Massively parallel DNA and RNA sequencing have become widely available, reducing the cost by several orders of magnitude and placing the capacity to generate gigabases to terabases of sequence data into the hands of individual investigators. These next-generation technologies have the potential to dramatically accelerate biological and biomedical research by enabling the comprehensive analysis of genomes and transcriptomes to become inexpensive, routine and widespread. The exploding volume of data has spurred the development of novel algorithmic approaches for primary analyses of sequence data in such areas as error correction, de novo genome assembly, novel transcript discovery, virus quasispecies assembly, etc. This workshop will bring together specialists to discuss the various mathematical and computational challenges presented by next-generation sequencing technologies.

Workshop topics of interest include but are not limited to:

• NGS error correction
• Read mapping
• Variant detection and genotyping
• Characterization of Structural Variants with NGS
• Haplotype assembly from NGS reads
• De novo transcriptome assembly
• Genome-assisted transcriptome reconstruction
• Transcriptome quantification
• Small RNA analysis
• De novo genome assembly from NGS reads
• Scaffolding and gap closure using paired NGS reads
• ChIP-Seq data analysis
• Whole-genome NGS-based association studies

This meeting is by invitation only. If you would like to inquire about the possibility of being invited, please contact the workshop chairs by May 10, 2013. One page abstracts of invited talks will be included in the ICCABS proceedings published in the IEEE Xplore Digital Library. Full length articles will be invited to a special issue of a major international journal following the workshop.

Workshop Registration Fees:

• IEEE Members: $350
• IEEE Non-members and late registration (after May 20, 2013): $450