

# Introduction to metabarcoding

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# Which is our question?

- ▶ Who is in there?
- ▶ What can they do?
- ▶ What are they doing?



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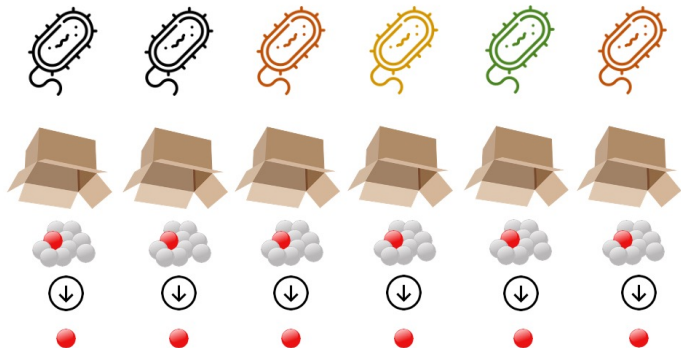


# Molecular barcoding

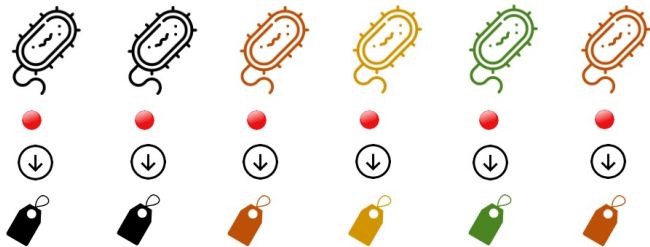




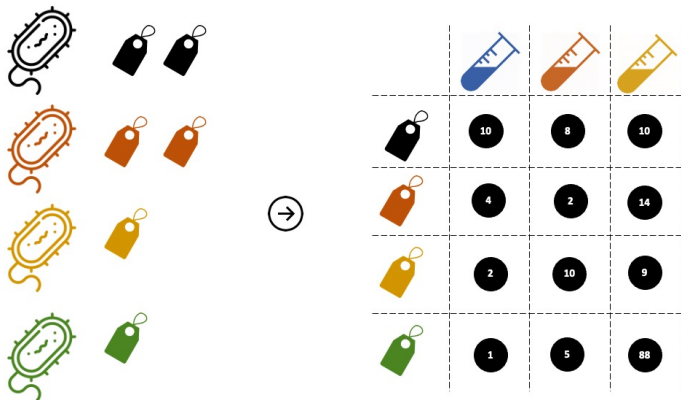
# Metabarcoding



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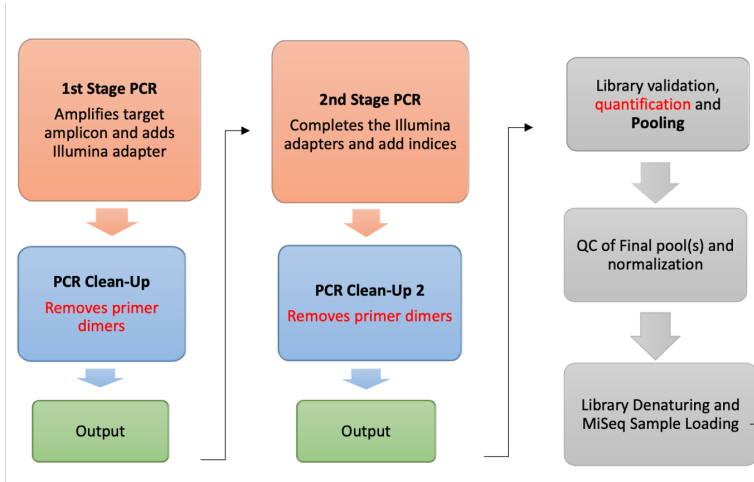
# Metabarcoding



# General workflow

1. Sample collection
2. DNA extraction
3. PCR amplification of our target
4. Adaptor ligation
5. Sequencing
6. Data analysis

# Library preparation workflow

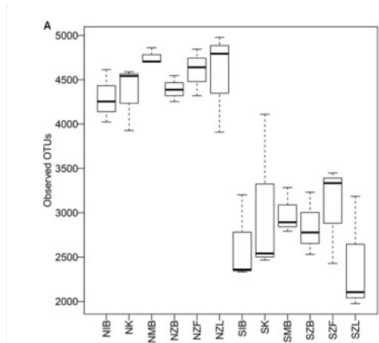


# Technical considerations - experimental design

- ▶ Target gene (specificity, resolution)
- ▶ Replicates (technical/biological)
- ▶ Sequencing depth
- ▶ Databases for taxonomy assignment
- ▶ Bias

# Technical considerations - DNA extraction

- ▶ DNA extraction introduces a bias in the final dataset
- ▶ A recent investigation on 322 studies shows they used 72 different methods. 14 did not report such info!



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# Technical considerations - PCR

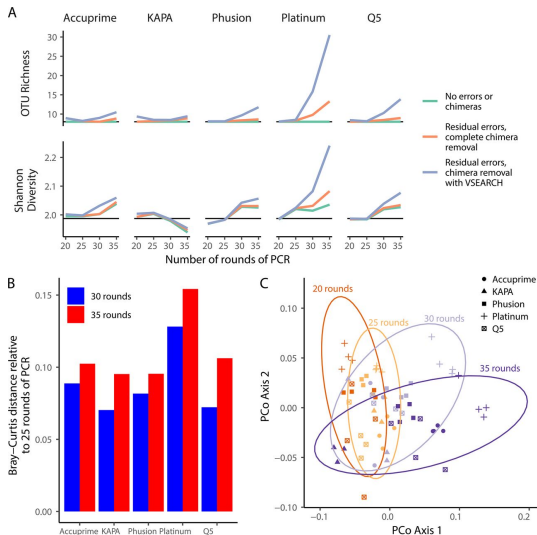
- ▶ Target gene
  - ▶ Who is our target? Bacteria, fungi, insects, fish, specific genus...
  - ▶ Is the resolution optimal for our question?
  - ▶ Are PCR primers available or we have to design them?
  - ▶ Is the taxonomy database available or we have to build a custom one?
- ▶ PCR bias
  - ▶ Use a Hi-Fi polymerase
  - ▶ Use optimal annealing temperature
  - ▶ Do not exaggerate with PCR cycles
  - ▶ Run multiple PCRs on the same sample



**CONSERVED REGIONS:** unspecific applications

**VARIABLE REGIONS:** group or species-specific applications

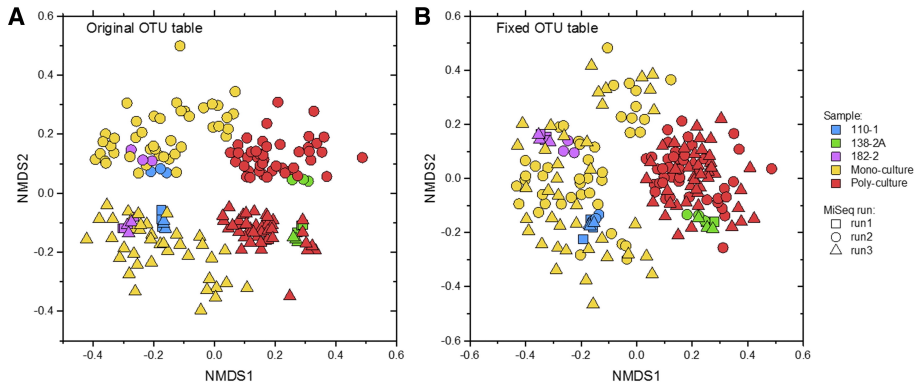
# Technical considerations - PCR



## Technical considerations - Library prep

- ▶ Which sequencing methodology will be a good fit for your research question?  
(read length/depth of sampling)
- ▶ How diverse is your system?

# Technical considerations - Sequencing run



# Control samples

- ▶ **Negative control 1.** Run molecular biology grade water throughout the pipeline. Pool it with the other samples even if you do not see amplification.
- ▶ **Negative control 2.** This is the negative control from your first PCR. If you see a band, discard the entire batch of samples and start again. If no band is observed, sequence anyway.
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