

Visiting Scholar Opportunity



Virus Genomics

Cancer Challenge

A small, but critical, part of the research at the National Cancer Institute (NCI) includes the study of cancer-causing viruses. Historically, the study of human and animal leukemia viruses at NCI led to the discovery, characterization, and translation to clinical utility of a multitude of oncogenes.

The understanding of these cancer-causing retroviruses primed NCI to become an epicenter of AIDS research. More recently, work on papilloma viruses has led to the development and widespread use of the first vaccine that will prevent cancer.

The ability to describe, characterize, and classify known, as well as unknown, cancer-causing viruses is expected to grow exponentially with the application of novel genomics technologies and techniques. However, viral genomics comes with its own set of bioinformatics challenges. Viruses can be difficult to isolate, sequence, and identify. Investigators are challenged with the task of distinguishing the viral genetic information from the genetic information of the host cells in which they propagate. Furthermore, even next-generation sequencing analysis pathways are not necessarily designed to utilize our knowledge of the behavior and characteristics of viruses within the host.

Clearly, a systems biology approach is needed if we are to achieve the level of understanding that enables better diagnostics and strategies for targeted therapies. Advancing the genomics of these cancer-causing viruses is an essential component of this more integrated approach.

Visiting Scholar Opportunity

The Visiting Scholar will work closely with researchers in the [Laboratory of Molecular Technology \(LMT\)](#), [Sequencing Facility \(SF\)](#), [AIDS and Cancer Virus Program \(ACVP\)](#), and [Advanced Biomedical Computing Center \(ABCC\)](#) to apply

state-of-the-art sequencing and analysis capabilities, and develop new analysis pathways and strategies designed specifically for cancer-causing viruses. The current opportunities focus on human papilloma viruses (HPV) and Kaposi's sarcoma herpesvirus (KSHV).

General Aspects of the Opportunity

Initially, our contributions to the research efforts on viral sequencing consisted of sequence determination followed by provision of the sequence data to investigators in other laboratories for use in their respective lines of investigation.



The Sequencing Facility houses the PacBio's SMRT system, which is a significant leap forward in DNA sequencing, since it can perform long-reads (on the order of 2,500 base pairs) on single molecules and determine sequence data in real time.

Now we are engaging in collaborative types of partnerships, in which the experimental design as well as the analytical work is approached as an integrated team effort. As a consequence, progress has accelerated on the number of fully sequenced KSHV genomes, as well as on the capacity to sequence viral genomes from clinical specimens.

Focus on KSHV and HPV

KSHV is an important cause of cancers in AIDS patients, especially in African populations, and HPV has a causative role in the etiology of specific cervical, anal, head, and neck cancers. These two types of viruses are excellent targets for further developing next-generation sequencing analysis capabilities. Planning is currently under way to type HPV strains and examine integration sites in patient samples. We are currently sequencing complete genomes in KSHV, utilizing raw throughput, amplification, and target capture technology strategies coupled with high-throughput sequencing.

As part of an integrated project team, the Visiting Scholar will have an opportunity to deepen experience with state-of-the-art sequencing and will play a seminal role in the bioinformatics component of the research efforts. Our laboratory has access to biospecimens that are difficult to obtain, and there exists a high level of interest in using the data derived from these studies in clinical settings. The residency is expected to lead to additional opportunities for follow-on collaborations, and to the acceleration of the translation of new understanding to clinical practice.

Who Should Apply?

We seek postdoctoral fellows or early-career scientists with a background in bioinformatics and experience in genomics or virology (preferably all three).