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Extracting the reaction network buried in single Molecule Time Series of Epidermal Growth Factor Receptor and Grb2

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Bio-molecules system work and function across different spatial and temporal scales. Recent developments in single molecule (SM) experiments manifest the detailed dynamics of these multi-scale biophysical systems in the molecular level. We apply a recently developed model-free time series analysis methodology directly to the SM experimental data to illustrate the underlying multi-scale dynamics. Without a priori assumptions, our method can determine the sequence of conformation states and the corresponding state-space network (SSN) which captures the hidden multi-scale protein dynamics in details.

In this presentation, the multi-state reactions between epidermal growth factor receptor (EGFR) and Grb2 probed by SM measurements will be considered in detail to demonstrate the SSN construction scheme and its essential features. The dissociation kinetics between Grb2 and EGFR is independent on the concentration of Grb2 but it is inverse in associate case. Analytically we are already developed the auto-correlation function of symbolic time series and dwell time series which will proof the accuracy of our SSN's precision. We expect that the outcomes of our analysis can provide us with new insights toward the understanding of cell signaling processes in terms of single molecule time series.