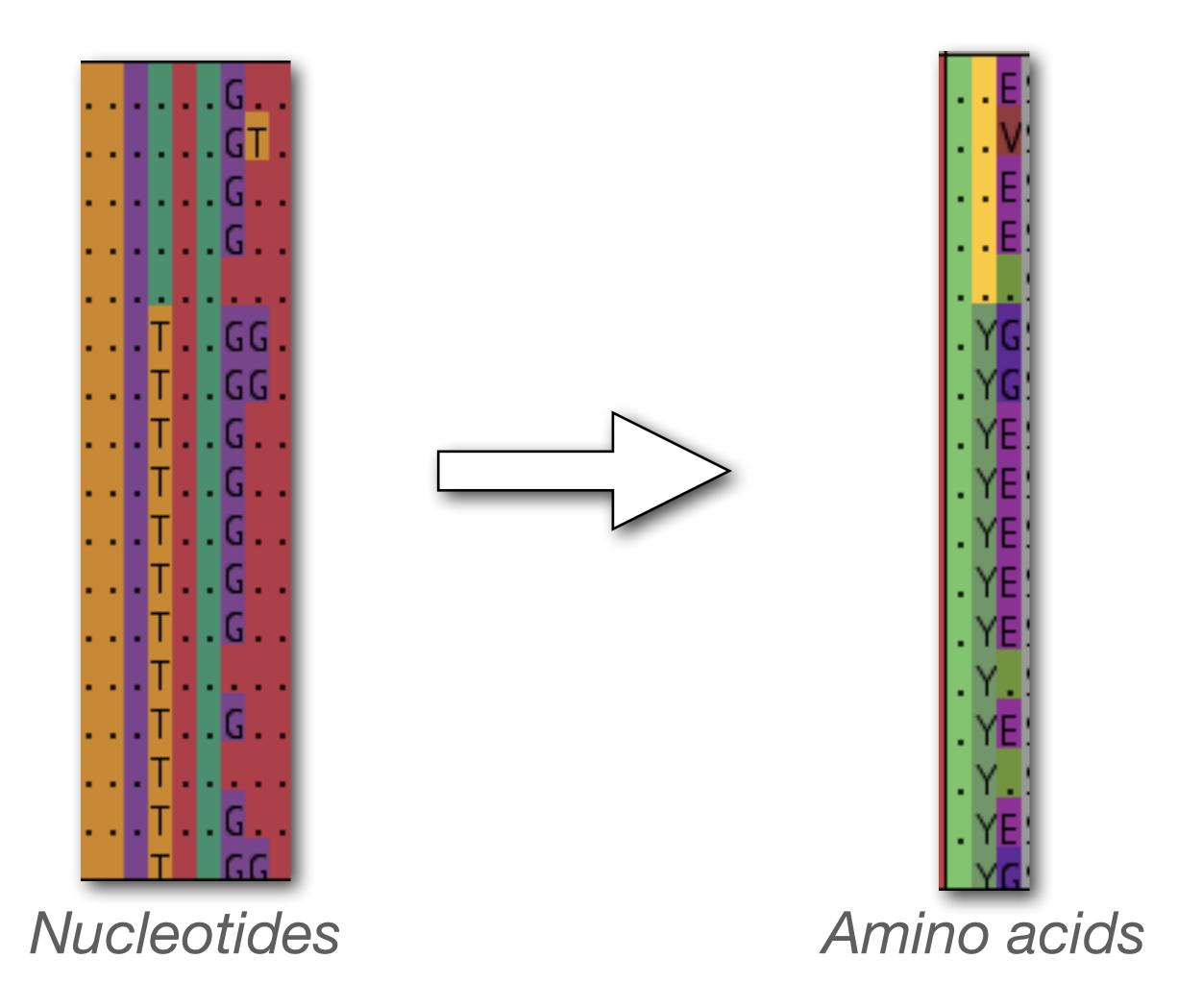
## Diversification: an antigenic site in H3N2 IAV hemagglutinin



## Molecular signatures of selection

- Because synonymous substitutions do not alter the protein, we often posit that they are neutral
- The **rate** of accumulation of synonymous substitutions (**dS**) can serve as the neutral background evolutionary rate
- We can compare the rate of accumulation of non-synonymous substitutions (dN), which alter the
  protein sequence, to dS and use their ratio to classify the nature of the evolutionary process

$$dS \sim \frac{\text{number of fixed synonymous mutations}}{\text{proportion of random mutations that are synonymous}}$$

$$dN \sim \frac{\text{number of fixed non-synonymous mutations}}{\text{proportion of random mutations that are non-synonymous}}$$