

## Supporting Information

### Model Robustness

In order to test the robustness of our results, we varied both the kinetic parameters in our model, as well as altering the structure of the equations themselves. We then resimulated the resulting Spo0J/Soj dynamics. We found that our results were substantially insensitive to many, though not all, of the perturbations:

- We tested the effects of varying the membrane/nucleoid diffusion constants: in the wild type model  $D_3$  was set to zero. However, setting it equal to  $0.006 \mu\text{m}^2 \text{s}^{-1}$  (the same as the other membrane/nucleoid diffusion constants) did not appreciably alter our results (with the exception of widening the Soj membrane distribution, see Fig. 5). Setting  $D_4 = D_5 = 0 \mu\text{m}^2 \text{s}^{-1}$  also did not significantly alter the model dynamics. However, setting  $D_2 = 0 \mu\text{m}^2 \text{s}^{-1}$  did destroy the Soj relocations. The key point here is that the membrane/nucleoid diffusion constants must be small compared to the cytoplasmic diffusion constants; with the exception of removing Soj nucleoid diffusion altogether, their precise values appear to be unimportant. Varying the cytoplasmic diffusion of Soj also had only a weak effect on the Soj dynamics: any diffusion constant larger than about  $D_1 = 1 \mu\text{m}^2 \text{s}^{-1}$  yielded significant Soj relocations.
- We also varied the reaction rates: Soj relocations persisted even when  $k_1, k_2, k_3, k_5, \sigma_1, \sigma_2$  were each separately increased by a factor of 2. However, increasing  $k_4, k_6$  by a factor of 2 did abolish the relocations. Separately reducing  $k_4, k_6, \sigma_3$  by a factor of two again led to Soj relocations. Hence, the Soj relocations are fairly robust to changes in the kinetic constants. The variations in  $k_1, k_2, k_3, k_4, \sigma_1, \sigma_2$

were performed on the Spo0J19 mutant model I and the variations in  $k_5$ ,  $k_6$ ,  $\sigma_3$  on the wild type model.

- We altered the exponents governing the cooperativity of the Soj binding/unbinding dynamics. Setting either of  $\sigma_1$ ,  $\sigma_3$  to zero, with all other parameters having their wild type values, suppressed the Soj relocations. Setting  $\sigma_2$  to zero abolished relocations in simulations of the Spo0J19 mutant (both models). Cooperativity therefore appears to be an important element in generating realistic Soj dynamics. However, provided the  $\sigma$  terms are nonzero, there is still flexibility in the choice of the exponents in the cooperativity terms (previously set equal to two for the  $\sigma_1$ ,  $\sigma_3$  terms, and unity for the  $\sigma_2$  term). For example, using otherwise wild type parameters, but setting the exponent to 1.5 for the  $\sigma_1$ ,  $\sigma_2$  terms, and with  $\sigma_1$  and  $\sigma_2$  increased by factors of 10 and 40, also yielded Soj relocations albeit of an increased frequency and reduced amplitude. Using an exponent of 2.5 for the  $\sigma_1$ ,  $\sigma_2$  terms, and with  $\sigma_1$  and  $\sigma_2$  reduced by factors of 20 and 10, yielded relocations similar to those in the wild type model.
- We also tested several variations on the nature of the cooperative Soj unbinding from the nucleoid. For example, we altered the model so that the Spo0J condensation process was cooperative, meaning that the Spo0J condensed preferentially where condensed Spo0J was already present. A high local density of condensed Spo0J could then be responsible for the cooperativity in the Soj expulsion process. However, despite some effort, these modifications suppressed the Soj dynamics. Hence we currently favor our model where the Soj catalyzes its own disassociation in the presence of condensed Spo0J. However, given the complexity of the Spo0J/chromosome condensation we cannot rule out the possibility that this failure is a consequence of an over-simplification in our

modelling. To test this point further more data is needed so that more realistic models can be constructed of the Spo0J/chromosome reorganization dynamics.

- Adding protein production and degradation with a Soj half-life of 30 minutes did not significantly alter the dynamics in simulated wild type cells.
- We also tested a model where the requirement that Soj first bind to the polar membrane before rebinding to the nucleoid was relaxed. In this implementation there was only a single species of cytoplasmic Soj. This form was assumed able to bind to either the nucleoid or MinD/polar membrane (using the same  $k_1$ ,  $k_5$  terms as in the wild type model equations): these regions simply competed for Soj binding. However, using this modified model, we were unable to reproduce the results found in experiments. The difficulty here is that in order to obtain relocations in simulated wild type cells, the Soj must be able to bind relatively easily to any given nucleoid. However, in filamentous cells, this has the consequence that it is easy for the Soj to diffuse away and populate nucleoids well away from polar regions. In essence, the presence of extra Soj binding sites close to the poles is insufficient to “pin” the Soj close to the pole and prevent the Soj from diffusing away. Finally, we mention that this model is also made less likely by experimental results in *minD* mutants, where membrane Soj binding is prevented and the Soj dynamics virtually abolished (at least in exponential phase). This behavior is not what one would expect if the MinD/polar membrane were simply competing for Soj binding.

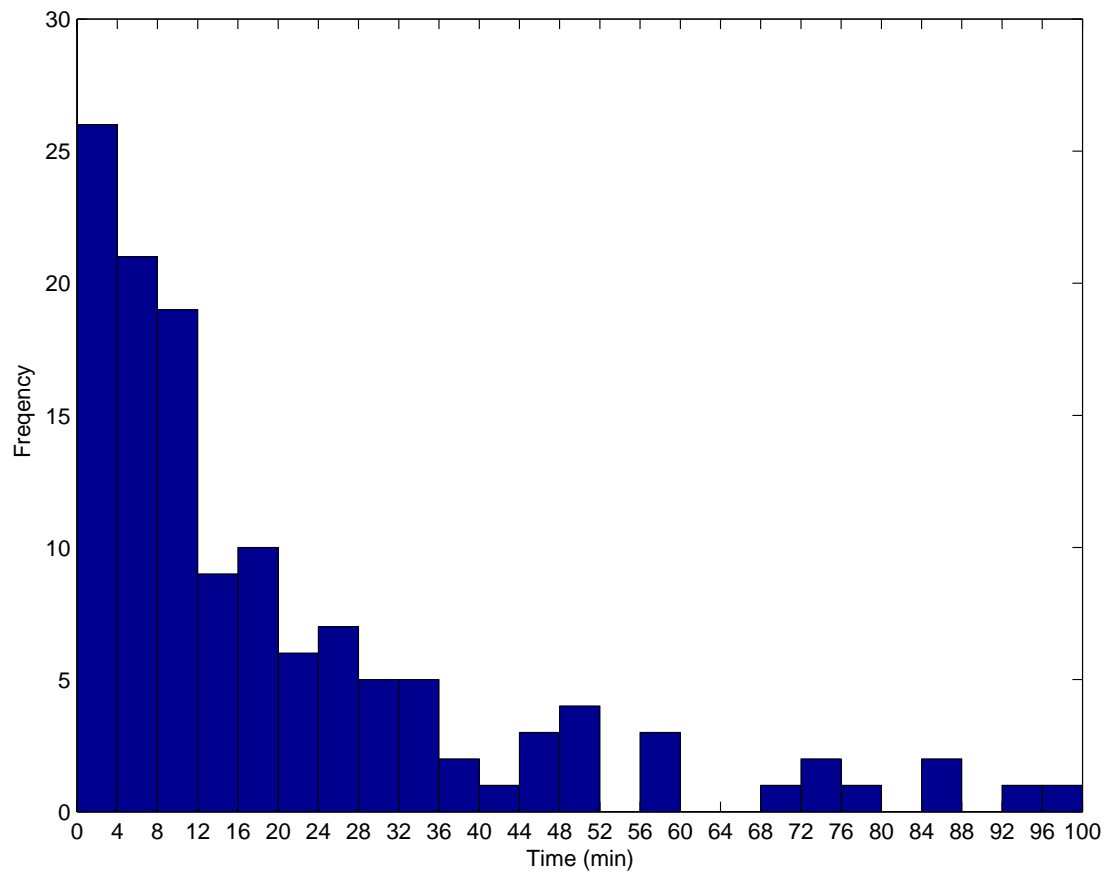
### **Supporting Figures**

**Fig. 4.** Histogram of the Soj relocation period, for wild type simulations where Soj was seen to relocate at least once over a simulated period of 100 minutes. Note the

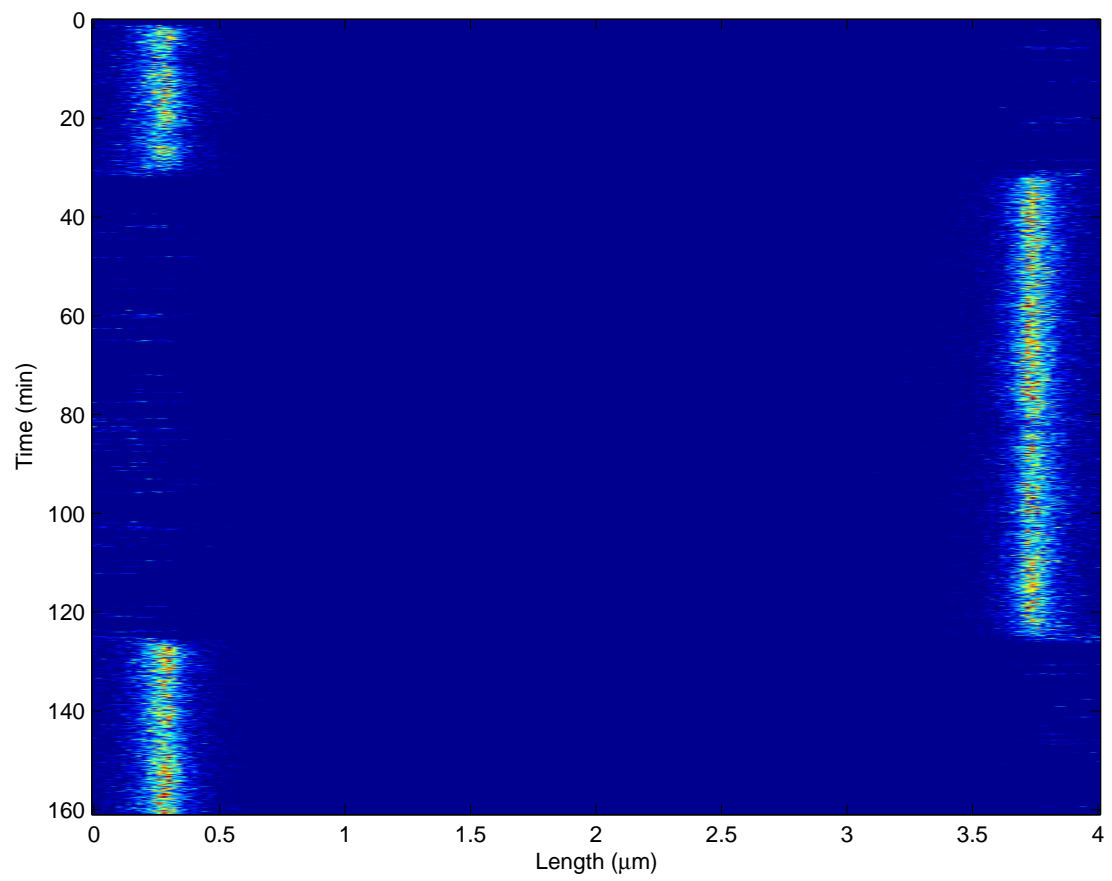
absence of any peak, reminiscent of a characteristic period. This is consistent with our analysis of the Soj relocations as being noise driven “escape” events.

**Fig. 5.** (A) Space-time plots of membrane bound Soj, and (B) both membrane and nucleoid bound Soj, for the case where  $D_3=0.006 \mu\text{m}^2 \text{s}^{-1}$ , with otherwise wild type parameters; bright colors represent high concentrations on a nucleoid or polar membrane. Notice that the membrane bound Soj forms tight clusters close to the cell poles, and that these clusters are offset from the nucleoid bound Soj clusters.

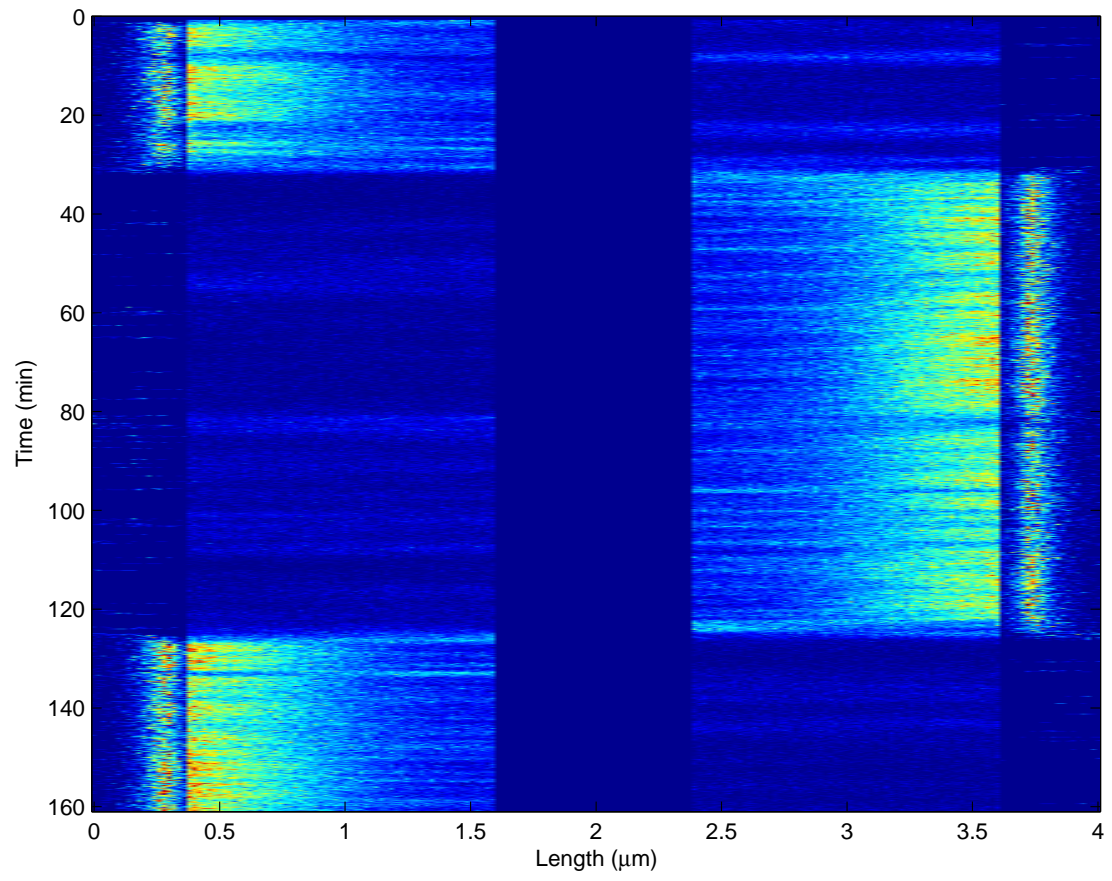
**Fig. 6.** Typical data for the number of Soj proteins on each nucleoid as a function of time, from simulated cell with copy numbers of Soj and Spo0J equal to 3000 but with otherwise wild type parameters. Note the rather regular dynamics, punctuated by periods with far more random dynamics.



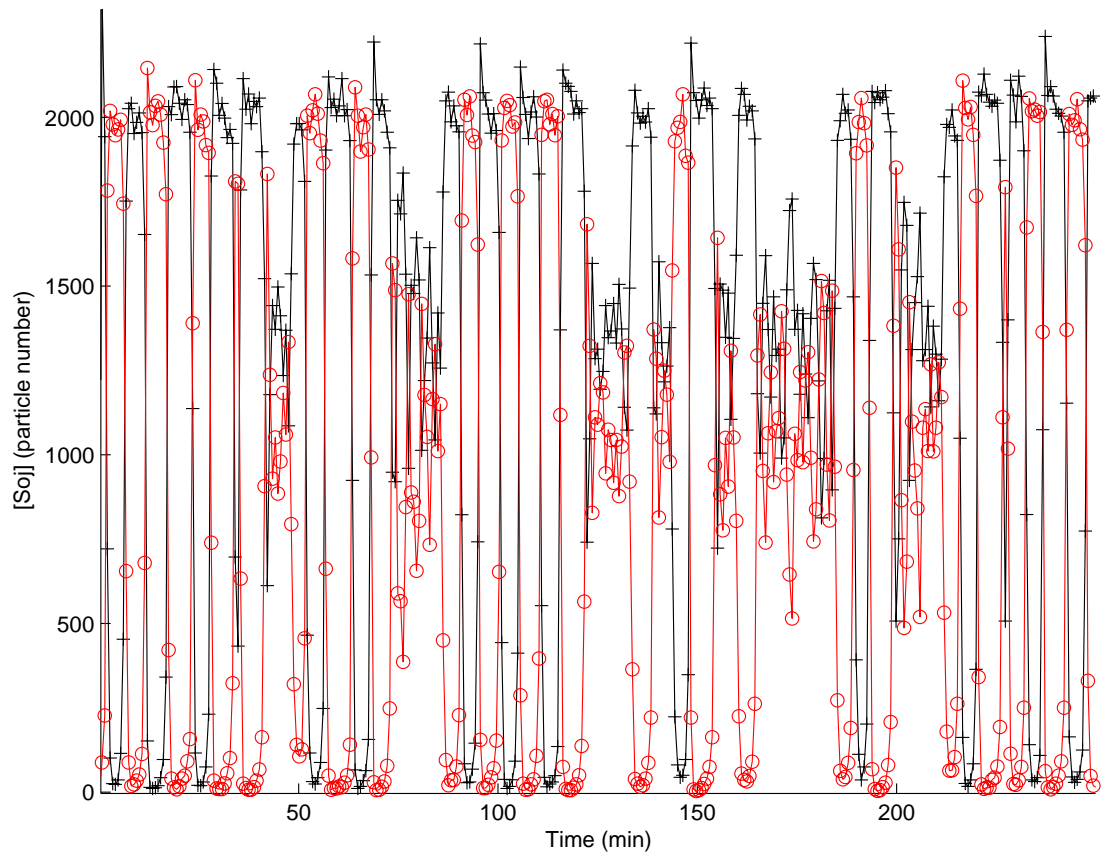
**Fig. 4**



**Fig. 5A**



**Fig. 5B**



**Fig. 6**