

Minion Bioinformatics

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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