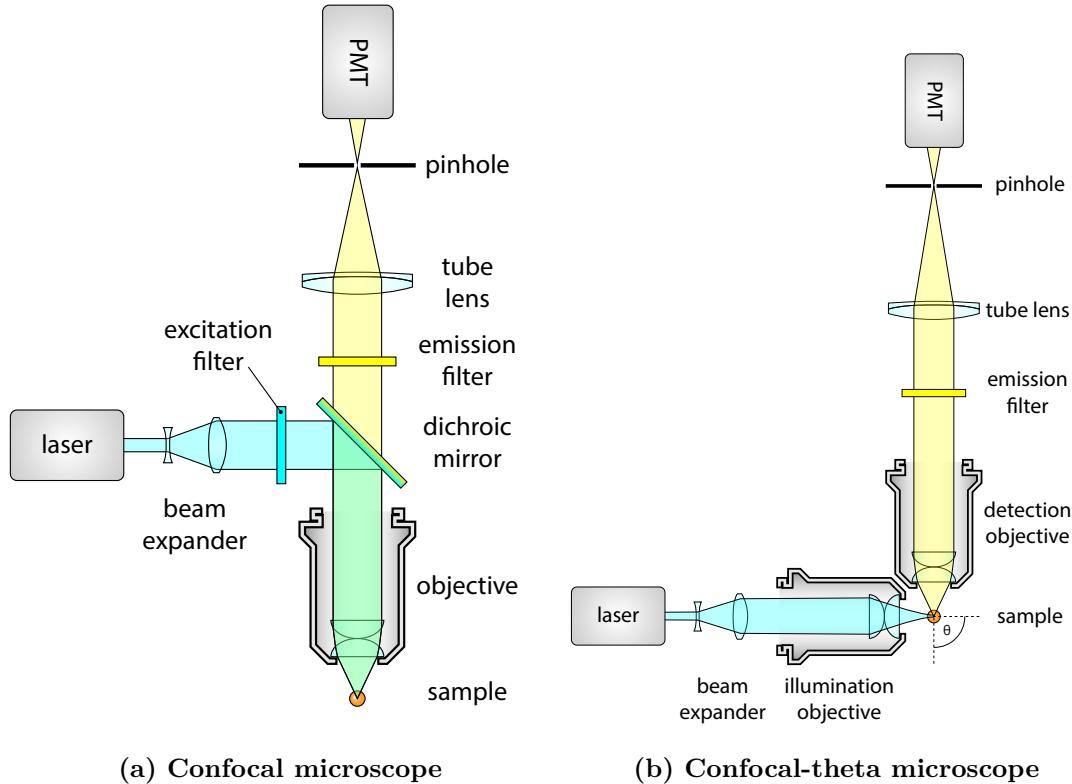
**Figure 1.6: Resolution of a wide-field microscope.** Axial (blue) and lateral (red) resolutions of a wide-field microscope are shown with respect to the numerical aperture (NA). Resolutions are calculated with  $\lambda = 510\text{nm}$ , the emission maximum of GFP and  $n = 1.33$ , the refractive index of water, for water dipping objectives.

the significant differences in lateral and axial resolution for any objective (Fig. 1.6). Especially for low NAs, this can be significant, a factor of  $\sim 20$  difference. For higher ( $>0.8$ ) NAs the axial resolution increases faster than the lateral, however they will only be equal when  $\alpha = 180^\circ$ . This means that isotropic resolution with a single lens is only possible if the lens is collecting all light emitting from the sample, which seems hardly possible, and would be highly impractical. For commonly used high NA objectives the lateral to axial ratio will still be around 3–6.

Instead of using a single lens to achieve isotropic resolution, it's more practical to image the sample from multiple directions to complement the missing information from different views. When rotating the sample  $90^\circ$  for example, the lateral direction of the second view will correspond to the axial direction of the first view. If rotation is not possible, using multiple objectives can also achieve similar result, such as in the case of Multi-Imaging Axis Microscopy (MIAM) [25, 26]. This microscope consisted of 4 identical objectives arranged in a tetrahedral fashion to collect as much light as possible from multiple directions, and provide isotropic 3D resolution, albeit at the expense of extremely difficult sample handling, since the sample was completely surrounded by objectives from all directions.

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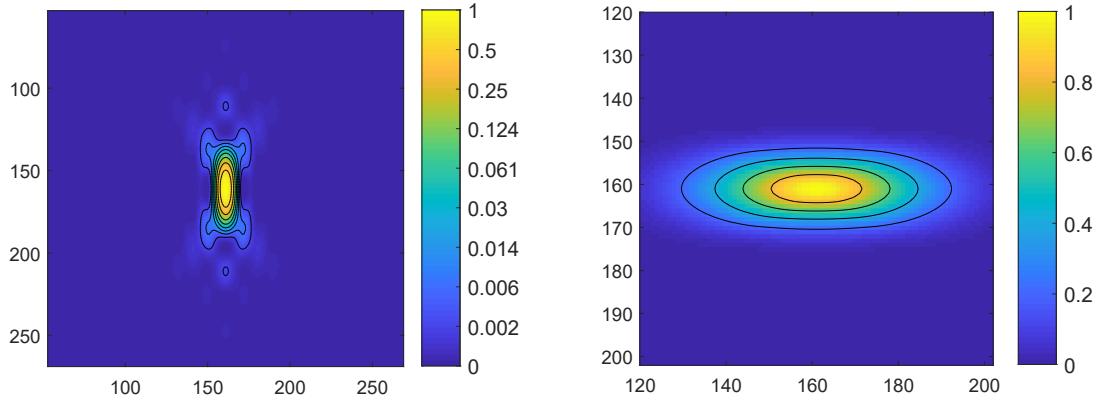
**Figure 1.7: Basic optical components of a confocal laser scanning and confocal-theta microscope.** Both type of microscopes use confocal images detection, which means that a pinhole is used to exclude light coming from out of focus points. Light intensity is measured by a photomultiplier for every voxel in the region of interest. The final image is generated on a computer using the positions and recorded intensity values. A regular confocal microscope (1.7a) uses the same objective for illumination and detection, while a confocal-theta microscope (1.7b) uses a second objective that is rotated by  $\vartheta$  around the focus. In this case,  $\vartheta = 90^\circ$ .

### 1.2.1 Confocal laser scanning microscopy

Confocal laser scanning microscopy (CLSM) [27, 28] addresses most of the problems of wide-field microscopy we mentioned in the previous section. It is capable of optical sectioning by rejecting out of focus light, which makes it a true 3D imaging technique. Furthermore, the light rejection also massively reduces out of focus background, and increases contrast.

This is achieved by two significant modifications compared to the wide-field optical path. To be able to reject the out of focus light, an adjustable pinhole is placed at the focus of the tube lens. Light rays originating from the focal point will meet at this position, and are able to pass through the pinhole, however out-of-focus light will converge either before or after the aperture, and thus the aperture blocks these rays. To maximize the fluorescence readout efficiency for the single focal point, a photomultiplier tube is used instead of an area sensor (Fig. 1.7a).

To maximize the signal from the focal point, the illumination light is also focused



**Figure 1.8: Axial cross section of the PSF and OTF of a confocal laser scanning microscope.** Simulated PSF and OTF for a laser scanning confocal microscope with a water immersion objective ( $n = 1.33$ ).  $NA = 1.1$ ,  $\lambda = 510\text{ nm}$

here by coupling an expanded laser beam through the back aperture of the objective. This not only increases illumination efficiency (since other, not detected points are not illuminated), but has the added benefit of increasing the resolution as well. This is due to the combined effect of illumination and detection PSFs as described in Eq. 1.14 (Fig. 1.8). For Gaussian-like PSFs, the final resolution (along a single direction) can be calculated in the following way:

$$\frac{1}{\delta_{sys}^2} = \frac{1}{\delta_{ill}^2} + \frac{1}{\delta_{det}^2}, \quad (1.15)$$

where  $\delta_{ill}$  and  $\delta_{det}$  are the resolutions for the illumination and detection, respectively. Since the same objective is used for both illumination and detection, and the difference in wavelength is almost negligible,  $\delta_{ill} = \delta_{det} = \delta$ , the final system resolution will be:

$$\delta_{sys} = \frac{1}{\sqrt{2}}\delta. \quad (1.16)$$

This means that the distinguishable features in a confocal microscope are  $\sim 0.7$  times smaller than in a wide-field microscope using the same objective.

Because of the different detection method in a confocal microscope, direct image formation on an area sensor is not possible, since at any given time, only a single point is interrogated in the sample. Instead, it's necessary to move the illumination and detection point in synchrony (or in a simpler, albeit slower solution, to move the sample) to scan the entire field of view. The image can be later computationally reconstructed by a computer program that records the fluorescence intensity of every point of the field of view, and displays these values as a raster image.

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### 1.2.2 Confocal-theta microscopy

Although confocal microscopy already has 3D capabilities, its axial resolution is still limited compared to the lateral, since it uses only one objective. An alternative realization of the confocal microscope, the confocal theta microscope [29] introduces a second objective to the system, that is used to illuminate the sample (Fig. 1.7b). Since this decouples the illumination and detection, using a filter cube is no longer necessary. The second objective is rotated by  $\theta$  around the focus, this is where the name of this setup originates from.

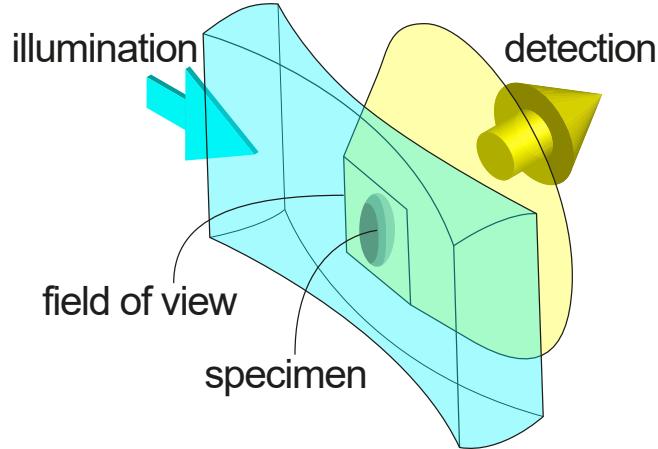
As in the case of standard confocal microscopy, the system PSF is improved by the illumination pattern. Here, however, the axial direction of the detection coincides with the lateral direction of the illumination, which results in a dramatic improvement of axial resolution compared to standard confocal microscopy. Lateral resolution will also be increased, but by a smaller extent, resulting in an almost isotropic PSF, and equal axial and lateral resolutions (Fig. ??).

Although this is a big improvement to confocal microscopy in terms of resolution, this technique did not reach a widespread adoption as it complicates sample handling, while still suffering from two big drawbacks of confocal microscopy techniques that limits its live imaging capabilities.

Imaging live specimens for an extended period of time with confocal microscopy although possible [30, 31], is not ideal. For each voxel imaged, a large portion of the specimen has to be illuminated, which results in a very high dose of radiation on the samples. This can be as much as 30–100 times larger, than the dose used for the actual imaging [32]. Illumination with high power of laser for an extended time frame can result in bleaching the fluorophores, which in turn will lower the signal at later times. Furthermore, any absorbed photon has the possibility to disrupt the chemical bonds inside the specimen, which can lead to phototoxic effects. Moreover, the usage of the pinhole although increases resolution, also decreases the detectable signal intensity, thus has a negative impact on image contrast [33].

## 1.3 Light-sheet microscopy

A selective-plane illumination microscope (SPIM) uses a light-sheet to illuminate only a thin section of the sample (Fig. 1.9). This illumination plane is perpendicular to the imaging axis of the detection objective and coincides with the focal plane. This way, only the section in focus will be illuminated, thus providing much better signal to noise ratio. In case of conventional wide-field fluorescence microscopy, where the whole specimen is illuminated, light scattering from different regions contributes to a significant background noise. With selective-plane illumination, this problem is intrinsically solved, and it also



**Figure 1.9: Basic concept of single-plane illumination microscopy.** The sample is illuminated from the side by laser light shaped to a light-sheet (blue). This illuminates the focal plane of the detection lens, that collects light in a wide-field mode (yellow). The image is recorded, and the sample is translated through the light-sheet to acquire an entire 3D stack.

provides a true sectioning capability. This makes SPIM especially suitable for 3D imaging.

The main principle behind single plane illumination microscopy, that is illuminating the sample from the side by a very thin light-sheet, dates back to the early 20<sup>th</sup> century, when Siedentopf and Zsigmondy first described the ultramicroscope [34]. This microscope used sunlight as an illumination source, that was guided through a precision slit to generate a thin light-sheet. This allowed Zsigmondy to visualize gold nanoparticles floating in and out of the light-sheet. Since these particles are much smaller than the wavelength of the light, the device was called an ultramicroscope. His studies with colloids, and the development of the ultramicroscope led Zsigmondy to win the Nobel Prize in 1925.

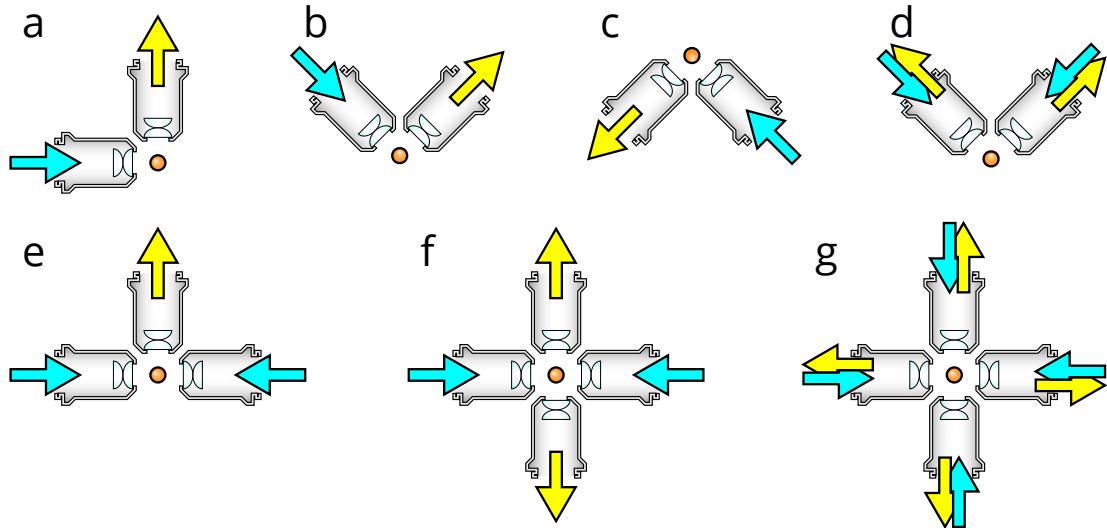
After Zsigmondy, this method was forgotten until rediscovered in the 1990s, when Voie *et al.* constructed their Orthogonal-plane Fluorescent Optical Sectioning (OPFOS) microscope [35]. They used it to image a fixed, optically cleared and fluorescently labelled guinea pig cochlea. In order to acquire a 3D dataset, the sample was illuminated from the side with a light-sheet generated by a cylindrical lens, then rotated around the center axis to obtain multiple views. Although they only reached a lateral resolution around 10 µm and axial resolution of 26 µm, this method allowed them to generate a 3D reconstruction of the cochlea [36].

Later, in 2002, Fuchs *et al.* developed Thin Light-Sheet Microscopy (TLSM) [37] and used this technique to investigate the microbial life in seawater samples without disturbing their natural environment (by e.g. placing them on a coverslip). Their light-sheet was similar to the one utilized in OPFOS, being 23 µm thin, and providing a 1 mm × 1 mm field of view.

Despite these early efforts, the method did not gain larger momentum. The real

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**Figure 1.10: Different optical arrangements for light-sheet microscopy.** (a) Original SPIM design with a single lens for detection and illumination. [38] (b) Upright SPIM to allow for easier sample mounting such as using a petri dish (iSPIM, [39, 40, J1]). (c) Inverted SPIM, where the objectives are below the sample, which is held by a thin foil [J2]. (d) Dual-view version of the upright configuration, where both objective can be used for illumination and detection (disPIM, [41]). (e) Multidirectional-SPIM (mSPIM) for even illumination of the sample with two objectives for illumination [42]. (f) Multi-view SPIM with two illumination and detection objectives for *in toto* imaging of whole embryos (MuVi-SPIM [3], SimView [4], Four-lens SPIM [43]). (g) A combination of (d) and (f), using four identical objectives, where both can illuminate and detect in a sequential manner, to achieve isotropic resolution without sample rotation (IsoView [44]).

breakthrough in light-sheet imaging happened at EMBL in 2004, where Huisken *et al.* [38] combined the advantages of endogenous fluorescent proteins and the optical sectioning capability of light-sheet illumination to image Medaka fish embryos, and the complete embryonic development of a *Drosophila melanogaster* embryo. They called this Selective-Plane Illumination Microscopy (SPIM), and it quickly became popular to investigate developmental biological questions.

Since then, light-sheet based imaging has gained more and more popularity, as it can be adapted and applied to a wide variety of problems. Although sample mounting can be challenging because of the objective arrangement, this can also be an advantage, since new microscopes can be designed with the sample in mind [45, J3] (Fig. 1.10). This made it possible to adapt the technique for numerous other specimens, such as zebrafish larvae [46], *C. elegans* embryos [40], mouse brain [5], and even mouse embryos [J2, 47, 48].

As many of these specimens require very different conditions and mounting techniques, these microscopes have been adapted to best accommodate them. An upright objective arrangement for example (Fig 1.10b) allows imaging samples on a coverslip, while its inverted version is well suited for mouse embryos, where a foil is separating them from the immersion medium (Fig. 1.10c). A modified version of the upright arrangement allows for multi-view imaging using both objectives for illumination and detection in a

sequential manner (Fig. 1.10d) [49].

For larger samples, to achieve a more even illumination, two objectives can be used from opposing directions to generate two light-sheets (Fig. 1.10e) [42]. This arrangement can further be complemented by a second detection objective, to achieve parallelized multi-view imaging (Fig. 1.10f) [3, 4, 43]. For ultimate speed, 4 identical objectives can be used to achieve almost instantaneous views from 4 different directions by using all objectives for illumination and detection (Fig 1.10g) [44].

Furthermore, because of the wide-field detection scheme it is possible to combine SPIM with many superresolution techniques, such as single molecule localization [50], STED [51], RESOLFT [J1], or structured illumination [6, 52, 53].

#### **1.3.1 Optics of light-sheet microscopy**

Since illumination and detection for light-sheet microscopy are decoupled, two independent optical paths are implemented.

The detection unit of a SPIM is basically equivalent to a detection unit of a wide-field microscope, without a dichroic mirror (Fig. 1.11). Most important components are the objective together with the tube lens, filter wheel, and a sensor, typically a CCD or sCMOS camera.

One of the most important aspects that determine the resolution of the microscope is the detection objective. Since imaging biological specimens usually requires a water-based solution, the objectives also need to be directly submerged in the medium to minimize spherical aberrations. Since the refraction index of water ( $n = 1.33$ ) is greater than the refraction index of air, these objectives tend to have a higher NA, which results in higher resolution. The final resolution, however, also depends on the pixel size of the sensor which determines the spatial sampling rate of the image.

Although image quality and resolution greatly depends on the detection optics, the real strength of light-sheet microscopy, the inherent optical sectioning is due to the specially designed illumination pattern, that confines light to the vicinity of the detection focal plane.

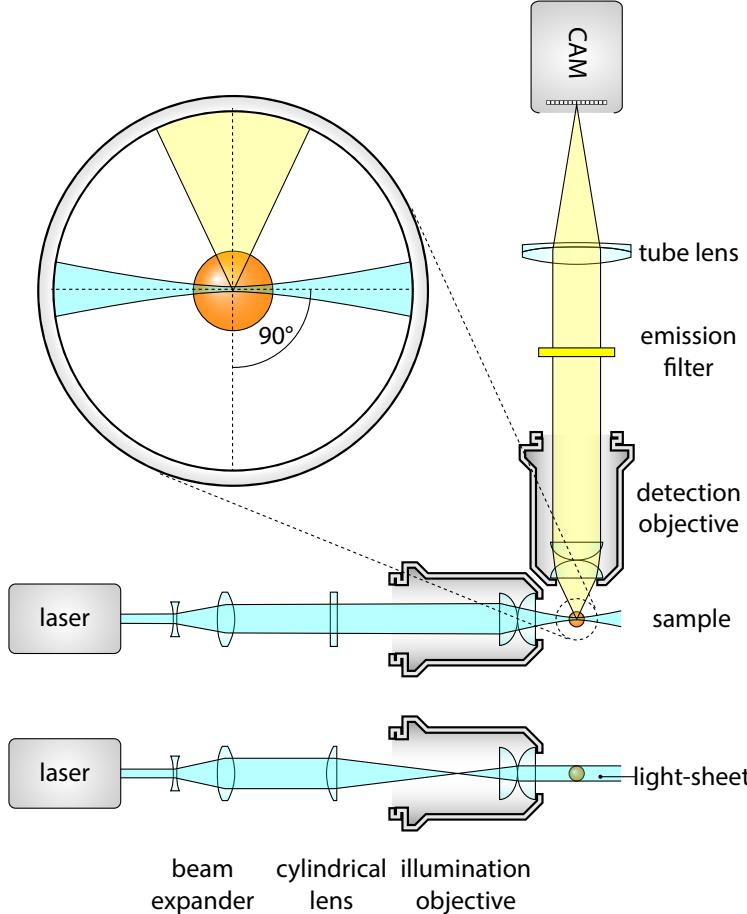
There are two most commonly used options to generate a light-sheet: either by using a cylindrical lens, to illuminate the whole field of view with a static light-sheet, as in the original SPIM concept [38]; or by quickly scanning a thin laser beam through the focal plane, thus resulting in a virtual light-sheet [46].

#### **1.3.2 Static light-sheet illumination**

For a static light-sheet, the normally circular Gaussian laser beam needs to be shaped in an astigmatic manner, i.e. either expanded or squeezed along one direction, to shape it into a sheet instead of a beam. This effect can be achieved by using a cylindrical lens,

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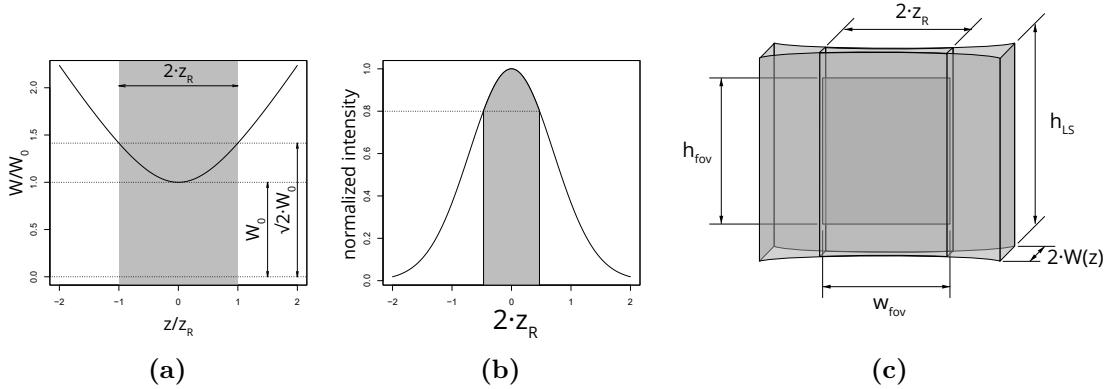
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**Figure 1.11: Basic optical components of a SPIM.** A dedicated illumination objective is used to generate the light sheet, which is an astigmatic Gaussian beam, focuses along one direction. Astigmatism is introduced by placing a cylindrical lens focusing on the back focal plane of the objective. Detection is performed at a right angle, with a second, detection objective. Scattered laser light is filtered, and a tube lens forms the image on an area sensor, such as an sCMOS camera.

which as the name suggests has a curvature in one direction, but is flat in the other, thus focusing a circular beam to a sheet.

However, to achieve light-sheets that are thin enough, one would need to use cylindrical lenses with a very short focal length, and these are hardly accessible in well corrected formats. For this reason, it's more common to use a longer focal length cylindrical lens in conjunction with a microscope objective, which is well corrected for chromatic and spherical aberrations [54]. This way, the light-sheet length, thickness and width can be adjusted for the specific imaging tasks.



**Figure 1.12: Light-sheet dimensions.** 1.12a The width and thickness of the field of view depends on the Rayleigh length of the beam ( $z_{R,y}$ ) and the beam waist ( $W_0$ ). 1.12b Height of the field of view is determined by the Gaussian profile of the astigmatic beam. 1.12c shows a light sheet, with the field of view indicated. Since the light-sheet intensity is uneven, the field of view has to be confined to a smaller region.

## Light-sheet dimensions

The shape of the illumination light determines the optical sectioning capability and the field of view of the microscope, so it is important to be able to quantify these measures. The most commonly used illumination source is a laser beam coupled to a single mode fiber, thus its properties can be described by Gaussian beam optics.

For paraxial waves, i.e. waves with nearly parallel wave front normals, a general wave equation can be approximated with the paraxial Helmholtz equation [55]

$$\nabla_T^2 U + i2k \frac{\partial U}{\partial z} = 0 \quad (1.17)$$

where  $\nabla_T^2 = \frac{\partial^2}{\partial x^2} + \frac{\partial^2}{\partial y^2}$ ,  $U(\vec{r})$  is the wave function,  $k = \frac{2\pi}{\lambda}$  is the wavenumber and  $z$  is in the direction of the light propagation.

A simple solution to this differential equation is the Gaussian beam:

$$U(r, z) = A_0 \cdot \frac{W_0}{W(z)} \cdot e^{-\frac{r^2}{W^2(z)}} \cdot e^{-i \cdot \phi(r, z)} \quad (1.18)$$

where  $A_0$  is the amplitude of the wave,  $W_0$  is the radius of the beam waist (the thinnest location on the beam),  $r = \sqrt{x^2 + y^2}$  is the distance from the center of the beam,  $W(z)$  is the radius of the beam  $z$  distance from the waist, and  $\phi(r, z)$  is the combined phase part of the wave-function (Fig. 1.12a). Furthermore:

$$W(z) = W_0 \sqrt{1 + \left(\frac{z}{z_R}\right)^2} \quad (1.19)$$

where the parameter  $z_R$  is called the Rayleigh-range, and is defined the following way:

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$$z_R = \frac{\pi W_0^2}{\lambda}. \quad (1.20)$$

Apart from the circular Gaussian beam, the elliptical Gaussian beam is also an eigenfunction of Helmholtz equation (1.17) which describes the beam shape after a cylindrical lens:

$$U(x, y, z) = A_0 \cdot \sqrt{\frac{W_{0,x}}{W_x(z - z_{0,x})}} \sqrt{\frac{W_{0,y}}{W_y(z - z_{0,y})}} \cdot e^{-\frac{x^2}{W_x^2(z - z_{0,x})}} \cdot e^{-\frac{y^2}{W_y^2(z - z_{0,y})}} \cdot e^{-i \cdot \phi(x, y, z)} \quad (1.21)$$

This beam still has a Gaussian profile along the  $x$  and  $y$  axes, but the radii ( $W_{0,x}$  and  $W_{0,y}$ ), and the beam waist positions ( $z_{0,x}$  and  $z_{0,y}$ ) are uncoupled, which results in an elliptical and astigmatic beam. The beam width can be now described by two independent equations for the two orthogonal directions:

$$W_x(z) = W_{0,x} \sqrt{1 + \left(\frac{z}{z_{R,x}}\right)^2} \quad \text{and} \quad W_y(z) = W_{0,y} \sqrt{1 + \left(\frac{z}{z_{R,y}}\right)^2}. \quad (1.22)$$

Since the beam waist is different along the two axes, the Rayleigh range is also different:

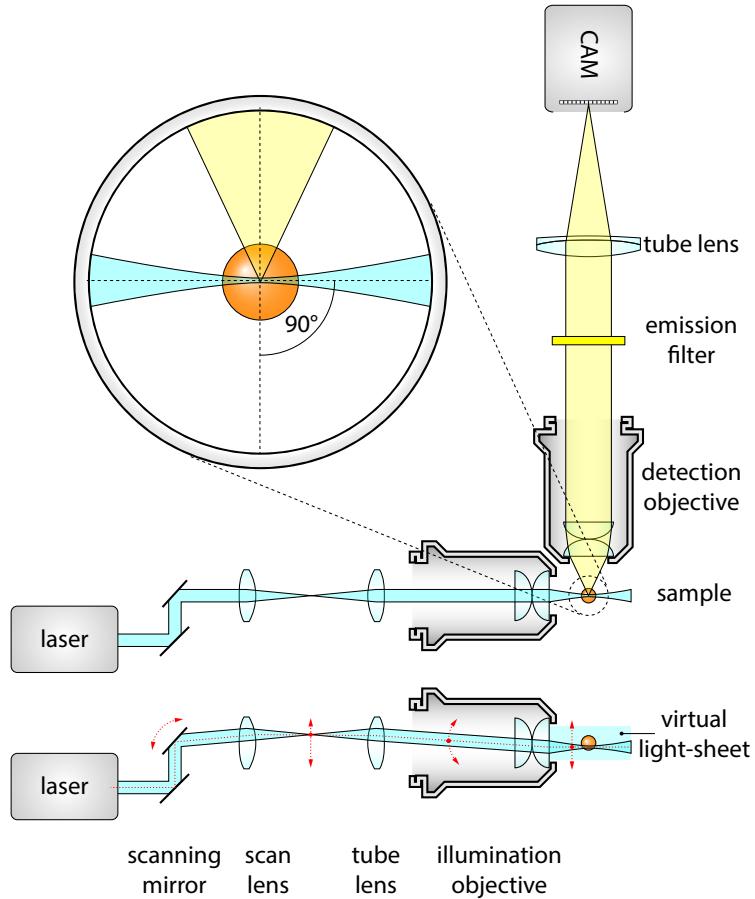
$$z_{R,x} = \frac{\pi W_{x,0}^2}{\lambda}, \quad z_{R,y} = \frac{\pi W_{y,0}^2}{\lambda}. \quad (1.23)$$

Based on these equations, the light-sheet dimensions and usable field of view (fov) can be specified (Fig. 1.12c). The light-sheet thickness will depend on the beam waist,  $W_{0,y}$  (if we assume the cylindrical lens is focusing along  $y$ ), and the length of the light-sheet can be defined as twice the Rayleigh range,  $2 \cdot z_{R,y}$ . As these are coupled (see Eq. 1.23), having a thin light-sheet for better sectioning also means the length of it will be relatively short. Fortunately, because of the quadratic relation, to increase the field of view by a factor of two, the light-sheet thickness only needs to increase by a factor of  $\sqrt{2}$ .

Light-sheet height is determined by the intensity profile of the beam along the vertical axis (Fig. 1.12b). Since this is a Gaussian function (see Eq. 1.18), only a small part in the middle can be used for imaging, because towards the sides the intensity dramatically drops. To allow a maximum 20% drop of intensity at the edges, the light-sheet height is  $h_{fov} = 2 \cdot 0.472 \cdot W_{x,0}$ .

### 1.3.3 Digitally scanned light-sheet illumination

Although generating a static light-sheet is relatively straightforward, with the simple addition of a cylindrical lens to the light path, it has some drawbacks. As already mentioned in the previous section, the light intensity distribution along the field of view is



**Figure 1.13: DSLM illumination.** DSLM illuminates a specimen by a circularly-symmetric beam that is scanned over the field of view. This creates a virtual light-sheet, which illuminates a section of a specimen just like the SPIM. Light-sheet in DSLM is uniform over the whole field of view and its height can be dynamically altered by changing the beam scan range.

not constant, as the light-sheet is shaped from a Gaussian beam. Furthermore, along the lateral direction of the light-sheet the illumination NA is extremely low, resulting in effectively collimated light. Because of this, shadowing artifacts can deteriorate the image quality [42].

A more flexible way of creating a light-sheet is by scanning a focused beam in the focal plane to generate a virtual light-sheet (digital scanned light-sheet microscopy, DSLM [46]). Although this method might require higher peak intensities, it solves both drawbacks of the cylindrical lens illumination. By scanning the beam, the light-sheet height can be freely chosen, and a homogenous illumination will be provided. Focusing the beam in all directions evenly introduces more angles in the lateral direction as well, which shortens the length of the shadows.

The basic optical layout of a DSLM is shown on Fig. 1.13. A galvanometer controlled mirror is used to alter the beam path that can quickly turn around its axis which will

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result in an angular sweep of the laser beam. To change the angular movement to translation, a scan lens is used to generate an intermediate scanning plane. This plane is then imaged to the specimen by the tube lens and the illumination objective, resulting in a scanned focused beam at the detection focal plane. The detection unit is identical to the wide-field detection scheme, similarly to the static light-sheet illumination. By scanning the beam at a high frequency, a virtual light-sheet is generated, and the fluorescent signal is captured by a single exposure on the camera, resulting in an evenly illuminated field of view.

### **1.4 Light-sheet microscopy for mouse imaging**

Because of its optical sectioning capabilities, combined with the high specificity of fluorescent labels, confocal microscopy has been the go-to technique for decades in biological research. Even though it has some drawbacks, important discoveries have been made using this technique, as live imaging is not always necessary.

Especially using cell cultures, or fixed specimens, confocal microscopy has been used to investigate X chromosome inactivation [56], the role of amyloid  $\beta$ -peptide in Alzheimer's disease [57], the role of Oct4 [58] and Sox2 [59] in the self-renewal of pluripotent stem cells, just to highlight a few.

Live imaging capabilities of confocal microscopy are, however, limited. This is mostly due to the illumination scheme: to collect information from a single point, almost the whole embryo has to be illuminated. This unwanted illumination can easily lead to bleaching of the fluorophores, and also to phototoxic effects that can prevent further embryonic development. The point scanning nature of image acquisition also implies an inherent constraint to the maximum imaging speed, as it can be only increased at the expense of reducing signal intensity (Fig. 1.1).

One improvement to address both of these drawbacks is the use of a spinning disk with a specific pattern (also called Nipkow disk) of holes to generate multiple confocal spots at the same time [60]. If these spots are far enough from each other, confocal rejection of out-of-focus light can still occur. As the disk is spinning, the hole pattern will sweep the entire field of view, eventually covering all points [61]. The image is recorded by an area detector, such as a CCD or EM-CCD, which speeds up image acquisition [62].

Although out-of-focus illumination is still an issue, spinning disk confocal microscopy was successfully used to investigate the mechanisms of symmetry breaking in early mouse embryonic development [63], and the mechanisms leading to the first cell fate specification that will differentiate extraembryonic tissue from the embryo proper [31, 64, 65]. Even though these studies were carried out with live embryos, only a few hours of continuous imaging is possible before the accumulation of phototoxic effects arrests development

[66]. Compared to this, just the pre-implantation phase of mouse embryonic development spans 3 days, and the full development is 18 days [67].

### 1.4.1 Imaging pre-implantation

Pre-implantation is the first phase of mouse embryonic development, that starts right after fertilization. The embryo in this phase is still in the oviduct, travelling towards the uterus, where it will implant to the uterine wall. The developmental stage between fertilization and the implantation is called the pre-implantation stage. Here the embryo divides, and already the first cell fate specifications start when forming the trophoectoderm (TE) and the inner cell mass (ICM) at the blastocyst stage. ICM cells will form the embryo proper, while TE cell will contribute to the formation of the extraembryonic tissues.

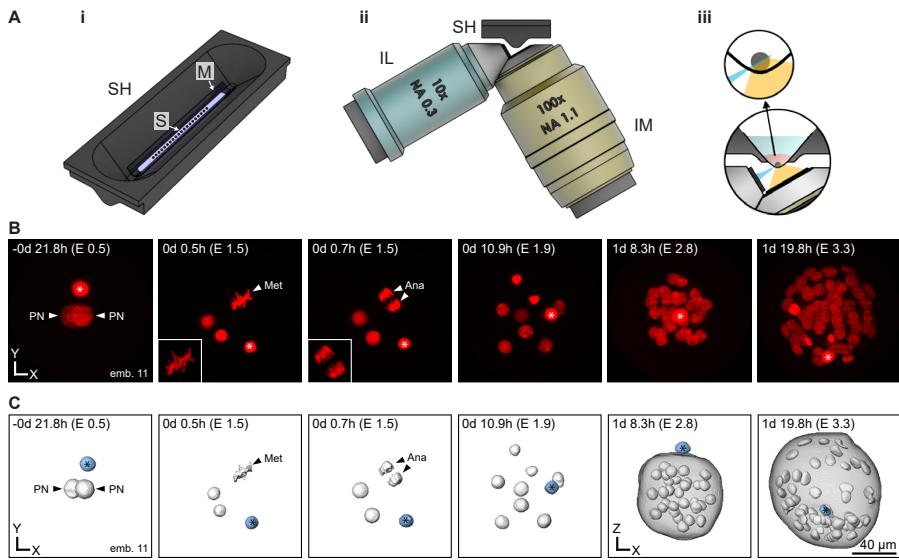
During this process the embryo is still self-sufficient, which makes it possible to image this stage in an *ex vivo* embryo culture by providing the proper conditions [68]. Long term imaging, however, is extremely challenging due to the very high light sensitivity of the specimens. Imaging these embryos in a confocal microscope will lead to incomplete development, even if the imaging frequency is minimized to every 15 mins [J2].

Imaging for just a few hours is already enough to investigate important processes, such as cell fate patterning [69]. Other approaches aim to lower the phototoxicity by either using 2-photon illumination which operates at longer wavelengths [70–72], or by lowering imaging frequency as a compromise [73]. These approaches, however either require highly specialized equipment, such as an ultra short pulsed laser, or is compromising on the time resolution.

Light-sheet microscopy, on the other hand, drastically lowers phototoxic effect by using a much more efficient illumination scheme (see Sec. 1.3), and thus makes a better use of the photon budget. Using this technique, it is possible to image the full pre-implantation development at high spatial and temporal resolution without any negative impact on the developmental process. Such a microscope was developed by Strnad *et al.* at EMBL [J2], who used it to understand when exactly is the first cell fate specification decided in the embryonic cells.

As a mouse embryo culture is not compatible with the standard agarose-based sample mounting techniques, a completely new approach was taken, which resulted in a microscope designed around the sample. The sample holder forming a V-shape was built with a bottom window, and it is lined with a thin FEP (fluorinated ethylene propylene) foil that supports the embryos (Fig. 1.14A, i). This arrangement allows the utilization of the standard microdrop embryo culture, while providing proper viewing access for the objectives. As the embryos are relatively small (100 µm) and transparent, a single illumination and single detection objective arrangement is enough for high quality imaging.

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**Figure 1.14: Inverted light-sheet microscope for multiple early mouse embryo imaging..** (i) A sample holder (SH), containing a transparent FEP membrane (M) allows multiple embryo samples (S) to be placed in line for multisample imaging. (ii) Inverted objective orientation with side view of the sample holder. One possible configuration is to use a  $10\times 0.3$  NA illumination objective (IL) and another  $100\times 1.1$  NA detection objective placed at a right angle to the illumination. (iii) Close up on side view of sample on FEP membrane with both objectives. Since the FEP membrane is transparent on water, it provides no hindrance to the illumination beam in penetrating the sample or for the emitted fluorescence on reaching the detection objective. (B) Still images of one particular timelapse experiment, and (C) corresponding segmented nuclei. The star depicts the polar body. Adapted from Strnad *et al.* [J2]

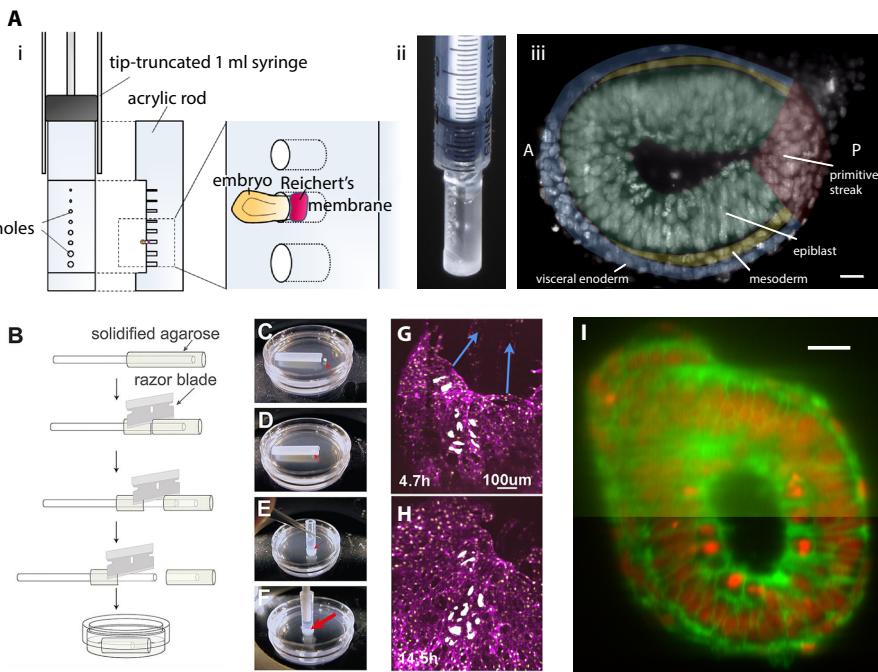
A low resolution ( $\text{NA}=0.3$ ) objective is used to generate the scanned light-sheet, and a high resolution ( $\text{NA}=1.1$ ) objective is detecting the fluorescence at  $50\times$ magnification (Fig 1.14A, ii). As the foil is curved, it allows unrestricted access to the embryo, while separating the imaging medium from the immersion liquid (Fig. 1.14A, iii). Furthermore, its refractive index is matching the refractive index of water, so optical aberrations are minimized.

Using this setup, Strnad *et al.* were able to pinpoint the exact timing of the first cell fate decision that leads either to ICM or TE cells. More than 100 embryos expressing nuclear (H2B-mCherry) and membrane (mG) markers were imaged for the entire 3 days of pre-implantation development (Fig. 1.14B). The image quality was good enough to segment all nuclei in the embryos (Fig. 1.14C), and track them from 1 to 64 cell stage, building the complete lineage tree. Based on the lineage trees, and the final cell fate assignments, it was determined that at the 16 cell stage the final specification is already decided, while earlier than this it is still random.

### 1.4.2 Imaging post-implantation development

After the initial 3 days of pre-implantation, the embryo undergoes the implantation process, during which it is inaccessible to microscopical investigations. Although a new method was recently developed that allows *in vitro* culturing of the embryos embedded

## 1.4 Light-sheet microscopy for mouse imaging



**Figure 1.15: Imaging mouse post-implantation development.** (A) (i, ii) Mounting technique for E5.5 to E6.5 embryos. A tip-truncated 1 mL syringe holds an acrylic rod, cut and drilled with holes of different size in order to best fit the mouse embryo by its Reichert's membrane, leaving the embryo free inside the medium. (iii) Maximum intensity projection of a 13  $\mu\text{m}$  slice at 78  $\mu\text{m}$  from distal end of an E6.5 mouse embryo. The different tissues corresponding to the rudimentary body plan are annotated. Scale bar: 20  $\mu\text{m}$ . (B) For stages ranging between E6.5 and E8.5, mounting using a hollow agarose cylinder has also successfully been proposed. Optimal sizes for the corresponding embryonic stage to be imaged can be produced, so that the embryo can grow with least hindrance. (C–F) Steps for mounting the mouse embryo inside the agarose cylinder. The inner volume of the cylinder can be filled with optimal medium, allowing the much larger chamber volume to have less expensive medium. (G–H) Example images of a 9.8 h timelapse with the mounting shown in (B) where the expansion of the yolk sac can be observed in direction of the blue arrows. (I) In order to aid multiview light-sheet setups in overcoming the higher scattering properties of embryos at this stage, and to allow faster and easier data recording, electronic confocal slit detection allows better quality images to be taken at shorter acquisition times. Scale bar: 20  $\mu\text{m}$ . Adapted from Ichikawa *et al.* [47], Udan *et al.* [48] and de Medeiros and Norlin *et al.* [74].

in a 3D gel [75], this has not reached wider adoption yet. Because of this, developmental processes during implantation have only been investigated in fixed embryos.

Following the implantation process, at the post-implantation phase, *ex vivo* embryo culturing becomes possible again [76, 77], and these embryos can be kept alive for several days in an artificial environment. During this process especially interesting stages are the late blastocyst ( $\sim$ E4.5), gastrulation ( $\sim$ E6.5), and somite formation ( $\sim$ E8.5). Before live imaging techniques became available, these stages were mostly investigated using *in situ* visualization techniques to shed light on several developmental processes [78]. Many pathways playing important roles have been identified this way, however live imaging is still necessary to validate these results, and ensure continuity in the same specimen [79].

Light-sheet microscopy is a good choice for imaging these stages, just like in the case of pre-implantation embryos. These embryos, however, present new challenges for sample handling and culturing. Owing to their extreme sensitivity, dissection can be difficult,

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especially for earlier stages (E4.5). Furthermore, since the embryo is also growing during development, gel embedding is not an option, as this might constrain proper development. Thus, special handling and mounting techniques had to be developed in order to allow live 3D imaging of these specimens.

Ichikawa *et al.* [47] designed a custom mounting apparatus manufactured from acrylic in the shape of a rod that fits in a standard 1 mL syringe with its tip truncated (Fig. 1.15A, i). In the rod several holes were drilled with different sizes that can accommodate different sized embryos, which are held by an extraembryonic tissue, the Reichert's membrane (Fig. 1.15A, ii). Mounting this way doesn't disturb the embryo itself, and it can freely develop in the culturing medium, while it is also stationary for the purpose of imaging. Using this technique, Ichikawa *et al.* were able to image through several stages of development, including interkinetic nuclear migration at stages E5.5–6.5 (Fig. 1.15A, iii).

A second method of sample mounting for light-sheet imaging was developed by Udan *et al.* who were able to record a full 24 h time-lapse of living embryos focusing on the gastrulation and yolk sac formation processes (Fig. 1.15G–I). Their mounting technique comprised of producing a hollow agarose container shaped like a cylinder that could support the embryo from below without constraining its growth (Fig. 1.15B–F).

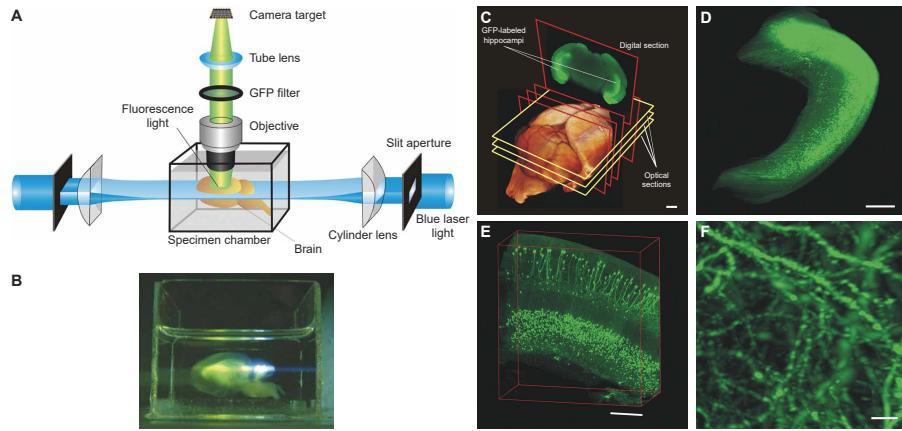
Another consideration to keep in mind, is the growing size of the embryo. As it gets bigger, illumination is less efficient, and scattering can dominate at larger depths. As mentioned in earlier (Sec. 1.3) this can be alleviated by multi-view imaging: illuminating and detecting from multiple directions. Electronic confocal slit detection can further improve the signal to noise ratio by rejecting unwanted scattered light, which allows deeper imaging in large specimens, even up to E7.5 (Fig. 1.15I) [74].

### 1.4.3 Imaging adult mice

Imaging adult mice is especially interesting for answering neurobiological questions. Since development is over at this stage, the use of an environmental chamber is no longer necessary. The biggest challenge for imaging these samples is their size, as they are centimeters in size instead of less than a millimeter in the embryonic stage. Furthermore, the tissues of adult mice are much more opaque which severely limits imaging depth. Light-sheet microscopy can already deal with large specimens, however to achieve (sub)cellular resolution for an entire brain for example, multiple recording have to be stitched together after acquisition [80].

Light scattering and absorption depends on the tissue composition, and also imaging depth. Especially the brain with the high concentration of lipids in the myelinated fibers pose a real challenge for imaging. Live imaging is usually performed with 2-photon microscopy which can penetrate the tissue up to 800  $\mu\text{m}$  [81]. Using fixed samples, however,

## 1.4 Light-sheet microscopy for mouse imaging



**Figure 1.16: Imaging adult mouse brain with light-sheet microscopy..** (A) Schematics of the ultramicroscope for brain imaging. The specimen is embedded in clearing medium to ensure necessary imaging depth. Illumination is applied from two sides to achieve even illumination for the whole field of view. Light-sheet is generated by a slit aperture flowed by a cylindrical lens. The specimen is imaged from the top using wide-field detection method. (B) Photograph of the imaging chamber with a mounted cleared specimen and light-sheet illumination. (C) Surface rendering of a whole mouse brain, reconstructed from 550 optical sections. GFP and autofluorescence signal was imaged. Hippocampal pyramidal and granule cell layers are visible in the digital section. Scale bar: 1 mm. Objective: Planapoachromat 0.5×. (D) Reconstruction of an excised hippocampus from 410 sections. Note that single cell bodies are visible. Scale bar: 500 µm. Objective: Fluar 2.5×. (E) 3D reconstruction of a smaller region of an excised hippocampus from 132 sections. Scale bar: 200 µm. Objective: Fluar 5×. (F) 3D reconstruction of CA1 pyramidal cells imaged with a higher resolution objective (LD-Plan Neofluar 20× NA 0.4) in a whole hippocampus (430 sections). Dendritic spines are also visible, even though usually a higher NA objective (>1.2) is required to visualize these. Scale bar: 5 µm. Adapted from Dodt *et al.* [5].

the scattering problem can be eliminated by the use of tissue clearing methods.

Tissue clearing is a process that removes and/or substitutes scattering and absorbing molecules by a chemical process while keeping the tissue structure intact and preserving fluorescence. The most dominant contributors to these effects are the proteins and lipids. Proteins in the cells locally change the refractive index of the tissue which leads to scattering, while lipids absorb the light. Clearing methods tackle these problems by chemically removing and substituting lipids by certain types of gel, and immersing the whole sample in a medium with higher refractive index to match the optical properties of proteins. Numerous methods have been developed for tissue clearing, such as ScaleA2 [82], 3DISCO [83, 84], ClearT2 [85], SeeDB [86], CLARITY [87, 88], CUBIC [89] and iDISCO [90].

The first combination of optical clearing and light-sheet microscopy for whole brain imaging was performed by Dodt *et al.* using a custom ultramicroscope consisting of two opposing illumination arms and a single detection with an objective from above (Fig. 1.16A). The light-sheets were positioned horizontally, and the cleared samples could be placed in a transparent imaging chamber filled with the clearing medium (Fig. 1.16B). Imaging was performed from both top and bottom after rotating the sample 180°. By changing the detection lens, it is possible to adapt the system to different samples: low magnification is capable of imaging the whole brain (Fig. 1.16C), while for smaller,

## **1. LIVE IMAGING IN THREE DIMENSIONS**

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dissected parts, such as the hippocampus, higher magnification with higher resolution is more appropriate (Fig. 1.16D). With this configuration individual cell-cell contacts can be recognized (Fig. 1.16E), and even dendritic spines can be visualized (Fig. 1.16F).

Although light-sheet microscopy is highly suitable for imaging cleared specimens, even entire mice [91], brain imaging in live animals is more challenging due to the standard two-objective setup of a conventional SPIM microscope. Two light-sheet based methods, however offer a solution for this, axial plane optical microscopy (APOM) [92] and swept confocally-aligned planar excitation (SCAPE) [93] both use only a single objective to generate a light-sheet and detect the fluorescence as well. This is done by rotating the detection plane at an intermediate image (APOM), or by rotating both the light-sheet and detection plane simultaneously (SCAPE).

## Chapter 2

# Dual Mouse-SPIM

mammalian development chromosome segregation cell specification symmetry breaking  
signaling pathways human infertility congenital diseases

current mouse-SPIM [J2] already is very good for answering many of these questions  
resolution from beads: diSPIM [41] combine these two plus also [94]

advantages: immersion liquid and culture medium separated open-top sample holder  
allow standard microdrop *in vitro* embryo culture row of embryos - high throughput dual  
color imaging environmental chamber allows live imaging for 3 days, every  
follow chromosomes by tracking kinetochores

from lattice paper: “because photodamage mechanisms that scale supralinearly with  
peak intensity have been identified for both visible [95] and two-photon [96] excitation.”

### 2.1 Microscope design principles

In order to address the challenges outlined in the previous section, we propose a new light-sheet microscope design for imaging pre-implantation development at high resolution. The design is guided by the following requirements:

1. subcellular, isotropic resolution
2. high light collection efficiency
3. live embryo compatible

From these requirements the strongest is the live compatibility

#### 2.1.1 Light collection efficiency of an objective

Resolution is not the only parameter of concern when designing a new microscope setup. We also have to consider light collection efficiency, since many application, especially live imaging applications require a tight photon budget. This means a single fluorophore

## 2. DUAL MOUSE-SPIM

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can only emit so many times before it undergoes an irreversible chemical reaction, i.e. it bleaches. The more we can collect of these photons, the more information we gain, and altogether the efficiency is higher.

Photon collection efficiency also defines single molecule localization accuracy, since the signal to noise ratio will depend on the square of the number of collected photons. This is why it's important to also maximize light collection efficiency.

Let's define light collection efficiency  $\eta$  as the ratio of collected photons and all emitted photons:

$$\eta = \frac{N_{\text{collected}}}{N_{\text{emitted}}}$$

Since we can assume that the direction of photons emitted from a fluorescent molecule are random, the light collection efficiency will correspond to the solid angle subtended by the objective front lens at the focal point. To calculate this, let's consider the unit sphere centered at the focal point, and calculate the surface area of the spherical cap corresponding to the objective acceptance angle  $\alpha$  (Fig. 2.1a). The area of the cap can be expressed as a function of the angle:

$$A_{\text{cap}} = 2\pi r^2(1 - \cos \alpha)$$

The surface area of the full sphere is calculated as:

$$A_{\text{sph}} = 4\pi r^2$$

For both equations  $r$  is the radius of the sphere. From here, the light collection efficiency can be calculated as:

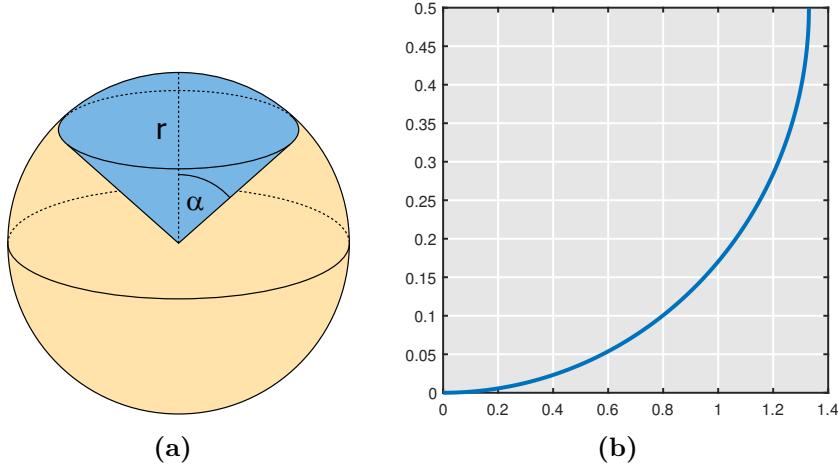
$$\eta = \frac{N_{\text{collected}}}{N_{\text{emitted}}} = \frac{A_{\text{cap}}}{A_{\text{sph}}} = \frac{1 - \cos \alpha}{2}$$

Some more calculations: (Fig. 2.1b).

### 2.1.2 Multi-view resolution

here a figure with rotating 2 psfs

In order to maximize light-collection efficiency and resolution, we opted for a high-NA water dipping objective, the Nikon CFI75 Apo LWD 25x/1.1w model. Two of these arranged in 120° allows for twice improved light collection efficiency compared to the 0.8 NA configuration in 90° alignment, with further improved lateral resolution along 2 axes (Figure 2.2). In the next section I will describe the design considerations for illumination and detection optics to achieve optimal sample illumination.



**Figure 2.1: Light collection efficiency of an objective.** (a) Light collection efficiency is the ratio of photons collected by the objective and all emitted photons. If the fluorophores are emitted randomly in all directions, it will be the surface ratio of the conical section (blue) to the whole sphere. (b) Light collection efficiency ( $\eta$ ) as a function of the numerical aperture (NA)

### 2.1.3 Light-sheet design

To allow for flexibility in the field of view height, even illumination, reduced stripes, and potential for confocal line detection, we opted to use the beam scanning technique to generate a virtual light-sheet. The effective focal length of the Nikon 25x objective, given the 200 mm focal length tube lens is

$$f_o = \frac{f_{tl}}{M} = \frac{200 \text{ mm}}{25} = 8 \text{ mm}, \quad (2.1)$$

and the back aperture diameter is 17.6 mm.

To generate the tilted light-sheet as shown on Fig. 2.3, the illumination beam will need to be displaced by

$$\delta = f_o \cdot \tan 30^\circ = 4.62 \text{ mm} \quad (2.2)$$

Since the Gaussian beam is not uniform, only a smaller portion of it can be used to maintain even illumination (Figure 1.12c). Because the size of an early mouse embryo is around 80  $\mu\text{m}$ , we require the length and the height of the light-sheet to be at least 100  $\mu\text{m}$ .

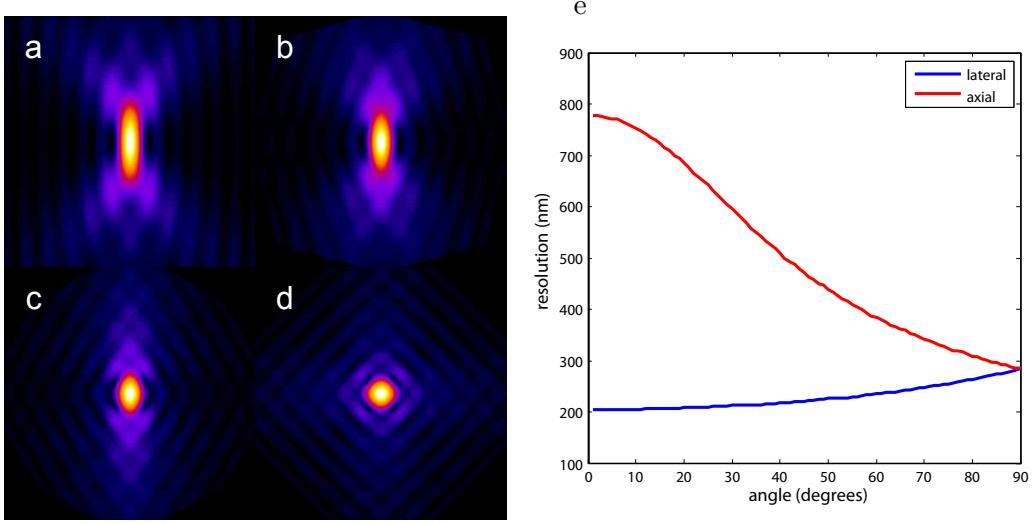
#### The length and thickness of the light-sheet

As we saw in section 1.3.2, the length of the light-sheet is determined by the Rayleigh-range of the beam in the  $zy$  plane. Since  $l_{fov} = 2 \cdot z_R = 100 \mu\text{m}$

$$z_R = 50 \mu\text{m} \quad (2.3)$$

## 2. DUAL MOUSE-SPIM

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**Figure 2.2: Lateral and axial resolution of a multi-view optical system.** a) Simulated PSF for a single view. b)-d) Simulated compound PSF of two views aligned in b) 30, c) 60 and d) 90 degrees to each other. e) Axial and lateral resolution of a dual-view setup depending on the rotation angle of the two objectives. Parameters used for calculations: NA=1.1,  $\lambda_{ex} = 488\text{nm}$ ,  $\lambda_{det} = 510\text{nm}$ ,  $n = 1.333$  for water immersion.

Since the Rayleigh range and the diameter of the beam waist are coupled, the light-sheet thickness can be calculated after rearranging Equation 1.23

$$2 \cdot W_0 = 2 \cdot \sqrt{\frac{z_R \cdot \lambda}{\pi}} = 5.57 \mu\text{m} \quad (2.4)$$

when  $\lambda = 488\text{ nm}$  for GFP excitation. As the beam width for these calculations is defined as  $1/e^2$  of the peak intensity, we also calculate the more commonly used FWHM:

$$\text{FWHM} = W_0 \cdot \sqrt{2 \ln 2} = 3.28 \mu\text{m}. \quad (2.5)$$

From this, the divergence angle of the beam is

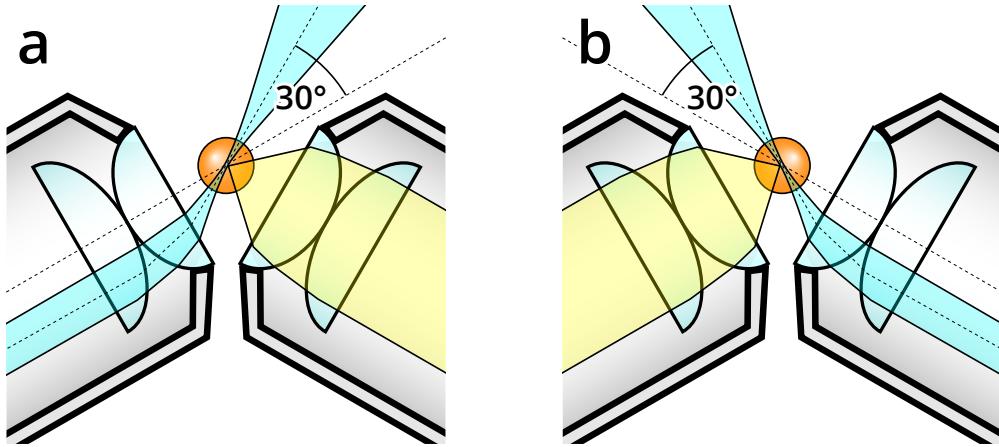
$$\theta_0 = \frac{\lambda}{\pi W_0, y} = 55.74 \text{ mrad} \quad (2.6)$$

This means, the numerical aperture needed to produce this light-sheet is:

$$\text{NA}_{ls} = n \cdot \sin(\theta_0) = 0.0743 \quad (2.7)$$

Since  $\text{NA} = 1.1$ , and the diameter of the back aperture is  $d = 17.6\text{ mm}$  and the divergence angle  $\theta_0 \ll 1$ , using paraxial approximation, the necessary beam width at the back focal plane in the  $y$  direction is

$$b_y = d \cdot \frac{\text{NA}_{ls}}{\text{NA}} = 1.19 \text{ mm} \quad (2.8)$$



**Figure 2.3: Dual view concept with high NA objectives.** To achieve multi-view detection while maximizing resolution and light collection efficiency, two high NA objectives are placed in  $120^\circ$  arrangement. To be able to overlap the light-sheet with the focal plane, the light-sheet is tilted  $30^\circ$ . Because of the high NA objectives, this tilt does not effect the illumination quality. The objectives are used in an alternating sequence for illumination and detection.

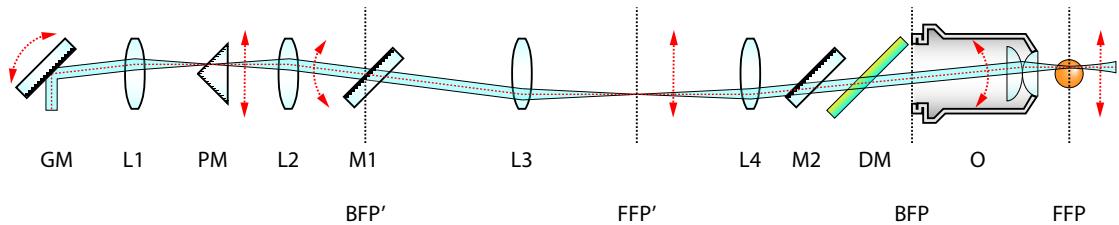
Thus, to generate a light-sheet with appropriate length to cover a whole mouse pre-implantation embryo, the laser beam diameter should be  $b = 1.19\text{ mm}$ . Larger than this will result in a more focused beam, and a shorter light-sheet, while a smaller diameter beam will have worse optical sectioning capabilities.

### The height of the light-sheet

The height can be adjusted by changing the beam scanning amplitude with the galvo mirror. To scan the entire field of view of  $\sim 270\text{ }\mu\text{m}$ , the scanning angle range at the back focal plane of the objective will need to be  $\theta = \tan^{-1}(270/2/f_o) = \pm 0.967^\circ$ .

## 2.2 Optical layout

design principles: highest isotropic resolution, highest light collection efficiency possible  
 $2 \times 0.8\text{ NA}$  water dipping in  $90^\circ$  multi-view deconvolve Gaussian fit  $\sigma_{xyz} = 135$   $2 \times 1.1\text{ NA}$  water dipping in  $120^\circ$  multi-view deconvolved Gaussian fit  $\sigma_z = 135$ , and  $\sigma_{xy} = 82.2$  simulations from PSF generator! put here



**Figure 2.4: Simplified schematics for illumination.**

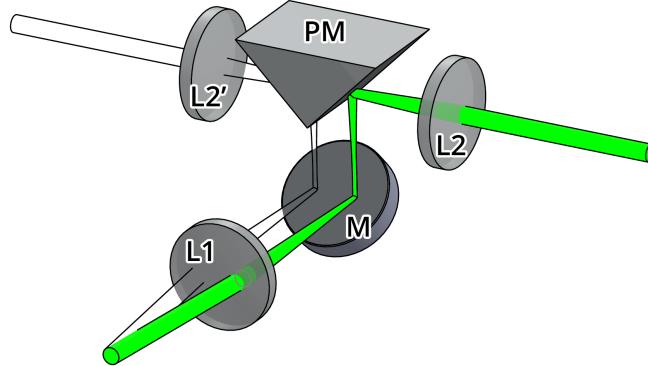
## 2. DUAL MOUSE-SPIM

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When designing the optical layout of the setup, we had two principles in mind: simplicity and efficiency. Because of the symmetrical design it is possible that

### 2.2.1 Illumination

#### Beam splitter unit



**Figure 2.5: Illumination branch splitting block.** 3D model of the custom designed splitter block used in the illumination branch. Depending on the horizontal beam position at the lower port, the beam will be reflected either to the right or to the left. Because of the mirror alignment, the beam is rotated 90 degrees.

### 2.2.2 Detection

#### Light combining unit

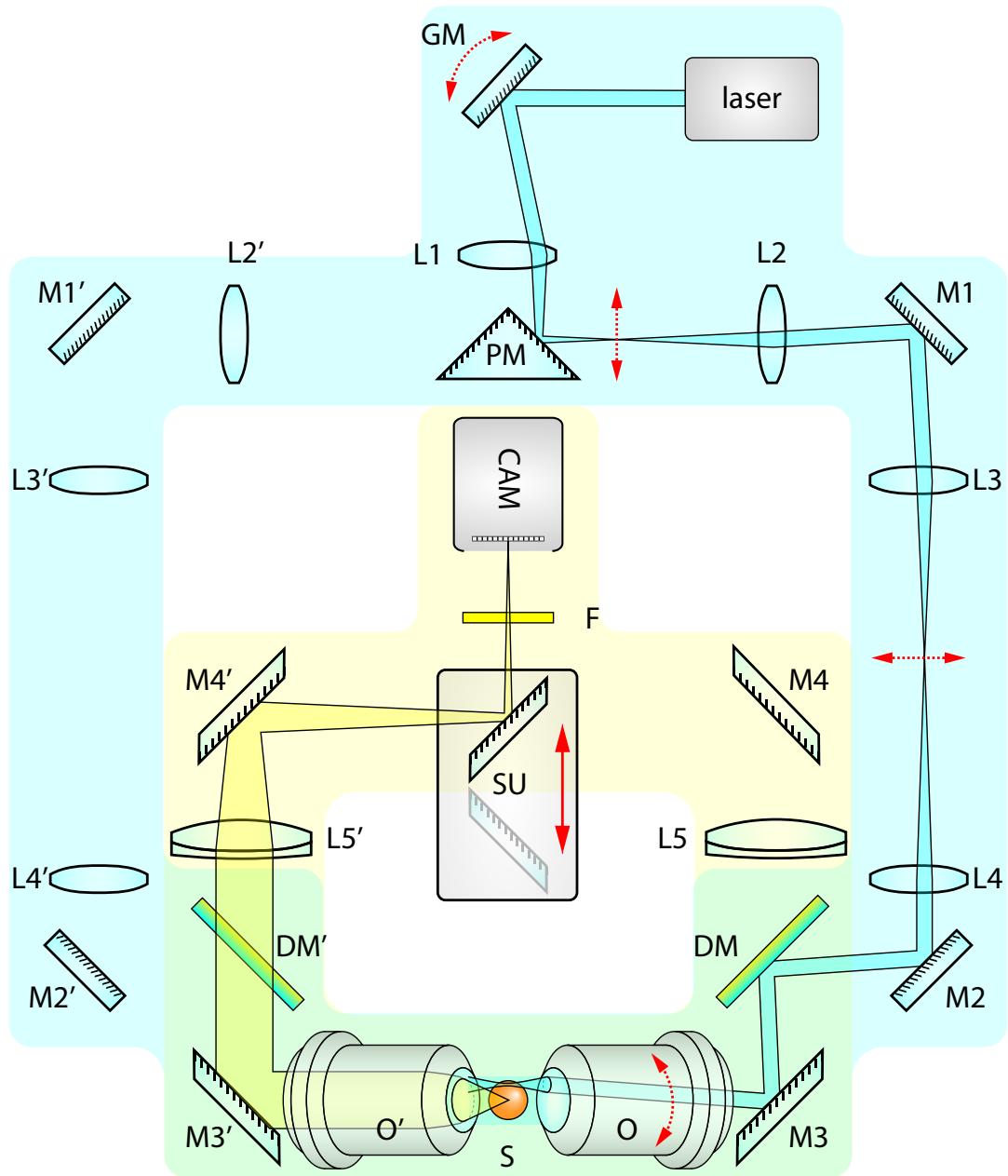
## 2.3 Optical alignment

Precise alignment of the illumination and detection paths are crucial for high quality imaging, and has a pronounced importance for high magnification and high resolution optical systems. The DualMouse SPIM contains two illumination and detection paths that share many common elements, which makes alignment a \*important?\* process. The final aim for the alignment is to perfectly overlap the light-sheets with the detection focal planes, and to optimize ...

### 2.3.1 Alignment of illumination branches

The two illumination branches start with a common light source, a single mode fiber coupled to laser combiner, and they also share a galvanometric mirror that performs the beam scanning to generate the virtual light-sheet. Likewise shared is a scan lens focusing on the galvo mirror (GM), and the illumination splitter unit (PM, see Section 2.2.1).

Alignment for the illumination arms are done in three steps. First the laser beam is aligned on the first rail that holds the galvo, lens L1, and the splitter unit PM. This



**Figure 2.6: Dual Mouse SPIM optical layout.** The microscope consists of two main parts, the illumination branches (blue) and detection branches (yellow). For both illumination and detection there are two identical paths implemented. Illumination direction can be changed by applying a different offset to the galvo mirror, which in turn will direct the beam to the opposite face of the prism mirror. L1 and L2 will then image the galvo on M1. Using L3 as a scan lens, and L4 as a tube lens, the scanned beam is coupled to the objective path by quad band dichroic mirror (DM) CAM – camera, DM – dichroic mirror, F – filter wheel, L – lens, M – mirror, O – objective, PM – prism mirror, S – sample, SU – switcher unit

is performed by two kinematic mirrors placed between the fiber output and the galvo mirror. Using these two mirrors it's possible to freely align the beam along all 4 degrees of freedom: translation in two orthogonal directions, and rotation around two orthogonal

## **2. DUAL MOUSE-SPIM**

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axes. Beam alignment on the rail is tested by two irises at the two ends of the rail, if the beam passes through both of them we consider it centered and straight on the optical axis.

After the beam is aligned on the first rail, lens L1 and the splitter unit PM are placed in the measured positions to image the galvo mirror on mirror M1 using lenses L1 and L2. Correct positioning of the splitter unit along the rail is crucial, since this will affect the lateral position and tilt of the beam exiting the unit. To some extent, this can also be compensated by adjusting the two mirrors before the galvo mirror, but is avoided if possible as this will also displace the beam from the center of the galvo mirror.

### **Adjusting beam position.**

Beam position can be adjusted by either translating the beam in a conjugated image plane, or by rotating the beam in a conjugated back focal plane. The setup was designed in a way, that BFP' coincides with mirror M2. This mirror is mounted in a gimbal mirror mount, allowing to rotate the mirror exactly around its center, which avoids unwanted translational movements, and results in pure rotation of the beam. Lens L3 is positioned exactly 1 focal length from the mirror, thus acting as a scan lens, and transforming the rotational movements to translation. This translation is further imaged and demagnified by the tube lens L4 and the objective O.

**Adjusting beam tilt** Beam tilt can be adjusted by

### **Adjusting beam axial position.**

**Adjusting scanning plane angle.** After the beam is properly aligned, i.e. it is in focus, and in the center of field of view, it is still necessary to check if the scanning direction is parallel to the imaging plane. It is possible that the beam is in focus in the center position, but when moved up or down it drifts out of focus due to a tilted scanning angle. This tilt can be compensated by mirror M1, that is placed at the conjugated back focal plane BFP'. Between lenses L3 and L4 a magnified version of the light-sheet will be visible, and the tilt can be checked by placing an alignment target in the optical path while scanning the beam. By tilting mirror M1 up or down, the scanning pattern not only moves up or down, but is also rotated if the mirror surface is not exactly vertical. Since M1 and GM are in conjugated planes, the tilt and offset can be performed independently. The tilt is first fixed by M1 while inspecting the target, and the beam is re-centered by changing the offset on the galvo mirror. Moving the galvo mirror will not introduce tilt, since in this case rotation axis is perpendicular to the reflection plane.

### 2.3.2 Alignment of detection branches

Since the detection path is equivalent to a wide-field detection scheme, its alignment is much simpler than that of the illumination branches. The only difference is the detection branch merging unit (see Sec. 2.2.2.) that features two moving mirrors. This, however doesn't effect the alignment procedure, since the movement direction is parallel to both mirror's surface, meaning that the exact position of the mirrors will not affect the image quality, as long as the mirrors are not clipping the image itself. Stability test were performed to confirm the consistent switching performance of the mirror unit before the final alignment took place (see Sec. 2.5.3).

The final alignment procedure

**Positioning the tube lens.** The position of the tube lens determines the focal plane the is being imaged on the camera sensor. Ideally, the tube lens' distance from the camera sensor is exactly the tube lens focal length, which will ensure the best imaging performance. If the tube lens distance is not correct, the focal plane will be slightly shifted in the axial direction. Although small shifts will not necessarily have detrimental effect on the image quality, because the light sheet can also be shifted accordingly. Because of the shifted focal and image planes, however, the magnification of the system will be affected, and will change depending on the amount of defocus. For this reason we aim for positioning the tube lens as close to the theoretical position as possible.

Our tube lens is a compound, achromatic lens with a center thickness of 12.5 mm, and edge thickness of 11.3 mm. Its effective focal length is 400 mm which will produce a 50x magnified image. Back focal length is 394.33 mm which we measured form the camera chip, and the lens was positioned at this theoretically optimal position.

**Adjusting correction collar.** The Nikon 25x objectives used for this setup have a built in correction ring that can be used to correct spherical aberrations resulting from refractive index differences when imaging samples behind a coverslip. This can be also effectively used to correct for any spherical aberrations occurring from imaging through the FEP foil. Although these aberrations are expected to be extremely low, due to the relatively thin, 50  $\mu\text{m}$  foil thickness, and the close matching of refractive index ( $n_{FEP} = 1.344$ ,  $n_{H_2O} = 1.333$ ), for optimal, aberration free image quality it can't be neglected.

The correction collars are adjusted by inspecting a gel suspended fluorescent bead specimen with the microscope, where the beads can act as a reporter of the point spread function of the microscope. The alignment can be performed "live" by inspecting the bead image quality for any aberrations. By gradually changing the correction collar, the ring are minimized on out of focus beads, and the peak intensity is maximized for in

## 2. DUAL MOUSE-SPIM

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focus beads. By moving the correction ring, the focal plane is also slightly shifted, which has to be compensated by shifting the light-sheet correspondingly to coincide with the correct imaging plane.

**Adjusting field of view.** To allow for proper sampling of the image, we use 50x magnification, which, combined with the 6.5  $\mu\text{m}$  pixel pitch of our sCMOS camera will result in a 0.13  $\mu\text{m}$  pixel size. The full field of view with this magnification is  $2048 \times 0.13 = 266.24 \mu\text{m}$ . The full field of view the objective provide, are larger than this, at 800  $\mu\text{m}$ . To ensure the best image quality, we align the center of the objective field of view on the camera sensor, since this region has the best optical properties in term of numerical aperture, aberration correction and field flatness.

Field of view alignment can be performed using mirror M4 just before the detection merging unit. To identify the center region of the field of view, diffuse white light is used to illuminate the entire sample chamber, and is imaged on the camera. Then, mirror M4 is adjusted until the top edge of the field of view becomes visible, *i.e.* where the illumination from the chamber is clipped. This will have a circular shape. Then, adjusting the mirror in the orthogonal direction, the left-right position of the field of view can be adjusted, by centering the visible arc on the camera sensor.

After the horizontal direction is centered, vertical centering is performed. This, however can't be centered the same way as the horizontal direction, since for that we would have to misalign the already aligned horizontal position. To determine the center, we move the field of view from the topmost position to the bottom. During this process the number of turns of the adjustment screw is counted (this can be done accurately by using a hex key). After reaching the far end of the field of view, the mirror movement is reversed, and the screw is turned halfway to reach the middle.

### 2.4 Control unit

Apart from the optics design, automation hardware and software is also a custom design. To be able to conduct high speed experiments and time-lapse recordings, a high level of automation, hardware and software integration is necessary. Our system comprises of two main components: a National Instruments embedded system (cRIO 9068), and a high performance workstation.

#### 2.4.1 Hardware

Various components need to be properly synchronized to operate the microscope. Illumination is performed with a multi-line laser combiner, light-sheet is generated by a galvo scanner For more details, see Appendix section A.

Equation 1.5

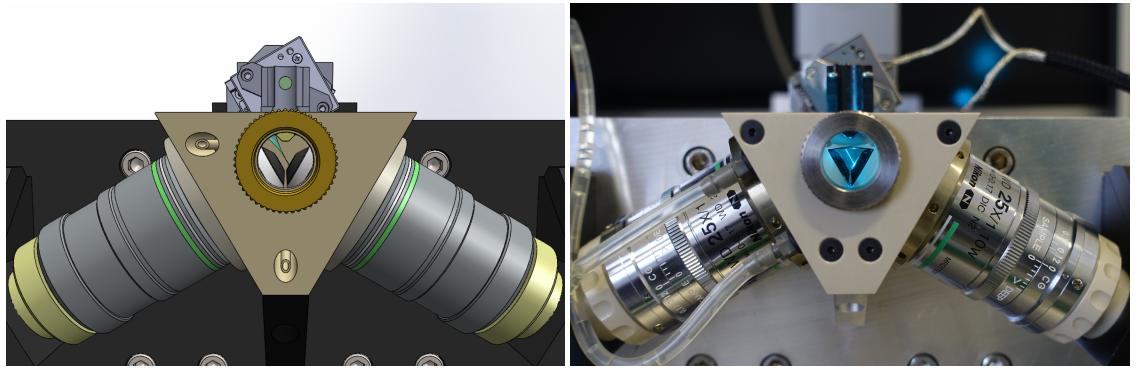
Figure 1.16

section 2.2.2

Table 3.4

#### 2.4.2 Software

### 2.5 Results



**Figure 2.7: Front view of the Dual Mouse-SPIM.**

Resolution for Lattice light-sheet [6]: 230 nm in x and 370 nm in z [44]

After the design phase, all custom parts were manufactured at the EMBL workshop, and I assembled the microscope on a NewPort X by X optical table (Fig. 2.7).

#### 2.5.1 Characterizing illumination profile

Since a Gaussian beam is used for illumination, its intensity profile is dependent on the axial position (Eq. 1.18). Although the total intensity at any cross section of the beam is constant, because of the divergent properties, the peak intensity varies. To assess any non-uniformities in the illumination pattern, I measured the illumination beam intensity for each view.

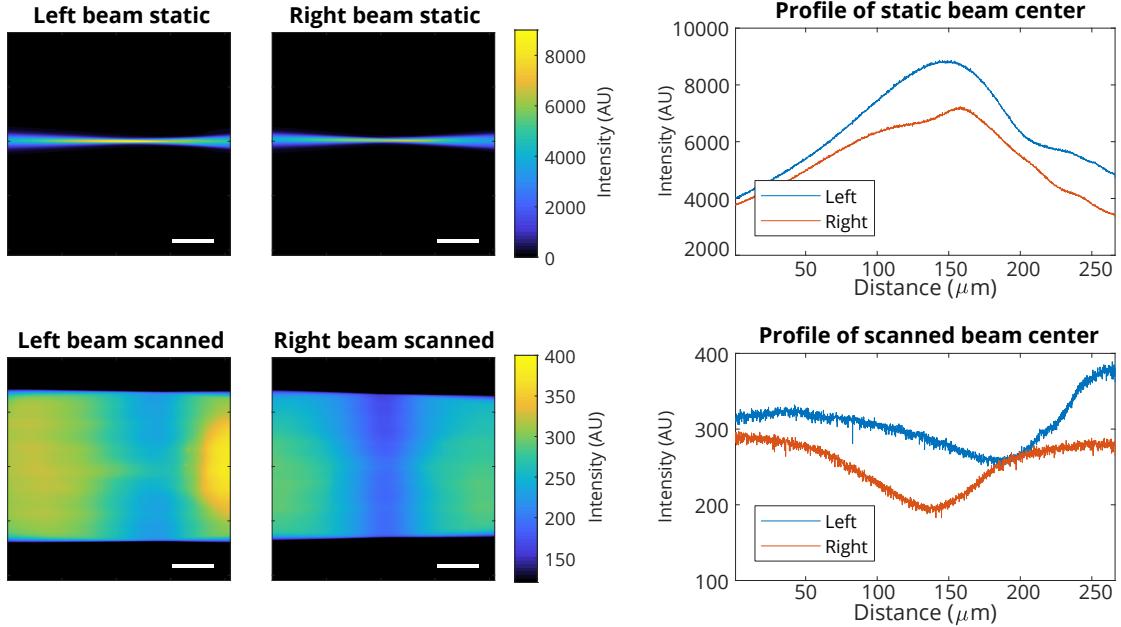
To visualize the beam, the chamber was filled with a fluorescent solution (methylene blue solution in distilled water). In order to increase the signal to noise ratio of these images, a long exposure time of 200 ms were used, and 500 images of each beam was averaged (Fig. 2.8).

#### 2.5.2 Resolution and point spread function measurement

To measure the resolution of the microscope, and characterize its optical performance I performed point spread function measurement using fluorescently labeled beads

## 2. DUAL MOUSE-SPIM

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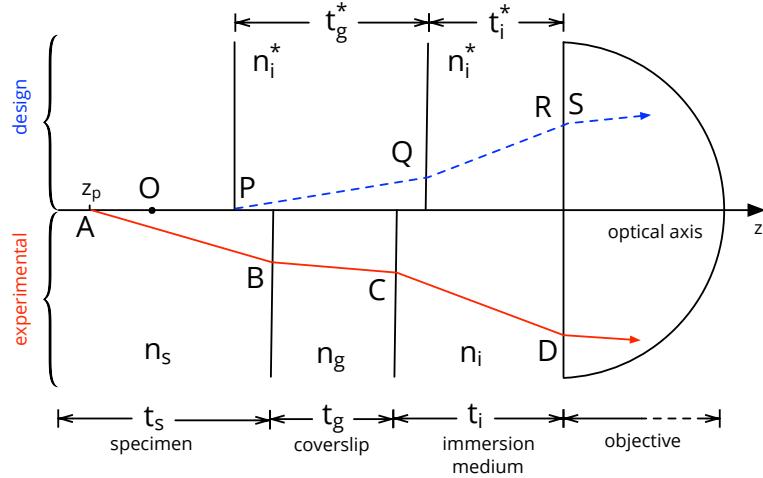


**Figure 2.8: Illumination beam profile.** Average of 50 stationary beam images for both left and right objectives (top left). Beam intensity profile along the center of each beam is plotted (top right). To simulate scanned beam illumination intensity, each beam image was averaged along the vertical axis (bottom left). Intensity profile of the projections are plotted (bottom right).

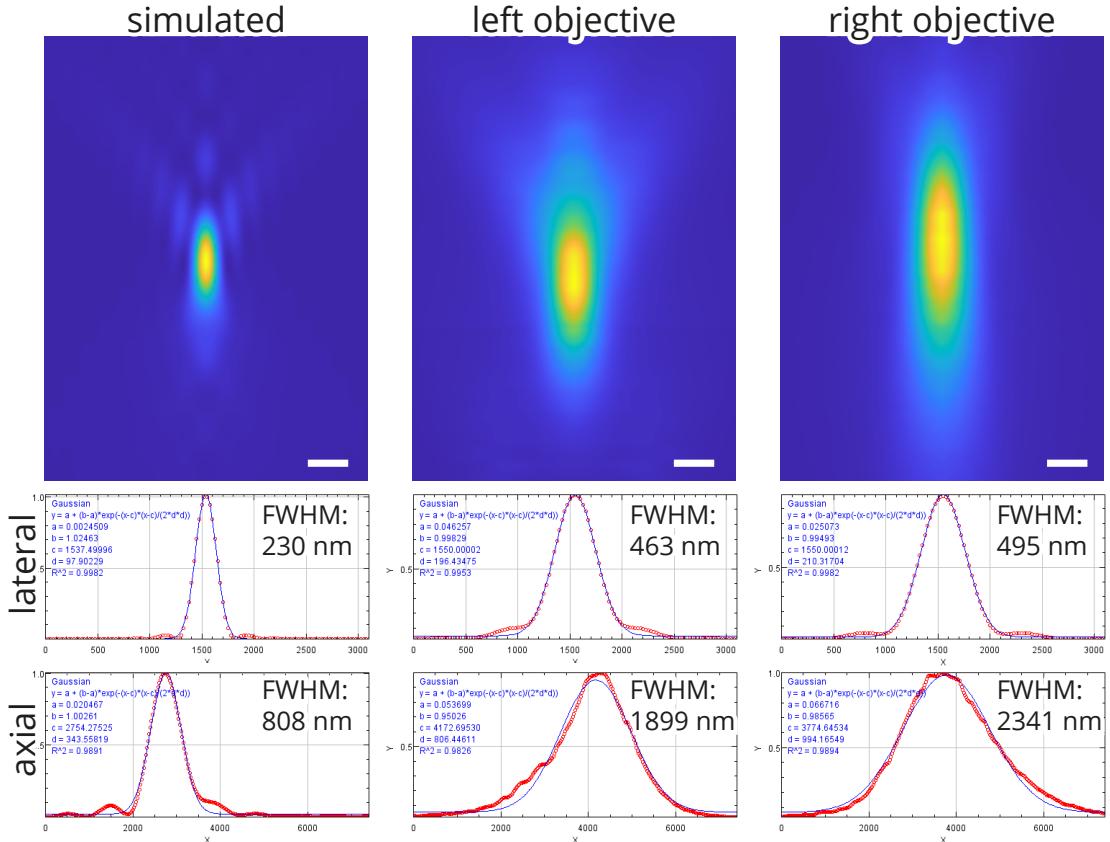
(TetraSpeck 500 nm, ThermoFisher). The beads were sonicated, and mixed with 0.8% GelRite solution at a final dilution of 1:1000. The gel was loaded in glass capillaries and allowed to cool. After the gel solidified, a ~1 mm piece was cut off and placed in the microscope sample holder.

In order to establish an ideal, reference PSF, we simulated the theoretical PSF of the microscope with the Gibson-Lanni model [97], using the MicroscPSF Matlab implementation [98]. The advantage of this model is that it accounts for any differences between the experimental conditions and the design parameters of the objective, and thus it can simulate any possible aberrations that should arise. The adjustable parameters are the following (Fig. 2.9):

### 2.5.3 Stability of view switcher unit



**Figure 2.9: Schematics for the Gibson-Lanni model.** The model is based on the differences in light propagation between the experimental (red) and design conditions (blue). The optical path length difference is calculated as follows:  $OPD = [ABCD] - [PQRS]$ . System properties are represented by vectors  $\mathbf{n} = (n_i, n_i^*, n_g, n_g^*, n_s)$  and  $\mathbf{t} = (t_i, t_i^*, t_g, t_g^*, t_s)$  for the refractive indices and path lengths respectively. Adapted from [98].



**Figure 2.10: Simulated and measured PSF of Dual Mouse-SPIM.** Top row: axial sections of simulated and measured point spread functions. Middle row: lateral intensity profile and Gaussian fit. Bottom row: Axial intensity profile and Gaussian fit. Simulations were performed based on the Gibson-Lanni model. Immersion medium and sample refractive index: 1.330, coverslip (FEP foil) refractive index: 1.344, coverslip distance: 1900  $\mu\text{m}$ , coverslip thickness: 50  $\mu\text{m}$ . Scale bar: 500 nm.

## **2. DUAL MOUSE-SPIM**

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## Chapter 3

# Image processing for multi-view microscopy

When using any kind of microscopy in research, image processing is a crucial part of the workflow. This is especially true for light-sheet microscopy, since it's capable imaging the same specimen for multiple days, producing immense amounts of data. A single overnight experiment of *Drosophila* development (which is a very typical use-case for light-sheet) can produce multiple terabytes of data. To see the real scales, let's consider the following imaging conditions:

camera	Hamamatsu Orca Flash 4
image size	8 MB
1 stack = 250 planes	2 GB
2 views	4 GB
Time-lapse: 16 h @ 2/min	7.5 TB
$n$ colors	$n \cdot 7.5$ TB

As it is apparent from this table,

### **3. IMAGE PROCESSING FOR MULTI-VIEW MICROSCOPY**

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#### **3.1 Multi-view image fusion**

##### **3.1.1 Registration**

**Image based registration**

**Bead based registration**

##### **3.1.2 Transformation**

**Rigid**

**Affine**

**Elastic**

##### **3.1.3 Image fusion**

**Average**

**Sigmoidal weighted average**

**Fourier mixing**

Huisken had something like this

**Wavelet-based fusion**

**Multi-view deconvolution**

[99] Uros thesis [100], [101] Spatially variant deconvolution

#### **3.2 Image compression**

Image compression is an important tool for everyday life, however it's rarely used in the context of scientific imaging because of fear of information loss. This preconception is mainly due to the famous blocking artifacts found in many highly compressed JPEG images, however not all image compression algorithms introduce artifacts, and in fact many lossless algorithms exist that would be suitable for such images. Nowadays, when data production is in an exponential growth compression is again in highlight, without it it would be extremely difficult to maintain many scientific projects that produce images at a high data rate.

In this paper I will review the basics of image compression based on Sayood's textbook, Introduction to Data Compression [102]. I will introduce some basics of information theory and entropy, followed by discussing two widely used entropy coding algorithms,

Huffman coding and arithmetic coding. Section 3 will be about transform coding, specifically Discrete Cosine Transform (DCT) and wavelet transform while also touching upon techniques based on differential pulse code modulation. Finally I will show how some of the most widely used image compression standards use these methods to achieve effective image compression.

#### 3.2.1 Entropy coding

##### Information and Entropy

"For the purpose of data compression it is useful to quantify the amount of *information* contained within a piece of data. The first rigorous definition of information was presented in an extremely influential paper by Shannon, published in two parts in 1948 [103, 104]."

"First, let's define the amount of self-information contained in the outcome of a random experiment:"

$$I(A) = \log_b \frac{1}{P(A)} = -\log_b P(A) \quad (3.1)$$

2 independent events:

$$P(A, B) = P(A) \cdot P(B) \quad (3.2)$$

self-information is additive:

$$I(A, B) = \log_b \frac{1}{P(A, B)} \quad (3.3)$$

$$= \log_b \frac{1}{P(A) \cdot P(B)} \quad (3.4)$$

$$= \log_b \frac{1}{P(A)} + \log_b \frac{1}{P(B)} \quad (3.5)$$

entropy for random variable  $X$  average or expected self-information for the random variable

$$H(X) = \sum_i P(A_i)I(A_i) = -\sum_i P(A_i) \log_b P(A_i) \quad (3.6)$$

entropy rate for data source  $S$  average information output by the data source

##### Huffman coding

Huffman coding is a prefix-free, optimal code that is widely used in data compression. It was developed by David A. Huffman as a course assignment on the first ever course on information theory at MIT, and was published shortly afterwards [105]. It is a variable length binary code which assigns different length codewords to letters of different probabilities. It is able to achieve optimal compression, which means the total length of the coded sequence will be minimal.

### 3. IMAGE PROCESSING FOR MULTI-VIEW MICROSCOPY

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**Table 3.1: Examples of a random binary code (#1) and a prefix-free binary code (#2).** Code #2 is uniquely decodable, while for code #1 it's necessary to introduce boundaries between codewords to be able to distinguish them.

Letter	Code #1	Code #2
$a_1$	0	10
$a_2$	11	11
$a_3$	00	00
$a_4$	10	010
$a_5$	111	011

Although it produces a variable length code which can introduce some issues with decoding, it is still uniquely decodable. It achieves this property by using prefix-free codewords, meaning that none of the codewords are prefixes of any other codewords. This property can be exploited when decoding the codeword, since during this procedure the number of bits for the next codeword can not be determined in advance. However if no codeword is a prefix of another codeword, by simply reading the successive bits one by one until we reach a valid codeword, it's possible to uniquely decode the message.

Let's take the example in Table 3.2. Five letters are coded in binary code by Code #1 and by Code #2. Code 1 is not a prefix code, and because of this when reading the encoded sequence we can not be sure when we reach the end of a codeword. Decoding the sequence 0000 for example could be interpreted as 4 letters of  $a_1$  or 2 letters of  $a_3$ .

The Huffman coding procedure is based on two observations regarding optimal and prefix-free codes:

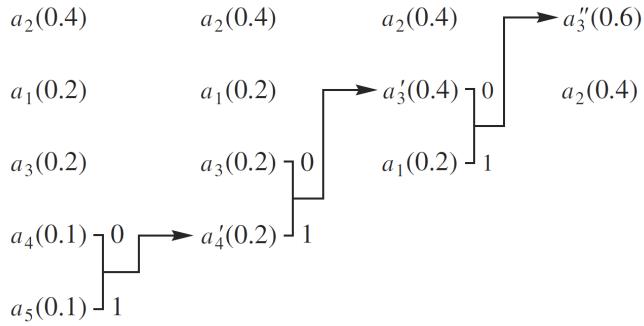
1. For a letter with higher frequency the code should produce shorter codewords, and for letters with lower frequency it should produce longer codewords.
2. In an optimum code, the two least frequent codewords should have the same lengths.

From these statements the first is trivial to see that is correct. If the more frequent letters would have longer codewords than the less frequent letters, the average codeword length (weighted by the probabilities) would be larger than in the opposite case. Thus, more frequent letters must not have longer codewords than less frequent letter.

The second statement at first glance might not be so intuitive, so let's consider the following situation. The two least frequent codewords do not have the same lengths, that is the least frequent is longer. However, because this is a prefix code, the second longest codeword is not a prefix of the longest codeword. This means, if we truncate the longest codeword to the same length as the second longest, they will still be distinct codes and uniquely decodable. This way we have a new coding scheme which requires less space on average to code the same sequence as the original code, from which we can conclude the original code was not optimal. Therefore, for an optimal code, statement 2 must be true.

Table 3.2: Huffman code table.

Letter	Probability	Codeword
$a_2$	0.4	$c(a_2)$
$a_1$	0.2	$c(a_2)$
$a_3$	0.2	$c(a_2)$
$a_4$	0.1	$c(a_2)$
$a_5$	0.1	$c(a_2)$



**Figure 3.1: Building the binary Huffman tree.** The letters are ordered by probability, these will be the final leave of the tree. To join the two branches at every iteration we join the two nodes with the smallest probability, and create a new common node with the sum of the probabilities. This process is continued until all nodes are joined in a root node with probability of 1. Now, if we traverse down the tree to each leaf, the codeword will be defined by their position.

To construct such a code, the following iterative procedure can be used. Let's consider an alphabet with five letters  $A = [a_1, a_2, a_3, a_4, a_5]$  with  $P(a_1) = P(a_3) = 0.2$ ,  $P(a_2) = 0.4$  and  $P(a_4) = P(a_5) = 0.1$  (Table 3.2). "The entropy for this source is 2.122 bits/symbol." Let's order the letters by probability, and consider the two least frequent. Since the codewords assigned to these should have the same lengths, "we can assign their codewords as"

$$\begin{aligned} c(a_4) &= \alpha_1 * 0 \\ c(a_5) &= \alpha_1 * 1 \end{aligned}$$

where  $c(a_i)$  is the assigned codeword for letter  $a_i$  and  $*$  denotes concatenation. Now we define a new alphabet  $A'$  with only four letters  $a_1, a_2, a_3, a'_4$ , where  $a'_4$  is a merged letter for  $a_4$  and  $a_5$  with the probability  $P(a'_4) = P(a_4) + P(a_5) = 0.2$ . We can continue this process of merging the letters until all of them are merged and we have only one letter left. Since this contains all of the original letters, its probability is 1. We can represent the end result in a binary tree (see Figure 3.1), where the leaves are the letter of the alphabet, nodes are the merged letters, and the codewords are represented by the path from the root node to each leaf (compare with Table 3.3). "The average length of this

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**Table 3.3: Huffman code table.**

Letter	Probability	Codeword
$a_2$	0.4	1
$a_1$	0.2	01
$a_3$	0.2	000
$a_4$	0.1	0010
$a_5$	0.1	0011

code is”

$$l = 0.4 \times 1 + 0.2 \times 2 + 0.2 \times 3 + 0.1 \times 4 + 0.1 \times 4 = 2.2 \text{ bits/symbol} \quad (3.7)$$

”A measure of the efficiency of this code is its redundancy—the difference between the entropy and the average length. In this case, the redundancy is 0.078 bits/symbol. The redundancy is zero when the probabilities are negative powers of two.”

#### Arithmetic coding

Although in this case the redundancy of the Huffman code is minimal, however in cases where a few symbols have vary high probability compared to the rest, the redundancy increases. This is simply because even for the most frequent letter the shortest codeword the Huffman code can produce is of length 1.

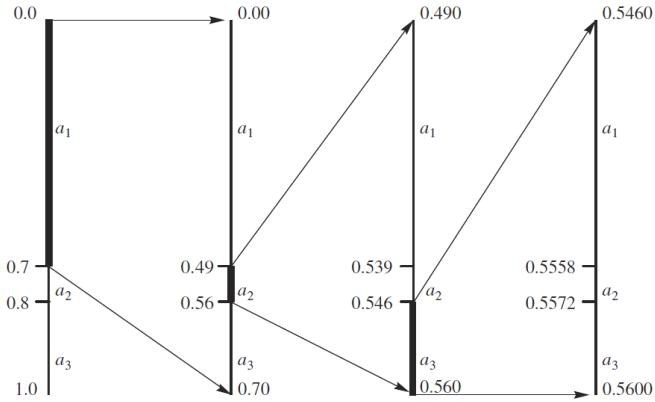
Let’s consider the following example: take alphabet  $A = [a_1, a_2]$  with  $P(a_1) = 0.95$  and  $P(a_2) = 0.05$ . The first order entropy for this source is  $-0.95 \log 0.95 - 0.05 \log 0.05 = 0.2864$  bits/symbol, however if we assign the Huffman code we will have to use  $c(a_1) = 0$  and  $c(a_2) = 1$ , which means the average length will be 1 bit/symbol. This means in order to code this sequence using a Huffman code, we will need more than 3 times the number of bits promised by the entropy.

To get around this fundamental limitation, a coding scheme must be used which does not use discrete codewords at all. Arithmetic coding is the most well-known example of such a scheme. The idea is due to Peter Elias. He developed it during the same course on information theory in which Huffman developed his coding method, but he never published it.

”In order to distinguish a sequence of symbols from another sequence of symbols we need to tag it with a unique identifier. One possible set of tags for representing sequences of symbols are the numbers in the unit interval  $[0,1)$ . Because the number of numbers in the unit interval is infinite, it should be possible to assign a unique tag to each distinct sequence of symbols. In order to do this, we need a function that will map sequences of symbols into the unit interval.”

Table 3.4: Example alphabet for arithmetic coding.

Letter	Probability
$a_1$	0.7
$a_2$	0.1
$a_3$	0.2


 Figure 3.2: Arithmetic coding scheme in practice with the alphabet from Table 3.4 on the sequence  $a_1, a_2, a_3$ .

"A straightforward algorithm to arithmetically encode a given input string is the following: Partition the unit interval  $[0, 1)$  into sub-intervals and assign one subinterval to each symbol in the input alphabet. The sizes of the sub-intervals are chosen to be proportional to the symbol frequencies. A string of symbols can be encoded by applying this process recursively: The sub-interval from the previous step is subdivided again using the same proportions. Figure 3.2. shows an example of arithmetic coding using the symbol frequencies given in Table 3.4."

This kind of coding although easy to understand, it's actually quite cumbersome to directly implement on a computer, where only a certain floating point precision can be achieved. For real life use this precision is often unsatisfactory, so some extra steps are involved in the coding.

Since after each step the next subinterval is a subset of the previous interval, if the coding interval after a certain number of steps is contained in either the upper or lower half of the unit interval it will remain there for the rest of the coding. We can exploit this fact by rescaling that interval to the unit interval and writing either a 0 or 1 bit to the output depending on the position of the subinterval. By continuing this scheme it's possible to reach arbitrary precision even using a computer.

The decoding process is analogous to encoding. The decoder keeps track of the current lower and upper bounds. It mimics the rescaling operations of the encoder based on the bits of the encoded binary number.

### 3. IMAGE PROCESSING FOR MULTI-VIEW MICROSCOPY

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#### 3.2.2 Transform coding

The methods outlined in the previous section are effective at compressing the data in an optimal way and reaching the first order entropy, however they assume nothing about the structure of the data. For image compression it's important to also consider this, since most images have a relatively high level of autocorrelation, meaning that neighboring values have a high chance of being similar, although not necessarily equal. Transform coding is a technique that by itself does not compress the data, however by exploiting some knowledge of the structure it transforms the data effectively reducing its first order entropy. When regular entropy coding is then performed on the transformed data, because of the reduced first-order entropy, these techniques can achieve a higher rate of compression. At decompression, after decoding the entropy coder, the reverse transformation is applied to reveal the original data. This section will introduce two of the most important algorithms for transform coding, Discrete Cosine Transform and Discrete Wavelet Transform.

#### Discrete Cosine Transform

Discrete Cosine Transform [106] is closely related to the well known Fourier transform. The main idea behind this is to represent a function by a weighted sum of different sine and cosine functions. This provides a different view, instead of looking at the data in the time domain, we gain information about the frequencies that compose the signal.

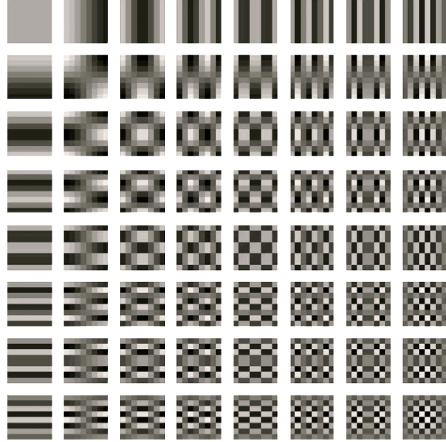
"Discrete Cosine Transform is a variant of the discrete Fourier transformation", however instead of making the signal periodic which can introduce large jumps at the edges, the signal is extended in a symmetric way. Since this will give a smooth transition even at the boundaries, the transform does not have to include so many high frequency components. Also, because of the symmetric extension, it's possible to represent the functions only by using the cosine bases, resulting in fewer coefficients. Overall, the DCT is much better suited for compression, than DFT.

The DCT base functions are defined in the following way:

$$c_{i,j} = s_i \cdot \cos \frac{(2j+1)i\pi}{2n} \quad \text{with } s_i = \begin{cases} \sqrt{\frac{1}{n}} & \text{if } i = 0 \\ \sqrt{\frac{2}{n}} & \text{otherwise} \end{cases} \quad (3.8)$$

"The scaling factors are chosen so that the  $L_2$  norm of each basis vector is 1 and so the transform is orthonormal. The inverse transform can therefore be found by simply transposing the transform matrix."

Applying the DCT to two dimensional functions, i.e. images is very similar to the two dimensional Fourier transform. The base functions are the outer products of the 1D base functions (Figure 3.3.), and the transform can actually be performed separately for



**Figure 3.3:** Basis functions of the  $8 \times 8$  2D DCT, computed as the outer product of the 1D basis vectors..

each dimension.

Computation effort in a naive implementation is  $O(n^2)$  but since DCT is based on the Fourier transform, an  $O(n \log n)$  algorithm is also possible, analogous to the fast Fourier transform. This is still larger than a linear scaling with the data size, which can be very inconvenient. Therefore, in practice the DCT is usually applied to smaller blocks of the image, such as  $4 \times 4$ ,  $8$  or  $16 \times 16$ .

Although DCT is an effective way of reducing the first-order entropy, it has a potential shortcoming by its use of floating point arithmetic. Because of the finite machine precision inherent rounding errors will occur, which means the reverse transformation can not generate the exact original data. For many application, such as photography, this still can be acceptable, but for scientific image data lossy compression is generally not accepted.

DCT-like integer-based variants in JPEG-XR, and H.264

### Discrete Wavelet Transform

”!!CHANGE THIS!!Methods based on Fourier analysis, such as the DCT introduced in the previous section, give excellent localization in frequency space: They tell us exactly which frequencies occur in the data, which is very useful for data compression. However, they give no spatial localization: They do not tell us where in the signal these frequencies occur. Every DCT base function affect the whole image domain!!UNTIL HERE!!”, which means distinct local structures can have a global effect on the final outcome. In case of an edge for example, it’s necessary to include a high frequency component with a large coefficient, but since every DCT base function has an impact on the whole domain, this will have to be compensated on smoother regions by also increasing the coefficients of other factors. This can negatively impact compression performance.

A solution for this is to use different base functions, namely ones with finite support.

### 3. IMAGE PROCESSING FOR MULTI-VIEW MICROSCOPY

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This way we will not only be able to get information about the frequency, but also about the localization of that frequency in some extent.

”!!!!One option for such a set of local basis functions, and certainly the most popular one, is the multi-resolution analysis based on wavelets. The term “multi-resolution analysis” in the context of wavelets was introduced in the late 1980s by Stéphane Mallat [107], though research on wavelets had been ongoing for several years before that.!!!!”

”The idea behind the wavelet multi-resolution analysis is to build a basis out of translated and scaled versions of one underlying function called the *mother wavelet*  $\psi$ . The mother wavelet is non-zero only in a small region, leading to the locality properties. It is translated to cover the whole domain. It also covers only a small frequency band, and is scaled to cover higher or lower frequencies. The family of translated and scaled functions  $\psi_{l,i}$  is generated from according to”

$$\psi_{l,i}(t) = \sqrt{2^l} \psi(2^l t - i), \quad l, i \in \mathbb{Z} \quad (3.9)$$

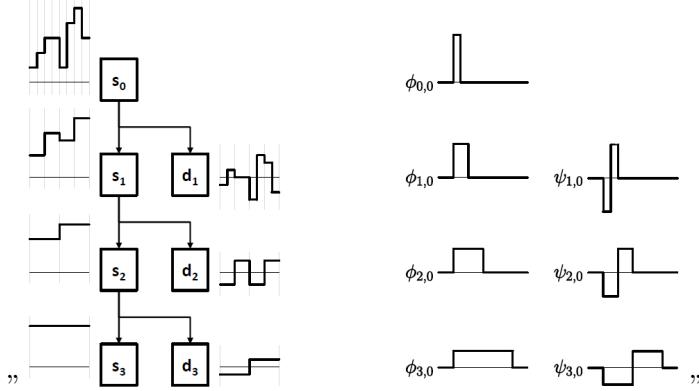
”Incrementing  $l$  halves the width of the resulting function, which thus corresponds to a higher frequency band. Changing  $i$  moves the function along the x axis. The size of each step scales with the width of the function, defined by  $l$ . The normalization factor  $\sqrt{2^l}$  is chosen so that the  $L_2$  norm stays constant. The mother wavelet can be chosen so that the  $\psi_{l,i}$  are pairwise orthogonal and thus form a basis of some function space. However, representing a function in this basis will generally require an infinite number of basis functions  $\psi_{l,i}$ : To represent a constant component, i.e. content of frequency zero, the wavelet must be infinitely scaled. To address this, it is necessary to introduce an additional scaling function  $\phi$  which complements the wavelet. It is scaled and translated the same way as the mother wavelet.”

The oldest wavelets are the Haar wavelets, and because of their simplicity, they provide a good example on how wavelet transformation works. The Haar wavelet scaling  $\phi$  and wavelet  $\psi$  functions are the following:

$$\phi(t) = \begin{cases} 1 & \text{if } 0 \leq t < 1 \\ 0 & \text{otherwise} \end{cases} \quad (3.10)$$

$$\psi(t) = \begin{cases} -1 & \text{if } 0 \leq t < \frac{1}{2} \\ 1 & \text{if } \frac{1}{2} \leq t < 1 \\ 0 & \text{otherwise} \end{cases} \quad (3.11)$$

”Clearly, all wavelet functions  $\psi_{l,i}$  are orthogonal. Additionally, the scaling functions  $\phi_{l,i}$  at a fixed level  $i$  are orthogonal. The scaling functions  $\phi_{l,i}$  are also orthogonal to the wavelet functions  $\psi_{k,i}$ ,  $k \geq l$  at the same and all finer levels.”



**Figure 3.4: Multi-resolution wavelet decomposition, using the Haar wavelets as an example.** Left: decomposition to multiple levels of low pass and high pass coefficients corresponding to the scaling and the wavelet functions respectively. Right: some of the base wavelet functions used for the decomposition.

"Figure 3.4. (left) schematically shows the decomposition of a signal into low-pass components corresponding to the scaling function, and high-pass components corresponding to the wavelet. The signal  $s_0$  can be represented by the translated scaling function at a finer scale  $l_0$ , "which can be decomposed to the sum of a coarser approximation  $s_1$  corresponding to the scaling function and the detail part  $d_1$  corresponding to the wavelet functions. This decomposition to a sum of coarser approximation and detail can be continued multiple times, thus resulting in the previously mentioned multi-resolution analysis.

Of course, for image compression applications, it is desirable to extend this transformation to a 2D version, that can be applied to the images before performing the arithmetic coding. Similarly to the DCT, the wavelet transform is also separable, and can be performed as a sequence of 1D transforms along different directions. Separable in a sense, that it does not matter in which order the individual 1D DWTs are applied to get the same 2D transformation.

JPEG [108], JPEG-LS [109] and JPEG2000 [110]

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**3.2.3 Differential pulse code modulation / LOCO-I?**

**3.3 Noise in light microscopy images**

**3.3.1 Photon shot noise**

**3.3.2 Camera noise**

**CCD**

**EM-CCD**

**sCMOS**

**3.3.3 Variance stabilization**

## Chapter 4

# Real-time, GPU accelerated image processing pipeline

### 4.1 GPU architecture

CUDA [111]

### 4.2 Live fusion

#### 4.2.1 MuVi-SPIM

#### 4.2.2 Bead based registration

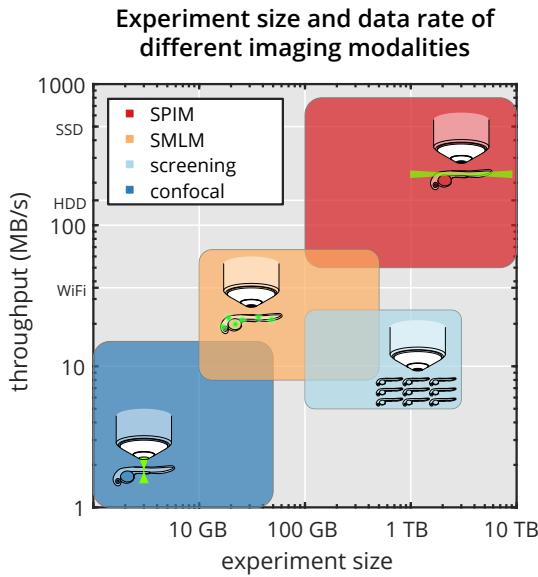
### 4.3 B<sup>3</sup>D image compression

B<sup>3</sup>D image compression high content screening [112–114] light-sheet (Sec. 1.3) single molecule localization microscopy [115–117] data handling is bottleneck [118–120] lossy compression not recommended for microscopy [121] KLB [122] jpeg compression so loss is not perceptible [102] big data viewer [123] Fiji [124]

FLIC [125] SFALIC [126] FELICS [127] Treib terrain editing [128] Treib turbulence [129] square root compression [130] noise and bias in square root compression [131] quantization [132] Anscombe [133] optimal inverse Anscombe [134, 135] optimal inverse generalized Anscombe [136]

## 4. REAL-TIME, GPU ACCELERATED IMAGE PROCESSING PIPELINE

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**Figure 4.1: Experiment sizes and data rate of different imaging modalities.** Comparison of single-plane illumination microscopy (SPIM, red rectangle), high-content screening (light blue), single molecule localization microscopy (SMLM, orange) and confocal microscopy (blue) by typical experiment size and data production rate (see also Table B1).

### 4.3.1 Data sizes in microscopy

### 4.3.2 Compression algorithm

### 4.3.3 Lossless compression performance

### 4.3.4 Swapping for WNL

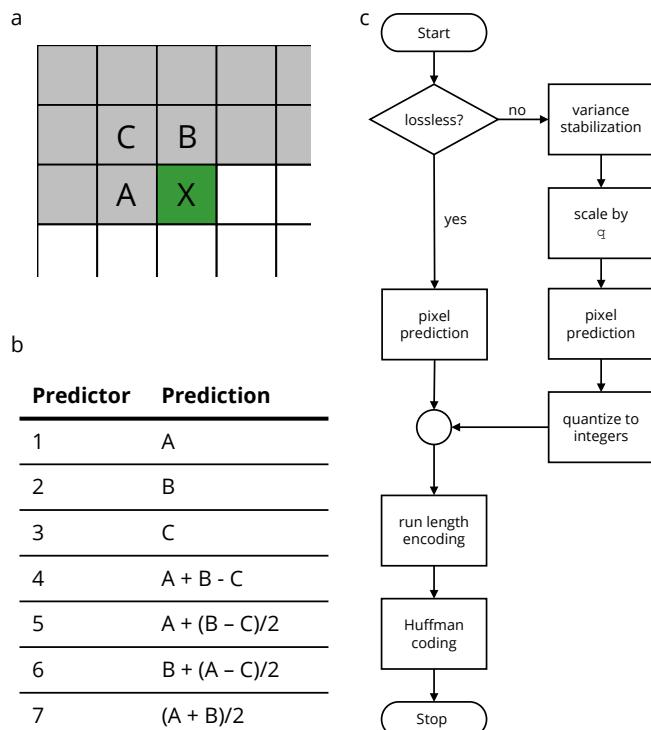
### 4.3.5 Benchmarking

## 4.4 Noise dependent lossy compression

## 4.5 Methods

### Compression benchmarking

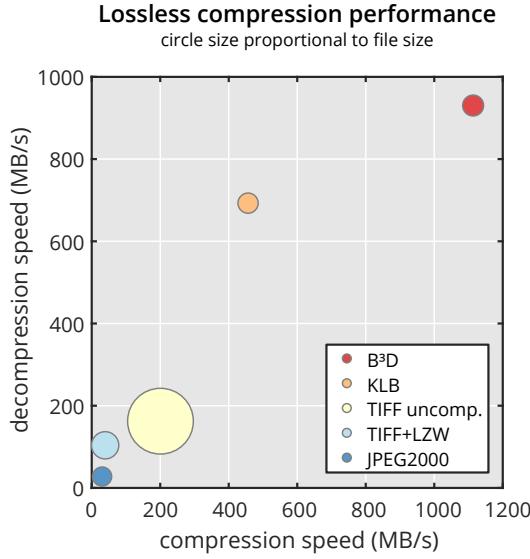
For all presented benchmarks, TIFF and JPEG2000 performance was measured through MATLAB's imwrite and imread functions, while KLB and B<sup>3</sup>D performance was measured in C++. All benchmarks were run on a computer featuring 32 processing cores (2×Intel Xeon E5-2620 v4), 128 GB RAM and an NVIDIA GeForce GTX 970 graphics processing unit. Read and write measurements were performed in RAM to minimize I/O overhead, and are an average of 5 runs.



**Figure 4.2: B<sup>3</sup>D algorithm schematics.** (a) Prediction context for pixel X, the next sample to be encoded. Three neighboring pixels are considered: left (A), top (B) and top left (C) neighbors. (b) Lossless JPEG predictors for X, based on the context showed in (a). The first three predictors are one-dimensional, while the rest are two-dimensional. Using a two dimensional predictor while increases complexity slightly, also increases the achievable compression ratio. We found that for fluorescence microscopy images predictor 7 performs best, hence its inclusion in the B<sup>3</sup>D algorithm. (c) Complete algorithm flowchart depicting the main stages of the compression. First, if the result should be lossless, pixel prediction is performed on the original image values. If within noise level mode is selected, the image noise is stabilized first (see "Supplementary Note"), which is then scaled by the quantization step q. Prediction is performed, and the prediction errors are rounded to the nearest integer. The prediction errors for both lossless and lossy modes are then run-length encoded, and finally Huffman coding is applied to effectively reduce data size. The output of the Huffman coder is saved as the compressed file.

## 4. REAL-TIME, GPU ACCELERATED IMAGE PROCESSING PIPELINE

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**Figure 4.3: Lossless compression performance.** Performance comparison of our B<sup>3</sup>D B<sup>3</sup>D compression algorithm (red circle) vs. KLB (orange), uncompressed TIFF (light yellow), LZW compressed TIFF (light blue) and JPEG2000 (blue) regarding write speed (horizontal axis), read speed (vertical axis) and file size (circle size). (see also Table B2).

### Light-sheet imaging

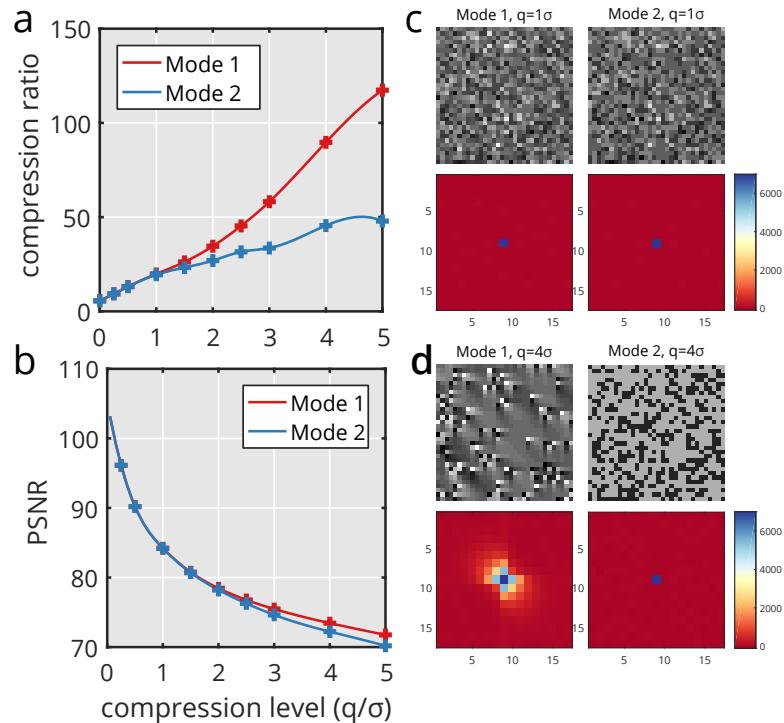
*Drosophila* embryos were imaged in our MuVi-SPIM setup [3] using the electronic confocal slit detection (eCSD) [74]. Embryos were collected on an agar juice plate, and dechorionated in 50% bleach solution for 1 min. The embryos were then mounted in a shortened glass capillary (Brand 100 µl) filled with 0.8% GelRite (Sigma-Aldrich), and pushed out of the capillary to be supported only by the gel.

### 3D nucleus segmentation

3D nucleus segmentation of *Drosophila* embryos was performed using Ilastik [137]. The original dataset was compressed at different quantization levels, then upsampled in z to obtain isotropic resolution. To identify the nuclei, we used the pixel classification workflow, and trained it on the uncompressed dataset. This training was then used to segment the compressed datasets as well. Segmentation overlap was calculated in Matlab ("Supplementary Code") using the Sørensen–Dice index [138, 139]:

$$QS = 2 |A \cap B| / (|A| + |B|) \quad (4.1)$$

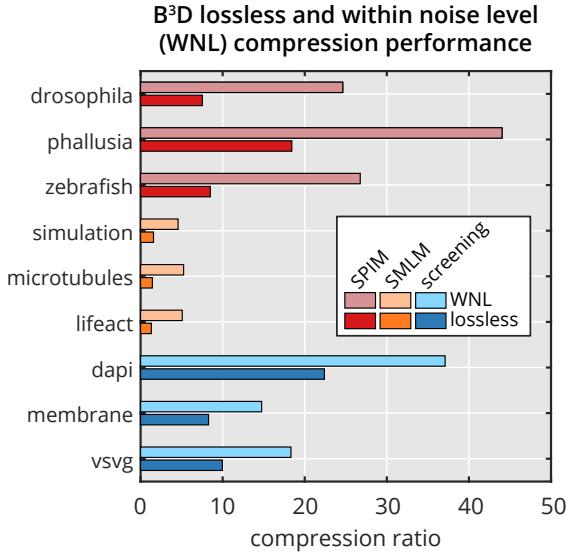
where the sets  $A$  and  $B$  represent the pixels included in two different segmentations.



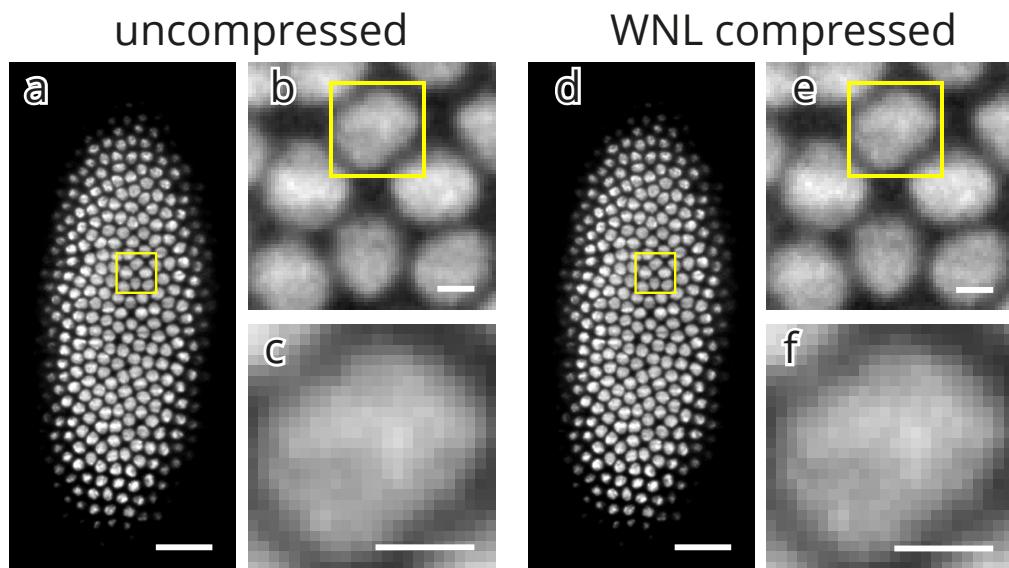
**Figure 4.4: Options for noise dependent lossy compression.** Comparing Mode 1 (prediction then quantization) and Mode 2 (quantization then prediction) of noise dependent lossy compression in terms of compression ratio, peak signal to noise ratio (PSNR) and spatial correlations introduced to random noise. (a) Compression ratio as a function of the quantization step for Mode 1 and Mode 2. (b) PSNR as a function of the quantization step for Mode 1 and Mode 2. (c, d) Random noise was compressed at various quantization steps both for Mode 1 and Mode 2. Autocorrelation was calculated for the compressed images to see whether the compression introduces any spatial correlation between the pixels. For  $q=1\sigma$  both modes are free of correlation (c, top: compressed images, bottom: autocorrelation), however, for  $q=2\sigma$  Mode 1 exhibits a correlation pattern (d, top left: compressed image, bottom left: autocorrelation) that is not present in Mode 2 (d, top right compressed image, bottom right: autocorrelation). For more discussion, see “Supplementary Note”.

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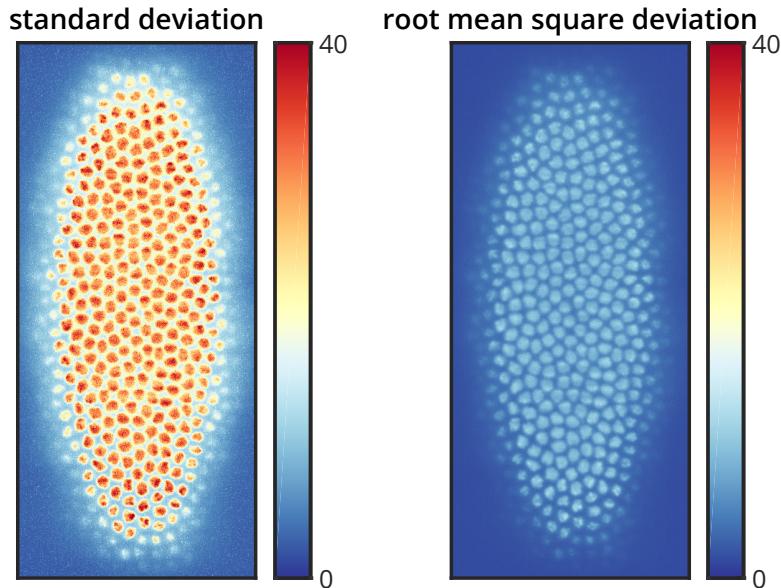
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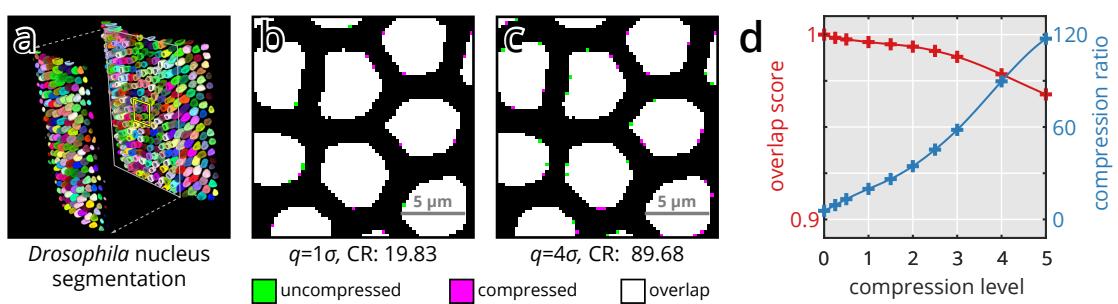
**Figure 4.5:** Within noise level compression performance. WNL compression performance compared with lossless performance for 9 different dataset representing 3 imaging modalities (SPIM, SMLM, screening). Compression ratio = original size / compressed size. For description of datasets see Table B3 in Appendix B.



**Figure 4.6:** Image quality of a WNL compressed dataset. WNL compression performance compared with lossless performance for 9 different dataset representing 3 imaging modalities (SPIM, SMLM, screening). Compression ratio = original size / compressed size. For description of datasets see Table B3.



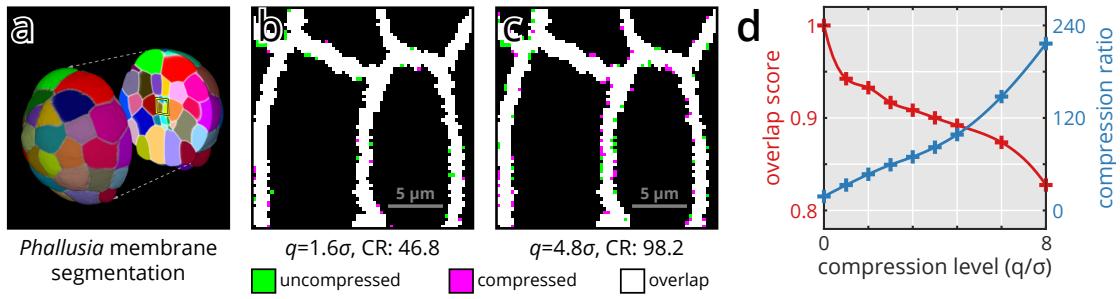
**Figure 4.7: Compression error compared to image noise.** To compare the difference arising from WNL compression to image noise, we imaged a single plane 100 times in a *Drosophila melanogaster* embryo expressing H2Av-mCherry nuclear marker at 38 ms intervals. The whole acquisition took 3.8 s, for which the sample can be considered stationary. To visualize image noise, the standard deviation was calculated for the uncompressed images (left). All images were then WNL compressed, and the root mean square deviation was calculated compared to the uncompressed images (right). The root mean square deviation on average is 3.18 times smaller than the standard deviation of the uncompressed images.



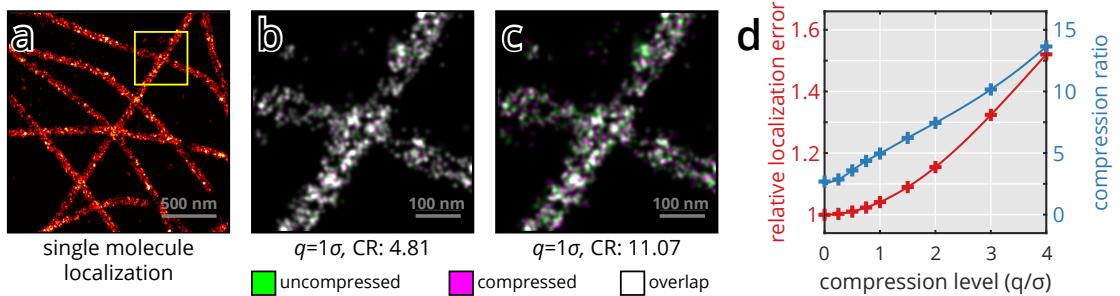
**Figure 4.8: Influence of noise dependent lossy compression on 3D nucleus segmentation.** A *Drosophila melanogaster* embryo expressing H2Av-mCherry nuclear marker was imaged in MuVi-SPIM [3], and 3D nucleus segmentation was performed ("Online Methods") (a). The raw data was subsequently compressed at increasingly higher compression levels, and segmented based on the training of the uncompressed data. To visualize segmentation mismatch, the results of the uncompressed (green) and compressed (magenta) datasets are overlaid in a single image (b, c; overlap in white). Representative compression levels were chosen at two different multiples of the photon shot noise, at  $q=1\sigma$  (b) and  $q=4\sigma$  (c). For all compression levels the segmentation overlap score ("Online Methods") was calculated and is plotted in (g) along with the achieved compression ratios.

## 4. REAL-TIME, GPU ACCELERATED IMAGE PROCESSING PIPELINE

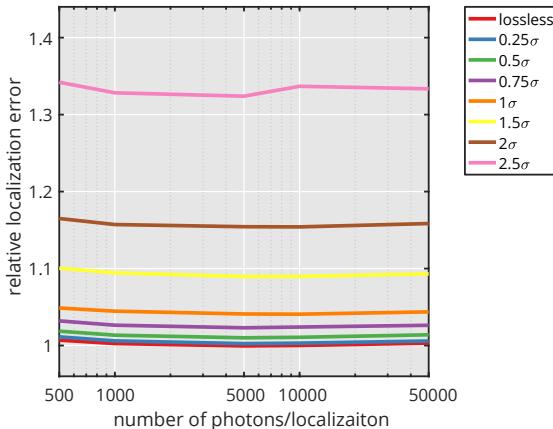
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**Figure 4.9: Influence of noise dependent lossy compression on 3D membrane segmentation.** A *Phallusia mammillata* embryo expressing PH-citrine membrane marker was imaged in MuVi-SPIM [3], and 3D membrane segmentation was performed (“Supplementary Methods”) (a). The raw data was subsequently compressed at increasingly higher compression levels, and segmented using the same settings as the uncompressed data. To visualize segmentation mismatch, the results of the uncompressed (green) and compressed (magenta) datasets are overlaid in a single image (b, c; overlap in white). Representative compression levels were chosen at two different multiples of the photon shot noise, at  $q=1.6\sigma$  (b) and  $q=4.8\sigma$  (c). For all compression levels the segmentation overlap score (“Supplementary Methods”) was calculated and is plotted in (d) along with the achieved compression ratios.



**Figure 4.10: Influence of noise dependent lossy compression on single-molecule localization.** Microtubules, immunolabeled with Alexa Fluor 647 were imaged by SMLM (a). The raw data was compressed at increasingly higher compression levels, and localized using the same settings as the uncompressed data. To visualize localization mismatch, the results of the uncompressed (green) and compressed (magenta) datasets are overlaid in a single image (b, c; overlap in white). Two representative compression levels were chosen at  $q=1\sigma$  (b) and  $q=4\sigma$  (c). To assess the effects of compression on localization precision, a simulated dataset with known emitter positions was compressed at various levels. For all compression levels the relative localization error (normalized to the Cramér–Rao lower bound) was calculated and is plotted in (d) along with the achieved compression factors.



**Figure 4.11: Change in localization error only depends on selected quantization step.** We simulated multiple datasets (“Supplementary Methods”) with different average photon numbers per localization. Background was kept at a constant average of 20 photons/pixel. Datasets were compressed at multiple compression levels (see legend), and localization error relative to the Cramér-Rao lower bound was calculated. The relative localization error only depends on the compression level, and not on the signal to background illumination ratio.

### 3D membrane segmentation

Raw MuVi-SPIM recordings of *Phallusia mammillata* embryos expressing PH-citrine membrane marker were kindly provided by Ulla-Maj Fiúza (EMBL, Heidelberg). Each recording consisted of 4 views at 90 degree rotations. The views were fused using an image based registration algorithm followed by a sigmoidal blending of the 4 views. The fused stack was then segmented using the MARS algorithm [140] with an hmin parameter of 10. The raw data (all 4 views) was compressed at different levels, and segmented using the same pipeline. Segmentation results were then processed in Matlab to calculate the overlap score for the membranes using the Sørensen–Dice index (“Supplementary Code”).

### Single-molecule localization imaging

In order to visualize microtubules, U2OS cells were treated as in [141] and imaged in a dSTORM buffer [142]. In brief, the cells were permeabilized and fixed with glutaraldehyde, washed, then incubated with primary tubulin antibodies and finally stained with Alexa Fluor 647 coupled secondary antibodies. The images were recorded on a home-built microscope previously described [141], in its 2D single-channel mode.

### Single-molecule localization data analysis

Analysis of single-molecule localization data was performed on a custom-written MATLAB software as in [143]. Pixel values were converted to photon counts according to measured offset and calibrated gain of the camera (EMCCD iXon, Andor). The back-

## **4. REAL-TIME, GPU ACCELERATED IMAGE PROCESSING PIPELINE**

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ground was estimated with a wavelet filter [144], background-subtracted images were thresholded and local maxima were detected on the same images. 7-pixel ROIs around the detected local maxima were extracted from the raw images and fitted with a GPU based MLE fitter [145]. Drift correction was performed based on cross-correlation. Finally, images were reconstructed by filtering out localizations with a high uncertainty ( $>30$  nm and large PSF ( $>150$  nm) and Gaussian rendering.

### **Simulation of single-molecule localization data**

Single molecule localization data was simulated in Matlab ( "Supplementary Code") by generating a grid of pixelated Gaussian spots with standard deviation of 1 pixel. With a pixel size of a 100 nm, this corresponds to a FWHM of 235.48 nm. The center of each spot was slightly offset from the pixel grid at 0.1 pixel increments in both x and y directions. To this ground truth image a constant value was added for illumination background, and finally Poisson noise was applied to the image. This process was repeated 10000 times to obtain enough images for adequate accuracy.

### **Code availability**

Code used for analyzing data, B<sup>3</sup>D source code and compiled binaries, including a filter plugin for HDF5, is available for download at <https://git.embl.de/balazs/B3D>.

# Chapter 5

## Discussion

### 5.1 New scientific results

**Thesis I.** *I have designed and constructed a new light-sheet microscope suitable for high sensitivity imaging of delicate samples. A novel arrangement of two high numerical aperture objectives in 120 degrees allows for near isotropic resolution while increasing light collection efficiency by a factor of two.*

Corresponding publications: [J3], [J2], [J1]

Live imaging of light sensitive specimens, such as a developing mouse embryo is a challenging task

**Thesis II.** *I have developed a GPU-based image processing pipeline for multi-view light-sheet microscopy that enables real time fusion of opposing views.*

Corresponding publications: [C1], [C2], [C3]

**Thesis III.** *I have developed a new image compression algorithm that enables noise dependent lossy compression of light microscopy images, and can reach a compression ratio of 100 fold while preserving the results of downstream data analysis steps.*

Corresponding publications: [J4], [C1], [C2], [C3]

All microscopy images contain inherent noise, that is

**Thesis IV.** *I have developed a new GPU-based image compression library,  $B^3D$ , that implements the algorithm described in Thesis III, and allows for real time compression of microscopy images with a throughput of up to 1 GB/s.*

Corresponding publications: [J4], [C1], [C2], [C3]

$B^3D$  is an efficient, GPU-based image compression library allowing lossless and noise dependent lossy compression of microscopy images. Since many high-speed microscopy

## **5. DISCUSSION**

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methods generate immense amounts of data, easily reaching terabytes per experiment, image compression is especially important to efficiently deal with such datasets.

# Acknowledgements

## **ACKNOWLEDGEMENTS**

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# Appendix A

## Bill of materials

### Bill of Materials

#### Optical components

- Lenses
  - 2×Nikon CFI75 Apo LWD 25x/1.10w water dipping objectives
  - 2×Nikon ITL200 200 mm tube lens
  - 2×200 mm x 25 mm Dia. achromatic lens (Edmunds Optics, #47-645)
  - 2×400 mm x 40 mm Dia. achromatic lens (Edmunds Optics, #49-281)
  - 2×75 mm x 25 mm Dia. achromatic lens (Edmunds Optics, #47-639)
- Filters
  - 2×BrightLine quad-edge dichroic beam splitter (Semrock, Di03-R405/488/561/635-t3-25x36)
  - EdgeBasic 488 nm long pass filter (Semrock, BLP01-488R-25)
  - BrightLine 525/50 band pass filter (Semrock, FF03-525/50-25)
  - EdgeBasic 561 nm long pass filter (Semrock, BLP02-561R-25)
  - RazorEdge 647 nm long pass filter (Semrock, LP02-647RU-25)
- Mirrors
  - 6×1” Broadband Dielectric Elliptical Mirror (Thorlabs, BBE1-E03)
  - 2×30 mm Broadband 1/10λ Mirror (OptoSigma, TFMS-30C05-4/11)
  - 10 Pack of 1” Protected Silver Mirrors (Thorlabs, PF10-03-P01-10)
  - Knife-Edge Right-Angle Prism Dielectric Mirror (Thorlabs, MRAK25-E02)

#### Mechanical components

- 40 mm travel range pneumatic cylinder (Airtac, HM-10-040)
- 5/2-way electric valve (Airtac, M-20-510-HN)
- 2×25 mm extended contact bearing steel stage (OptoSigma, TSDH-251C)
- 30x90 mm stainless steel slide (OptoSigma, IPWS-F3090)
- close proximity gimbal mirror mount (Thorlabs, GMB1/M)
- 30 mm cage elliptical mirror mount (Thorlabs, KCB1E)

## **APPENDIX A**

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### **Custom parts**

All parts are (anodized) aluminium, unless stated otherwise.

- 2×mirror holder block
- Front plate for objective, chamber and mirror mounting
- Imaging chamber (PEEK)
- Wedge ring and matching threads to fasten objectives
- Camera bridge
- Illumination splitter unit
- adapter plates to mount stages

### **Electronics**

- Embedded system (National Instruments, cRIO-9068) equipped with:
  - 2×C series digital I/O card (NI 9401)
  - 1×C Series 100 kS/s 4-channel Voltage Output Module (NI 9263)
  - 1×C Series 25 kS/s 16-channel Voltage Output Module (NI 9264)
- Omicron SOLE-3 laser combiner, with 488, 561 and 638 nm laser lines
- Andor Zyla 4.2 sCMOS Camera
- Galvanometric scanner mirror (Cambridge Technology, 6210B)
- 6 position filter wheel (Ludl Electronic Products, 96A361)
- Filter wheel controller unit (Ludl Electronic Products, MAC5000)
- 2 piezoelectric stages (Nanos Instruments, LPS-30-30-1-V2\_61-S-N)
- 2 stage controller boards (Nanos Instruments, BMC101)

# **Appendix B**

**Data sizes in microscopy**

**Lossless compression performnace**

**Benchmarking datasets**

## APPENDIX B

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	imaging device	image size	frame rate	data rate	data size
<b>SPIM</b>	2x sCMOS camera (e.g. Hamamatsu ORCA Flash4.0)	2048x2048	50/s	800 MB/s	10 TB
<b>SMLM</b>	2x EMCCD camera (e.g. Andor iXon Ultra 897)	512x512	56/s	56 MB/s	500 GB
<b>screening</b>	CCD camera (e.g. Hamamatsu ORCA-R2)	1344x1024	8.5s/	22 MB/s	5 TB
<b>confocal</b>	Zeiss LSM 880, 10 channels	512x512	5/s	12.5 MB/s	50 GB

**Table B1: Data sizes in microscopy.** Typical devices used for confocal microscopy, high-content screening, single-molecule localization microscopy and light-sheet microscopy and their data production characteristics. Data visualized on Figure 4.1

	write speed	read speed	CR	file size
<b>B<sup>3</sup>D</b>	1,115.08 MB/s	928.97 MB/s	9.861	100%
<b>KLB</b>	283.19 MB/s	619.95 MB/s	10.571	93.28%
<b>JPEG2000</b>	31.94 MB/s	26.38 MB/s	11.782	83.69%
<b>JPEG2000</b>	202.32 MB/s	161.08 MB/s	1.00	986.1%
<b>TIFF + LZW</b>	40.85 MB/s	102.37 MB/s	5.822	169.37%

**Table B2: Lossless compression performance.** B<sup>3</sup>D is compared with various popular lossless image compression methods regarding write speed, read speed and compression ratio (original size / compressed size). Data visualized on Figure 4.3.

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<b>Dataset name</b>	<b>Imaging modality</b>	<b>Description</b>	<b>Size (MB)</b>
<b>drosophila</b>	SPIM	dataset acquired in MuVi-SPIM of a Drosophila melanogaster embryo expressing H2Av-mCherry nuclear marker	494.53
<b>zebrafish</b>	SPIM	dataset acquired in MuVi-SPIM of a zebrafish embryo expressing b-actin::GCaMP6f calcium sensor	2,408.00
<b>phallusia</b>	SPIM	dataset acquired in MuVi-SPIM of a Phallusia mammillata embryo expressing PH-citrine membrane marker	1,323.88
<b>simulation</b>	SMLM	MT0.N1.LD-2D simulated dataset of microtubules labeled with Alexa Fluor 647 from SMLMS 2016 challenge	156.22
<b>microtubules</b>	SMLM	microtubules immuno-labeled with Alexa Fluor 674-bound antibodies in U2OS cells	1,643.86
<b>lifeact</b>	SMLM	actin network labeled with LifeAct-tdEOS in U2OS cells	3,316.15
<b>dapi</b>	screening	wide field fluorescence images of DAPI stained HeLa Kyoto cells [146]	1,005.38
<b>vsvg</b>	screening	wide field fluorescence images of CFP-tsO45G proteins in HeLa Kyoto cells [146]	1,005.38
<b>membrane</b>	screening	wide field fluorescence images of membrane localized CFP-tsO45G proteins labeled with AlexaFluor647 in HeLa Kyoto cells [146]	1,005.38

**Table B3: Datasets used for benchmarking compression performance.**

## **APPENDIX B**

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