

# Minion Bioinformatics

# Steps

1. Get reference library
2. Run “Bioinformatics”

ie go from sequences to species

# Get reference library

- I don't know how to do this
- not specific to minion - same steps regardless of lab/sequencer
- Mike Allen knows this and has instructions I can point you to

# Minion Bioinformatics Steps

- Base calling
- Concat fastqs
- Quality filter
- Length filter
- Primer match and trim
- Trim extra adapters
- Cluster sequences into MOTUs
- BLAST
- Remove contamination species
- Account for positive control
- Account for negative controls
- Compile and clean data

# How do we do bioinformatics?

Coding\*

# Why is it so annoying?

- Coding is a technical skill that needs to be learned
- Many different softwares
- Data is large

# What do we want to do?

- work to be able to use my code
- work through each thing step by step --> make your own pipeline