

# Key drivers of adaptation in rapidly evolving pathogens

- Zoonoses and transmission to new hosts (both species and individuals)
- Immune selection (CTL, innate, antibody)
- Development of drug resistance
- Virulence/transmissibility
- Host/pathogen arms-races, e.g. host antiviral factors
- **Most** of the time, **most** of the viral genome is conserved
- **Most** of the **observed variation** is “neutral”
- Changes that are **not neutral** are important to **detect early**, and, ideally, **predict**

# How much genomic variation is there in SARS-CoV-2?

- There are >4M genomes in GISAID and >1.3M NGS datasets in SRA for SARS-CoV-2
- At this point, nearly every genomic position has sequences with multiple allelic variants (AVs)

