

CORRECTION

# Correction: Bayesian inference and comparison of stochastic transcription elongation models

The *PLOS Computational Biology* Staff

There are a number of errors in the caption for [S1 Fig](#). The publisher apologizes for the errors. Please see the correct [S1 Fig](#) caption here.

## Supporting information

**S1 Fig. Simulations of the elongation pathway.** Each point is a single simulation of the full *rpoB* gene (4029 nt). Parameters on the x- and y-axis are sampled uniformly at random from the displayed range at the beginning of each trial. The z-axis of each plot (mean elongation velocity) is then measured from the respective simulation. [NTP] and  $F$  held constant at 1000  $\mu\text{M}$  and 0 pN respectively. (A): Relationship between  $\Delta G_i^\ddagger$  and  $k_{cat}$  with binding at equilibrium (Model 8). (B) Relationship between  $k_{bind}$  and  $k_{cat}$  for the kinetic binding model with translocation at equilibrium (Model 2). (C) Relationship between  $K_D$  and  $k_{bind}$  with translocation held at equilibrium (Model 2).  $K_D$  and  $k_{bind}$  sampled uniformly from specified range and velocity is measured. Samples with simulated velocities outside of the range 0.1–0.2 bp/s were discarded. [NTP] = 10  $\mu\text{M}$  and  $k_{cat} = 100 \text{ s}^{-1}$ . (PDF)



## Reference

1. Douglas J, Kingston R, Drummond AJ (2020) Bayesian inference and comparison of stochastic transcription elongation models. *PLoS Comput Biol* 16(2): e1006717. <https://doi.org/10.1371/journal.pcbi.1006717> PMID: 32059006

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