# mRNA Vaccine Sequence Design Using Discrete Optimization Techniques Applied to the SARS-CoV-2 Virus

Cross, Sarah (School: Keystone School)

Recent research in the treatment and prevention of disease has become dominated by a relatively new and revolutionary technique: mRNA. Although initially used to develop cancer prophylactics, its potential applications in the medical industry have expanded drastically, as it has massive advantages over conventional DNA techniques such as LAV(live attenuated viruses) by being much faster and safer to develop, providing precision in antigen design, and allowing researchers the ability to adapt vaccines to virus variations quickly and synthesize fully customizable treatments for patients. Technology is now at the point where we have the ability to form mRNA vaccine candidates using computational genetic simulations, creating full working prototypes before testing in the lab. By applying state-of-the-art techniques, bioinformaticians can encode for specific antigens such as the SARS-CoV-2 spike glycoprotein and compute vaccines for a virus and its potential mutations. A process that once required years of work and a lab now can be solved computationally in a matter of days. Constrained discrete optimization will be used to minimize a fitness function balancing both GC(guanine-cytosine) content and utilization of common codons in the human body to maximize mRNA levels and the formation of antibodies in the cell. The researcher will show that these results come very close to encoding for the BNT162b2 vaccine from the SARS-CoV-2 spike glycoprotein, with a 78.1% codon similarity and 90.7% nucleotide similarity. This discrete optimization method will be compared against those produced by that of a widely accepted codon mapping approach; the approach illustrated here enables greater levels of customization in vaccine design.