

Operational Taxonomic Unit (OTU)

**One of these things is
not like the other....**



A cluster of 16S rRNA reads with $\geq 97\%$
similarity to define “species”

Questions that can be answered by 16S sequencing:

- Which microbes are in my sample? What might they be doing?
- Is microbe X present at different levels between samples (differential abundance)?
- Why might one phylum be more abundant in this environment?

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