

**Undergraduate research opportunities (Winter/Summer 2024) for
Chemistry & Biochemistry/Biology//Physics/Chemical & Materials Engineering students**

***In silico* biomarker discovery for vaping-associated pulmonary inflammation**

(Differential gene expression, protein-protein interaction network, functional enrichment analysis)

In silico biomarker discovery is a valuable approach for identifying diagnostic or therapeutic markers associated with different diseases. The use of electronic cigarettes (e-cigarettes) or vape pens, known as vaping, has seen a surge in popularity as an alternative to traditional tobacco smoking. However, concerns have arisen about the potential health risks linked to vaping, particularly with respect to pulmonary health. Vaping-associated pulmonary inflammation has become a critical public health concern, especially in North America, necessitating the development of effective diagnostic and therapeutic biomarkers. In this context, the application of *in silico* biomarker discovery, which harnesses modern computational approaches, presents a promising avenue for identifying markers associated with this condition.

Our biomarker discovery team focuses on integration of omics and clinical data, and computational techniques for identification of biomarkers. The *in silico* biomarker discovery process is expected to yield a set of potential diagnostic or therapeutic markers associated with vaping-associated pulmonary inflammation. These markers may include genes, proteins, or metabolites that display significant dysregulation in individuals affected by this condition compared to healthy controls. Computational models may also be developed to predict an individual's risk of developing pulmonary inflammation based on their vaping behavior, genetic factors, and clinical data.

In the proposed research project, the student will collect comprehensive datasets containing omics and clinical data related to vaping-associated pulmonary inflammation, as well as control data. Moreover, the student will learn and use different databases, tools and techniques for differential gene expression, protein-protein interaction network, functional enrichment and pathway analysis. To facilitate this investigation, the student will have access to cutting-edge computing resources within the Centre for Research in Molecular Modeling (CERMM) and the Digital Research Alliance of Canada (formerly Compute Canada). Additionally, they will benefit from the collective expertise of our scientific and technical team, participate in team meetings, and engage in scientific discussions throughout the project's duration. This collaborative and technologically advanced environment will provide an ideal platform for the student to contribute meaningfully to the field of *in silico* biomarker discovery and their applications in diagnostics or therapeutics for vaping-associated pulmonary inflammation.

Keywords: biomarkers; DESeq2 analysis; differential gene expression; LIMMA; protein-protein interaction network; pathway analysis;