

Fitted parameters for the four-state models for kinesin yielding the velocity and randomness plots shown in Fig. 7

The parameters are as follows: First, requiring that the biochemical states (1), (2) and (3) be colocalized and fixing the substep distance at $d_0 = 0.15$ nm (equal to that for $N=2$) yields satisfactory fits to both $V(F_x, [\text{ATP}])$ and $r(F_x, [\text{ATP}])$ (see the solid curves in Fig. 7) when the zero-load rate constants are given by

$$\begin{aligned} k_0^0 &= 1.45 \mu\text{M}^{-1} \cdot \text{s}^{-1}, & w_1^0 &= 80 \text{ s}^{-1}, & u_1^0 &= 520 \text{ s}^{-1}, \\ w_2^0 &= 20 \text{ s}^{-1}, & u_2^0 &= 250 \text{ s}^{-1}, & w_3^0 &= 20 \text{ s}^{-1}, \\ u_3^0 &= 250 \text{ s}^{-1}, & k'_0 &= 0.03 \mu\text{M}^{-1} \cdot \text{s}^{-1}, & c_0 &= 0.5 \mu\text{M}, \end{aligned} \quad [11]$$

while the load distribution vectors, apart from $\theta_1^+ = \theta_2^\pm = \theta_3^- = 0$, are (with the factor $c_{\parallel} = 1.45$ incorporated in the z components)

$$\begin{aligned} \theta_0^+ d &= (1.15, 0, -0.35) \text{ nm}, & \theta_1^- d &= (-1.00, 0, -0.10) \text{ nm}, \\ \theta_3^+ d &= (0.42, 0, -0.35) \text{ nm}, & \theta_0^- d &= (7.63, 0, 0.80) \text{ nm}. \end{aligned} \quad [12]$$

The forward rates in **11** are similar to those found previously (see ref. 1 Eq. **14**); but the balance of the reverse rates is rather different as, of course, are the load distribution factors.

Next, imposing $\theta_1^+ = \theta_2^- = \theta_3^+ = \theta_0^- = 0$, which implies that states (1), (2) and (3), (4) are colocalized, and fixing $d_0 = 0.6$ nm yields the fit

$$\begin{aligned} k_0^0 &= 1.3 \mu\text{M}^{-1} \cdot \text{s}^{-1}, & w_1^0 &= 20 \text{ s}^{-1}, & u_1^0 &= 290 \text{ s}^{-1}, \\ w_2^0 &= 40 \text{ s}^{-1}, & u_2^0 &= 290 \text{ s}^{-1}, & w_3^0 &= 0.9 \text{ s}^{-1}, \\ u_3^0 &= 780 \text{ s}^{-1}, & k'_0 &= 7 \mu\text{M}^{-1} \cdot \text{s}^{-1}, & c_0 &= 70 \mu\text{M}, \end{aligned} \quad [13]$$

with the load distribution vectors (including the factor c_{\parallel})

$$\begin{aligned} \theta_0^+ d &= (0.90, 0, -0.25) \text{ nm}, & \theta_1^- d &= (-0.29, 0, -0.57) \text{ nm}, \\ \theta_2^+ d &= (0.29, 0, -0.32) \text{ nm}, & \theta_3^- d &= (7.30, 0, 1.14) \text{ nm}. \end{aligned} \quad [14]$$

See the dashed curves in Fig. 7.

Finally, when we impose the colocalization of states (2), (3) and (4), by setting $\theta_2^+ = \theta_3^\pm = \theta_0^- = 0$, and again take $d_0 = 0.6$ nm, the data are best fitted (see the dotted curves in Fig. 7) with the parameters

$$\begin{aligned} k_0^0 &= 1.65 \mu\text{M}^{-1} \cdot \text{s}^{-1}, & w_1^0 &= 4.0 \text{ s}^{-1}, & u_1^0 &= 290 \text{ s}^{-1}, \\ w_2^0 &= 5 \text{ s}^{-1}, & u_2^0 &= 1800 \text{ s}^{-1}, & w_3^0 &= 20 \text{ s}^{-1}, \\ u_3^0 &= 300 \text{ s}^{-1}, & k'_0 &= 55 \mu\text{M}^{-1} \cdot \text{s}^{-1}, & c_0 &= 1.0 \mu\text{M}, \end{aligned} \quad [15]$$

and the load distribution vectors

$$\begin{aligned} \theta_0^+ d &= (0.94, 0, -0.37) \text{ nm}, & \theta_1^- d &= (-0.33, 0, -0.54) \text{ nm}, \\ \theta_2^+ d &= (-0.16, 0, -0.14) \text{ nm}, & \theta_2^- d &= (7.75, 0, 1.05) \text{ nm}. \end{aligned} \quad [16]$$

This fit is considerably improved if one allows $d_0 = 1.1$ nm; but, as explained, such a relatively large value is excluded by the single-step observations (2,3).

References:

1. Fisher, M. E. & Kolomeisky, A. B. (2001) *Proc. Natl. Acad. Sci. USA* **98**, 7748-7753.
2. Carter, N. J. & Cross, R. A. (2005) *Nature* **435**, 308-312.
3. Nishiyama, M., Muto, E., Inoue, Y., Yanagida, T. & Higuchi, H. (2001) *Nature Cell Biol.* **3**, 425-428.