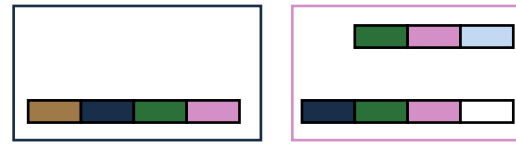
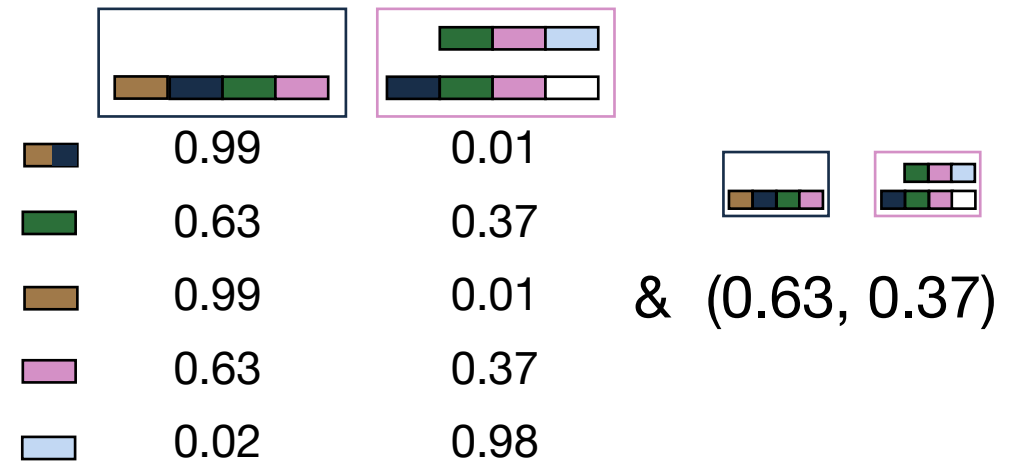


Reference
assemblies



Clustering the
assemblies
(PopPUNK)



**Probabilistic assignment &
abundance estimation (mSWEEP)**

Meta-
genomic reads

Exact pseudoalignment
(Themisto)

**Binning
(mGEMS)**

Assembly
(shovill)

Downstream genomic epidemiology