The Laboratory of Dr. Vijay Sankaran (www.bloodgenes.org) in the Division of Hematology/Oncology at Boston Children's Hospital and in the Medical and Population Genetics Program at the Broad Institute of MIT and Harvard are currently seeking applications from exceptional candidates for the position of:

Computational Biologist & Analyst

A successful applicant will work closely with both wet- and dry-lab scientists to elucidate the genetic underpinnings of normal human blood cell production and study how this process goes awry in genetic diseases. She or he will be involved in analyzing various large high-throughput sequencing data sets, applying basic and advanced statistical methods including modern machine learning techniques, communicating the results of these analyses clearly, and drafting manuscripts and grants of finished research projects. <u>Multiple opportunities will be available for a successful candidate to lead independent research projects.</u> Importantly, a successful candidate will be surrounded by friendly and extraordinary colleagues and mentors at the "world's most innovative intersection": http://bit.ly/1iyrx8T. In addition, this work provides an opportunity for the candidate to have an impact on real patients by identifying the genetic basis and potential therapeutic approaches for a number of childhood blood diseases.

Requirements:
- Highly motivated candidates at any level will be considered (BS, MS, or PhD in a computational science such as Mathematics, Computer Science, Computational Biology, Genetics, Statistics, or related fields).
- An understanding of basic biology with an emphasis on genetics and transcriptional regulation.
- A mastery of basic statistics (e.g. hypothesis testing, linear regression, non-parametric approaches, etc.) and either experience with or willingness to learn advanced statistical and machine learning techniques (e.g. variable selection by Lasso, clustering techniques, etc.).
- Demonstrated proficiency in either R or Python and familiarity with Unix and the command line. Ability to program in languages such as Java, C++, or Perl is a plus.
- Preference will be given to candidates with experience analyzing at least some of the following types of high-throughput data: exome sequencing, whole genome sequencing, RNA-seq, ChIP-seq, Ribosome Profiling, and CLIP-seq.
- A successful candidate will most importantly be highly self-motivated, demonstrate excellent interpersonal and communication skills, be organized and detail oriented, have an eagerness to learn and apply new techniques, and work well in a collaborative environment.

If interested, please email sankaran AT broadinstitute DOT org and attach the following:
- A cover letter
- Curriculum Vitae / Resumé
- A list of three references (references will only be contacted after speaking with the candidate)

Boston Children's Hospital is an equal opportunity employer.
Compensation will be commensurate with experience.