Single-Molecule Motility: Statistical Analysis and the Effects of Track Length on Quantification of Processive Motion

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Single-Molecule Motility Analysis

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Table S1: Solutions to Eq. 6 for a collection of potential microtubule length distributions

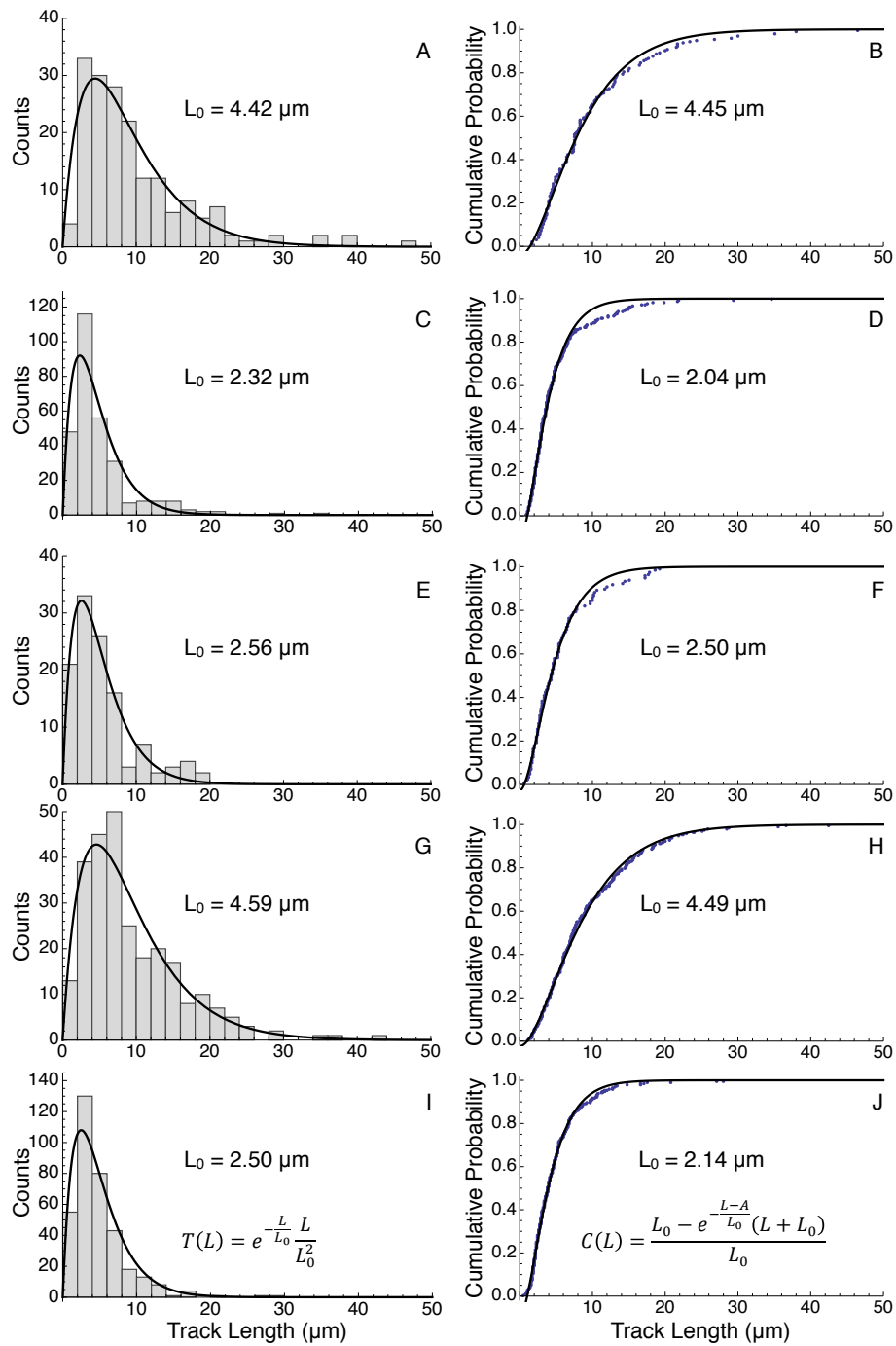|	Exponential	Schulz	Double Schulz*
α	L_0	$2L_0$	$2(a_1 L_{01} + a_2 L_{02})$
$T(L)$	$e^{-\frac{L}{L_0}}\frac{1}{L_0}$	$e^{-\frac{L}{L_0}}\frac{L}{L_0^2}$	$a_1 e^{-\frac{L}{L_{01}}}\frac{L}{L_{01}^2} + a_2 e^{-\frac{L}{L_{02}}}\frac{L}{L_{02}^2}$
$\langle x \rangle_{obs}$	$x_0\left(1 - \frac{x_0}{L_0 + x_0}\right)$	$x_0\left(1 - \frac{x_0(L_0 + 2x_0)}{2(L_0 + x_0)^2}\right)$	$x_0\left(1 - \frac{x_0}{\alpha}\left(\frac{a_1 L_{01}(L_{01} + 2x_0)}{(L_{01} + x_0)^2} + \frac{a_1 L_{02}(L_{02} + 2x_0)}{(L_{02} + x_0)^2}\right)\right)$

*With $a_1 + a_2 = 1$

FIGURE S1: Track length data represented and fitted as both histograms and cumulative frequency plots for Kin-1 on Taxol (A,B), Taxol Sheared (C,D), and GMPCPP (E,F) microtubules and Kin-2 on Taxol (G,H), and GMPCPP (I,J) microtubules. As with fits to cumulative frequency of motility data (Eq. 2), the cumulative distribution function for the Schulz distribution (plot inset) may require an offset parameter A to adjust for data not originating at the origin, which was validated by track distribution simulations. While the resultant characteristic track lengths measured in both analyses yield similar results, we employed the cumulative frequency results in our measurements (and in Table 2, main text) since the data is not course grained by binning.
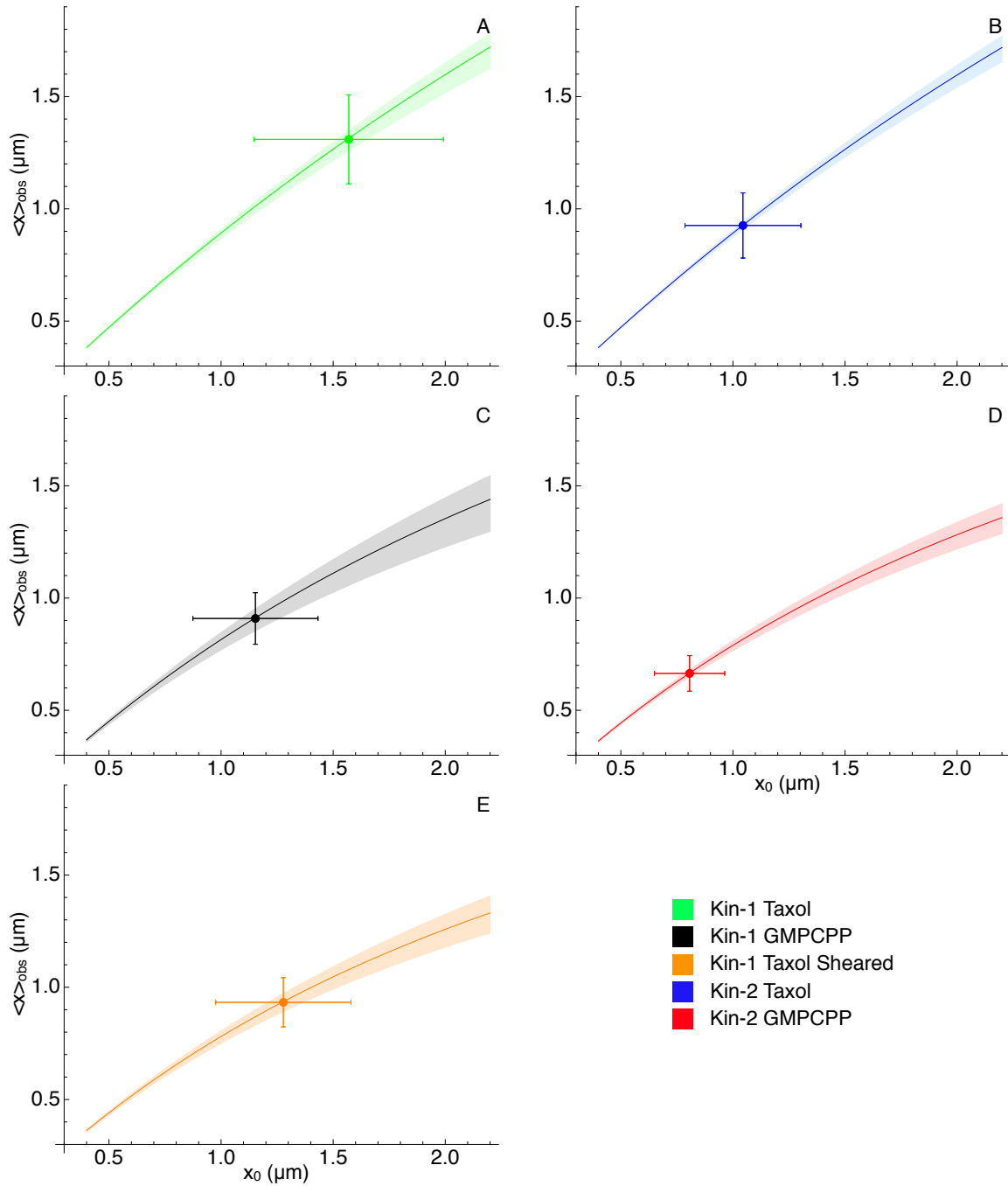
FIGURE S2: The magnitude of microtubule track uncertainty as computed via bootstrap of the microtubule length distributions for Kin-1 (A,C) and Kin-2 (B,D) on microtubule populations stabilized with either Taxol or GMPCPP, respectively, and Kin-1 on sheared Taxol stabilized microtubules (E). The 99% confidence region for the microtubule tracks is signified by the shaded regions about the solid curves (bootstrapped mean values). The median (dots) and 99% confidence intervals (error bars) are determined by a Gaussian fit to the corresponding one-dimensional histograms for x_{obs} and x_0.
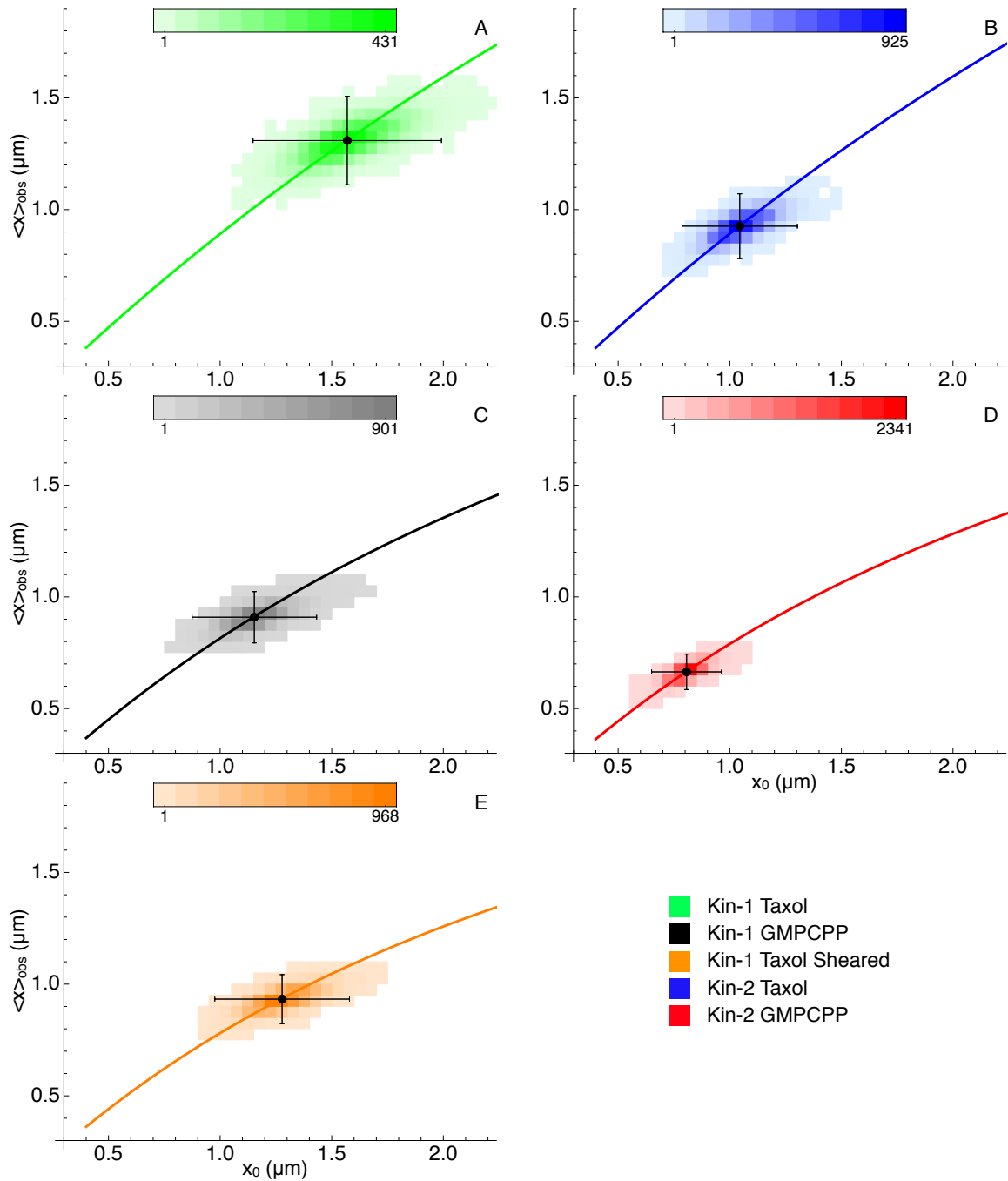
FIGURE S3: Density plots for the computation of x_0 via a complete sampling of both the x_{obs} and L_0 probability space for Kin-1 (A,C) and Kin-2 (B,D) on microtubule populations stabilized with either Taxol or GMPCPP, respectively, and Kin-1 on sheared Taxol stabilized microtubules (E). The median (black dots) and 99% confidence intervals (error bars) are determined by a Gaussian fit to the corresponding one-dimensional histograms for x_{obs} and x_0.
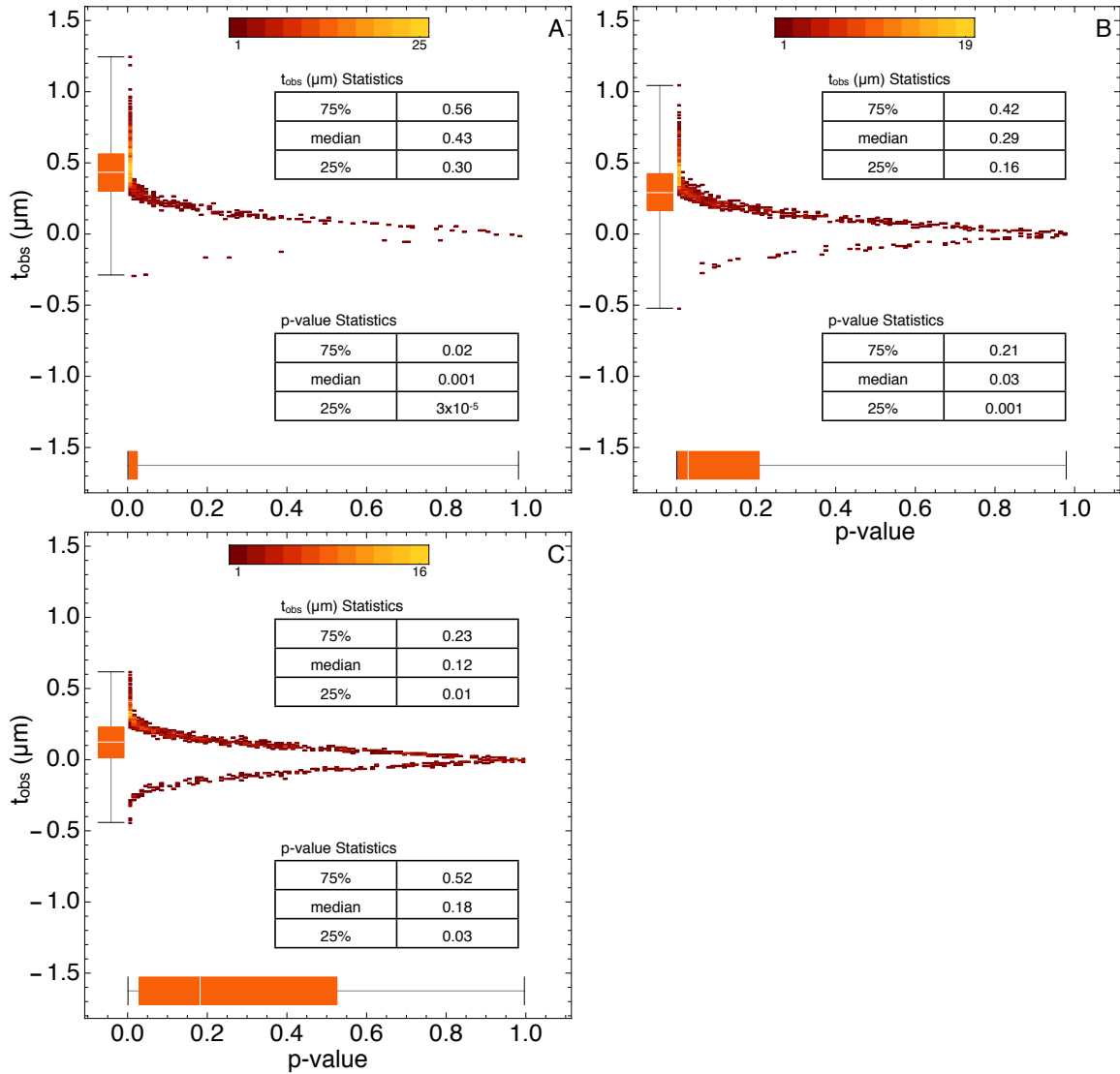
FIGURE S4: Parameter space search for the most probable difference (t_{obs}) and resultant p-value between calculated characteristic run lengths (x_0) for Kin-1 Taxol vs. GMPCPP (A), Kin-1 Taxol vs. Taxol Sheared (B) and Kin-1 Taxol Sheared vs. GMPCPP (C). The values diagramed by the whisker plots, including median, 25th and 75th percentiles are presented in the inset tables.
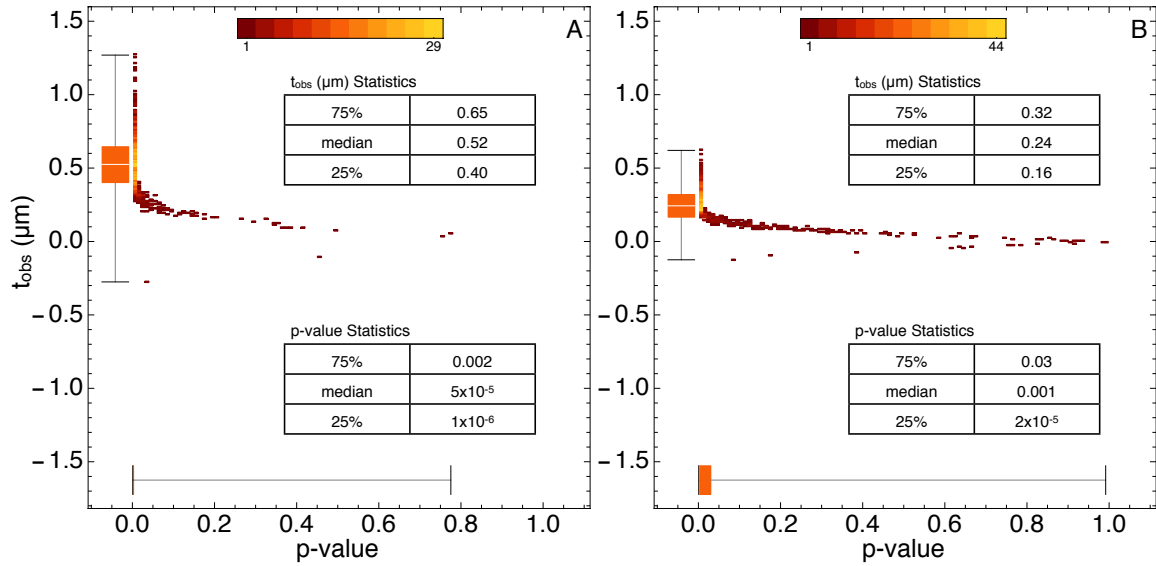
FIGURE S5: Parameter space search for the most probable difference (t_{obs}) and resultant p-value between calculated characteristic run lengths (x_0) for Kin-1 Taxol vs. Kin-2 Taxol (A) and Kin-2 Taxol vs. GMPCPP (B). The values diagramed by the whisker plots, including median, 25th and 75th percentiles are presented in the inset tables.