Calculating OTUs

 Distance matrix dist.seqs(fasta=example.final.fasta)

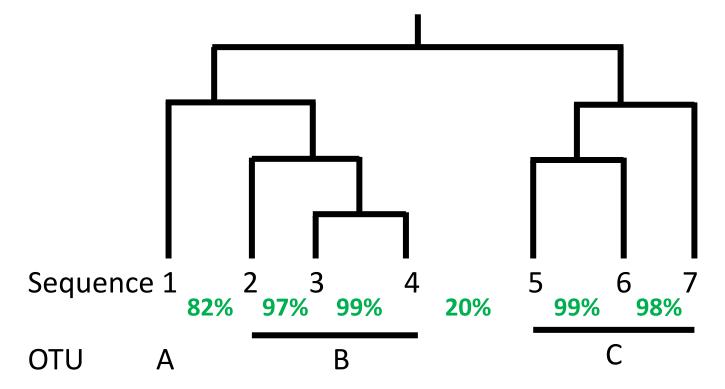
	Sequence1	Sequence2	Sequence3	Sequence4
Sequence1	0			
Sequence2	0.160	0		
Sequence3	0.153	0.158	0	
Sequence4	0.155	0.159	0.159	0

2. Cluster

cluster.split(column=example.final.dist,
count=example.final.count_table,
method=nearest)

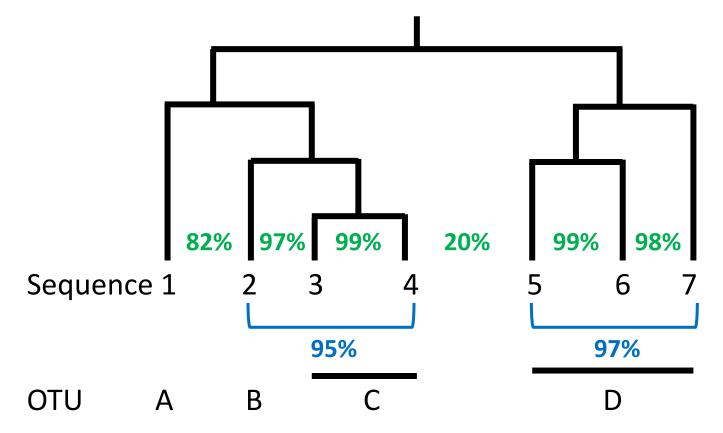
Clustering methods

- Nearest neighbor
 - Each of the sequences within an OTU are at most X% distant from the most similar sequence in the OTU.
 - Least conservation grouping = fewest OTUs

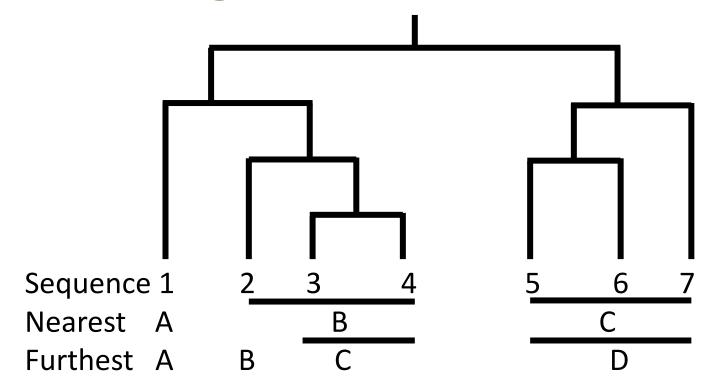


Clustering methods

- Furthest neighbor
 - All of the sequences within an OTU are at most X% distant from all of the other sequences within the OTU.
 - Most conservative grouping = most OTUs



Clustering methods



- Average neighbor
 - Middle ground between the other two algorithms.