Evolutionary Biology Metabarcoding Big Data wgs Next Generation Sequencing

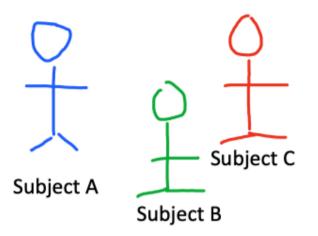
Bioinformatics Working Group

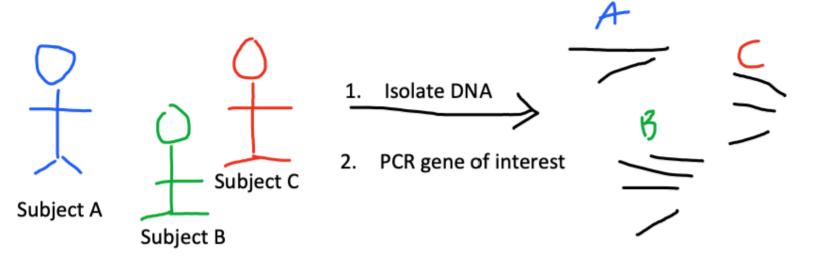


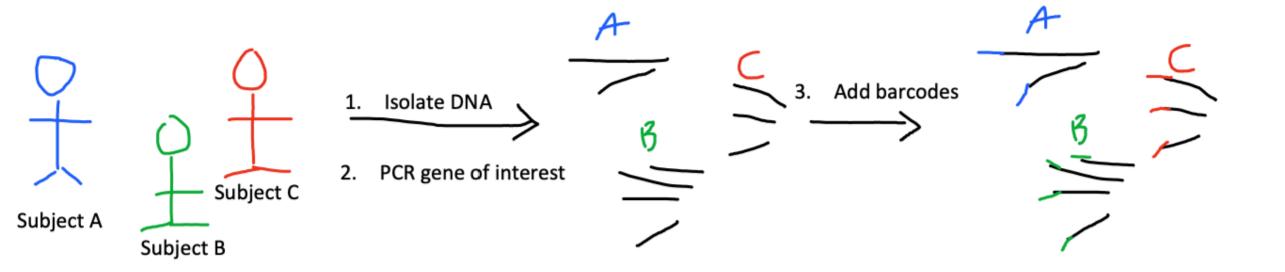
Taruna Schuelke
UC Santa Barbara
10 April 2019

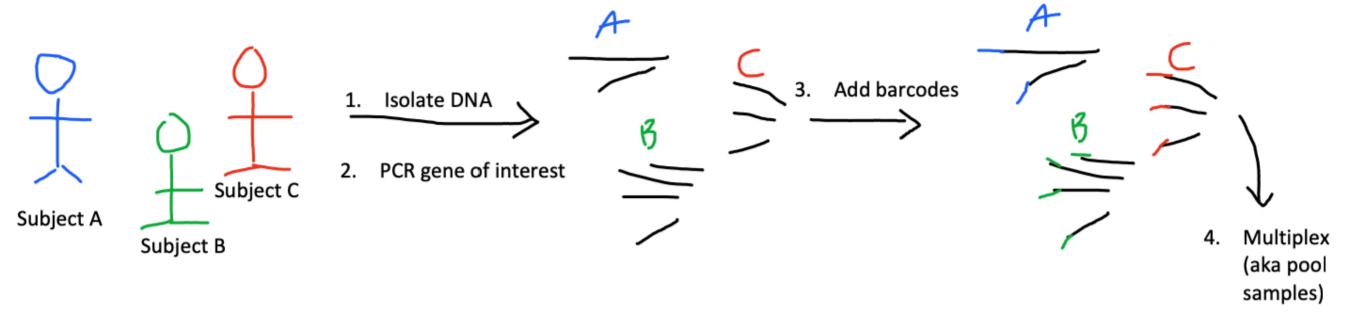
Objectives

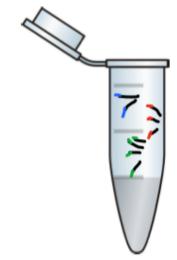
- 1. Wrap SSH keys
- 2. Overview of metabarcoding
- 3. QIIME2 terms
- 4. Download mock data
- 5. Github

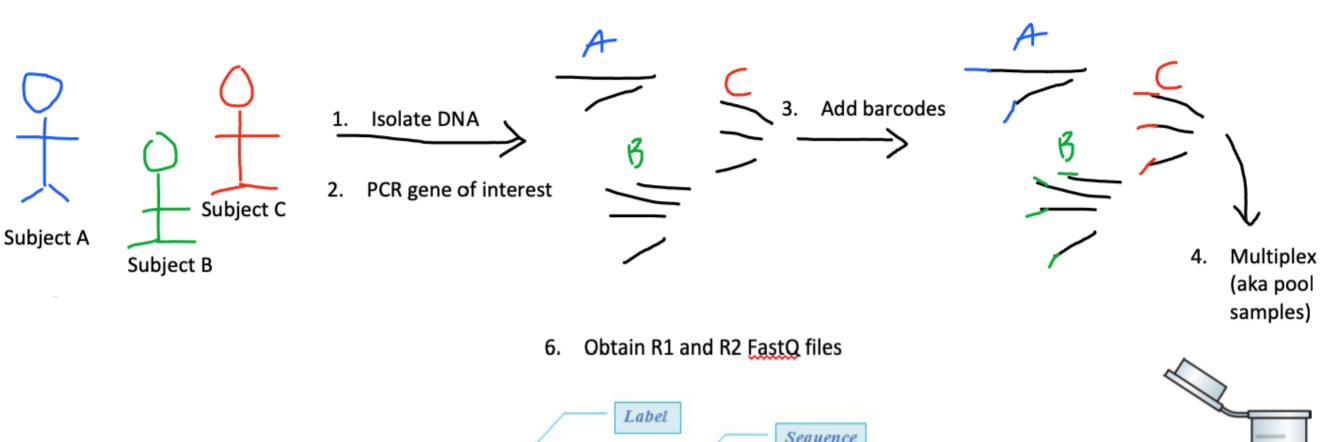


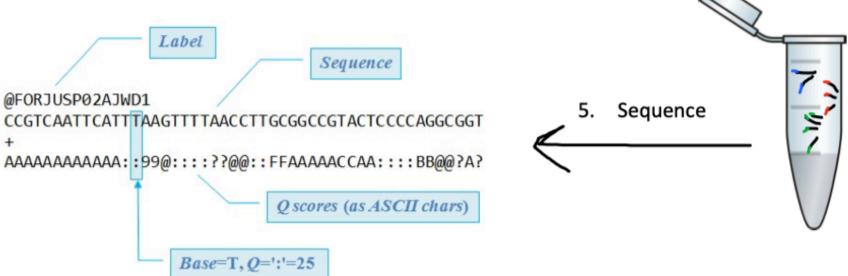


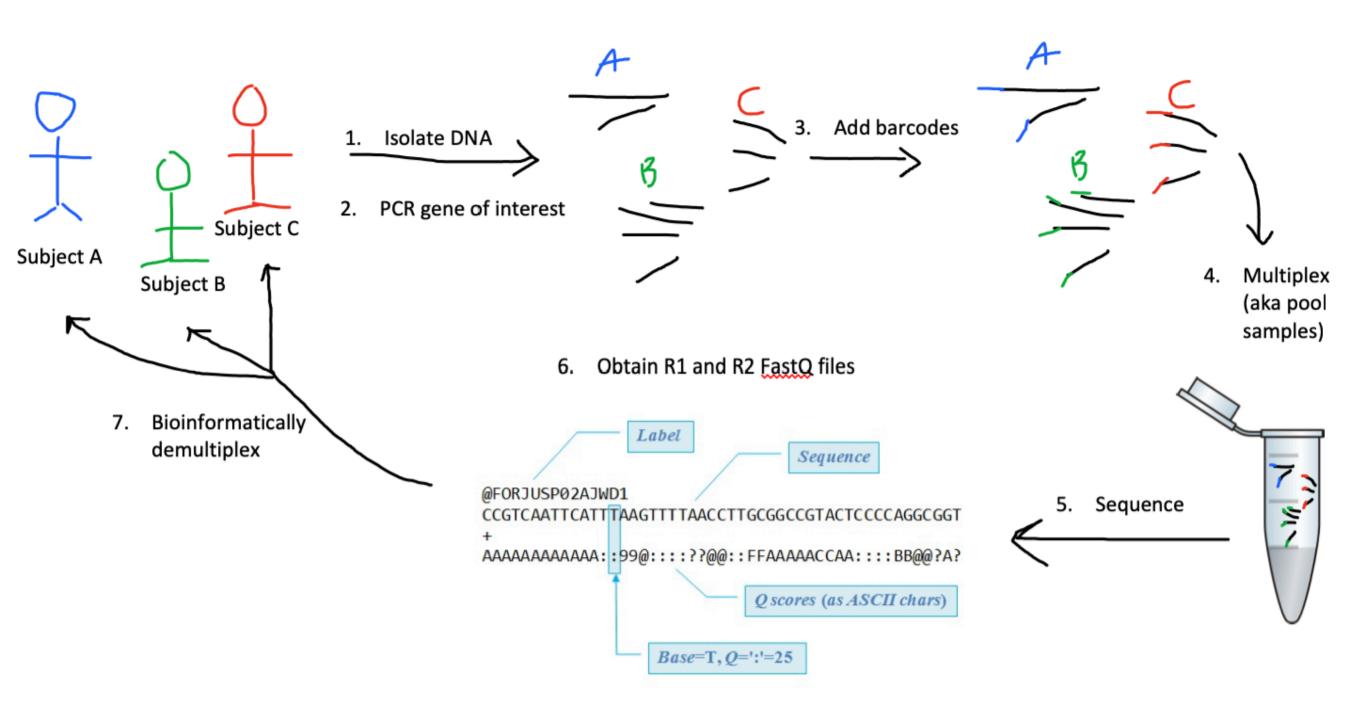


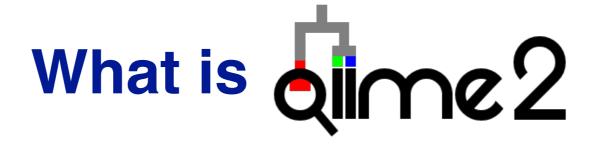












A pipeline for analyzing microbial diversity data.