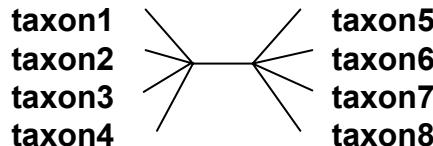
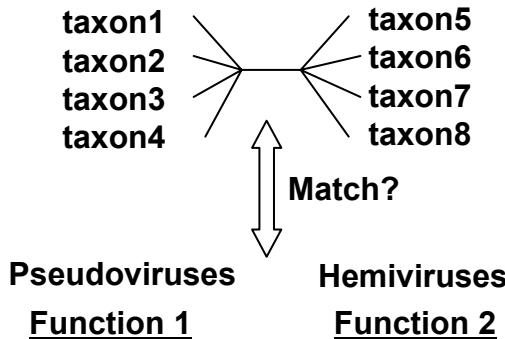


Amino Acid Alignment

Function 1
(half-tRNA priming) { taxon1 ...PRIMINGBYHALFTRNA...
taxon2 ...PRIMINGBYHALFTRNA ...
taxon3 ...PRIMINGBYHALFTRNA ...
taxon4 ...PRIMINGBYHALFTRNA ...

Function 2
(full-tRNA priming) { taxon5 ...PRIMINGBYFULLTRNA ...
taxon6 ...PRIMINGBYFULLTRNA ...
taxon7 ...PRIMINGBYFULLTRNA ...
taxon8 ...PRIMINGBYFULLTRNA ...

Tree from aligned sequences (split cluster)



Predefined functional split