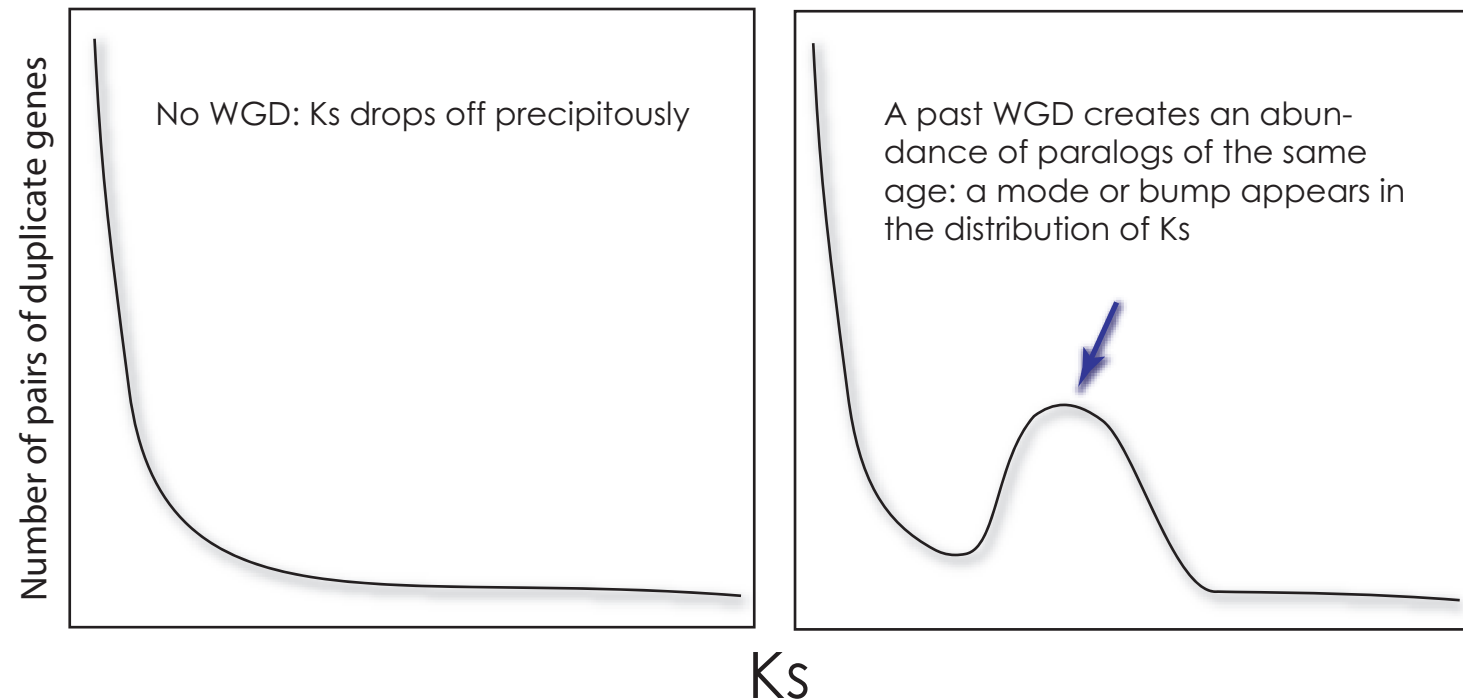


Determining the genome-wide distribution of K_s (silent site substitutions)

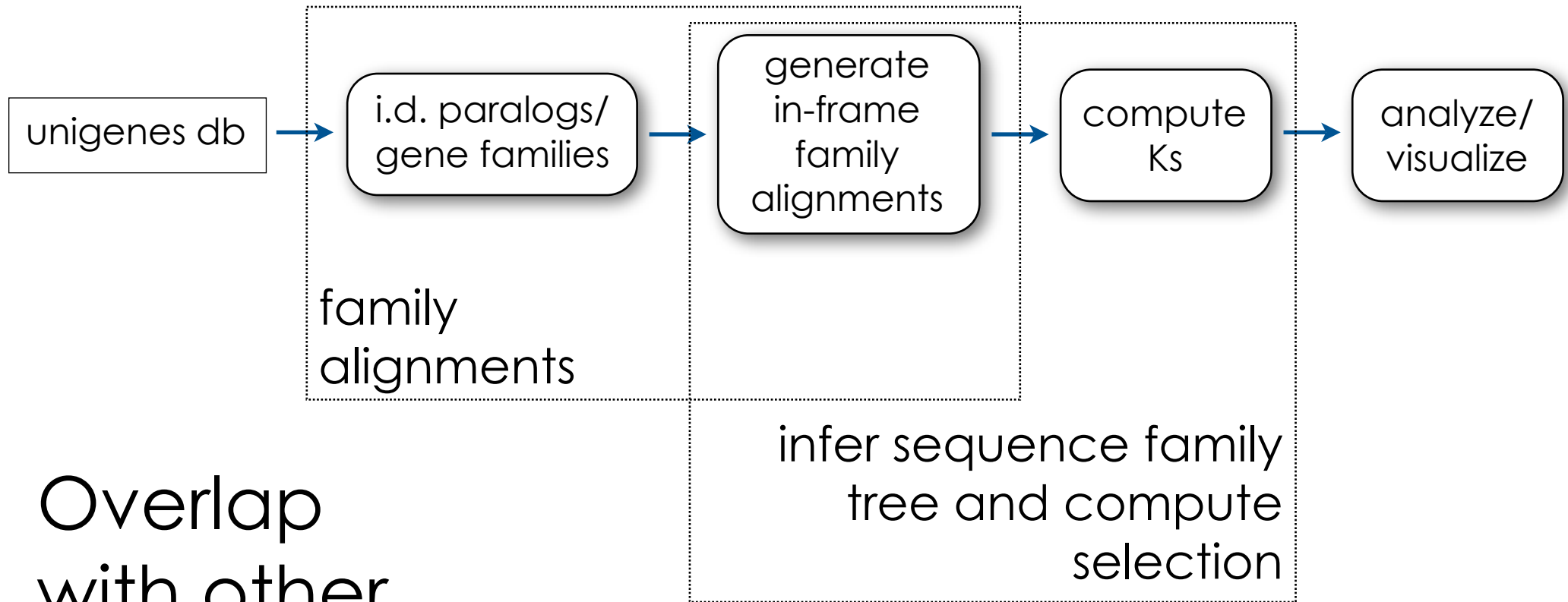


Uses “gene space” sequences: ESTs/unigenes

Standard analysis to study

- past whole genome duplication (WGD)
- broader studies of K_s and patterns in the evolution of duplicated genes and gene families
- studies of paralogs and homologs

Analysis pipeline: general terms



Overlap
with other
use-cases

Analysis pipeline: steps

