

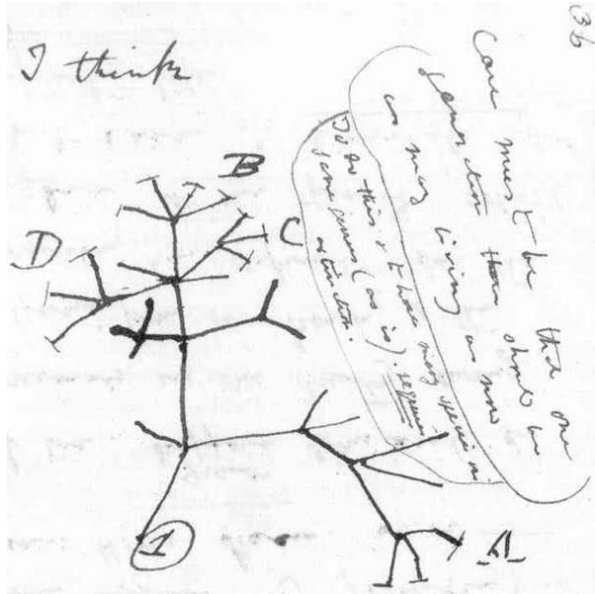


SMTB

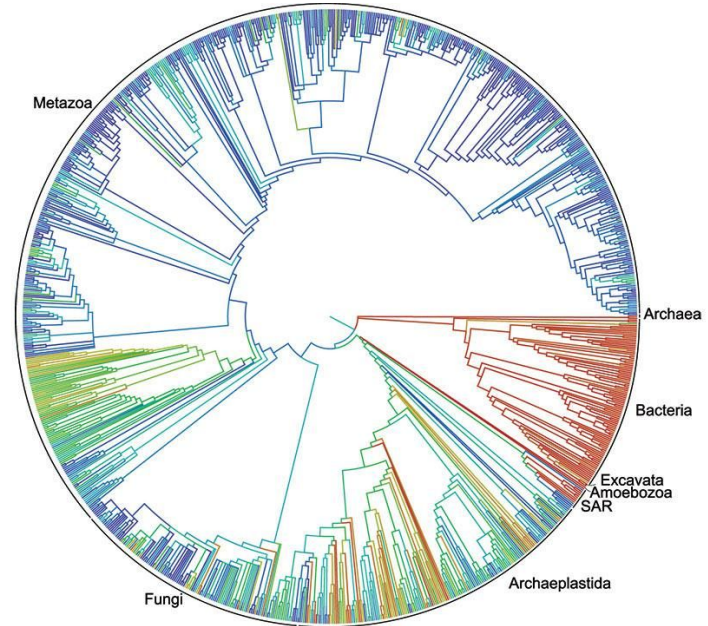
# Laboratory of Phylogenetic Reconstruction of Evolutionary Accidents (Lab PhREAc)

*Danilović Tea, Matach Dzmitry, González Somermeyer Louisa,  
Pal Arka, Riegler Stefan, Redondo Rodrigo*

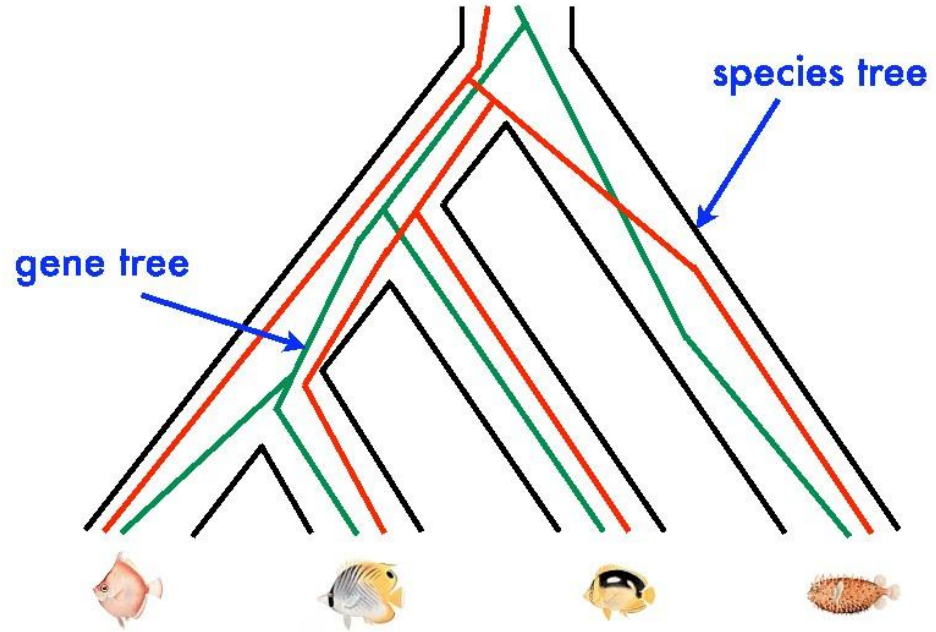
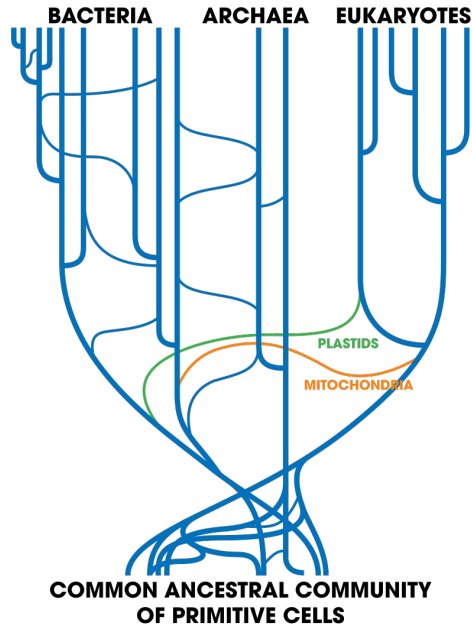
# The Rise (and Fall?) of Phylogenetics



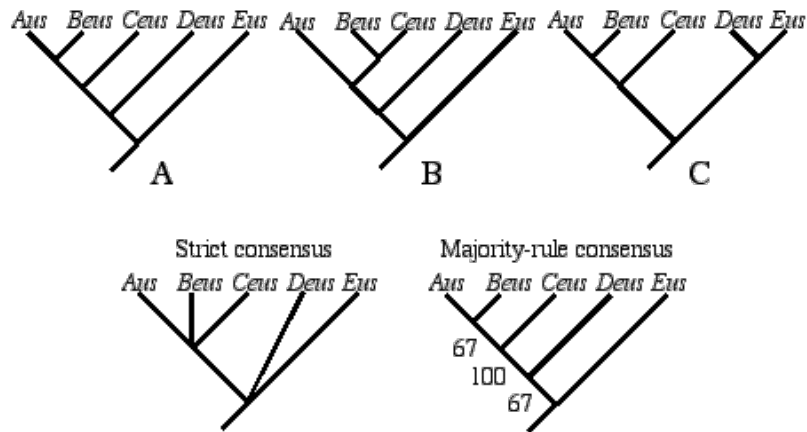
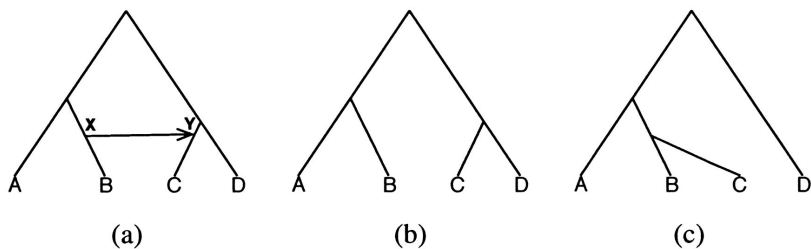
Charles Darwin (1837)



# The Rise (and Fall?) of Phylogenetics



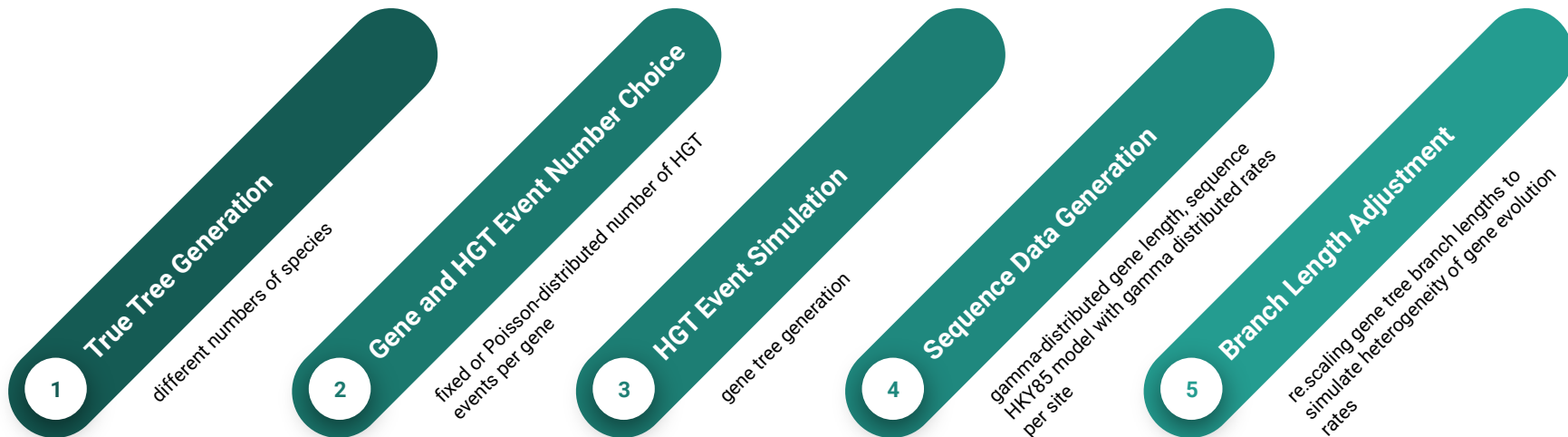
# Solving the Horizontal Gene Transfer Problem - Consensus Trees



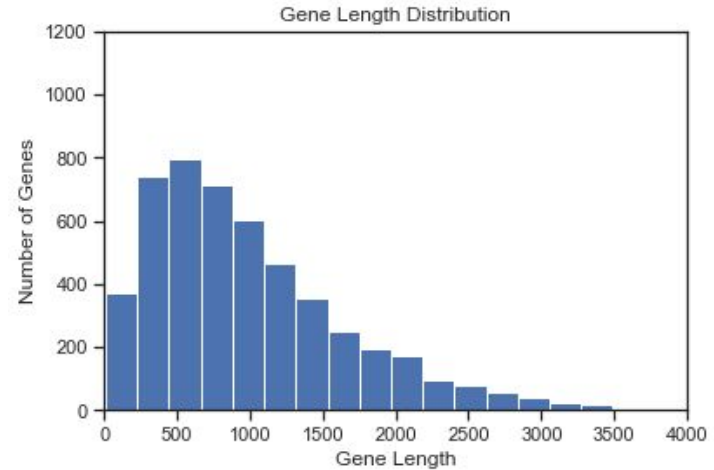
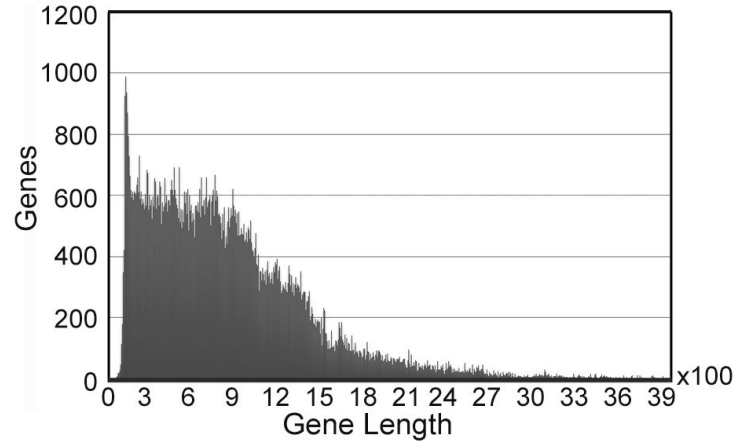
# General Framework



# Simulation Framework

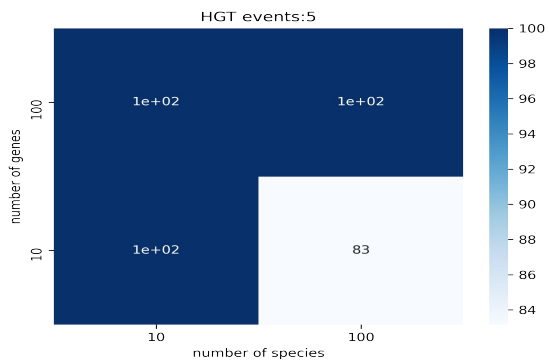
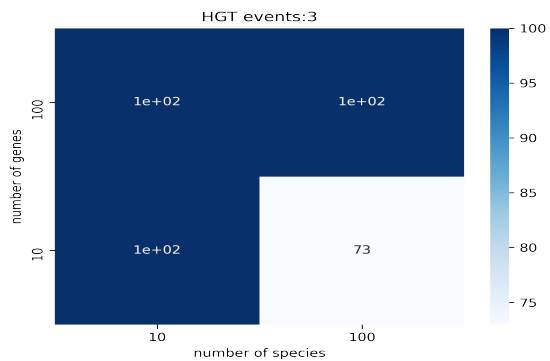
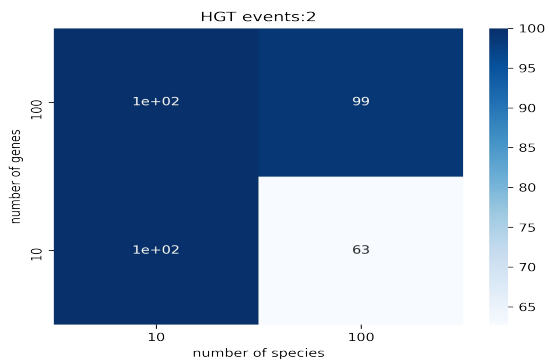
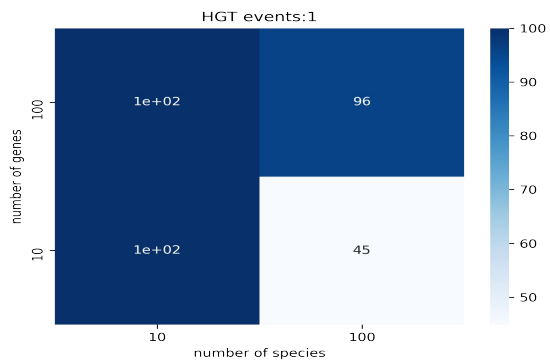


# Gene Length Distribution



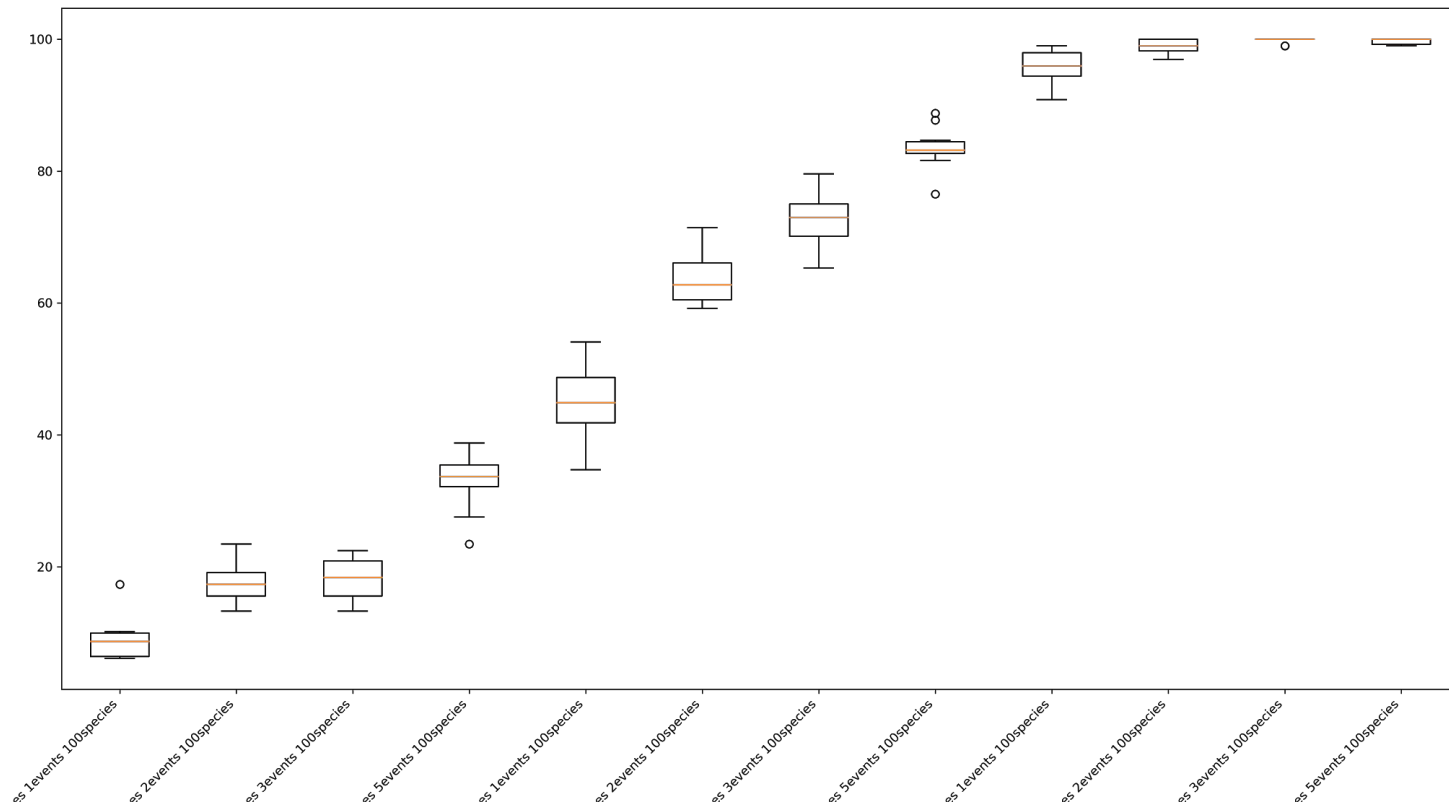
Yang et al. (2009) **More than 9,000,000 Unique Genes in Human Gut Bacterial Community: Estimating Gene Numbers Inside a Human Body.** PLOS ONE

# “Worst Case Scenario” Simulations





# “Worst Case Scenario” Simulations



# Realistic Simulations



# Outlook

- expanding the dataset
  - more genes
  - more species
  - more simulations
- optimizing phylogeny reconstruction
- comparing with Supertree/Supermatrix methods

**Thank you for your attention!**