analysis methods and demonstrate the method’s superiority in inferring correct HMM topology and kinetic parameters. We then apply the method to DNA polymerase binding and replication to identify tilt of multiple polymerases to a DNA overhang construct and to extract binding, dissociation, and polymerization kinetics. The presented statistical algorithm provides objective quantification of single-molecule trajectories and successfully identifies, segments, and analyses photophysical, dynamical, and stoichiometric ‘regimes’ within these trajectories. Our work illuminates important mechanisms in DNA replication and paves the way for experimental extension to studies of large complexes and molecular machines and to the field of single-molecule enzymology.

3030-Pos Board B800
Specification, Construction, and Exact Reduction of Finite State Transition System Models of Biochemical Processes
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Biochemical reactions may be viewed as discrete event processes characterized by a finite number of states and transitions. These processes may be modeled as finite state transition systems where state transitions represent individual reaction events. The time-evolution of the state occupancy probabilities of such systems is described by the master equation. Since these systems often involve a large number of interactions, it can be difficult to construct the master equation for a model describing a system, and since the resulting models can involve a huge number of states, solving the associated master equation can be difficult or impossible. Here, we describe a method for the specification, construction, and reduction of finite state transition system models of biochemical processes using the symmetry and invariant manifold reduction techniques. The method allows a user to specify transition rules using an intuitive graphical representation, and to automatically construct the transition matrix of a differential equation characterizing exactly the dynamics of a model, with a potentially significant reduction in dimension when compared to the full master equation of the model. The application of the method to a biological process is illustrated by models describing a hypothetical ion-channel at several levels of complexity.

3031-Pos Board B801
Reported Colligative Effects on Brain Energetically Consistent with Electrostriction
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Cellphone exposure reportedly alters brain EEG [1], blood flow [2] metabolism [3], and blood-brain barrier [4]. Others claim slight heating is the only plausible effect. We find deformation of soft tissue by electrostriction forces energetically possible. We consider a simple model of two hemispheres of fatty brain immersed in an aqueous fluid of higher dielectric constant. The polar fluid is attracted to regions of stronger electric field at the skull surface. The pressure pushing the hemispheres together could be transduced by pressure sensors between the hemispheres; cycling of the pressure might also cause damage akin to mechanical fatigue. Such forces are small but normally vanished due to neutral buoyancy. Assuming very soft tissue (rat brains soften as for the samples which were UV irradiated or annealed to 25K. Both the spectra were registered for the samples immediately after deposition as well as for the samples which were UV irradiated or annealed to 25K. Both the UV irradiation and the matrix annealing result in redistribution of the band intensities in the FTIR spectra. It allows us to distinguish spectral bands of different conformers. Assignment of the spectral bands was performed based on calculated vibrational spectra of the β-alanine conformers. As a result we detected presence of 4 β-alanine conformers were found at the MP2/aug-cc-pVDZ level of theory. But 10 of them are separated from lower energy conformers by low energy barriers and they can not present in the matrices. High-resolution FTIR spectra were registered for the samples immediately after deposition as well as for the samples which were UV irradiated or annealed to 25K. Both the UV irradiation and the matrix annealing result in redistribution of the band intensities in the FTIR spectra. It allows us to distinguish spectral bands of different β-alanine conformers. Assignment of the spectral bands was performed based on calculated vibrational spectra of the β-alanine conformers. As a result we detected presence of 4 β-alanine conformers in the Ar matrices. Further data about β-alanine conformational structure can be used in molecular dynamics simulations and also they can be useful for searching of β-alanine in the interstellar space. Key words: β-alanine, matrix isolation, quantum chemical calculations.