Combined Biostatistician/ Bioinformatician Position in Analysis of Pediatric Brain Cancer.

Do you have expertise in both biostatistics and bioinformatics in the analysis of genomic data, particularly of cancer? We’re looking for you!

We need to analyze and interpret data from a number of functional genomic mouse models of cancers that have been studied using next generation sequencing platforms (Illumina and 454).

The applicant will work with multiple investigators in a large-scale cancer genomics/genetics program to analyze insertional mutagenesis data to determine the genes and pathways driving particular cancers, or associated with a particular phenotype. The applicant will analyze these data using available software tools (and develop new scripts and pipelines when required), in collaboration with a professional bioinformatician, and will collaborate with experimental biologists to interpret the results.

The applicant will have a PhD or MSc in biostatistics, with prior experience in molecular biology, cell biology, biochemistry, molecular genetics, or a related discipline. Outstanding communication and teamwork skills are essential. Previous experience in experimental biology research and/or genomics data analysis will be favored in applicant selection. Programming skills in languages such as R, Perl, Python or Java are a plus. Prior experience with next generation sequencing data is an asset.

The work will be conducted at the Hospital for Sick Children and at the University of Toronto, both major international centres of genomics, proteomics and systems biology research, in the heart of Toronto. There will be ample opportunity for professional development. The applicant will be co-supervised by principal investigators involved in experimental cancer research and computational biology/bioinformatics.

Please send your CV and the names of 3 references to Michael Taylor at mdtaylor@sickkids.ca