

## SCI-121 – Medical Science For AI Engineering

### Emergence of new or re-emerging viruses

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Mutation contributes significantly to the emergence of new or re-emerging viruses in humans and animals by enabling viruses to adapt to changing environments and evade immune responses. Viral mutations occur primarily during replication when errors are introduced in the virus's genetic material, either RNA or DNA. Mutations can also arise from recombination events when two virus strains infect the same cell and exchange genetic material, generating new variants with mixed traits.

These mutations help viruses adapt by altering proteins crucial for infectivity and immune recognition. For example, changes in viral surface proteins can enhance a virus's ability to bind to host cells or reduce the effectiveness of antibodies generated by previous infections or vaccination, which allows the virus to evade immunity, spread more efficiently, or increase virulence, contributing to outbreaks or pandemics.

Influenza virus is a prime example in which mutations in hemagglutinin (HA) and neuraminidase (NA) proteins help the virus evade immunity and increase transmissibility. For instance, various nonsynonymous mutations in HA and NA proteins have been observed in recent Influenza A (H1N1)pdm09 strains, likely driven by immune selection pressure, leading to increased virulence and outbreak potential. These mutations can change antibody binding sites and the orientation to host receptors, thereby escaping immune detection and causing more severe infections.

Similarly, SARS-CoV-2, the virus causing COVID-19, has exhibited frequent mutations especially in the spike protein's receptor-binding domain (RBD) and other functional regions that mediate host entry. Specific mutations such as D614G and several others around the furin cleavage site have made the virus more transmissible and have contributed to the increase of variants with partial resistance to immunity from prior infection or vaccines. These adaptive changes enable the virus to persist in human populations despite public health interventions.

In summary, viral mutations driven by replication errors, host immune pressures, and recombination underpin the emergence of new or re-emerging viruses by enabling evasion of host defenses and adaptation to new hosts or environments. Influenza and SARS-CoV-2 provide compelling examples of how mutation assists viral evolution, affecting public health responses and vaccine development.

## References

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