



**BIG DATA**

# Interdisciplinary Data Sciences Consortium

\* IDSC Seminar Series \*

**November 20, 2015 1:30-2:30pm**

**Location: CPR 122**

**Presents**

**Dr. Feng Cheng**

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Adjunct Assistant Professor, Department of Biostatistics, College of Public Health  
University of South Florida  
12901 Bruce B. Downs Blvd., MDC 30 Room 3102B  
Tampa, FL, 33612-4749



## **Title: Introduction of Expression Microarray Data Analysis**

**Abstract:** The expression microarray technique is a high throughput genomic method in biology for investigating genome-wide transcriptional patterns. Expression microarrays can detect the expression levels of thousands of genes simultaneously and provide a global picture of biological systems. Microarray technology has revolutionized the way scientists examine genes, and it has been widely used in basic and clinical research accounting for more than 40,000 PubMed articles. The public microarray repositories such as NCBI GEO and EBI ArrayExpress databases now contain over 1,000,000 microarrays from more than 40,000 independent studies. The analysis of large amount of data from expression microarray is a very important topic in bioinformatics and computational biology. This talk will review expression microarray technique and its data analysis.



**Biography:** Dr. Feng Cheng is an Assistant Professor at the Department of Pharmaceutical Science in USF College of Pharmacy. Dr. Cheng received his first Ph.D. degree in computational medicinal chemistry at the Chinese Academy of Science (CAS) in 2003. After finishing his second PhD in bioinformatics at the University of Virginia in 2010, Dr. Cheng received his postdoctoral training at Yale University. In addition, He has four years of research experience in computational biology at The University of Illinois at Urbana Champaign and Rice University. Dr. Cheng has published over 40 research papers in prestigious journals including *Nature*, *Neuron*, and *Scientific Reports*. Presently, Dr. Cheng is an editor of the *Open Bioinformatics Journal* and *Journal of Bioinformatics and Computational Biomedicine*. Dr. Cheng has been serving as a peer reviewer for more than ten journals, such as *Journal of Theoretical Biology*, *Current Bioinformatics*, and *Current Computer Aided Drug Design*. Dr. Cheng researches mainly focus on applications of genomic data and bioinformatics method in clinical and basic research. He is also interested in computer-aided drug discovery and development.

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