

# **BUILDING A PHYLOGENETIC TREE**

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# **1. INTRODUCTION**

Feature	Character-Based Methods	Distance-Based Methods
Data Used	Individual characters (nucleotides, amino acids, morphological traits)	Overall genetic or morphological distances between pairs of organisms
Analysis Focus	How characters change (gained, lost, modified) throughout evolution	Pairwise similarity based on distance calculations
Tree Building Goal	Find the tree with the fewest evolutionary changes to explain the data	Build a tree that reflects the pairwise distances
Advantages	More detailed evolutionary information	Faster and computationally simpler
Disadvantages	Can be computationally expensive for large datasets	May lose information by condensing data into distances

# Distance-Based Methods

Sequence  
alignment

X: AAT TTG TCC

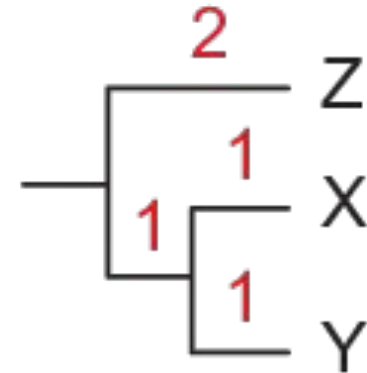
Y: AAT TTG TAA

Z: AAT TAA GGG

Pairwise genetic  
distance matrix

X	—		
Y	2	—	
Z	4	4	—
	X	Y	Z

Distance  
tree

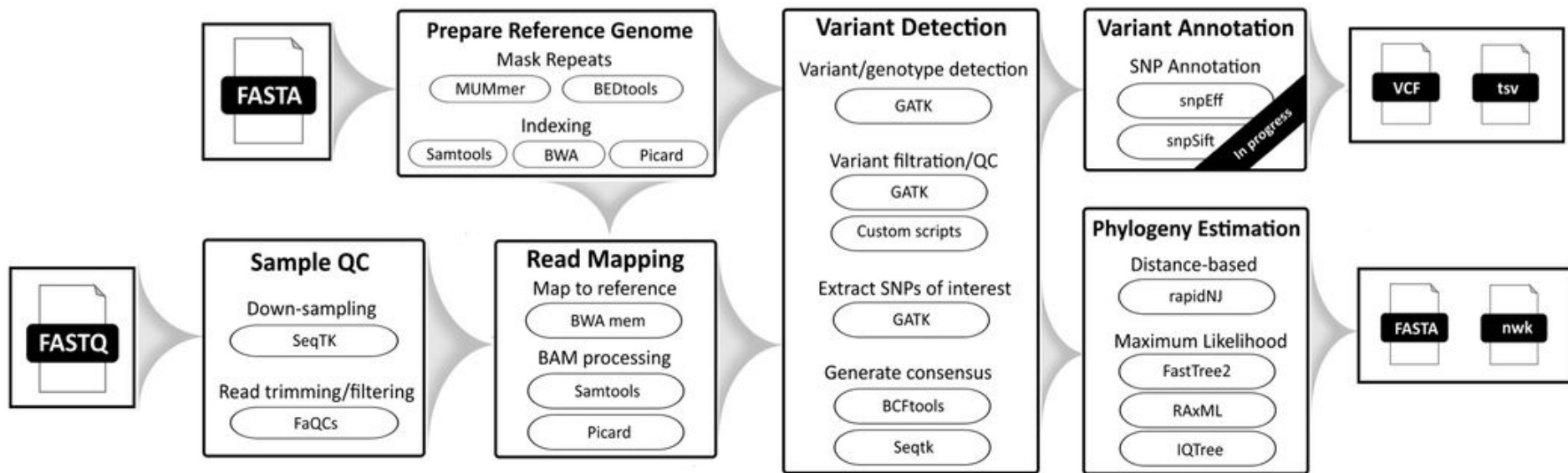


Feature	Character-Based Methods	Distance-Based Methods
<b>Examples of Methods</b>	Parsimony, Maximum Likelihood	Neighbor-Joining, UPGMA
<b>Tools</b>	Molecular Evolutionary Genetics Analysis (MEGA), FastTree2, RAxML, IQTree	MEGA, rapidNJ
<b>Visualization</b>	Molecular Evolutionary Genetics Analysis (MEGA), iTOL, ETE Toolkit TreeViewer, Microreact	

## **2. CASE STUDY**

# Whole-genome-sequencing bioinformatic pipeline

**Problem:** The fungal pathogen *Candida auris* is an emerging global health concern that can cause invasive infections, can spread rapidly in healthcare settings, and is characterized by high rates of antifungal drug resistance.





# Practice

[https://github.com/UeenHuynh/MGMA\\_2024/tree/main/lecture9/9.3\\_Building-a-Phylogenetic-Tree](https://github.com/UeenHuynh/MGMA_2024/tree/main/lecture9/9.3_Building-a-Phylogenetic-Tree)