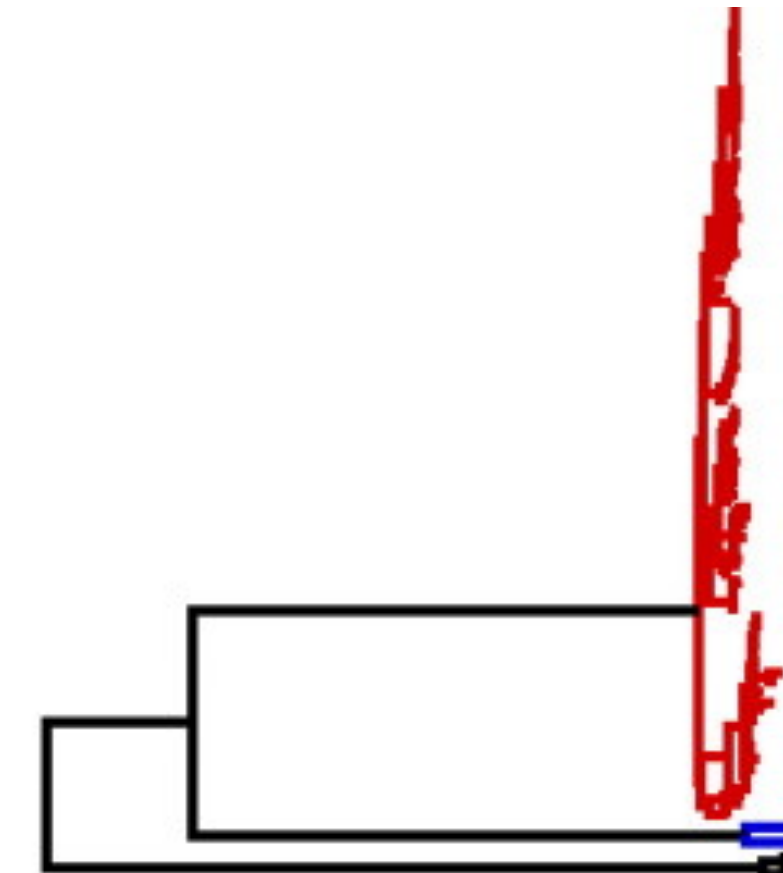


- Using models that do not vary selection pressure across lineages yields a patently false “*too young*” estimate for the origin of **measles** (about 600 years ago)
- This estimate is refuted by clear historical records which suggest

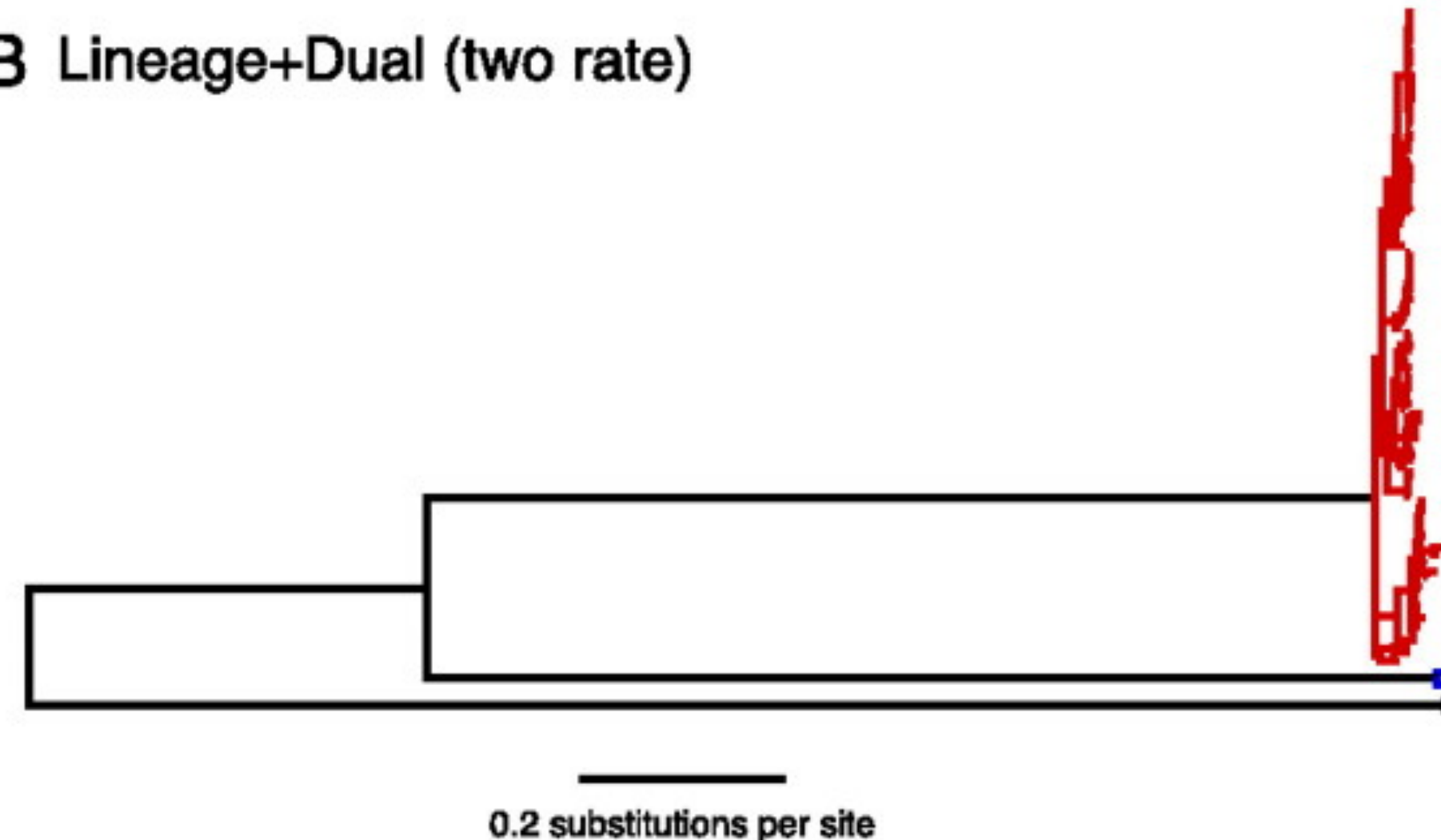
that measles is at least 1,500-5,000 years old

- *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

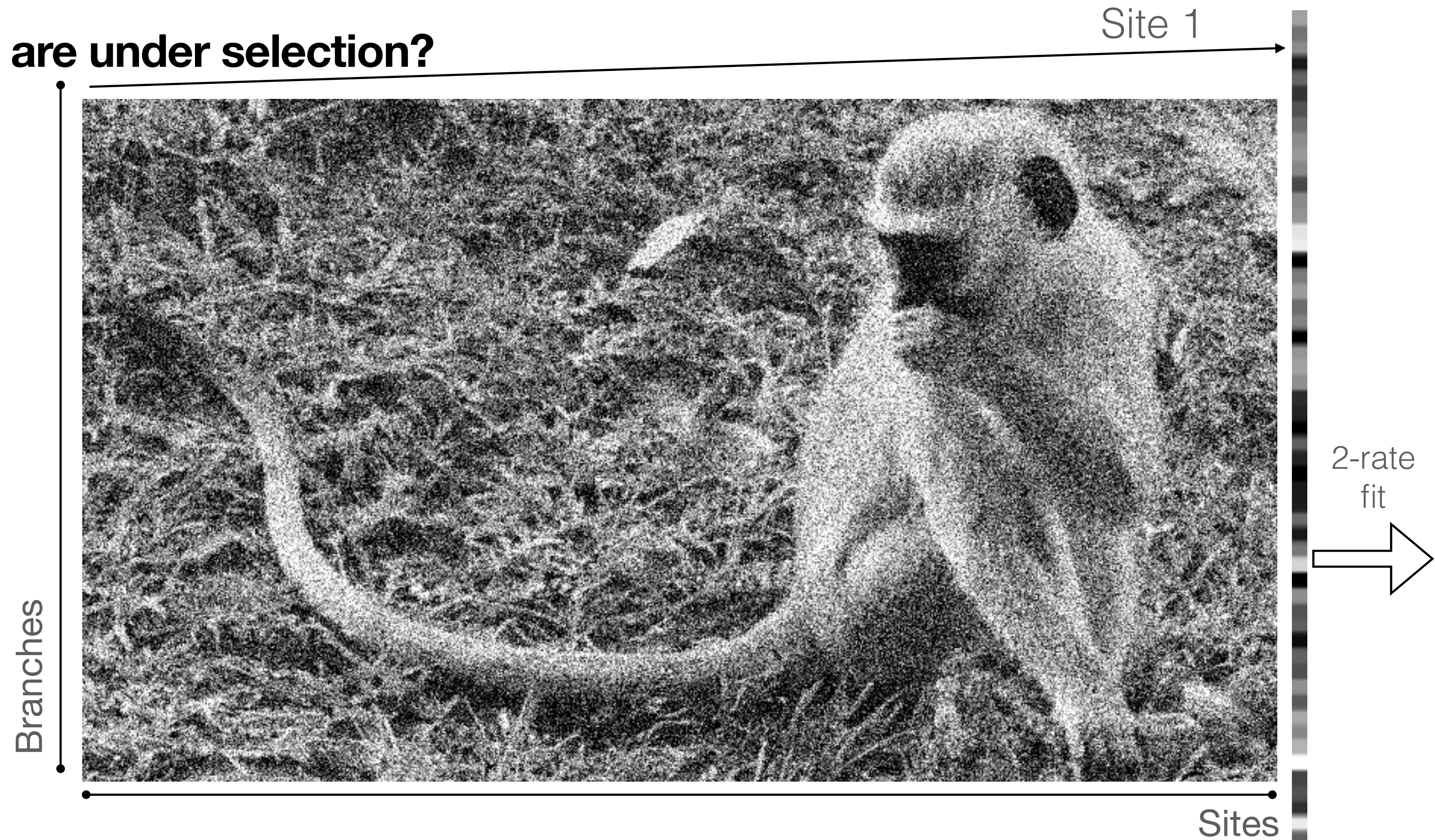
A GTR + Γ_4



B Lineage+Dual (two rate)



Which sites are under selection?



For each image column, is there a significant proportion of bright pixels, once the column has been reduced to 2 colors only?



[MEME]: at a given **site**, each branch is a draw from a 2-bin (d_S , d_N) distribution, which is inferred from that site only. Test if there is a proportion of branches with $d_N > d_S$ (LRT)