Data Collection	iMAP: Integrated Microbiome Data Analysis Pipeline
Sampling & DNA Sequencing	Gathering materials & Pre-processing Sequence processing & Taxonomic assignment & Preliminary analysis
TGCGCAAGCGGCCTCTAAGACAGGTGTGAACTCCCCGGGCTT TGGGCCACAGCCTGCACCCAGCCGCGCTGTGGGATGACAC GGCGGGCTGCGGGTTCGGGTTGAACCTCACCGC DNA sequencing	Gather required materials Get demultiplexed reads (FastQ files) Get sample metadata Clone iMAP repository Install required software Download reference DBs Verify folders and files Cluster OTUs & assign conserved taxonomy Read inspection Review per sample read depth Review read length Pick representative sequences Align to reference 16S rRNA gene alignment Review, screen and filter by sequence length Phylotypes approach Phylogeny approach Preliminary analysis OTU abundance Review, screen & filter by sequence 16S rRNA gene alignment Review, screen & filter by sequence 16S rRNA gene alignment Review, screen & filter by sequence 16S rRNA gene alignment Review, screen & filter by sequence 16S rRNA gene alignment Review, screen & filter by sequence 16S rRNA gene alignment Review of the taxonomy Preliminary analysis OTU abundance Alpha diversity
Library Preparation DNA Extraction Sampling & Recording	• Remove retained phiX reads • Remove poor alignments & chimeras • Inspect uniformity of sample identifiers • Review experimental variables • Review missing data • Review missing data • Remove poor alignments & chimeras • Phylogenetic annotation • Upload trees to iTOL viewer • Prepare annotation files • Add annotation files • Export annotated tree
Sample metadata	Progress Report 1 Progress Report 2 Progress Report 3 Progress Report 4 Metadata profiling Pre-processing Sequence-processing Preliminary analysis
Field & Wet Lab	Review-As-You-Go (RAYG): Progress Reports Summarizing Bioinformatics Analysis and Exploratory Visualization