

UNIVERSITY OF MACAU
FACULTY OF SCIENCE AND TECHNOLOGY
DEPARTMENT of
COMPUTER AND INFORMATION SCIENCE

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"High-Content Neuronal Image Analysis"

by

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Date: March 26, 2013 (TUESDAY)

Time: 2:30PM – 4:00PM

Venue: J315 (University of Macau)

Abstract

High-content neuronal screening has recently become a powerful high-throughput methodology for identifying and studying molecules or chemical compounds that regulate neuronal morphology, such as the patterns of neurite outgrowth and the size distributions of cell clusters. Such studies are expected to be an increasingly utilized approach in drug discovery and in vitro study of nervous systems. A typical high-content neuronal screening project generates hundreds of thousands high resolution images of neuronal cell cultures with highly complex morphology. It is of great challenge to reliably and automatically analyze a large quantity of such images. We have developed a robust image analysis method for automatically analyzing the complex morphology of neuronal cell cultures. This method has been one of the key innovations that enabled high-throughput genetic and drug discovery screening using neuronal cells.

Biography

Dr. Pengyu Hong is an Associate Professor of Computer Science at Brandeis University, Waltham MA, USA. He received his BS (1995) and MS (1997) in Computer Science from Tsinghua University and his PhD (2001) in Computer Science from University of Illinois at Urbana-Champaign. He was a post-doc fellow at the Department of Statistics at Harvard University from 2002 to 2004, and continued his post-doc training at the Department of Statistics at Stanford University in 2005. He then moved to Brandeis in 2005 as an Assistant Professor. His current research focuses on developing computational techniques for analyzing complex high-dimensional data (such as, EEG, high-content image analysis, microarray gene expression, mass spectrometry of glycans, and so on) and automatically inferring of biological networks from these datasets.

ALL ARE WELCOME!