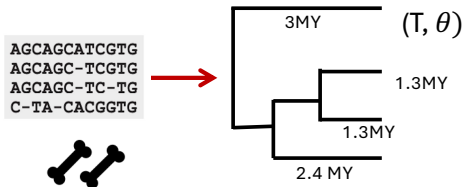


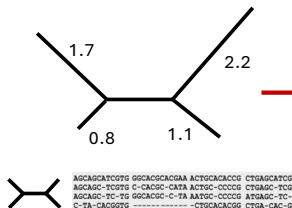
A)

## Traditional pipelines

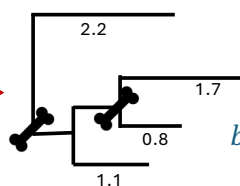
## Bayesian Analysis



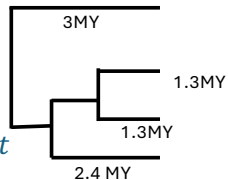
## Concatenation with ML



## Rooting



## ML Dating

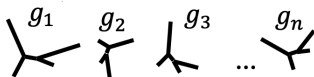


$$b_i = \mu_i \Delta t$$

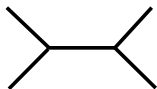
## New pipeline

## Gene tree estimation

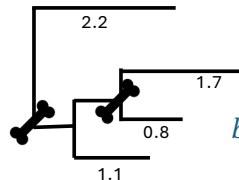
AGCAGCATCGTG GGCACGCACGAA ACTGCACACCG CTGAGCATCG  
AGCAGC-TCGTG C-CACGC-CATA ACTGC-CCCCG CTGAGC-TCG  
AGCAGC-TC-TG GGCACGC-C-TA AATGC-CCCCG ATGAGC-TC-  
C-TA-CACGGTG -----CTGCACACGG CTGA-CAC-G



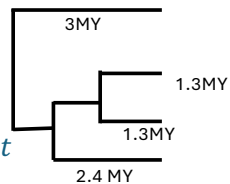
## Summary method



## SU branch length estimation + Rooting



## ML Dating



$$b_i = \mu_i \Delta t$$