

Constructing a *Bacteroides* species tree

- The genus *Bacteroides* is the most common and abundant bacterial genus in the human gut microbiome
- Horizontal gene transfer (HGT) is rampant
 - High diversity of mobile genetic elements
 - Many apparently transferred genetic regions are not associated with a known mobile element
 - HGT is inferred by comparing tree topologies
- Can we trust the *Bacteroides* “species tree”?

Robinson-Fouldes Scores

	CA-ML	Denoised CA-ML	ASTRAL	ASTRID
CA-ML	0			
Denoised CA-ML	0.42	0		
ASTRAL	0.45	0.57	0	
ASTRID	0.54	0.63	0.41	0

