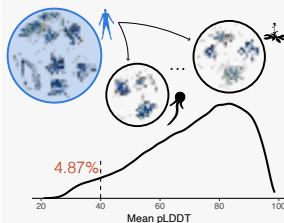


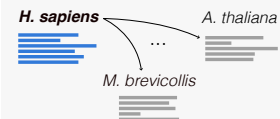
A. Input

1 seed species (*H. sapiens*)
+ 17 eukaryotic species

Excluding proteins with
poor quality structures

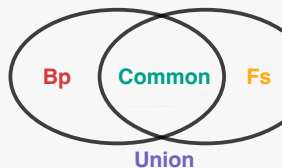


19,555 *H. sapiens* seeds vs
325,576 proteins

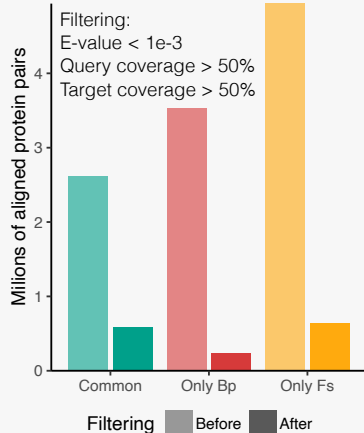


Foldseek (Fs)
BlastP (Bp)

B. Homology search

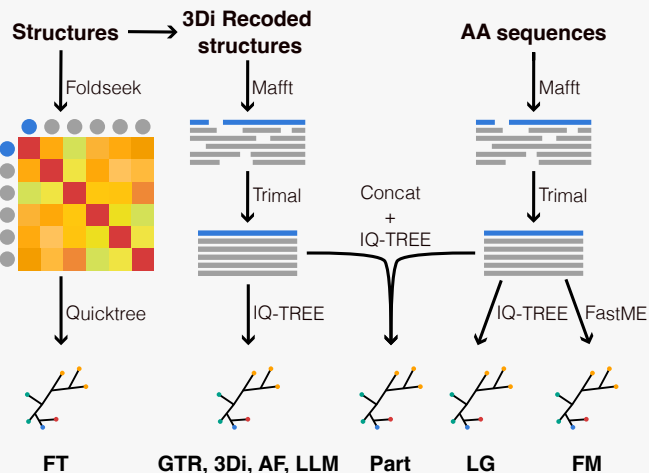


4 target sets
1000 seeds*



C. Tree reconstruction method

For each seed:



Performance Comparison

- Compare distance to species tree (RF distance)
- Compute Quartet Frequencies (Astral-PRO)
- Count gene duplications and losses (Notung)