To go with the flow: Molecular motors are a drag
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Appendix B

Spurious Effects On The Lattice

Spurious Effects

The motion of a single molecular motor bound to the cytoskeleton can be described via a biased diffusion. This is a combination of a driving velocity component derived from hydrolysing ATP, $V_0=(V_0,0,0)$, and a diffusive component, $g_i$. The motor velocity, $V_i$, is given by:

$$V_i = V_0 + g_i = \mu_{ii} \cdot F_0 + g_i.$$  \hfill (B.1)

In this equation, $\mu_{ii} = \mu_0 \hat{I}$, is the motor mobility with magnitude $\mu_0$ and $\hat{I}$ is an identity matrix, $F_0 = (F_0,0,0)$, is the force generated while a molecular motor hydrolyses ATP and the diffusive component, $g_i$, has the following mean and variance:

$$\langle g_i(t) \rangle = 0$$

$$\langle g_i(t)g_j(t') \rangle = 2D_{ij}\delta(t-t') = 2k_bT\mu_{ij}\delta(t-t').$$ \hfill (B.2)

Note that the hydrodynamic interaction contribution of the Langevin equation (see eq.4.1) is absent from equation B.1 as a motor exerts no hydrodynamic interactions on itself. In the d-lattice model that is used in chapter 4, the motor positions and displacements are restricted to lattice positions. During one simulation time step the motors are allowed to make a move of either zero (dwell), $\pm 1$ or $\pm 2$ lattice nodes in both x and y directions. To be able to map the Langevin equation on the lattice, the simulation parameters (see table 4.1 in chapter 4) are tuned to be of order one. A velocity that is too small would not utilise the full span of the mapping algorithm and a too large velocity would only trigger steps of maximum value. Moreover, the thermal energy has to be large enough to be able to reach the full displacement range of $\pm 2$ lattice nodes. In order to map equation B.1 on the lattice, the algorithm in Fig.B.1 is used (see chapter 4*).

*In the section: ‘Allowing For Larger Displacements’.
However, an unwanted side effect of mapping the shifted Gaussian distribution (eq.B.1*) on a lattice, is the appearance of spurious dynamics. This results in velocities that deviate from the expected (mean) value. Including the spurious effects, $\varepsilon$, into eq.B.1 yields:

$$ V_i = V_0 + g_i + \varepsilon = \langle V_0 \rangle + g_i. $$  \hspace{1cm} (B.3)

In this equation, the effective single motor velocity is given by:

$$ \langle V_0 \rangle = V_0 + \varepsilon. $$  \hspace{1cm} (B.4)

The spurious effects can be understood by means of Fig.B.2. In the absence of a net motor force, i.e. $V_0=0$, the Gaussian velocity distribution is symmetrical around zero (see Fig.B.2A) and it crosses the threshold values ($\pm 0.25$ and $\pm 1.5$ in Fig.B.1) for stepping forward or back with equal probability. Thus, for the simulation parameters that were determined in Table 4.1 in chapter 4, the mapping algorithm yields the expected average velocity of $\langle V_i \rangle = \langle g_i(t) \rangle = 0$.

However, as molecular motors can derive motion from hydrolysing ATP, the position of the average velocity is shifted corresponding to the single motor velocity, $V_0$, but the mapping algorithm remains the same. For example, in Fig.B.2B, the nominal motor velocity is $V_0=0.2$. The velocity mapping at this point is no longer symmetrical around the average velocity, thus random velocity deviations, $g_i$, in either positive or negative direction have different effects that on average do not cancel each other out. As in Fig.B.2B $V_0$ is close to the threshold (0.25), a small random displacement towards the

*The mean value is $V_0$. 

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threshold value suffices to cross it, whereas a small displacement in opposite direction of equal size will not yield a displacement. This results in an over or underestimation of the measured single motor velocity $\langle V_0 \rangle$. For $V_0=0.2$ this leads to an overestimation of the velocity. As shown in Fig.B.3A and B, this overestimation decreases with increasing mobility, $\mu_0$, and $V_0$. The mobility is a measure for the variance of the Gaussian velocity distribution. Therefore, the larger the mobility*, the broader the distribution (see eq.B.2). This improves the mapping on the lattice, as it effectively decreases the effect of the shift of the distribution’s mean and increases the probability for crossing the established thresholds in both positive and negative direction. The effect of increasing $V_0$ is shown in Fig.B.2C. The figure shows that choosing the motor velocity further away from the threshold at 0.25 decreases the spurious effects and approximately yields the single motor velocity. This is confirmed in Fig.B.3B, where the normalised single motor velocity is shown for different $V_0$. However, when $V_0$ approaches the next threshold at 1.5, the spurious lattice effect causes an underestimation of the velocity.

Fig.B.3C shows that the results from Fig.B.3A-B, are recovered when multiple motors are present in the system. Similar to the single motor data, the spurious effects increase with $V_0$ and $\mu_0$. In addition, the spurious dynamics increase with the motor concentration until they reach a maximum at $\phi_\mu=50\%$. The filament is modelled as an ASEP¹, where excluded volume is taken into account, and the motors predominantly walk in a forward direction. It is therefore more likely for a motor to collide with another motor when moving backward, against the direction of flow, than for moving forward. This means that, even though the mapping for multiple motors is calculated in the same way as for a single motor, the excluded volume effects in the system will not allow for every (trial) move. For increasing concentrations up to $\phi_\mu=50\%$ this effectively changes the shape of the velocity distribution as back stepping becomes less likely due to excluded volume effects. In the forward direction the effect will be less relevant as, on average, all motors walk in the same direction and the next lattice node is more likely to be free. However, at filament occupations beyond $\phi_\mu=50\%$ the average motor-motor separations become very small². Above $\phi_\mu=50\%$ displacements of $\pm 2$ become less probable because of space constraints. The magnitude of the spurious velocity increase is shown for different occupation fractions in Fig.B.3D. In this figure the spurious velocity deviation ($\langle V_0 \rangle$ minus the theoretical velocity for an ASEP model (eq.A.2)) is normalised using $\langle V_0 \rangle$. For the simulation settings that were used in chapter 4 to investigate hydrodynamic interactions ($V_0=0.4$, $\mu_0=0.3769$) the normalised spurious deviation, is found

*At constant $k_B T$.

¹This is a modified ASEP that allows for motor detachment from and attachment to the filament via Langmuir Kinetics. Moreover, the original model only allows for steps of $\pm 1$ lattice nodes per time step (see chapter 3).

²Assuming a homogeneous motor distributed along the bio-filament the free space between 2 motors can be calculated via: $x = \frac{(1-\phi_\mu)}{2\phi_\mu}$ (in lattice spacings $l$).
Figure B.2: A) Mapping of the single motor velocity distribution on the lattice in the absence of a net external force ($V_0=0$). The measured velocity ($\langle V_c \rangle$) corresponds to the nominal velocity. B) A Single motor moving with a velocity ($V_0=0.2$) close to the threshold value, for a move of +1 lattice node, yields a measured velocity larger than the theoretical velocity. C) The deviation of the single motor velocity from the nominal velocity decreases with increasing $V_0$.

to have a maximum value of 0.05 for $\phi_n=50\%$. This value is small with respect to the velocity increase via hydrodynamic interactions (compare with Fig.4.5A).
Discussion

Spurious lattice effects will appear when an symmetrical (around zero) mapping algorithm is used in combination with a shifted Gaussian distribution with finite mean. For a single motor, the magnitude of this effect can be controlled by ensuring that the variance of the distribution is large enough to sample the full mapping range. Moreover, choosing the velocity further away from the mapping thresholds minimises the
spurious effects. In addition, spurious dynamics effectively modify the variance of the distribution causing a small over or underestimation of the motor velocity. When multiple motors are present in the system, excluded volume effects influence the magnitude of the spurious effects. This causes larger deviations with increasing filament occupation fraction with a maximum value at filament $\phi_\mu=50\%$. The magnitude of the spurious dynamics are smaller than the magnitude of the motor velocity increase due to hydrodynamic interactions.