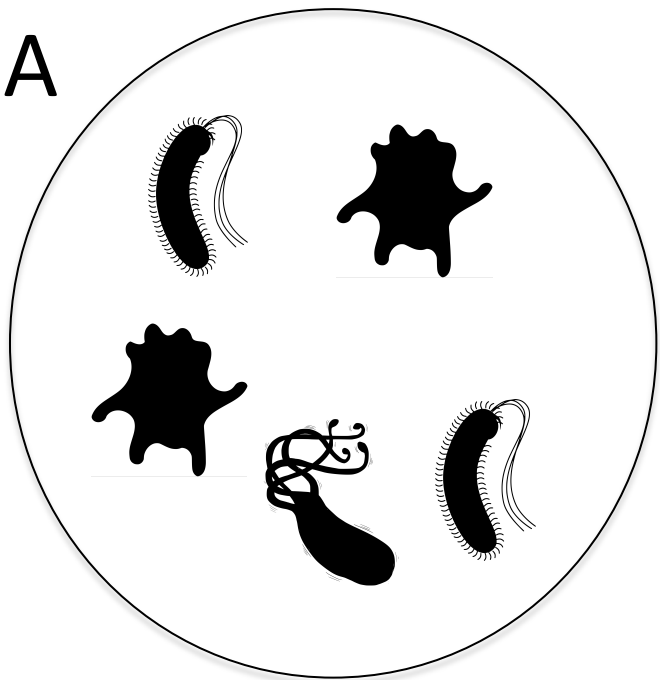
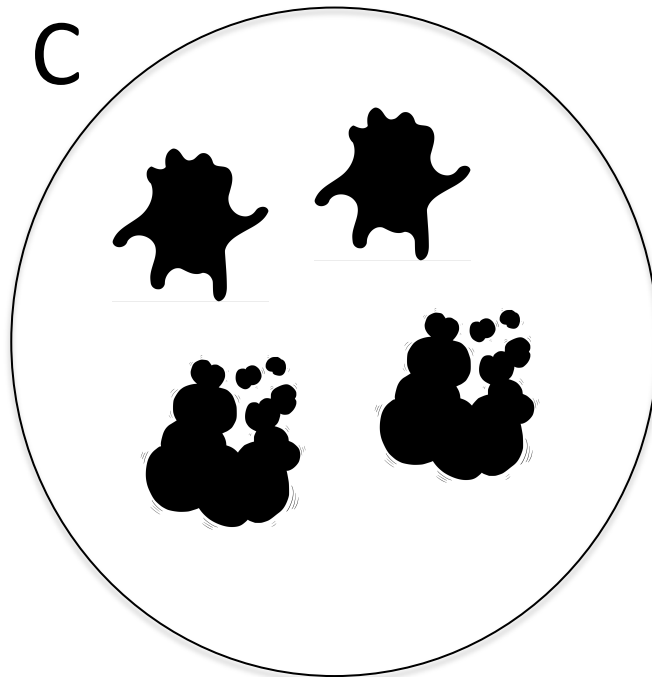


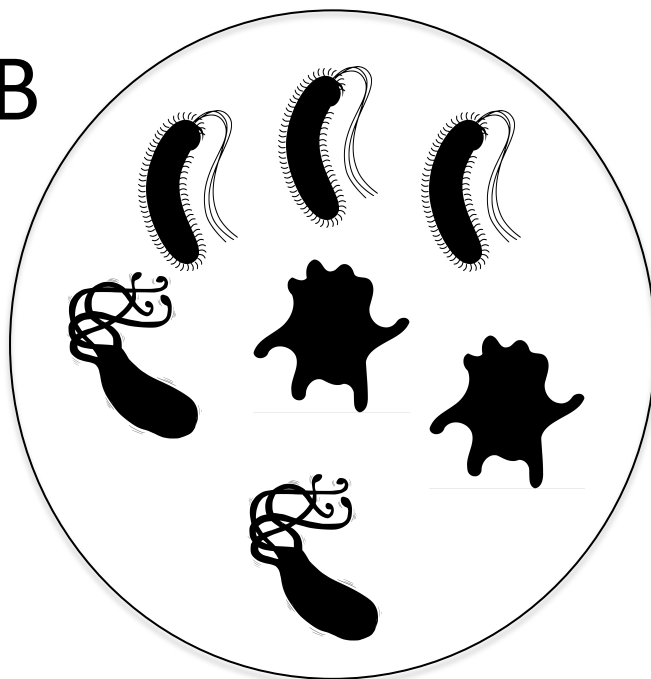
A



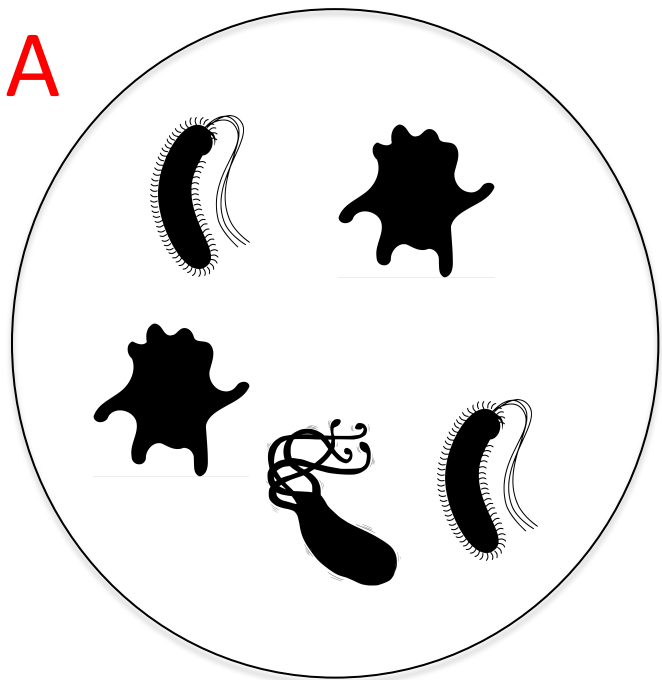
C



B

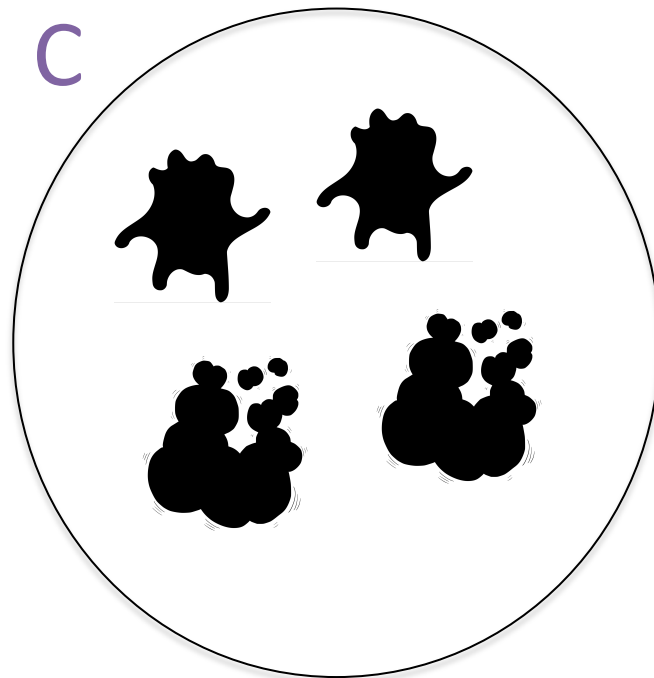


A



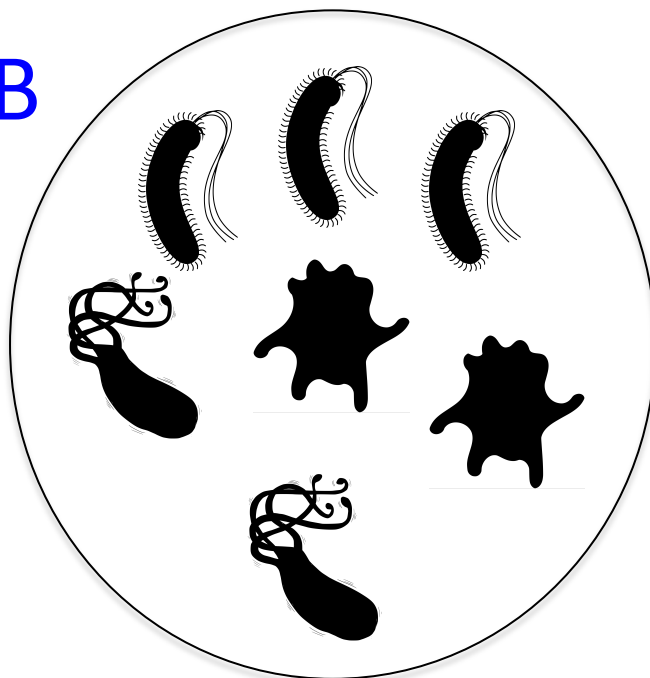
$$\alpha = 3$$

C

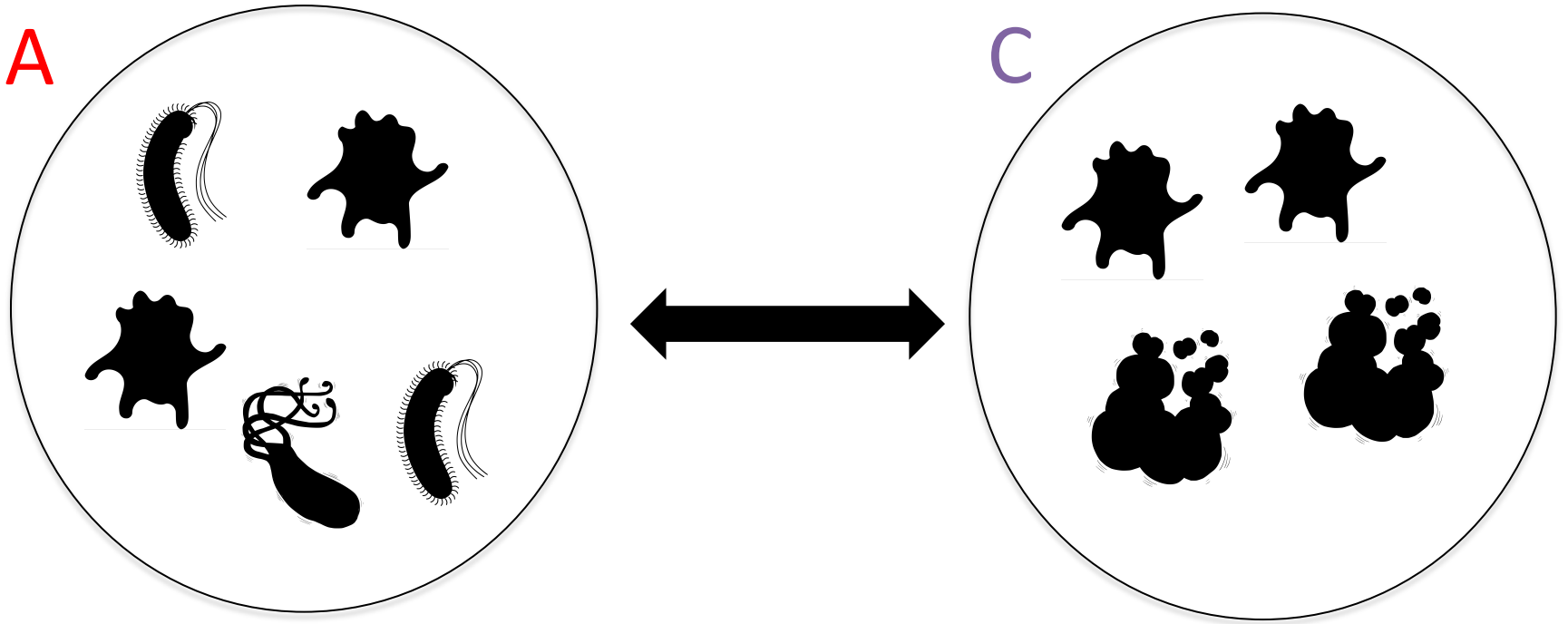


$$\alpha = 2$$

B



$$\alpha = 3$$



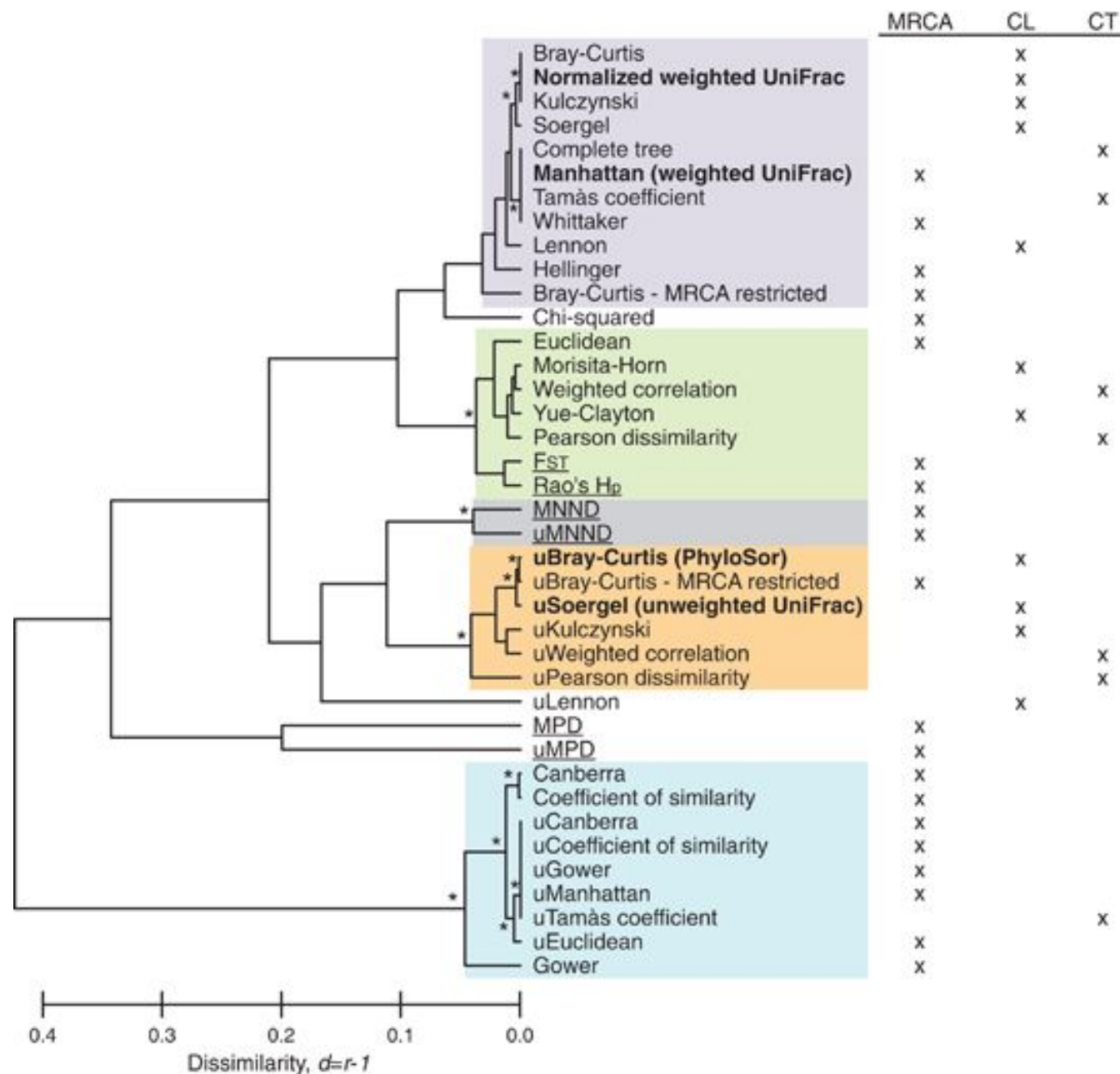
$$(\textcolor{red}{3}-\textcolor{purple}{1}) + (\textcolor{purple}{2}-\textcolor{red}{2}) = \beta 2$$

Classes of beta diversity tests

- **Quantitative**
 - Abundance based
(e.g., Bray Curtis,
Weighted Unifrac)
- **Qualitative**
 - Presence/absence
(e.g., Jaccard)

Classes of beta diversity tests

- **Quantitative**
 - Abundance based (e.g., Bray Curtis, Weighted Unifrac)
- **Qualitative**
 - Presence/absence (e.g., Jaccard)
- **Taxon based**
 - Frequency or count data (e.g., Bray Curtis)
- **Sequence based**
 - Genetic distance between aligned sequences (e.g., Fst)
- **Phylogeny based**
 - Computes distance between taxa using a phylogenetic tree (e.g., Unifrac)



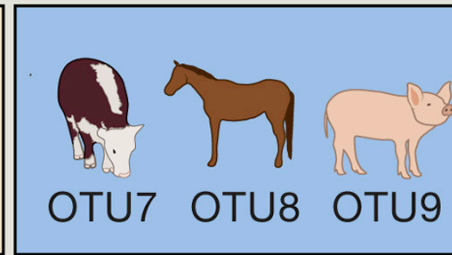
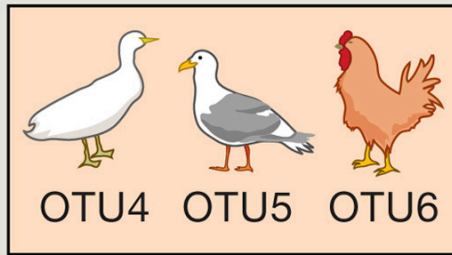
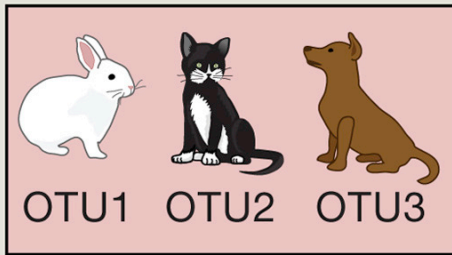
<https://www.nature.com/articles/ismej201288>

Bray Curtis

- Developed by J. Roger Bray and John T. Curtis (1957)
- **Compositional dissimilarity between two sites based on counts at each site**
- Ranges from 0 to 1:
 - 0 == two sites are the exact same
 - 1 == two sites are completely different

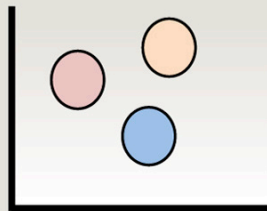
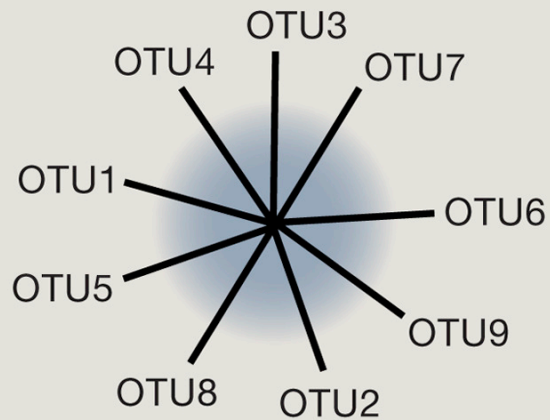
Unifrac

- Developed by Catherine Lozupone and Rob Knight (2005)
- Weighted (quantitative) or unweighted (qualitative)
- **Considers phylogenetic distance between organisms within a site**



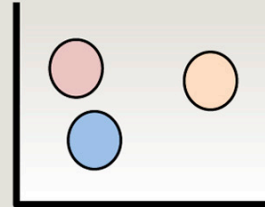
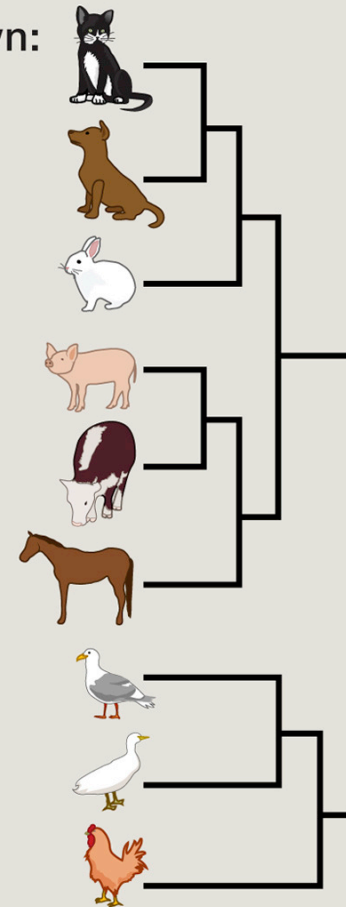
OTU phylogeny unknown:

Communities equidistant



OTU phylogeny known:

Bird community is less related



Things to consider

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- How robust is your data to different measures of beta diversity?

More reading

<https://aem.asm.org/content/71/12/8228>

<https://esajournals.onlinelibrary.wiley.com/doi/full/10.1002/ecs2.2100>

<https://www.ncbi.nlm.nih.gov/pubmed/22855211>

<https://www.ncbi.nlm.nih.gov/pubmed/22915830>