Yujiro Richard Yamada and Charles S. Peskin. 2009. A look-ahead model for the elongation dynamics of transcription. *Biophys. J.* 96:3015–3031.

Because of a computational error, the curves labeled w = 1 in Figs. 6 and 7 are incorrect, i.e., they do not correspond to the parameters that give the best fit to the data for the case w = 1. All of the other curves (w = 2, 3, 4) in both figures are correct. The corrected figures are shown below.

Although the fit of the case w = 1 to the data now appears better than before, it remains true that the fit to data is worst for w = 1 and best for w = 4, of the four cases considered. It should also be noted that the best-fit result in the case w = 1 is achieved only by allowing the forward rate constant to become unrealistically large (indeed, essentially infinite) so that the waiting time distribution becomes monoexponential (straight line on the semilogarithmic plot of Fig. 6), in contrast to the data.

We thank Andrew Matteson for calling our attention to this error.

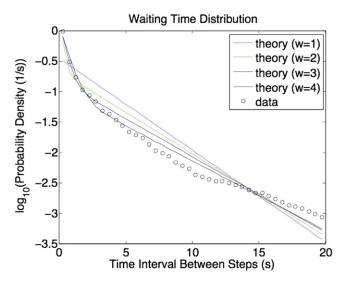


Figure 6

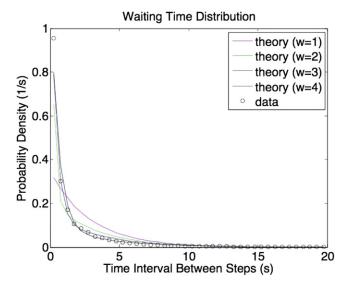


Figure 7