Memorial Sloan Kettering Cancer Center™

We are seeking a highly motivated candidate, interested in statistical and computational cancer genomics, for a position as a postdoctoral fellow. This position will focus on the integration of large-scale sequencing data from public (such as TCGA) and local resources to understand the relationship between germline and somatic variants and phenotypic outcomes.

Applicants should hold a PhD degree in biostatistics, statistics, bioinformatics, or a related field, ideally with experience in NGS sequencing data analysis including whole-exomes and whole-genomes and familiarity with standard NGS variant detection and annotation tools. The successful candidate should have solid methodological training in statistics, be comfortable working with large data sets, proficient in at least one of the statistical programming languages R/Matlab/Python and have experience working on Unix/Linux systems and basic shell scripting. The successful applicant will be supervised jointly by Drs Colin Begg and Ronglai Shen. To apply, send a cover letter, cv, and the names of 3 references to Katherine Cheung at wongk1@mskcc.org: Memorial Sloan Kettering Cancer Center, 485 Lexington Avenue, New York, NY 10017.