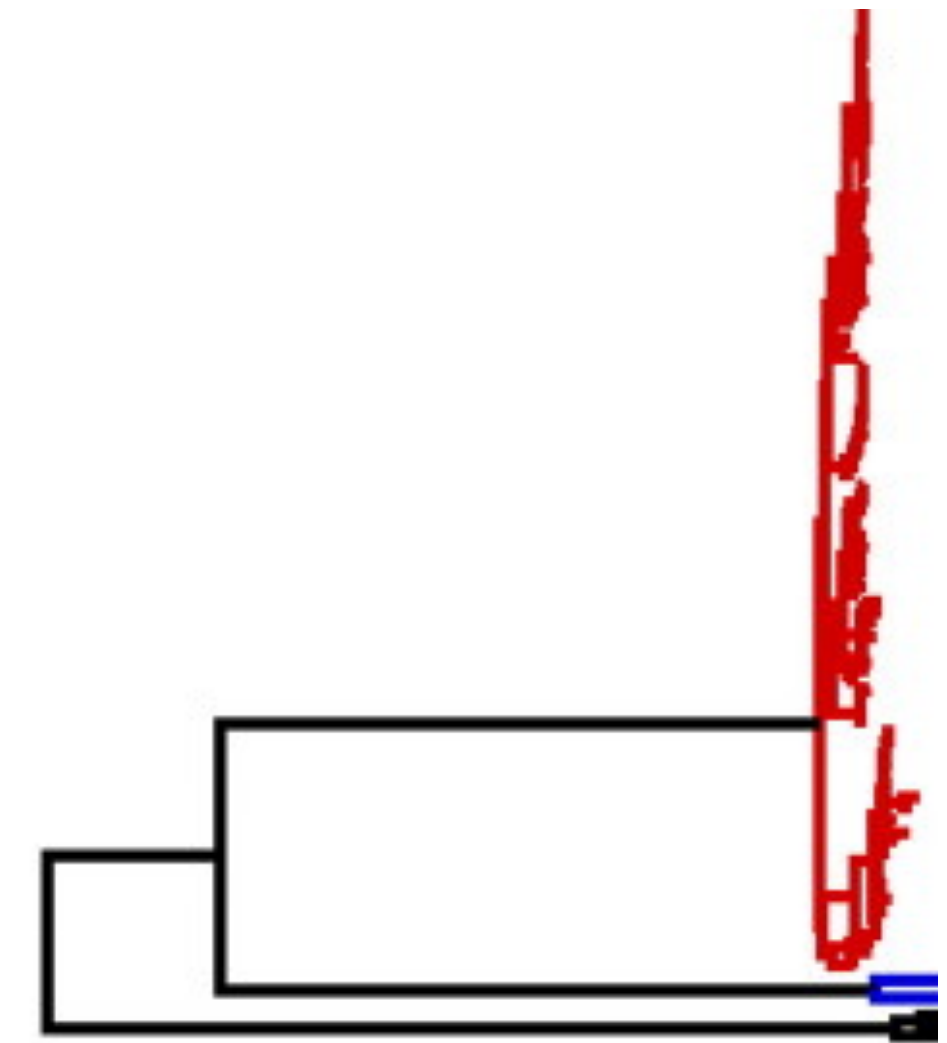
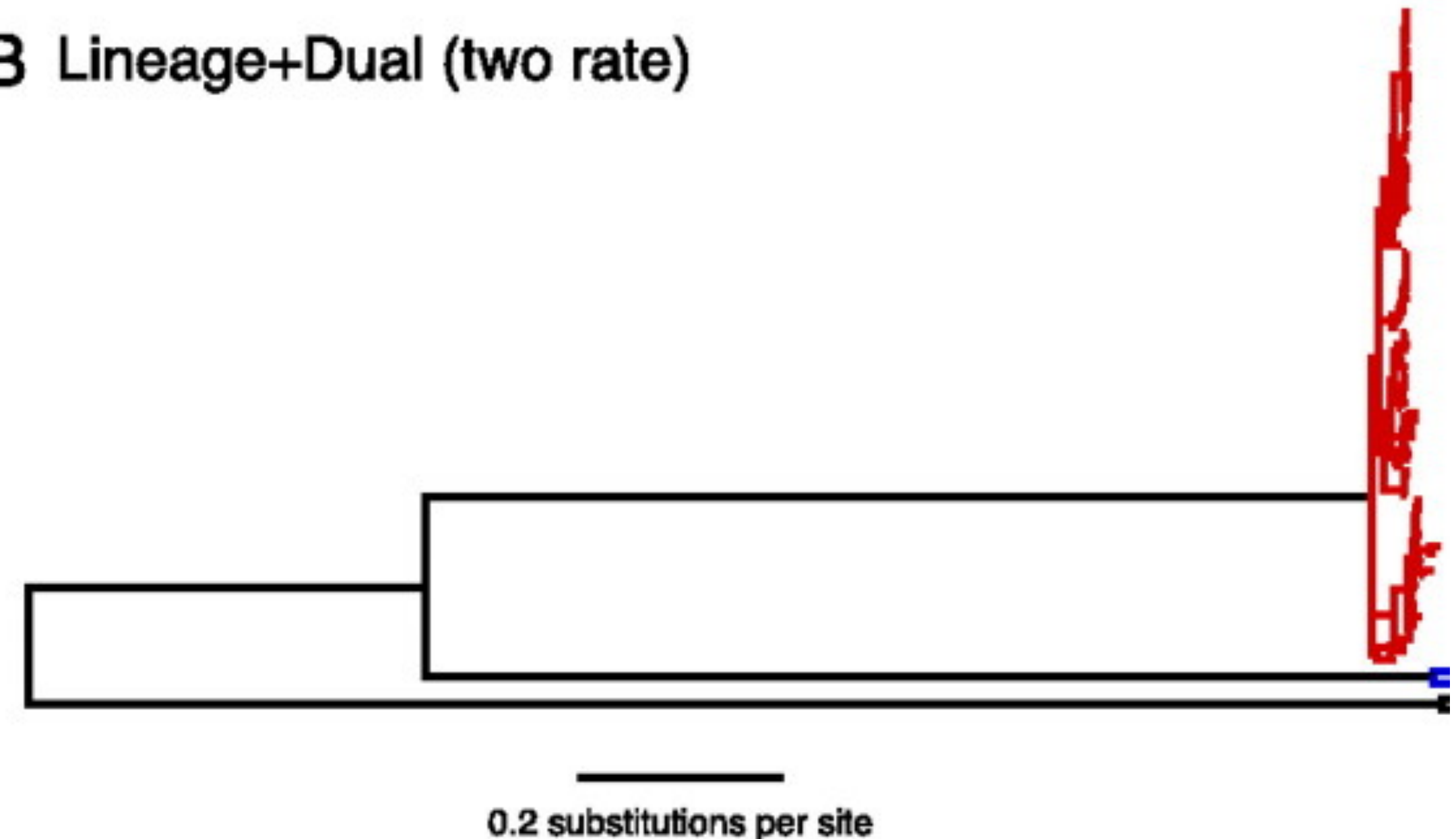


- Using models that do not vary selection pressure across lineages yields a patently false “*too young*” estimate for the origin of **measles** (about 600 years ago)
- This estimate is refuted by clear historical records which suggest that measles is at least 1,500-5,000 years old
  - *This includes a treatise by a Persian physician Rhazes about **differential diagnosis of measles and smallpox** published circa 600 AD.*
- Same patterns found for corona-viruses, ebola, avian influenza and herpesvirus

A GTR +  $\Gamma_4$



B Lineage+Dual (two rate)



# Interpreting dN/dS for intra-host and intra-species pathogen

- **dN/dS** can be estimated for all sorts of sequence data (e.g., it has been done for cancer SNP data)
- Traditional interpretation of dN/dS is based on the assumption that **substitution ~ fixation**
- Not the same for intra-species / intra-host pathogens
  - Much of variation is due to polymorphism, or even dead-end mutations
  - This is because selection has not had a chance to “filter” mutations (except for patently deleterious ones)
  - This often manifests as differences in selective “regimes” between tips and internal branches