



American Society for Quality (www.asq.org) – Washington DC and Maryland Metro, Section 509 (www.asq509.org)

Biomed/Biotech Special Interest Group (SIG) Meeting
(<http://www.asq509.org/ht/d/sp/i/31557/pid/31557>)

“Effectively Applying Sequencing Technology for Translational Cancer Research”

To be presented by

Wenming Xiao, MS, PhD

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Staff Scientist

Center for Cancer Research

National Cancer Institute, US NIH

Thursday, June 26, 2014

6:00 – 6:20 PM – Networking; Pizza/drink

6:20 – 8:45 PM – Program

8:45 – 9:00 PM – Door-prizes drawing; Networking

Online Registration site: <http://www.asq509.org/ht/d/DoSurvey/i/35817>

Open to Public –

\$5: non-ASQ members to cover pizza/drink cost;

Free: ASQ members, veterans, senior citizens, teachers, students, interns, residents, postdocs, FDA Commissioner’s Fellows, MJ-DC members, NTUAADC members, CAPA members, CCACC volunteers/employees, FAPAC members, CBA members, AAGEN members, Commissioned Corp officers, and current job-seekers.

Location: Kelly’s Deli Conference Center, 7519 Standish Place, Rockville (Derwood, for GPS users), MD 20855

Registration Deadline: Please register by **Thursday noon, June 26, 2014.**

Question: Please contact Dr. C.J. George Chang, Chair of Biomed/Biotech SIG, ASQ509; gchang2008@yahoo.com or 240-793-8425 (cell).

Driving directions: By Cars: From I-270 (N or S bound): Take Exit 9A and exit from the FIRST right exit; turn left (east) onto Shady Grove Dr.; turn right (south) onto Rockville Pike (**Route 355**); turn left (east) onto East Gude Dr.; turn left (north) immediately onto Crabb’s Branch Dr.; turn left (west) immediately onto Standish Place. The first building on your right side is 7519 Standish Place; open parking). **The venue is on the first floor with its entrance opposite to the left side of building main entrance.** **By Metro trains:** Off from Red Line **Shady Grove Station**, and take RideOn **Route 59 TOWARD ROCKVILLE** and get off from “**Calhoun Place**” stop. Standish Place is next to the Bus stop. Our venue is within 2 min of walking distance from the stop.

Summary:

Rapid evolving of sequencing technology not only increases the throughputs, simplifies sample processing, and lowers assay cost, but also makes variety of applications readily available for research community. The advance of this technology enables us to perform large cohort study in various diseases, such as NCI's TCGA, TARGET, and CGCI projects that search for somatic mutations in dozens of human cancer. These projects allow an unbiased analysis of genome-wide genetic alteration of cancers. The discoveries from these projects and many other studies have changed our traditional classification of diseases. Patients thought to be belonging to a same disease group can now be separated into many subgroups based on their genetic mutation markers. Newly stratified patient groups would then be linked to different clinic outcome and responsiveness to therapeutics agents, which is the foundation for precision and personalized medicine.

We will have an overview of evolution of sequencing technology, the concept and techniques for key sequencing platforms, and the advantages and challenges. We will also introduce major applications of using sequencing technology in biological research and issues in data analysis. Finally, our speaker will use his personal experience as an example to demonstrate how sequencing technology would help us in finding genetic mutations in cancers that not only enable us to understand biological pathways and mechanism of cancer development, but also allow us to select patients for specific drug treatment.

Presenter's Bio: Wenming Xiao, MS, PhD

Dr. Wenming Xiao received his bachelor in biology from Xiamen University in 1989 and master in genetics from the Institute of Microbiology, Chinese Academy of Science in 1992. Later on, he moved to United States and finished PhD program in molecular genetics from the Medical College of Wisconsin in 1997 and master program in computer science from Marquette University in 1998. From 1998 to 2005, Dr. Xiao was **bioinformatics scientist** in Gene Logic, MetriGenix, and Celera Genomics. Since 2005, he joined the National Institute of Health as a **contractor** and now as a **staff scientist** at Center for Cancer Research, National Cancer Institute, NIH. Dr. Xiao has numerous publications in peer-reviewed journals such as Nature, PNAS, N. Engl. J. Med, and Cancer Cell. In 2010, he received the NIH director award and NIH merit award for his contribution in **Lymphoma Leukemia Molecular Profiling Program**.

During his early career in industry, Dr. Xiao defined and developed IT infrastructure and software/database solutions for genomics and microarray data. His recent focus is to develop informatics tools in supporting next generation sequencing (NGS) technology for intramural research at the NIH for various applications, such as genome assembly, ChIP-Seq, RNA-Seq, Exome-Seq, and digital gene expression.

This Biomed/Biotech SIG event is cosponsored by the Monte Jade Science and Technology Association of Greater Washington (www.MonteJadeDC.org) and NTU Alumni Association at DC (www.ntuaadc.org).