

TU DRESDEN

ADVANCED PRACTICAL COURSE

LAB REPORT

Biomolecular Motors

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1 Introduction

1.1 Kinesin-1: Cell's workhorses

All life forms in our universe are made of cells. To understand the mechanisms in and between those elementary building blocks of life is a real fundamental aim of biology, biochemistry and biophysics. But understanding these tiny but really complex structures also means understanding thousands of finely tuned mechanisms that are essential for survival of a cell. One necessary condition for most of these processes is a *directional* (not statistical!) motion of cell components. For example the segregation of chromosomes during cell division would not work with brownian motion alone. Fortunately there are so called *motor proteins* as kinesin, dynein and myosin that are responsible for this kind of motion appearing in many transport-mechanisms.

In the following experiment we will investigate *kinesin-1*, a motor protein moving along *microtubule* filaments. For that purpose we will measure their velocity and the mean run length. But at first some basic knowledge.

Microtubules (MTs) are a component of the cytoskeleton that can be depicted with the "cell's highway" because they form basically the ground where the motorproteins can walk on. Their basic building blocks are the $\alpha - / \beta$ -tubulin heterodimers that polymerise longitudinally in an periodic structure with a repeat-length of 8 nm. They form a structure of hollow-cylinders having an outer diameter of 25 nm. Because the binding between the subunits is reversible MTs show a highly dynamic growing behavior that is necessary to build those "roads" as flexible as possible. Later we have to surpass this effect. The directed motion on the MTs is enabled by the structural polarity of the tubulin-dimers. Figure 1 shows the strucutre of the MTs.[01]

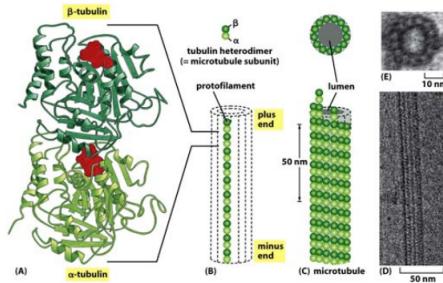


Figure 1: Structure of the microtubules[01]

Kinesin-1 is a motor-protein that moves along the MT transporting different types of cargo (e.g. vesicles, mitochondria, chromosomes) in the cells. It consists of two identical subunits that are winded into each other. For the motion from the minus-end to the plus-end of the MTs it uses the strucutural polarity of the tubulin-subunits binding its motor domain just to the β -tubulin parts. So it moves in discrete steps of $\Delta x = 8$ nm exerting a force of $F = 5$ pN to the MT-surface powered by the hydrolysis of an ATP-molecule during each step. The ATP-hydrolysis leads to an energy-emission of $E_{ATP} = 101 \cdot 10^{-21}$ J while the motorproteins do a work of $W_{MP} = F \cdot \Delta x = 4 \cdot 10^{-20}$ J. This means an efficiency of $\eta = W_{MP}/E_{ATP} = 39.60\%$.[01] The mechanochemical cycle of kinesin-1 is visualised in Figure 2:

1.2 Fluorescence Microscopy

In Flourescence microscopy the emission of light by an marked assay is used. More accurate, an electron in an excited singlet state in an excited orbital in a molecule is paired by the contrary spin to the second electron in the ground-state orbital. The return to the ground state is allowed by spin

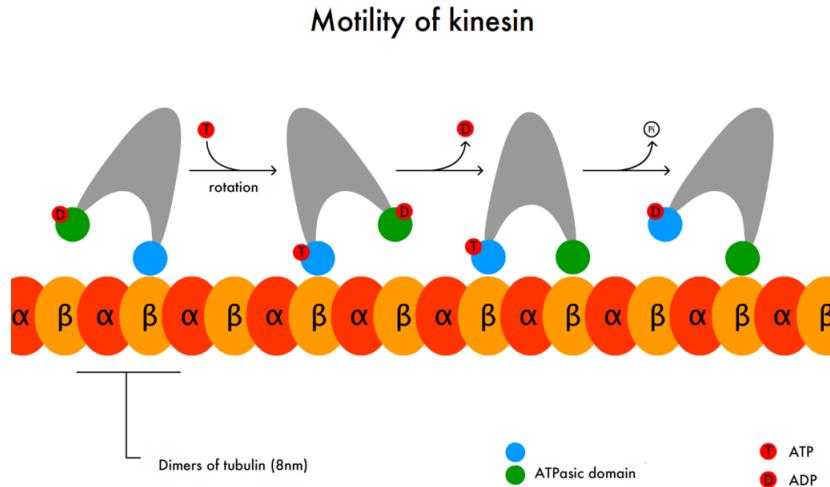


Figure 2: Mechanochemical cycle of Kinesin-1:
Absorbing of ATP, Emitting of ADP, ATP Hydrolysis[03]

(pauli principle). This appears rapidly with an emission rate of about 10^8 s^{-1} by the emmission of a photon.

1.2.1 Flourescent markers

There are two types of flourescent markers: intrinsic and extrinsic. The intrinsic ones appear naturally in the sample (for example chlorophyll). Extrensic markers are added to the probes, when flourescence does not appear naturally (e.g. flourescein). In a conjugated p-electron-system they have delocalized electrons. In this system, the first excitation energy of the molecule is comparatively low, so it can be stimulated by visible light. In this expermient, microtubules where marked with rhodamine and the motor proteins by green flourescence protein (GFP).

1.2.2 Total internal reflection Flourescence Mircroscopy

Total internal reflection flourescence (TIRF) microscopy is used in this experiment. The base of this methodology is the total internal reflection. It can be detected when a beam of light travels from a medium with high refractive index to a medium with a low one under an angle bigger than the critical angle α_c . Even though the beam is totally reflected, a field is generated, which decays exponentially. It reaches typically 100 nm into the medium with the lower refractive index. This distance is useful, because it naturally creates a way to limit the volume where flourophores get excited. Instead of the illumination of the whole probe, which would create some noise, lower the contrast between the probes and the background (because the background is also illuminated), it reduces the background illumination and increase the contrast between the assays one wants to see and the background.

2 Experimental procedure

2.1 Making of the Kinesin-1-stepping assay

We started the experiment with preparing the specimen that is visualised schematically in Figure 3. For that we got a hydrophobic object holder where several organic substances later will bind to. Two

flow channels were formed by placing 3 stripes of some synthetic material on the slide that seal the channels under the coverslip after a short heating procedure. Then these channels were flooded by several chemicals. At first we filled in the *BRB80* buffersolution. That is necessary to hold the pH-Value approximately constant. Then we put the *Anti- β -tubulin antibodies* in the channel that bind the microtubules to the surface of the object holder. The experiment of our group unfortunately failed probably because of using a too thin antibody-solution in this step. For hindering proteins other than the microtubules to bind to the surface of the slide we now wash the channel with some blocker-substances: *F127* and *Casein*. Because microtubules are highly dynamic filaments we have to stabilise them some how. For this purpose we combine our BRB buffersolution with *taxol* that prevents the depolymerisation of tubulin. So finally we can put the rhodamine-labeled *microtubules* and the *kinesin-1 motorproteins* that are dyed with GFP in the channel. The kinesin-solution is enriched with *MgATP* that is the 'fuel' of the motorprotein's motion. Additionally a *glucose-based antifade-cocktail* is used to suppress the reaction of free-radicals created by strongly excited fluorophores with free-oxygen of about a factor 2. This is necessary to reduce the photobleaching and the damaging of the proteins.

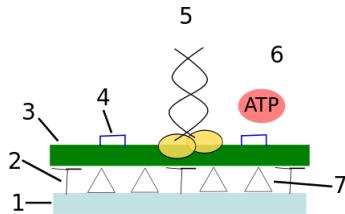


Figure 3: Schematic sketch of the stepping assay.

1-Hydrophobic slide, 2-Anti- β -tubulin antibody,

3-MT, 4-Taxol stabilisator, 5-motor-protein,

6-ATP - 'fuel', 7-block substances (F127, Casein)

Now we are ready for taking the movies of our stepping-assay.

2.2 Stream acquisition

First the experimental supervisor placed the flow cell holder on the microscope stage. We used an oil objective which has to touch the bottom of the flow cell. The objective has a magnification of 100x and a numerical aperture of 1,46. After the assay was fixed we used a Software called MetaMorph. We chose the camera button. We used a digital Camera by Andor which took greyscaled pictures. Its resolution is 2.6 MPixel with 512x512 pixels. The size of one pixel ist $256 \mu\text{m}^2$. According to the meta data of the movies and pictures the chosen additional magnification of the camera is 1.0x. This means, the pixel size is the original pixel size of the camera. If it had been 2.5x, we could have seen 2.5 times less, so a pixel would have been $A = 256 \mu\text{m}^2 / 2.5 = 102.4 \mu\text{m}^2$. So we took the TRITC filter and the lamp on the taskbar and watched the live images token by the camera. We searched and focused a cutout where we could see enough MTs. Unfortunately our assay showed that no MT's were fixed in it, so we could not take any pictures. Maybe this was caused by a too thin microtubule- or antibody-solution. We used the assay of our co-workers instead.

After we focused the MTs, we stopped live imaging and took pictures of the MTs luminescated by rhodamine. After that we take the GFP filter and choose the laser illumination. Then we choose again live imaging ("show live"). The TIRF angle will be adjusted. Again we choose the TRITC filter on the taskbar, the lamp illumination and take live imaging. We move to a new field of view, focus properly and take an image of the MTs such as in figure 4.

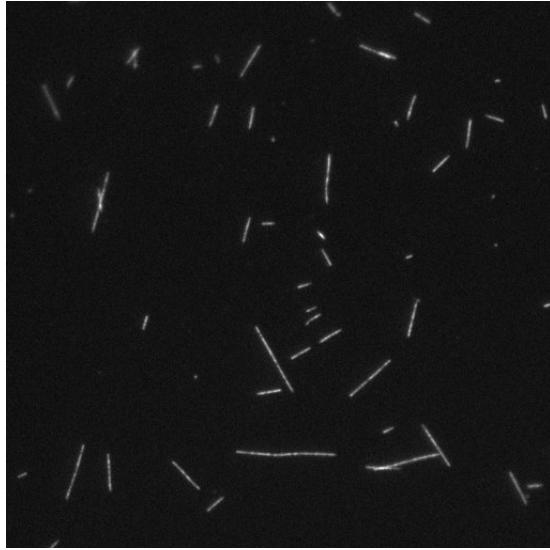


Figure 4: Example of an image, where we focused on the MTs

Then we save an image of this position. We now switched again to the GFP filter, selected the laser as light source and take live imaging. We can see moving motors. We stop live imaging and take a movie via the acquire button. The number of frames we took is 1000. For one frame the camera needs 150 ms, so at the end one we wait 150 s per video stream. We took 8 movies. When all streams are collected, one can do the data processing with FIESTA. There you can mark the possible trajectories of the motor proteins (as seen in figure 5) and the software will calculate pieces of the picture where the height is the time dimension and the width is the movement. If there is motion, one can mark up the lines and get the time which was needed for the marked distance (see figure 6).

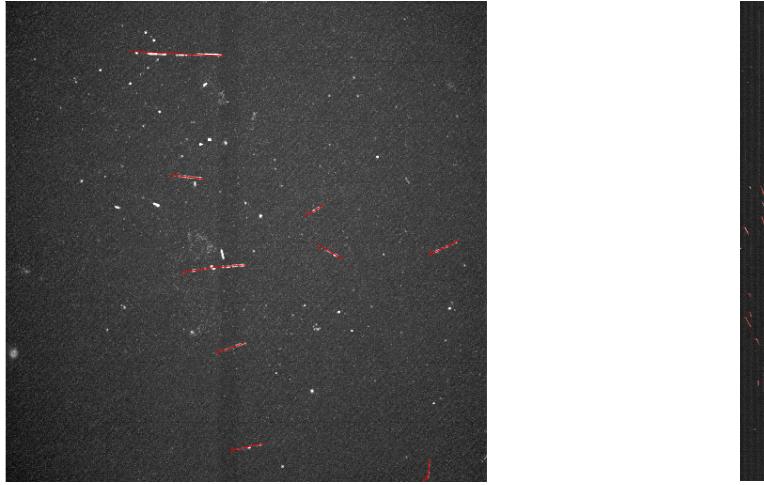


Figure 5: first step marking of the micro-tubules

Figure 6: marking of the trajectories of the motor proteins

3 Data Analysis

According to the data evaluation, we got $N = 204$ events. That means, we got 204 times a distance, a time and a velocity which are distributed.

3.1 Data evaluation of velocity

We think, the velocity is a gaussian distribution. This assumption can be proven by a student's t-test. But we only have one set of data.

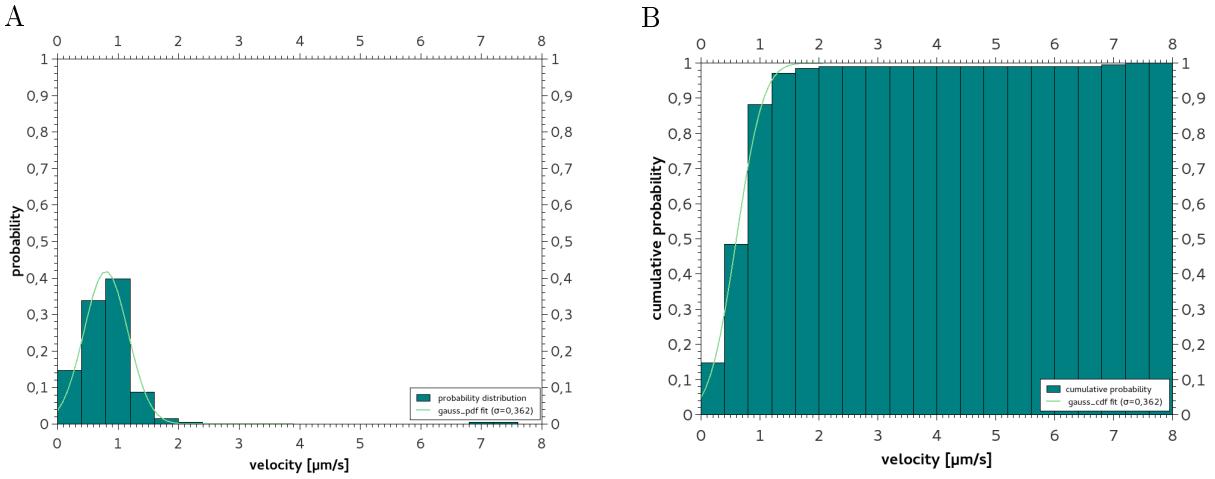


Figure 7: **A:** Histogram of the relative velocity distribution. **B:** Histogram of the cululative velocity distribution

The mean of the velocity \bar{v} , its standard deviation $\sigma_{\bar{v}}$ and the standard error of the mean velocity $\Delta\bar{v}$ can be calculated by a data analysis tool. We used an Origin like software called qtiplot, which calculates column statistics, which are not influenced by binning, because that are the measured raw data. These include the searched values. In general one can calculate these values as following:

$$\bar{v} = N^{-1} \sum_{i=1}^N v_i, \quad \sigma_{\bar{v}} = \sqrt{\sum_{i=1}^N \frac{(v_i - \bar{v})^2}{N-1}}, \quad \Delta\bar{v} = \frac{\sigma_{\bar{v}}}{\sqrt{N}}$$

So we get:

$$\bar{v} = (0.87 \pm 0.05) \frac{\mu\text{m}}{\text{s}}, \quad \sigma_{\bar{v}} = 0.72 \frac{\mu\text{m}}{\text{s}}$$

To minimize the error one could easily take more measurements. According to the law of large numbers the measured mean velocity would converge to the expactation value. With an infinite number of measurements we would get the exact result. Also we could use software which marks the traces, which would create a unit law of marking. As a human being, one cannot see every trace and one can not mark every trace the way. This is caused by a diameter of the traces which is not infinite. The means, one could easily stretch the distance walked by the kinesin by marking from on edge to the diagonal opposite edge. An automation would avoid these errors.

3.2 Data evaluation of run length

Now we are going to figure out what distance D a motorprotein covers on a single microtubule before releasing itself. For that we also use the data acquired by the streamed films. One frame of the stream corresponds to 150 ms. With that and the determined velocity $\bar{v} = (0.87 \pm 0.05) \mu\text{m/s}$ we can calculate the minimal distance we can measure with our streaming-system (and also the minimal bin-size): $d_{min} = \bar{v} \cdot 1 \text{ FRAME} = 0.12 \mu\text{m} \cong 0.2 \mu\text{m}$. Therefore all of the measured distances which are below that value cannot be reasonable and they will be ignored in our statistics - anyway they will appear as first bin in the histogram for the sake of completeness. We rounded the value of d_{min} up because we want to choose a smooth bin-width. Finally we decided the bin width to be $w_{bin} = 0.4 \mu\text{m} \cong 2 \cdot d_{min}$. We estimated this using the **Square-root choice**[02] which says that the number of bins is $k = \lfloor \sqrt{N} \rfloor$ where $N = 204$ is the number of samples.

Considering these facts we got the following results. At first the mean distance and its statistical error:

$$\bar{D} = (1.1 \pm 0.1) \mu\text{m}$$

The figures (8) and (9) visualise the distribution of the measured distances:

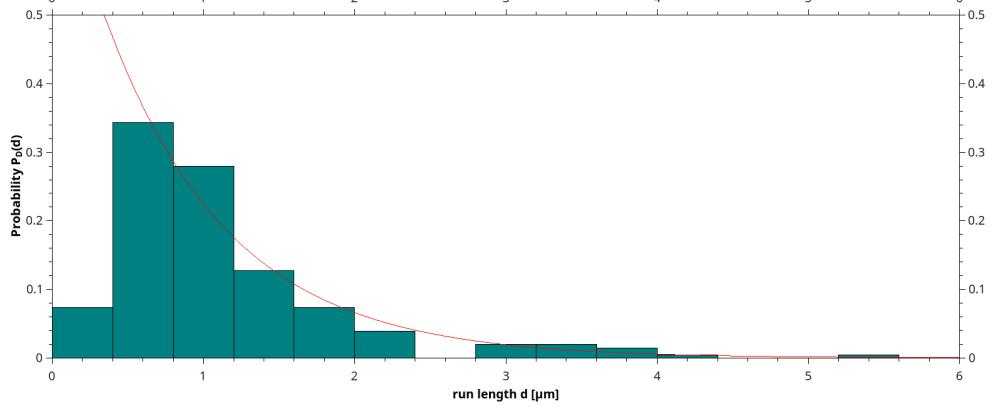


Figure 8: Probility distribution of the measured run length.

The very first bin is ignored from the exponential fitting

Because all invalid values fall into the first bin, it will be disregarded in the exponential fit of the probability function $P_D(d)$ and in the cumulative probability. We consider this fact by using an offset $d_0 = w_{bin} = 2 \cdot d_{min} = 0.4 \mu\text{m}$ in the exponential fit of the probability distribution. So the fit equation becomes:

$$P_D(d) = A \cdot e^{-\kappa \cdot (d-d_0)}$$

with the fit parameters:

$$A = 0.37 \pm 0.02$$

$$\kappa = (1.2 \pm 0.1) \mu\text{m}^{-1}$$

$$d_0 = 0.4 \mu\text{m} = \text{const.}$$

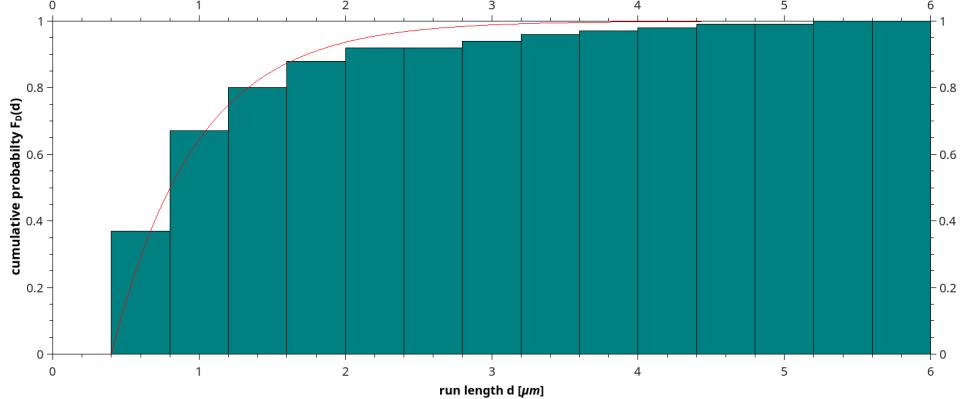


Figure 9: Cumulative probability disregarding the 'invalid' values with $d < d_0$

For the cumulative distribution function $F_D(d) = P_D(D \leq d)$ we use the fit equation:

$$F_D(d) = 1 - e^{-k \cdot (d-d_0)}$$

and extract the fit parameters:

$$k = (1.7 \pm 0.4) \mu\text{m}^{-1}$$

$$d_0 = 0.4 \mu\text{m} = \text{const.}$$

With that equation we can choose an arbitrary confidence level $F_D(d) \stackrel{!}{=} \pi(d) \in [0, 1]$ which gives the probability of the run length D to be less or equal than given d . If we invert this function we

get the *characteristic run length* $d = \pi^{-1}(\pi(d))$:

$$d(\pi) = d_0 + \ln((1 - \pi)^{-1/k})$$

$$\Delta d(\pi) = \left| \frac{\partial d}{\partial k} \Delta k \right| = \left| \frac{\Delta k}{k} \cdot (d_0 - d) \right|$$

We calculate this length for some characteristic values of π that correspond to the confidence levels of the Gaussian normal distribution for finding the value of the random variable x in an intervall around the exepnected value: $x \in [-n\sigma + \mu, n\sigma + \mu]$, $n = 1, 2, 3$:

n	π	$d(\pi)$ [μm]	$\Delta d(\pi)$ [μm]
1	0.6827	1.1	0.2
2	0.9545	2.2	0.4
3	0.9973	3.9	0.8

We prefered the cdf-method to the pdf-method because we can check our result for given π just by looking at the histogram without an additional integration. The deviation of the pdf-fit with respect to the histogram is also larger than in the cdf. We could minimise the error Δd easily by taking more samples. We also should have avoided motorprotein-trajectories that are too 'short' to minimise the amount of values within the first bin. Also the magnification of the camera could be choosed larger to follow the trajectories better in the software.

4 Discussion and conclusions

In this experiment we quantified the *velocity* v and the characteristic *run length* d (confidence level: 68.27 %) of *Kinesin-1 motor proteins* by doing a kinesin-1 stepping assay:

$$v = (0.87 \pm 0.05) \mu\text{m/s}$$

$$d = (1.1 \pm 0.2) \mu\text{m}$$

Those results fit good to the values given in literature: $v_{lit} = 0.8 \mu\text{m/s}$ [01] and $D_{lit} = 0.8 \mu\text{m}$ [04].

5 Appendix

6 References

References

- [01] S. Diez. *Advanced practical course - Experiment MMC*, Dresden, 2015
- [02] <https://en.wikipedia.org/wiki/Histogram> [November 20, 2015]
- [03] <https://en.wikipedia.org/wiki/Kinesin> [November 22, 2015]
- [04] C.Leduc et al. *Detection of fractional steps in cargo movement by the collective operation of kinesin-1 motors*. Stanford. May 2007