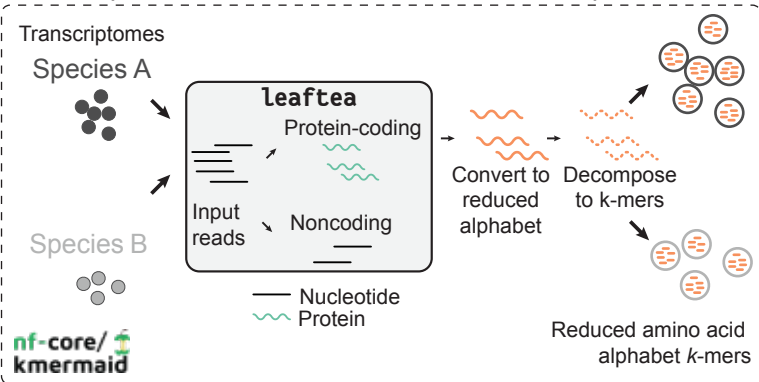
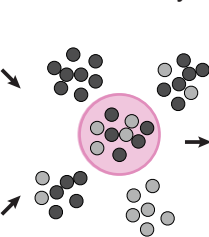


## Subsample amino acid k-mers from each transcriptome



## Cluster on k-mer similarity



## Perform differential k-mer expression and query for functional annotation

