- Sensitive dN/dS (ω) models can "zoom-in" on small fractions of alignments

- Those could (should*) be real biological features indicative of accelerated evolutionary rates

- But they can (and often appare to be) artifacts due to MSA/sequence quality issues

- These apparent issues remain even after applying current state-of-the-art MSA/filtering tools (e.g. PRANK, PREQUAL) in this space

- Need a method to separate the signal from the noise

- What are some obvious **evolutionary** features of the noise?

- We developed this method out of necessity, because the signal was being overwhelmed by the noise in high-throughput screens for selection.

- Let's examine another example (from Zoonomia), where we downsample the genes down to 16 species (using **treemer**)

- Two genes that show evidence of episodic positive diversifying selection

  - One likely "real"

  - One likely "not real"

  - How can we tell?