S5-03

System biological model of circulation : from cell to system

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A new multi-scale system biological model incorporating a cell model to global circulation mechanism is proposed to analyze cardiovascular physiology. Electrophysiology of a cardiac cell is numerically approximated using a mathematical model of human ventricular myocyte. Ion transports across cell membrane initiated by action potential induce excitation-contraction mechanism in the cell model via the mechanism of cross bridge dynamics. Negroni and Lascano model (NL model) is employed to compute the tension by the cross bridges closely related to on calcium dynamics in cytoplasm. To convert the tension in cell level into contraction force of cardiac muscle, we assume a thin-walled hemispheric shape for the geometric model of ventricle. A lumped parameter model with 6 compartments is utilized to compute the systemic circulation interacting with the cardiac cell mechanism. Computed results using the present multi-scale model are well compared with the existing ones. Especially it is shown that the typical characteristics of heart mechanics, such as pressure-volume relation, stroke volume and ejection fraction, can be generated by the present multi-scale system biological model from cell to system.

S5-04

ECgene: The Genome Portal Site for Alternative Splicing

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Alternative splicing (AS) is an important mechanism of modulating gene function and expression in mammals. Recent study shows that approximately 70% of human genes show AS events. AS is closely related to pharmacogenomics and many diseases. We developed a genome portal site for alternative splicing, ECgene (Gene modeling by EST Clustering; http://genome.ewha.ac.kr/ECgene) that shows gene structure, function, and expression. It produces gene models by combining genome-based sequence clustering and transcript assembly procedures. The sequence clustering is quite similar to the NCBI's UniGene procedure (genome-based version), but ECgene uses graph theory to generate gene models in addition. ECgene web site provides various tools for analyzing gene structure and function. The genome browser adds ECgene models as custom tracks of the UCSC genome browser. ASviewer is specifically designed to show differences in the gene structure and functional domains at a glance. We provide two methods of analyzing gene expression - SAGE-based or EST-based. SAGE tag for each transcript is extracted and tag frequencies represent quantitative gene expression pattern. The EST-based method analyzes the cDNA libraries of the cluster member sequences. ASmodeler allows users to build gene models using their own sequences. Currently, we support human, mouse, and rat genomes.