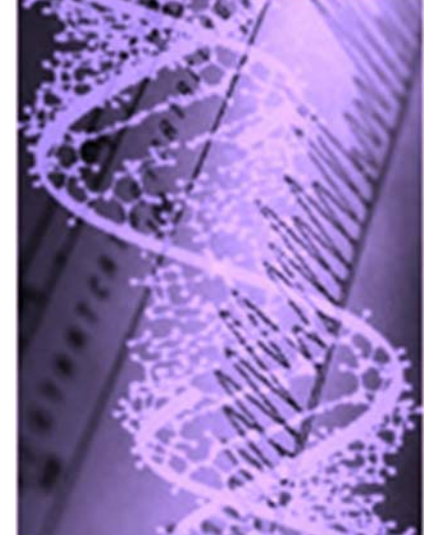


Joshua Singer (Neurobiology) CH - Retinal Microcircuitry: Night vision represents a remarkable feat of signal processing: the absorption of only a few photons by an array of thousands of rod photoreceptors somehow generates a visual response. In mammals, a specialized collection of interneurons transfers rod signals to ganglion cells, the output cells of the retina; this microcircuit is called the rod pathway. The rod pathway is anatomically well-characterized, but little is known about the nature of signal transfer between its component neurons. In particular, we do not understand how the signal generated by rod photoreceptors is passed across multiple synapses (both chemical and electrical) without being contaminated and degraded by synaptic noise. My laboratory addresses this issue by studying the physiology of the interneurons in the rod pathway: specifically, rod bipolar cells and All amacrine cells. Most of the experiments we perform involve electrical recordings from visually identified neurons in a mammalian retinal slice preparation. These recordings have allowed us to study the membrane properties of rod bipolars and All amacrine cells as well as chemical synaptic transmission between rod bipolars and AIs and electrical coupling between AIs. Recently, we have become interested in integrating computational models into our studies. These models will be generated in the NEURON programming environment and will be constrained by morphological and electrophysiological data acquired by our laboratory. Specifically, we would like to examine signal processing by groups of electrically coupled All amacrine cells to understand how the rod pathway maintains the high signal-to-noise ratio required for night vision and how it is optimized to encode small rod signals with a great degree of reproducibility.

D. Martin Watterson (Molecular Pharmacology & Biological Chemistry) CH – uses an interdisciplinary approach to study fundamental biological processes and mechanisms of pathophysiology. His laboratory has identified new approaches to therapeutic intervention in areas of unmet medical need, the approach centers around integrative chemical biology, medicinal chemistry, and computational biology interdigitated with molecular genetics and animal models of disease.



RESEARCH DAY

NOVEMBER 16TH, 2007



Master's Program in Computational Biology & Bioinformatics
Available research projects for CBB students
Technological Institute – L324
November 16, 2007

Rex Chisholm (Center for Genetic Medicine) CH - studies the myosins, a class of molecular motors that interact with actin to power cell motility and facilitate a wide range of processes ranging from intracellular transport to cardiac and skeletal muscle contraction. Myosin motors have been linked to numerous human diseases, including hypertrophic cardiomyopathy, the leading cause of sudden death in otherwise healthy adults. Dr. Chisholm is the Principal Investigator for the dictyBase resource, a development platform of a genome database for *Dictyostelium discoideum*, a NIH-supported model organism. dictyBase provides integrated access to the annotated *Dictyostelium* genome sequence, curated literature, and functional genomics data through their website. **Daniel Schneider**, a part-time CBB student, works with Dr. Chisholm and Dr. Kibbe on the dictyBase project.

Ann Harris (Pediatrics) CH - Regulation of expression of the CFTR gene, which when mutated causes Cystic Fibrosis, is complex and poorly understood. The CFTR mRNA and protein show patterns of expression in vivo that are tightly regulated both temporally, during development, and spatially in different tissues. However, elements in the basal promoter do not confer accurate temporal and spatial expression on transgenes and very little is known about other regulatory elements that confer tissue specificity on CFTR expression. We have generated data over the past several years that implicate intronic sequences in tissue specific regulation of CFTR expression. The sequences are located many kilobases away from the basal promoter; hence, it is important to establish their mechanism of action within chromatin and how they influence gene expression. We propose to utilize bioinformatic approaches to interrogate individual regulatory elements and their combined role in global regulation of CFTR chromatin structure.

Aggelos Katsaggelos (Electrical Engineering and Computer Science) EV – Dr. Katsaggelos and Dr. Sotirios Tsiftaris are interested in the analysis of signal processing for bioinformatics-related research. Dr. **Sotirios Tsiftaris** will be presenting a research poster, "Signal Processing and Biology Meet at IVPL".

Andreas Matoushek (Biochemistry, Molecular Biology, and Cell Biology) EV – Dr. Matoushek is interested in the mechanisms of macromolecular machines, particularly the mechanism by which proteins are unfolded by translocases and proteases.

Richard Morimoto (Biochemistry, Molecular Biology, and Cell Biology) EV – Dr. Morimoto and his laboratory are interested primarily in "Chaperone Networks and Mechanisms of Protein Conformational Disease".

Ishwar Radhakrishnan (Biochemistry, Molecular Biology, & Cell Biology) EV - Research in the Radhakrishnan lab is directed towards clarifying the basis for how proteins function in the cell with particular emphasis on the sequence and structural requirements that govern non-covalent interactions with other biomolecules. We combine traditional experimental approaches with informatics approaches. Central to the informatics endeavors is the development and application of computational tools to mine sequence and high-resolution structural data. One such tool that we have developed in the lab is called [MONSTER](#). Extensions to this tool are envisaged including integration with complementary tools to facilitate higher-order analyses of biomolecular complexes including automatic detection of complex motifs and patterns and structure prediction of novel interacting proteins/biomolecules.

Denise Scholtens (Preventive Medicine) CH – Dr. Scholtens is currently developing methodology for the analysis of high-dimensional data, the analysis of factorial designed microarray experiments and local modeling of protein complexes. Dr. Scholtens will present her work today, entitled "Hypergraph Models for Systems Biology Data".

Hans-Georg Simon (Pediatrics) CH – The Simon laboratory is interested in the formation of the emergence of biological information. The laboratory uses a range of molecular techniques to clone and engineer genes, biochemical techniques to determine the encoded protein structure and function, cell biological techniques to visualize subcellular localizations of mRNA and protein, and bioinformatics to identify gene pathway association and regulation. For functionally testing gene *in vivo*, we are employing retroviral gene-transfer, antisense knock-down, and genetic knock-out approaches.