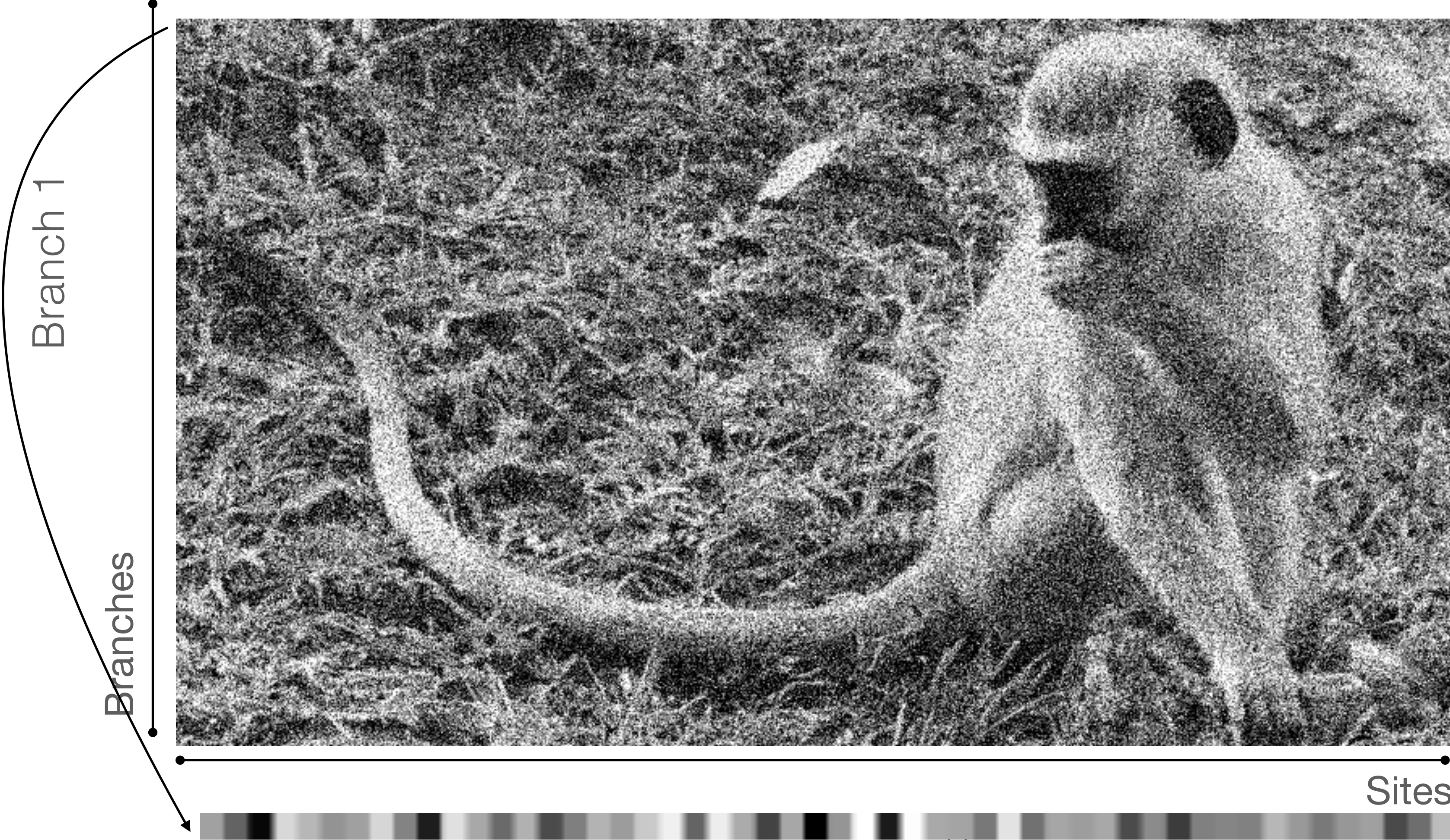# Any questions on the previous material?

We covered the following methods in HyPhy: FitMG94, BUSTED

This estimates a mean gene-wide dN/dS (with FitMG94)

Or estimates dN/dS through a branch-site method (with BUSTED)

Which branches are under selection?

Branch 1

Branches

Sites

3-rate fit

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

🌲 [aBSREL]: at a given branch, each site is a draw from an N-bin (dN/dS) distribution, which is inferred from all data for the branch. Test if there is a proportion of sites with dN/dS > 1 (LRT). **N** is derived adaptively from the data.