Eric Allain
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I am a clinical specialist at Vitalité Health Network and Adjunct Professor in the Department of Chemistry and Biochemistry at the Université de Moncton. Prior to my appointment, I was a Post-Doctoral Fellow in Bioinformatics at the Atlantic Cancer Research Institute in Moncton.

Cancer cells arise when the genetic material of cells is damaged leading to abnormal behaviour including uncontrolled growth. The genetic material in all cells consists of two related types of molecules (termed DNA and RNA) that together control all functions of a cell. Recent technologies that sequence the component parts of DNA and RNA allow rapid and accurate measurement of changes to both DNA and RNA. Being able to assess changes that have occurred in cancer cells is an important tool to determine the precise type of cancer and how best to treat the cancer. As a Clinical Specialist in the clinical Genetics Division at Vitalité Health Network in Moncton, I help develop tools for DNA and RNA sequencing that can help physicians understand cancer-cell behavior in blood cancer (termed leukemia). Currently, approved methods for measuring DNA and RNA only target or examine a small portion of the genetic material that is already known to exhibit abnormalities. As our knowledge of leukemia progresses, this approach to testing defined portions of the genetic material will undoubtedly overlook abnormalities since discoveries are constantly revealing new abnormalities associated with leukemia that are not yet included within our tests. I want to take advantage of newer technologies that can measure most potential abnormalities in the genetic material of leukemia cancer cells. Thus, the main goal is development of methods that first capture leukemia cells from the blood of cancer patients and then use sophisticated computer programs to search for huge numbers of abnormalities at one time. My focus will be on the most frequent adult leukemia termed Chronic Lymphocytic Leukemia (CLL). My research program will first establish a method for capturing CLL cells from blood by adapting well-known procedures for this task. Sequencing technology will then be combined with computer software to scan the genetic material of cancer cells for abnormalities. The cost and effectiveness of our strategy will then be compared to current hospital-approved testing methods. Measuring both molecules involved in genetic control will achieve clearer results. This research will impact the speed and comprehensiveness of leukemia characterization and will provide more information for the physician while using fewer resources than current methods. This research will use state-of-the-art technology to benefit patients by providing caregivers timely, accurate information about the patient's cancer and improve patient outcomes.

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