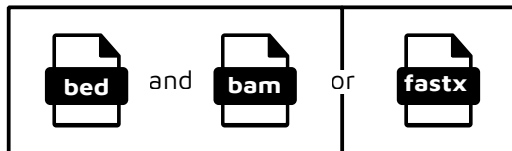


Predict orthologs of Reads



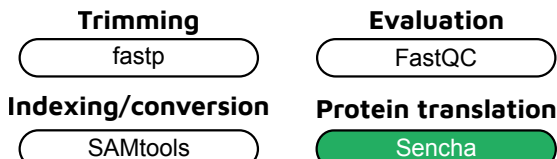
Predict orthologs of k-mer hashes



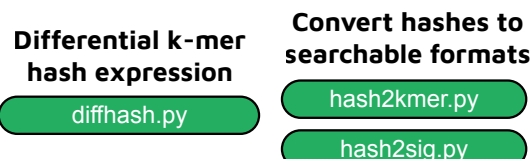
Reference
Proteome



Preprocess reads



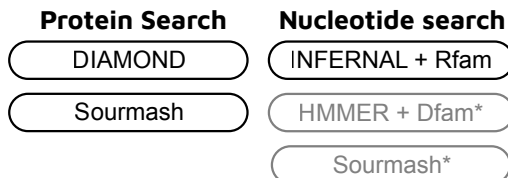
Preprocess k-mer hashes



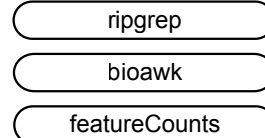
Existing tool

Novel tool

Search for functional annotations



Count differential k-mers in genes



bam

*To be added

Reporting

MultiQC

Files for downstream analyses

