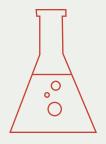
#### THE BIOMEDICAL INFORMATICS STUDENT CLUB

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# Solving the Maize











## **GUEST SPEAKER**

Dr Jer-Ming Chia Solutions Architect, Cycle Computing LLC

## **WHEN**

Thurs, Oct 23, 2014

## TIME

1:00 PM - 2:00 PM

## **PLACE**

Namm 523

To RSVP contact
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cuny.edu

### **ABSTRACT**

DNA-sequencing technologies has rapidly transformed genomics research in recent years, not only because of the exponentially increasing throughput of DNA sequencing machines, but more importantly, because it has applications that reaches almost all aspects of biology and medicine. While these sequencing-based assays have been embraced readily, the high-dimensionality and large volumes of generated data remain daunting to many. One of Dr Chia's primary interests is to develop computational tools and algorithms that reduce data complexity, and lower the barrier that prevents researchers from interacting with the data readily.

Dr Chia is a senior architect and cloud-computing specialist for Cycle Computing. He uses elastic cloud clusters that are designed to scale and meet the ever increasing high-throughput sequencing analytical workloads.

He has analyzed next generation sequencing data to uncover genetic variants associated with female infertility and designed systems for understanding the biological context of these variants. He has also been a project manager for the plant science domain of the Department of Energy's Knowledgebase for Systems Biology initiative where he was responsible for managing the 20-member plant science team. Dr Chia was technical lead and co-lead author in several highly successful next-generation sequencing-based, genetic diversity projects in maize and grape.

