

FIG. 6: The SSN for a simple Markovian protein folding-unfolding example with past sub-sequence length equal to (A) zero, (B) one and (C) two. The past sub-sequences that have the same transition probabilities are grouped as the same state, represented by circles. The directed links between states are labeled with the resulting conformation and with its transition probability shown inside the parenthesis.

FIG. 7: The statistical complexity as a function of L_{past} for the time series of $\mathbf{A}^{(3)}$ and $\mathbf{D}^{(j)}$ ($j = 1, 2, 3$) of the delay-time time series τ of ET single-molecule measurement for Fre/FAD complex. This analysis clearly shows that $\mathbf{D}^{(2)}$ and $\mathbf{D}^{(3)}$ are Markovian whereas $\mathbf{A}^{(3)}$ is non-Markovian.

FIG. 8: Autocorrelation functions of $\mathbf{A}^{(3)}$ and $\mathbf{D}^{(j)}$ ($j = 1, 2, 3$) of the delay-time time series τ of ET single-molecule measurement for Fre/FAD complex. The results indicate that $\mathbf{A}^{(j)}$ capture all the nonstationarity of τ with timescale longer than 2^j .

FIG. 9: k_I/k_{\max} vs $\log P_I$ for each multiscale SSNs, $\varepsilon^{A^{(4)},D^{(4)},D^{(3)}}$, $\varepsilon^{A^{(6)},D^{(6)},D^{(5)}}$ and $\varepsilon^{A^{(8)},D^{(8)},D^{(7)}}$ for the protein conformational fluctuation of the Fre/FAD complex. Notice the divergence into two classes of k_I/k_{\max} for $\log P_I \gtrsim -10$, and the consistency of such divergence for time steps less than 2^8 .