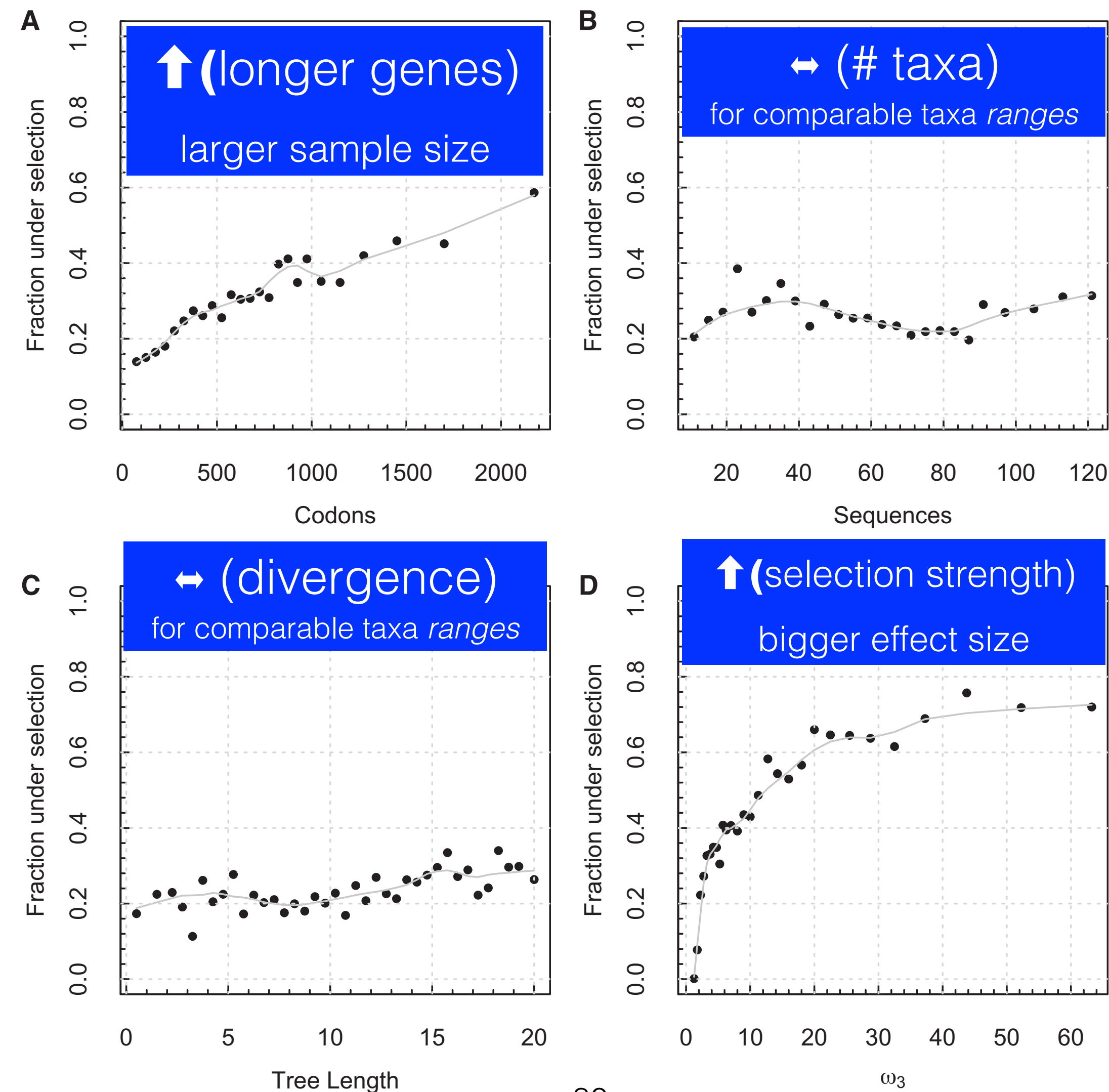


# Where does the power come from for BUSTED?

## *An analysis of ~9,000 curated gene alignments from selectome.unil.ch*



# 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)