Time	event	group
8:30-8:50	Registration and presentation equipment check	
8:50-9:00	opening	
9:00-9:18	Investigating the role of telopeptides in collagen self-assembly with microrheology Tuba Altindal, Marjan Shayegan and Nancy R. Forde Department of Physics, Simon Fraser University Collagen-based structures are what confer to connective tissues in vertebrates their integrity and strength. Self-assembly of collagen into fibrils and higher-order structures can be mimicked in vitro when the appropriate conditions are met. It has long been known that fibril formation kinetics can be slowed down considerably by proteolytic removal of telopeptides – short non-helical fragments flanking the triple-helical domain of a collagen[1,2]. Based on competitive binding assays, it has also been suggested that there could be transient interactions between telopeptides and the collagen triple-helix, conferring telopeptides their catalytic role in fibrillogenesis[3]. However, the mechanism of interaction between telopeptides and collagen molecules is still unknown. Here, we describe the results of the experiments where we probed the local viscoelasticity of collagen solutions with intact and removed telopeptides using optical-tweezers-based microrhelogy. We find that the removal of telopeptides significantly reduces elasticity of collagen solutions at timescales from ~10 msec to ~1 sec. Telopeptides have previously been postulated to bind transiently to specific sites on the collagen triple helix in solution[1, 3], and thus may facilitate the otherwise less probable encounter of two collagen molecules in proper register. Our microrheology experiments provide direct evidence of increased strength and duration of interprotein contact arising from the presence of telopeptides, critical in catalyzing self-assembly of fibrillar collagen systems. [1] N. Kuznetsova and S. Leikin, J. Biol. Chem. 274, 36083 (1999) [2] W.D. Comper and A. Veis, Biopolymers 16, 2113 (1977) [3] D.J. Prockop and A. Fertala, J. Biol. Chem. 273, 15598 (1998)	Talk session 1
9:18-9:36	Solving a jigsaw puzzle: Combining high-resolution crystal structures of ion channel domains and low-resolution cryo-EM Kelvin Lau and Filip Van Petegem Department of Molecular Biology and Biochemistry, University of British Columbia The ryanodine receptor is the largest ion channel known. It is responsible for the release of calcium ions from the intracellular stores of the sarcoplasmic/endoplasmic reticulum. The release of calcium signals for a wide assortment of cellular processes, most importantly, muscle contraction in skeletal and cardiac tissue. Only two regions of this receptor have been described by high-resolution crystal structures. In addition these two domains have been docked into low-resolution cryo-EM structures. Here, I will present a novel domain x-ray crystal structure of the ryanodine receptor from both skeletal and cardiac isoforms. Stability of the wild-type versus those of mutants will be discussed. The docked location of the domain within the whole channel may suggest its functional properties.	
9:36-10:54	Form and function of vertebrate photoreceptors Novales Flamarique, Inigo Department of Biological Sciences, Simon Fraser University	

	Vertebrate photoreceptors are commonly distinguished based on the shape of their outer segments: those of cones taper, whereas the ones from rods do not. The functional advantages of cone taper, a common occurrence in vertebrate retinas, have remained elusive. Here, this topic was investigated using theoretical analyses aimed at revealing structure–function relationships in photoreceptors. Geometrical optics combined with spectrophotometric and morphological data were used to support the analyses and to test predictions. Three functions were considered for correlations between taper and functionality. The first function proposed that outer segment taper serves to compensate for self-screening of the visual pigment contained within. The second function linked outer segment taper to compensation for a signal-to-noise ratio decline along the longitudinal dimension. Both functions were supported by the data: real cones taper more than required for these compensatory roles. The third function related outer segment taper to the optical properties of the inner compartment whereby the primary determinant was the inner segment's ability to concentrate light via its ellipsoid. In support of this idea, the rod/cone ratios of primarily diurnal animals were predicted based on a principle of equal light flux gathering between photoreceptors. In addition, ellipsoid concentration factor, a measure of ellipsoid ability to concentrate light onto the outer segment, correlated positively with outer segment taper expressed as a ratio of characteristic lengths, where critical taper was the yardstick. Depending on a light-funneling property and the presence of focusing organelles such as oil droplets, cone outer segments can be reduced in size to various degrees. The main conclusion from this study was that outer segment taper is but one component of a miniaturization process that reduces metabolic costs while improving signal detection. Compromise solutions in the various retinas and retinal regions occur between ellipsoid size and acuity, on the one hand, and faster response time and reduced light sensitivity, on the other.	
10:54-10:12	Enthalpy-Entropy Compensation: Messy Data, Real Effect Eric Mills Physics and Astronomy Department, University of British Columbia In a wide variety of soft systems the measured enthalpy and the entropy changes upon some perturbation move in step with each other, so that the change in free energy is much less than either. This may indicate some deep principle in the thermodynamics of soft or biological systems, but efforts to understand this have been confounded by the nature of the uncertainty in the enthalpy and entropy, which is so large and correlated that it renders many measurements statistically insignificant. We look at this problem using data on two-state proteins, to shed light on enthalpy-entropy compensation and the perils of reading too much into your data.	
10:12-10:45	Surprise (game or activity yet to be decided about)	
10:45-11:00	Coffee Break	
11:00-12:15	Keynote talk	
12:15-13:00	LUNCH and presentation equipment check	
13:00-13:18	Characterizing dynamic protein localization throughout the bacterial cell cycle at the proteome scale Nathan J. Kuwada and Paul A. Wiggins Departments of Physics and Bioengineering University of Washington, Seattle, WA, USA	Talk sessi on 2

	Bacteria exhibit a surprising complexity of subcellular organization despite the absence of membrane-bound organelles and cytoskeletal motor proteins. To characterize localization dynamics throughout the cell cycle at a proteome scale, we combine time-lapse fluorescence microscopy and automated image analysis to capture the cell-cycle localization dynamics of nearly every protein in E. coli with non-diffuse localization. For each protein we capture hundreds of complete cell cycles, which facilitates both the quantitative analysis of cell cycle dynamics and cell-to-cell variation in protein localization. Global analysis reveals many subtle yet significant variations in spatiotemporal localization behavior. In addition, although cell division in E. coli was long believed to be essentially symmetric, we have discovered many examples of non-trivial protein partitioning at cell division. This observation in E. coli suggests that processes like asymmetric cell division, which plays a central role in development, have primitive precursors in bacterial cells with even the simplest life cycles.	
13:18-13:36	Shahzad Ghanbarian, Department of Physics and Astronomy, University of British Columbia We present the results of molecular dynamics simulations of electrostatic interaction between two DNA double strands. In particular we study a simple model for B-DNA with helical charge pattern in the presence of divalent mobile ions. The effective force on each molecule depends on the central distance and on the relative orientation of two DNAs. We explore the role of solvation effects and the resulting deviations from Coulomb's law on the nanoscale on the interaction between two DNA strands. A coarse- grained ion-phosphate potential can be constructed from all-atom simulations. This function can be parameterized in order to reproduce the structure of counter ions in detailed atomistic solvent model and in the presence of DNA. Successes and limitations of this approach for capturing ion-ion correlation effects will be discussed.	
13:36-13:54	Volume Profiles as a Tool for Probing the Transition States of Protein Folding Heather Wiebe and Noham Weinberg Department of Chemistry, Simon Fraser University Within the framework of transition state theory (TST), the kinetics of large-scale conformational changes in proteins and other biomolecules is described in terms of transition states (TS). The volumetric properties of TS's are expressed as the logarithmic pressure derivatives of the rate constants, known as activation volumes $\Delta V(TS) = -RT(\partial \ln k / \partial P)$. Experimental activation volumes are available for a number of protein systems.[1] According to TST, activation volumes can be identified as the difference in volume between the TS and reactant species $\Delta V(TS) = V(TS) - V(R)$. The concept of volume profile $\Delta V(y)$, describing how the volume of a molecular system varies along its reaction coordinate y, is widely used in discussing the mechanisms of high pressure reactions. Volume profiles can be calculated theoretically using our recently developed method[2] based on molecular dynamics (MD) simulations. If the position y(TS) of the TS along the reaction coordinate is unknown, it can be found by locating $\Delta V(TS)$ on the MD-generated volume profile: $\Delta V(y) = \Delta V(TS)$. We illustrate this approach by its successful application to the unfolding of a model chain system. [1] For example, G. J. A. Vidugiris et al, Biochemistry, 1995, 34, 4909 [2]H. Wiebe et al, J. Phys. Chem. C, 2012, 116, 2240	

13:54-14:12	3D reaction-diffusion modeling of conifer embryo development David Holloway Mathematics, British Columbia Institute of Technology Experimental work at UBC, UVic and BCIT has shown that cotyledons (embryonic 'seed leaves') in conifers form with a constant spacing, such that larger embryos have more cotyledons. We have also used hormone disruption to alter the patterning. I will describe recent work on modelling the spacing phenomena as two coupled reaction-diffusion mechanisms, with the first mechanism establishing an annular pattern within which the cotyledons can be formed by the second (hormone-dependent) mechanism.	
14:12-14:40	Coffee and cookies break	
14:40-14:58	An adaptive, patient-specific treatment approach for EGFR-driven, stage IV lung cancer. Philip Gerlee, Ben Creelan, Lori Hazelhurst, Jill Gallaher, Joshua Scurll, Hildur Knutsdottir, Olya Grove, Dan Nichol, Marc Sturrock Department of Mathematics and Statistics, University of British Columbia Lung cancer is the leading cause of cancer-related mortality in Canada and the United States. It can typically be classified at the molecular level by oncogene mutations that drive the cancer, with one such mutation occurring in the EGFR oncogene. Standard of care for patients suffering from stage IV (metastatic) non-small cell lung cancer (NSCLC) that is being driven by an EGFR oncogene mutation is to give the patient an EGFR tyrosine kinase inhibitor (TKI) such as Erlotnib, but unfortunately most patients develop acquired resistance to the drug within a year or so, and survival rates are poor, with median survival time less than two years. Hildur Knutsdottir and I will present a $50,000-grant-winning model aimed at tackling this problem, which we developed as part of a team at the Integrated Mathematical Oncology (IMO) Workshop on Personalized Medicine at the Moffitt Cancer Center, Tampa, Florida in November 2013. We first simplified the EGFR pathway down to five key genes and subsequently developed a model that describes the evolutionary dynamics of the number of cell clones harbouring various combinations of gene mutations or amplifications. Using a threshold tumour burden as an indicator of patient death, we proceeded to use a genetic algorithm to predict a locally optimal sequence of drug combination therapies to maximize patients' survival times. When simulated on a cohort of 100 virtual patients, our model's selected treatment schedule predicted a prolongation of survival by an average of 45 days compared with standard of care Erlotnib. Moreover, our model allows for new patient data to be fed back into the model every time new data (e.g. imaging) is available from a patient, thus allowing the model to be continually refined and increasingly personalized for individual patients.	Talk sessi on 3
14:58-15:16	3D reaction-diffusion modeling of conifer embryo development David Holloway Mathematics, British Columbia Institute of Technology Experimental work at UBC, UVic and BCIT has shown that cotyledons (embryonic 'seed leaves') in conifers form with a constant spacing, such that larger embryos have more cotyledons. We have also used hormone disruption to alter the patterning. I will describe recent work on modelling the spacing phenomena as two coupled reaction-diffusion mechanisms, with the first mechanism establishing an annular pattern within which the cotyledons	

	can be formed by the second (hormone-dependent) mechanism.	
15:16-15:34	Time dependant Electrical Impedance Spectroscopy of Salivary glands Parvind K Grewal [1, 2], Steven Thomas[2], Anand Karvat[2], Farid Golnaraghi[1], Jeff Liu [2], Krishnan Kalpagam [2] and Kirpal S Kohli [2, 3] [1] Mechatronic Systems Engineering, Simon Fraser University, Surrey, Canada [2] BC cancer Agency, Fraser Valley Cancer Centre, Surrey, Canada [3] E-mail any correspondence to: kkohli@bccancer.bc.ca Xerostomia is a known side effect of radiation therapy patients undergoing head and neck radiotherapy. Electrical Impedance Spectroscopy (EIS) has a potential to better understand the mechanism of salivary production and related cellular changes due to radiation tissue damage. In present study the electrical impedance is measured using an impedance spectroscope HF2IS from Zurich instruments (“Zurich Instruments”). The electrodes are circular Ag/AgCl 2mm electrodes from Vermed. These are non-polarizable and generate less than 10μV noise, hence preferred for skin surface measurements. This paper discusses the use of superficially placed cutaneous electrodes for EIS measurement of salivary glands output and the challenges related to signal drift that needs to be better accounted for.	
15:34-15:45	Results of surprise	
15:45-17:00	Poster Session, Wine	