Postdoctoral Fellow

Cancer Computational Biology

Email: lawrence@broadinstitute.org

URL: http://personal.broadinstitute.org/lawrence/

URL: http://www.massgeneral.org/cancer/research/researchlab.aspx?id=1740

Unique opportunity to join an interdisciplinary team bridging the Harvard Medical School, the Massachusetts General Hospital, and the Broad Institute of Harvard and MIT. The **Lawrence Lab** at the Massachusetts General Hospital Cancer Center seeks well-qualified candidates to join a team of computational biologists working at the forefront of cancer research and treatment. We use computation as a powerful microscope to study both the fundamental biology of cancer initiation and progression, as well the diagnosis and treatment of cancer patients in the hospital setting.

Current research interests of the Lawrence Lab:

- **Cancer driver genes**: tumors grow because of specific driver mutations that deactivate tumor suppressors or activate oncogenes. We are working to complete our understanding of the full catalog of cancer's "box of tricks".
- **Resistance to targeted therapies:** single drugs targeting specific driver mutations can be effective for a while, but the cancer invariably discovers a work-around. We are actively investigating mechanisms of drug resistance and how to combat it.
- **Single-cell sequencing**: New approaches allow us to dissect a tumor down to single cells and investigate the RNA expression or DNA mutations in each cell. Understanding intratumoral heterogeneity is shedding new light on cancer progression and patient outcomes.
- **Liquid biopsies**: novel state-of-the-art technologies are starting to allow us to monitor the progression of cancer (both before, during, and after treatment) through a simple blood draw. We are actively working to overcome analytical challenges inherent in the study of circulating tumor cells (CTCs) and cell-free circulating tumor DNA (ctDNA).
- **Mutational processes**: our genomes accumulate mutations from environmental agents such as ultraviolet radiation and tobacco smoke, as well as from intrinsic processes like errors during DNA replication. Studying these mutational background patterns can tell us what repair pathways are broken in a specific tumor, perhaps pointing the way to an effective genotoxic therapy. We are working to develop novel DNA sequencing technologies for studying mutagenesis in model systems.

Required skills

- Ph.D. in one of Computational Biology, Bioinformatics, Biology, Computer Science, Mathematics, Physics, or a related field.
- Independent, self-motivated drive to push research forward.
- Strong publication record: first-author publication(s) in well-respected peer-reviewed journals.
- Excellent programming skills (using any of Matlab, R, Java, Python, Perl, C, etc.)
- Nimble approach to programming and data analysis, with an emphasis on simple, intuitive, reasoning: quickly open unfamiliar datasets, generate simple visualizations to project the data onto our brains as usefully as possible, to stimulate hypothesis generation and the next steps of the analysis.
- Comfort using Word, Excel, Powerpoint to communicate results between team members.
- Ability to work together with multi-disciplinary teams comprising physicians, biologists, statisticians, and software engineers.
- Fluency in spoken and written English
- Experience in "machine learning" welcomed

About the employer

Massachusetts General Hospital (MGH), consistently rated among the top three hospitals in the nation by *U. S. News and World Report*, is located in the heart of Boston, Massachusetts. The Center for Cancer Research (CCR) is the engine for discovery for the MGH Cancer Center. Working together, the CCR science faculty and the Hospital's renowned clinical staff are recognized worldwide as pioneers in the new field of "personalized medicine", based on the realization that every human tumor has unique characteristics, and that understanding those characteristics can provide vital information about disease progression and help predict the success or failure of today's therapies. Researchers in the CCR are also deeply involved in the creation and development of "smart drugs" that target specific disease pathways to produce new, more effective anti-cancer drugs, potentially with fewer side effects.