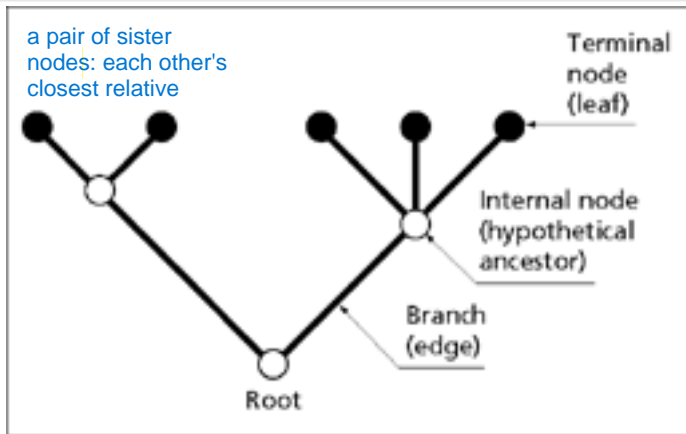
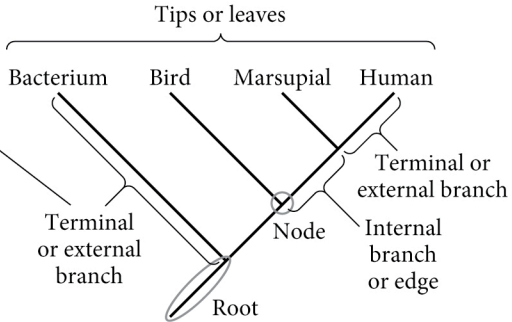
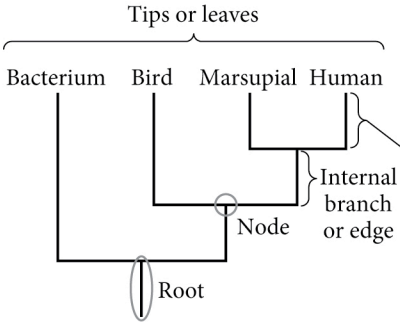
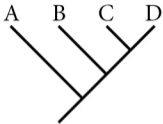


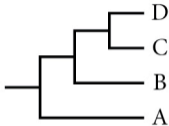
# Tree Terminology



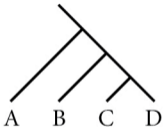




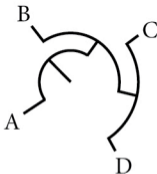
Diagonal (up)



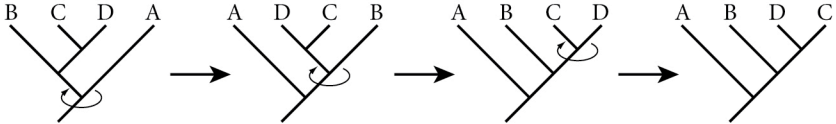
Rectangular (right)



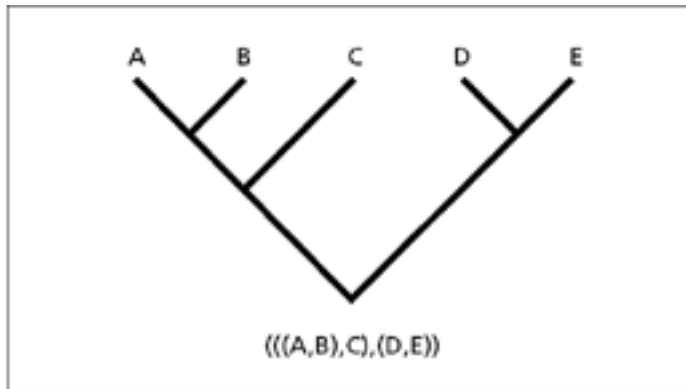
Diagonal (down)



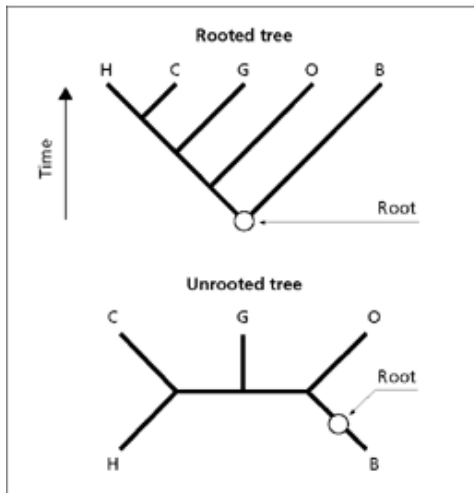
Circle



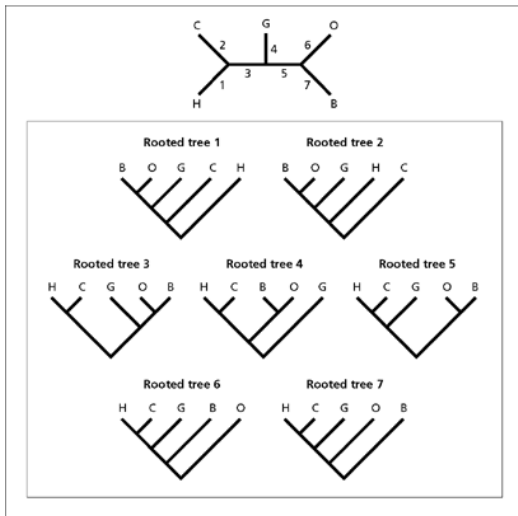
# The Newick Tree Format



## Rooted and Unrooted Trees

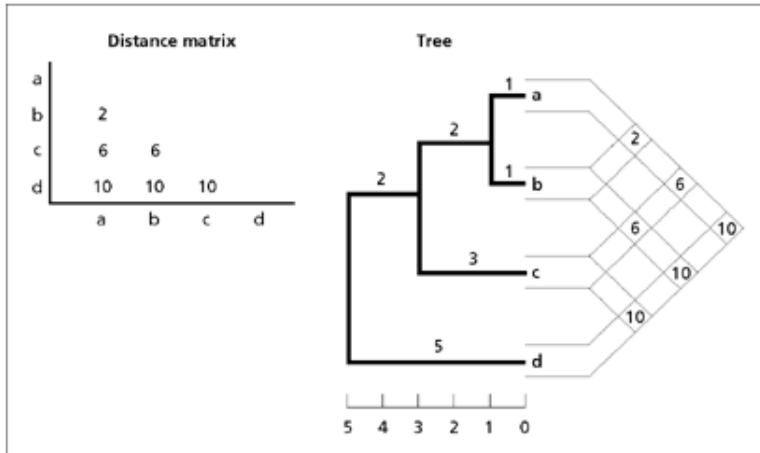


## Rooted and Unrooted Trees (Cont'd)



# Tree Distances

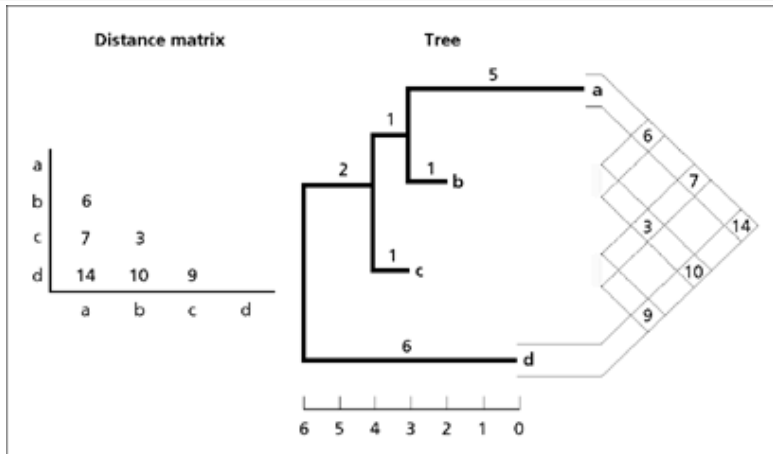
## Ultrametric Distance



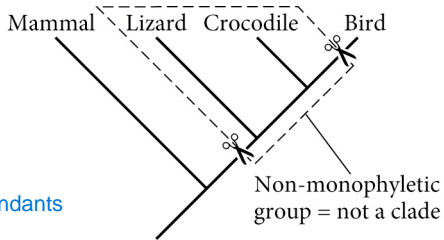
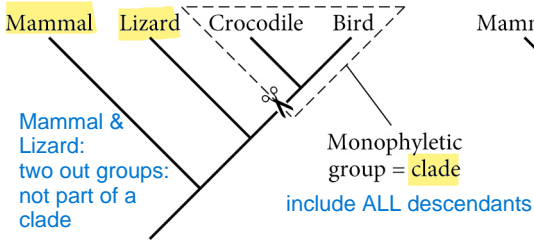


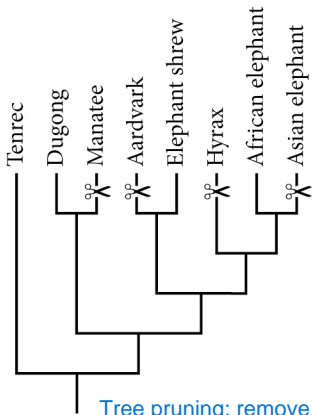
# Tree Distances

## Additive Distance

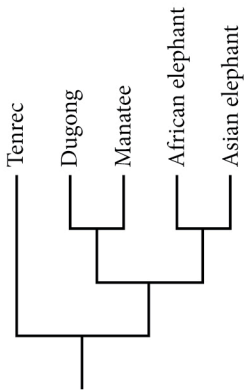
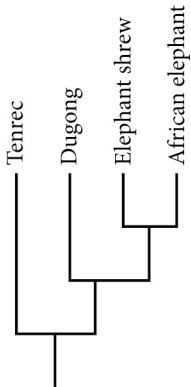
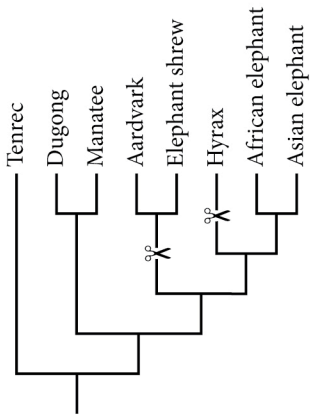






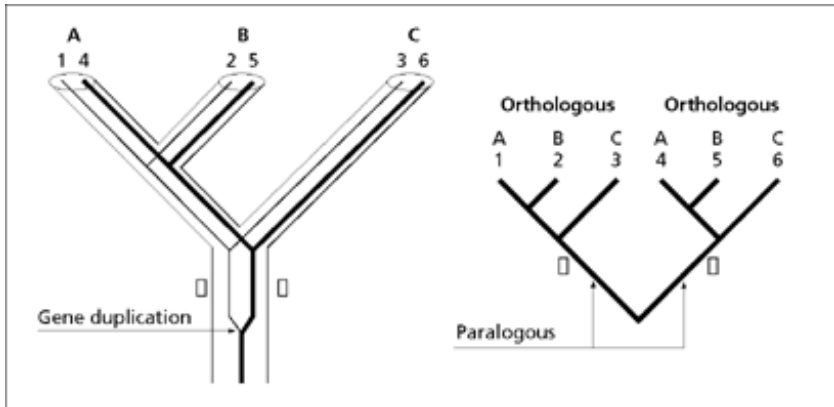


Tree pruning: remove ALL descendants of a branch



# Gene Tree and Species Tree

## Orthology and Paralogy



homologs

orthologs

paralogs

orthologs

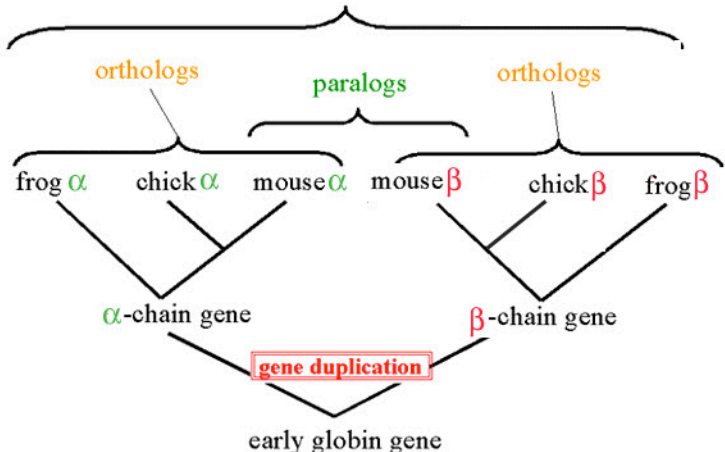
frog  $\alpha$  chick  $\alpha$  mouse  $\alpha$  mouse  $\beta$  chick  $\beta$  frog  $\beta$

$\alpha$ -chain gene

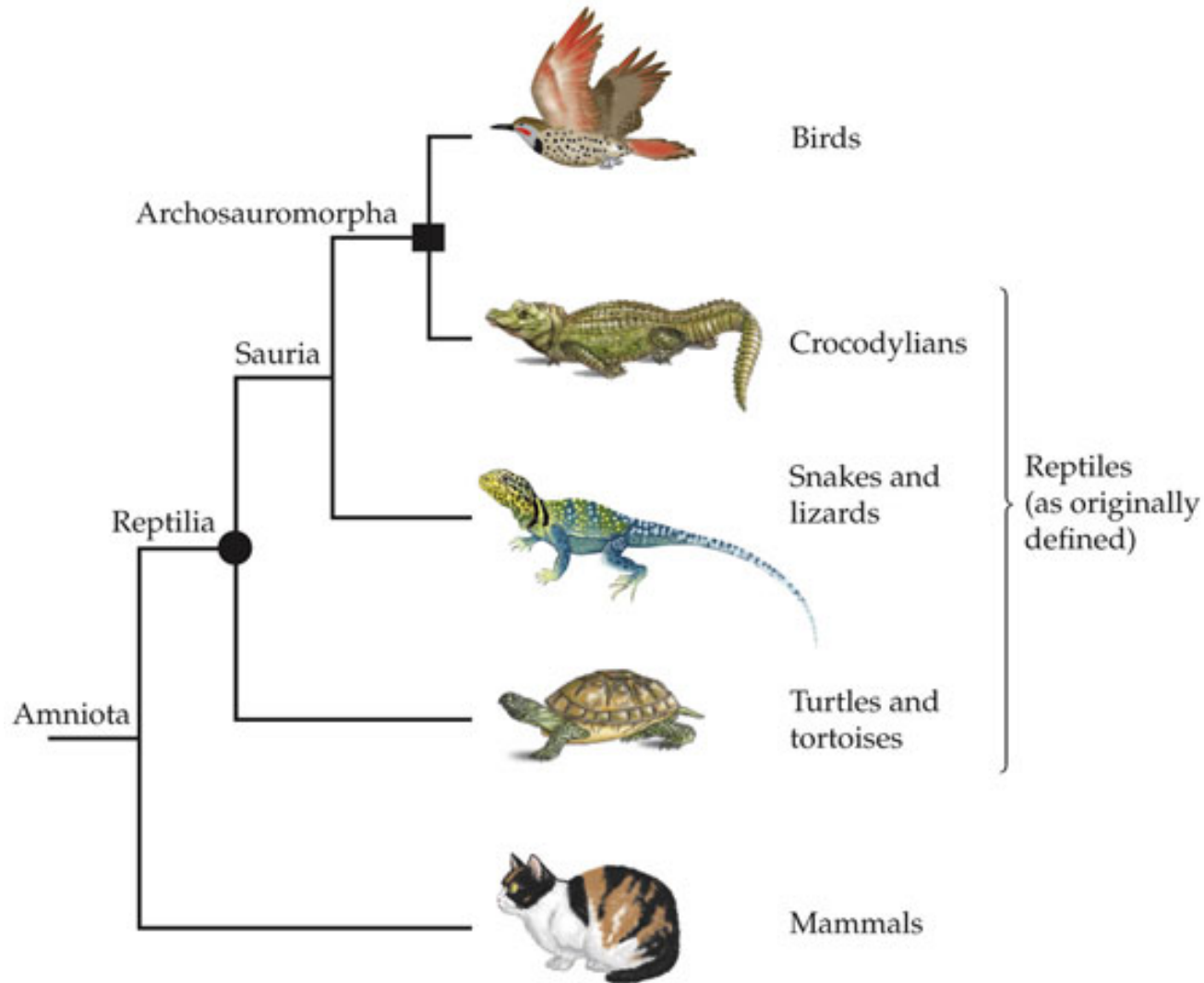
$\beta$ -chain gene

gene duplication

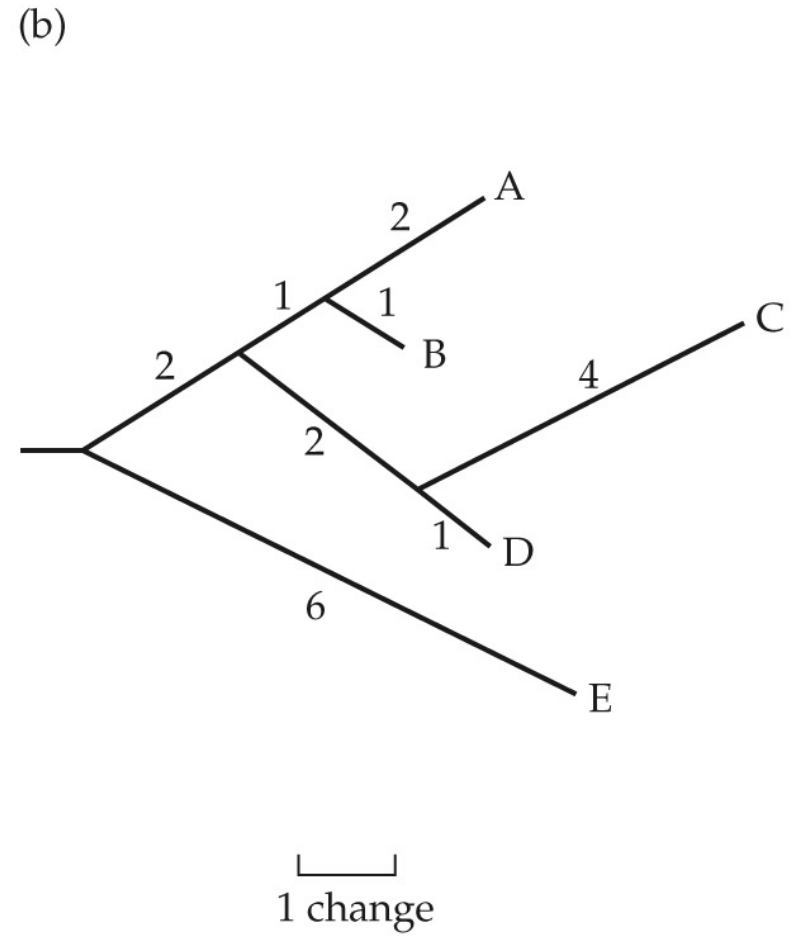
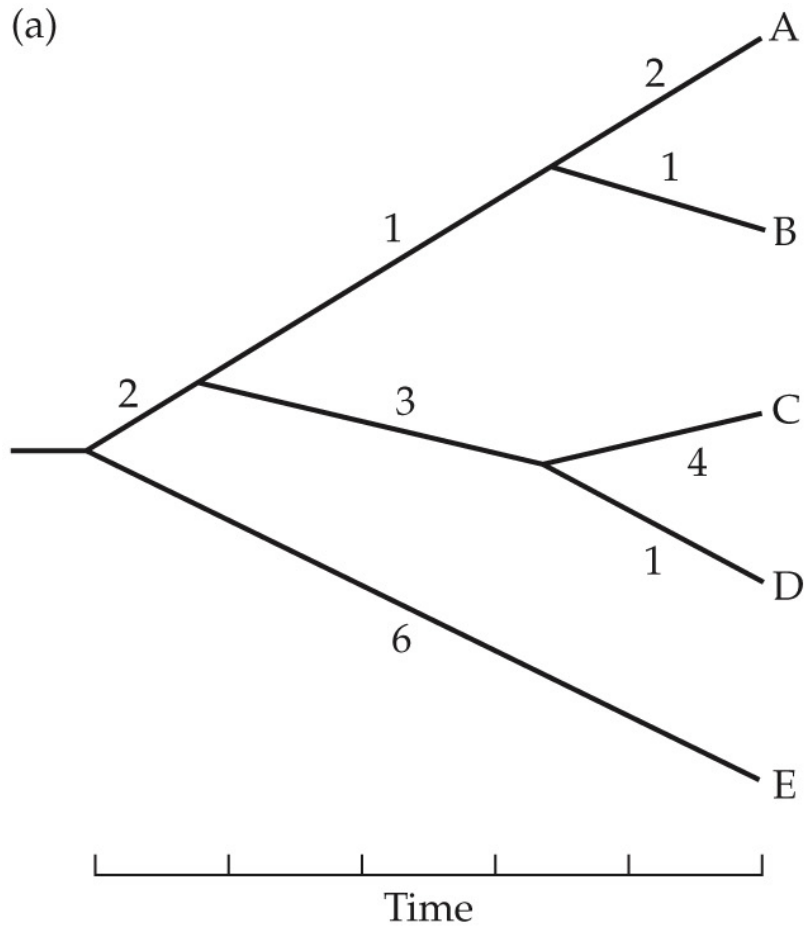
early globin gene



# Monophyletic & Paraphyletic Groups

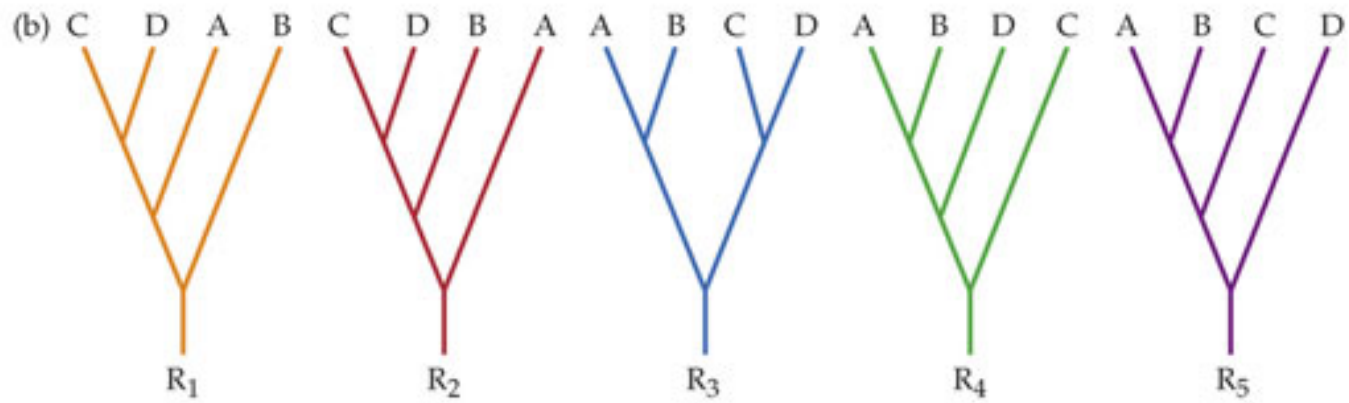
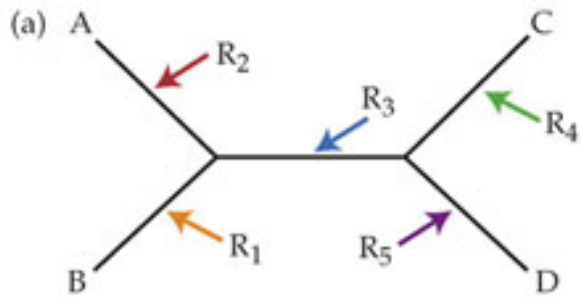


# Scaled & Un-scaled Trees



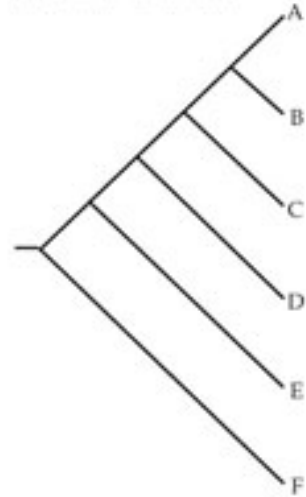


# Rooted and Unrooted Trees

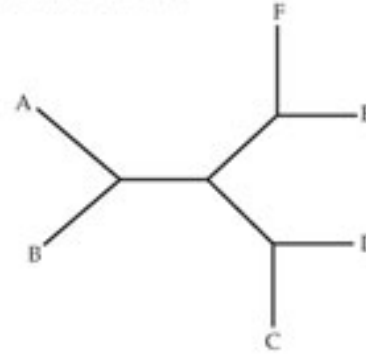


# Newick Tree Format

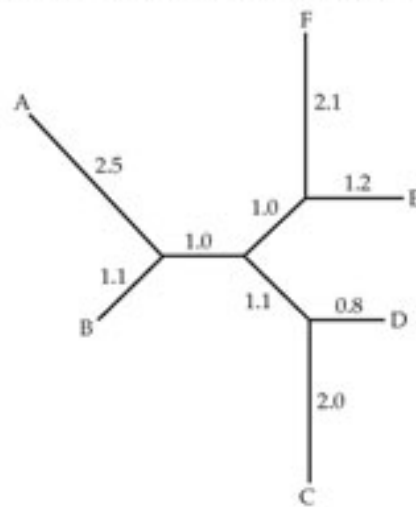
(a)  
 (((((A,B),C),D),E),F);



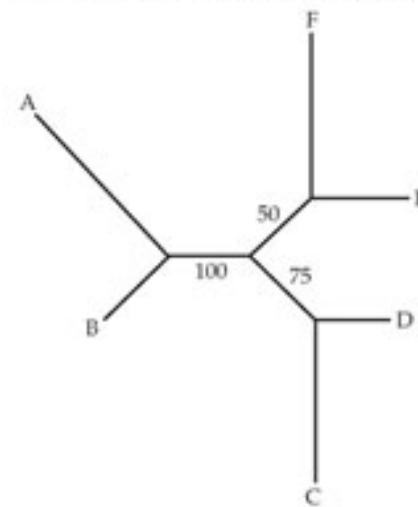
(b)  
 ((A,B),(C,D),(E,F));



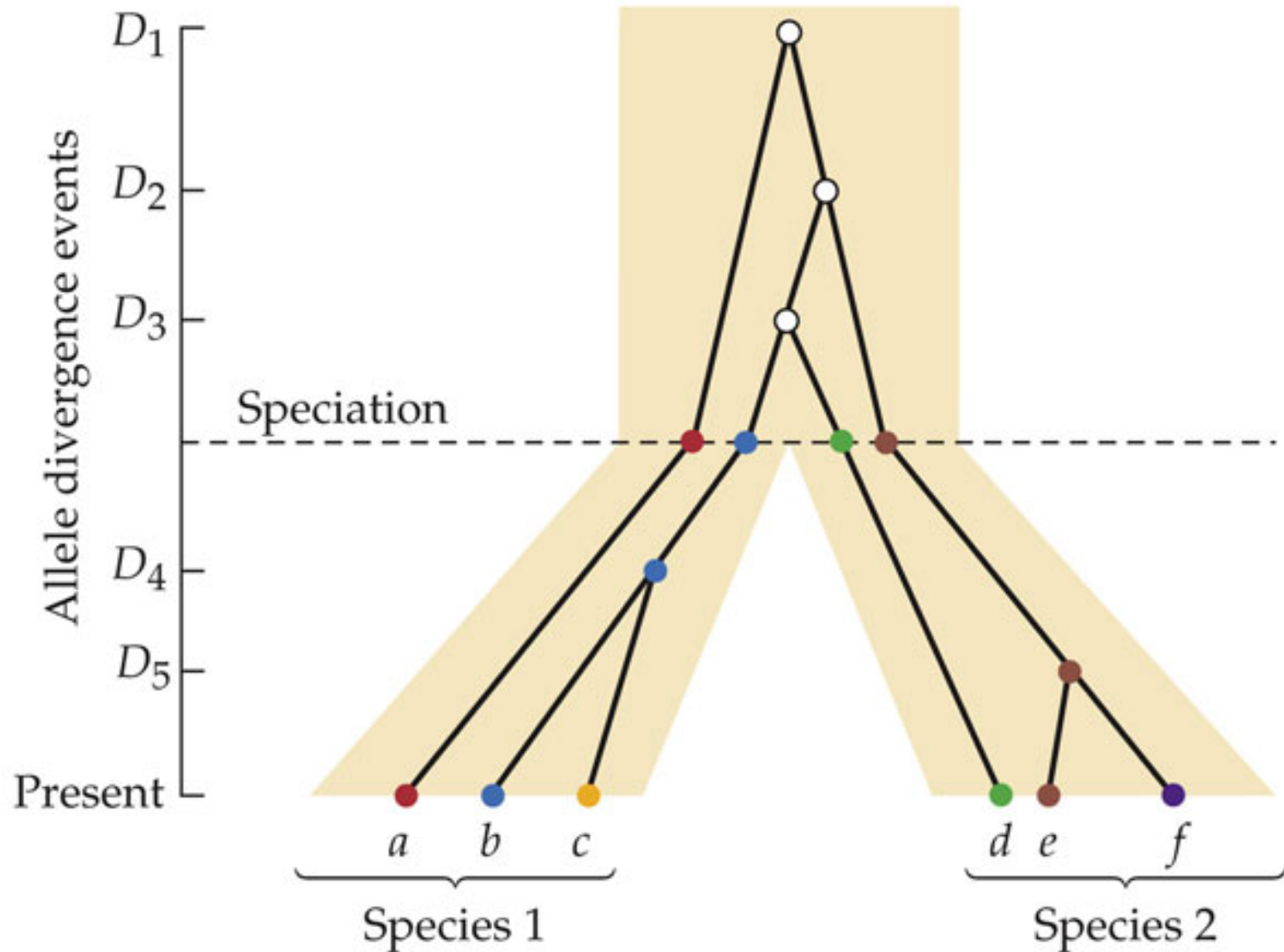
(c)  
 ((A:2.5,B:1.1):1.0,(C:2.0,D:0.8):1.1,(E:1.2,F:2.1):1.0);



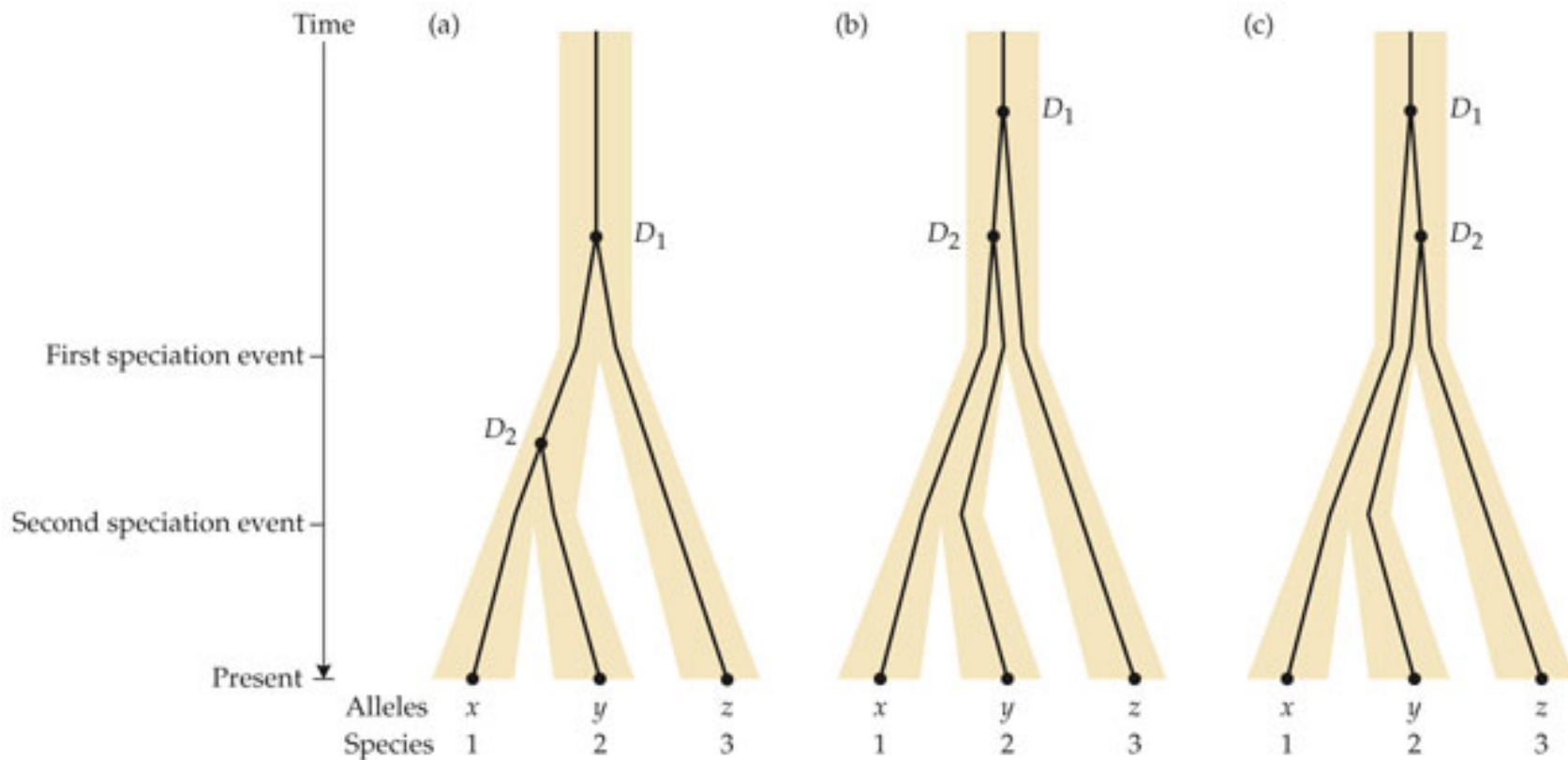
(d)  
 ((A:2.5,B:1.1):1.0,[100],[C:2.0,D:0.8):1.1[75],[E:1.2,F:2.1):1.0[50]]);



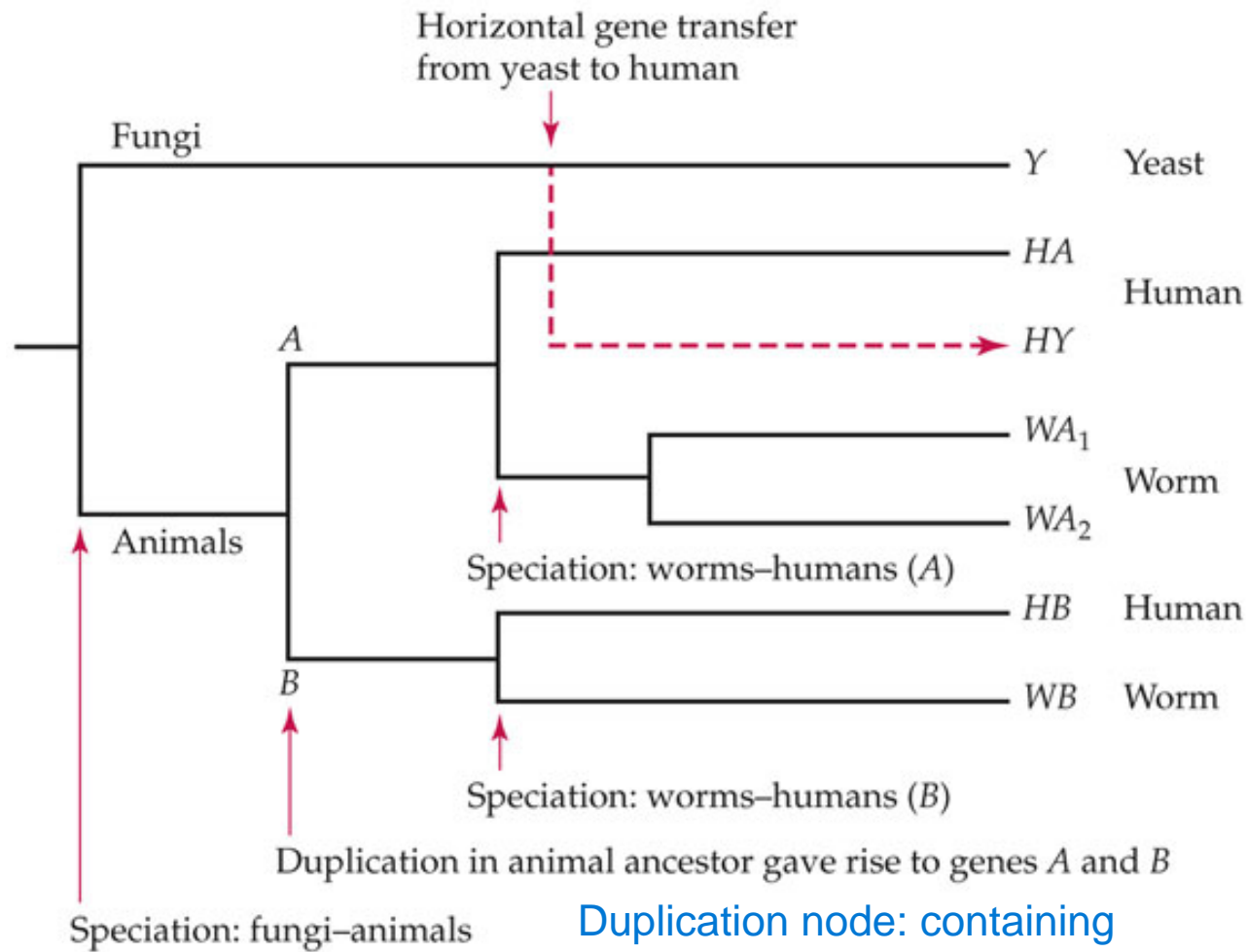
# Incomplete Lineage Sorting



# Gene Tree vs Species Tree



# Orthology vs Paralogy



Duplication node: containing overlapping species between two descendant clades

Collapse a branch: shrink its length to 0 (towards parent node, without removing any descendants)

