

# Questions about the previous material?



We covered the FEL and SLAC selection analyses, site-level methods

- Fixed Effects Likelihood (**FEL**)
  - A simpler alternative to MEME (looks for pervasive selection)
  - May be more suited for smaller datasets or datasets of low divergence
- Single Likelihood Ancestor Counting (**SLAC**)
  - A counting-based approach
  - Good for data exploration and visualization

# It is not unexpected that site-level positive results can occur when a gene-level test does not yield a positive result

- **Lack of power for the global test:** if the proportion of sites under selection is very small, a mixture-model test, like BUSTED, will miss it.
- **Model violations:** MEME supplies much more flexible distributions of  $dN/dS$  over sites; compared to alignment-wide k-bin ( $k=3$ ) BUSTED distribution.
- **False positives at site-level:** our site-level tests have good statistical properties, but each positive site result could be a false positive; FWER correction would make site-level tests too conservative.
- **Summary:** gene-level selection tests need a minimal proportion of sites to be under selection to be powered; site-level tests should not be used to make inferences about gene-level selection.