SE&T Colloquium Series-Fall 2011

Speaker	Dr. Il-Hyung Cho Department of Computer Science and Information Systems
Title	***GenSAS-An Online Integrated Genome Sequence Annotation Pipeline***
Abstract	Advances in DNA sequencing technology have significantly reduced the costs associated with sequencing an organism's genome. However, the operating costs of hardware, software, and labor to analyze the sequence data are still too high for most users to process in house. Henceforth, most of the current bioinformatics applications used by bench scientists will be accessible through a Web environment. While there are many individual web-based tools available for gene annotation, there is no one-stop website where biologists can run several gene prediction tools and display the results in a graphic viewer for further manual curation. In this talk we present GenSAS, the Genome Sequence Annotation Server, a JavaScript-based framework of gene prediction and comparative sequence similarity applications for structural and functional sequence annotation. GenSAS is unique in that it offers a website with a single graphical interface for running multiple structural and functional annotation tools, visualization and manual curation of genome. GenSAS improves the overall performance by distributing the work between the server and client machine and supports a streamlined workflow that further simplifies the tasks and reduces the overall processing time. We present its functionality, the technology used in implementing each functionality, and software architecture of the overall implementation.
Date	Tuesday, October 4
Time	4:10-5:00pm
Place	Pioneer 240
	Refreshments will be served at 4:00pm.