

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 binding 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

Scott M. Bugenhagen, Daniel A. Beard.

Medical College of Wisconsin, Milwaukee, WI, USA.

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 Cellphone Effects on Brain Energetically Consistent with Electrostriction

William J. Bruno^{1,2}.

¹Los Alamos National Laboratory, Los Alamos, NM, USA, ²New Mexico Consortium, Los Alamos, NM, USA.

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 vanish due to neutral buoyancy. Assuming very soft tissue (rat brains soften with age) and published tissue permittivities, we find the energy difference $\Delta U = (\epsilon_1^{-1} - \epsilon_2^{-1}) S V / 2c$ from displacing a volume V of 1 cc of fluid by a nearby cell tower or wi-fi computer causing incident power density S of one mW/m^2 creates deformation that slightly exceeds thermal noise. Data modulations cannot be transduced by the slow-moving fluid, but pulse modulations (used to reduce mobile devices' duty cycles) can. Blood also has a higher dielectric constant than brain, so there would be a force on the blood brain barrier. Sharp et al. [5] similarly invoked photon pressure as the basis for microwave hearing [6]. Lower frequency fields are better shielded by the skin, but the effect might explain headache from a pulsed low-frequency electric field [7].

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3032-Pos Board B802

Global Sensitivity Analysis of Arrhythmic Risk Biomarkers in Cardiac Single Cell Models

Anna A. Sher¹, Paul Carter¹, Blair Bethwaite², Denis Noble¹, David Abramson², David J. Gavaghan¹.

¹Oxford University, Oxford, United Kingdom, ²Monash University, Melbourne, Australia.

Global sensitivity analysis is critical in understanding the role of ionic currents variability in modulating cellular electrophysiological properties of ventricular myocytes as well as in assessing the cardiac single cell arrhythmic risk biomarkers. This work involves a systematic investigation into the sensitivity of various preclinical cellular biomarkers of arrhythmic risk to changes in ionic current conductances and kinetics. We compare local and global sensitivity analysis approaches. The nonlinearity of the system is confirmed to play an important role when considering the effect of parameters on markers that involve information from different frequencies. In the case of such biomarkers as action potential duration (APD), maxima Ca_i and Na_i concentrations, we find no significant changes in the overall order of the parameters' significance between local and global sensitivity studies. However, even for these single frequency markers we are able to give a more precise relative contribution of each parameter. Importantly, in the case of maximum S1-S2 slope marker, which integrates the information across a spectrum of frequencies of electrical stimuli, we find significant changes in the order of parameters as compared to the previously used methods for studying the sensitivity of cellular biomarkers. Moreover, the models consistently identify the L-type Calcium current (ICaL) as one of the dominant currents affecting the plateau of the action potential. Furthermore, in consistency with experimental data, the simulation results show that variation in conductances and kinetics of other channels does not affect the significance of ICaL's contribution. We demonstrate the critical role of global (vs local) sensitivity analysis in providing insights into the sensitivity of preclinical biomarkers, and hence mechanisms of repolarization and their rate dependence.

3033-Pos Board B803

Low Temperature Matrix Isolation IR-Spectroscopy and Quantum Chemical Study of β -Alanine Structure

Daryna Smyrnova¹, Stepan Stepanian².

¹The Katholieke Universiteit Leuven, Leuven, Belgium, ²B.Verkin Institute for Low Temperature Physics and Engineering of the National Academy of Sciences of Ukraine, Kharkiv, Ukraine.

In this study we have focused on conformational structure of the β -alanine molecule isolated in low-temperature argon matrices. The main purpose was to determine the set of the β -alanine conformers, which can occur in the matrices. Matrix isolation FTIR-spectroscopy was combined with quantum chemical calculations performed by the MP2 and DFT(B3LYP) methods using the aug-cc-pVDZ and aug-cc-pVTZ basis sets. Gibbs free energies of the β -alanine conformers also were calculated at the CCSD(T)/CBS level of theory.

Totally 21 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 matrixes. 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 matrixes. 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.

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Atomistic Simulation Studies of the Permeation of Organic Molecules Through Lipid Membranes

Zahleh Ghaemi Bafghi¹, Alessandro Laio¹, Paolo Carloni².

¹SISSA (Scuola Internazionale Superiore di Studi Avanzati), Trieste, Italy,

²German Research School for Simulation Sciences, Jülich, Germany.

For drugs with intracellular targets the process of permeation through the membrane is of fundamental importance (A. Malkia, et al., Euro J of Pharm