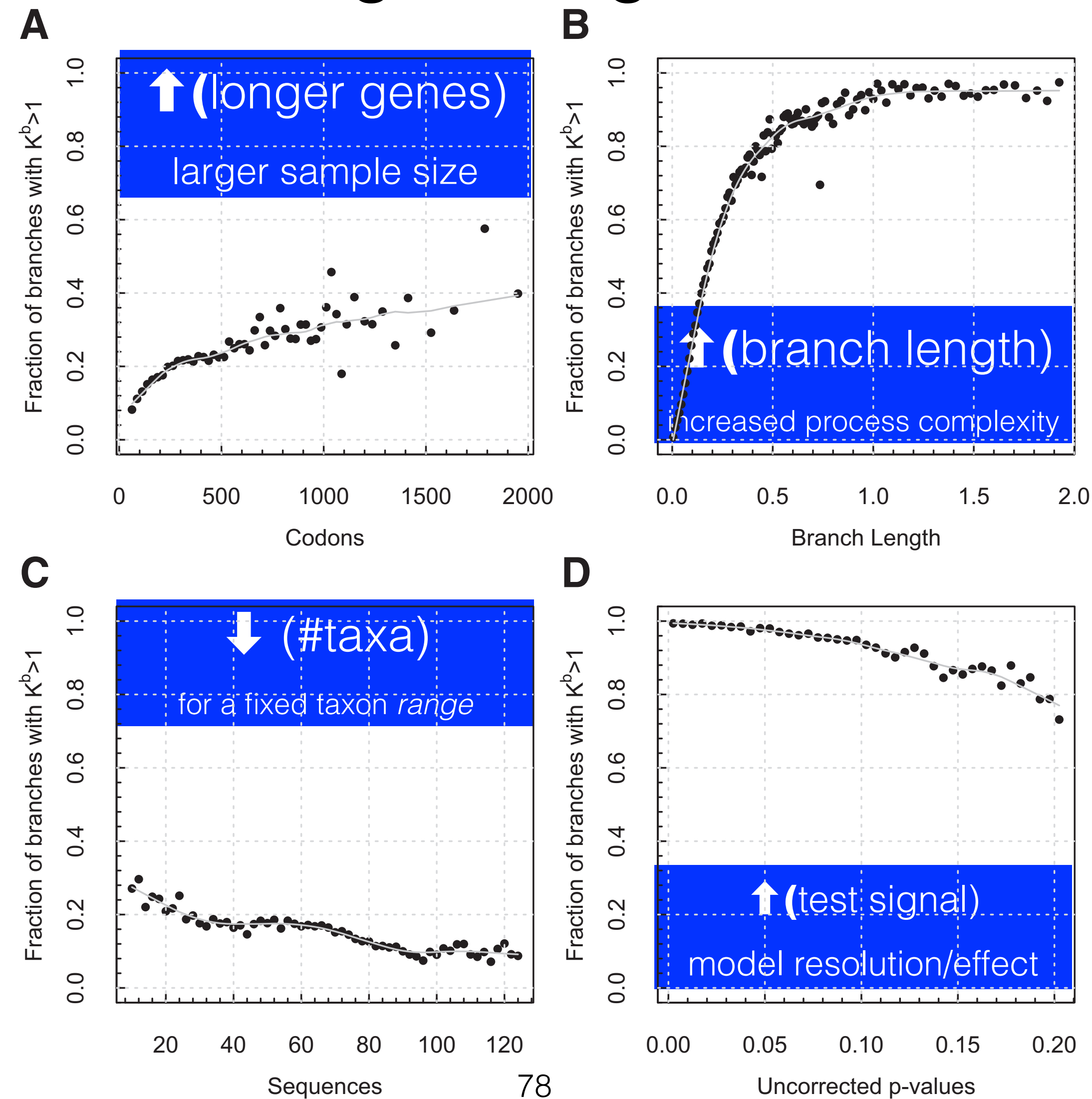


# Correlates of evolutionary complexity

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



# Unanticipated effects of bad modeling assumptions

- Models that fail to account for significant shifts in selective pressures through lineages also significantly underestimate branch lengths
- An instructive example is long-range molecular dating of pathogens, where recent isolates (e.g., 30-50 years of sampling) are used to extrapolate the date when a particular pathogen had emerged
- This creates the situation when terminal branches in the tree have relatively high dN/dS (within-host level evolution), while deep interior branches have very low dN/dS (long term conservation)