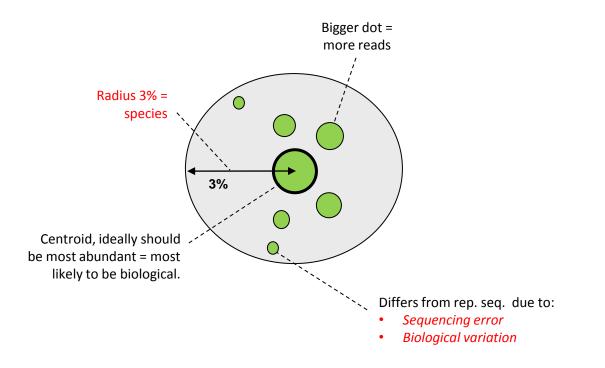
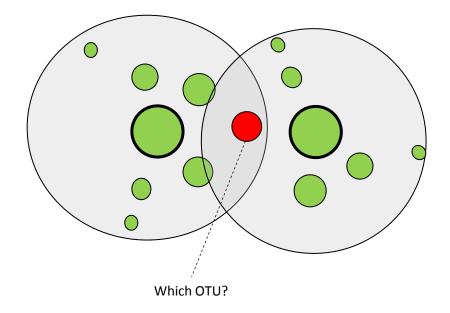
CHALLENGES IN OTU CLUSTERING Robert Edgar

Independent scientist robert@drive5.com www.drive5.com

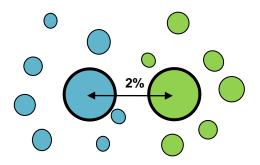
OTUs: Huse "dot plots"



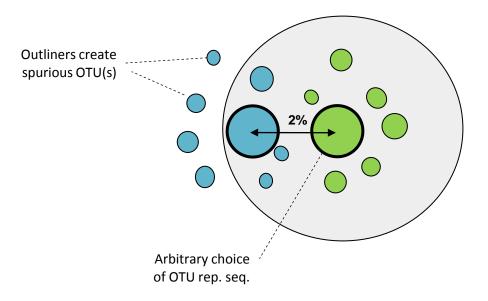
Ambiguous assignments



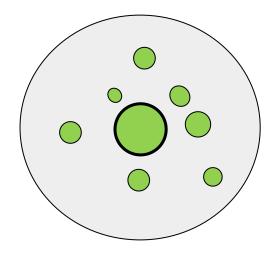
Abundant sequences <3% different



Abundant sequences <3% different

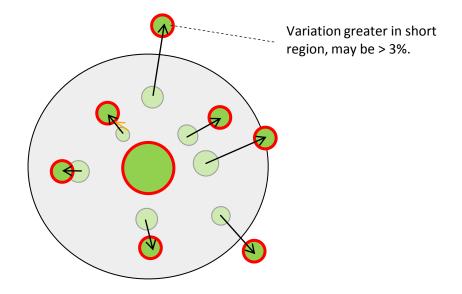


Full-length 16S gene (~1500nt)

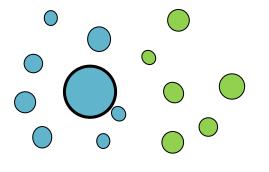


Full-length 16S gene (~1500nt)

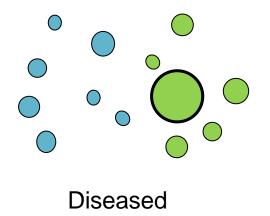
Next-gen reads of hypervariable region (~300nt)



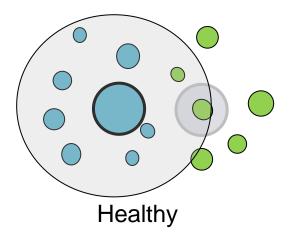
Variation between populations

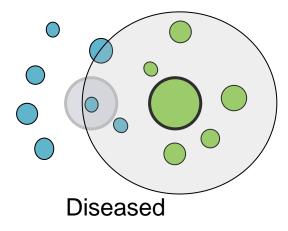


Healthy

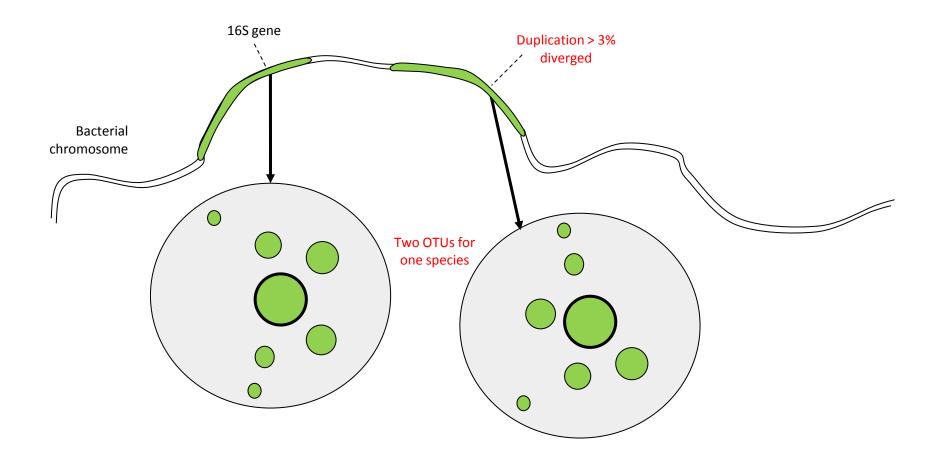


Variation between populations



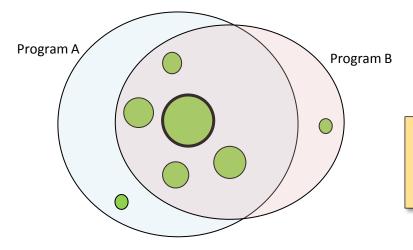


Paralogs and segmental duplications



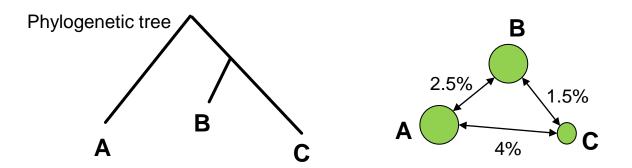
Alignment variation and defining % identity



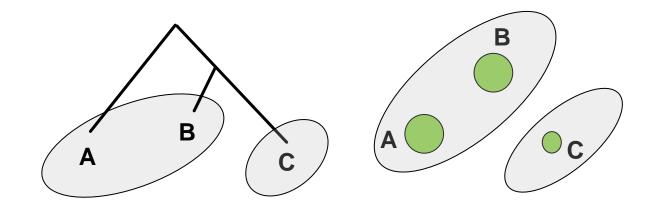


Different programs produce different results from the same algorithm & same input data because alignments and %id definition vary. This can bias validation, e.g. *Schloss & Westcott (2011) AEM*.

Hard to define an OTU or an optimal set of OTUs



Hard to define an OTU or an optimal set of OTUs



Optimal OTUs per Schloss & Westcott's MCC measure can be non-monophyletic.

- OTUs are hacks
- Do not exist in nature
- Cannot be defined and validated robustly
- But can still be useful!