Conformational Transition

To consider the process of protein structure unfolding and refolding (or structure conversion), we add a new reaction to the original model, i.e. $A \xleftarrow{k_2} B$, where $A$ represents proteins with specific conformations before fibrillation, $B$ is proteins with specific conformations after fibrillation, and $k_2$ represent the forward and backward reaction rates of structure conversion, respectively. Here, all terms concerning $m(t)$ in Eq. 1 should be replaced by $m_B(t)$ -- the concentration of monomers in conformation $B$. If we further assume that monomers in conformations $A$ and $B$ are in fast equilibrium compared to other fibrillation processes, such that $k_1m_A(t) = k_2m_B(t)$, we will recover Eq. 1 by defining

$$
\begin{align*}
  \frac{k_1}{k_1 + k_2} k_+ \\
  \left(\frac{k_1}{k_1 + k_2}\right)^n k_n
\end{align*}
$$

A comparison of numerical solutions of the original model and the extended models is presented in Figure S1.
As we can see that even the fast equilibrium approximation is so strictly satisfied, our above treatment is still valid as long as enough unfolded monomers can be provided for fiber elongation process (the red and black lines). However, if the reaction rates for protein structure conversion are lowered further more, the results produced by considering protein structure unfolding and refolding will greatly differ from the original case (the purple and green lines.).
FIGURES

Figure S1. Comparison of numerical solutions of the original model and extended model under different reaction rates for protein structure conversion. The blue crosses represent the solution of the original model based on Eq. 1, with parameters of $k_+ = 5 \times 10^4 \text{M}^{-1}\text{s}^{-1} \quad k_- = 2 \times 10^{-8} \text{s}^{-1} \quad k_n = 2 \times 10^{-5} \text{M}^{-1}\text{s}^{-1} \quad n_c = 2 \quad$ and $m_{\text{tot}} = 5 \times 10^{-6} \text{M}$. The numerical solutions of the extended model are calculated under four different sets of reaction rates for protein structure conversion, i.e. $k_1 = 10^{-2} \text{M}^{-1}\text{s}^{-1} \quad k_2 = 9.9 \times 10^{-1} \text{M}^{-1}\text{s}^{-1}$ (red solid line); $k_1 = 10^{-3} \text{M}^{-1}\text{s}^{-1} \quad k_2 = 9.9 \times 10^{-2} \text{M}^{-1}\text{s}^{-1}$ (black dotted line); $k_1 = 10^{-4} \text{M}^{-1}\text{s}^{-1} \quad k_2 = 9.9 \times 10^{-3} \text{M}^{-1}\text{s}^{-1}$ (purple dashed line); and $k_1 = 10^{-5} \text{M}^{-1}\text{s}^{-1} \quad k_2 = 9.9 \times 10^{-4} \text{M}^{-1}\text{s}^{-1}$ (green dashed and dotted line). Examples with even higher reaction rates of $k_1, k_2$, which will give similar plots as the red solid line, are not further shown for simplicity. Other model parameters are fixed as $k_+ = 5 \times 10^6 \text{M}^{-1}\text{s}^{-1}, k_- = 2 \times 10^{-8} \text{s}^{-1}, k_n = 2 \times 10^{-1} \text{M}^{-1}\text{s}^{-1} \quad m_{\text{tot}} = 5 \times 10^{-6} \text{M}$ and $n_c = 2.$
Figure S2. The log-log correlation between the experimental data, taken from eight Type-I amyloid proteins (the yeast prion Sup35 NW region, Csg B\textsubscript{trunc}, Ure2 protein, β2-microglobulin, stefin B, α-synucleins, WW domain and insulin), and the estimated data via Eqs. 5 and 6 separately. (A) Correlation for the half-time of fiber formation $t_{1/2}$ with a Pearson correlation coefficient $r = 0.95$. (B) Correlation for the apparent fiber growth $k_{app}$ with a Pearson correlation coefficient $r = 0.94$. 