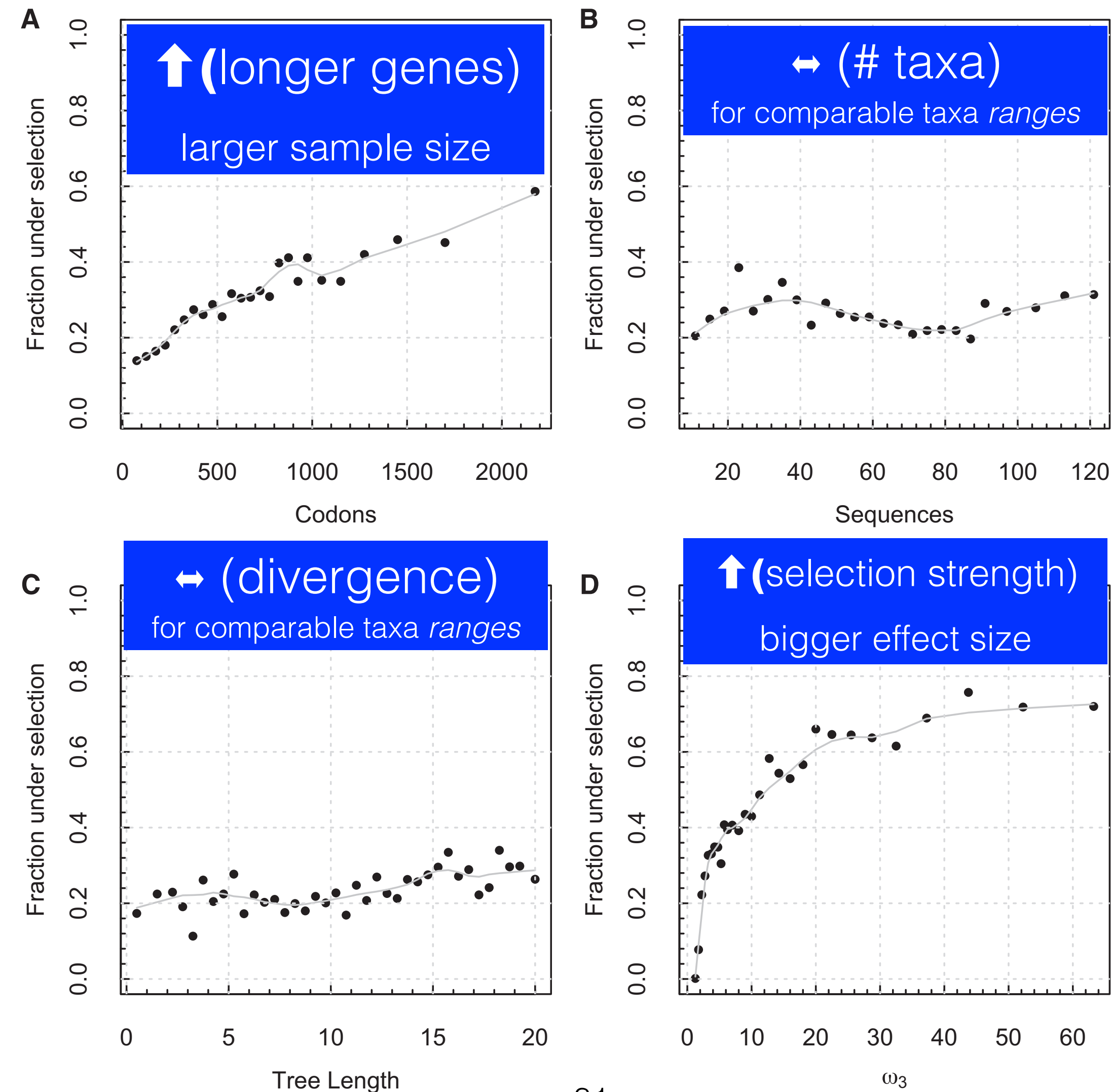


Where does the power come from for BUSTED?

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

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

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