

The capacity for scientific innovation is inexorably linked to the capacity for scientific leadership. Both require a strong personal constitution to sustain the pursuit of ideas which contravene established dogma, and the ability to inspire collaborators and funding agencies to join you in that pursuit.

The foundations of my leadership stem from my experience as the President of the Varsity Outdoor Club (VOC), a 103 year-old and the largest recreational club at the University of British Columbia. As president I led a 12-person executive team which brought mountaineering, rock-climbing, ski-touring and hiking to thousands of students, safely and sustainably. I applied these experiences of forging a tight-knit and inter-dependent executive as **Co-Founder of the genomics hackathon collective, *hackseq* ([www.hackseq.com](http://www.hackseq.com))**. *hackseq* began as a satellite event to the 2016 American Society of Human Genetics meeting and has grown each subsequent year. We have raised over \$125,000 of sponsorship funding, including a \$50,000 National Science Foundation grant in partnership with the 2020 RNA Society Meeting. Each event is a 72-hour collaborative team challenge with 8-14 teams or 60-110 individuals, in which the team lead (usually a graduate-student or post-doc) proposes an innovative genomics idea and with an interdisciplinary team, attempts to realise it. I am the longest serving organizer of *hackseq*, involved in *hackseq* (2016), *hackseq18* (2018), and *hackseqRNA* (2020) and I led teams at *hackseq17*, *hackseq19*, and *hackseqRNA*. My *hackseq17* team, bioSyntax, won the competition and we subsequently published a 2018 paper based on our software in *BMC Bioinformatics*, one of the six publications to result from a *hackseq* event.

Personally, this endeavour culminated at *hackseqRNA* where **I initiated and led the Serratus team**, an international collaboration between 13 scientists. The goal of *Serratus* ([www.serratus.io](http://www.serratus.io)) was to create the computing infrastructure capable of searching >50 million gigabytes of public sequencing data and identify every coronavirus sequence. The objective was to ensure that the global research community fighting the current pandemic may benefit from the richest possible coronavirus sequence diversity to aid in vaccine and therapeutics development. I personally secured \$197,000 CAD of funding which was applied exclusively to the massive cloud-computing resources necessary to perform such an ultra-deep sequence search. In total, we assembled >11,000 coronaviruses and so far have discovered 6 new species of corona-like or coronaviruses, some radically diverged from previously known coronaviruses. The pre-print describing this work is available on bioRxiv, and we are awaiting reviews from our submission to *Nature*.

It is with this leadership experience that I advance this research proposal. **I initiated and led the proposed foundational research on rRNA variation**, of my own volition, and in addition to my regular doctoral work. This required writing the grants to fund this research, and establishing the collaborations with the Morin, Wieden and Landthaler laboratories to realize our recent *Cell Reports* publication. I believe this research contains further unrealized potential and deep insights into the mechanisms of eukaryotic translation.

Receiving the Banting Fellowship will accelerate the development of this work into a full-fledged research program and support this advancement to ultimately benefit Canadians diagnosed with cancer.