

Experiment protocol

Biomolecular Motors: From Cellular Function to Nanotechnology

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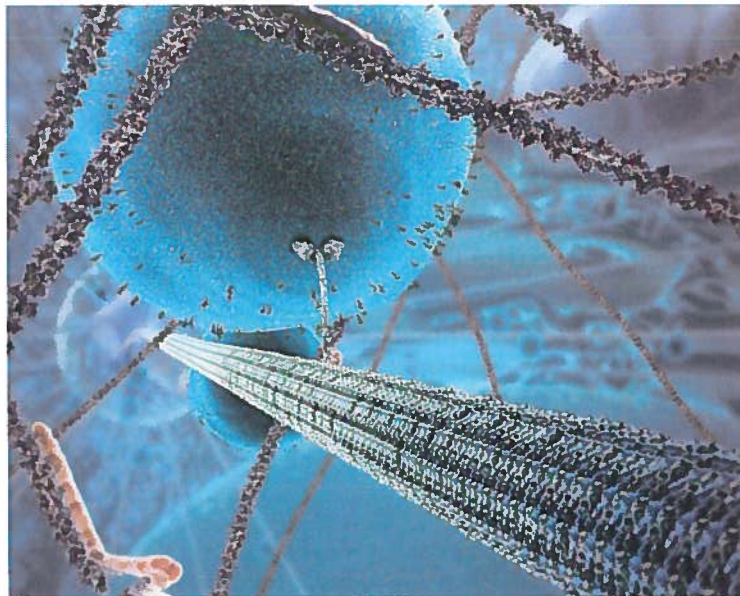


Figure 1: Kinesin-1 with cargo on microtubules [2]

Nice one!

1

- You understood what we did nicely
- The format of the presented evaluation was good!
- There were some small flaws with the statistics.
- Your english can be a bit improved.
- overall great 8.5 points

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1 Basics

Proteins are the basis of every living organism. They perform all types of work inside the cells. In this experiment, the interaction of the cytoskeletal motor protein kinesin-1 with microtubule filaments is investigated at two different temperatures. Most of the following principles are described in the used script. [1]

1.1 Microtubules

Microtubules are hollow polymer-cylinders. They are highly dynamic filaments, always shrinking or growing, which serve as tracks for active intercellular transport. Microtubules consists of tubulin subunits, which give the tubules a plus and minus end, which allow a directed transport. A illustration of them can be seen in figure 1. *→ where is figure 1? ah ok u*
In this experiment, the dynamic of the tubules is stopped by Taxol, which connects to the ends of them. The microtubules are labeled with rhodamine to provide red fluorescence for observation. ✓

1.2 Kinesin-1

Kinesin-1 is a motor protein which transports cargo around the cell. It consists of two identical, connected subunits which both have a head, a stalk and a tail, as can be seen in figure 1. *no two head units with one stalk + tail*
The head serves as motor, the tail as cargoholder.

The movement of kinesin-1 is accomplished through bipedal walk along microtubules: one head moves in front, the other stays connected to the microtubule. For each step, the kinesin-1 "consumes" one ATP-molecule to deliver the required energy. In this way the protein manages to accomplish a velocity of $0.8 \mu\text{m/s}$. However, with a probability of 1% both heads disconnect, resulting in a detachment of the microtubule after an average way length of $0.8 \mu\text{m}$.

In this experiment, the kinesin-1 proteins are labeled with GFP to provide green fluorescence. The used assay is a stepping assay, meaning that the kinesin-1 walk on the affixed microtubules. ✓

1.3 Fluorescence microscopy

To investigate the proteins fluorescence microscopy is used. The rhodamine and the GFP are excited by light: One of their electrons enters an excited orbital. This electron has the opposite spin of the remaining electron in the ground-state orbital. The molecules begin to vibrate and lose thermic energy in the process. After around 10^{-8} seconds the excited electron jumps back to the ground state and emits a photon. Because of the lost energy, the emitted photon has a larger wavelength then the absorbed one and can *was; always use past tense.*

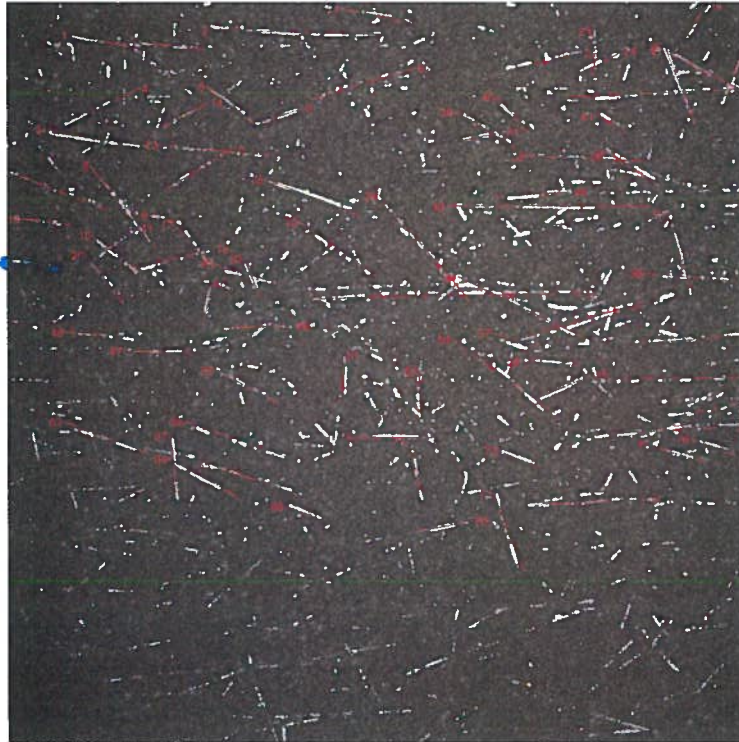
2 Experimental procedure

↑ always use the same description

be distinguished from the laser light. Through this the tubules and proteins with the excited molecules can be observed.

To limit the fluorescing volume and gain a clearer picture, Total Internal Reflection Fluorescence Microscopy is used. The exciting laser light is totally reflected before they enter the object. However, an evanescent wave still enters the object. Thus, only the first few microtubules and kinesin-1 are illuminated.

coverslip surface



* better say only objects in close distance (e.g. ~200nm in z) are illuminated.

Figure 2: Marking of microtubules in FIESTA for analysis

2 Experimental procedure

was investigated

The movement of kinesin-1 has to be researched at two different temperatures: 25°C and 37°C. At first one prepares a flow-cell: two pieces of glass – one hydrophobic, one hydrophilic to provide a better flow of the liquids – are fused with 3 pieces of parafilm to form two channels (one as a backup). Then the channels are flushed with BRB80 – this is done after every flushing, to wash the channels, keep them wet and provide a good environment for the experiment. Afterwards Anti-Tubulin antibodies, to bind the microtubules in the channels, and F127, to prevent the binding of the kinesin-1 with the glass, is injected next. After this the microtubules, are flushed in. After a waiting

↓ now we waited

3 Data and analysis

time of around 1h the kinesin-1 final solution, which includes the kinesin-1, ~~nutrients~~ for both the microtubules and the kinesin-1 and ATP for the movement of the kinesin-1, is injected into the channel.

antibody cocktail + ATP
observe the stepping of kinesin-1 molecules on MTs we used ...

To see the behaviour the samples are researched with a TIRF-microscope with a magnification of 100x and a camera pixel-size of $16 \mu m^2$. At first a ~~photo~~ of the microtubules is taken at normal light, to determine the position of the microtubules. After this a 1000-frames video is taken under green laser light, to see the movement of the kinesin-1. The data-analysis is done using the FIESTA-program which is contributed. The clearly visible positions of the microtubules are manually marked, as one can see in figure 2. After that the computer will track of moving particles on those lines, and trajectories have to be selected by hand. One example can be seen in figure 3. For each temperature 200-500 recognizable trajectories of the kinesin-1 are marked. The program FIESTA then calculates the velocity and run-length from those trajectories, using the vertical axis as time and the horizontal axis as place.

was acquired

its blue but green emission

3 Data and analysis

and tracks of kinesin-1

? During After During TIRF-exposure, ...

After the laserlight shone on our probes, the microtubules dissolved. This happened both for the main and the backup-channel of the flow-cell. Because time was short, the experiment couldn't be redone. The reason for this problem was probably the kinesin-1 final solution (which contained ~~nutrients~~ and stabilizers), which was tarnished, even though this solution was reproduced after the first failure. Because the second group, which did their experiment on the same day, had the same problem, it probably wasn't an experimentation error, but the basic liquids were suspected to be tarnished. As we had no usable experimental data of ourselves, the following data-analysis is performed with data of a former group. The extraction of the data by using FIESTA was performed by us. ✓

We acquired the following amount of movement incidents:

25°C : 546

37°C : 513 ✓

3.1 Velocity

Histograms of the velocities are shown in figure 4. They resemble normal distributions, however, the performance of a Shapiro-Wilk-test gives back a value of $W = 0.8$, which isn't enough to verify this claim. Other tests gave similar results. However, from a thermodynamical view this distribution has to be normal. To make sure that this is

is not

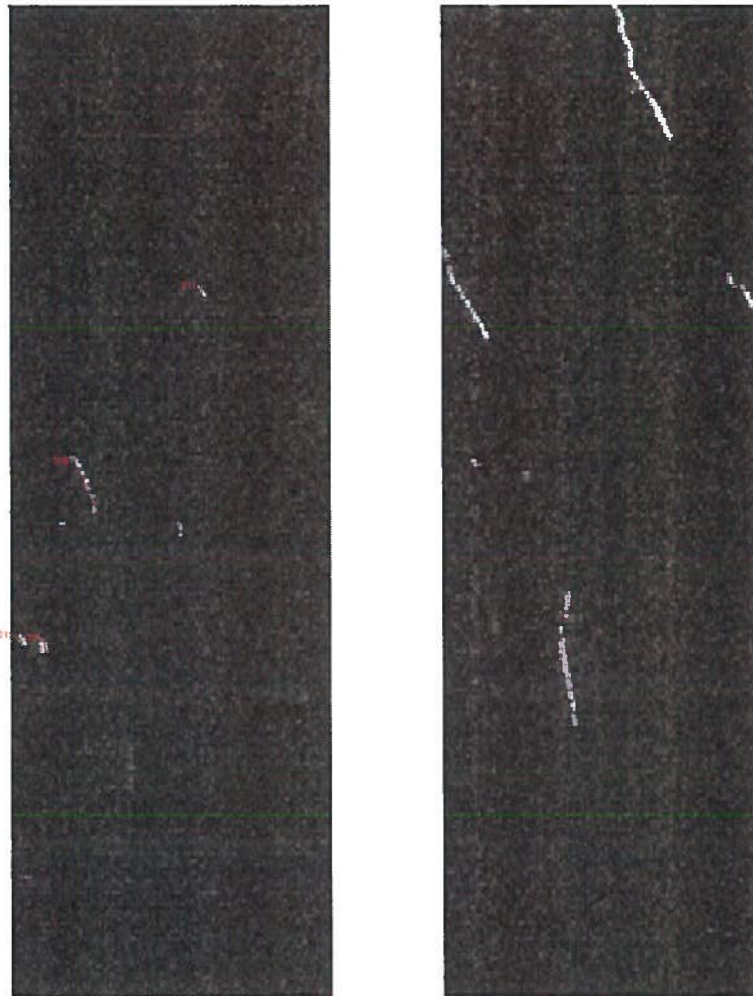


Figure 3: Marking of kinesin-1 in FIESTA; the horizontal axis describes the place of the kinesin-1 on the beforehand marked microtubules, the vertical axis is the time

really the case, a bigger amount of incidents would be necessary. The calculated mean velocities with their standard deviations as errors are:

$$\begin{aligned} v_{25^{\circ}\text{C}} &= (1.0 \pm 0.5) \mu\text{m/s} \\ v_{37^{\circ}\text{C}} &= (1.4 \pm 0.6) \mu\text{m/s} \end{aligned} \quad \left. \begin{array}{l} \text{0.9} \pm 0.3 \text{ from w1} \\ \text{if you have the fit} \\ \text{state it!} \end{array} \right\}$$

These velocities seem to be higher than the literature value for kinesin-1 movement, which is $0.8 \mu\text{m/s}$. However, as the errors are very big, the literature values lie inside the error-range. A comparison of the two mean velocities leads to the claim, that the true mean velocities differ for $0.4 \mu\text{m/s}$, the velocity of kinesin-1 in higher temperature

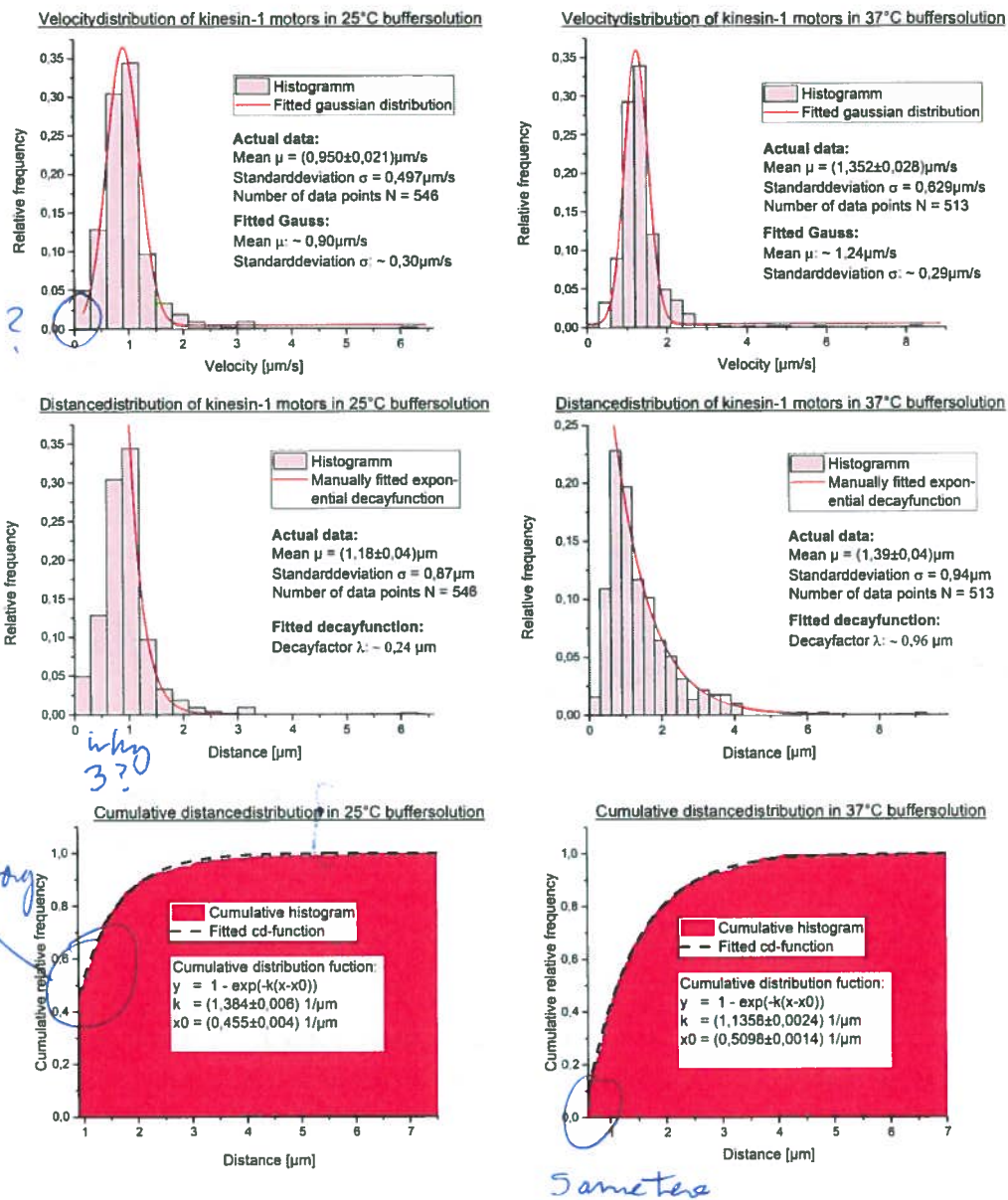


Figure 4: Chosen bin size: $0.3 \mu\text{m/s}$
 top-left: Normalized velocity of kinesin-1 at 25°C ;
 top-right: Normalized velocity of kinesin-1 at 37°C ;
 chosen bin size: $0.3 \mu\text{m}$
 mid-left: Normalized run-length of kinesin-1 at 25°C ;
 mid-right: Normalized run-length of kinesin-1 at 37°C ;
 chosen bin size: 8 nm
 bottom-left: Cumulative run-length of kinesin-1 at 25°C ;
 bottom-right: Cumulative run-length of kinesin-1 at 37°C

seems to be higher. The performance of a Welch-test leads to a two-sided t-value of 0.956, which is bigger than 0.05. Therefore, the claim cannot be falsified.

TIRF-microscope is a very exact measurement, the gained pictures are very accurate, as can be seen in figure 2. Errors come mainly from the lack of sufficient incidents and the evaluation with FIESTA. Because the marking of microtubules and of kinesin-1-tracks was done manually, errors are inevitable. Normally, these errors should cancel each other statistically, however, as three different people did the evaluation of the data, this doesn't need to be the case. Another big error of the analysis should therefore be the lack of marked slow proteins: As very slow moving particles weren't marked, because they could be dead proteins or errors of the picture, very slow moving kinesin-1 are ignored.

3.2 Run-length

The histograms of the run-length can also be found in figure 4. These distributions can be fitted with an exponential fit. We fitted without using the first three bins for 25°C and without using the first two bins for 37°C. The first bins aren't reliable, as the slowest moving kinesin-1 weren't marked, as explained above. The formula for the fit is:

for exponential $y = A \cdot \exp\left[-\frac{x}{\lambda}\right]$ $y = a(1 - e^{-bx})^c$

not consistent!
the bin size you are according
your resolution, and only
this one
you can
neglect!

The calculated mean run-lengths with their standard deviation as errors are:

$$l_{25^\circ C} = (1.2 \pm 0.9) \mu m$$

$$l_{37^\circ C} = (1.4 \pm 0.9) \mu m$$

then you plot or
derive $\lambda_{25^\circ C}$, $\lambda_{37^\circ C}$

Again the claim is, that the true mean velocities differ for the same value than the measured mean velocities, in this case $l_{37^\circ C}$ is 0.2 μm bigger than $l_{25^\circ C}$. The Welch-test gives a two-sided t-value of 0.818. Because of this, the claim also cannot be neglected.

which means what same or not? is it needed
I don't understand
what you are
saying. "

To achieve an exacter value and lessen the error, the cumulative distribution function for the run-lengths is now calculated and fitted. To grant a better visibility of the result, the chosen bin size is much smaller. The plots can be seen in figure 4. The formula for the fit is:

$$y = 1 - e^{-k(x-x_0)}$$

For this formula the mean value is calculated like this[3]:

$$\bar{x} = \frac{1}{k} \quad \checkmark$$

And it's error with the Gauss' uncertainty propagation:

$$\Delta x = \left| \frac{-1}{k^2} \Delta k \right|$$

Thus, the following values are achieved:

$$\begin{aligned} \bar{l}_{25^\circ C} &= (0.7225 \pm 0.0031) \mu m \\ \bar{l}_{37^\circ C} &= (0.8804 \pm 0.0019) \mu m \end{aligned}$$

These values are in the vicinity of the literature value for movement of kinesin-1 on microtubules, which is $0.8 \mu m$.

3.3 Interaction-time

To achieve further insight in the dependence of kinesin-1 movement from temperature, the interaction-time of kinesin-1 with microtubules is also calculated, using the measured data. This is done using the following simple formula:

$$t_{interaction} = \frac{l_{run-length}}{v_{kinesin}}$$

The error is calculated with Gauss:

$$\Delta t_{interaction} = \sqrt{\left(\frac{\Delta l_{run-length}}{v_{kinesin}} \right)^2 + \left(-\frac{l_{run-length}}{v_{kinesin}^2} \Delta v_{kinesin} \right)^2}$$

Thus, the values for the interaction-time are:

$$\begin{aligned} t_{interaction; 25^\circ C} &= (0.72 \pm 0.36) s \\ t_{interaction; 37^\circ C} &= (0.6 \pm 0.4) s \end{aligned}$$

These values indicate, that, while velocity and run-length are rising with temperature, the interaction-time with the microtubules is shrinking. However, because of the big uncertainty, further measurements would be necessary to prove this.

are you sure?

4 Discussion

$$v_{25^{\circ}C} = (1.0 \pm 0.5) \mu m/s$$

$$v_{37^{\circ}C} = (1.4 \pm 0.6) \mu m/s$$

$$\bar{l}_{25^{\circ}C} = (0.7225 \pm 0.0031) \mu m$$

$$\bar{l}_{37^{\circ}C} = (0.8804 \pm 0.0019) \mu m$$

$$t_{interaction;25^{\circ}C} = (0.72 \pm 0.36) s$$

$$t_{interaction;37^{\circ}C} = (0.6 \pm 0.4) s$$

The data indicates, that velocity and run-length are rising with temperature while the interaction-time is shrinking. The performed t-tests solidify this claim. To truly verify it, more measurements are necessary because more incidents would lead to a smaller uncertainty for the velocity, which is the main reason for the big uncertainty of the interaction-time.

Problems of this experiment involve mainly the lack of sufficient incidents to achieve real normal distributions for the velocity and lessen the existing errors and the manual analysis with FIESTA, which doesn't allow to differentiate between dead kinesin-1, impurities in the probe and slow moving kinesin-1.

Our own experimental set-up also suffered from not-stabilized microtubules, either because of bad work or, more likely, because the used materials were damaged. This is suspected, because remaking of the stabilization and nutrient-giving solution didn't make a difference and another group suffered from the same problem at the same time.

4.1 Conclusion

In this experiment we managed to achieve data of the interaction of kinesin-1 with microtubules both at room- and at body-temperature. We saw, that kinesin-1 probably move faster and over longer distances at body-temperature, which is helpful for inner-cell transport. Without motor-proteins like kinesin-1, nutrients for the cell-components could only be transported by diffusion. This is a good method over short distances, but over long distances it needs an incredible large amount of time. Therefore, the motor-proteins are helpful, as even the more distant regions, for example the axon terminals of neuron cells, are reached in a usable amount of time. ✓

References

- [1] http://www.bcube-dresden.de/fileadmin/www.bcube-dresden.de/uploads/diez/Versuch__MMC__WS2016__Anleitung__small.pdf 03.11.2016 12:00 o'clock
- [2] <http://ww1.prweb.com/prfiles/2009/09/08/140163/XVIVOHarvardKinesinMidView.jpg> 02.11.2016 18:00 o'clock
- [3] https://en.wikipedia.org/wiki/Exponential_distribution 02.11.2016 17:30 o'clock

